

(12) STANDARD PATENT
(19) AUSTRALIAN PATENT OFFICE

(11) Application No. **AU 2017250304 B2**

(54) Title
Compositions and methods for selective protein expression

(51) International Patent Classification(s)
C07K 14/725 (2006.01) **C12N 15/62** (2006.01)

(21) Application No: **2017250304** (22) Date of Filing: **2017.04.14**

(87) WIPO No: **WO17/181119**

(30) Priority Data

(31) Number	(32) Date	(33) Country
62/322,931	2016.04.15	US
62/481,094	2017.04.03	US

(43) Publication Date: **2017.10.19**

(44) Accepted Journal Date: **2023.08.17**

(71) Applicant(s)
Novartis AG;The Trustees of the University of Pennsylvania

(72) Inventor(s)
Golosov, Andrei;Guimaraes, Carla;Motz, Gregory;Milone, Michael;Ellebrecht, Christoph;Payne, Aimee S.

(74) Agent / Attorney
Davies Collison Cave Pty Ltd, Level 15 1 Nicholson Street, MELBOURNE, VIC, 3000, AU

(56) Related Art
WO 00/23602 A2
JIE SUN ET AL, "The quest for spatio-temporal control of CAR T cells", CELL RESEARCH - XIBAO YANJIU, GB, CN, (2015-12-17), vol. 25, no. 12, pages 1281 - 1282
WO 2017/024318 A1
AJAMETE KAYKAS ET AL, "Mutant Frizzled 4 associated with vitreoretinopathy traps wild-type Frizzled in the endoplasmic reticulum by oligomerization", NATURE CELL BIOLOGY, GB, (2003-12-14), vol. 6, no. 1, pages 52 - 58
RIVERA V M ET AL, "REGULATION OF PROTEIN SECRETION THROUGH CONTROLLED AGGREGATION IN THE ENDOPLASMIC RETICULUM", SCIENCE, AMERICAN ASSOCIATION FOR THE ADVANCEMENT OF SCIENCE, (2000-01-01), vol. 287, pages 826 - 830
LUIS QUINTINO ET AL, "Functional Neuroprotection and Efficient Regulation of GDNF Using Destabilizing Domains in a Rodent Model of Parkinson's Disease", MOLECULAR THERAPY, US, (2013-12-01), vol. 21, no. 12, pages 2169 - 2180
HOKYUNG K CHUNG ET AL, "Tunable and reversible drug control of protein production via a self-excising degron", NATURE CHEMICAL BIOLOGY, Basingstoke, (2015-07-27), vol. 11, no. 9, pages 713 - 720
M. R. PRATT ET AL, "Small-molecule-mediated rescue of protein function by an inducible proteolytic shunt", PROCEEDINGS NATIONAL ACADEMY OF SCIENCES PNAS, US, (2007-07-03), vol. 104, no. 27, pages 11209 - 11214
WO 01/57242 A2

YUSUKE MIYAZAKI ET AL, "Destabilizing Domains Derived from the Human Estrogen Receptor", JOURNAL OF THE AMERICAN CHEMICAL SOCIETY, US, (2012-03-07), vol. 134, no. 9, pages 3942 - 3945

MICHAEL C JENSEN ET AL, "Design and implementation of adoptive therapy with chimeric antigen receptor-modified T cells", IMMUNOLOGICAL REVIEWS., US, (2013-12-13), vol. 257, no. 1, Special Issue,, pages 127 - 144



(51) International Patent Classification:

C12N 15/62 (2006.01) C07K 14/725 (2006.01)

(21) International Application Number:

PCT/US2017/027778

(22) International Filing Date:

14 April 2017 (14.04.2017)

(25) Filing Language:

English

(26) Publication Language:

English

(30) Priority Data:

62/322,931	15 April 2016 (15.04.2016)	US
62/481,094	03 April 2017 (03.04.2017)	US

(71) Applicants: **NOVARTIS AG** [CH/CH]; Lichstrasse 35, CH-4056 Basel (CH). **THE TRUSTEES OF THE UNIVERSITY OF PENNSYLVANIA** [US/US]; 3160 Chestnut Street, Suite 200, Philadelphia, PA 19104 (US).

(72) Inventors; and

(71) Applicants (*for US only*): **GOLOSOV, Andrei** [—/US]; Novartis Institutes for BioMedical Research, Inc., 100 Technology Square, Cambridge, MA 02139 (US). **GUIMARAES, Carla** [PT/US]; Novartis Institutes for BioMedical Research, Inc., 100 Technology Square, Cambridge, MA 02139 (US). **MOTZ, Gregory** [US/US]; 83 Greene St., Quincy, MA 02170 (US). **MILONE, Michael** [US/US]; 314 Surrey Road, Cherry Hill, NJ 08002 (US). **ELLEBRECHT, Christoph, T.** [DE/US]; 415 S. 13th Street, Philadelphia, PA 19147 (US). **PAYNE, Aimee, S.** [US/US]; 536 Hamilton Road, Merion Station, PA 19066 (US).

(74) Agent: **COLLAZO, Diana, M.** et al.; Lando & Anastasi, LLP, Riverfront Office Park, One Main Street, Suite 1100, Cambridge, MA 02142 (US).

(81) Designated States (*unless otherwise indicated, for every kind of national protection available*): AE, AG, AL, AM,

(54) Title: COMPOSITIONS AND METHODS FOR SELECTIVE PROTEIN EXPRESSION

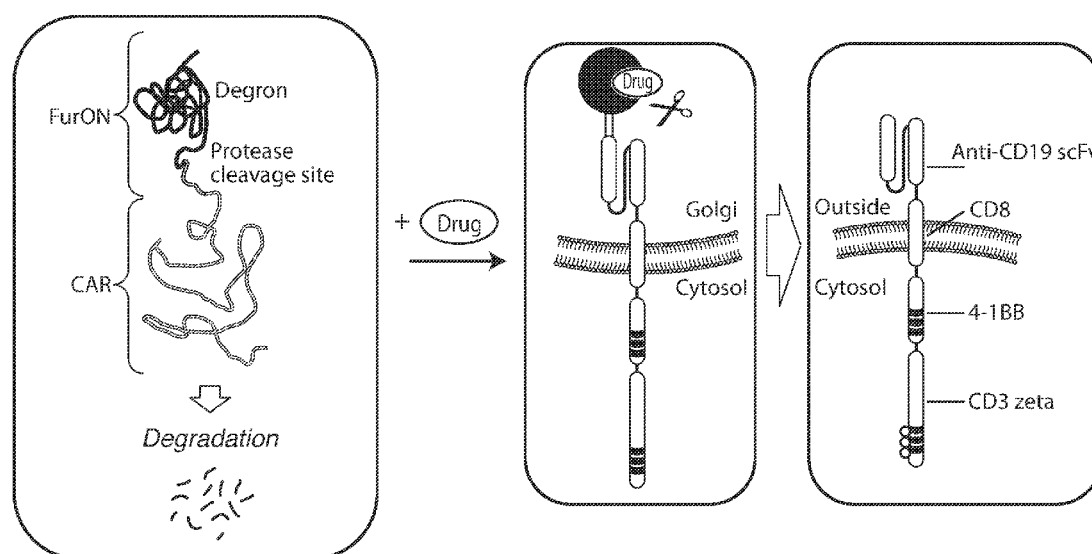


FIG. 25

(57) **Abstract:** Provided herein are fusion proteins including two protein domains separated by a heterologous protease cleavage site, wherein a first of the protein domains is a conditional expression domain. Thus, the fusion proteins comprise three essential elements: a conditional expression domain, a domain containing the protein of interest, and a protease cleavage domain separating the two. Also provided herein are methods for treating autoantibody and alloantibody-mediated diseases or conditions in a subject by targeting B cells with anti-B cell modified T cells. In one embodiment, a chimeric antigen receptor (CAR) modified T cell is selectively ablated in a subject after adoptive transfer. Pharmaceutical compositions comprising the temporally regulated CAR modified T cell are also described herein.



AO, AT, AU, AZ, BA, BB, BG, BH, BN, BR, BW, BY, BZ, CA, CH, CL, CN, CO, CR, CU, CZ, DE, DJ, DK, DM, DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IR, IS, JP, KE, KG, KH, KN, KP, KR, KW, KZ, LA, LC, LK, LR, LS, LU, LY, MA, MD, ME, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PA, PE, PG, PH, PL, PT, QA, RO, RS, RU, RW, SA, SC, SD, SE, SG, SK, SL, SM, ST, SV, SY, TH, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, ZA, ZM, ZW.

- (84) Designated States** (*unless otherwise indicated, for every kind of regional protection available*): ARIPO (BW, GH, GM, KE, LR, LS, MW, MZ, NA, RW, SD, SL, ST, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, RU, TJ, TM), European (AL, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HR, HU, IE, IS, IT, LT, LU, LV, MC, MK, MT, NL, NO, PL, PT, RO, RS, SE, SI, SK, SM, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, KM, ML, MR, NE, SN, TD, TG).

Declarations under Rule 4.17:

- *as to applicant's entitlement to apply for and be granted a patent (Rule 4.17(ii))*
- *as to the applicant's entitlement to claim the priority of the earlier application (Rule 4.17(iii))*

Published:

- *with international search report (Art. 21(3))*
- *before the expiration of the time limit for amending the claims and to be republished in the event of receipt of amendments (Rule 48.2(h))*
- *with sequence listing part of description (Rule 5.2(a))*

(88) Date of publication of the international search report:

04 January 2018 (04.01.2018)

COMPOSITIONS AND METHODS FOR SELECTIVE PROTEIN EXPRESSION

RELATED APPLICATIONS

This application claims priority to U.S. Serial No.: 62/322,931, filed April 15, 2016, and U.S. Serial No.: 62/481,094 filed April 3, 2017, the entire contents of each of these applications is incorporated herein by
5 reference.

SEQUENCE LISTING

The instant application contains a Sequence Listing which has been submitted electronically in ASCII format and is hereby incorporated by reference in its entirety. Said ASCII copy, created on April 14, 2017, is named N2067-7128WO_SL.txt and is 2,326,027 bytes in size.

BACKGROUND OF THE INVENTION

A variety of constructs have been developed to enable selective expression of a desired protein of interest. Recent constructs have been tested which incorporate a domain engineered to degrade in the absence of a stabilizing ligand (known in the art as “degrons”). Other constructs incorporate a domain engineered to aggregate in the absence of a deaggregating ligand (e.g., an aggregation domain). Such
15 domains can be fused to proteins of interest to permit selective expression of such proteins only in the presence of the stabilizing or deaggregating ligand.

Degrans and aggregation domains known in the art can, in certain circumstances, have certain disadvantages associated with disrupting the desired function of the protein of interest due to the size and/or conformation of the fusion protein. Such disadvantages can be particularly evident when the
20 protein of interest is a transmembrane protein. Thus, there is a need for improving the degran/aggregation domain technology. Furthermore, a need exists for methods of modifying T cells to treat various diseases and conditions such as but not limited to cancer, autoimmunity and alloimmunity without permanently modifying or suppressing the immune system.

SUMMARY OF THE INVENTION

In one aspect, the invention features fusion proteins including two protein domains separated by a heterologous protease cleavage site (e.g., a protease cleave site that is cleaved by a mammalian intracellular or extracellular protease), wherein a first of the protein domains is a conditional expression domain, e.g., a degradation domain or an aggregation domain, and the second protein is a protein of interest, e.g., a transmembrane protein (e.g., a CAR).

In some embodiments, the conditional expression domain is a degradation domain, e.g., a degradation domain as described herein. Without wishing to be bound by theory, in some embodiments, the

degradation domain is unstable and/or unable to fold into a stable conformation in the absence of an expression compound, e.g., a stabilization compound. The misfolded/unfolded degradation domain can be degraded by intracellular degradation pathways along with the other domain(s) of the fusion protein (see, for example, Figure 25). In the presence of the expression compound, the degradation domain is able to fold into a stable conformation and is less susceptible to intracellular degradation pathways, e.g., relative to the degradation domain in the absence of the expression compound. Thus, the level and/or rate of cell surface expression or extracellular expression of the fusion protein is enhanced, e.g., by at least 2-, 3-, 4-, 5-, 6-, 7-, 8-, 9-, 10-, 20-, or 30-fold, in the presence of the expression compound relative to the absence of the expression compound. In some embodiments, once the degradation domain of the fusion protein assumes a proper conformation, the heterologous cleavage site is exposed, leading to removal of the degradation domain, and thus, freeing the second protein domain.

In other embodiments, the conditional expression domain is an aggregation domain. Without wishing to be bound by theory, in some embodiments in the absence of expression compound, e.g., deaggregation compound, the aggregation domain of the fusion protein associates with one or more other aggregation domains into oligomers and aggregates (see, for example, Figure 26). The aggregated fusion protein can be sequestered in the cellular compartment in which it is aggregated. In the presence of expression compound, e.g., deaggregation compound, the aggregation domains dissociate from one another, and the fusion proteins are solubilized (e.g., assumes a monomeric configuration). Thus, the level and/or rate of cell surface expression or extracellular expression of the fusion protein is enhanced, e.g., by at least 2-, 3-, 4-, 5-, 6-, 7-, 8-, 9-, 10-, 20-, or 30-fold, in the presence of the expression compound relative to the absence of the expression compound. In some embodiments, once the aggregation domain of the fusion protein is solubilized, the heterologous cleavage site is exposed, leading to removal of the aggregation domain, and thus, freeing the second protein domain.

In any of the foregoing aspects and embodiments, the fusion protein includes a first protein domain that is or comprises a conditional expression domain, e.g., a degradation domain or an aggregation domain, and a second protein domain that is or comprises a protein of interest, e.g., a transmembrane protein (e.g., a CAR), wherein the first and the second domains of the fusion protein are separated by a heterologous protease cleavage site (e.g., a protease cleavage site that is cleaved by a mammalian intracellular or extracellular protease). In some embodiments, the conditional expression domain, e.g., the degradation or the aggregation domain, is located N-terminal to the second protein domain. In certain embodiments, the fusion protein further includes a signal peptide N-terminal to the degradation domain.

In one aspect, the invention pertains to a fusion protein, comprising two protein domains separated by a heterologous protease cleavage site, wherein a first of said protein domains is a conditional expression domain, and a second of said protein domains is a transmembrane protein, wherein the conditional expression domain has a first state associated with a first level of surface expression and/or extracellular expression of the fusion protein and a second state associated with a second level of surface expression

and/or extracellular expression of the fusion protein, wherein the second level is increased, e.g., by at least 2, 3, 4, 5, 10, 20 or 30 fold over the first level in the presence of an expression compound.

In another aspect, the invention pertains to a fusion protein, comprising two protein domains separated by a heterologous protease cleavage site, wherein a first of said protein domains is a conditional expression domain, and a second of said protein domains is a transmembrane protein, wherein the heterologous protease cleavage site is a furin cleavage site, provided that the furin cleavage site does not comprise the amino acid sequence SARNRQKR (SEQ ID NO: 981).

In another aspect, the invention pertains to a fusion protein, comprising two protein domains separated by a heterologous protease cleavage site, wherein a first of said protein domains is a conditional expression domain, and a second of said protein domains is a chimeric antigen receptor (CAR).

In some embodiments, the conditional expression domain is a degradation domain.

In some embodiments, the conditional expression domain is an aggregation domain.

In some embodiments, the fusion protein comprises two protein domains separated by a heterologous protease cleavage site, wherein the first of said protein domains (also referred to herein as the first protein domain) is or comprises a degradation domain, e.g., a degradation domain as described herein, and the second of said protein domains (also referred to herein as the second protein domain) is a protein of interest. In one embodiment, the protein of interest is a transmembrane protein, e.g., a CAR.

In some embodiments, the degradation domain is chosen from an estrogen receptor (ER) domain, an FKB protein (FKBP) domain or an dihydrofolate reductase (DHFR).

In some embodiments, the degradation domain has a first state associated with a first level of surface expression and/or extracellular expression of the fusion protein and a second state associated with a second level of surface expression and/or extracellular expression of the fusion protein, wherein the second level is increased, e.g., by at least 2, 3, 4, 5, 10, 20 or 30 fold over the first level in the presence of a stabilization compound.

In certain embodiments, the degradation domain is derived from an estrogen receptor. For example, the degradation domain can comprise an amino acid sequence selected from SEQ ID NO: 58 or a sequence having at least 90%, 95%, 97%, 98%, or 99% identity thereto, or SEQ ID NO: 121 or a sequence having at least 90%, 95%, 97%, 98%, or 99% identity thereto. In some embodiments, the degradation domain comprises an amino acid sequence selected from SEQ ID NO: 58 or SEQ ID NO: 121. When the degradation domain is derived from an estrogen receptor, the stabilization compound can be selected from Bazedoxifene or 4-hydroxy tamoxifen (4-OHT). In some embodiments, the stabilization compound is Bazedoxifene. Tamoxifen and Bazedoxifene are FDA approved drugs, and thus are safe to use in a human.

In certain embodiments, the degradation domain is derived from an FKB protein (FKBP). For example, the degradation domain can comprise an amino acid sequence of SEQ ID NO: 56 or a sequence having at least 90%, 95%, 97%, 98%, or 99% identity thereto. In some embodiments, the degradation domain comprises SEQ ID NO: 56. When the degradation domain is derived from a FKBP, the stabilization compound can be Shield-1.

In some embodiments, the degradation domain is derived from dihydrofolate reductase (DHFR). In some embodiments, the degradation domain comprises an amino acid sequence selected from SEQ ID NO: 57 or a sequence having at least 90%, 95%, 97%, 98%, or 99% identity thereto. In some embodiments, the degradation domain comprises SEQ ID NO: 57. When the degradation domain is derived from a DHFR, the stabilization compound can be Trimethoprim.

In other embodiments, the degradation domain is not derived from an FKB protein or estrogen receptor.

In some embodiments, the fusion protein comprises two protein domains separated by a heterologous protease cleavage site, wherein the first of said protein domains (also referred to herein as the first protein domain) is or comprises an aggregation domain, e.g., an aggregation domain as described herein, and the second of said protein domains (also referred to herein as the second protein domain) is a protein of interest. In one embodiment, the protein of interest is a transmembrane protein, e.g., a CAR.

In some embodiments, the fusion protein comprises two protein domains separated by a heterologous protease cleavage site, wherein a first of said protein domains is an aggregation domain, and a second of said protein domains is a transmembrane protein, wherein the aggregation domain has a first state associated with a first level of surface expression and/or extracellular expression of the fusion protein and a second state associated with a second level of surface expression and/or extracellular expression of the fusion protein, and wherein the second level is increased, e.g., by at least 2, 3, 4, 5, 10, 20 or 30 fold over the first level in the presence of a deaggregation compound.

In some embodiments, the fusion protein, comprises two protein domains separated by a heterologous protease cleavage site, wherein a first of said protein domains is an aggregation domain, and a second of said protein domains is a transmembrane protein, wherein the heterologous protease cleavage site is a furin cleavage site, provided that the furin cleavage site does not comprise the amino acid sequence SARNRQKR (SEQ ID NO: 981).

In some embodiments, the fusion protein, comprises two protein domains separated by a heterologous protease cleavage site, wherein a first of said protein domains is an aggregation domain, and a second of said protein domains is a chimeric antigen receptor (CAR).

In some embodiments, the aggregation domain comprises 1, 2, 3, 4, 5, 6, 7, 8, or more repeats of a dimerization domain, e.g., a homodimerization or a heterodimerization domain.

In some embodiments, the aggregation domain is from an FKB protein (FKBP).

In some embodiments, the aggregation domain is an FKBP F36M domain.

In some embodiments, the aggregation domain is from an FKB protein (FKBP) and comprises an amino acid sequence that is at least 90, 95, 97, 98, 99, or 100% identical to either of SEQ ID NOs: 975 or 976.

- 5 In some embodiments, the fusion protein comprises a further 2nd, 3rd, 4th, 5th, 6th, 7th, 8th, 9th, or 10th aggregation domain.

In some embodiments, the 2nd, 3rd, 4th, 5th, 6th, 7th, 8th, 9th, or 10th aggregation domain is the same type of aggregation domain as the first aggregation domain.

In some embodiments, the aggregation domain forms homodimers with the same aggregation domain.

- 10 In some embodiments, the fusion protein comprises a plurality of aggregation domains, wherein the plurality comprises more than one, e.g., two, types of aggregation domains, and a first type of aggregation domain forms heterodimers with a second type of aggregation domain.

In some embodiments, the fusion protein comprises 2, 4, 6, 8, or 10 aggregation domains, wherein the fusion protein comprises equal numbers of the first type of aggregation domain and the second type of aggregation domain.

- 15 In some embodiments, the aggregation domains are disposed in the fusion protein in an alternating order of first type and second type, e.g., first, second, first, second, or second, first, second, first.

In some embodiments, said deaggregation compound is selected from FK506, rapamycin, AP22542, AP21998, and Shield-1 when the fusion protein comprises an aggregation domain derived from FKB protein (FKBP), e.g., FKBP F36M.

- 20 In some embodiments, said heterologous cleavage site is cleaved by a mammalian intracellular protease.

In some embodiments, said cleavage site is cleaved by a protease selected from the group consisting of furin, PCSK1, PCSK5, PCSK6, PCSK7, cathepsin B, Granzyme B, Factor XA, Enterokinase, genenase, sortase, precision protease, thrombin, TEV protease, and elastase 1.

- 25 In some embodiments, said cleavage site comprises a polypeptide having an cleavage motif selected from the group consisting of RX(K/R)R consensus motif, RXXX[KR]R consensus motif, RRR consensus motif, I-E-P-D-X consensus motif (SEQ ID NO: 35), Glu/Asp-Gly-Arg, Asp-Asp-Asp-Asp-Lys (SEQ ID NO: 36), Pro-Gly-Ala-Ala-His-Tyr (SEQ ID NO: 37), LPXTG/A consensus motif, Leu-Glu-Val-Phe-Gln-Gly-Pro (SEQ ID NO: 38), Leu-Val-Pro-Arg-Gly-Ser (SEQ ID NO: 40), E-N-L-Y-F-Q-G (SEQ ID NO: 41), and
- 30 [AGSV]-x (SEQ ID NO: 42).

In some embodiments, said cleavage site is cleaved by furin.

In some embodiments, the fusion protein comprises a furin cleavage site selected from RTKR (SEQ ID NO: 123); GTGAEDPRPSRKRRSLGDVG (SEQ ID NO: 125); GTGAEDPRPSRKRR (SEQ ID NO: 127); LQWLEQQVAKRRTKR (SEQ ID NO: 129); GTGAEDPRPSRKRRSLGG (SEQ ID NO: 131);
 5 GTGAEDPRPSRKRRSLG (SEQ ID NO: 133); SLNLTESHNSRKKR (SEQ ID NO: 135); or CKINGYPKRGRKRR (SEQ ID NO: 137).

In some embodiments, the fusion protein comprises a furin cleavage site selected from GTGAEDPRPSRKRRSLGDVG (SEQ ID NO: 125); or GTGAEDPRPSRKRR (SEQ ID NO: 127).

In some embodiments, the fusion protein comprises the furin cleavage site of
 10 GTGAEDPRPSRKRRSLGDVG (SEQ ID NO: 125).

In some embodiments, said heterologous protease cleavage site is cleaved by a mammalian extracellular protease.

In some embodiments, said mammalian extracellular protease is selected from the group consisting of Factor XA, Enterokinase, genenase, sortase, precision protease, thrombin, TEV protease, and elastase
 15 1.

In some embodiments, said cleavage site comprises a polypeptide having an amino acid sequence selected from the group consisting of Glu/Asp-Gly-Arg, Asp-Asp-Asp-Asp-Lys (SEQ ID NO: 36), Pro-Gly-Ala-Ala-His-Tyr (SEQ ID NO: 37), LPXTG/A consensus motif, Leu-Glu-Val-Phe-Gln-Gly-Pro (SEQ ID NO: 38), Leu-Val-Pro-Arg-Gly-Ser (SEQ ID NO: 40), E-N-L-Y-F-Q-G (SEQ ID NO: 41), and [AGSV]-x (SEQ ID
 20 NO: 42).

In any of the foregoing aspects and embodiments, the heterologous cleavage site is cleaved by furin, PCSK1, PCSK5, PCSK6, PCSK7, cathepsin B, Granzyme B, Factor XA, Enterokinase, genenase, sortase, precision protease, thrombin, TEV protease, or elastase 1. For example, the protease cleave site can include a polypeptide having an cleavage motif selected from RX(K/R)R consensus motif,
 25 RXXX[KR]R consensus motif, RRX consensus motif, I-E-P-D-X consensus motif (SEQ ID NO: 35), Glu/Asp-Gly-Arg, Asp-Asp-Asp-Asp-Lys (SEQ ID NO: 36), Pro-Gly-Ala-Ala-His-Tyr (SEQ ID NO: 37), LPXTG/A consensus motif, Leu-Glu-Val-Phe-Gln-Gly-Pro (SEQ ID NO: 38), Leu-Val-Pro-Arg-Gly-Ser (SEQ ID NO: 40), E-N-L-Y-F-Q-G (SEQ ID NO: 41), or [AGSV]-x (SEQ ID NO: 42). In certain
 30 embodiments, the mammalian extracellular protease is selected from Factor XA, Enterokinase, genenase, sortase, precision protease, thrombin, TEV protease, or elastase 1 (e.g., the cleavage site can include a polypeptide having an amino acid sequence selected from Glu/Asp-Gly-Arg, Asp-Asp-Asp-Asp-Lys (SEQ ID NO: 36), Pro-Gly-Ala-Ala-His-Tyr (SEQ ID NO: 37), LPXTG/A consensus motif, Leu-

Glu-Val-Phe-Gln-Gly-Pro (SEQ ID NO: 38), Leu-Val-Pro-Arg-Gly-Ser (SEQ ID NO: 40), E-N-L-Y-F-Q-G (SEQ ID NO: 41), or [AGSV]-x (SEQ ID NO: 42)).

In some embodiments, the fusion protein described herein includes a furin cleavage site. In some embodiments, the fusion proteins described herein include any one of furin cleavage sites listed in Table

20. In some embodiments, the fusion proteins described herein include a furin cleavage site selected from RTKR (SEQ ID NO: 123) or a sequence having at least 90%, 95%, 97%, 98%, or 99% identity thereto; GTGAEDPRPSRKRRSLGDVG (SEQ ID NO: 125) or a sequence having at least 90%, 95%, 97%, 98%, or 99% identity thereto; GTGAEDPRPSRKRR (SEQ ID NO: 127) or a sequence having at least 90%, 95%, 97%, 98%, or 99% identity thereto; LQWLEQQVAKRRTKR (SEQ ID NO: 129) or a sequence having at least 90%, 95%, 97%, 98%, or 99% identity thereto; GTGAEDPRPSRKRRSLGG (SEQ ID NO: 131) or a sequence having at least 90%, 95%, 97%, 98%, or 99% identity thereto; GTGAEDPRPSRKRRSLG (SEQ ID NO: 133) or a sequence having at least 90%, 95%, 97%, 98%, or 99% identity thereto; SLNLTESHNSRKKR (SEQ ID NO: 135) or a sequence having at least 90%, 95%, 97%, 98%, or 99% identity thereto; or CKINGYPKRGRKRR (SEQ ID NO: 137) or a sequence having at least 90%, 95%, 97%, 98%, or 99% identity thereto. In some embodiments, the fusion proteins described herein include a furin cleavage site selected from GTGAEDPRPSRKRRSLGDVG (SEQ ID NO: 125) or a sequence having at least 90%, 95%, 97%, 98%, or 99% identity thereto, or GTGAEDPRPSRKRR (SEQ ID NO: 127) or a sequence having at least 90%, 95%, 97%, 98%, or 99% identity thereto. In some embodiments, the fusion proteins described herein include the furin cleavage site of GTGAEDPRPSRKRRSLGDVG (SEQ ID NO: 125) or a sequence having at least 90%, 95%, 97%, 98%, or 99% identity thereto.

In some embodiments, the fusion proteins described herein include a furin cleavage site selected from RTKR (SEQ ID NO: 123); GTGAEDPRPSRKRRSLGDVG (SEQ ID NO: 125); GTGAEDPRPSRKRR (SEQ ID NO: 127); LQWLEQQVAKRRTKR (SEQ ID NO: 129); GTGAEDPRPSRKRRSLGG (SEQ ID NO: 131); GTGAEDPRPSRKRRSLG (SEQ ID NO: 133); SLNLTESHNSRKKR (SEQ ID NO: 135); or CKINGYPKRGRKRR (SEQ ID NO: 137). In some embodiments, the fusion proteins described herein include a furin cleavage site selected from GTGAEDPRPSRKRRSLGDVG (SEQ ID NO: 125) or GTGAEDPRPSRKRR (SEQ ID NO: 127). In some embodiments, the fusion proteins described herein include the furin cleavage site of GTGAEDPRPSRKRRSLGDVG (SEQ ID NO: 125).

In some embodiments, the conditional expression domain, e.g., aggregation domain or degradation domain, is located N-terminal to said second protein domain or C-terminal to said second protein domain.

In some embodiments, said fusion protein further comprises a signal peptide N-terminal to said conditional expression domain, e.g., aggregation domain or degradation domain. In some embodiments, the fusion protein further comprises a linker positioned between the signal peptide and said conditional

expression domain, e.g., aggregation domain or degradation domain. In some embodiments, the linker is a linker in any fusion protein listed in Tables 23 and 24.

In some embodiments, the fusion protein comprises an amino acid sequence of any fusion protein listed in Tables 22, 23, or 24.

- 5 In any of the foregoing aspects and embodiments, a second of the protein domains is a transmembrane protein (e.g., a transmembrane receptor). In any of the foregoing aspects, the transmembrane receptor can be, e.g., a synthetic protein (e.g., a chimeric antigen receptor). Chimeric antigen receptors can include, e.g., in a N-terminal to C-terminal direction, an antigen binding domain, a transmembrane domain, and one or more intracellular signaling domains. The signaling domain may include one or more
- 10 primary signaling domains (e.g., a CD3-zeta stimulatory domain) and, optionally, one or more costimulatory signaling domains (e.g., an intracellular domain from a costimulatory protein selected from CD27, CD28, 4-1BB (CD137), OX40, GITR, CD30, CD40, ICOS, BAFFR, HVEM, ICAM-1, lymphocyte function-associated antigen-1 (LFA-1), CD2, CDS, CD7, CD287, LIGHT, NKG2C, NKG2D, SLAMF7, NKp80, NKp30, NKp44, NKp46, CD160, B7-H3, or a ligand that specifically binds CD83).
- 15 In certain of the above embodiments, the antigen binding domain is an scFv. Also, the antigen binding domain may binds an antigen selected from CD19; CD123; CD22; CD30; CD171; CS-1; C-type lectin-like molecule-1, CD33; epidermal growth factor receptor variant III (EGFRvIII); ganglioside G2 (GD2); ganglioside GD3; TNF receptor family member B cell maturation (BCMA); Tn antigen ((Tn Ag) or (GalNAcα-Ser/Thr)); prostate-specific membrane antigen (PSMA); Receptor tyrosine kinase-like orphan
- 20 receptor 1 (ROR1); Fms-Like Tyrosine Kinase 3 (FLT3); Tumor-associated glycoprotein 72 (TAG72); CD38; CD44v6; Carcinoembryonic antigen (CEA); Epithelial cell adhesion molecule (EPCAM); B7H3 (CD276); KIT (CD117); Interleukin-13 receptor subunit alpha-2; Mesothelin; Interleukin 11 receptor alpha (IL-11Ra); prostate stem cell antigen (PSCA); Protease Serine 21; vascular endothelial growth factor receptor 2 (VEGFR2); Lewis(Y) antigen; CD24; Platelet-derived growth factor receptor beta (PDGFR-
- 25 beta); Stage-specific embryonic antigen-4 (SSEA-4); CD20; Folate receptor alpha; Receptor tyrosine-protein kinase ERBB2 (Her2/neu); Mucin 1, cell surface associated (MUC1); epidermal growth factor receptor (EGFR); neural cell adhesion molecule (NCAM); Prostase; prostatic acid phosphatase (PAP); elongation factor 2 mutated (ELF2M); Ephrin B2; fibroblast activation protein alpha (FAP); insulin-like growth factor 1 receptor (IGF-I receptor), carbonic anhydrase IX (CAIX); Proteasome (Prosome,
- 30 Macropain) Subunit, Beta Type, 9 (LMP2); glycoprotein 100 (gp100); oncogene fusion protein including breakpoint cluster region (BCR) and Abelson murine leukemia viral oncogene homolog 1 (Abl) (bcr-abl); tyrosinase; ephrin type-A receptor 2 (EphA2); Fucosyl GM1; sialyl Lewis adhesion molecule (sLe); ganglioside GM3; transglutaminase 5 (TGS5); high molecular weight-melanoma-associated antigen (HMWMAA); o-acetyl-GD2 ganglioside (OAcGD2); Folate receptor beta; tumor endothelial marker 1
- 35 (TEM1/CD248); tumor endothelial marker 7-related (TEM7R); claudin 6 (CLDN6); thyroid stimulating hormone receptor (TSHR); G protein-coupled receptor class C group 5, member D (GPCR5D);

- chromosome X open reading frame 61 (CXORF61); CD97; CD179a; anaplastic lymphoma kinase (ALK); Polysialic acid; placenta-specific 1 (PLAC1); hexasaccharide portion of globoH glycosphingolipid (GloboH); mammary gland differentiation antigen (NY-BR-1); uroplakin 2 (UPK2); Hepatitis A virus cellular receptor 1 (HAVCR1); adrenoceptor beta 3 (ADRB3); pannexin 3 (PANX3); G protein-coupled receptor 20 (GPR20); lymphocyte antigen 6 complex, locus K 9 (LY6K); Olfactory receptor 51E2 (OR51E2); TCR Gamma Alternate Reading Frame Protein (TARP); Wilms tumor protein (WT1); Cancer/testis antigen 1 (NY-ESO-1); Cancer/testis antigen 2 (LAGE-1a); Melanoma-associated antigen 1 (MAGE-A1); ETS translocation-variant gene 6, located on chromosome 12p (ETV6-AML); sperm protein 17 (SPA17); X Antigen Family, Member 1A (XAGE1); angiopoietin-binding cell surface receptor 2 (Tie 2); melanoma cancer testis antigen-1 (MAD-CT-1); melanoma cancer testis antigen-2 (MAD-CT-2); Fos-related antigen 1; tumor protein p53 (p53); p53 mutant; prostein; surviving; telomerase; prostate carcinoma tumor antigen-1, melanoma antigen recognized by T cells 1; Rat sarcoma (Ras) mutant; human Telomerase reverse transcriptase (hTERT); sarcoma translocation breakpoints; melanoma inhibitor of apoptosis (ML-IAP); ERG (transmembrane protease, serine 2 (TMPRSS2) ETS fusion gene); N-Acetyl glucosaminyl-transferase V (NA17); paired box protein Pax-3 (PAX3); Androgen receptor; Cyclin B1; v-myc avian myelocytomatosis viral oncogene neuroblastoma derived homolog (MYCN); Ras Homolog Family Member C (RhoC); Tyrosinase-related protein 2 (TRP-2); Cytochrome P450 1B1 (CYP1B1); CCCTC-Binding Factor (Zinc Finger Protein)-Like, Squamous Cell Carcinoma Antigen Recognized By T Cells 3 (SART3); Paired box protein Pax-5 (PAX5); proacrosin binding protein sp32 (OY-TES1); lymphocyte-specific protein tyrosine kinase (LCK); A kinase anchor protein 4 (AKAP-4); synovial sarcoma, X breakpoint 2 (SSX2); Receptor for Advanced Glycation Endproducts (RAGE-1); renal ubiquitous 1 (RU1); renal ubiquitous 2 (RU2); legumain; human papilloma virus E6 (HPV E6); human papilloma virus E7 (HPV E7); intestinal carboxyl esterase; heat shock protein 70-2 mutated (mut hsp70-2); CD79a; CD79b; CD72; Leukocyte-associated immunoglobulin-like receptor 1 (LAIR1); Fc fragment of IgA receptor (FCAR or CD89); Leukocyte immunoglobulin-like receptor subfamily A member 2 (LILRA2); CD300 molecule-like family member f (CD300LF); C-type lectin domain family 12 member A (CLEC12A); bone marrow stromal cell antigen 2 (BST2); EGF-like module-containing mucin-like hormone receptor-like 2 (EMR2); lymphocyte antigen 75 (LY75); Glypican-3 (GPC3); Fc receptor-like 5 (FCRL5); or immunoglobulin lambda-like polypeptide 1 (IGLL1).
- 30 In some embodiments, the fusion protein comprises an antigen binding domain that binds CD19. In some embodiments, the fusion protein comprises an antigen binding domain comprising an amino acid sequence selected from any one of SEQ ID NOs: 356-368 or 381. In some embodiments, the fusion protein comprises a chimeric antigen receptor comprising an amino acid sequence selected from any one of SEQ ID NOs: 897, 902, 907, 912, 917, 922, 927, 932, 937, 942, 947, 952, 956.
- 35 In some embodiments, the fusion protein comprises an antigen binding domain that binds CD123. In some embodiments, the fusion protein comprises an antigen binding domain comprising an amino acid

sequence selected from any one of SEQ ID NOs: 751, 756, 761, or 766. In some embodiments, the fusion protein comprises a chimeric antigen receptor comprising an amino acid sequence selected from any one of SEQ ID NOs: 750, 755, 760, or 765.

5 In some embodiments, the fusion protein comprises an antigen binding domain that binds BCMA. In some embodiments, the fusion protein comprises an antigen binding domain comprising an amino acid sequence selected from any one of SEQ ID NOs: 382, 386, 390, 394, 398, 402, 406, 410, 414, 418, 422, 426, 430, 434, 438, 442, 446, 450, 454, 458, 462, 466, 470, 474, 478, 482, 486, 490, 494, 498, 502, 506, 510, 514, 518, 522, 528, 531, 534, or 537. In some embodiments, the fusion protein comprises a chimeric antigen receptor comprising an amino acid sequence selected from any one of SEQ ID NOs:
10 789, 791, 793, 795, 797, 799, 801, 803, 805, 807, 809, 811, 813, 815, 817, 819, 821, 823, 825, 827, 829, 831, 833, 835, 837, 839, 841, 843, 845, 847, 849, 851, 853, 855, 857, or 859.

In some embodiments, the fusion protein comprises an antigen binding domain that binds CD20. In some embodiments, the fusion protein comprises an antigen binding domain comprising an amino acid sequence located at positions 470-712 or 470-939 of SEQ ID NO: 3033. In some embodiments, the
15 fusion protein comprises a chimeric antigen receptor comprising an amino acid sequence of SEQ ID NO: 3033.

Cells, nucleic acids and method of making the fusion proteins

In another aspect, the invention features a cell, e.g., a host cell including any one of the foregoing fusion
20 proteins. In some embodiments, the cell, e.g., the host cell, is an immune cell, e.g., an immune effector cell. In some embodiments, the cell is a T cell or an NK cell.

In yet another aspect, the invention features a nucleic acid (e.g., an mRNA or DNA molecule) encoding any one of the foregoing fusion proteins. In another aspect, the invention features a vector (e.g., a viral vector (such as a lentiviral vector)) containing such a nucleic acid. The invention also features a viral
25 particle including such a viral vector.

In yet another aspect, the invention features a cell, e.g., host cell (e.g., a human T cell) containing any of the foregoing vectors, nucleic acids, or fusion proteins.

In certain embodiments, the cell further includes a protease capable of cleaving the heterologous protease cleavage site. In certain embodiments, the host cell can further include a stabilization
30 compound (e.g., Bazedoxifene, Shield1 or 1 μ M 4-OHT (4-hydroxy tamoxifen)) wherein said degradation domain assumes a conformation permissive to cellular degradation in the absence of said stabilization compound.

In some embodiments, in the absence of an expression compound, e.g., a stabilization compound, the fusion protein is degraded by cellular degradation pathways, e.g., at least 50%, 60%, 70%, 80%, 90% or greater of the fusion protein is degraded.

5 In some embodiments, in the absence of an expression compound, e.g., deaggregation compound, the fusion protein is in an aggregated state in the cell, e.g., in the endoplasmic reticulum or the cytosol, e.g., at least 50%, 60%, 70%, 80%, 90% or greater is in the aggregated state.

In some embodiments, said cell further comprises an expression compound, e.g., a stabilization compound.

10 In some embodiments, the conditional expression domain, e.g., degradation domain, assumes a conformation more resistant to cellular degradation in the presence of the expression compound, e.g., stabilization compound, relative to a conformation in the absence of the expression compound.

In some embodiments, the conformation of the fusion protein is more permissive to cleavage at the heterologous protease cleavage site in the presence of the expression compound, e.g., stabilization compound, relative to a conformation in the absence of the expression compound.

15 In some embodiments, the level of cell surface expression or extracellular expression of the fusion protein is greater, e.g., 2, 3, 4, 5, 6, 7, 8, 9, 10, 20, or 30 fold greater, than the level of cell surface expression or extracellular expression of the fusion protein in a cell not comprising an expression compound, e.g., a stabilization compound.

20 In some embodiments, said cell further comprises an expression compound, e.g., a deaggregation compound.

In some embodiments, the conditional expression domain, e.g., aggregation domain, assumes a conformation more resistant to oligomerization or aggregation in the presence of the expression compound, e.g., deaggregation compound, relative to a conformation in the absence of the expression compound.

25 In some embodiments, the conformation of the fusion protein is more permissive to cleavage at the heterologous protease cleavage site in the presence of the expression compound, e.g., deaggregation compound, relative to a conformation in the absence of the expression compound.

30 In some embodiments, the level of cell surface expression or extracellular expression of the fusion protein is greater, e.g., 2, 3, 4, 5, 6, 7, 8, 9, 10, 20, or 30 fold greater, than the level of cell surface expression or extracellular expression of the fusion protein in a cell not comprising an expression compound, e.g., a deaggregation compound.

In yet another aspect, a method of making a fusion protein as described herein is disclosed. The method includes providing a cell, e.g., a host cell as described herein, e.g., a host cell comprising any of the foregoing vectors, nucleic acids, or fusion proteins, under conditions suitable for expression.

In another aspect, the invention also features a method of conditionally expressing a protein of interest.

5 In one embodiment, the protein of interest is a transmembrane protein, e.g., a CAR.

In some embodiments, the invention also features a method for conditionally expressing a protein of interest, transmembrane protein, or CAR on the surface of a cell (e.g., an immune cell, e.g., a host cell).

The method includes:

10 providing a cell, e.g., an immune cell (e.g., a host cell) comprising a fusion protein or a nucleic acid encoding the fusion protein (e.g., any of the fusion proteins described herein);

contacting the fusion protein or the cell comprising said fusion protein with an expression compound, wherein:

15 (a) in the presence of said expression compound, the surface expression of said protein of interest, transmembrane protein, or CAR is increased, e.g., 2, 3, 4, 5, 6, 7, 8, 9, 10, 20, or 30 fold greater, relative a reference value, e.g., relative to the level of surface expression of said protein of interest, transmembrane protein, or CAR in the absence of said expression compound; and

20 (b) in the absence of said expression compound, the surface expression of said protein of interest, transmembrane protein, or CAR is substantially decreased, e.g., e.g., 2, 3, 4, 5, 6, 7, 8, 9, 10, 20, or 30 fold less, relative a reference value, e.g., relative relative to the level of surface expression of said protein of interest, transmembrane protein, or CAR in the presence of the expression compound.

25 In some embodiments, the presence of said expression compound is associated with, e.g., causes, a change in conformation of the conditional expression domain from a first folding state to second folding state, wherein the first folding state is more susceptible to degradation, e.g., cellular degradation, or aggregation relative to the second folding state.

In some embodiments, the presence of said expression compound exposes the heterologous protease cleavage site, e.g., to a greater extent, e.g., 2, 3, 4, 5, 6, 7, 8, 9, 10, 20, or 30 fold greater, relative the exposure of the protease cleavage site in the absence of said expression compound.

30

In some embodiments, the invention also features a method of conditionally expressing a protein of interest, transmembrane protein, or CAR, said method comprising contacting a cell, e.g., a host cell and/or a cell described herein, with a stabilization compound, wherein:

(a) in the presence of said stabilization compound,

(i) said degradation domain assumes a conformation more resistant to cellular degradation relative to a conformation in the absence of the stabilization compound,

thereby resulting in cleavage of said degradation domain from said protein of interest, transmembrane protein, or CAR and the expression of said protein of interest, transmembrane protein, or CAR; and

- 5 (b) in the absence of said stabilization compound, said degradation domain assumes a conformation more permissive to cellular degradation relative to a conformation in the presence of stabilization compound, thereby resulting in degradation of said protein of interest, transmembrane protein, or CAR.

In some embodiments, said cell is contacted with said stabilization compound ex vivo.

In some embodiments, said cell is contacted with said stabilization compound in vivo.

- 10 In some embodiments, the invention also features a method of conditionally expressing a protein of interest, transmembrane protein, or CAR, said method comprising contacting a cell, e.g., a host cell and/or a cell described herein, with a deaggregation compound, wherein:

(a) in the presence of said deaggregation compound,

- 15 (i) said aggregation domain assumes a conformation more resistant to aggregation or oligomerization relative to a conformation in the absence of the deaggregation compound,

thereby resulting in cleavage of said aggregation domain from said protein of interest, transmembrane protein, or CAR and the expression of said protein of interest, transmembrane protein, or CAR; and

- 20 (b) in the absence of said deaggregation compound, said aggregation domain assumes a conformation more permissive to aggregation or oligomerization relative to a conformation in the presence of the deaggregation compound, thereby resulting in aggregation of said protein of interest, transmembrane protein, or CAR.

In some embodiments, said cell is contacted with said deaggregation compound ex vivo.

In some embodiments, said cell is contacted with said deaggregation compound in vivo.

- 25 In yet another aspect, the invention features a method of treating a subject having a disease associated with expression of a tumor antigen, including administering to the subject an effective amount of any of the foregoing host cells, wherein the second protein is a chimeric antigen receptor and includes, in a N-terminal to C-terminal direction, an antigen binding domain, a transmembrane domain, and one or more intracellular signaling domains and the antigen binding domain specifically binds the tumor antigen. In yet another aspect, the invention features a method of treating an autoantibody or alloantibody disease or
30 condition, the method comprising administering to the subject an effective amount of the foregoing host

cell, wherein said second protein is a chimeric antigen receptor and comprises, in a N-terminal to C-terminal direction, an antigen binding domain, a transmembrane domain, and one or more intracellular signaling domains and said antigen binding domain specifically binds an antigen specific of said autoantibody or alloantibody disease. In such methods, the host cell can be either autologous or non-autologous, e.g., allogeneic, to the subject. Such methods can further include the step of contacting the host cell, in vivo or ex vivo, with the foregoing stabilization compounds.

In some embodiments, the cell is contacted with an expression compound, and:

(a) in the presence of said expression compound,

(i) said conditional expression domain assumes a conformation more resistant to cellular degradation or aggregation relative to a conformation in the absence of said expression compound, thereby resulting in cleavage of said conditional expression domain from said chimeric antigen receptor (CAR) and the expression of said CAR; and

(b) in the absence of said expression compound, said conditional expression domain assumes a conformation more permissive to cellular degradation or aggregation relative to a conformation in the presence of said expression compound, thereby resulting in degradation or aggregation of said fusion protein.

In some embodiments, the cell, e.g., host cell, is contacted with a stabilization compound, and:

(a) in the presence of said stabilization compound,

(i) said degradation domain assumes a conformation more resistant to cellular degradation relative to a conformation in the absence of said stabilization compound,

thereby resulting in cleavage of said degradation domain from said chimeric antigen receptor (CAR) and the expression of said CAR; and

(b) in the absence of said stabilization compound, said degradation domain assumes a conformation more permissive to cellular degradation relative to a conformation in the presence of said stabilization compound, thereby resulting in degradation of said fusion protein.

In some embodiments, said stabilization compound is selected from Bazedoxifene or 4-hydroxy tamoxifen (4-OHT) when the fusion protein comprises a degradation domain derived from estrogen receptor.

In some embodiments, said stabilization compound is Shield-1 when the fusion protein comprises a degradation domain derived from an FKB protein.

In some embodiments, the cell is contacted with a deaggregation compound, and:

(a) in the presence of said deaggregation compound,

(i) said aggregation domain assumes a conformation more resistant to aggregation or oligomerization relative to a conformation in the absence of said deaggregation compound,

thereby resulting in cleavage of said aggregation domain from said chimeric antigen receptor (CAR) and the expression of said CAR; and

(b) in the absence of said deaggregation compound, said aggregation domain assumes a conformation more permissive to aggregation or oligomerization relative to a conformation in the presence of said deaggregation compound, thereby resulting in aggregation of said fusion protein.

In some embodiments, said deaggregation compound is selected from FK506, rapamycin, AP22542, and AP21998 when the fusion protein comprises an aggregation domain derived from FKB protein (FKBP), e.g., FKBP F36M.

In some embodiments, the autoantibody disease or condition is selected from the group consisting of bullous pemphigoid, epidermolysis bullosa acquisita, p200 pemphigoid, linear IgA bullous dermatosis, other pemphigoid group diseases, dermatitis herpetiformis, celiac disease, myasthenia gravis, Goodpasture's syndrome, granulomatosis with polyangiitis and other ANCA+ vasculitides, autoimmune limbic encephalitis, anti-N-methyl-D-aspartate receptor encephalitis, neuromyelitis optica, autoimmune hemolytic anemia, autoantibody-associated end-organ damage in lupus and other connective tissue diseases (due to anti-dsDNA, anti-Ro, and other autoantibodies), Graves' and Hashimoto's thyroiditis, anti-insulin antibodies in diabetes, anti-insulin receptor antibodies in autoimmune hypoglycemia, cryoglobulinemia, rheumatoid arthritis, multiple sclerosis, Sjogren's syndrome, dermatomyositis, anti-Fc-epsilon receptor antibodies in chronic idiopathic urticaria, anti-folate receptor antibodies, anti-endothelial receptor or anti-adrenergic receptor antibodies in pulmonary arterial hypertension, refractory hypertension, dilated cardiomyopathy, an autoinflammatory syndrome, neuromyelitis optica, Goodpasture's syndrome, anti-NMDAR encephalitis, AIHA, ITP, TTP, Graves'/Hashimoto's disease, Primary biliary cirrhosis, Neonatal lupus, Maternal autoabs causing T cell destruction, Pulmonary alveolar proteinosis, Anti-folate receptor, Chronic inflammatory demyelinating polyneuropathy, and Idiopathic membranous nephropathy. In some embodiments, the alloantibody disease or condition is an immune reaction in response to an organ transplant, blood transfusion, pregnancy, or protein replacement therapy.

In some embodiments, the cancer is mesothelioma (e.g., malignant pleural mesothelioma), e.g., in a subject who has progressed on at least one prior standard therapy; lung cancer (e.g., non-small cell lung cancer, small cell lung cancer, squamous cell lung cancer, or large cell lung cancer); pancreatic cancer (e.g., pancreatic ductal adenocarcinoma, or metastatic pancreatic ductal adenocarcinoma (PDA), e.g., in

a subject who has progressed on at least one prior standard therapy); esophageal adenocarcinoma, ovarian cancer (e.g., serous epithelial ovarian cancer, e.g., in a subject who has progressed after at least one prior regimen of standard therapy), breast cancer, colorectal cancer, bladder cancer or any combination thereof.

5

In some embodiments, the disease associated with expression of a tumor antigen is a cancer.

In some embodiments, the disease associated with expression of the tumor antigen is a hematological cancer, e.g., a hematological cancer chosen from a leukemia or lymphoma.

10 In some embodiments, the cancer is chosen from: chronic lymphocytic leukemia (CLL), mantle cell lymphoma (MCL), multiple myeloma, acute lymphoid leukemia (ALL), Hodgkin lymphoma, B-cell acute lymphoid leukemia (BALL), T-cell acute lymphoid leukemia (TALL), small lymphocytic leukemia (SLL), B cell prolymphocytic leukemia, blastic plasmacytoid dendritic cell neoplasm, Burkitt's lymphoma, diffuse large B cell lymphoma (DLBCL), DLBCL associated with chronic inflammation, chronic myeloid leukemia, myeloproliferative neoplasms, follicular lymphoma, pediatric follicular lymphoma, hairy cell leukemia, 15 small cell- or a large cell-follicular lymphoma, malignant lymphoproliferative conditions, MALT lymphoma (extranodal marginal zone lymphoma of mucosa-associated lymphoid tissue), Marginal zone lymphoma, myelodysplasia and myelodysplastic syndrome, non-Hodgkin lymphoma, plasmablastic lymphoma, plasmacytoid dendritic cell neoplasm, Waldenstrom macroglobulinemia, splenic marginal zone lymphoma, splenic lymphoma/leukemia, splenic diffuse red pulp small B-cell lymphoma, hairy cell leukemia-variant, 20 lymphoplasmacytic lymphoma, a heavy chain disease, plasma cell myeloma, solitary plasmacytoma of bone, extraosseous plasmacytoma, nodal marginal zone lymphoma, pediatric nodal marginal zone lymphoma, primary cutaneous follicle center lymphoma, lymphomatoid granulomatosis, primary mediastinal (thymic) large B-cell lymphoma, intravascular large B-cell lymphoma, ALK+ large B-cell lymphoma, large B-cell lymphoma arising in HHV8-associated multicentric Castleman disease, primary 25 effusion lymphoma, B-cell lymphoma, acute myeloid leukemia (AML), or unclassifiable lymphoma.

In some embodiments, the cancer is chosen from MCL, CLL, ALL, Hodgkin lymphoma, AML, or multiple myeloma.

In yet another aspect, the invention features a fusion protein, cell, nucleic acid, viral particle, or vector described herein for use as a medicament.

30 In yet another aspect, the invention features a fusion protein, cell, nucleic acid, vector, or method described herein for use in the treatment of a disease expressing a tumor antigen.

Methods and compositions for use in treating autoantibody or alloantibody disease

In one aspect, the invention features methods of treating an autoantibody or alloantibody disease or condition in a subject in need thereof comprising administering an effective amount of a pharmaceutical composition comprising a modified T cell to the subject, wherein the modified T cell comprises a nucleic acid comprising a suicide gene and a nucleic acid encoding a chimeric antigen receptor (CAR)

5 comprising an anti-B cell binding domain, a transmembrane domain, a costimulatory domain and an intracellular signaling domain. In another aspect, the invention features methods of treating an autoantibody or alloantibody disease or condition in a subject in need thereof comprising administering an effective amount of a pharmaceutical composition comprising a modified T cell to the subject, wherein the modified T cell comprises a nucleic acid encoding a dimerization domain and a chimeric antigen receptor
10 (CAR) comprising an anti-B cell binding domain, a transmembrane domain, a costimulatory domain and an intracellular signaling domain.

In some embodiments, the suicide gene encodes the amino acid sequence selected from the group consisting of SEQ ID NOs: 3005-3007.

In some embodiments, the suicide gene further comprises a dimerization domain comprising the amino
15 acid sequence selected from the group consisting of SEQ ID NO: 3013 and 3014.

In some embodiments, the dimerization domain comprises the amino acid sequence of SEQ ID NO: 980.

In some embodiments, the dimerization domain further comprises a furin cleavage site comprising the amino acid sequence of SEQ ID NO: 980.

In some embodiments, the CAR further comprises a signal peptide.

20 In some embodiments, the signal peptide comprises the amino acid sequence of SEQ ID NO: 3035.

In some embodiments, administering the effective amount comprises activating the modified T cell to effect cytotoxic function against B cells.

In some embodiments, the method further comprises activating a suicide gene product of the suicide gene to induce cell death of the modified T cell.

25 In some embodiments, activating the suicide gene product further comprises administering a dimerization agent to promote dimerization of the suicide gene product.

In some embodiments, activating the suicide gene product occurs after the modified T cell exerts cytotoxic function against B cells.

In some embodiments, activating the suicide gene product occurs after an onset of an adverse reaction in
30 the subject to the modified T cell.

In some embodiments, the method further comprises repressing activation of a suicide gene product of the suicide gene to repress cell death of the modified T cell.

In some embodiments, repressing activation of the suicide gene product further comprises administering a solubilizing agent to prevent dimerization of the suicide gene product.

- 5 In some embodiments, administering the solubilizing agent occurs concurrently with administration of the modified T cell and continues as the modified T cell exerts cytotoxic function against B cells.

In some embodiments, administering the solubilizing agent is ceased after an onset of an adverse reaction in the subject to the modified T cell.

- 10 In some embodiments, the anti-B cell binding domain of the CAR comprises an antibody selected from the group consisting of a monoclonal antibody, a polyclonal antibody, a synthetic antibody, human antibody, humanized antibody, single domain antibody, single chain variable fragment, and antigen-binding fragments thereof.

- 15 In some embodiments, the anti-B cell binding domain of the CAR specifically binds a B cell marker selected from the group consisting of CD19, BCMA, CD20, CD21, CD27, CD38, CD138 and any combination thereof.

In some embodiments, the anti-B cell binding domain of the CAR specifically binds a B cell marker selected from the group consisting of CD20, CD21, CD27, CD38, CD138, any combination thereof, and at least one surface marker selectively found on a pro-B cell, pre-B cell, immature B cell, mature B cell, memory B cell, and plasma cell.

- 20 In some embodiments, the intracellular domain of the CAR comprises dual signaling domains.

In some embodiments, the costimulatory domain is selected from the group consisting of CD3, CD27, CD28, CD83, CD86, CD127, 4-1BB, 4-1BBL, PD1, PD1L, T cell receptor (TCR), any derivative or variant thereof, any synthetic sequence thereof that has the same functional capability, and any combination thereof.

- 25 In some embodiments, the method further comprises administering a solubilizing agent to prevent dimerization of the CAR.

In some embodiments, administering the solubilizing agent occurs concurrently with administration of the modified T cell and continues as the modified T cell exerts cytotoxic function against B cells.

- 30 In some embodiments, administering the solubilizing agent is ceased after an onset of an adverse reaction in the subject to the modified T cell.

In some embodiments, the autoantibody disease or condition is selected from the group consisting of bullous pemphigoid, epidermolysis bullosa acquisita, p200 pemphigoid, linear IgA bullous dermatosis, other pemphigoid group diseases, dermatitis herpetiformis, celiac disease, myasthenia gravis, Goodpasture's syndrome, granulomatosis with polyangiitis and other ANCA+ vasculitides, autoimmune limbic encephalitis, anti-N-methyl-D-aspartate receptor encephalitis, neuromyelitis optica, autoimmune hemolytic anemia, autoantibody-associated end-organ damage in lupus and other connective tissue diseases (due to anti-dsDNA, anti-Ro, and other autoantibodies), Graves' and Hashimoto's thyroiditis, anti-insulin antibodies in diabetes, anti-insulin receptor antibodies in autoimmune hypoglycemia, cryoglobulinemia, rheumatoid arthritis, multiple sclerosis, Sjogren's syndrome, dermatomyositis, anti-Fc-epsilon receptor antibodies in chronic idiopathic urticaria, anti-folate receptor antibodies, anti-endothelial receptor or anti-adrenergic receptor antibodies in pulmonary arterial hypertension, refractory hypertension, dilated cardiomyopathy, and an autoinflammatory syndrome.

In some embodiments, the alloantibody disease or condition is an immune reaction in response to an organ transplant, blood transfusion, pregnancy, and protein replacement therapy.

In some embodiments, the modified T cell is further modified by deleting a gene selected from the group consisting of a T cell receptor (TCR) chain, a major histocompatibility complex protein, and any combination thereof.

In some embodiments, the modified T cell is further modified before administration to the subject in need thereof.

In some embodiments, the modified T cell is further modified by inducing a CRISPR/Cas system.

In one aspect, the invention features a pharmaceutical composition formulated for use in a method described herein, the composition comprising a modified T cell comprising a nucleic acid encoding a suicide gene and a nucleic acid encoding a chimeric antigen receptor (CAR) comprising an anti-B cell binding domain, a transmembrane domain, a costimulatory domain and an intracellular signaling domain.

In one aspect, the invention features a pharmaceutical composition formulated for use in a method described herein, the composition comprising a modified T cell comprising a nucleic acid encoding a dimerization domain and a chimeric antigen receptor (CAR) comprising an anti-B cell binding domain, a transmembrane domain, a costimulatory domain and an intracellular signaling domain.

In some embodiments, the suicide gene encodes the amino acid sequence selected from the group consisting of SEQ ID NOs: 3005-3007.

In some embodiments, the suicide gene further comprises a dimerization domain comprising the amino acid sequence selected from the group consisting of SEQ ID NOs: 3013 and 3014.

In some embodiments, the dimerization domain comprises the amino acid sequence of SEQ ID NO: 980.

In some embodiments, the dimerization domain further comprises a furin cleavage site comprising the amino acid sequence of SEQ ID NO: 980.

In some embodiments, the CAR further comprises a signal peptide.

- 5 In some embodiments, the signal peptide comprises the amino acid sequence of SEQ ID NO: 3035.

In some embodiments, the composition further comprises an inducing agent to induce activation of the suicide gene.

In some embodiments, the modified T cell lacks at least one gene encoding a T cell receptor (TCR) chain, and a major histocompatibility complex protein.

- 10 In one aspect, the invention features an isolated nucleic acid sequence comprising a nucleic acid sequence comprising (i) a suicide gene comprising a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 3001-3004; and (ii) a nucleic acid sequence encoding a chimeric antigen receptor (CAR) comprising an anti-B cell binding domain, a transmembrane domain, a costimulatory domain and an intracellular signaling domain.

- 15 In some embodiments, the isolated nucleic acid sequence comprises SEQ ID NO: 3018, 3020, 3024, 3026, 3028 or 3030.

In one aspect, the invention features an isolated polypeptide comprising (i) an amino acid sequence encoded by a suicide gene wherein the amino acid sequence is selected from the group consisting of SEQ ID NOs: 3005-3007; and (ii) a chimeric antigen receptor (CAR) comprising an anti-B cell binding domain, a transmembrane domain, a costimulatory domain and an intracellular signaling domain.

- 20

In some embodiments, the isolated polypeptide comprises an amino acid sequence of SEQ ID NO: 3019, 3021, 3026, 3028, 3030 or 3034.

In one aspect, the invention features an isolated nucleic acid sequence comprising (i) a nucleic acid encoding a dimerization domain; and (ii) a chimeric antigen receptor (CAR) comprising an anti-B cell binding domain, a transmembrane domain, a costimulatory domain and an intracellular signaling domain.

- 25

In some embodiments, the dimerization domain comprises the amino acid sequence of SEQ ID NO: 980.

In some embodiments, the isolated nucleic acid sequence comprises SEQ ID NO: 977 or 3032.

In one aspect, the invention features an isolated polypeptide comprising (i) a dimerization domain; and (ii) a chimeric antigen receptor (CAR) comprising an anti-B cell binding domain, a transmembrane domain, a costimulatory domain and an intracellular signaling domain.

- 30

In some embodiments, the isolated polypeptide comprises an amino acid sequence of SEQ ID NO: 978 or 3033.

BRIEF DESCRIPTION OF THE DRAWINGS

5 **FIG. 1** is a graph showing expression of PCSK (proprotein convertase) family members in primary human T cells. The expression of the PCSK family members was measured by qRT-PCR. RNA was harvested from normal donor T cells on days 0, 4, and 11 following stimulation with anti-CD3/anti-CD28 activation beads. An additional group was supplemented with 100 U/mL IL-2 during culture and RNA was harvested on day 11.

10 **FIG. 2** is a series of graphs showing compound-dependent CAR expression in Jurkat T cells transduced with an anti-CD19 scFv CAR construct fused to the indicated furin degradation domain (FKBP_{FD}, ER α _{FD}, or DHFR_{FD}) followed by treatment with the corresponding stabilizing compound. FKBP_{FD} transduced cells treated with 1 μ M Shield1; ER α _{FD} transduced cells treated with 1 μ M Bazedoxifene; DHFR_{FD} transduced cells treated with 1 mM Trimethoprim (TMP). Expression of the anti-CD19 scFv is inducible by the
15 stabilizing compound. Black=UTD (untransduced cells); Gray=construct, no compound; White=construct, with compound.

FIG. 3 is a graph showing kinetics of CAR expression in Jurkat T cells transduced with an anti-CD19 scFv CAR construct fused to the indicated furin degradation domain (FKBP_{FD} or ER α _{FD}) following addition of a stabilization compound. The FKBP_{FD} transduced cells were treated with 1 μ M Shield1 and the ER α _{FD}
20 transduced cells were treated with 1 μ M 4-OHT (4-hydroxy tamoxifen) for the time indicated; and CAR expression was determined by FACS.

FIG. 4 is a series of histograms showing a furin degon domain ER α _{FD} can regulate CAR19 expression in a Bazedoxifene -dependent manner in primary human T cells, and that stabilization is enhanced in the presence of IL-2 in vitro. Primary human T cells were transduced with ER α _{FD} domain fused to an anti-
25 CD19 scFv CAR construct. 100 U/mL IL-2 was added on day 9 following activation with anti-CD3/CD28 stimulation beads. Bazedoxifene was added on day 10, and CAR expression was determined by FACS on day 11.

FIG. 5 is a pair of graphs showing kinetics of CAR expression following compound washout in primary T cells transduced with CAR construct fused to a furin degradation domain. Primary human T cells were
30 transduced with the indicated furin degradation domain (FKBP_{FD} or ER α _{FD}) fused to an anti-CD19 scFv CAR construct. 100 U/mL IL-2 was added on day 9 following activation with anti-CD3/CD28 stimulation beads. Bazedoxifene was added on day 10, and T cells were frozen on day 11. T cells were thawed,

extensively washed, and placed in culture for the times indicated followed by determination of CAR expression by FACS.

FIG. 6 is a series of plots showing multiple ER α targeting drugs stabilize FurOn CARTs. Jurkat T cells were transduced with ER α _{FD} degradation domain fused to an anti-CD19 scFv CAR construct followed by treatment with the indicated compounds for 24 hours. ER α targeting drugs used were: 10 μ M 4-OHT, 1 μ M Bazedoxifene, or 1 μ M Lasofoxifene.

FIG. 7 is a graph showing dose response of ER α _{FD} fused CAR expression to Bazedoxifene. Primary human T cells were transduced with ER α _{FD} degradation domain fused to an anti-CD19 scFv CAR construct or the parental CD19 CAR construct. 100 U/mL IL-2 was added on day 9 following activation with anti-CD3/CD28 stimulation beads, and T cells were frozen on day 11. T cells were thawed and placed in culture with Bazedoxifene for 48 hours at the concentrations indicated. CAR expression was determined by FACS.

FIG. 8 is a pair of graphs showing compound-dependent target specific cell killing by ER-alpha based FurON CART. Primary human T cells were transduced with ER α _{FD} degradation domain fused to an anti-CD19 scFv CAR construct or the parental CD19 CAR construct. 100 U/mL IL-2 and Bazedoxifene were added on day 9 following activation with anti-CD3/CD28 stimulation beads, and T cells were frozen on day 11. T cells were thawed and incubated for 20 hours with the indicated luciferized cell line targets, K562 (CD19-) or NALM6 (CD19+). Percent killing was determined by analysis of remaining luciferase activity.

FIG. 9 is a pair of graphs showing compound-dependent target specific cell killing by FKBP based FurON CART. Primary human T cells were transduced with FKBP_{FD} furin degradation domain fused to an anti-CD19 scFv CAR construct or the parental CD19 CAR construct. 100 U/mL IL-2 and Shield1 were added on day 9 following activation with anti-CD3/CD28 stimulation beads, and T cells were frozen on day 11. T cells were thawed and incubated for 20 hours with the indicated luciferized cell line targets, K562 (CD19-) or NALM6 (CD19+). Percent killing was determined by analysis of remaining luciferase activity.

FIG. 10 is a pair of graphs showing compound-dependent cytokine production of ER-alpha FurOn CART. Primary human T cells were transduced with ER α _{FD} furin degradation domain fused to an anti-CD19 scFv CAR construct or the parental CD19 CAR construct. 100 U/mL IL-2 and Bazedoxifene were added on day 9 following activation with anti-CD3/CD28 stimulation beads, and T cells were frozen on day 11. T cells were thawed and incubated with the indicated cell line targets for 20 hrs. Supernatants were harvested and analyzed by cytokine bead array.

FIG. 11 is a graph showing compound dependent proliferation of ER-alpha FurOn CART. Primary human T cells were transduced with ER α _{FD} degradation domain fused to an anti-CD19 scFv CAR construct or the parental CD19 CAR construct. 100 U/mL IL-2 and Bazedoxifene were added on day 9 following activation

with anti-CD3/CD28 stimulation beads, and T cells were frozen on day 11. T cells were thawed and incubated with the indicated cell line targets for 4 days. T cell FurON-CAR numbers were analyzed by FACS.

FIGs. 12A-12B are representative immunoblots showing the degree of furin cleavage across the various tested furin cleavage sites in ER α -FurON CAR19 constructs. The tested furin cleavage sites are: #105 – LQWLEQQVAKRRTKR (SEQ ID NO: 129); #106 – GTGAEDPRPSRKRRSLGDVG (SEQ ID NO: 125); #107 – GTGAEDPRPSRKRRSLGG (SEQ ID NO: 131); #108 – GTGAEDPRPSRKRRSLG (SEQ ID NO: 133); #102 – SLNLTESHNSRKRR (SEQ ID NO: 135); #103 – GTGAEDPRPSRKRR (SEQ ID NO: 127); #104 – CKINGYPKRGRKRR (SEQ ID NO: 137); #73 – RTKR (SEQ ID NO: 123).

FIG. 13 is a table showing the furon (furin degra) domain regulates CAR19 expression in a stabilizing compound-dependent manner in human primary T cells, but had no impact on cell viability and cell proliferation.

FIG. 14 is a series of line graphs showing that CAR19 with the furin degra domain kills CD19+ tumor cells in a stabilizing compound dose-dependent manner and is noninferior to the parental CAR construct.

FIG. 15 is a bar graph showing primary human T cells expressing ER α FurON CAR19 secrete IFN γ in the presence of CD19+ tumor cells, in a manner that is stabilizing compound dose-dependent and is noninferior to the parental CAR construct.

FIG. 16 is a series of bar graphs showing primary human T cells expressing ER α FurON CAR19 proliferate in the presence of CD19+ tumor cells, in a manner that is stabilizing compound-dependent and is noninferior to the parental CAR19 construct.

FIG. 17 is a series of graphs showing that the tested FurON domains regulate CAR19 expression in Jurkat cells in a compound-dependent manner, regardless of the number of mutations; and no CAR surface expression is detected in the absence of stabilizing compound.

FIG. 18 is a table showing that the FurON domain regulates CAR19 expression in a stabilizing compound- and IL-2-dependent manner in human primary T cells. No surface CAR expression is detected in the absence of the stabilizing compound bazedoxifene, when the FurON moiety is fused to CAR19.

FIGs. 19A-19B are line graphs showing that CART cells expressing FurON CAR19, comprising a limited number of mutations in the degra domain, kill CD19+ tumor cells, in a stabilizing compound- and target-dependent manner and is noninferior to the parental CAR construct.

FIG. 20 is a bar graph showing that CART cells expressing FurON CAR19, comprising a limited number of mutations in the degron domain, secrete cytokines in the presence of CD19+ tumor cells, in a manner that is stabilizing compound-dependent and is noninferior to the parental CAR construct.

FIG. 21 is a bar graph showing that CD3+ T cells comprising FurON CAR19 proliferate in the presence of CD19+ tumor cells, in a manner that is stabilizing compound-dependent and is noninferior to the parental CAR construct.

FIG. 22 is a series of graphs showing that the FurON domain regulates CAR123 expression in primary human T cells, in a stabilizing compound-dependent manner.

FIG. 23 is a series of bar graphs showing that CART cells expressing FurON CAR123 kill CD123+ tumor cells, in a stabilizing compound- and target-dependent manner and is noninferior to the parental CAR construct.

FIG. 24 is a series of bar graphs showing that CART cells expressing FurON CAR123 secrete cytokines in the presence of CD123+ tumor cells, in a manner that is stabilizing compound-dependent and is noninferior to the parental CAR construct.

FIG. 25 is a schematic showing an exemplary fusion protein comprising a degradation domain (degron), protease cleavage site, and a second protein domain (a CAR), and the change in degradation of the fusion protein in the presence of a drug, e.g., stabilization compound.

FIG. 26 is a schematic showing an exemplary fusion protein comprising four copies of an aggregation domain (FKBP12F36M), a protease cleavage site (Furin site), and a second protein domain (ScFv with cytoplasmic tail), and the change in aggregation of the fusion protein in the presence of a compound, e.g., deaggregation compound. This figure is an exemplary illustration of a regulatory on-CAR system, which is yet another embodiment to control the cell surface expression and hence function of the CAR. The CAR is expressed downstream of modified FKBP12 domains, separated by a furin site. Without a solubilizing compound present, the CAR molecules spontaneously aggregate in the endoplasmic reticulum and a reduced number of CAR molecules, e.g., no CAR molecule, can egress to the surface of the T cell. This results in a reduced CAR mediated T cell function, e.g., no CAR mediated T cell function. When the solubilizing compound is present, the CAR aggregation domains are separated and aggregation is prevented. A furin site which is located N-terminal of the scFv becomes accessible for cleavage. After removal of the aggregation domains by furin in the late Golgi apparatus, CAR molecules egress to the surface of the T cells and CAR mediated T cell function can occur.

FIG. 27 is an illustration of an anti-CD19 or anti-CD20 chimeric antigen receptor construct with a suicide switch (inducible caspase-9 or iCasp9 or iC9), collectively referred to as CD19 sCAR or CD20 sCAR, designed to cause complete but transient B cell depletion. CD19/CD20 sCAR T cells exert their

therapeutic effect by depleting B cells upon infusion. Subsequent treatment with small molecule compounds allow caspase-9 to dimerize and activate caspase activity to induce suicide of CD19/CD20 sCAR T cells, thereby allowing B cell repopulation to occur.

5 **FIG. 28** is an illustration of a reversible caspase-9 suicide cassette, which is another embodiment of a caspase-9 suicide cassette. In the CD19/CD20 revCAR system, caspase-9 is constitutively expressed and spontaneously dimerizes, thus inducing apoptosis as the default in CD19 revCAR T cells. In the presence of a small molecule compound that solubilizes the caspase-9 molecules (i.e., inhibits dimerization), caspase activity is inhibited. Thus, small molecule solubilizer treatment inhibits caspase-9 activity during expansion and infusion of revCAR T cells, and withdrawal of the small molecule solubilizer
10 results in activation of caspase-9 activity and suicide of revCAR T cells, thereby allowing B cell repopulation to occur.

FIGS. 29A-29F are a series of graphs showing efficient expression of CD19 sCAR, CD19revCAR, and CD20 CAR constructs in primary human T cells.

15 **FIG. 30** is a graph showing specific killing in vitro by CD19 sCARs. Nalm6 is a B cell line that expresses CD19 (wt, wildtype). CD19 sCAR T cells killed CD19+ Nalm6 cells, whereas nontransduced (NTD) T cells or T cells expressing a control sCAR (negative control) did not recognize Nalm6 wt cells .

FIG. 31 is a graph showing specific and robust elimination of CD19 sCAR T cells after activation of the caspase-9 suicide switch with AP20187. CAR T cells were incubated in the presence of the indicated concentrations of AP20187 for 16 hours at 37°C. Dead cells were detected with live/dead-violet dye and
20 quantified by flow cytometry. Only T cells that expressed the inducible caspase were eliminated (FMC63 iC9 or CD19 sCAR, as well as iC9 control CAR). T cells that did not express control CAR were not affected (nontransduced, NTD, or a control CAR not expressing iC9).

FIG. 32 is a graph showing that CD19 sCAR T cells expressing the inducible caspase-9 are effective in vivo. NSG mice were injected with 1×10^6 CD19+ Nalm6 cells. Five days later, mice were treated either
25 with CD19 CAR T cells that express an inducible caspase-9 or with non-transduced control T cells.

FIG. 33 is a graph showing detection of CD19 sCAR T cells expressing an inducible caspase-9 in the blood and spleen by flow cytometry at the conclusion of the in vivo experiment, indicating engraftment.

FIG. 34 is a series of graph depicting Killing assay: CD20sCAR, 20revCAR and CD20 onCAR. 4h chromium release assay to assess killing of Nalm6 cell that were previously engineered to express
30 CD20. Kwt = K562 wild-type cells that are CD20 negative and serve as irrelevant target to demonstrate specific killing. CD20sCAR, 20revCAR and CD20 onCAR show equivalent and specific killing of the CD20+ target cells. On-CAR was tested in presence of 500nM Shield-1.

FIG. 35 is a series of histograms demonstrating that the absence of solubilizing FKBP ligand (e.g. shield-1) inhibits CAR function. Shown is the percent reduction of killing in absence of shield-1 compared to killing in presence of 500nM shield-1. Jeko cells express CD20. At lower E:T ratio's the On-CAR function is strongly inhibited if no FKBP ligand is present.

- 5 **FIG. 36** is series of graphs illustrating the modulation of CAR surface expression with FKBP ligand Shield-1. CD20 on-CAR T cells were stained for CAR expression and the mean fluorescence intensity (MFI, assessed by flow cytometry) of the CAR signal was plotted against the Shield-1 concentration. Shield-1 results in a dose-dependent increase in CAR expression. Absence of Shield-1 results in ~60% reduction of CD20 on-CAR expression (bottom graph).
- 10 **FIG. 37** is a series of flow cytometry graphs depicting the titration of Shield-1 in CD19rev CAR. CD19rev CAR T cells (~38% transduced) were incubated in different doses of Shield-1 for 24h to assess dose-dependent caspase-9 activation. The remaining CAR+ cells were quantified by flow cytometry. In the CD19revCAR system, lower doses of Shield-1 result in higher caspase-9 activation and increased apoptosis (lower proportion of CAR+ cells).
- 15 **FIG. 38** is a graph depicting the *in vivo* assessment of apoptosis efficiency in anti CD19 revCAR T cells. Nalm6 cells (expressing click-beetle luciferase) that are CD19 positive were injected (i.v.) into NSG mice on day 0. On day 4, the mice were injected with CD19 targeting revCAR, 19sCAR, or irrelevant (nontransduced) T cells. Bioluminescence signals of Nalm6 cells were quantified at indicated time points. revCAR treated mice were injected twice with 10mg/kg aquashield-1 at indicated time points, these
- 20 injections were anticipated to be insufficient to keep the revCAR T cells alive. Therefore the bioluminescence curve for revCAR and NTD mice is vastly overlapping, indicating sufficient *in vivo* apoptosis of revCAR T cells.
- FIG. 39** is a series of a schematic timeline and a graph showing the *in vivo* efficacy of CD19 revCAR T cells. Nalm6 cells (expressing click-beetle luciferase) that are CD19 positive were injected (i.v.) into NSG
- 25 mice on day 0. On day 4, the osmotic infusion pumps were implanted into the mice to secrete aquashield-1 at a dose of 20mg/kg/day. CD19rev CAR T cells were injected 4 hours after successful pump implantation (Bottom graph, black arrow). Bioluminescence signals of Nalm6 cells was quantified at indicated time points. The infusion pumps secreted aquashield-1 for 7 days, after which the bioluminescence of Nalm6 cells started to rise (CD19 revCAR curves).
- 30 **FIG. 40** is a series of flow cytometry graphs depicting that the suicide activation results in peripheral depletion of the suicide CAR T cells. Mice were injected with Nalm6 cells and after 5 days were treated with 19s CAR T cells. CD19s CAR T cells were sorted before injection based on scFV expression. Flow plots show peripheral T cells (CD3+, CD45+) on day 8 and day26. CD19 sCAR T cells were depleted on day 10 by injection of AP1903 (10mg/kg). In the AP1903 treated mice, the 2 plots on the left show that T

cells are hardly detectable after suicide activation and In the vehicle treated mice, the 2 plots on the right showed stable T cell percentages.

FIG. 41 is a series of graphs demonstrating that suicide activation results in the peripheral depletion of sCAR T cells. The quantification of T cells was done from several mice. Mice were treated with AP1903 on day 10 to deplete sCAR T cells. After treatment the T cell percentages drop in the AP1903 group as opposed to the vehicle treated group.

FIG. 42 is a series of images and graphs demonstrating that suicide activation results in the depletion of sCAR T cells from lymphoid organs. Top image sections: spleens of mice were harvested >2 weeks after AP1903 treatment and stained for human CD3; in AP1903 treated mice, T cells are not detectable as opposed to vehicle treated mice. Bottom graph: quantitative PCR was performed to detect sCAR T cells in spleens of AP1903 and vehicle treated mice, demonstrating near-total sCAR absence in most mice.

FIG. 43 is a series of a schematic timeline and graphs showing that using BT (bone marrow, liver, thymus) mice as host requires 'universal' T cells lacking TCR and MHC expression. T cells were transduced on day 1 after activation with CD19 sCAR encoding lentivirus, the cells were electroporated with Cas9 guide RNA on day 3 (10ug/10⁶ cells) and again electroporated on day 4 with guide RNAs targeting the TCRbeta chain and beta-2 microglobulin. Flow plots show sCAR19 expression in 45.2% of the cells 10 days after activation and double knock-out for TCRbeta and beta-2 microglobulin in ~20% of the cells. The schematic outlines the timeline for T cell production.

FIG. 44 is a schematic timeline of the experimental design of the in vivo experiment of the present invention. Using BT (bone marrow, liver, and thymus) mice for assessment of universal sCAR function in a non-oncology mouse model. Human fetal bone marrow and thymus were implanted into NSG mice on day -91. Validation of engraftment was done by flow cytometry on day -27. Universal T cells expressing CD19 sCAR T cells were injected on day 0, B cell depletion was assessed on day 10 and mice were treated with AP1903 (3 daily injections with 10mg/kg). sCAR survival was assessed with qPCR.

FIG. 45 is a series of flow cytometry graphs depicting that 'Universal' sCAR T cells deplete peripheral B cells in non-autologous BT (bone marrow, liver, and thymus) mice. Universal CAR T cells were able to deplete human B cells in a non-cancer humanized mouse model. Flow plots on day 0 and day 10 demonstrate complete absence of CD19 positive cells in the peripheral circulation.

FIG. 46 is a graph showing that the universal sCAR T cells can be depleted with AP1903 treatment. A quantitative PCR was performed to detect sCAR T cells in peripheral blood of AP1903 and vehicle treated mice, demonstrating near-total sCAR absence in 2/3 mice. A qPCR from peripheral blood WPRE copy number was performed with a gDNA, 4 weeks after AP1903 treatment.

FIG. 47 is a graph showing that CD19+ NALM6 tumor growth was inhibited in mice infused with CART19, or infused with FurON CART19 and treated with BZA, with or without cotreatment with IL2.

DETAILED DESCRIPTION

5 In general, the invention features the regulated expression of recombinant fusion proteins. This regulation features expression of fusion proteins containing a protein of interest fused to a conditional expression domain, e.g., degradation domain (frequently termed a “degron” in the art) or an aggregation domain. Typically, such degradation domains fold into a stable confirmation only in the presence of a specific ligand (e.g., a soluble ligand or a ligand tethered to the fusion protein). In the absence of such a
10 ligand, the degradation domain assumes a disorganized structure, leading to degradation of the entire fusion protein by native intracellular mechanisms. Typically, such aggregation domains associate into oligomers and/or aggregates in the absence of a specific ligand (e.g., a soluble ligand or a ligand tethered to the fusion protein), leading to the aggregation and/or sequestration of the entire fusion protein. The invention is based on the insight that the degradation domain or aggregation domain can be separated
15 from the protein of interest by a cleavage site (e.g., a protease cleavage site) when expressed under stabilizing conditions (e.g., in the presence of a stabilization compound) or deaggregating conditions (e.g., in the presence of a deaggregation compound). Thus, in the absence of a cognate protease, the fusion protein comprising a degradation domain will escape degradation only in the presence of the stabilizing compound and the fusion protein comprising an aggregation domain will escape aggregation only in the
20 presence of the deaggregation compound. However, once the cleavage site is cleaved by a cognate protease, the presence of a stabilizing compound or deaggregating compound is no longer necessary to allow the protein of interest to escape degradation or aggregation because it is no longer associated with the degradation domain or aggregation domain. Thus, at the time of initial expression, the fusion protein comprising a degradation domain is susceptible to degradation and the fusion protein comprising an
25 aggregation domain is susceptible to aggregation, however, once the cleavage has occurred, the resulting protein of interest can be otherwise indistinguishable from its non-fusion protein counterpart.

The fusion proteins of the invention thus have three essential elements: a conditional expression domain (e.g., degradation domain or aggregation domain), a domain containing the protein of interest, and a cleavage domain separating the two. Within each of these elements, the specific domains are
30 interchangeable and discussed below. Notably, the fusion protein can be arranged such that conditional expression domain is located either N-terminal or C-terminal to the protein of interest. However, in certain embodiments, the conditional expression domain is N-terminal to the protein of interest. In such embodiments, where the conditional expression domain is a degradation domain, the degradation domain, where disorganized, targets the entire fusion protein for degradation prior to the cleavage of the
35 cleavage domain. In case of a C-terminal fusion, the protease cleavage site has to be oriented towards

the compartment where the protease resides. In the particular case of furin, the C-terminal degron needs to face the lumen of the endoplasmic reticulum and Golgi.

DEFINITIONS

As used herein, the term “conditional expression domain” refers to a domain of a fusion protein that has a first state and a second state, e.g., states of aggregation or conformational states, e.g., states of stabilization/destabilization, or states of folding/misfolding. The first state is associated with, causes, or mediates cell surface expression or extracellular expression of one or more (e.g., all) portions of the fusion protein at a first rate or level and the second state is associated with, causes, or mediates cell surface expression or extracellular expression of one or more (e.g., all) portions of the fusion protein at a second rate or level. Absent an expression compound, when expressed in a cell of interest, a large fraction of the fusion protein comprising a conditional expression domain is not detectable either on the cell surface or extracellularly. Conversely, in the presence of an expression compound, surface expression and/or extracellular expression of one or more (e.g., all) domains of the fusion protein is substantially increased. Thus, a conditional expression domain is identifiable by the following characteristics: (1) it is not naturally occurring in the context of the fusion protein; (2) surface expression and/or extracellular expression is regulated co-translationally or post-translationally; (3) the rate of surface expression and/or extracellular expression is substantially increased in the presence of an expression compound. In embodiments, a conditional expression domain is a degradation domain, for example, as described herein. In other embodiments, a conditional expression domain is an aggregation domain, for example as described herein. In embodiments, the fusion protein comprising the conditional expression domain comprises a chimeric antigen receptor (CAR), for example, as described herein. In embodiments, the fusion protein comprises a heterologous protease cleavage site disposed between the conditional expression domain and a second domain. In such embodiments, in the absence of an expression compound, the protease cleavage site of a large fraction of the fusion proteins is not accessible by the cognate protease, and the cellular fate of the fusion protein is directed by the conditional expression domain. In the presence of an expression compound, the protease cleavage site of a large fraction of the fusion proteins become accessible to the cognate protease, the conditional expression domain is cleaved from the fusion protein, and the cellular fate of the remainder of the fusion protein proceeds as is uninterrupted by the conditional expression domain.

As used herein, the term “aggregation domain” refers to a domain of a fusion protein that causes intracellular aggregation of the fusion protein. Absent a deaggregation compound, when expressed in a cell of interest, a large fraction of the fusion protein comprising an aggregation domain is present in aggregates which, for example, are sequestered within the cell before reaching mature expression, for example, before being expressed on the surface of the cell or before being secreted extracellularly. Conversely, in the presence of a deaggregation compound, surface expression and/or extracellular expression of one or more (e.g., all) domains of the fusion protein is substantially increased. Thus, an

aggregation domain is identifiable by the following characteristics: (1) it is not naturally occurring in the context of the fusion protein; (2) surface expression and/or extracellular expression is regulated co-translationally or post-translationally; (3) the rate of surface expression and/or extracellular expression is substantially increased in the presence of a deaggregation compound. In embodiments, the aggregation domain comprises one or more, e.g., 1, 2, 3, 4, 5, 6, 7, or more repeats of a dimerization domain. In embodiments, the dimerization domain is a homodimerization domain. In other embodiments, the dimerization domain is a heterodimerization domain.

As used herein, the term “expression compound” refers to a compound that, when added to a cell expressing a fusion protein comprising a conditional expression domain, binds to a conditional expression domain and results in increased surface expression and/or extracellular expression of one or more (e.g., all) domains of the fusion protein. Expression compounds can be naturally occurring or synthetic.

As used herein, the term “deaggregation compound” refers to a compound that, when added to a cell expressing a fusion protein comprising an aggregation domain, binds to an aggregation domain and results in increased surface expression and/or extracellular expression of one or more (e.g., all) domains of the fusion protein. Deaggregation compounds can be naturally occurring or synthetic.

By the term “degradation domain” is meant a domain of a fusion protein that assumes a stable conformation when expressed in the presence of a stabilizing compound. Absent the stable conformation when expressed in a cell of interest, a large fraction of degradation domains (and, typically, any protein to which they are fused) will be degraded by endogenous cellular machinery. Notably, a degradation domain is not a naturally occurring domain of a protein but is rather engineered to be unstable absent contact with the stabilizing compound. Thus, a degradation domain is identifiable by the following characteristics: (1) it is not naturally occurring; (2) its expression is regulated co-translationally or post-translationally through increased or decreased degradation rates; (3) the rate of degradation is substantially decreased in the presence of a stabilizing compound. In some embodiments, the degradation domain does not lead to aggregation of the fusion proteins. In some embodiments, absent a stabilizing compound, the degradation domain or other domain of the fusion protein is not substantially detectable in or on the cell.

As used herein, the terms “deaggregation” and “disaggregation” are used interchangeably.

As used herein, a “fusion protein” or “chimeric protein” refers to a protein created through the joining of two or more heterologous protein domains into a single, continuous protein.

By the term “heterologous” is meant a domain (e.g., a protein domain) that has a different origin (i.e., does not naturally occur fused to at least one of the other referenced domains) than one or more protein domains to which it is fused. Furthermore, by “heterologous protease cleavage site” is meant a protease cleavage site that is not cleaved by any domain of the fusion protein in which it is present.

By “protease” is meant a protein that cleaves another protein based on the presence of a cleavage site in the to-be-cleaved protein.

By “intracellular protease” is meant a protease that is natively expressed inside a cell of interest.

By “extracellular protease” is meant a protease that is natively expressed in an organism (e.g., a mammal) and secreted or exposed to the outside of cells (e.g., in the blood or the surface of the skin).

By “stabilization compound” or “stabilizing compound” is meant a compound that, when added to a cell expressing a degradation domain, stabilizes the degradation domain and decreases the rate at which it is subsequently degraded. Stabilization compounds or stabilizing compounds can be naturally occurring or synthetic.

The term “a” and “an” refers to one or to more than one (i.e., to at least one) of the grammatical object of the article. By way of example, “an element” means one element or more than one element.

The term “about” when referring to a measurable value such as an amount, a temporal duration, and the like, is meant to encompass variations of $\pm 20\%$ or in some instances $\pm 10\%$, or in some instances $\pm 5\%$, or in some instances $\pm 1\%$, or in some instances $\pm 0.1\%$ from the specified value, as such variations are appropriate to perform the disclosed methods.

The term “Chimeric Antigen Receptor” or alternatively a “CAR” refers to a recombinant polypeptide construct comprising at least an extracellular antigen binding domain, a transmembrane domain and a cytoplasmic signaling domain (also referred to herein as “an intracellular signaling domain”) comprising a functional signaling domain derived from a stimulatory molecule as defined below. In some embodiments, the domains in the CAR polypeptide construct are in the same polypeptide chain, e.g., comprise a chimeric fusion protein. In some embodiments, the domains in the CAR polypeptide construct are not contiguous with each other, e.g., are in different polypeptide chains, e.g., in regulatable chimeric antigen receptor (RCAR).

In one aspect, the stimulatory molecule is the zeta chain associated with the T cell receptor complex. In one aspect, the cytoplasmic signaling domain comprises a primary signaling domain (e.g., a primary signaling domain of CD3-zeta). In one aspect, the cytoplasmic signaling domain further comprises one or more functional signaling domains derived from at least one costimulatory molecule as defined below. In one aspect, the costimulatory molecule is chosen from 4-1BB (i.e., CD137), CD27, ICOS, and/or CD28. In one aspect, the CAR comprises a chimeric fusion protein comprising an extracellular antigen binding domain, a transmembrane domain and an intracellular signaling domain comprising a functional signaling domain derived from a stimulatory molecule. In one aspect, the CAR comprises a chimeric fusion protein comprising an extracellular antigen binding domain, a transmembrane domain and an intracellular signaling domain comprising a functional signaling domain derived from a co-stimulatory molecule and a

functional signaling domain derived from a stimulatory molecule. In one aspect, the CAR comprises a chimeric fusion protein comprising an extracellular antigen binding domain, a transmembrane domain and an intracellular signaling domain comprising two functional signaling domains derived from one or more co-stimulatory molecule(s) and a functional signaling domain derived from a stimulatory molecule. In one aspect, the CAR comprises a chimeric fusion protein comprising an extracellular antigen binding domain, a transmembrane domain and an intracellular signaling domain comprising at least two functional signaling domains derived from one or more co-stimulatory molecule(s) and a functional signaling domain derived from a stimulatory molecule. In one aspect the CAR comprises an optional leader sequence at the amino-terminus (N-ter) of the CAR fusion protein. In one aspect, the CAR further comprises a leader sequence at the N-terminus of the extracellular antigen binding domain, wherein the leader sequence is optionally cleaved from the antigen recognition domain (e.g., a scFv) during cellular processing and localization of the CAR to the cellular membrane.

A CAR that comprises an antigen binding domain (e.g., a scFv, or TCR) that targets, e.g., binds to, a specific antigen X, such as those described herein, is also referred to as XCAR, X-CAR or X-targeting CAR. For example, a CAR that comprises an antigen binding domain that targets CD19 is referred to as CD19CAR.

The term "signaling domain" refers to the functional portion of a protein which acts by transmitting information within the cell to regulate cellular activity via defined signaling pathways by generating second messengers or functioning as effectors by responding to such messengers. In some aspects, the signaling domain of the CAR described herein is derived from a stimulatory molecule or co-stimulatory molecule described herein, or is a synthesized or engineered signaling domain.

The term "antibody," as used herein, refers to a protein, or polypeptide sequence derived from an immunoglobulin molecule which specifically binds with an antigen. Antibodies can be polyclonal or monoclonal, multiple or single chain, or intact immunoglobulins, and may be derived from natural sources or from recombinant sources. Antibodies can be tetramers of immunoglobulin molecules.

The term "antibody fragment" refers to at least one portion of an intact antibody, or recombinant variants thereof, and refers to the antigen binding domain, e.g., an antigenic determining variable region of an intact antibody, that is sufficient to confer recognition and specific binding of the antibody fragment to a target, such as an antigen. Examples of antibody fragments include, but are not limited to, Fab, Fab', F(ab')₂, and Fv fragments, scFv antibody fragments, linear antibodies, single domain antibodies such as sdAb (either VL or VH), camelid VHH domains, and multi-specific antibodies formed from antibody fragments such as a bivalent fragment comprising two Fab fragments linked by a disulfide bridge at the hinge region, and an isolated CDR or other epitope binding fragments of an antibody. An antigen binding fragment can also be incorporated into single domain antibodies, maxibodies, minibodies, nanobodies, intrabodies, diabodies, triabodies, tetrabodies, v-NAR and bis-scFv (see, e.g., Hollinger and Hudson,

Nature Biotechnology 23:1126-1136, 2005). Antigen binding fragments can also be grafted into scaffolds based on polypeptides such as a fibronectin type III (Fn3)(see U.S. Patent No.: 6,703,199, which describes fibronectin polypeptide minibodies).

The term “scFv” refers to a fusion protein comprising at least one antibody fragment comprising a variable region of a light chain and at least one antibody fragment comprising a variable region of a heavy chain, wherein the light and heavy chain variable regions are contiguously linked via a short flexible polypeptide linker, and capable of being expressed as a single chain polypeptide, and wherein the scFv retains the specificity of the intact antibody from which it is derived. Unless specified, as used herein an scFv may have the VL and VH variable regions in either order, e.g., with respect to the N-terminal and C-terminal ends of the polypeptide, the scFv may comprise VL-linker-VH or may comprise VH-linker-VL.

The term “complementarity determining region” or “CDR,” as used herein, refers to the sequences of amino acids within antibody variable regions which confer antigen specificity and binding affinity. For example, in general, there are three CDRs in each heavy chain variable region (e.g., HCDR1, HCDR2, and HCDR3) and three CDRs in each light chain variable region (LCDR1, LCDR2, and LCDR3). The precise amino acid sequence boundaries of a given CDR can be determined using any of a number of well-known schemes, including those described by Kabat et al. (1991), “Sequences of Proteins of Immunological Interest,” 5th Ed. Public Health Service, National Institutes of Health, Bethesda, MD (“Kabat” numbering scheme), Al-Lazikani et al., (1997) JMB 273,927-948 (“Chothia” numbering scheme), or a combination thereof. Under the Kabat numbering scheme, in some embodiments, the CDR amino acid residues in the heavy chain variable domain (VH) are numbered 31-35 (HCDR1), 50-65 (HCDR2), and 95-102 (HCDR3); and the CDR amino acid residues in the light chain variable domain (VL) are numbered 24-34 (LCDR1), 50-56 (LCDR2), and 89-97 (LCDR3). Under the Chothia numbering scheme, in some embodiments, the CDR amino acids in the VH are numbered 26-32 (HCDR1), 52-56 (HCDR2), and 95-102 (HCDR3); and the CDR amino acid residues in the VL are numbered 26-32 (LCDR1), 50-52 (LCDR2), and 91-96 (LCDR3). In a combined Kabat and Chothia numbering scheme, in some embodiments, the CDRs correspond to the amino acid residues that are part of a Kabat CDR, a Chothia CDR, or both. For instance, in some embodiments, the CDRs correspond to amino acid residues 26-35 (HCDR1), 50-65 (HCDR2), and 95-102 (HCDR3) in a VH, e.g., a mammalian VH, e.g., a human VH; and amino acid residues 24-34 (LCDR1), 50-56 (LCDR2), and 89-97 (LCDR3) in a VL, e.g., a mammalian VL, e.g., a human VL.

The portion of the CAR of the invention comprising an antibody or antibody fragment thereof may exist in a variety of forms where the antigen binding domain is expressed as part of a contiguous polypeptide chain including, for example, scFv antibody fragments, linear antibodies, single domain antibodies such as sdAb (either VL or VH), camelid VHH domains, a humanized antibody, a bispecific antibody, an antibody conjugate (Harlow et al., 1999, In: Using Antibodies: A Laboratory Manual, Cold Spring Harbor Laboratory Press, NY; Harlow et al., 1989, In: Antibodies: A Laboratory Manual, Cold Spring Harbor,

New York; Houston et al., 1988, Proc. Natl. Acad. Sci. USA 85:5879-5883; Bird et al., 1988, Science 242:423-426). In one aspect, the antigen binding domain of a CAR of the invention comprises an antibody fragment. In a further aspect, the CAR comprises an antibody fragment that comprises a scFv.

As used herein, the term "binding domain" or "antibody molecule" (also referred to herein as "anti-target
5 (e.g., CD19) binding domain") refers to a protein, e.g., an immunoglobulin chain or fragment thereof, comprising at least one immunoglobulin variable domain sequence. The term "binding domain" or "antibody molecule" encompasses antibodies and antibody fragments. In an embodiment, an antibody molecule is a multispecific antibody molecule, e.g., it comprises a plurality of immunoglobulin variable domain sequences, wherein a first immunoglobulin variable domain sequence of the plurality has binding
10 specificity for a first epitope and a second immunoglobulin variable domain sequence of the plurality has binding specificity for a second epitope. In an embodiment, a multispecific antibody molecule is a bispecific antibody molecule. A bispecific antibody has specificity for no more than two antigens. A bispecific antibody molecule is characterized by a first immunoglobulin variable domain sequence which has binding specificity for a first epitope and a second immunoglobulin variable domain sequence that
15 has binding specificity for a second epitope.

The term "antibody heavy chain," refers to the larger of the two types of polypeptide chains present in antibody molecules in their naturally occurring conformations, and which normally determines the class to which the antibody belongs.

The term "antibody light chain," refers to the smaller of the two types of polypeptide chains present in
20 antibody molecules in their naturally occurring conformations. Kappa (κ) and lambda (λ) light chains refer to the two major antibody light chain isotypes.

The term "recombinant antibody" refers to an antibody which is generated using recombinant DNA technology, such as, for example, an antibody expressed by a bacteriophage or yeast expression system. The term should also be construed to mean an antibody which has been generated by the synthesis of a
25 DNA molecule encoding the antibody and which DNA molecule expresses an antibody protein, or an amino acid sequence specifying the antibody, wherein the DNA or amino acid sequence has been obtained using recombinant DNA or amino acid sequence technology which is available and well known in the art.

The term "immunoglobulin" or "Ig," as used herein is defined as a class of proteins, which function as
30 antibodies. Antibodies expressed by B cells are sometimes referred to as the BCR (B cell receptor) or antigen receptor. The five members included in this class of proteins are IgA, IgG, IgM, IgD, and IgE. IgA is the primary antibody that is present in body secretions, such as saliva, tears, breast milk, gastrointestinal secretions and mucus secretions of the respiratory and genitourinary tracts. IgG is the most common circulating antibody. IgM is the main immunoglobulin produced in the primary immune
35 response in most subjects. It is the most efficient immunoglobulin in agglutination, complement fixation,

and other antibody responses, and is important in defense against bacteria and viruses. IgD is the immunoglobulin that has no known antibody function, but may serve as an antigen receptor. IgE is the immunoglobulin that mediates immediate hypersensitivity by causing release of mediators from mast cells and basophils upon exposure to allergen.

- 5 The term “antigen” or “Ag” refers to a molecule that provokes an immune response. This immune response may involve either antibody production, or the activation of specific immunologically-competent cells, or both. The skilled artisan will understand that any macromolecule, including virtually all proteins or peptides, can serve as an antigen. Furthermore, antigens can be derived from recombinant or genomic DNA. A skilled artisan will understand that any DNA, which comprises a nucleotide sequences or a partial
10 nucleotide sequence encoding a protein that elicits an immune response therefore encodes an “antigen” as that term is used herein. Furthermore, one skilled in the art will understand that an antigen need not be encoded solely by a full length nucleotide sequence of a gene. It is readily apparent that the present disclosure includes, but is not limited to, the use of partial nucleotide sequences of more than one gene and that these nucleotide sequences are arranged in various combinations to encode polypeptides that
15 elicit the desired immune response. Moreover, a skilled artisan will understand that an antigen need not be encoded by a “gene” at all. It is readily apparent that an antigen can be generated or can be derived from a biological sample, or might be macromolecule besides a polypeptide. Such a biological sample can include, but is not limited to a tissue sample, a tumor sample, a cell or a fluid with other biological components.
- 20 The term “autoantigen” means, in accordance with the present invention, any self-antigen which is recognized by the immune system as being foreign. Autoantigens comprise, but are not limited to, cellular proteins, phosphoproteins, cellular surface proteins, cellular lipids, nucleic acids, glycoproteins, including cell surface receptors.

“Autoantibody” refers to an antibody that is produced by a B cell specific for an autoantigen.

- 25 The term “autoantibody disease” as used herein is defined as a disorder that results from an autoantibody immune response. An autoantibody disease is the result of an inappropriate and excessive response production of autoantibodies. Examples of autoantibody diseases include but are not limited to, bullous pemphigoid, epidermolysis bullosa acquisita, p200 pemphigoid, linear IgA bullous dermatosis, other pemphigoid group diseases, dermatitis herpetiformis, celiac disease, myasthenia gravis, Goodpasture’s
30 syndrome, granulomatosis with polyangiitis and other ANCA+ vasculitides, autoimmune limbic encephalitis, anti-N-methyl-D-aspartate receptor encephalitis, neuromyelitis optica, autoimmune hemolytic anemia, autoantibody-associated end-organ damage in lupus and other connective tissue diseases (due to anti-dsDNA, anti-Ro, and other autoantibodies), Graves’ and Hashimoto’s thyroiditis, anti-insulin antibodies in diabetes, anti-insulin receptor antibodies in autoimmune hypoglycemia, cryoglobulinemia,
35 rheumatoid arthritis, multiple sclerosis, Sjogren’s syndrome, dermatomyositis, anti-Fc-epsilon receptor

antibodies in chronic idiopathic urticaria, anti-folate receptor antibodies, anti-endothelial receptor or anti-adrenergic receptor antibodies in pulmonary arterial hypertension, refractory hypertension, dilated cardiomyopathy, and autoinflammatory syndromes such as IgG4-related disease, among others.

5 The term “autoimmune disease” as used herein is defined as a disorder or condition that results from an antibody mediated autoimmune response against autoantigens. An autoimmune disease results in the production of autoantibodies that are inappropriately produced and/or excessively produced to a self-antigen or autoantigen.

The term “autologous” refers to any material derived from the same individual to whom it is later to be re-introduced into the individual.

10 The term “anti-tumor effect” or “anti-tumor activity” refers to a biological effect which can be manifested by various means, including but not limited to, e.g., a decrease in tumor volume, a decrease in the number of tumor cells, a decrease in the number of metastases, an increase in life expectancy, decrease in tumor cell proliferation, decrease in tumor cell survival, or amelioration of various physiological symptoms associated with the cancerous condition. An “anti-tumor effect” can also be manifested by the ability of
15 the peptides, polynucleotides, cells and antibodies of the invention in prevention of the occurrence of tumor in the first place.

The term “allogeneic” refers to any material derived from a different animal of the same species as the individual to whom the material is introduced. Two or more individuals are said to be allogeneic to one another when the genes at one or more loci are not identical. In some aspects, allogeneic material from
20 individuals of the same species may be sufficiently unlike genetically to interact antigenically

The term “xenogeneic” refers to a graft derived from an animal of a different species.

The term “apheresis” as used herein refers to an extracorporeal process by which the blood of a donor or patient is removed from the donor or patient and passed through an apparatus that separates out selected particular constituent(s) and returns the remainder to the circulation of the donor or patient, *e.g.*,
25 by retransfusion. Thus, in the context of “an apheresis sample” refers to a sample obtained using apheresis.

The term “cleavage” refers to the breakage of covalent bonds, such as in the backbone of a nucleic acid molecule or the hydrolysis of peptide bonds. Cleavage can be initiated by a variety of methods, including, but not limited to, enzymatic or chemical hydrolysis of a phosphodiester bond. Both single-stranded
30 cleavage and double-stranded cleavage are possible. Double-stranded cleavage can occur as a result of two distinct single-stranded cleavage events. DNA cleavage can result in the production of either blunt ends or staggered ends. In certain embodiments, fusion polypeptides may be used for targeting cleaved double-stranded DNA.

The term “cancer” or “tumor” refers to a disease characterized by the uncontrolled growth of aberrant cells. Cancer includes all types of cancerous growths or oncogenic processes, metastatic tissues or malignantly transformed cells, tissues or organs irrespective of the histopathologic type or stage of invasiveness. Cancer cells can spread locally or through the bloodstream and lymphatic system to other parts of the body. Examples of various cancers are described herein and include but are not limited to, breast cancer, prostate cancer, ovarian cancer, cervical cancer, skin cancer, pancreatic cancer, colorectal cancer, renal cancer, liver cancer, brain cancer, lymphoma, leukemia, lung cancer and the like.

The term “CRISPR/CAS,” “clustered regularly interspaced short palindromic repeats system,” or “CRISPR” refers to DNA loci containing short repetitions of base sequences. Each repetition is followed by short segments of spacer DNA from previous exposures to a virus. Bacteria and archaea have evolved adaptive immune defenses termed CRISPR-CRISPR-associated (Cas) systems that use short RNA to direct degradation of foreign nucleic acids. In bacteria, the CRISPR system provides acquired immunity against invading foreign DNA via RNA-guided DNA cleavage.

In the type II CRISPR/Cas system, short segments of foreign DNA, termed “spacers” are integrated within the CRISPR genomic loci and transcribed and processed into short CRISPR RNA (crRNA). These crRNAs anneal to trans-activating crRNAs (tracrRNAs) and direct sequence-specific cleavage and silencing of pathogenic DNA by Cas proteins. Recent work has shown that target recognition by the Cas9 protein requires a “seed” sequence within the crRNA and a conserved dinucleotide-containing protospacer adjacent motif (PAM) sequence upstream of the crRNA-binding region.

To direct Cas9 to cleave sequences of interest, crRNA-tracrRNA fusion transcripts, hereafter referred to as “guide RNAs” or “gRNAs” may be designed, from human U6 polymerase III promoter. CRISPR/CAS mediated genome editing and regulation, highlighted its transformative potential for basic science, cellular engineering and therapeutics.

The term “CRISPRi” refers to a CRISPR system for sequence specific gene repression or inhibition of gene expression, such as at the transcriptional level.

“Derived from” as that term is used herein, indicates a relationship between a first and a second molecule. It generally refers to structural similarity between the first molecule and a second molecule and does not connote or include a process or source limitation on a first molecule that is derived from a second molecule. For example, in the case of an intracellular signaling domain that is derived from a CD3zeta molecule, the intracellular signaling domain retains sufficient CD3zeta structure such that it has the required function, namely, the ability to generate a signal under the appropriate conditions. It does not connote or include a limitation to a particular process of producing the intracellular signaling domain, e.g., it does not mean that, to provide the intracellular signaling domain, one must start with a CD3zeta sequence and delete unwanted sequence, or impose mutations, to arrive at the intracellular signaling domain.

The phrase “disease associated with expression of a tumor antigen” includes, but is not limited to, a disease associated with expression of a tumor antigen as described herein or condition associated with cells which express a tumor antigen as described herein including, e.g., proliferative diseases such as a cancer or malignancy or a precancerous condition such as a myelodysplasia, a myelodysplastic syndrome or a preleukemia; or a noncancer related indication associated with cells which express a tumor antigen as described herein. In one aspect, a cancer associated with expression of a tumor antigen as described herein is a hematological cancer. In one aspect, a cancer associated with expression of a tumor antigen as described herein is a solid cancer. Further diseases associated with expression of a tumor antigen described herein include, but not limited to, e.g., atypical and/or non-classical cancers, malignancies, precancerous conditions or proliferative diseases associated with expression of a tumor antigen as described herein. Non-cancer related indications associated with expression of a tumor antigen as described herein include, but are not limited to, e.g., autoimmune disease, (e.g., lupus), inflammatory disorders (allergy and asthma) and transplantation.

The term “conservative sequence modifications” refers to amino acid modifications that do not significantly affect or alter the binding characteristics of the antibody or antibody fragment containing the amino acid sequence. Such conservative modifications include amino acid substitutions, additions and deletions. Modifications can be introduced into an antibody or antibody fragment of the invention by standard techniques known in the art, such as site-directed mutagenesis and PCR-mediated mutagenesis. Conservative amino acid substitutions are ones in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (e.g., lysine, arginine, histidine), acidic side chains (e.g., aspartic acid, glutamic acid), uncharged polar side chains (e.g., glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine, tryptophan), nonpolar side chains (e.g., alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine), beta-branched side chains (e.g., threonine, valine, isoleucine) and aromatic side chains (e.g., tyrosine, phenylalanine, tryptophan, histidine). Thus, one or more amino acid residues within a CAR of the invention can be replaced with other amino acid residues from the same side chain family and the altered CAR can be tested using the functional assays described herein.

The term “stimulation,” refers to a primary response induced by binding of a stimulatory molecule (e.g., a TCR/CD3 complex or CAR) with its cognate ligand (or tumor antigen in the case of a CAR) thereby mediating a signal transduction event, such as, but not limited to, signal transduction via the TCR/CD3 complex or signal transduction via the appropriate NK receptor or signaling domains of the CAR. Stimulation can mediate altered expression of certain molecules, such as downregulation of TGF- β , and/or reorganization of cytoskeletal structures, and the like.

The term “stimulatory molecule,” refers to a molecule expressed by an immune effector cell (e.g., a T cell, NK cell, B cell) that provides the cytoplasmic signaling sequence(s) that regulate activation of the immune

effector cell in a stimulatory way for at least some aspect of the immune effector cell signaling pathway, e.g., the T cell signaling pathway. In one aspect, the signal is a primary signal that is initiated by, for instance, binding of a TCR/CD3 complex with an MHC molecule loaded with peptide, and which leads to mediation of a T cell response, including, but not limited to, proliferation, activation, differentiation, and the like. A primary cytoplasmic signaling sequence (also referred to as a "primary signaling domain") that acts in a stimulatory manner may contain a signaling motif which is known as immunoreceptor tyrosine-based activation motif or ITAM. Examples of an ITAM containing primary cytoplasmic signaling sequence that is of particular use in the invention includes, but is not limited to, those derived from CD3 zeta, common FcR gamma (FCER1G), Fc gamma RIIa, FcR beta (Fc epsilon R1b), CD3 gamma, CD3 delta, CD3 epsilon, CD5, CD22, CD79a, CD79b, CD278 (also known as "ICOS"), FcεRI, DAP10, DAP12, and CD66d. In a specific CAR of the invention, the intracellular signaling domain in any one or more CARs of the invention comprises an intracellular signaling sequence, e.g., a primary signaling sequence of CD3-zeta. In a specific CAR of the invention, the primary signaling sequence of CD3-zeta is the sequence provided as SEQ ID NO:18, or the equivalent residues from a non-human species, e.g., mouse, rodent, monkey, ape and the like. In a specific CAR of the invention, the primary signaling sequence of CD3-zeta is the sequence as provided in SEQ ID NO:20, or the equivalent residues from a non-human species, e.g., mouse, rodent, monkey, ape and the like.

The term "antigen presenting cell" or "APC" refers to an immune system cell such as an accessory cell (e.g., a B-cell, a dendritic cell, and the like) that displays a foreign antigen complexed with major histocompatibility complexes (MHC's) on its surface. T-cells may recognize these complexes using their T-cell receptors (TCRs). APCs process antigens and present them to T-cells.

An "intracellular signaling domain," as the term is used herein, refers to an intracellular portion of a molecule. The intracellular signaling domain generates a signal that promotes an immune effector function of the CAR-expressing cell, e.g., a CART cell or CAR-expressing NK cell. Examples of immune effector function, e.g., in a CART cell or CAR-expressing NK cell, include cytolytic activity and helper activity, including the secretion of cytokines. While the entire intracellular signaling domain can be employed, in many cases it is not necessary to use the entire chain. To the extent that a truncated portion of the intracellular signaling domain is used, such truncated portion may be used in place of the intact chain as long as it transduces the effector function signal. The term intracellular signaling domain is thus meant to include any truncated portion of the intracellular signaling domain sufficient to transduce the effector function signal.

In an embodiment, the intracellular signaling domain can comprise a primary intracellular signaling domain. Exemplary primary intracellular signaling domains include those derived from the molecules responsible for primary stimulation, or antigen dependent stimulation. In an embodiment, the intracellular signaling domain can comprise a costimulatory intracellular domain. Exemplary costimulatory intracellular signaling domains include those derived from molecules responsible for costimulatory signals, or antigen

independent stimulation. In an embodiment, the intracellular signaling domain is synthesized or engineered. For example, in the case of a CAR-expressing immune effector cell, e.g., CART cell or CAR-expressing NK cell, a primary intracellular signaling domain can comprise a cytoplasmic sequence of a T cell receptor, a primary intracellular signaling domain can comprise a cytoplasmic sequence of a T cell receptor, and a costimulatory intracellular signaling domain can comprise cytoplasmic sequence from co-receptor or costimulatory molecule.

A primary intracellular signaling domain can comprise a signaling motif which is known as an immunoreceptor tyrosine-based activation motif or ITAM. Examples of ITAM containing primary cytoplasmic signaling sequences include, but are not limited to, those derived from CD3 zeta, common FcR gamma (FCER1G), Fc gamma RIIa, FcR beta, CD3 gamma, CD3 delta, CD3 epsilon, CD5, CD22, CD79a, CD79b, CD278 ("ICOS"), FcεRI CD66d, DAP10 and DAP12.

The term "zeta" or alternatively "zeta chain", "CD3-zeta" or "TCR-zeta" is defined as the protein provided as GenBank Acc. No. BAG36664.1, or the equivalent residues from a non-human species, e.g., mouse, rodent, monkey, ape and the like, and a "zeta stimulatory domain" or alternatively a "CD3-zeta stimulatory domain" or a "TCR-zeta stimulatory domain" is defined as the amino acid residues from the cytoplasmic domain of the zeta chain that are sufficient to functionally transmit an initial signal necessary for T cell activation. In one aspect the cytoplasmic domain of zeta comprises residues 52 through 164 of GenBank Acc. No. BAG36664.1 or the equivalent residues from a non-human species, e.g., mouse, rodent, monkey, ape and the like, that are functional orthologs thereof. In one aspect, the "zeta stimulatory domain" or a "CD3-zeta stimulatory domain" is the sequence provided as SEQ ID NO:18. In one aspect, the "zeta stimulatory domain" or a "CD3-zeta stimulatory domain" is the sequence provided as SEQ ID NO:20. Also encompassed herein are CD3 zeta domains comprising one or more mutations to the amino acid sequences described herein, e.g., SEQ ID NO: 20.

The term "costimulatory molecule" refers to the cognate binding partner on a T cell that specifically binds with a costimulatory ligand, thereby mediating a costimulatory response by the T cell, such as, but not limited to, proliferation. Costimulatory molecules are cell surface molecules other than antigen receptors or their ligands that are required for an efficient immune response. Costimulatory molecules include, but are not limited to an MHC class I molecule, a TNF receptor protein, an Immunoglobulin-like protein, a cytokine receptor, an integrin, a signaling lymphocytic activation molecule (SLAM protein), an activating NK cell receptor, BTLA, a Toll ligand receptor, OX40, CD2, CD7, CD27, CD28, CD30, CD40, CDS, ICAM-1, LFA-1 (CD11a/CD18), 4-1BB (CD137), B7-H3, CDS, ICAM-1, ICOS (CD278), GITR, BAFTR, LIGHT, HVEM (LIGHTR), KIRDS2, SLAMF7, NKp80 (KLRP1), NKp44, NKp30, NKp46, CD19, CD4, CD8alpha, CD8beta, IL2R beta, IL2R gamma, IL7R alpha, ITGA4, VLA1, CD49a, ITGA4, IA4, CD49D, ITGA6, VLA-6, CD49f, ITGAD, CD11d, ITGAE, CD103, ITGAL, CD11a, LFA-1, ITGAM, CD11b, ITGAX, CD11c, ITGB1, CD29, ITGB2, CD18, LFA-1, ITGB7, NKG2D, NKG2C, TNFR2, TRANCE/RANKL, DNAM1 (CD226), SLAMF4 (CD244, 2B4), CD84, CD96 (Tactile), CEACAM1, CRTAM, Ly9 (CD229), CD160

(BY55), PSGL1, CD100 (SEMA4D), CD69, SLAMF6 (NTB-A, Ly108), SLAM (SLAMF1, CD150, IPO-3), BLAME (SLAMF8), SELPLG (CD162), LTBR, LAT, GADS, SLP-76, PAG/Cbp, CD19a, and a ligand that specifically binds with CD83.

5 A costimulatory intracellular signaling domain or costimulatory signaling domain can be the intracellular portion of a costimulatory molecule. The intracellular signaling domain can comprise the entire intracellular portion, or the entire native intracellular signaling domain, of the molecule from which it is derived, or a functional fragment thereof.

10 The term "4-1BB" refers to a member of the TNFR superfamily with an amino acid sequence provided as GenBank Acc. No. AAA62478.2, or the equivalent residues from a non-human species, e.g., mouse, rodent, monkey, ape and the like; and a "4-1BB costimulatory domain" is defined as amino acid residues 214-255 of GenBank Acc. No. AAA62478.2, or the equivalent residues from a non-human species, e.g., mouse, rodent, monkey, ape and the like. In one aspect, the "4-1BB costimulatory domain" is the sequence provided as SEQ ID NO:14 or the equivalent residues from a non-human species, e.g., mouse, rodent, monkey, ape and the like.

15 The term "immune response" as used herein is defined as a cellular response to an antigen that occurs when lymphocytes identify antigenic molecules as foreign and induce the formation of antibodies and/or activate lymphocytes to remove the antigen.

20 When "an immunologically effective amount," "an autoimmune disease-inhibiting effective amount," or "therapeutic amount" is indicated, the precise amount of the compositions of the present invention to be administered can be determined by a physician or researcher with consideration of individual differences in age, weight, tumor size, extent of infection or metastasis, and condition of the patient (subject).

25 "Immune effector cell," as that term is used herein, refers to a cell that is involved in an immune response, e.g., in the promotion of an immune effector response. Examples of immune effector cells include T cells, e.g., alpha/beta T cells and gamma/delta T cells, B cells, natural killer (NK) cells, natural killer T (NKT) cells, mast cells, and myeloid-derived phagocytes.

30 "Immune effector function or immune effector response," as that term is used herein, refers to function or response, e.g., of an immune effector cell, that enhances or promotes an immune attack of a target cell. E.g., an immune effector function or response refers to a property of a T or NK cell that promotes killing or the inhibition of growth or proliferation, of a target cell. In the case of a T cell, primary stimulation and co-stimulation are examples of immune effector function or response.

The term "effector function" refers to a specialized function of a cell. Effector function of a T cell, for example, may be cytolytic activity or helper activity including the secretion of cytokines.

The term “encoding” refers to the inherent property of specific sequences of nucleotides in a polynucleotide, such as a gene, a cDNA, or an mRNA, to serve as templates for synthesis of other polymers and macromolecules in biological processes having either a defined sequence of nucleotides (e.g., rRNA, tRNA and mRNA) or a defined sequence of amino acids and the biological properties resulting therefrom. Thus, a gene, cDNA, or RNA, encodes a protein if transcription and translation of mRNA corresponding to that gene produces the protein in a cell or other biological system. Both the coding strand, the nucleotide sequence of which is identical to the mRNA sequence and is usually provided in sequence listings, and the non-coding strand, used as the template for transcription of a gene or cDNA, can be referred to as encoding the protein or other product of that gene or cDNA.

Unless otherwise specified, a “nucleotide sequence encoding an amino acid sequence” includes all nucleotide sequences that are degenerate versions of each other and that encode the same amino acid sequence. The phrase nucleotide sequence that encodes a protein or a RNA may also include introns to the extent that the nucleotide sequence encoding the protein may in some version contain an intron(s).

The term “effective amount” or “therapeutically effective amount” are used interchangeably herein, and refer to an amount of a compound, formulation, material, or composition, as described herein effective to achieve a particular biological result.

The term “endogenous” refers to any material from or produced inside an organism, cell, tissue or system.

The term “exogenous” refers to any material introduced from or produced outside an organism, cell, tissue or system.

The term “expression” refers to the transcription and/or translation of a particular nucleotide sequence driven by a promoter.

The term “transfer vector” refers to a composition of matter which comprises an isolated nucleic acid and which can be used to deliver the isolated nucleic acid to the interior of a cell. Numerous vectors are known in the art including, but not limited to, linear polynucleotides, polynucleotides associated with ionic or amphiphilic compounds, plasmids, and viruses. Thus, the term “transfer vector” includes an autonomously replicating plasmid or a virus. The term should also be construed to further include non-plasmid and non-viral compounds which facilitate transfer of nucleic acid into cells, such as, for example, a polylysine compound, liposome, and the like. Examples of viral transfer vectors include, but are not limited to, adenoviral vectors, adeno-associated virus vectors, retroviral vectors, lentiviral vectors, and the like.

The term “expression vector” refers to a vector comprising a recombinant polynucleotide comprising expression control sequences operatively linked to a nucleotide sequence to be expressed. An expression vector comprises sufficient cis-acting elements for expression; other elements for expression

can be supplied by the host cell or in an in vitro expression system. Expression vectors include all those known in the art, including cosmids, plasmids (e.g., naked or contained in liposomes) and viruses (e.g., lentiviruses, retroviruses, adenoviruses, and adeno-associated viruses) that incorporate the recombinant polynucleotide.

- 5 The term “lentivirus” refers to a genus of the Retroviridae family. Lentiviruses are unique among the retroviruses in being able to infect non-dividing cells; they can deliver a significant amount of genetic information into the DNA of the host cell, so they are one of the most efficient methods of a gene delivery vector. HIV, SIV, and FIV are all examples of lentiviruses.

- 10 The term “lentiviral vector” refers to a vector derived from at least a portion of a lentivirus genome, including especially a self-inactivating lentiviral vector as provided in Milone et al., *Mol. Ther.* 17(8): 1453–1464 (2009). Other examples of lentivirus vectors that may be used in the clinic, include but are not limited to, e.g., the LENTIVECTOR® gene delivery technology from Oxford BioMedica, the LENTIMAX™ vector system from Lentigen and the like. Nonclinical types of lentiviral vectors are also available and would be known to one skilled in the art.

- 15 The term “homologous” or “identity” refers to the subunit sequence identity between two polymeric molecules, e.g., between two nucleic acid molecules, such as, two DNA molecules or two RNA molecules, or between two polypeptide molecules. When a subunit position in both of the two molecules is occupied by the same monomeric subunit; e.g., if a position in each of two DNA molecules is occupied by adenine, then they are homologous or identical at that position. The homology between two
20 sequences is a direct function of the number of matching or homologous positions; e.g., if half (e.g., five positions in a polymer ten subunits in length) of the positions in two sequences are homologous, the two sequences are 50% homologous; if 90% of the positions (e.g., 9 of 10), are matched or homologous, the two sequences are 90% homologous.

- “Humanized” forms of non-human (e.g., murine) antibodies are chimeric immunoglobulins,
25 immunoglobulin chains or antibody fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. For the most part, humanized antibodies and antibody fragments thereof are human immunoglobulins (recipient antibody or antibody fragment) in which residues from a complementary-determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species
30 (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity, and capacity. In some instances, Fv framework region (FR) residues of the human immunoglobulin are replaced by corresponding non-human residues. Furthermore, a humanized antibody/antibody fragment can comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. These modifications can further refine and optimize antibody or antibody fragment
35 performance. In general, the humanized antibody or antibody fragment thereof will comprise substantially

all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or a significant portion of the FR regions are those of a human immunoglobulin sequence. The humanized antibody or antibody fragment can also comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human

5 immunoglobulin. For further details, see Jones et al., *Nature*, 321: 522-525, 1986; Reichmann et al., *Nature*, 332: 323-329, 1988; Presta, *Curr. Op. Struct. Biol.*, 2: 593-596, 1992.

"Fully human" refers to an immunoglobulin, such as an antibody or antibody fragment, where the whole molecule is of human origin or consists of an amino acid sequence identical to a human form of the antibody or immunoglobulin.

10 The term "isolated" means altered or removed from the natural state. For example, a nucleic acid or a peptide naturally present in a living animal is not "isolated," but the same nucleic acid or peptide partially or completely separated from the coexisting materials of its natural state is "isolated." An isolated nucleic acid or protein can exist in substantially purified form, or can exist in a non-native environment such as, for example, a host cell.

15 In the context of the present disclosure, the following abbreviations for the commonly occurring nucleic acid bases are used. "A" refers to adenosine, "C" refers to cytosine, "G" refers to guanosine, "T" refers to thymidine, and "U" refers to uridine.

The term "operably linked" or "transcriptional control" refers to functional linkage between a regulatory sequence and a heterologous nucleic acid sequence resulting in expression of the latter. For example, a first nucleic acid sequence is operably linked with a second nucleic acid sequence when the first nucleic acid sequence is placed in a functional relationship with the second nucleic acid sequence. For instance, a promoter is operably linked to a coding sequence if the promoter affects the transcription or expression of the coding sequence. Operably linked DNA sequences can be contiguous with each other and, e.g., where necessary to join two protein coding regions, are in the same reading frame.

25 The term "parenteral" administration of an immunogenic composition includes, e.g., subcutaneous (s.c.), intravenous (i.v.), intramuscular (i.m.), or intrasternal injection, intratumoral, or infusion techniques.

The term "nucleic acid" or "polynucleotide" refers to deoxyribonucleic acids (DNA) or ribonucleic acids (RNA) and polymers thereof in either single- or double-stranded form. Unless specifically limited, the term encompasses nucleic acids containing known analogues of natural nucleotides that have similar binding properties as the reference nucleic acid and are metabolized in a manner similar to naturally occurring nucleotides. Unless otherwise indicated, a particular nucleic acid sequence also implicitly encompasses conservatively modified variants thereof (e.g., degenerate codon substitutions), alleles, orthologs, SNPs, and complementary sequences as well as the sequence explicitly indicated. Specifically, degenerate codon substitutions may be achieved by generating sequences in which the third

position of one or more selected (or all) codons is substituted with mixed-base and/or deoxyinosine residues (Batzer et al., Nucleic Acid Res. 19:5081 (1991); Ohtsuka et al., J. Biol. Chem. 260:2605-2608 (1985); and Rossolini et al., Mol. Cell. Probes 8:91-98 (1994)).

5 The terms "peptide," "polypeptide," and "protein" are used interchangeably, and refer to a compound comprised of amino acid residues covalently linked by peptide bonds. A protein or peptide must contain at least two amino acids, and no limitation is placed on the maximum number of amino acids that can comprise a protein's or peptide's sequence. Polypeptides include any peptide or protein comprising two or more amino acids joined to each other by peptide bonds. As used herein, the term refers to both short chains, which also commonly are referred to in the art as peptides, oligopeptides and oligomers, for
10 example, and to longer chains, which generally are referred to in the art as proteins, of which there are many types. "Polypeptides" include, for example, biologically active fragments, substantially homologous polypeptides, oligopeptides, homodimers, heterodimers, variants of polypeptides, modified polypeptides, derivatives, analogs, fusion proteins, among others. A polypeptide includes a natural peptide, a recombinant peptide, or a combination thereof.

15 The term "promoter" refers to a DNA sequence recognized by the synthetic machinery of the cell, or introduced synthetic machinery, required to initiate the specific transcription of a polynucleotide sequence.

The term "promoter/regulatory sequence" refers to a nucleic acid sequence which is required for expression of a gene product operably linked to the promoter/regulatory sequence. In some instances,
20 this sequence may be the core promoter sequence and in other instances, this sequence may also include an enhancer sequence and other regulatory elements which are required for expression of the gene product. The promoter/regulatory sequence may, for example, be one which expresses the gene product in a tissue specific manner.

The term "constitutive" promoter refers to a nucleotide sequence which, when operably linked with a
25 polynucleotide which encodes or specifies a gene product, causes the gene product to be produced in a cell under most or all physiological conditions of the cell.

The term "inducible" promoter refers to a nucleotide sequence which, when operably linked with a polynucleotide which encodes or specifies a gene product, causes the gene product to be produced in a cell substantially only when an inducer which corresponds to the promoter is present in the cell.

30 The term "tissue-specific" promoter refers to a nucleotide sequence which, when operably linked with a polynucleotide encodes or specified by a gene, causes the gene product to be produced in a cell substantially only if the cell is a cell of the tissue type corresponding to the promoter.

The terms “cancer associated antigen” or “tumor antigen” interchangeably refers to a molecule (typically a protein, carbohydrate or lipid) that is expressed on the surface of a cancer cell, either entirely or as a fragment (e.g., MHC/peptide), and which is useful for the preferential targeting of a pharmacological agent to the cancer cell. In some embodiments, a tumor antigen is a marker expressed by both normal

5 cells and cancer cells, e.g., a lineage marker, e.g., CD19 on B cells. In some embodiments, a tumor antigen is a cell surface molecule that is overexpressed in a cancer cell in comparison to a normal cell, for instance, 1-fold over expression, 2-fold overexpression, 3-fold overexpression or more in comparison to a normal cell. In some embodiments, a tumor antigen is a cell surface molecule that is inappropriately synthesized in the cancer cell, for instance, a molecule that contains deletions, additions or mutations in

10 comparison to the molecule expressed on a normal cell. In some embodiments, a tumor antigen will be expressed exclusively on the cell surface of a cancer cell, entirely or as a fragment (e.g., MHC/peptide), and not synthesized or expressed on the surface of a normal cell. In some embodiments, exemplary tumor antigens include: CD19; CD123; CD22; CD30; CD171; CS-1; C-type lectin-like molecule-1, CD33; epidermal growth factor receptor variant III (EGFRvIII); ganglioside G2 (GD2); ganglioside GD3; TNF

15 receptor family member B cell maturation (BCMA); Tn antigen ((Tn Ag) or (GalNAc α -Ser/Thr)); prostate-specific membrane antigen (PSMA); Receptor tyrosine kinase-like orphan receptor 1 (ROR1); Fms-Like Tyrosine Kinase 3 (FLT3); Tumor-associated glycoprotein 72 (TAG72); CD38; CD44v6; Carcinoembryonic antigen (CEA); Epithelial cell adhesion molecule (EPCAM); B7H3 (CD276); KIT (CD117); Interleukin-13 receptor subunit alpha-2; Mesothelin; Interleukin 11 receptor alpha (IL-11Ra);

20 prostate stem cell antigen (PSCA); Protease Serine 21; vascular endothelial growth factor receptor 2 (VEGFR2); Lewis(Y) antigen; CD24; Platelet-derived growth factor receptor beta (PDGFR-beta); Stage-specific embryonic antigen-4 (SSEA-4); CD20; Folate receptor alpha; Receptor tyrosine-protein kinase ERBB2 (Her2/neu); Mucin 1, cell surface associated (MUC1); epidermal growth factor receptor (EGFR); neural cell adhesion molecule (NCAM); Prostase; prostatic acid phosphatase (PAP); elongation factor 2 mutated (ELF2M); Ephrin B2; fibroblast activation protein alpha (FAP); insulin-like growth factor 1

25 receptor (IGF-I receptor), carbonic anhydrase IX (CAIX); Proteasome (Prosome, Macropain) Subunit, Beta Type, 9 (LMP2); glycoprotein 100 (gp100); oncogene fusion protein consisting of breakpoint cluster region (BCR) and Abelson murine leukemia viral oncogene homolog 1 (Abl) (bcr-abl); tyrosinase; ephrin type-A receptor 2 (EphA2); Fucosyl GM1; sialyl Lewis adhesion molecule (sLe); ganglioside GM3;

30 transglutaminase 5 (TGS5); high molecular weight-melanoma-associated antigen (HMWMAA); o-acetyl-GD2 ganglioside (OAcGD2); Folate receptor beta; tumor endothelial marker 1 (TEM1/CD248); tumor endothelial marker 7-related (TEM7R); claudin 6 (CLDN6); thyroid stimulating hormone receptor (TSHR); G protein-coupled receptor class C group 5, member D (GPRC5D); chromosome X open reading frame 61 (CXORF61); CD97; CD179a; anaplastic lymphoma kinase (ALK); Polysialic acid; placenta-specific 1

35 (PLAC1); hexasaccharide portion of globoH glycosphingolipid (GloboH); mammary gland differentiation antigen (NY-BR-1); uroplakin 2 (UPK2); Hepatitis A virus cellular receptor 1 (HAVCR1); adrenoceptor beta 3 (ADRB3); pannexin 3 (PANX3); G protein-coupled receptor 20 (GPR20); lymphocyte antigen 6

complex, locus K 9 (LY6K); Olfactory receptor 51E2 (OR51E2); TCR Gamma Alternate Reading Frame Protein (TARP); Wilms tumor protein (WT1); Cancer/testis antigen 1 (NY-ESO-1); Cancer/testis antigen 2 (LAGE-1a); Melanoma-associated antigen 1 (MAGE-A1); ETS translocation-variant gene 6, located on chromosome 12p (ETV6-AML); sperm protein 17 (SPA17); X Antigen Family, Member 1A (XAGE1);

5 angiopoietin-binding cell surface receptor 2 (Tie 2); melanoma cancer testis antigen-1 (MAD-CT-1); melanoma cancer testis antigen-2 (MAD-CT-2); Fos-related antigen 1; tumor protein p53 (p53); p53 mutant; prostatein; surviving; telomerase; prostate carcinoma tumor antigen-1, melanoma antigen recognized by T cells 1; Rat sarcoma (Ras) mutant; human Telomerase reverse transcriptase (hTERT); sarcoma translocation breakpoints; melanoma inhibitor of apoptosis (ML-IAP); ERG (transmembrane

10 protease, serine 2 (TMPRSS2) ETS fusion gene); N-Acetyl glucosaminyl-transferase V (NA17); paired box protein Pax-3 (PAX3); Androgen receptor; Cyclin B1; v-myc avian myelocytomatosis viral oncogene neuroblastoma derived homolog (MYCN); Ras Homolog Family Member C (RhoC); Tyrosinase-related protein 2 (TRP-2); Cytochrome P450 1B1 (CYP1B1); CCCTC-Binding Factor (Zinc Finger Protein)-Like, Squamous Cell Carcinoma Antigen Recognized By T Cells 3 (SART3); Paired box protein Pax-5 (PAX5);

15 proacrosin binding protein sp32 (OY-TES1); lymphocyte-specific protein tyrosine kinase (LCK); A kinase anchor protein 4 (AKAP-4); synovial sarcoma, X breakpoint 2 (SSX2); Receptor for Advanced Glycation Endproducts (RAGE-1); renal ubiquitous 1 (RU1); renal ubiquitous 2 (RU2); legumain; human papilloma virus E6 (HPV E6); human papilloma virus E7 (HPV E7); intestinal carboxyl esterase; heat shock protein 70-2 mutated (mut hsp70-2); CD79a; CD79b; CD72; Leukocyte-associated immunoglobulin-like receptor

20 1 (LAIR1); Fc fragment of IgA receptor (FCAR or CD89); Leukocyte immunoglobulin-like receptor subfamily A member 2 (LILRA2); CD300 molecule-like family member f (CD300LF); C-type lectin domain family 12 member A (CLEC12A); bone marrow stromal cell antigen 2 (BST2); EGF-like module-containing mucin-like hormone receptor-like 2 (EMR2); lymphocyte antigen 75 (LY75); Glypican-3 (GPC3); Fc receptor-like 5 (FCRL5); immunoglobulin lambda-like polypeptide 1 (IGLL1); TNF receptor family

25 member; Fms-Like Tyrosine Kinase 3 (FL T3); CD10; CD19; CD20; CD21; CD22; CD23; CD24; CD25; CD37; CD38; CD53; CD72; CD73; CD74; CD75; CD77; CD79a; CD79b; CD80; CD81; CD82; CD83; CD84; CD85; ROR1; BCMA; CD86; CD179b; CD1a; CD1b; CD1c; CD1d; CD2; CD5; CD6; CD9; CD11a; CD11b; CD11c; CD17; CD18; CD26; CD27; CD29; CD30; CD31; CD32a; CD32b; CD35; CD38; CD39; CD40; CD44; CD45; CD45RA; CD45RB; CD45RC; CD45RO; CD46; CD47; CD48; CD49b; CD49c;

30 CD49d; CD50; CD52; CD54; CD55; CD58; CD60a; CD62L; CD63; CD63; CD68 CD69; CD70; CD85E; CD85I; CD85J; CD92; CD95; CD97; CD98; CD99; CD100; CD102; CD108; CD119; CD120a; CD120b; CD121b; CD122; CD124; CD125; CD126; CD130; CD132; CD137; CD138; CD139; CD147; CD148; CD150; CD152; CD162; CD164; CD166; CD167a; CD170; CD175; CD175s; CD180; CD184; CD185; CD192; CD196; CD197; CD200; CD205; CD210a; CDw210b; CD212; CD213a1; CD213a2; CD215;

35 CD217; CD218a; CD218b; CD220; CD221; CD224; CD225; CD226; CD227; CD229; CD230; CD232; CD252; CD253; CD257; CD258; CD261; CD262; CD263; CD264; CD267; CD268; CD269; CD270; CD272; CD274; CD275; CD277; CD279; CD283; CD289; CD290; CD295; CD298; CD300a; CD300c;

CD305; CD306; CD307a; CD307b; CD307c; CD307d; CD307e; CD314; CD315; CD316; CD317; CD319; CD321; CD327; CD328; CD329; CD338; CD351; CD352; CD353; CD354; CD355; CD357; CD358; CD360; CD361; CD362; CD363; and a peptide of any of these antigens presented on MHC. Particularly preferred antigens include: CD19, CD20, CD22, FcRn5, FcRn2, BCMA, CS-1, CD138, CLDN6, mesothelin, EGFRvIII, CD123, CD33 and CLL-1. In some embodiments, the CARs of the present disclosure includes CARs comprising an antigen binding domain (e.g., antibody or antibody fragment) that binds to a MHC presented peptide. Normally, peptides derived from endogenous proteins fill the pockets of Major histocompatibility complex (MHC) class I molecules, and are recognized by T cell receptors (TCRs) on CD8 + T lymphocytes. The MHC class I complexes are constitutively expressed by all nucleated cells. In cancer, virus-specific and/or tumor-specific peptide/MHC complexes represent a unique class of cell surface targets for immunotherapy. TCR-like antibodies targeting peptides derived from viral or tumor antigens in the context of human leukocyte antigen (HLA)-A1 or HLA-A2 have been described (see, e.g., Sastry et al., J Virol. 2011 85(5):1935-1942; Sergeeva et al., Blood, 2011 117(16):4262-4272; Verma et al., J Immunol 2010 184(4):2156-2165; Willemsen et al., Gene Ther 2001 8(21) :1601-1608 ; Dao et al., Sci Transl Med 2013 5(176) :176ra33 ; Tassev et al., Cancer Gene Ther 2012 19(2):84-100). For example, TCR-like antibody can be identified from screening a library, such as a human scFv phage displayed library. Accordingly, the present disclosure provides CARs that comprise an antigen binding domain that binds to a MHC presented peptide of a molecule selected from the group of WT1, NY-ESO-1, LAGE-1a, MAGE-A1 and RAGE-1.

The term "flexible polypeptide linker" or "linker" as used in the context of a scFv refers to a peptide linker that consists of amino acids such as glycine and/or serine residues used alone or in combination, to link variable heavy and variable light chain regions together. In one embodiment, the flexible polypeptide linker is a Gly/Ser linker and comprises the amino acid sequence (Gly-Gly-Gly-Ser)_n, where n is a positive integer equal to or greater than 1, for example, n=1, n=2, n=3, n=4, n=5 and n=6, n=7, n=8, n=9 or n=10 (SEQ ID NO:28). In one embodiment, the flexible polypeptide linkers include, but are not limited to, (Gly₄ Ser)₄ (SEQ ID NO:29) or (Gly₄ Ser)₃ (SEQ ID NO:30). In another embodiment, the linkers include multiple repeats of (Gly₂Ser), (GlySer) or (Gly₃Ser) (SEQ ID NO:31). Also included within the scope of the invention are linkers described in WO2012/138475, incorporated herein by reference).

As used herein, a 5' cap (also termed an RNA cap, an RNA 7-methylguanosine cap or an RNA m⁷G cap) is a modified guanine nucleotide that has been added to the "front" or 5' end of a eukaryotic messenger RNA shortly after the start of transcription. The 5' cap consists of a terminal group which is linked to the first transcribed nucleotide. Its presence is critical for recognition by the ribosome and protection from RNases. Cap addition is coupled to transcription, and occurs co-transcriptionally, such that each influences the other. Shortly after the start of transcription, the 5' end of the mRNA being synthesized is bound by a cap-synthesizing complex associated with RNA polymerase. This enzymatic complex catalyzes the chemical reactions that are required for mRNA capping. Synthesis proceeds as a multi-step

biochemical reaction. The capping moiety can be modified to modulate functionality of mRNA such as its stability or efficiency of translation.

As used herein, "in vitro transcribed RNA" refers to RNA, preferably mRNA, that has been synthesized in vitro. Generally, the in vitro transcribed RNA is generated from an in vitro transcription vector. The in vitro
5 transcription vector comprises a template that is used to generate the in vitro transcribed RNA.

As used herein, a "poly(A)" is a series of adenosines attached by polyadenylation to the mRNA. In the preferred embodiment of a construct for transient expression, the polyA is between 50 and 5000 (SEQ ID NO: 32), preferably greater than 64, more preferably greater than 100, most preferably greater than 300 or 400. Poly(A) sequences can be modified chemically or enzymatically to modulate mRNA functionality
10 such as localization, stability or efficiency of translation.

As used herein, "polyadenylation" refers to the covalent linkage of a polyadenylyl moiety, or its modified variant, to a messenger RNA molecule. In eukaryotic organisms, most messenger RNA (mRNA) molecules are polyadenylated at the 3' end. The 3' poly(A) tail is a long sequence of adenine nucleotides (often several hundred) added to the pre-mRNA through the action of an enzyme, polyadenylate
15 polymerase. In higher eukaryotes, the poly(A) tail is added onto transcripts that contain a specific sequence, the polyadenylation signal. The poly(A) tail and the protein bound to it aid in protecting mRNA from degradation by exonucleases. Polyadenylation is also important for transcription termination, export of the mRNA from the nucleus, and translation. Polyadenylation occurs in the nucleus immediately after transcription of DNA into RNA, but additionally can also occur later in the cytoplasm. After transcription
20 has been terminated, the mRNA chain is cleaved through the action of an endonuclease complex associated with RNA polymerase. The cleavage site is usually characterized by the presence of the base sequence AAUAAA near the cleavage site. After the mRNA has been cleaved, adenosine residues are added to the free 3' end at the cleavage site.

As used herein, "transient" refers to expression of a non-integrated transgene for a period of hours, days
25 or weeks, wherein the period of time of expression is less than the period of time for expression of the gene if integrated into the genome or contained within a stable plasmid replicon in the host cell.

As used herein, the terms "treat", "treatment" and "treating" refer to the reduction or amelioration of the progression, severity and/or duration of a proliferative disorder, or the amelioration of one or more symptoms (preferably, one or more discernible symptoms) of a proliferative disorder resulting from the
30 administration of one or more therapies (e.g., one or more therapeutic agents such as a CAR of the invention). In specific embodiments, the terms "treat," "treatment" and "treating" refer to the amelioration of at least one measurable physical parameter of a proliferative disorder, such as growth of a tumor, not necessarily discernible by the patient. In other embodiments the terms "treat", "treatment" and "treating" - refer to the inhibition of the progression of a proliferative disorder, either physically by, e.g., stabilization of
35 a discernible symptom, physiologically by, e.g., stabilization of a physical parameter, or both. In other

embodiments the terms “treat”, “treatment” and “treating” refer to the reduction or stabilization of tumor size or cancerous cell count.

The term “signal transduction pathway” refers to the biochemical relationship between a variety of signal transduction molecules that play a role in the transmission of a signal from one portion of a cell to another portion of a cell. The phrase “cell surface receptor” includes molecules and complexes of molecules capable of receiving a signal and transmitting signal across the membrane of a cell.

The term “subject” is intended to include living organisms in which an immune response can be elicited (e.g., mammals, human). A “subject” or “patient,” as used therein, may be a human or non-human mammal. Non-human mammals include, for example, livestock and pets, such as ovine, bovine, porcine, canine, feline and murine mammals. Preferably, the subject is human.

The term, a “substantially purified” cell refers to a cell that is essentially free of other cell types. A substantially purified cell also refers to a cell which has been separated from other cell types with which it is normally associated in its naturally occurring state. In some instances, a population of substantially purified cells refers to a homogenous population of cells. In other instances, this term refers simply to cell that have been separated from the cells with which they are naturally associated in their natural state. In some aspects, the cells are cultured in vitro. In other aspects, the cells are not cultured in vitro.

The term “suicide gene” as used herein refers to a suicide or apoptosis-inducing gene operably linked to a promoter, which may be constitutive or inducible. Examples of a suicide gene include, but are not limited to, a herpes simplex virus thymidine kinase (HSV-TK), the cytoplasmic domain of Fas, a caspase such as caspase-8 or caspase-9, cytosine deaminase, E1A, FHIT, and other known suicide or apoptosis-inducing genes.

The term “suicide gene product” or “suicide domain” as used herein refers to the expression product of the suicide gene.

The term “therapeutic” as used herein means a treatment. A therapeutic effect is obtained by reduction, suppression, remission, or eradication of a disease state.

The term “tolerance” or “immune tolerance” as used herein refers to a state in which a subject has a reduced or absent immune response to a specific antigen or group of antigens to which the subject is normally responsive to. Tolerance is achieved under conditions that suppress the immune reaction and is not just the absence of an immune response. In an embodiment, tolerance in a subject can be characterized by one or more of the following: a decreased level of a specific immunological response (e.g., mediated by antigen-specific effector T lymphocytes, B lymphocytes, or antibody); a delay in the onset or progression of a specific immunological response; or a reduced risk of the onset or progression of a specific immunological response, as compared to untreated subjects.

The term “prophylaxis” as used herein means the prevention of or protective treatment for a disease or disease state.

The term “transfected” or “transformed” or “transduced” refers to a process by which exogenous nucleic acid is transferred or introduced into the host cell. A “transfected” or “transformed” or “transduced” cell is one which has been transfected, transformed or transduced with exogenous nucleic acid. The cell includes the primary subject cell and its progeny.

The term “specifically binds,” refers to an antibody, or a ligand, which recognizes and binds with a cognate binding partner (e.g., a stimulatory and/or costimulatory molecule present on a T cell) protein present in a sample, but which antibody or ligand, does not substantially recognize or bind other molecules in the sample.

“Refractory” as used herein refers to a disease, e.g., cancer, that does not respond to a treatment. In embodiments, a refractory cancer can be resistant to a treatment before or at the beginning of the treatment. In other embodiments, the refractory cancer can become resistant during a treatment. A refractory cancer is also called a resistant cancer.

“Relapsed” or “relapse” as used herein refers to the return or reappearance of a disease (e.g., cancer) or the signs and symptoms of a disease such as cancer after a period of improvement or responsiveness, e.g., after prior treatment of a therapy, e.g., cancer therapy. The initial period of responsiveness may involve the level of cancer cells falling below a certain threshold, e.g., below 20%, 1%, 10%, 5%, 4%, 3%, 2%, or 1%. The reappearance may involve the level of cancer cells rising above a certain threshold, e.g., above 20%, 1%, 10%, 5%, 4%, 3%, 2%, or 1%. For example, e.g., in the context of B-ALL, the reappearance may involve, e.g., a reappearance of blasts in the blood, bone marrow (> 5%), or any extramedullary site, after a complete response. A complete response, in this context, may involve < 5% BM blast. More generally, in an embodiment, a response (e.g., complete response or partial response) can involve the absence of detectable MRD (minimal residual disease). In an embodiment, the initial period of responsiveness lasts at least 1, 2, 3, 4, 5, or 6 days; at least 1, 2, 3, or 4 weeks; at least 1, 2, 3, 4, 6, 8, 10, or 12 months; or at least 1, 2, 3, 4, or 5 years.

Ranges: throughout this disclosure, various aspects of the invention can be presented in a range format. It should be understood that the description in range format is merely for convenience and brevity and should not be construed as an inflexible limitation on the scope of the invention. Accordingly, the description of a range should be considered to have specifically disclosed all the possible subranges as well as individual numerical values within that range. For example, description of a range such as from 1 to 6 should be considered to have specifically disclosed subranges such as from 1 to 3, from 1 to 4, from 1 to 5, from 2 to 4, from 2 to 6, from 3 to 6 etc., as well as individual numbers within that range, for example, 1, 2, 2.7, 3, 4, 5, 5.3, and 6. As another example, a range such as 95-99% identity, includes

something with 95%, 96%, 97%, 98% or 99% identity, and includes subranges such as 96-99%, 96-98%, 96-97%, 97-99%, 97-98% and 98-99% identity. This applies regardless of the breadth of the range.

FUSION PROTEINS

Provided herein are fusion proteins including two protein domains separated by a heterologous protease cleavage site (e.g., a protease cleavage site that is cleaved by a mammalian intracellular or extracellular protease), wherein a first of the protein domains is a conditional expression domain, e.g., a degradation domain or an aggregation domain. In some embodiments, the fusion proteins described herein comprise three essential elements: a conditional expression domain, e.g., a degradation domain or an aggregation domain, a domain containing the protein of interest, and a protease cleavage domain separating the two. These elements can be arranged such that the conditional expression domain, e.g., a degradation domain or an aggregation domain, is located either N-terminal or C-terminal to the protein of interest.

In some embodiments, the fusion protein described herein includes a furin cleavage site. In some embodiments, the fusion proteins described herein include any one of furin cleavage sites listed in Table 20. In some embodiments, the fusion proteins described herein include a furin cleavage site selected from RTKR (SEQ ID NO: 123); GTGAEDPRPSRKRRSLGDVG (SEQ ID NO: 125) or a sequence having at least 90%, 95%, 97%, 98%, or 99% identity thereto; GTGAEDPRPSRKRR (SEQ ID NO: 127) or a sequence having at least 90%, 95%, 97%, 98%, or 99% identity thereto; LQWLEQQVAKRRTKR (SEQ ID NO: 129) or a sequence having at least 90%, 95%, 97%, 98%, or 99% identity thereto; GTGAEDPRPSRKRRSLGG (SEQ ID NO: 131) or a sequence having at least 90%, 95%, 97%, 98%, or 99% identity thereto; GTGAEDPRPSRKRRSLG (SEQ ID NO: 133) or a sequence having at least 90%, 95%, 97%, 98%, or 99% identity thereto; SLNLTESHNSRKRR (SEQ ID NO: 135) or a sequence having at least 90%, 95%, 97%, 98%, or 99% identity thereto; or CKINGYPKGRKRR (SEQ ID NO: 137) or a sequence having at least 90%, 95%, 97%, 98%, or 99% identity thereto. In some embodiments, the fusion proteins described herein include a furin cleavage site selected from GTGAEDPRPSRKRRSLGDVG (SEQ ID NO: 125) or a sequence having at least 90%, 95%, 97%, 98%, or 99% identity thereto, or GTGAEDPRPSRKRR (SEQ ID NO: 127) or a sequence having at least 90%, 95%, 97%, 98%, or 99% identity thereto. In some embodiments, the fusion proteins described herein include the furin cleavage site of GTGAEDPRPSRKRRSLGDVG (SEQ ID NO: 125) or a sequence having at least 90%, 95%, 97%, 98%, or 99% identity thereto.

In some embodiments, the fusion proteins described herein include a furin cleavage site selected from RTKR (SEQ ID NO: 123); GTGAEDPRPSRKRRSLGDVG (SEQ ID NO: 125); GTGAEDPRPSRKRR (SEQ ID NO: 127); LQWLEQQVAKRRTKR (SEQ ID NO: 129); GTGAEDPRPSRKRRSLGG (SEQ ID NO: 131); GTGAEDPRPSRKRRSLG (SEQ ID NO: 133); SLNLTESHNSRKRR (SEQ ID NO: 135); or CKINGYPKGRKRR (SEQ ID NO: 137). In some embodiments, the fusion proteins described herein include a furin cleavage site selected from GTGAEDPRPSRKRRSLGDVG (SEQ ID NO: 125) or

GTGAEDPRPSRKRR (SEQ ID NO: 127). In some embodiments, the fusion proteins described herein include the furin cleavage site of GTGAEDPRPSRKRRSLGDVG (SEQ ID NO: 125).

In some embodiments, the fusion protein described herein includes a furin degnon (FurON) domain, which comprises two components: a degnon or degradation domain, which is a mutated protein domain unable to acquire a proper conformation in the absence of a small molecule ligand, and a furin cleavage site.

The furin degnon domain can be fused to a protein of interest that is expressed in the endoplasmic reticulum. The N- and/ or C-termini of the protein of interest can be used as site of fusion, provided that the furin degnon domain faces the lumen of the endoplasmic reticulum. The protein of interest can be either a membrane protein (regardless of the number of transmembrane domains) or a soluble protein.

The orientation of the furin cleavage site relative to the degnon domain should be such that the cleavage results in the separation of the furin degnon domain and protein of interest. In the absence of the small molecule ligand or stabilization compound, the furin degnon domain leads to the destabilization or degradation of the entire fusion protein. In the presence of the small molecule ligand or stabilization compound, the fusion protein is spared from degradation. The furin degnon domain is mutated such that the affinity to its natural endogenous ligand is abolished; the affinity to the small molecule ligand or stabilization compound is preserved; and protein instability is conferred when the small molecule is absent.

In some embodiments, the degnon or degradation domain is derived from a protein listed in Table 21. In some embodiments, the degnon or degradation domain is derived from an estrogen receptor. In some embodiments, the degnon or degradation domain comprises an amino acid sequence selected from SEQ ID NO: 58 or a sequence having at least 90%, 95%, 97%, 98%, or 99% identity thereto, or SEQ ID NO: 121 or a sequence having at least 90%, 95%, 97%, 98%, or 99% identity thereto. In some embodiments, the degnon or degradation domain comprises an amino acid sequence selected from SEQ ID NO: 58 or SEQ ID NO: 121.

In some embodiments, the degnon or degradation domain is derived from an FKB protein (FKBP). In some embodiments, the degradation domain comprises an amino acid sequence of SEQ ID NO: 56 or a sequence having at least 90%, 95%, 97%, 98%, or 99% identity thereto. In some embodiments, the degradation domain comprises an amino acid sequence of SEQ ID NO: 56.

In some embodiments, the degnon or degradation domain is derived from dihydrofolate reductase (DHFR). In some embodiments, the degradation domain comprises an amino acid sequence selected from SEQ ID NO: 57 or a sequence having at least 90%, 95%, 97%, 98%, or 99% identity thereto. In some embodiments, the degradation domain comprises an amino acid sequence selected from SEQ ID NO: 57. In some embodiments, the degnon or degradation domain is not derived from an FKB protein, estrogen receptor, or DHFR.

PROTEINS OF INTEREST

The fusion proteins of the invention can include virtually any protein of interest. In certain preferred embodiments, the protein of interest can be a transmembrane protein (e.g., a transmembrane receptor).

The format of the fusion proteins of the invention are of particular use in such transmembrane proteins

because inclusion of an intact conditional expression domain, e.g., degradation domain or, e.g., aggregation domain, on the N-terminus of a transmembrane receptor would possibly result in disruption of the activity of the protein of interest, while inclusion on the C-terminus may result in poor regulation of the protein of interest (because, e.g., integration into the membrane may result in sufficient stabilization of the protein or degradation domain to avoid degradation and/or aggregation). One example of a class of proteins of interest is Chimeric Antigen T Cell Receptors as described in the section below.

CHIMERIC ANTIGEN RECEPTOR

In some embodiments, the protein of interest is a chimeric antigen receptor (CAR), wherein the CAR comprises an antigen binding domain (e.g., antibody or antibody fragment, TCR or TCR fragment) that binds to a tumor antigen as described herein, a transmembrane domain (e.g., a transmembrane domain described herein), and an intracellular signaling domain (e.g., an intracellular signaling domain described herein) (e.g., an intracellular signaling domain comprising a costimulatory domain (e.g., a costimulatory domain described herein) and/or a primary signaling domain (e.g., a primary signaling domain described herein)). CAR nucleic acid constructs, encoded proteins, containing vectors, host cells, pharmaceutical compositions, and methods of administration and treatment related to the present disclosure are disclosed in detail in International Patent Application Publication No. WO2015142675, which is incorporated by reference in its entirety.

In some embodiments, the protein of interest is a chimeric antigen receptor (CAR), wherein the CAR comprises an antigen binding domain (e.g., antibody or antibody fragment, TCR or TCR fragment) that binds to a tumor-supporting antigen (e.g., a tumor-supporting antigen as described herein), a transmembrane domain (e.g., a transmembrane domain described herein), and an intracellular signaling domain (e.g., an intracellular signaling domain described herein) (e.g., an intracellular signaling domain comprising a costimulatory domain (e.g., a costimulatory domain described herein) and/or a primary signaling domain (e.g., a primary signaling domain described herein)). In some embodiments, the tumor-supporting antigen is an antigen present on a stromal cell or a myeloid-derived suppressor cell (MDSC). In other aspects, the invention features polypeptides encoded by such nucleic acids and host cells containing such nucleic acids and/or polypeptides.

In some embodiments, a CAR molecule comprises at least one intracellular signaling domain selected from a CD137 (4-1BB) signaling domain, a CD28 signaling domain, a CD27 signaling domain, an ICOS

signaling domain, a CD3zeta signal domain, or any combination thereof. In some embodiments, a CAR molecule comprises at least one intracellular signaling domain selected from one or more costimulatory molecule(s) selected from CD137 (4-1BB), CD28, CD27, or ICOS.

5 The present invention, in some aspects, also includes a method of modifying a T cell with a chimeric antigen receptor (CAR) and a suicide gene. Thus, the present invention encompasses a nucleic acid encoding a CAR or a modified T cell comprising a CAR, wherein the CAR includes an antigen binding domain, a transmembrane domain and an intracellular domain.

Example of CARs are described in U.S. Patent Nos.: 8,911,993, 8,906,682, 8,975,071, 8,916,381, 9,102,760, 9,101,584, and 9,102,761, all of which are incorporated herein by reference in their entireties.

10 Sequences of non-limiting examples of various components that can be part of a CAR molecule are listed in Table 2, where “aa” stands for amino acids, and “na” stands for nucleic acids that encode the corresponding peptide.

Table 2. Sequences of various components of CAR (aa – amino acids, na – nucleic acids that encodes the corresponding protein)

SEQ ID NO	description	Sequence
1	EF-1 promoter	CGTGAGGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATC GCCCACAGTCCCCGAGAAGTTGGGGGAGGGGTCCGGCAAT TGAACCGGTGCCTAGAGAAGGTGGCGCGGGGTAAACTGGG AAAGTGATGTCGTGTACTGGCTCCGCCTTTTTCCCGAGGGT GGGGGAGAACCGTATATAAGTGCAGTAGTCGCCGTGAACGT TCTTTTCGCAACGGGTTTGCCGCCAGAACACAGGTAAGTG CCGTGTGTGGTTCCCGCGGGCCTGGCCTCTTACGGGTTAT GGCCCTTGCGTGCCTTGAATTACTTCCACCTGGCTGCAGTA CGTGATTCTTGATCCCGAGCTTCGGGTTGGAAGTGGGTGGG AGAGTTCGAGGCCTTGCGCTTAAGGAGCCCCTTCGCCTCGT GCTTGAGTTGAGGCCTGGCCTGGGCGCTGGGGCCGCCGCG TGCGAATCTGGTGGCACCTTCGCGCCTGTCTCGCTGCTTTC GATAAGTCTCTAGCCATTTAAATTTTTGATGACCTGCTGCG ACGCTTTTTTCTGGCAAGATAGTCTTGTAATGCGGGCCAA GATCTGCACACTGGTATTTTCGGTTTTTGGGGCCGCGGGCGG CGACGGGGCCCGTGCCTCCAGCGCACATGTTCCGGCGAGG CGGGGCCTGCGAGCGCGGCCACCGAGAATCGGACGGGGG TAGTCTCAAGCTGGCCGGCCTGCTCTGGTGCCTGGCCTCGC GCCGCCGTGTATCGCCCCGCCCTGGGCGGCAAGGCTGGCC CGGTCCGCACCAAGTTGCGTGAGCGGAAAGATGGCCGCTTC CCGGCCCTGCTGCAGGGAGCTCAAAATGGAGGACGCGGCG CTCGGGAGAGCGGGCGGGTGAGTCACCCACACAAAGGAAA AGGGCCTTTCGGTCCCTCAGCCGTCGCTTCATGTGACTCCAC GGAGTACCGGGCGCCGTCCAGGCACCTCGATTAGTTCTCGA GCTTTTGGAGTACGTCGTCTTTAGGTTGGGGGAGGGGTTT TATGCGATGGAGTTTCCCACACTGAGTGGGTGGAGACTGA AGTTAGGCCAGCTTGGCACTTGATGTAATTCTCCTTGAATT

		TGCCCTTTTTGAGTTTGGATCTTGGTTCATTCTCAAGCCTCA GACAGTGGTTCAAAGTTTTTTCTTCCATTTCAAGGTGTCGTG A
2	Leader (aa)	MALPVTALLLPLALLLHAARP
3	Leader (na)	ATGGCCCTGCCTGTGACAGCCCTGCTGCTGCCTCTGGCTCT GCTGCTGCATGCCGCTAGACCC
33	Leader (na)	ATGGCCCTCCCTGTACCGCCCTGCTGCTTCCGCTGGCTCT TCTGCTCCACGCCGCTCGGCCC
4	CD 8 hinge (aa)	TTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFA CD
5	CD8 hinge (na)	ACCACGACGCCAGCGCCGCGACCAACACCGGCGCCCA CCATCGCGTTCGACGCCCTGTCCCTGCGCCAGAGGCGTG CCGGCCAGCGGCGGGGGGCGCAGTGACACGAGGGGGCT GGACTTCGCCTGTGAT
6	Ig4 hinge (aa)	ESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVS VLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQ VYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN YKTTTPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEAL HNHYTQKSLSLGLKGM
7	Ig4 hinge (na)	GAGAGCAAGTACGGCCCTCCCTGCCCCCTTGCCCTGCCC CCGAGTTCCTGGGCGGACCCAGCGTGTTCTGTTCCTGTTCCCCC AAGCCCAAGGACACCCTGATGATCAGCCGGACCCCGAGG TGACCTGTGTGGTGGTGGACGTGTCCCAGGAGGACCCGA GGTCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCAC AACGCCAAGACCAAGCCCCGGGAGGAGCAGTTCAATAGCA CCTACCGGGTGGTGTCCGTGCTGACCGTGTGCACAGGA CTGGCTGAACGGCAAGGAATACAAGTGTAAAGGTGTCCAACA AGGGCCTGCCAGCAGCATCGAGAAAACCATCAGCAAGGC CAAGGGCCAGCCTCGGGAGCCCCAGGTGTACACCCTGCCC CCTAGCCAAGAGGAGATGACCAAGAACCAGGTGTCCCTGAC CTGCCTGGTGAAGGGCTTCTACCCAGCGACATCGCCGTG GAGTGGGAGAGCAACGGCCAGCCCGAGAACAACACTACAAGA CCACCCCCCTGTGCTGGACAGCGACGGCAGCTTCTTCCTG TACAGCCGGCTGACCGTGGACAAGAGCCGGTGGCAGGAGG GCAACGTCTTTAGCTGCTCCGTGATGCACGAGGCCCTGCAC AACCACTACACCCAGAAGAGCCTGAGCCTGTCCCTGGGCAA GATG
8	IgD hinge (aa)	RWPESPKAQASSVPTAQPAEGSLAKATTAPATTRNTGRGGE EKKKEKEKEEQEERETKTPECPSTHTQPLGVYLLTPAVQDLWLR DKATFTCFVVGSDLKDAHLTWEVAGKVPTGGVEEGLLERHSN GSQSQHSRLTLPRSLWNAGTSVTCTLNHPSLPPQRLMALREP AAQAPVKLSLNLASSDPPEAASWLLCEVSGFSPNILLMWLE DQREVNTSGFAPARPPPQPGSTTFWAWSVLRVPAPPSPQPAT YTCVVSHEDSRTLLNASRSLEVSYVTDH
9	IgD hinge (na)	AGGTGGCCCGAAAGTCCCAAGGCCAGGCATCTAGTGTTCC TACTGCACAGCCCCAGGCAGAAAGGCAGCCTAGCCAAAGCTA CTACTGCACCTGCCACTACGCGCAATACTGGCCGTGGCGG GGAGGAGAAGAAAAAGGAGAAAGAGAAAGAAGAACAGGAA GAGAGGGAGACCAAGACCCCTGAATGTCCATCCCATAACCA GCCGCTGGGCGTCTATCTCTTGACTCCCGCAGTACAGGACT TGTGGCTTAGAGATAAGGCCACCTTTACATGTTTCGTCTGG GCTCTGACCTGAAGGATGCCCATTTGACTTGGGAGGTTGCC GGAAAGGTACCCACAGGGGGGGTTGAGGAAGGGTTGCTGG AGCGCCATTCCAATGGCTCTCAGAGCCAGCACTCAAGACTC

		ACCCTTCCGAGATCCCTGTGGAACGCCGGGACCTCTGTCAC ATGTACTCTAAATCATCCTAGCCTGCCCCACAGCGTCTGAT GGCCCTTAGAGAGCCAGCCGCCAGGCACCAGTTAAGCTTA GCCTGAATCTGCTCGCCAGTAGTGATCCCCCAGAGGCCGCC AGCTGGCTCTTATGCGAAGTGTCCGGCTTTAGCCCGCCCAA CATCTTGCTCATGTGGCTGGAGGACCAGCGAGAAGTGAACA CCAGCGGCTTCGCTCCAGCCCGGCCCCACCCAGCCGGG TTCTACCACATTCTGGGCCTGGAGTGTCTTAAGGGTCCCAG CACCACCTAGCCCCCAGCCAGCCACATACACCTGTGTTGTG TCCCATGAAGATAGCAGGACCCTGCTAAATGCTTCTAGGAG TCTGGAGGTTTCCTACGTGACTGACCATT
10	GS hinge/linker (aa)	GGGGSGGGGS
11	GS hinge/linker (na)	GGTGGCGGAGGTTCTGGAGGTGGAGGTTCC
12	CD8TM (aa)	IYIWAPLAGTCGVLLSLVITLYC
13	CD8 TM (na)	ATCTACATCTGGGCGCCCTTGGCCGGGACTTGTGGGGTCCT TCTCCTGTCACTGGTTATCACCTTTACTGC
34	CD8 TM (na)	ATCTACATTTGGGCCCCTCTGGCTGGTACTTGCGGGTCCT GCTGCTTTCACCTCGTGATCACTCTTTACTGT
14	4-1BB intracellular domain (aa)	KRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCEL
15	4-1BB intracellular domain (na)	AAACGGGGCAGAAAGAACTCCTGTATATATTCAAACAACCA TTTATGAGACCAGTACAACTACTCAAGAGGAAGATGGCTGT AGCTGCCGATTTCCAGAAGAAGAAGAGGAGGATGTGAACT G
118	4-1BB intracellular domain (na)	AAGCGCGGTCGGAAGAAGCTGCTGTACATCTTTAAGCAACC CTTCATGAGGCCTGTGCAGACTACTCAAGAGGAGGACGGCT GTTTCATGCCGTTCCAGAGGAGGAGGAAGGCGGCTGCGA ACTG
16	CD27 (aa)	QRRKYRSNKGESPVPAEPCRYSCPREEEGSTIPIQEDYRKPE PACSP
17	CD27 (na)	AGGAGTAAGAGGAGCAGGCTCCTGCACAGTGACTACATGAA CATGACTCCCCGCCGCCCGGGCCCACCCGCAAGCATTAC CAGCCCTATGCCCCACCACGCGACTTCGCAGCCTATCGCTC C
18	CD3-zeta (aa)	RVKFSRSADAPAYKQGQNLQYLNELNLGRREEYDVLDRRRGRD PEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRG KGHDGLYQGLSTATKDTYDALHMQALPPR
19	CD3-zeta (na)	AGAGTGAAGTTCAGCAGGAGCGCAGACGCCCCCGCGTACA AGCAGGGCCAGAACCAGCTCTATAACGAGCTCAATCTAGGA CGAAGAGAGGAGTACGATGTTTTGGACAAGAGACGTGGCCG GGACCCTGAGATGGGGGGAAAGCCGAGAAGGAAGAACCCT CAGGAAGGCCTGTACAATGAAGTGCAGAAAGATAAGATGGC GGAGGCCTACAGTGAGATTGGGATGAAAGGCGAGCGCCGG AGGGGCAAGGGGCACGATGGCCTTTACCAGGGTCTCAGTA CAGCCACCAAGGACACCTACGACGCCCTTCACATGCAGGCC CTGCCCCCTCGC
119	CD3-zeta (na)	CGCGTGAAATTAGCCGCAGCGCAGATGCTCCAGCCTACAA GCAGGGGCAGAACAGCTCTACAACGAACTCAATCTTGGTC GGAGAGAGGAGTACGACGTGCTGGACAAGCGGAGAGGACG GGACCCAGAAATGGGCGGGAAGCCGCGCAGAAAGAATCCC

		CAAGAGGGCCTGTACAACGAGCTCCAAAAGGATAAGATGGC AGAAGCCTATAGCGAGATTGGTATGAAAGGGGAACGCAGAA GAGGCAAAGGCCACGACGGACTGTACCAGGGACTCAGCAC CGCCACCAAGGACACCTATGACGCTCTTCACATGCAGGCC TGCCGCCTCGG
20	CD3-zeta (aa)	RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRD PEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRG KGHDGLYQGLSTATKDTYDALHMQALPPR
21	CD3-zeta (na)	AGAGTGAAGTTCAGCAGGAGCGCAGACGCCCCCGCGTACC AGCAGGGCCAGAACCAGCTCTATAACGAGCTCAATCTAGGA CGAAGAGAGGAGTACGATGTTTTGGACAAGAGACGTGGCCG GGACCCTGAGATGGGGGGAAAGCCGAGAAGGAAGAACCCT CAGGAAGGCCTGTACAATGAAGTGCAGAAAGATAAGATGGC GGAGGCCTACAGTGAGATTGGGATGAAAGGCGAGCGCCGG AGGGGCAAGGGGCACGATGGCCTTTACCAGGGTCTCAGTA CAGCCACCAAGGACACCTACGACGCCCTTCACATGCAGGCC CTGCCCCCTCGC
22	linker	GGGGS
23	linker	GGTGGCGGAGGTTCTGGAGGTGGAGGTTCC
24	PD-1 extracellular domain (aa)	Pgwldspdrpwnpptfspallvtegdnatftcsfntsesfvlnwyrmspsnqtdklaa fpedrsqpgqdcfrvrlpngrdfhmsvrrrnsdgtlclgaislapkaqikeslraelrvt erraevpahpspsprpagqfqlv
25	PD-1 extracellular domain (na)	Cccgatggttctgactctccgatcgcccggtggaatccccaaccttctaccggca ctcttggtgtgactgaggcgataatgcgacctcacgtgctcgttccaacacctccga atcattcgtgctgaactggtaccgcatgagcccgtaaccagaccgacaagctcgccg cgttccggaagatcggtcgcaaccgggacaggattgtcggttccgctgactcaactgc cgaatggcagagactccacatgagcgtggtccgctaggcgaaacgactccggga cctacctgtcggagccatctcgtggtcgccctaaggcccaaatcaaagagagcttgagg gccgaactgagagtaccgagcgcagagctgaggtgccaactgcacatccatccccat cgccctggcctgcgggcgagtttcagaccctggc
26	PD-1 CAR (aa) with signal	Malpvtallplallhaarppgwldspdrpwnpptfspallvtegdnatftcsfntsesfv lnwyrmspsnqtdklaafpedrsqpgqdcfrvrlpngrdfhmsvrrrnsdgtlclg aislapkaqikeslraelrvterraevptahpspsprpagqfqlvtttpprptpaptiasq plslrpeacrpaaggavhtrglfdiaywapltagtclgllslvitlyckrgrklllyfkpfm rpvqttqeedgcscrfeeeeeggcclrvkfsrsadapaykqgnqlynelnlgrreeydv dkrrgrdpemggkprknpqeglynelqkdkmaeayseigmkgerrrgkghdglyqgl statkdydalhmqalppr
27	PD-1 CAR (na)	Atggccctccctgtcactgacctctctccctcgactcctgctccacgcccgtagacc accggatggttctgactctccgatcgcccggtggaatccccaaccttctaccggca ctcttggtgtgactgaggcgataatgcgacctcacgtgctcgttccaacacctccga atcattcgtgctgaactggtaccgcatgagcccgtaaccagaccgacaagctcgccg cgttccggaagatcggtcgcaaccgggacaggattgtcggttccgctgactcaactgc cgaatggcagagactccacatgagcgtggtccgctaggcgaaacgactccggga cctacctgtcggagccatctcgtggtcgccctaaggcccaaatcaaagagagcttgagg gccgaactgagagtaccgagcgcagagctgaggtgccaactgcacatccatccccat cgccctggcctgcgggcgagtttcagaccctggcaccactccggcgccgccc accgactccggcccaactatcgagaccagccctgtcgtgaggccggaagcatgc cgccctgcccggagggtgctgtcataccggggattggacttcgcatgcacatctac atttggtcctctcgccggaactgtggtgctccttctgctccttggtcatccctgtactg caagcggggtcggaaaaagcttctgtacatttcaagcagccctcatgaggcccggtgca aaccaccaggaggaggacggtgctcctgcccgttcccgaagaggaagaaggag gttgcgagctgcgctgaagtctccggagcgcgagccccgcctataagcaggg ccagaaccagctgtacaacgaactgaacctgggacggcggaagagtgtgct ggacaagcggcgccgggaccccgaaatggcggaagcctagaagaagaa ccctcaggaaggcctgtataacgagctgcagaaggacaagatggccgaggcctactc

		cgaaattgggatgaagggagagcggcgaggggaaaggggcacgacggcctgtac caaggactgtccaccgccaccaaggacacatacgatgccctgcacatgcaggcccttc cccctcgc
28	linker	(Gly-Gly-Gly-Ser) _n , where n = 1-10
29	linker	(Gly ₄ Ser) ₄
30	linker	(Gly ₄ Ser) ₃
31	linker	(Gly ₃ Ser)
32	polyA	[a] ₅₀₋₅₀₀₀
39	PD1 CAR (aa)	<u>Pgwildspdrpwnpptfspallvtegdnatftcsfsntsesfvlnwyrmspsnqtdklaa</u> <u>fpedrsqpggdcrfrvtqlpngrdfhmsvvrarrndsgtylcaislakpakikeslraelrvt</u> <u>erraeavptahpspsprpagqfqlvtttpaprpptpaptiasqplslrpeacrpaaggavht</u> <u>rgldfacdiyiwaplagtcgvllslvitlyckgrkkilyifkqpfmrpvqttqeedgcscrfee</u> <u>eeggcelrvkfsrsadapaykqggnqlynelnlgrreeydvldkrrgrdpemggkprkn</u> <u>pqeglynelqkdkmaeayseigmkgerrrgkghdglyqglstatkdtydalhmqalppr</u>
120	ICOS intracellular domain (aa)	TKKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTL
1111	ICOS intracellular domain (na)	ACAAAAAAGAAGTATTCATCCAGTGTGCACGACCCTAACGGT GAATACATGTTTCATGAGAGCAGTGAACACAGCCAAAAAATCC AGACTCACAGATGTGACCCTA
972	ICOS TM domain (aa)	TTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFA CDFWLPIGCAAFVVVCILGCILICWL
973	ICOS TM domain (na)	ACCACGACGCCAGCGCCGCGACCACCAACACCGGCGCCCA CCATCGCGTCGCAGCCCCTGTCCCTGCGCCAGAGGCGTG CCGGCCAGCGCGGGGGGCGCAGTGCACACGAGGGGGCT GGACTTCGCCTGTGATTTCTGGTTACCCATAGGATGTGCAG CCTTTGTTGTAGTCTGCATTTTGGGATGCATACTTATTTGTTG GCTT
124	CD28 intracellular domain (aa)	RSKRSRLLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRS
1113	CD28 intracellular domain (na)	AGGAGTAAGAGGAGCAGGCTCCTGCACAGTGACTACATGAA CATGACTCCCCGCCGCCCGGGCCACCCGCAAGCATTAC CAGCCCTATGCCCCACCACGCGACTTCGCAGCCTATCGCTC C

In specific aspects, a CAR construct comprises a scFv domain, wherein the scFv may be preceded by an optional leader sequence such as provided in SEQ ID NO: 2, and followed by an optional hinge sequence such as provided in SEQ ID NO:4 or SEQ ID NO:6 or SEQ ID NO:8 or SEQ ID NO:10, a transmembrane region such as provided in SEQ ID NO:12, an intracellular signalling domain that includes any one of SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO: 120, or SEQ ID NO: 124, and a CD3 zeta sequence that includes SEQ ID NO: 18 or SEQ ID NO: 20, e.g., wherein the domains are contiguous with and in the same reading frame to form a single fusion protein.

In one aspect, an exemplary CAR constructs comprise an optional leader sequence (e.g., a leader sequence described herein), an extracellular antigen binding domain (e.g., an antigen binding domain described herein), a hinge (e.g., a hinge region described herein), a transmembrane domain (e.g., a transmembrane domain described herein), and an intracellular stimulatory domain (e.g., an intracellular stimulatory domain described herein). In one aspect, an exemplary CAR construct comprises an

optional leader sequence (e.g., a leader sequence described herein), an extracellular antigen binding domain (e.g., an antigen binding domain described herein), a hinge (e.g., a hinge region described herein), a transmembrane domain (e.g., a transmembrane domain described herein), an intracellular costimulatory signaling domain (e.g., a costimulatory signaling domain described herein) and/or an intracellular primary signaling domain (e.g., a primary signaling domain described herein).

An exemplary leader sequence is provided as SEQ ID NO: 2. An exemplary hinge/spacer sequence is provided as SEQ ID NO: 4 or SEQ ID NO: 6 or SEQ ID NO: 8 or SEQ ID NO: 10. An exemplary transmembrane domain sequence is provided as SEQ ID NO: 12. An exemplary sequence of the intracellular signaling domain of the 4-1BB protein is provided as SEQ ID NO: 14. An exemplary sequence of the intracellular signaling domain of CD27 is provided as SEQ ID NO: 16. An exemplary sequence of the intracellular signaling domain of ICOS is provided as SEQ ID NO: 120. An exemplary sequence of the intracellular signaling domain of CD28 is provided as SEQ ID NO: 124. An exemplary CD3zeta domain sequence is provided as SEQ ID NO: 18 or SEQ ID NO: 20.

The nucleic acid sequences coding for the desired molecules can be obtained using recombinant methods known in the art, such as, for example by screening libraries from cells expressing the nucleic acid molecule, by deriving the nucleic acid molecule from a vector known to include the same, or by isolating directly from cells and tissues containing the same, using standard techniques. Alternatively, the nucleic acid of interest can be produced synthetically, rather than cloned.

Antigen Binding Domain

In one aspect, a chimeric antigen receptor (CAR) comprises a target-specific binding element otherwise referred to as an antigen binding domain. The choice of moiety depends upon the type and number of ligands that define the surface of a target cell. For example, the antigen binding domain may be chosen or engineered to recognize a ligand that acts as a cell surface marker on target cells associated with a particular disease state, e.g., a tumor antigen associated with a particular cancer (e.g., an antigen binding domain that binds to a tumor antigen). In other embodiments, the antigen binding domain is chosen or engineered to recognize normal B cells, or a subpopulation of B cells, for depleting normal B cells or a target B cell population (e.g., an antigen binding domain that binds to a B cell antigen).

The antigen binding domain can be any domain that binds to the antigen including but not limited to a monoclonal antibody, a polyclonal antibody, a recombinant antibody, a bispecific antibody, a conjugated antibody, a human antibody, a humanized antibody, and a functional fragment thereof, including but not limited to a single-domain antibody such as a heavy chain variable domain (VH), a light chain variable domain (VL) and a variable domain (VHH) of camelid derived nanobody, and to an alternative scaffold known in the art to function as antigen binding domain, such as a recombinant fibronectin domain, a T cell receptor (TCR), a recombinant TCR with enhanced affinity, or a fragment thereof, e.g., single chain TCR, and the like. In some instances, it is beneficial for the antigen binding domain to be derived from the same

species in which the CAR will ultimately be used in. For example, for use in humans, it may be beneficial for the antigen binding domain of the CAR to comprise human or humanized residues for the antigen binding domain of an antibody or antibody fragment.

In some embodiments, the antigen binding domain of the encoded CAR molecule comprises an antibody, an antibody fragment, an scFv, a Fv, a Fab, a (Fab')₂, a single domain antibody (SDAB), a VH or VL domain, a camelid VHH domain or a bi-functional (e.g. bi-specific) hybrid antibody (e.g., Lanzavecchia et al., Eur. J. Immunol. 17, 105 (1987)).

In some embodiments, the antigen binding domain of the encoded CAR molecule comprises an scFv. In some instances, scFvs can be prepared according to method known in the art (see, for example, Bird et al., (1988) Science 242:423-426 and Huston et al., (1988) Proc. Natl. Acad. Sci. USA 85:5879-5883). ScFv molecules can be produced by linking VH and VL regions together using flexible polypeptide linkers.

In one aspect, the antigen binding domain of the CAR is a scFv antibody fragment that is humanized compared to the murine sequence of the scFv from which it is derived.

In one aspect, the antigen binding domain of a CAR of the invention (e.g., a scFv) is encoded by a nucleic acid molecule whose sequence has been codon optimized for expression in a mammalian cell. In one aspect, entire CAR construct of the invention is encoded by a nucleic acid molecule whose entire sequence has been codon optimized for expression in a mammalian cell. Codon optimization refers to the discovery that the frequency of occurrence of synonymous codons (i.e., codons that code for the same amino acid) in coding DNA is biased in different species. Such codon degeneracy allows an identical polypeptide to be encoded by a variety of nucleotide sequences. A variety of codon optimization methods is known in the art, and include, e.g., methods disclosed in at least US Patent Numbers 5,786,464 and 6,114,148. In one embodiment, the CAR comprises an antigen binding domain that binds to a B cell. Cell surface markers selectively found on B cells may act as an antigen that binds to the antigen binding domain of the CAR. The anti-B cell antigen binding domain can include any domain that binds to the B cell and may include, but is not limited to, a monoclonal antibody, a polyclonal antibody, a synthetic antibody, a human antibody, a humanized antibody, a non-human antibody, and any fragment thereof. Thus, in one embodiment, the antigen binding domain portion comprises a mammalian antibody or a fragment thereof, such as a single chain variable fragment (scFv). The antigen binding domain may bind one or more antigens, such as, but not limited to, any surface marker selectively found on a B cell, such as a pro-B cell, pre-B cell, immature B cell, mature B cell, memory B cell, and plasma cell. In one embodiment, the antigen binding domain binds at least one antigen, such as CD19, BCMA, and any combination thereof. In another embodiment, the antigen binding domain binds at least one antigen, such as CD20, CD21, CD27, CD38, CD138, , and any combination thereof. In some instances, it is beneficial for the antigen binding domain to be derived from the same species in which the CAR will ultimately be used in. For example, for use in humans, it may be beneficial for the antigen binding domain

of the CAR to comprise a human antibody, humanized antibody as described elsewhere herein, or a fragment thereof.

Tumor antigens

- 5 In some embodiments, an antigen binding domain of the CAR specifically targets a tumor antigen. There are two classes of tumor antigens (tumour antigens, TA) that can be targeted by CARs: (1) a tumor antigen that is expressed on the surface of cancer cells; and (2) a tumor antigen that itself is intracellular, however, a fragment of such antigen (peptide) is presented on the surface of the cancer cells by MHC (major histocompatibility complex).
- 10 In one embodiment, the tumor antigen is expressed on both normal cells and cancer cells, but is expressed at lower levels on normal cells. In one embodiment, the method further comprises selecting a CAR that binds a tumor antigen with an affinity that allows the cell engineered to express the CAR to bind and kill the cancer cells expressing a tumor antigen but less than 30%, 25%, 20%, 15%, 10%, 5% or less of the normal cells expressing a tumor antigen are killed, e.g., as determined by an assay described
- 15 herein. For example, a killing assay such as flow cytometry based on Cr51 CTL can be used. In one embodiment, the selected CAR has an antigen binding domain that has a binding affinity K_D of 10^{-4} M to 10^{-8} M, e.g., 10^{-5} M to 10^{-7} M, e.g., 10^{-6} M or 10^{-7} M, for the target antigen. In one embodiment, the selected antigen binding domain has a binding affinity that is at least five-fold, 10-fold, 20-fold, 30-fold, 50-fold, 100-fold or 1,000-fold less than a reference antibody, e.g., an antibody described herein.
- 20 Accordingly, a cell can be engineered to express a CAR comprising an antigen binding domain that can target, e.g., bind to, any one of the exemplary tumor antigens (tumour antigens): CD123, CD30, CD171, CS-1, CLL-1 (CLECL1), CD33, EGFRvIII, GD2, GD3, Tn Ag, sTn Ag, Tn-O-Glycopeptides, Stn-O-Glycopeptides, PSMA, FLT3, FAP, TAG72, CD44v6, CEA, EPCAM, B7H3, KIT, IL-13Ra2, Mesothelin, IL-11Ra, PSCA, VEGFR2, LewisY, PDGFR-beta, PRSS21, SSEA-4, Folate receptor alpha, ERBB2
- 25 (Her2/neu), MUC1, EGFR, NCAM, Prostase, PAP, ELF2M, Ephrin B2, IGF-I receptor, CAIX, LMP2, gp100, bcr-abl, tyrosinase, EphA2, Fucosyl GM1, sLe, GM3, TGS5, HMWMAA, o-acetyl-GD2, Folate receptor beta, TEM1/CD248, TEM7R, CLDN6, TSHR, GPRC5D, CXORF61, CD97, CD179a, ALK, Plsialic acid, PLAC1, GloboH, NY-BR-1, UPK2, HAVCR1, ADRB3, PANX3, GPR20, LY6K, OR51E2, TARP, WT1, NY-ESO-1, LAGE-1a, legumain, HPV E6,E7, MAGE-A1, MAGE A1, ETV6-AML, sperm
- 30 protein 17, XAGE1, Tie 2, MAD-CT-1, MAD-CT-2, Fos-related antigen 1, p53, p53 mutant, prostein, survivin and telomerase, PCTA-1/Galectin 8, MelanA/MART1, Ras mutant, hTERT, sarcoma translocation breakpoints, ML-IAP, ERG (TMPRSS2 ETS fusion gene), NA17, PAX3, Androgen receptor, Cyclin B1, MYCN, RhoC, TRP-2, CYP1B1, BORIS, SART3, PAX5, OY-TES1, LCK, AKAP-4, SSX2, RAGE-1, human telomerase reverse transcriptase, RU1, RU2, intestinal carboxyl esterase, mut hsp70-2, LAIR1,
- 35 FCAR, LILRA2, CD300LF, CLEC12A, BST2, EMR2, LY75, GPC3, FCRL5, IGLL1, CD10, CD19, CD20,

CD21, CD22, CD23, CD24, CD25, CD37, CD38, CD53, CD72, CD73, CD74, CD75, CD77, CD79a, CD79b, CD80, CD81, CD82, CD83, CD84, CD85, ROR1, BCMA, CD86, and CD179b. Other B cell antigens that can be targeted by a CAR described herein include: CD1a, CD1b, CD1c, CD1d, CD2, CD5, CD6, CD9, CD11a, CD11b, CD11c, CD17, CD18, CD26, CD27, CD29, CD30, CD31, CD32a, CD32b, CD35, CD38, CD39, CD40, CD44, CD45, CD45RA, CD45RB, CD45RC, CD45RO, CD46, CD47, CD48, CD49b, CD49c, CD49d, CD50, CD52, CD54, CD55, CD58, CD60a, CD62L, CD63, CD63, CD68 CD69, CD70, CD85E, CD85I, CD85J, CD92, CD95, CD97, CD98, CD99, CD100, CD102, CD108, CD119, CD120a, CD120b, CD121b, CD122, CD124, CD125, CD126, CD130, CD132, CD137, CD138, CD139, CD147, CD148, CD150, CD152, CD162, CD164, CD166, CD167a, CD170, CD175, CD175s, CD180, CD184, CD185, CD192, CD196, CD197, CD200, CD205, CD210a, CDw210b, CD212, CD213a1, CD213a2, CD215, CD217, CD218a, CD218b, CD220, CD221, CD224, CD225, CD226, CD227, CD229, CD230, CD232, CD252, CD253, CD257, CD258, CD261, CD262, CD263, CD264, CD267, CD268, CD269, CD270, CD272, CD274, CD275, CD277, CD279, CD283, CD289, CD290, CD295, CD298, CD300a, CD300c, CD305, CD306, CD307a, CD307b, CD307c, CD307d, CD307e, CD314, CD315, CD316, CD317, CD319, CD321, CD327, CD328, CD329, CD338, CD351, CD352, CD353, CD354, CD355, CD357, CD358, CD360, CD361, CD362, CD363 and peptides of these antigens presented on MHC.

In some embodiments, the antigen binding domain of a CAR targets a tumor antigen that is associated with a solid tumor, e.g., expressed by a solid tumor cell, referred to herein as a solid tumor associated antigen, e.g., an antigen associated with mesothelioma (e.g., malignant pleural mesothelioma), lung cancer (e.g., non-small cell lung cancer, small cell lung cancer, squamous cell lung cancer, or large cell lung cancer), pancreatic cancer (e.g., pancreatic ductal adenocarcinoma), esophageal adenocarcinoma, ovarian cancer, breast cancer, colorectal cancer and bladder cancer or any combination thereof. In one embodiment, the disease is pancreatic cancer, e.g., metastatic pancreatic ductal adenocarcinoma (PDA), e.g., in a subject who has progressed on at least one prior standard therapy. In one embodiment, the disease is mesothelioma (e.g., malignant pleural mesothelioma), e.g., in a subject who has progressed on at least one prior standard therapy. In one embodiment, the disease is ovarian cancer, e.g., serous epithelial ovarian cancer, e.g., in a subject who has progressed after at least one prior regimen of standard therapy.

Examples of tumor associated antigens (e.g., solid tumor antigens) include, without limitation: EGFRvIII, mesothelin, GD2, Tn antigen, sTn antigen, Tn-O-Glycopeptides, sTn-O-Glycopeptides, PSMA, CD97, TAG72, CD44v6, CEA, EPCAM, KIT, IL-13Ra2, leguman, GD3, CD171, IL-11Ra, PSCA, MAD-CT-1, MAD-CT-2, VEGFR2, LewisY, CD24, PDGFR-beta, SSEA-4, folate receptor alpha, ERBBs (e.g., ERBB2), Her2/neu, MUC1, EGFR, NCAM, Ephrin B2, CAIX, LMP2, sLe, HMWMAA, o-acetyl-GD2, folate receptor beta, TEM1/CD248, TEM7R, FAP, Legumain, HPV E6 or E7, ML-IAP, CLDN6, TSHR, GPRC5D, ALK, Polysialic acid, Fos-related antigen, neutrophil elastase, TRP-2, CYP1B1, sperm protein 17, beta

human chorionic gonadotropin, AFP, thyroglobulin, PLAC1, globoH, RAGE1, MN-CA IX, human telomerase reverse transcriptase, intestinal carboxyl esterase, mut hsp 70-2, NA-17, NY-BR-1, UPK2, HAVCR1, ADRB3, PANX3, NY-ESO-1, GPR20, Ly6k, OR51E2, TARP, GFR α 4, and a peptide of any of these antigens presented on MHC.

- 5 In an embodiment, the antigen binding domain of a CAR binds to human mesothelin. In an embodiment, the antigen binding domain is a murine scFv domain that binds to human mesothelin, e.g., SS1 as shown in Table 3. In an embodiment, the antigen binding domain is a humanized antibody or antibody fragment, e.g., scFv domain, derived from the murine SS1 scFv. In an embodiment, the antigen binding domain is a human antibody or antibody fragment that binds to human mesothelin. Exemplary human scFv
- 10 domains (and their sequences) and the murine SS1 scFv that bind to mesothelin are provided in Table 3. CDR sequences are underlined. The scFv domain sequences provided in Table 3 include a light chain variable region (VL) and a heavy chain variable region (VH). The VL and VH are attached by a linker comprising the sequence GGGGSGGGGSGGGGS (SEQ ID NO: 30) (e.g., as shown in SS1 scFv domains) or GGGGSGGGGSGGGGSGGGGS (SEQ ID NO: 29) (e.g., as shown in M1, M2, M3, M4, M5,
- 15 M6, M7, M8, M9, M10, M11, M12, M13, M14, M15, M16, M17, M18, M19, M20, M21, M22, M23, or M24 scFv domains). The scFv domains listed in Table 3 are in the following orientation: VL-linker-VH.

Table 3. Antigen binding domains that bind to mesothelin

Tumor antigen	Name	Amino acid sequence	SEQ ID NO:
mesothelin	M5 (human)	QVQLVQSGAEVEKPGASVKVSCKASGYTFTDYYMHVVRQAPGQ GLEWMGWINPNSGGTNYAQKFQGRVTMTRDTSISTAYMELSRLR SDDTAVYYCASGWDFDYWGQGLTVTVSSGGGGSGGGGSGGGG SGGGGSDIVMTQSPSSLSASVGDRVTITCRASQSIRYYLSWYQQK PGKAPKLLIYTASILQNGVPSRFSGSGSGTDFTLTISLQPEDFATY YCLQTYTTPDFGPGTKVEIK	201
mesothelin	M11 (human)	QVQLQQSGAEVKKPGASVKVSCKASGYTFTGYMHVVRQAPGQ GLEWMGWINPNSGGTNYAQNFQGRVTMTRDTSISTAYMELRRLR SDDTAVYYCASGWDFDYWGQGLTVTVSSGGGGSGGGGSGGGG SGGGGSDIRMTQSPSSLSASVGDRVTITCRASQSIRYYLSWYQQK PGKAPKLLIYTASILQNGVPSRFSGSGSGTDFTLTISLQPEDFATY YCLQTYTTPDFGPGTKVEIK	202
mesothelin	ss1 (murine)	QVQLQQSGPELEKPGASVKISCKASGYSFTGYTMNWVKQSHGKS LEWIGLITPYNGASSYNQKFRGKATLTVDKSSSTAYMDLLSLTSED SAVYFCARGGYDGRGFDYWGGQTTVTVSSGGGGSGGGGSGGGG GSDIELTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGTS PKRWIYDTSKLASGVPGRFSGSGSGNSYSLTISSVEAEDDATYYC QQWSGYPLTFGAGTKLEI	203
mesothelin	M1 (human)	QVQLQQSGAEVKKPGASVKVSCKASGYTFTGYMHVVRQAPGQ GLEWMGRINPNSGGTNYAQKFQGRVTMTRDTSISTAYMELSRLR SEDTAVYYCARGRYYGMDVWGQGMVTVSSGGGGSGGGGSGG	204

		GGSGGGGSEIVLTQSPATLSLSPGERATISCRASQSVSSNFAWYQ QRPQGAPRLLIYDASNRAIGIPPRFSGSGSGTDFTLTISSELEPEDF AAYYCHQRSNWLYTFGQGTKVDIK	
mesothelin	M2 (human)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHVVRQAPGQ GLEWMGWINPNSGGTNYAQKFQGRVTMTRDTSISTAYMELSRLR SDDTAVYYCARDLRRTVVTPRAYYGMDVWGQGTITVTVSSGGGG SGGGGSGGGGSGGGGSDIQLTQSPSTLSASVGDRTITCQASQD ISNSLNWYQQKAGKAPKLLIYDASTLETGVPSPRFSGSGSGTDFTSFT ISSLPEDIATYYCQQHDNLPLTFGQGTKVEIK	205
mesothelin	M3 (human)	QVQLVQSGAEVKKPGAPVKVSCKASGYTFTGYYMHVVRQAPGQ GLEWMGWINPNSGGTNYAQKFQGRVTMTRDTSISTAYMELSRLR SDDTAVYYCARGEWGDSYYDYWGQGTITVTVSSGGGGSGGGG SGGGGSGGGGSDIVLTQTPSSLSASVGDRTITCRASQSINTYLN WYQHKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISLQP EDFATYYCQQSFPLTFGGGKLEIK	206
mesothelin	M4 (human)	QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYWMHVVRQVPGK GLVWVSRINTDGGSTTTTADSVGRFTISRDNANKNTLYLQMNSLRD DDTAVYYCVGGHWAIVWGQGTITVTVSSGGGGSGGGGSGGGGS GGGGSDIQTQSPSTLSASVGDRTITCRASQSIDRLAWYQQKP GKAPKLLIYKASSLESGVPSRFSGSGSGTEFTLTISLQPDFAVY YCQQYGHLPMTFGQGTKVEIK	207
mesothelin	M6 (human)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMHVVRQAPGQ GLEWMGIINPSSGGSTSYAQKFQGRVTMTRDTSTSTVYMELSSLR EDTAVYYCARYRLIAVAGDYGGYGMVWGQGTMTVTVSSGGGG GGGGSGGGGSGGGGSDIQTQSPSSVASVGDRTITCRASQGV GRWLAWYQQKPGTAPKLLIYAASLTQSGVPSRFSGSGSGTDFTLT INNLPEDFATYYCQQANSFPLTFGGGTRLEIK	208
mesothelin	M7 (human)	QVQLVQSGGGVQVQGRSLRLSCAASGFTFSSYAMHVVRQAPGK GLEWVAVISYDGSNKYYADSVKGRFTISRDNANKNTLYLQMNSLRA EDTAVYYCARWKVSSSSPAFDYWGQGTITVTVSSGGGGSGGGGS GGGGSGGGGSEIVLTQSPATLSLSPGERAILSCRASQSVYTKYL WYQQKPGQAPRLLIYDASTRATGIPDRFSGSGSGTDFTLTINRLEP EDFAVYYCQHYGGSPLITFGQGTREIK	209
mesothelin	M8 (human)	QVQLQQSGAEVKKPGASVKVSCKTSGYPFTGYSLHWVRQAPGQ GLEWMGWINPNSGGTNYAQKFQGRVTMTRDTSISTAYMELSRLR SDDTAVYYCARDHYGGNSLFYWGQGTITVTVSSGGGGSGGGGS GGGGSGGGGSDIQLTQSPSSISASVGDVTSITCRASQDSGTWLA WYQQKPGKAPNLLMYDASTLEDGVPSPRFSGSASGTEFTLTVNRL QPEDSATYYCQQYNSYPLTFGGGKVDIK	210
mesothelin	M9 (human)	QVQLVQSGAEVKKPGASVEVSCKASGYTFTSYMHVVRQAPGQ GLEWMGIINPSSGGSTGYAQKFQGRVTMTRDTSTSTVHMESSLR SEDTAVYYCARGGYSSSSDAFDIWGQGTMTVTVSSGGGGSGGGG SGGGGSGGGGSDIQTQSPSSLSASVGDRTITCRASQDISSALA WYQQKPGTTPKLLIYDASSLESGVPSRFSGSGSGTDFTLTISLQP EDFATYYCQQFSSYPLTFGGGTRLEIK	211
mesothelin	M10 (human)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQG LEWMGWISAYNGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLRS DDTAVYYCARVAGGIYGGYGMVWGQGTITVTVSSGGGGSGGGG	212

		SGGGGSGGGGSDIVMTQTPDSLAVSLGERATISCKSSHSVLYNR NNKNYLAWYQQKPGQPPKLLFYWASTRKSGVPDRFSGSGSGTD FTLTSSSLQPEDFATYFCQQTQTFPLTFGQGTRLEIN	
mesothelin	M12 (human)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQ GLEWMGRINPNSGGTNYAQKFQGRVTMTTDTSTSTAYMELRSLR SDDTAVYYCARTTTSYAFDIWGQGTMTVTVSSGGGGSGGGGSGG GGSGGGGSDIQLTQSPSTLSASVGDRVITICRASQSISTWLAWYQ QKPGKAPNLLIYKASTLESGVPSRFSGSGSGTEFTLTSSSLQPDF ATYYCQQYNTYSPYTFGQGTKLEIK	213
mesothelin	M13 (human)	QVQLVQSGGGLVKPGGSLRLSCEASGFIFSDYYMGWIRQAPGKG LEWVSYIGRSGSSMYADSVKGRFTFSRDNAKNSLYLQMNSLRA EDTAVYYCAASPVVAATEDFQHWGQGTMTVTVSSGGGGSGGGGSG GGGGSGGGGSDIVMTQTPATLSLSPGERATLSCRASQSVTSNYL AWYQQKPGQAPRLLLFGASTRATGIPDRFSGSGSGTDFTLTINRL EPEDFAMYYCQQYGSAPVTFGQGTKLEIK	214
mesothelin	M14 (human)	QVQLVQSGAEVRAPGASVKISCKASGFTFRGYYIHWVRQAPGQG LEWMGIINPSGGSRAYAQKFQGRVTMTTRDTSTSTVYMELSSLRSD DTAMYYCARTASCGGDCYYLDYWGGGTMTVTVSSGGGGSGGGGSG GGGGSGGGGSDIQTQSPPTLSASVGDRVITICRASENVNIWL AWYQQKPGKAPKLLIYKSSSLASGVPSRFSGSGSGAEFTLTSSSLQ PDFATYYCQQYQSYPLTFGGGTKVDIK	215
mesothelin	M15 (human)	QVQLVQSGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGK GLEWVSGISWNSSGSIYADSVKGRFTISRDNKNSLYLQMNSLRA EDTAVYYCAKDGSSSWWGYFDYWGGGTMTVTVSSGGGGSGGGG SGGGGGSSSELTQDPAVSVALGQTVRITCQGDALRSYYASWYQ QKPGQAPMLVIYGKNNRPSGIPDRFSGSDSGDTASLTITGAQAED EADYYCNSRDSSGYPVFGTGKVTVL	216
mesothelin	M16 (human)	EVQLVESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGK GLEWVSGISWNSSGSTGYADSVKGRFTISRDNKNSLYLQMNSLRA AEDTALYYCAKDSSSWYGGGSAFDIWGQGTMTVTVSSGGGGSGG GGSGGGGSSSELTQEPAVSVALGQTVRITCQGDLSRYYASWYQ QKPGQAPVLVIFGRSRPSGIPDRFSGSSSGNTASLIITGAQAED ADYYCNSRDNTANHYVFGTGKLTVL	217
mesothelin	M17 (human)	EVQLVESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGK GLEWVSGISWNSSGSTGYADSVKGRFTISRDNKNSLYLQMNSLRA AEDTALYYCAKDSSSWYGGGSAFDIWGQGTMTVTVSSGGGGSGG GGSGGGGSSSELTQDPAVSVALGQTVRITCQGDLSRYYASWYQ QKPGQAPVLVIYGKNNRPSGIPDRFSGSSSGNTASLTITGAQAED EADYYCNSRGSSGNHYVFGTGKVTVL	218
mesothelin	M18 (human)	QVQLVQSGGGLVQPGGSLRLSCAASGFTFSSYWMHWVRQAPGK GLVWVSRINSDGSSTSYADSVKGRFTISRDNKNTLYLQMNSLRA EDTAVYYCVRTGWVGSYYYYMDVWGKTTVTVSSGGGGSGGGG SGGGGGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVSSN YLAWYQQKPGQPPRLIYDVSTRATGIPARFSGGGSGTDFTLTSS LEPEDFAVYYCQQRSNWPPWTFGQGTKVEIK	219
mesothelin	M19 (human)	QVQLVQSGGGVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGK GLEWVAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQMNSLRA EDTAVYYCAKGYSRYYYGMDVWGQGTMTVTVSSGGGGSGGGG	220

		SGGGGSGGGGSEIVMTQSPATLSLSPGERAILSCRASQSVYTKYL GWYQQKPGQAPRLLIYDASTRATGIPDRFSGSGSGTDFTLTINRLE PEDFAVYYCQHYGGSPLITFGQGTKVDIK	
mesothelin	M20 (human)	QVQLVQSGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGK GLEWVSAISGSGGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRA EDTAVYYCAKREAAAGHDWYFDLWGRGTLVTVSSGGGGSGGGG SGGGGSGGGGSDIRVTQSPSSLSASVGDRVITICRASQSSSYLN WYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQ PEDFATYYCQQSYSIPLTFGGGKVEIK	221
mesothelin	M21 (human)	QVQLVQSWAEVKKPGASVKVSCASGYTFTSYMHVVRQAPGQ GLEWMGIINPSGGSTSYAQKFQGRVTMTRDTSTSTVYMELSNLRS EDTAVYYCARSPRVTGTFDYWGQGLTVTVSSGGGGSGGGGSG GGGGSGGGGSDIQLTQSPSTLSASVGDRVITICRASQSSSWLAWY QQKPGKAPKLLIYKASSLESQVPSRFSGSGSGTEFTLTISSLQPD FATYYCQQYSSYPLTFGGGTRLEIK	222
mesothelin	M22 (human)	QVQLVQSGAEVRRPGASVKISCRASGDTSTRHYIHWLRQAPGQG PEWMGVINPTTGPATGSPAYAQMLQGRVTMTRDTSTRTVYME LR SLRFEDTAVYYCARSVVGRSAPYYFDYWGGQGLTVTVSSGGGG GGGGSGGGGSDIQTQSPSSLSASVGDRVITICRASQGI SDYSAWYQQKPGKAPKLLIYAASLTQSGVPSRFSGSGSGTDFTLT ISYLQSEDFATYYCQQYSSYPLTFGGGKVDIK	223
mesothelin	M23 (human)	QVQLQQSGAEVKKPGASVKVSCASGYTFTNYYMHVVRQAPGQ GLEWMGIINPSGGYTTYAQKFQGRVTMTRDTSTSTVYMESSLRS EDTAVYYCARIRSCGGDCYYFDNWGGQGLTVTVSSGGGGSGGGG SGGGGSGGGGSDIQLTQSPSTLSASVGDRVITICRAENVNIWLA WYQQKPGKAPKLLIYKSSSLASQVPSRFSGSGSGAEFTLTISSLQ DDFATYYCQQYQSYPLTFGGGKVDIK	224
mesothelin	M24 (human)	QITLKESGPALVKPTQTLTCTFSGFSLSTAGVHVGVIRQPPGKA LEWLALISWADDKRYRPSRLSDITRVTSKDQVLSMTNMQPED TATYYCALQGFDDGYEAWGPGTLVTVSSGGGGSGGGGSGGGG SGGGGSDIVMTQSPSSLSASAGDRVITICRASRGISSALAWYQQK PGKPPKLLIYDASSLESQVPSRFSGSGSGTDFTLTIDSLEPEDFAT YYCQQSYSTPWTFGGGKVDIK	225

The CDR sequences of the scFv domains of the mesothelin antigen binding domains provided in Table 3 are shown in Table 4 for the heavy chain variable domains and in Table 5 for the light chain variable domains.

Table 4. Amino acid sequences for the heavy chain (HC) CDR1, CDR2, and CDR3 regions of human anti-mesothelin scFvs

Descrip.	HC-CDR1	SEQ ID NO:	HC-CDR2	SEQ ID NO:	HC-CDR3	SEQ ID NO:
M5	GYTFTDYMH	226	WINPNSGGTNYAQKFQG	227	GWDFDY	228
M11	GYTFTGYMH	229	WINPNSGGTNYAQNFQG	230	GWDFDY	228
SS1	GYSFTGYTMN	231	LITPYNGASSYNQKFRG	232	GGYDGRGFDY	233

M1	GYTFTGYMH	229	RINPNSGGTNYAQKFQG	234	GRYYGMDV	235
M2	GYTFTGYMH	229	WINPNSGGTNYAQKFQG	227	DLRRTVVTTPRAYY GMDV	236
M3	GYTFTGYMH	229	WINPNSGGTNYAQKFQG	227	GEWDGSYYYYDY	237
M4	GFTFSSYWMH	238	RINTDGSTTTYADSVEG	239	GHWAV	240
M6	GYTFTSYMH	241	IINPSGGSTSYAQKFQ	242	YRLIAVAGDYYYY GMDV	243
M7	GFTFSSYAMH	244	VISYDGSNKYYADSVKG	245	WKVSSSSPAFDY	246
M8	GYPFTGYSLH	247	WINPNSGGTNYAQKFQG	227	DHYGGNSLFY	248
M9	GYTFTSYMH	241	IINPSGGSTGYAQKFQG	249	GGYSSSSDAFDI	250
M10	GYTFTSYGIS	251	WISAYNGNTNYAQKLQ	252	VAGGIYYYYGMD V	253
M12	GYTFTGYMH	229	RINPNSGGTNYAQKFQG	234	TTTSYAFDI	254
M13	GFIFSDYYMG	255	YIGRSGSSMYADSVKG	256	SPVVAATEDFQH	257
M14	GFTFRGYYIH	258	IINPSGGSRAYAQKFQG	259	TASCGGDCYYLD Y	260
M15	GFTFDDYAMH	261	GISWNSGSIGYADSVK	262	DGSSWSWGYF DY	263
M16	GFTFDDYAMH	261	GISWNSGSTGYADSVKG	264	DSSSWYGGGSAF DI	265
M17	GFTFDDYAMH	261	GISWNSGSTGYADSVKG	264	DSSSWYGGGSAF DI	265
M18	GFTFSSYWMH	238	RINS DGSSYADSVKG	266	TGWVGSYYYYMD V	267
M19	GFTFSSYGMH	268	VISYDGSNKYYADSVKG	245	GYSRYYYYYGMDV	269
M20	GFTFSSYAMS	270	AISGSGGSTYYADSVKG	271	REAAAGHDWYFD L	272
M21	GYTFTSYMH	241	IINPSGGSTSYAQKFQG	273	SPRVTTGYFDY	274
M22	GDTSTRHYIH	275	VINPTTGPATGSPAYAQ MLQG	276	SVVGRSAPYYFD Y	277
M23	GYTFTNYMH	278	IINPSGGYTTTAAQKFQG	279	IRSCGGDCYYFDN	280
M24	GFSLSTAGVH VG	281	LISWADDKRYRPSLRS	282	QGF DGYEAN	283

Table 5. Amino acid sequences for the light chain (LC) CDR1, CDR2, and CDR3 regions of human anti-mesothelin scFvs

Description	LC-CDR1	SEQ ID NO:	LC-CDR2	SEQ ID NO:	LC-CDR3	SEQ ID NO:
M5	RASQSIRYYLS	284	TASILQN	285	LQTYTTPD	286
M11	RASQSIRYYLS	284	TASILQN	285	LQTYTTPD	286
SS1	SASSSVSYM	287	DTSKLS	288	QQWSGYPLT	289
M1	RASQSVSSNFA	290	DASNRAT	291	HQRSNWLYT	292
M2	QASQDISNSLN	293	DASTLET	294	QQHDNLPLT	295
M3	RASQSINTYLN	296	AASSLQS	297	QQSFSPLT	298
M4	RASQSIDRLA	299	KASSLES	300	QQYGHLPMT	301
M6	RASQGVGRWLA	302	AASTLQS	303	QQANSFPLT	304
M7	RASQSVYTKYLG	305	DASTRAT	306	QHYGGSPLIT	307
M8	RASQDSGTWLA	308	DASTLED	309	QQYNSYPLT	310
M9	RASQDISSALA	311	DASSLES	312	QQFSSYPLT	313
M10	KSSHVLYNRNNKNYLA	314	WASTRKS	315	QQTQTFPLT	316
M12	RASQSISTWLA	317	KASTLES	318	QQYNTYSPYT	319
M13	RASQSVTSNYLA	320	GASTRAT	321	QQYGSAPVT	322
M14	RASENVNIWLA	323	KSSSLAS	324	QQYQSYPLT	325
M15	QGDALRSYYAS	326	GKNNRPS	327	NSRDSSGYPV	328
M16	QGDALRSYYAS	329	GRSRRPS	330	NSRDNTANHYV	331
M17	QGDALRSYYAS	329	GKNNRPS	327	NSRGSSGNHYV	332
M18	RASQSVSSNYLA	333	DVSTRAT	334	QQRSNWPPWT	335
M19	RASQSVYTKYLG	305	DASTRAT	306	QHYGGSPLIT	307
M20	RASQSISSYLN	336	AASSLQS	297	QQSYSIPLT	337
M21	RASQSISSWLA	338	KASSLES	300	QQYSSYPLT	339
M22	RASQGISDYS	340	AASTLQS	303	QQYYSYPLT	341
M23	RASENVNIWLA	323	KSSSLAS	324	QQYQSYPLT	325
M24	RASRGISSALA	342	DASSLES	312	QQSYSTPWT	343

Any known anti-mesothelin binding domain, from, for example, a known antibody, bispecific molecule or CAR, may be suitable for use in the CAR of the present invention. For example, the antigen binding domain against mesothelin is or may be derived from an antigen binding, e.g., CDRs or VH and VL, of an antibody, antigen-binding fragment or CAR described in, e.g., PCT publication WO2015/090230. In
 5 embodiments, the antigen binding domain against mesothelin is or is derived from an antigen binding portion, e.g., CDRs or VH and VL, of an antibody, antigen-binding fragment, or CAR described in, e.g., PCT publication WO1997/025068, WO1999/028471, WO2005/014652, WO2006/099141, WO2009/045957, WO2009/068204, WO2013/142034, WO2013/040557, or WO2013/063419.

In one embodiment, the mesothelin binding domain comprises one or more (e.g., all three) light chain complementary determining region 1 (LC CDR1), light chain complementary determining region 2 (LC CDR2), and light chain complementary determining region 3 (LC CDR3) of a mesothelin binding domain described herein, e.g., provided in Table 3 or 5, and/or one or more (e.g., all three) heavy chain complementary determining region 1 (HC CDR1), heavy chain complementary determining region 2 (HC CDR2), and heavy chain complementary determining region 3 (HC CDR3) of a mesothelin binding
 10 domain described herein, e.g., provided in Table 3 or 4. In one embodiment, the mesothelin binding domain comprises one, two, or all of LC CDR1, LC CDR2, and LC CDR3 of any amino acid sequences as provided in Table 5; and one, two or three of all of HC CDR1, HC CDR2 and HC CDR3, of any amino acid acid sequences as provided in Table 4.

In one embodiment, the mesothelin binding domain comprises a light chain variable region described
 20 herein (e.g., in Table 3) and/or a heavy chain variable region described herein (e.g., in Table 3). In one embodiment, the mesothelin binding domain is a scFv comprising a light chain and a heavy chain of an amino acid sequence listed in Table 3. In an embodiment, the mesothelin binding domain (e.g., an scFv) comprises: a light chain variable region comprising an amino acid sequence having at least one, two or three modifications (e.g., substitutions, e.g., conservative substitutions) but not more than 30, 20 or 10
 25 modifications (e.g., substitutions, e.g., conservative substitutions) of an amino acid sequence of a light chain variable region provided in Table 3, or a sequence with 95-99% identity with an amino acid sequence provided in Table 3; and/or a heavy chain variable region comprising an amino acid sequence having at least one, two or three modifications (e.g., substitutions, e.g., conservative substitutions) but not more than 30, 20 or 10 modifications (e.g., substitutions, e.g., conservative substitutions) of an amino
 30 acid sequence of a heavy chain variable region provided in Table 3, or a sequence with 95-99% identity to an amino acid sequence provided in Table 3.

In one embodiment, the mesothelin binding domain comprises an amino acid sequence selected from any one of SEQ ID NOs: 201-225; or an amino acid sequence having at least one, two or three modifications (e.g., substitutions, e.g., conservative substitutions) but not more than 30, 20 or 10
 35 modifications (e.g., substitutions, e.g., conservative substitutions) to any of the aforesaid sequences; or a sequence with 95-99% identity to any of the aforesaid sequences. In one embodiment, the mesothelin

binding domain is a scFv, and a light chain variable region comprising an amino acid sequence described herein, e.g., in Table 3, is attached to a heavy chain variable region comprising an amino acid sequence described herein, e.g., in Table 3, via a linker, e.g., a linker described herein. In one embodiment, the mesothelin binding domain includes a (Gly4-Ser)_n linker, wherein n is 1, 2, 3, 4, 5, or 6, preferably 4 (SEQ ID NO: 967). The light chain variable region and heavy chain variable region of a scFv can be, e.g., in any of the following orientations: light chain variable region-linker-heavy chain variable region or heavy chain variable region-linker-light chain variable region.

In an embodiment, the antigen binding domain of a CAR, e.g., a CAR expressed by a cell of the invention, binds to human EGFRvIII. In an embodiment, the antigen binding domain is a murine scFv domain that binds to human EGFRvIII such as, e.g., mu310C. In an embodiment, the antigen binding domain is a humanized antibody or antibody fragment, e.g., scFv domain, derived from the murine mu310C scFv. Exemplary humanized scFv domains (and their sequences) and murine SS1 scFv that bind to EGFRvIII are provided in Table 6.

In an embodiment, the antigen binding domain of a CAR binds to human claudin 6 (CLDN6). In an embodiment, the antigen binding domain is a murine scFv domain that binds to human CLDN6. In an embodiment, the antigen binding domain is a humanized antibody or antibody fragment. Exemplary scFv domains (and their sequences) that bind to CLDN6 are provided in Table 6. The scFv domain sequences provided in Table 6 include a light chain variable region (VL) and a heavy chain variable region (VH). The VL and VH are attached by a linker comprising the sequence GGGGSGGGGSGGGGSGGGGS (SEQ ID NO: 29), e.g., in the following orientation: VL-linker-VH.

Table 6. Antigen binding domains that bind to the tumor antigen EGFRvIII or CLDN6

Tumor antigen	Name	Amino acid sequence	SEQ ID NO:
EGFR vIII	huscFv1	Eiqlvqsgaevkkpgatvkisckgsgfniedyyihwvqqapgkglewmgridpendetk ygpifqgrvitadtstntvymelsslrsestavyycfrggvywgqgtvtvssggggsggg gsgggsggggsdvmtqspdslavslgeratinckssqslldsdgktylnwlqqkpgqp pkrlislvskldsgvpdrfsgsgsgtdftltisslqaedvavyycwqgthfpgtfgggtkveik	344
EGFR vIII	huscFv2	Dvmtqspdslavslgeratinckssqslldsdgktylnwlqqkpgqpkrllislvskldsgv pdrfsgsgsgtdftltisslqaedvavyycwqgthfpgtfgggtkveikggggsgggsggg gsggggseiqlvqsgaevkkpgatvkisckgsgfniedyyihwvqqapgkglewmgrid pendetkygpifqgrvitadtstntvymelsslrsestavyycfrggvywgqgtvtvss	345
EGFR vIII	huscFv3	Eiqlvqsgaevkkpgeslriskgsgfniedyyihwvrqmpgkglewmgridpendetk ygpifqghvtisadtsintvylqwsslkasdtamyycafrggvywgqgtvtvssggggsg ggsgggsggggsdvmtqspslpvtlqgpasickssqslldsdgktylnwlqrrpg qsrllislvskldsgvpdrfsgsgsgtdftlkisrveaedvgvyycwqgthfpgtfgggtkvei k	346
EGFR vIII	huscFv4	Dvmtqspslpvtlqgpasickssqslldsdgktylnwlqrrpgqsrllislvskldsgvp drfsgsgsgtdftlkisrveaedvgvyycwqgthfpgtfgggtkveikggggsgggsggg	347

		gsggggseiqlvqsgaevkpkgeslrisccksgsfniedyihwvrqmpgkglewmgrid pendetkygpifqghvtisadtsintvylqwsslkasdtamycafrggvywgqgtvtvss	
EGFR vIII	huscFv5	Eiqlvqsgaevkpkpgatvkiscksgsfniedyihwvqqapgkglewmgridpendetk ygpifqgrvtitadtstntvymelsslrstedavyycfrggvywgqgtvtvssggggsggg gsgggsggggsdvmtqspislplvtlqgpasisckssqslldsdgktylnwlqqrpgqs prrlislvsldsgvpdrfsgsgsgtdftlkisrveadvgyycwqgthfpgtfgggtkveik	348
EGFR vIII	huscFv6	Eiqlvqsgaevkpkgeslrisccksgsfniedyihwvrqmpgkglewmgridpendetk ygpifqghvtisadtsintvylqwsslkasdtamycafrggvywgqgtvtvssggggsg ggsgggsggggsdvmtqspdslavslgeratinckssqslldsdgktylnwlqqrpgq qppkrlislvsldsgvpdrfsgsgsgtdftltisslqaedvavyycwqgthfpgtfgggtkve k	349
EGFR vIII	huscFv7	Dvmtqspdslavslgeratinckssqslldsdgktylnwlqqrpgqppkrlislvsldsgv pdrfsgsgsgtdftltisslqaedvavyycwqgthfpgtfgggtkveikggggsgggsggg gsggggseiqlvqsgaevkpkgeslrisccksgsfniedyihwvrqmpgkglewmgrid pendetkygpifqghvtisadtsintvylqwsslkasdtamycafrggvywgqgtvtvss	350
EGFR vIII	huscFv8	Dvmtqspislplvtlqgpasisckssqslldsdgktylnwlqqrpgqppkrlislvsldsgv drfsgsgsgtdftlkisrveadvgyycwqgthfpgtfgggtkveikggggsgggsggg gsggggseiqlvqsgaevkpkpgatvkiscksgsfniedyihwvqqapgkglewmgrid pendetkygpifqgrvtitadtstntvymelsslrstedavyycfrggvywgqgtvtvss	351
EGFR vIII	Mu310C	eiqlqqsgaelvkpgasvklstcsgsfniedyihwvqrteggglewgridpendetkygp ifqgratitadtssntvylqlssltseadvyycafrggvywgpgtltvssggggsgggsgg ggshmdvmtqspiltvaigqsasisckssqslldsdgktylnwlqqrpgqspkrlislvs ldsgvpdrftgsgsgtdftlrisrveadlgiyycwqgthfpgtfgggtkleik	352
Claudin6	muMAB 64A	EVQLQQSGPELVKPGASMKISCKASGYSTGYTMNWVKQSHG KNLEWIGLINPYNGGTIYNQKFKGKATLTVDKSSSTAYMELLSLT SEDSAVYYCARDYGFVLDYWGGQTTLTVSSGGGGSGGGGSG GGGSGGGGSQIVLTQSPSIMSVSPGEKVTITCSASSSVSYMHW FQQKPGTSPKLCIYSTSNLASGVPARFSGRSGTSYSLTISRVA AEDAATYYCQQRSNYPWPWFGGGTKLEIK	353
Claudin6	mAb206- LCC	EVQLQQSGPELVKPGASMKISCKASGYSTGYTMNWVKQSHG KNLEWIGLINPYNGGTIYNQKFKGKATLTVDKSSSTAYMELLSLT SEDSAVYYCARDYGFVLDYWGGQTTLTVSSGGGGSGGGGSG GGGSGGGGSQIVLTQSPAIMSASPGEKVTITCSASSSVYLHWF QQKPGTSPKLWVYSTSNLPSGVPARFSGSGSGTSYSLTISRME AEDAATYYCQQRSIYPWPWFGGGTKLEIK	354
Claudin6	mAb206- SUBG	EVQLQQSGPELVKPGASMKISCKASGYSTGYTMNWVKQSHG KNLEWIGLINPYNGGTIYNQKFKGKATLTVDKSSSTAYMELLSLT SEDSAVYYCARDYGFVLDYWGGQTTLTVSSGGGGSGGGGSG GGGSGGGGSQIVLTQSPSIMSVSPGEKVTITCSASSSVSYMHW FQQKPGTSPKLGIYSTSNLASGVPARFSGRSGTSYSLTISRVA AEDAATYYCQQRSNYPWPWFGGGTKLEIK	355

In one embodiment, the EGFRvIII binding domain comprises one or more (e.g., all three) light chain complementary determining region 1 (LC CDR1), light chain complementary determining region 2 (LC CDR2), and light chain complementary determining region 3 (LC CDR3) of an EGFRvIII binding domain described herein, e.g., provided in Table 6, and/or one or more (e.g., all three) heavy chain complementary determining region 1 (HC CDR1), heavy chain complementary determining region 2 (HC

5

CDR2), and heavy chain complementary determining region 3 (HC CDR3) of an EGFRvIII binding domain described herein, e.g., provided in Table 6.

In one embodiment, the EGFRvIII binding domain comprises a light chain variable region described herein (e.g., in Table 6) and/or a heavy chain variable region described herein (e.g., in Table 6). In one embodiment, the EGFRvIII binding domain is a scFv comprising a light chain and a heavy chain of an amino acid sequence listed in Table 6. In an embodiment, the EGFRvIII binding domain (e.g., an scFv) comprises: a light chain variable region comprising an amino acid sequence having at least one, two or three modifications (e.g., substitutions, e.g., conservative substitutions) but not more than 30, 20 or 10 modifications (e.g., substitutions, e.g., conservative substitutions) of an amino acid sequence of a light chain variable region provided in Table 6, or a sequence with 95-99% identity with an amino acid sequence provided in Table 6; and/or a heavy chain variable region comprising an amino acid sequence having at least one, two or three modifications (e.g., substitutions, e.g., conservative substitutions) but not more than 30, 20 or 10 modifications (e.g., substitutions, e.g., conservative substitutions) of an amino acid sequence of a heavy chain variable region provided in Table 6, or a sequence with 95-99% identity to an amino acid sequence provided in Table 6.

In one embodiment, the EGFRvIII binding domain comprises an amino acid sequence selected from any one of SEQ ID NOs: 344-352; or an amino acid sequence having at least one, two or three modifications (e.g., substitutions, e.g., conservative substitutions) but not more than 30, 20 or 10 modifications (e.g., substitutions, e.g., conservative substitutions) to any of the aforesaid sequences; or a sequence with 95-99% identity to any of the aforesaid sequences. In one embodiment, the EGFRvIII binding domain is a scFv, and a light chain variable region comprising an amino acid sequence described herein, e.g., in Table 6, is attached to a heavy chain variable region comprising an amino acid sequence described herein, e.g., in Table 6, via a linker, e.g., a linker described herein. In one embodiment, the EGFRvIII binding domain includes a (Gly4-Ser)_n linker, wherein n is 1, 2, 3, 4, 5, or 6, preferably 4 (SEQ ID NO: 967). The light chain variable region and heavy chain variable region of a scFv can be, e.g., in any of the following orientations: light chain variable region-linker-heavy chain variable region or heavy chain variable region-linker-light chain variable region.

In one embodiment, the Claudin6 binding domain comprises one or more (e.g., all three) light chain complementary determining region 1 (LC CDR1), light chain complementary determining region 2 (LC CDR2), and light chain complementary determining region 3 (LC CDR3) of a Claudin6 binding domain described herein, e.g., provided in Table 6, and/or one or more (e.g., all three) heavy chain complementary determining region 1 (HC CDR1), heavy chain complementary determining region 2 (HC CDR2), and heavy chain complementary determining region 3 (HC CDR3) of a Claudin6 binding domain described herein, e.g., provided in Table 6.

In one embodiment, the Claudin-6 binding domain comprises a light chain variable region described herein (e.g., in Table 6) and/or a heavy chain variable region described herein (e.g., in Table 6). In one embodiment, the Claudin-6 binding domain is a scFv comprising a light chain and a heavy chain of an amino acid sequence listed in Table 6. In an embodiment, the Claudin-6 binding domain (e.g., an scFv)

5 comprises: a light chain variable region comprising an amino acid sequence having at least one, two or three modifications (e.g., substitutions, e.g., conservative substitutions) but not more than 30, 20 or 10 modifications (e.g., substitutions, e.g., conservative substitutions) of an amino acid sequence of a light chain variable region provided in Table 6, or a sequence with 95-99% identity with an amino acid sequence provided in Table 6; and/or a heavy chain variable region comprising an amino acid sequence
10 having at least one, two or three modifications (e.g., substitutions, e.g., conservative substitutions) but not more than 30, 20 or 10 modifications (e.g., substitutions, e.g., conservative substitutions) of an amino acid sequence of a heavy chain variable region provided in Table 6, or a sequence with 95-99% identity to an amino acid sequence provided in Table 6.

In one embodiment, the Claudin6 binding domain comprises an amino acid sequence selected from any
15 one of SEQ ID NOs: 353-355; or an amino acid sequence having at least one, two or three modifications (e.g., substitutions, e.g., conservative substitutions) but not more than 30, 20 or 10 modifications (e.g., substitutions, e.g., conservative substitutions) to any of the aforesaid sequences; or a sequence with 95-99% identity to any of the aforesaid sequences. In one embodiment, the Claudin6 binding domain is a scFv, and a light chain variable region comprising an amino acid sequence described herein, e.g., in
20 Table 6, is attached to a heavy chain variable region comprising an amino acid sequence described herein, e.g., in Table 6, via a linker, e.g., a linker described herein. In one embodiment, the Claudin6 binding domain includes a (Gly4-Ser)_n linker, wherein n is 1, 2, 3, 4, 5, or 6, preferably 4 (SEQ ID NO: 967). The light chain variable region and heavy chain variable region of a scFv can be, e.g., in any of the following orientations: light chain variable region-linker-heavy chain variable region or heavy chain
25 variable region-linker-light chain variable region.

In one embodiment, an antigen binding domain against GD2 is an antigen binding portion, e.g., CDRs, of an antibody described in, e.g., Mujoo et al., Cancer Res. 47(4):1098-1104 (1987); Cheung et al., Cancer Res 45(6):2642-2649 (1985), Cheung et al., J Clin Oncol 5(9):1430-1440 (1987), Cheung et al., J Clin Oncol 16(9):3053-3060 (1998), Handgretinger et al., Cancer Immunol Immunother 35(3):199-204 (1992).

30 In some embodiments, an antigen binding domain against GD2 is an antigen binding portion of an antibody selected from mAb 14.18, 14G2a, ch14.18, hu14.18, 3F8, hu3F8, 3G6, 8B6, 60C3, 10B8, ME36.1, and 8H9, see e.g., WO2012033885, WO2013040371, WO2013192294, WO2013061273, WO2013123061, WO2013074916, and WO201385552. In some embodiments, an antigen binding domain against GD2 is an antigen binding portion of an antibody described in US Publication No.:
35 20100150910 or PCT Publication No.: WO 2011160119.

In one embodiment, an antigen binding domain against the Tn antigen, the sTn antigen, a Tn-O-glycopeptide antigen, or a sTn-O-glycopeptide antigen is an antigen binding portion, e.g., CDRs, of an antibody described in, e.g., US 2014/0178365, US8,440,798, EP 2083868 A2, Brooks et al., PNAS 107(22):10056-10061 (2010), and Stone et al., OncoImmunology 1(6):863-873(2012).

- 5 In one embodiment, an antigen binding domain against PSMA is an antigen binding portion, e.g., CDRs, of an antibody described in, e.g., Parker et al., Protein Expr Purif 89(2):136-145 (2013), US 20110268656 (J591 ScFv); Frigerio et al, European J Cancer 49(9):2223-2232 (2013) (scFvD2B); WO 2006125481 (mAbs 3/A12, 3/E7 and 3/F11) and single chain antibody fragments (scFv A5 and D7).

- 10 In one embodiment, an antigen binding domain against CD97 is an antigen binding portion, e.g., CDRs, of an antibody described in, e.g., US6,846,911; de Groot et al., J Immunol 183(6):4127-4134 (2009); or an antibody from R&D:MAB3734.

In one embodiment, an antigen binding domain against TAG72 is an antigen binding portion, e.g., CDRs, of an antibody described in, e.g., Hombach et al., Gastroenterology 113(4):1163-1170 (1997); and Abcam ab691.

- 15 In one embodiment, an antigen binding domain against CD44v6 is an antigen binding portion, e.g., CDRs, of an antibody described in, e.g., Casucci et al., Blood 122(20):3461-3472 (2013).

In one embodiment, an antigen binding domain against CEA is an antigen binding portion, e.g., CDRs, of an antibody described in, e.g., Chmielewski et al., Gastroenterology 143(4):1095-1107 (2012).

- 20 In one embodiment, an antigen binding domain against EPCAM is an antigen binding portion, e.g., CDRs, of an antibody selected from MT110, EpCAM-CD3 bispecific Ab (see, e.g., clinicaltrials.gov/ct2/show/NCT00635596); Edrecolomab; 3622W94; ING-1; and adecatumumab (MT201).

In one embodiment, an antigen binding domain against KIT is an antigen binding portion, e.g., CDRs, of an antibody described in, e.g., US7915391, US20120288506, and several commercial catalog antibodies.

- 25 In one embodiment, an antigen binding domain against IL-13Ra2 is an antigen binding portion, e.g., CDRs, of an antibody described in, e.g., WO2008/146911, WO2004087758, several commercial catalog antibodies, and WO2004087758.

In one embodiment, an antigen binding domain against CD171 is an antigen binding portion, e.g., CDRs, of an antibody described in, e.g., Hong et al., J Immunother 37(2):93-104 (2014).

- 30 In one embodiment, an antigen binding domain against PSCA is an antigen binding portion, e.g., CDRs, of an antibody described in, e.g., Morgenroth et al., Prostate 67(10):1121-1131 (2007) (scFv 7F5);

Nejatollahi et al., J of Oncology 2013(2013), article ID 839831 (scFv C5-II); and US Pat Publication No. 20090311181.

In one embodiment, an antigen binding domain against MAD-CT-2 is an antigen binding portion, e.g., CDRs, of an antibody described in, e.g., PMID: 2450952; US7635753.

- 5 In one embodiment, an antigen binding domain against Folate receptor alpha is an antigen binding portion, e.g., CDRs, of the antibody IMG853, or an antibody described in US20120009181; US4851332, LK26: US5952484.

In one embodiment, an antigen binding domain against ERBB2 (Her2/neu) is an antigen binding portion, e.g., CDRs, of the antibody trastuzumab, or pertuzumab.

- 10 In one embodiment, an antigen binding domain against MUC1 is an antigen binding portion, e.g., CDRs, of the antibody SAR566658.

In one embodiment, the antigen binding domain against EGFR is antigen binding portion, e.g., CDRs, of the antibody cetuximab, panitumumab, zalutumumab, nimotuzumab, or matuzumab.

- 15 In one embodiment, an antigen binding domain against NCAM is an antigen binding portion, e.g., CDRs, of the antibody clone 2-2B: MAB5324 (EMD Millipore)

In one embodiment, an antigen binding domain against CAIX is an antigen binding portion, e.g., CDRs, of the antibody clone 303123 (R&D Systems).

In one embodiment, an antigen binding domain against Fos-related antigen 1 is an antigen binding portion, e.g., CDRs, of the antibody 12F9 (Novus Biologicals).

- 20 In one embodiment, an antigen binding domain against SSEA-4 is an antigen binding portion, e.g., CDRs, of antibody MC813 (Cell Signaling), or other commercially available antibodies.

In one embodiment, an antigen binding domain against PDGFR-beta is an antigen binding portion, e.g., CDRs, of an antibody Abcam ab32570.

- 25 In one embodiment, an antigen binding domain against ALK is an antigen binding portion, e.g., CDRs, of an antibody described in, e.g., Mino-Kenudson et al., Clin Cancer Res 16(5):1561-1571 (2010).

In one embodiment, an antigen binding domain against polysialic acid is an antigen binding portion, e.g., CDRs, of an antibody described in, e.g., Nagae et al., J Biol Chem 288(47):33784-33796 (2013).

In one embodiment, an antigen binding domain against PLAC1 is an antigen binding portion, e.g., CDRs, of an antibody described in, e.g., Ghods et al., Biotechnol Appl Biochem 2013 doi:10.1002/bab.1177.

In one embodiment, an antigen binding domain against GloboH is an antigen binding portion of the antibody VK9; or an antibody described in, e.g., Kudryashov V et al, Glycoconj J.15(3):243-9 (1998), Lou et al., Proc Natl Acad Sci USA 111(7):2482-2487 (2014) ; MBr1: Bremer E-G et al. J Biol Chem 259:14773-14777 (1984).

- 5 In one embodiment, an antigen binding domain against NY-BR-1 is an antigen binding portion, e.g., CDRs of an antibody described in, e.g., Jager et al., Appl Immunohistochem Mol Morphol 15(1):77-83 (2007).

- In one embodiment, an antigen binding domain against sperm protein 17 is an antigen binding portion, e.g., CDRs, of an antibody described in, e.g., Song et al., Target Oncol 2013 Aug 14 (PMID: 23943313);
10 Song et al., Med Oncol 29(4):2923-2931 (2012).

In one embodiment, an antigen binding domain against TRP-2 is an antigen binding portion, e.g., CDRs, of an antibody described in, e.g., Wang et al, J Exp Med. 184(6):2207-16 (1996).

In one embodiment, an antigen binding domain against CYP1B1 is an antigen binding portion, e.g., CDRs, of an antibody described in, e.g., Maecker et al, Blood 102 (9): 3287-3294 (2003).

- 15 In one embodiment, an antigen binding domain against RAGE-1 is an antigen binding portion, e.g., CDRs, of the antibody MAB5328 (EMD Millipore).

In one embodiment, an antigen binding domain against human telomerase reverse transcriptase is an antigen binding portion, e.g., CDRs, of the antibody cat no: LS-B95-100 (Lifespan Biosciences)

- In one embodiment, an antigen binding domain against intestinal carboxyl esterase is an antigen binding
20 portion, e.g., CDRs, of the antibody 4F12: cat no: LS-B6190-50 (Lifespan Biosciences).

In one embodiment, an antigen binding domain against mut hsp70-2 is an antigen binding portion, e.g., CDRs, of the antibody Lifespan Biosciences: monoclonal: cat no: LS-C133261-100 (Lifespan Biosciences).

- In one embodiment, an antigen binding domain against MAD-CT-2 is an antigen binding portion, e.g.,
25 CDRs, of an antibody described in, e.g., PMID: 2450952; US7635753.

- In one embodiment, the antigen binding domain comprises one, two three (e.g., all three) heavy chain CDRs, HC CDR1, HC CDR2 and HC CDR3, from an antibody listed above, and/or one, two, three (e.g., all three) light chain CDRs, LC CDR1, LC CDR2 and LC CDR3, from an antibody listed above. In one embodiment, the antigen binding domain comprises a heavy chain variable region and/or a variable light
30 chain region of an antibody listed above.

In some embodiments, the antigen binding domain of a CAR targets a tumor antigen that is an antigen expressed on a myeloid tumor (either a surface antigen or presented by MHC), and a cell comprising such a CAR recognizes a myeloid tumor antigen.

5 In an embodiment, the myeloid tumor antigen is an antigen that is preferentially or specifically expressed on the surface of a myeloid tumor cell.

In one embodiment, the antigen-binding domain of a CAR can be chosen such that a myeloid tumor population is targeted. Alternatively, when targeting of more than one type of myeloid tumor is desired, an antigen binding domain that targets a myeloid tumor antigen that is expressed by more than one, e.g., all, of the myeloid tumors to be targeted can be selected.

10 A CAR can target the following additional tumor antigens: CD123, CD34, Flt3, CD33 and CLL-1. In embodiments, the tumor antigen is selected from CD123, CD33 and CLL-1. In some embodiments, the tumor antigen is CD123. In some embodiments, the tumor antigen is CD33. In some embodiments, the tumor antigen is CD34. In some embodiments, the tumor antigen is Flt3. In embodiments, the tumor antigen is CLL-1. In embodiments, the antigen binding domain targets the human antigen.

15 In one aspect, the antigen-binding domain of a CAR binds to CD123, e.g., human CD123. Any known CD123 binding domain may be used in the invention. In one embodiment, an antigen binding domain against CD123 is an antigen binding portion, e.g., CDRs or VH and VL, of an antibody, antigen-binding fragment or CAR described in, e.g., PCT publication WO2014/130635. In one embodiment, an antigen binding domain against CD123 is an antigen binding portion, e.g., CDRs or VH and VL, of an antibody, antigen-binding fragment or CAR described in, e.g., PCT publication WO/2016/028896. In one
20 embodiment, an antigen binding domain against CD123 is an antigen binding portion, e.g., CDRs, of an antibody, antigen-binding fragment, or CAR described in, e.g., PCT publication WO1997/024373, WO2008/127735 (e.g., a CD123 binding domain of 26292, 32701, 37716 or 32703), WO2014/138805 (e.g., a CD123 binding domain of CSL362), WO2014/138819, WO2013/173820, WO2014/144622,
25 WO2001/66139, WO2010/126066 (e.g., the CD123 binding domain of any of Old4, Old5, Old17, Old19, New102, or Old6), WO2014/144622, WO2016/028896, or US2009/0252742. In embodiments, the antigen binding domain is or is derived from a murine anti-human CD123 binding domain. In embodiments, the antigen binding domain is a humanized antibody or antibody fragment, e.g., scFv domain. In an embodiment, the antigen binding domain is a human antibody or antibody fragment that
30 binds to human CD123. In embodiments, the antigen binding domain is an scFv domain which includes a light chain variable region (VL) and a heavy chain variable region (VH). The VL and VH may attached by a linker described herein, e.g., comprising the sequence GGGGSGGGGSGGGGS (SEQ ID NO: 30), and may be in any orientation, e.g., VL-linker-VH, or VH-linker-VL.

In some embodiments, the antigen binding domain that binds to CD123 is a scFv domain. In some
35 embodiments, the antigen binding domain that binds to CD123 is a murine scFv domain. In an

embodiment, the antigen binding domain that binds to CD123 is a human or humanized scFv domain. Exemplary scFv domains (and their sequences) that bind to CLDN6 are provided in Table 19. The scFv domain sequences provided in Table 19 include a light chain variable region (VL) and a heavy chain variable region (VH). The VL and VH are attached by a linker comprising the sequence

5 GGGGSGGGGSGGGGSGGGGS (SEQ ID NO: 29), e.g., in the following orientation: VL-linker-VH. In one embodiment, the CD123 binding domain comprises an amino acid sequence selected from any one of SEQ ID NOs: 751, 756, 761, or 766; or an amino acid sequence having at least one, two or three modifications (e.g., substitutions, e.g., conservative substitutions) but not more than 30, 20 or 10 modifications (e.g., substitutions, e.g., conservative substitutions) to any of the aforesaid sequences; or a
10 sequence with 95-99% identity to an amino acid sequence selected from any one of SEQ ID NOs: 751, 756, 761, or 766.

In one aspect, the antigen-binding domain of a CAR binds to CD33, e.g., human CD33. Any known CD33 binding domain may be used in the invention. In one embodiment, an antigen binding domain against CD33 is an antigen binding portion, e.g., CDRs or VH and VL, of an antibody, antigen-binding
15 fragment or CAR described in, e.g., PCT publication WO2016/014576 or US Patent Publication 2016-0096892-A1, the contents of which are incorporated herein in their entirety. In one embodiment, an antigen binding domain against CD33 is an antigen binding portion of or derived from Gemtuzumab ozogamicin (e.g., comprising an antigen binding domain comprising one or more, e.g., one, two, or three, CDRs of the heavy chain variable domain and/or one or more, e.g., one, two, or three, CDRs of the light
20 chain variable domain, or the VH or VL, or the scFv sequence, of the scFv sequence of Gemtuzumab ozogamicin) (previously marketed as Mylotarg), e.g., Bross et al., Clin Cancer Res 7(6):1490-1496 (2001) (Gemtuzumab Ozogamicin, hP67.6). In one embodiment, an antigen binding domain against CD33 is an antigen binding portion of or derived from (e.g., comprising an antigen binding domain comprising one or more, e.g., one, two, or three, CDRs of the heavy chain variable domain and/or one or more, e.g., one,
25 two, or three, CDRs of the light chain variable domain, or the VH or VL, or the scFv sequence) of the scFv sequence encoded by GenBank reference no. AM402974.1 (See, Wang et al., *Mol. Ther.*, vol. 23:1, pp. 184-191 (2015), hereby incorporated by reference. In one embodiment, an antigen binding domain against CD33 is an antigen binding portion, e.g., CDRs, of an antibody described in, e.g., Caron et al., Cancer Res 52(24):6761-6767 (1992) (Lintuzumab, HuM195), Lapusan et al., Invest New Drugs
30 30(3):1121-1131 (2012) (AVE9633), Aigner et al., Leukemia 27(5): 1107-1115 (2013) (AMG330, CD33 BiTE), Dutour et al., Adv hematol 2012:683065 (2012), and Pizzitola et al., Leukemia doi:10.1038/Lue.2014.62 (2014). In embodiments, the antigen binding domain is or is derived from a murine anti-human CD33 binding domain. In embodiments, the antigen binding domain is a humanized antibody or antibody fragment, e.g., scFv domain. In an embodiment, the antigen binding domain is a
35 human antibody or antibody fragment that binds to human CD33. In embodiments, the antigen binding domain is an scFv domain which includes a light chain variable region (VL) and a heavy chain variable region (VH). The VL and VH may attached by a linker described herein, e.g., comprising the sequence

GGGGSGGGSGGGGS (SEQ ID NO: 30), and may be in any orientation, e.g., VL-linker-VH, or VH-linker-VL.

In one aspect, the antigen-binding domain of a CAR binds to CLL-1, e.g., human CLL-1. Any known CLL-1 binding domain may be used in the invention. In one embodiment, an antigen binding domain against CLL-1 is an antigen binding portion, e.g., CDRs or VH and VL, of an antibody, antigen-binding fragment or CAR described in, e.g., PCT publication WO2016/014535 or US Patent Publication 2016-0051651-A1, the contents of which are incorporated herein in their entirety. In one embodiment, an antigen binding domain against CLL-1 is an antigen binding portion, e.g., CDRs, of an antibody available from R&D, ebiosciences, Abcam, for example, PE-CLL1-hu Cat# 353604 (BioLegend); and PE-CLL1 (CLEC12A) Cat# 562566 (BD). In embodiments, the antigen binding domain is or is derived from a murine anti-human CLL-1 binding domain. In embodiments, the antigen binding domain is a humanized antibody or antibody fragment, e.g., scFv domain. In an embodiment, the antigen binding domain is a human antibody or antibody fragment that binds to human CLL-1. In embodiments, the antigen binding domain is an scFv domain which includes a light chain variable region (VL) and a heavy chain variable region (VH). The VL and VH may attached by a linker described herein, e.g., comprising the sequence GGGGSGGGSGGGGS (SEQ ID NO: 30), and may be in any orientation, e.g., VL-linker-VH, or VH-linker-VL.

In some embodiments, the antigen binding domain of a CAR targets a B-Cell antigen. In an embodiment, the B cell antigen is an antigen that is preferentially or specifically expressed on the surface of the B cell. The antigen can be expressed on the surface of any one of the following types of B cells: progenitor B cells (e.g., pre-B cells or pro-B cells), early pro-B cells, late pro-B cells, large pre-B cells, small pre-B cells, immature B cells, e.g., naïve B cells, mature B cells, plasma B cells, plasmablasts, memory B cells, B-1 cells, B-2 cells, marginal-zone B cells, follicular B cells, germinal center B cells, or regulatory B cells (Bregs).

The present disclosure provides CARs that can target the following antigens: CD19; CD123; CD22; CD30; CD171; CS-1; C-type lectin-like molecule-1, CD33; epidermal growth factor receptor variant III (EGFRvIII); ganglioside G2 (GD2); ganglioside GD3; TNF receptor family member B cell maturation (BCMA); Tn antigen ((Tn Ag) or (GalNAc α -Ser/Thr)); prostate-specific membrane antigen (PSMA); Receptor tyrosine kinase-like orphan receptor 1 (ROR1); Fms-Like Tyrosine Kinase 3 (FLT3); Tumor-associated glycoprotein 72 (TAG72); CD38; CD44v6; Carcinoembryonic antigen (CEA); Epithelial cell adhesion molecule (EPCAM); B7H3 (CD276); KIT (CD117); Interleukin-13 receptor subunit alpha-2; Mesothelin; Interleukin 11 receptor alpha (IL-11Ra); prostate stem cell antigen (PSCA); Protease Serine 21; vascular endothelial growth factor receptor 2 (VEGFR2); Lewis(Y) antigen; CD24; Platelet-derived growth factor receptor beta (PDGFR-beta); Stage-specific embryonic antigen-4 (SSEA-4); CD20; Folate receptor alpha; Receptor tyrosine-protein kinase ERBB2 (Her2/neu); Mucin 1, cell surface associated (MUC1); epidermal growth factor receptor (EGFR); neural cell adhesion molecule (NCAM); Prostase;

prostatic acid phosphatase (PAP); elongation factor 2 mutated (ELF2M); Ephrin B2; fibroblast activation protein alpha (FAP); insulin-like growth factor 1 receptor (IGF-I receptor), carbonic anhydrase IX (CAIX); Proteasome (Prosome, Macropain) Subunit, Beta Type, 9 (LMP2); glycoprotein 100 (gp100); oncogene fusion protein consisting of breakpoint cluster region (BCR) and Abelson murine leukemia viral oncogene homolog 1 (Abl) (bcr-abl); tyrosinase; ephrin type-A receptor 2 (EphA2); Fucosyl GM1; sialyl Lewis adhesion molecule (sLe); ganglioside GM3; transglutaminase 5 (TGS5); high molecular weight-melanoma-associated antigen (HMWMAA); o-acetyl-GD2 ganglioside (OAcGD2); Folate receptor beta; tumor endothelial marker 1 (TEM1/CD248); tumor endothelial marker 7-related (TEM7R); claudin 6 (CLDN6); thyroid stimulating hormone receptor (TSHR); G protein-coupled receptor class C group 5, member D (GPRC5D); chromosome X open reading frame 61 (CXORF61); CD97; CD179a; anaplastic lymphoma kinase (ALK); Polysialic acid; placenta-specific 1 (PLAC1); hexasaccharide portion of globoH glycosphingolipid (GloboH); mammary gland differentiation antigen (NY-BR-1); uroplakin 2 (UPK2); Hepatitis A virus cellular receptor 1 (HAVCR1); adrenoceptor beta 3 (ADRB3); pannexin 3 (PANX3); G protein-coupled receptor 20 (GPR20); lymphocyte antigen 6 complex, locus K 9 (LY6K); Olfactory receptor 51E2 (OR51E2); TCR Gamma Alternate Reading Frame Protein (TARP); Wilms tumor protein (WT1); Cancer/testis antigen 1 (NY-ESO-1); Cancer/testis antigen 2 (LAGE-1a); Melanoma-associated antigen 1 (MAGE-A1); ETS translocation-variant gene 6, located on chromosome 12p (ETV6-AML); sperm protein 17 (SPA17); X Antigen Family, Member 1A (XAGE1); angiopoietin-binding cell surface receptor 2 (Tie 2); melanoma cancer testis antigen-1 (MAD-CT-1); melanoma cancer testis antigen-2 (MAD-CT-2); Fos-related antigen 1; tumor protein p53 (p53); p53 mutant; prostatein; surviving; telomerase; prostate carcinoma tumor antigen-1, melanoma antigen recognized by T cells 1; Rat sarcoma (Ras) mutant; human Telomerase reverse transcriptase (hTERT); sarcoma translocation breakpoints; melanoma inhibitor of apoptosis (ML-IAP); ERG (transmembrane protease, serine 2 (TMPRSS2) ETS fusion gene); N-Acetyl glucosaminyl-transferase V (NA17); paired box protein Pax-3 (PAX3); Androgen receptor; Cyclin B1; v-myc avian myelocytomatosis viral oncogene neuroblastoma derived homolog (MYCN); Ras Homolog Family Member C (RhoC); Tyrosinase-related protein 2 (TRP-2); Cytochrome P450 1B1 (CYP1B1); CCCTC-Binding Factor (Zinc Finger Protein)-Like, Squamous Cell Carcinoma Antigen Recognized By T Cells 3 (SART3); Paired box protein Pax-5 (PAX5); proacrosin binding protein sp32 (OY-TES1); lymphocyte-specific protein tyrosine kinase (LCK); A kinase anchor protein 4 (AKAP-4); synovial sarcoma, X breakpoint 2 (SSX2); Receptor for Advanced Glycation Endproducts (RAGE-1); renal ubiquitous 1 (RU1); renal ubiquitous 2 (RU2); legumain; human papilloma virus E6 (HPV E6); human papilloma virus E7 (HPV E7); intestinal carboxyl esterase; heat shock protein 70-2 mutated (mut hsp70-2); CD79a; CD79b; CD72; Leukocyte-associated immunoglobulin-like receptor 1 (LAIR1); Fc fragment of IgA receptor (FCAR or CD89); Leukocyte immunoglobulin-like receptor subfamily A member 2 (LILRA2); CD300 molecule-like family member f (CD300LF); C-type lectin domain family 12 member A (CLEC12A); bone marrow stromal cell antigen 2 (BST2); EGF-like module-containing mucin-like hormone receptor-like 2 (EMR2); lymphocyte antigen 75 (LY75); Glypican-3 (GPC3); Fc receptor-like 5 (FCRL5);

immunoglobulin lambda-like polypeptide 1 (IGLL1); TNF receptor family member; Fms-Like Tyrosine Kinase 3 (FL T3); CD10, CD19, CD20, CD21, CD22, CD23, CD24, CD25, CD37, CD38, CD53, CD72, CD73, CD74, CD75, CD77, CD79a, CD79b, CD80, CD81, CD82, CD83, CD84, CD85, ROR1, BCMA, CD86, and CD179b. Other B cell antigens that can be targeted by a CAR described herein include:

5 CD1a, CD1b, CD1c, CD1d, CD2, CD5, CD6, CD9, CD11a, CD11b, CD11c, CD17, CD18, CD26, CD27, CD29, CD30, CD31, CD32a, CD32b, CD35, CD38, CD39, CD40, CD44, CD45, CD45RA, CD45RB, CD45RC, CD45RO, CD46, CD47, CD48, CD49b, CD49c, CD49d, CD50, CD52, CD54, CD55, CD58, CD60a, CD62L, CD63, CD63, CD68 CD69, CD70, CD85E, CD85I, CD85J, CD92, CD95, CD97, CD98, CD99, CD100, CD102, CD108, CD119, CD120a, CD120b, CD121b, CD122, CD124, CD125, CD126,
10 CD130, CD132, CD137, CD138, CD139, CD147, CD148, CD150, CD152, CD162, CD164, CD166, CD167a, CD170, CD175, CD175s, CD180, CD184, CD185, CD192, CD196, CD197, CD200, CD205, CD210a, CDw210b, CD212, CD213a1, CD213a2, CD215, CD217, CD218a, CD218b, CD220, CD221, CD224, CD225, CD226, CD227, CD229, CD230, CD232, CD252, CD253, CD257, CD258, CD261, CD262, CD263, CD264, CD267, CD268, CD269, CD270, CD272, CD274, CD275, CD277, CD279,
15 CD283, CD289, CD290, CD295, CD298, CD300a, CD300c, CD305, CD306, CD307a, CD307b, CD307c, CD307d, CD307e, CD314, CD315, CD316, CD317, CD319, CD321, CD327, CD328, CD329, CD338, CD351, CD352, CD353, CD354, CD355, CD357, CD358, CD360, CD361, CD362, and CD363.

In another embodiment, the antigen targeted by the CAR is chosen from CD19, BCMA, CD20, CD22, FcRn5, FcRn2, CS-1 and CD138. In an embodiment, the antigen targeted by the CAR is CD19. In an
20 embodiment, the antigen targeted by the CAR is CD20. In an embodiment, the antigen targeted by the CAR is CD22. In an embodiment, the antigen targeted by the CAR is BCMA. In an embodiment, the antigen targeted by the CAR is FcRn5. In an embodiment, the antigen targeted by the CAR is FcRn2. In an embodiment, the antigen targeted by the CAR is CS-1. In an embodiment, the antigen targeted by the CAR is CD138.

25 In one embodiment, the antigen-binding domain of a CAR, e.g., the CAR expressed by a cell of the invention (e.g., a cell that also expresses a CAR), can be chosen such that a preferred B cell population is targeted. For example, in an embodiment where targeting of B regulatory cells is desired, an antigen binding domain is selected that targets an antigen that is expressed on regulatory B cells and not on other B cell populations, e.g., plasma B cells and memory B cells. Cell surface markers expressed on
30 regulatory B cells include: CD19, CD24, CD25, CD38, or CD86, or markers described in He et al., 2014, *J Immunology Research*, Article ID 215471. When targeting of more than one type of B cells is desired, an antigen binding domain that targets an antigen that is expressed by all of the B cells to be targeted can be selected.

In an embodiment, the antigen-binding domain of a CAR, e.g., the CAR expressed by a cell of the
35 invention, binds to CD19. CD19 is found on B cells throughout differentiation of the lineage from the pro/pre-B cell stage through the terminally differentiated plasma cell stage. In an embodiment, the

antigen binding domain is a murine scFv domain that binds to human CD19, e.g., CTL019 (e.g., SEQ ID NO: 356). In an embodiment, the antigen binding domain is a humanized antibody or antibody fragment, e.g., scFv domain, derived from the murine CTL019 scFv. In an embodiment, the antigen binding domain is a human antibody or antibody fragment that binds to human CD19. Exemplary scFv domains (and their sequences, e.g., CDRs, VL and VH sequences) that bind to CD19 are provided in Table 7 and Table 15A. The scFv domain sequences provided in Table 7 include a light chain variable region (VL) and a heavy chain variable region (VH). The VL and VH are attached by a linker comprising the sequence GGGGSGGGGSGGGGS (SEQ ID NO: 30), e.g., in the following orientation: VL-linker-VH.

Table 7. Antigen Binding domains that bind CD19

Antigen	Name	Amino Acid Sequence	SEQ ID NO:
CD19	muCTL019	DIQMTQTTSSLSASLGDRVTISCRASQDISKYLNWYQQKPDGTVKLLI YHTSRLHSGVPSRFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLP YTFGGGKLEITGGGGSGGGGSGGGGSEVKLQESGPGLVAPSQSL VTCTVSGVSLPDYGVSWIRQPPRGKLEWLGVIWGSETTYNSALKSR LTIKDNSKSQVFLKMNSLQTDDTAIYYCAKHHYYGGSYAMDYWGQG TSVTVSS	356
CD19	huscFv1	EIVMTQSPATLSLSPGERATLSCRASQDISKYLNWYQQKPGQAPRLLI YHTSRLHSGIPARFSGSGSGTDYTLTISSLPEDFAVYFCQQGNTLPY TFGQGTKLEIKGGGGSGGGGSGGGGSGVQLQESGPGLVKPSSETLSL TCTVSGVSLPDYGVSWIRQPPGKLEWIGVIWGSETTYSSSLKSRV TISKDNSKNQVSLKLSSVTAADTAVYYCAKHHYYGGSYAMDYWGQG TLVTVSS	357
CD19	huscFv2	EIVMTQSPATLSLSPGERATLSCRASQDISKYLNWYQQKPGQAPRLLI YHTSRLHSGIPARFSGSGSGTDYTLTISSLPEDFAVYFCQQGNTLPY TFGQGTKLEIKGGGGSGGGGSGGGGSGVQLQESGPGLVKPSSETLSL TCTVSGVSLPDYGVSWIRQPPGKLEWIGVIWGSETTYQSSSLKSRV TISKDNSKNQVSLKLSSVTAADTAVYYCAKHHYYGGSYAMDYWGQG TLVTVSS	358
CD19	huscFv3	QVQLQESGPGLVKPSSETLSLTCTVSGVSLPDYGVSWIRQPPGKLE WIGVIWGSETTYSSSLKSRVTISKDNSKNQVSLKLSSVTAADTAVYY CAKHHYYGGSYAMDYWGQGLTVTVSSGGGGSGGGGSGGGGSEIV MTQSPATLSLSPGERATLSCRASQDISKYLNWYQQKPGQAPRLLIYH TSRLHSGIPARFSGSGSGTDYTLTISSLPEDFAVYFCQQGNTLPYTF GQGTKLEIK	359
CD19	huscFv4	QVQLQESGPGLVKPSSETLSLTCTVSGVSLPDYGVSWIRQPPGKLE WIGVIWGSETTYQSSSLKSRVTISKDNSKNQVSLKLSSVTAADTAVYY CAKHHYYGGSYAMDYWGQGLTVTVSSGGGGSGGGGSGGGGSEIV MTQSPATLSLSPGERATLSCRASQDISKYLNWYQQKPGQAPRLLIYH TSRLHSGIPARFSGSGSGTDYTLTISSLPEDFAVYFCQQGNTLPYTF GQGTKLEIK	360
CD19	huscFv5	EIVMTQSPATLSLSPGERATLSCRASQDISKYLNWYQQKPGQAPRLLI YHTSRLHSGIPARFSGSGSGTDYTLTISSLPEDFAVYFCQQGNTLPY TFGQGTKLEIKGGGGSGGGGSGGGGSGGGGSGVQLQESGPGLVK PSETLSLTCTVSGVSLPDYGVSWIRQPPGKLEWIGVIWGSETTYSS SSLKSRVTISKDNSKNQVSLKLSSVTAADTAVYYCAKHHYYGGSYAM DYWGQGLTVTVSS	361
CD19	huscFv6	EIVMTQSPATLSLSPGERATLSCRASQDISKYLNWYQQKPGQAPRLLI YHTSRLHSGIPARFSGSGSGTDYTLTISSLPEDFAVYFCQQGNTLPY	362

		TFGQGTKLEIKGGGGSGGGGSGGGGSGGGGSSQVQLQESGPGLVK PSETLSLTCTVSGVSLPDYGVSWIRQPPGKGLEWIGVIWGSETTYQ SSLKSRVTISKDNSKNQVSLKLSSVTAADTAVYYCAKHHYYGGSYAM DYWGQGTTLTVSS	
CD19	huscFv7	QVQLQESGPGLVKPSETLSLTCTVSGVSLPDYGVSWIRQPPGKGLE WIGVIWGSETTYSSSLKSRVTISKDNSKNQVSLKLSSVTAADTAVYY CAKHHYYGGSYAMDYWGQGTTLTVSSGGGGSGGGGSGGGGSGG GGSEIVMTQSPATLSLSPGERATLSCRASQDISKYLNWYQQKPGQAP RLLIYHTSRLHSGIPARFSGSGSGTDYTLTISSLQPEDFAVYFCQQGN TLPYTFGQGTKLEIK	363
CD19	huscFv8	QVQLQESGPGLVKPSETLSLTCTVSGVSLPDYGVSWIRQPPGKGLE WIGVIWGSETTYQSSSLKSRVTISKDNSKNQVSLKLSSVTAADTAVYY CAKHHYYGGSYAMDYWGQGTTLTVSSGGGGSGGGGSGGGGSGG GGSEIVMTQSPATLSLSPGERATLSCRASQDISKYLNWYQQKPGQAP RLLIYHTSRLHSGIPARFSGSGSGTDYTLTISSLQPEDFAVYFCQQGN TLPYTFGQGTKLEIK	364
CD19	huscFv9	EIVMTQSPATLSLSPGERATLSCRASQDISKYLNWYQQKPGQAPRLLI YHTSRLHSGIPARFSGSGSGTDYTLTISSLQPEDFAVYFCQQGNTLPY TFGQGTKLEIKGGGGSGGGGSGGGGSGGGGSSQVQLQESGPGLVK PSETLSLTCTVSGVSLPDYGVSWIRQPPGKGLEWIGVIWGSETTYN SSLKSRVTISKDNSKNQVSLKLSSVTAADTAVYYCAKHHYYGGSYAM DYWGQGTTLTVSS	365
CD19	Hu scFv10	QVQLQESGPGLVKPSETLSLTCTVSGVSLPDYGVSWIRQPPGKGLE WIGVIWGSETTYNSSLKSRVTISKDNSKNQVSLKLSSVTAADTAVYY CAKHHYYGGSYAMDYWGQGTTLTVSSGGGGSGGGGSGGGGSGG GGSEIVMTQSPATLSLSPGERATLSCRASQDISKYLNWYQQKPGQAP RLLIYHTSRLHSGIPARFSGSGSGTDYTLTISSLQPEDFAVYFCQQGN TLPYTFGQGTKLEIK	366
CD19	Hu scFv11	EIVMTQSPATLSLSPGERATLSCRASQDISKYLNWYQQKPGQAPRLLI YHTSRLHSGIPARFSGSGSGTDYTLTISSLQPEDFAVYFCQQGNTLPY TFGQGTKLEIKGGGGSGGGGSGGGGSSQVQLQESGPGLVKPSETLSL TCTVSGVSLPDYGVSWIRQPPGKGLEWIGVIWGSETTYNSSLKSRV TISKDNSKNQVSLKLSSVTAADTAVYYCAKHHYYGGSYAMDYWGQ TLTVSS	367
CD19	Hu scFv12	QVQLQESGPGLVKPSETLSLTCTVSGVSLPDYGVSWIRQPPGKGLE WIGVIWGSETTYNSSLKSRVTISKDNSKNQVSLKLSSVTAADTAVYY CAKHHYYGGSYAMDYWGQGTTLTVSSGGGGSGGGGSGGGGSEIV MTQSPATLSLSPGERATLSCRASQDISKYLNWYQQKPGQAPRLLIYH TSRLHSGIPARFSGSGSGTDYTLTISSLQPEDFAVYFCQQGNTLPYTF GQGTKLEIK	368

The CDR sequences of the scFv domains of the CD19 antigen binding domains provided in Table 7 are shown in Tables 8 and 15B for the heavy chain variable domains and in Tables 9 and 15C for the light chain variable domains. "ID" stands for the respective SEQ ID NO for each CDR.

5 **Table 8.** Heavy Chain Variable Domain CDRs

Description	FW	HCDR1	SEQ ID NO	HCDR2	SEQ ID NO	HCDR3	SEQ ID NO
murine_CART19		GVSLPDYGV	369	VIWGSETTYNSALKS	370	HHYYGGSYAMDY	371

humanized_CART19 a	VH4	GVSLPDYGV	369	VIWGSETTTY SS SLKS	372	HYYYGGSYAMDY	371
humanized_CART19 b	VH4	GVSLPDYGV	369	VIWGSETTTY QS SLKS	373	HYYYGGSYAMDY	371
humanized_CART19 c	VH4	GVSLPDYGV	369	VIWGSETTYNS S SLKS	374	HYYYGGSYAMDY	371

Table 9. Light Chain Variable Domain CDRs

Description	FW	LCDR1	SEQ ID NO	LCDR2	SEQ ID NO	LCDR3	SEQ ID NO
murine_CART19		RASQDISKYL	375	HTSRLHS	376	QQGNTLPYT	377
humanized_CART19 a	VK3	RASQDISKYL	375	HTSRLHS	376	QQGNTLPYT	377
humanized_CART19 b	VK3	RASQDISKYL	375	HTSRLHS	376	QQGNTLPYT	377
humanized_CART19 c	VK3	RASQDISKYL	375	HTSRLHS	376	QQGNTLPYT	377

In an embodiment, the antigen binding domain comprises an anti-CD19 antibody, or fragment thereof, e.g., an scFv. For example, the antigen binding domain comprises a variable heavy chain and a variable light chain listed in Table 10. The linker sequence joining the variable heavy and variable light chains can be any of the linker sequences described herein, or alternatively, can be GSTSGSGKPGSGEGSTKG (SEQ ID NO: 378). The light chain variable region and heavy chain variable region of a scFv can be, e.g., in any of the following orientations: light chain variable region-linker-heavy chain variable region or heavy chain variable region-linker-light chain variable region.

Table 10. Additional Anti-CD19 antibody binding domains

Ab Name	VH Sequence	VL Sequence
SJ25-C1	QVQLLESGAELVRPGSSVKISCKASGYAFSSYWMNWVKQRPGQGLEWIGQIYPGDGDTNYNGKFKGQATLTADKSSSTAYMQLSGLTSEDSAVYSCARKTISSVVDYFYDYWGQGT	ELVLTQSPKFMSTSVGDRVSVTCKASQNVGTNVAWYQQKPGQSPKPLIYSATYRNSGVPDRFTGSGSGTDFTLTITNVQSKDLADYFYFCQYNRYPYTSGGGTKLEIKRRS (SEQ ID NO: 380)
	ScFv Sequence	
SJ25-C1 scFv	QVQLLESGAELVRPGSSVKISCKASGYAFSSYWMNWVKQRPGQGLEWIGQIYPGDGDTNYNGKFKGQATLTADKSSSTAYMQLSGLTSEDSAVYSCARKTISSVVDYFYDYWGQGTGSGSGKPGSGEGSTKGELVLTQSPKFMSTSVGDRVSVTCKASQNVGTNVAWYQQKPGQSPKPLIYSATYRNSGVPDRFTGSGSGTDFTLTITNVQSKDLADYFYFCQYNRYPYTSGGGTKLEIKRRS (SEQ ID NO: 381)	

In one embodiment, the CD19 binding domain comprises one or more (e.g., all three) light chain complementary determining region 1 (LC CDR1), light chain complementary determining region 2 (LC CDR2), and light chain complementary determining region 3 (LC CDR3) of a CD19 binding domain described herein, e.g., provided in Table 7 or 9, and/or one or more (e.g., all three) heavy chain complementary determining region 1 (HC CDR1), heavy chain complementary determining region 2 (HC CDR2), and heavy chain complementary determining region 3 (HC CDR3) of a CD19 binding domain described herein, e.g., provided in Table 7 or 8. In one embodiment, the CD19 binding domain comprises one, two, or all of LC CDR1, LC CDR2, and LC CDR3 of any amino acid sequences as provided in Table 9, incorporated herein by reference; and one, two or all of HC CDR1, HC CDR2, and HC CDR3 of any amino acid sequences as provided in Table 8.

In one embodiment, the CD19 binding domain comprises a light chain variable region described herein (e.g., in Table 7 or 10) and/or a heavy chain variable region described herein (e.g., in Table 7 or 10). In one embodiment, the CD19 binding domain is a scFv comprising a light chain and a heavy chain of an amino acid sequence listed in Table 7 or 10. In an embodiment, the CD19 binding domain (e.g., an scFv) comprises: a light chain variable region comprising an amino acid sequence having at least one, two or three modifications (e.g., substitutions, e.g., conservative substitutions) but not more than 30, 20 or 10 modifications (e.g., substitutions, e.g., conservative substitutions) of an amino acid sequence of a light chain variable region provided in Table 7 or 10, or a sequence with 95-99% identity with an amino acid sequence provided in Table 7 or 10; and/or a heavy chain variable region comprising an amino acid sequence having at least one, two or three modifications (e.g., substitutions, e.g., conservative substitutions) but not more than 30, 20 or 10 modifications (e.g., substitutions, e.g., conservative substitutions) of an amino acid sequence of a heavy chain variable region provided in Table 7 or 10, or a sequence with 95-99% identity to an amino acid sequence provided in Table 7 or 10.

In one embodiment, the CD19 binding domain comprises an amino acid sequence selected from any one of SEQ ID NOs: 356-368 and 381; or an amino acid sequence having at least one, two or three modifications (e.g., substitutions, e.g., conservative substitutions) but not more than 30, 20 or 10 modifications (e.g., substitutions, e.g., conservative substitutions) to any of the aforesaid sequences; or a sequence with 95-99% identity to any of the aforesaid sequences. In one embodiment, the CD19 binding domain is a scFv, and a light chain variable region comprising an amino acid sequence described herein, e.g., in Table 7 or 10, is attached to a heavy chain variable region comprising an amino acid sequence described herein, e.g., in Table 7 or 10, via a linker, e.g., a linker described herein. In one embodiment, the CD19 binding domain includes a (Gly4-Ser)_n linker, wherein n is 1, 2, 3, 4, 5, or 6, preferably 4 (SEQ ID NO: 967). The light chain variable region and heavy chain variable region of a scFv can be, e.g., in any of the following orientations: light chain variable region-linker-heavy chain variable region or heavy chain variable region-linker-light chain variable region.

Any known CAR, e.g., the CD19 antigen binding domain of any known CAR, in the art can be used in accordance with the instant invention to construct a CAR. For example, LG-740; CAR described in the US Pat. No. 8,399,645; US Pat. No. 7,446,190; Xu et al., Leuk Lymphoma. 2013 54(2):255-260(2012); Cruz et al., Blood 122(17):2965-2973 (2013); Brentjens et al., Blood, 118(18):4817-4828 (2011);

- 5 Kochenderfer et al., Blood 116(20):4099-102 (2010); Kochenderfer et al., Blood 122 (25):4129-39(2013); and 16th Annu Meet Am Soc Gen Cell Ther (ASGCT) (May 15-18, Salt Lake City) 2013, Abst 10. In one embodiment, an antigen binding domain against CD19 is an antigen binding portion, e.g., CDRs, of a CAR, antibody or antigen-binding fragment thereof described in, e.g., PCT publication WO2012/079000; PCT publication WO2014/153270; Kochenderfer, J.N. et al., J. Immunother. 32 (7), 689-702
 10 (2009); Kochenderfer, J.N., et al., Blood, 116 (20), 4099-4102 (2010); PCT publication WO2014/031687; Bejcek, Cancer Research, 55, 2346-2351, 1995; or U.S. Patent No. 7,446,190.

- In an embodiment, the antigen-binding domain of a CAR, e.g., the CAR expressed by a cell of the invention, binds to BCMA. BCMA is found preferentially expressed in mature B lymphocytes. In an embodiment, the antigen binding domain is a murine scFv domain that binds to human BCMA. In an
 15 embodiment, the antigen binding domain is a humanized antibody or antibody fragment, e.g., scFv domain, that binds human BCMA. In an embodiment, the antigen binding domain is a human antibody or antibody fragment that binds to human BCMA. Exemplary scFv domains (and their sequences, e.g., CDRs, VL and VH sequences) that bind to BCMA are provided in Table 11, Table 12, Table 13 and Table 14. The scFv domain sequences provided in Table 11 and Table 12 include a light chain variable region
 20 (VL) and a heavy chain variable region (VH). The VL and VH are attached by a linker, e.g., in the following orientation: VH-linker-VL.

Table 11. Antigen Binding domains that bind BCMA

The amino acid sequences variable heavy chain and variable light chain sequences for each scFv is also provided.

Name/ Description	SEQ ID NO:	Sequence
139109		
139109- aa ScFv domain	382	EVQLVESGGGLVQPGGSLRLSCAVSGFALSNHGMSWVRRAPGKGLEW VSGIVYSGSTYYAASVKGRFTISRDNRSRNTLYLQMNSLRPEDTAIYYCSA HGGESDVWGQGTTVTVSSASGGGGSGGRASGGGGSDIQLTQSPSSLS ASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRF SGSGSGTDFTLTISLQPEDFATYYCQQSYSTPYTFGQGTKVEIK
139109- nt ScFv domain	383	GAAGTGCAATTGGTGAATCAGGGGGAGGACTTGTGCAGCCTGGAG GATCGCTGAGACTGTCATGTGCCGTGTCCGGCTTTGCCCTGTCCAAC CACGGGATGTCCTGGGTCCGCCGCGCCTGGAAAGGGCCTCGAAT GGGTGTCGGGTATTGTGTACAGCGGTAGCACCTACTATGCCGCATCC GTGAAGGGGAGATTACCATCAGCCGGGACAACCTCCAGGAACACTCT GTACCTCCAAATGAATTCGCTGAGGCCAGAGGACACTGCCATCTACT ACTGCTCCGCGCATGGCGGAGAGTCCGACGTCTGGGGACAGGGGA CCACCGTGACCGTGTCTAGCGCGTCCGGCGGAGGCGGCAGCGGGG

		GTCGGGGCATCAGGGGGGCGGGCGGATCGGACATCCAGCTCACCCAGTC CCCGAGCTCGCTGTCCGCCTCCGTGGGAGATCGGGTCACCATCACG TGCCGCGCCAGCCAGTCGATTTCTCTACCTGAACTGGTACCAACA GAAGCCCGGAAAAGCCCCGAAGCTTCTCATCTACGCCGCCTCGAGC CTGCAGTCAGGAGTGCCCTCACGGTTCTCCGGCTCCGGTTCCGGTA CTGATTTACCCCTGACCATTTCTCCCTGCAACCGGAGGACTTCGCT ACTTACTACTGCCAGCAGTCGTA CTCCACCCCTACACTTTCCGGACAA GGCACCAAGGTCGAAATCAAG
139109- aa VH	384	EVQLVESGGGLVQPGGSLRLSCAVSGFALSNHGMSWVRRAPGKGLEW VSGIVYSGSTYYAASVKGRFTISRDNSENRLYLQMNSLRPEDTAIYYCSA HGGESDVWGQGTTVTVSS
139109- aa VL	385	DIQLTQSPSSLSASVGDRTITCRASQSISSYLNWYQQKPGKAPKLLIYA ASSLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYSTPYTFG QGTKVEIK
139103		
139103- aa ScFv domain	386	QVQLVESGGGLVQPGRSLRLSCAASGFTFSNYAMSWVRQAPGKGLGW VSGISRSGENTYYADSVKGRFTISRDNSENRLYLQMNSLRDEDTAVYYC ARSPAHHYGGMDVWGQGTTVTVSSASGGGGSGGRASGGGGSDIVLTQ SPGTLSLSPGERATLSCRASQSISSSFLAWYQQKPGQAPRLLIYGASRR ATGIPDRFSGSGSGTDFTLTISRLEPEDSAVYYCQYHSSPSWTFGQGT KLEIK
139103- nt ScFv domain	387	CAAGTGCAACTCGTGGAATCTGGTGGAGGACTCGTGCAACCCGGAA GATCGCTTAGACTGTCTGTGCCGCCAGCGGGTTCACTTTCTCGAAC TACGCGATGTCCTGGGTCCGCCAGGCACCCGGAAAGGGAAGTCCGGT GGGTGTCCGGCATTTCCTGGTCCGGCGAAAATACCTACTACGCCGA CTCCGTGAAGGGCCGCTTCAACATCTCAAGGGACAACAGCAAAAACA CCCTGTACTTGCAAATGAACTCCCTGCGGGATGAAGATACAGCCGTG TACTATTGCGCCCGGTGCGCTGCCATTACTACGGCGGAATGGACGT CTGGGGACAGGGAACCACTGTGACTGTCAGCAGCGCGTCCGGTGGC GGCGGCTCAGGGGGTCCGGCCCTCCGGGGGGGGAGGGTCCGACATC GTGCTGACCCAGTCCCCGGGAACCTGAGCCTGAGCCCGGGAGAGC GCGCGACCCTGTGATGCCGGGCATCCCAGAGCATTAGCTCCTCTTT CTCGCCTGGTATCAGCAGAAGCCCGGACAGGCCCGGAGGCTGCTGA TCTACGGCGCTAGCAGAAGGGCTACCGGAATCCCAGACCGGTTCTC CGGCTCCGGTTCCGGGACCGATTTCACCCTTACTATCTCGCGCCTGG AACCTGAGGACTCCGCCGTCTACTACTGCCAGCAGTACCACTCATCC CCGTCGTGGACGTTCCGACAGGGCACCAAGCTGGAGATTAAG
139103- aa VH	388	QVQLVESGGGLVQPGRSLRLSCAASGFTFSNYAMSWVRQAPGKGLGW VSGISRSGENTYYADSVKGRFTISRDNSENRLYLQMNSLRDEDTAVYYC ARSPAHHYGGMDVWGQGTTVTVSS
139103- aa VL	389	DIVLTQSPGTLSLSPGERATLSCRASQSISSSFLAWYQQKPGQAPRLLIY GASRRATGIPDRFSGSGSGTDFTLTISRLEPEDSAVYYCQYHSSPSWT FGQGTKLEIK
139105		
139105- aa ScFv domain	390	QVQLVESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEW VSGISWNSGSIGYADSVKGRFTISRDNKNSLYLQMNSLRAEDTALYYC SVHSFLAYWGQGLTVTVSSASGGGGSGGRASGGGGSDIVMTQTPLSLP VTPGEPASISCRSSQSLLSNGYNYLDWYLQKPGQSPQLLIYLGSNRAS GVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPYTFGQGTKV EIK
139105- nt ScFv domain	391	CAAGTGCAACTCGTGAATCCGGTGGAGGTCTGGTCCAACCTGGTAG AAGCCTGAGACTGTCTGTGCGGCCAGCGGATTCACTTTGATGACT ATGCTATGCACTGGGTGCGGCAGGCCCGAGGAAAGGGCCTGGAATG GGTGTCCGGGAATTAGCTGGAACCTCCGGGTCCATTGGCTACGCCGAC TCCGTGAAGGGCCGCTTACCATCTCCCGCGACAACGCAAAGAACTC

		CCTGTACTTGCAAATGAACTCGCTCAGGGCTGAGGATACCGCGCTGT ACTACTGCTCCGTGCATTCTTCCTGGCCTACTGGGGACAGGGA CTGGTCACCGTGTGAGCGCCTCCGGCGGCGGGGGCTCGGGTGA CGGGCCTCGGGCGGAGGGGGGTCCGACATCGTGATGACCCAGACC CCGCTGAGCTTGCCCGTGACTCCCGGAGAGCCTGCATCCATCTCCT GCCGGTCATCCCAGTCCCTTCTCCACTCCAACGGATACAACCTC GACTGGTACCTCCAGAAGCCGGGACAGAGCCCTCAGCTTCTGATCTA CCTGGGGTCAAATAGAGCCTCAGGAGTGCCGGATCGGTTTACGCGGA TCTGGTTCGGGAACCTGATTTCACTCTGAAGATTTCCCGCGTGGAAGC CGAGGACGTGGGCGTCTACTACTGTATGCAGGCGCTGCAGACCCCC TATACCTTCGGCCAAGGGACGAAAGTGGAGATCAAG
139105- aa VH	392	QVQLVESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEW VSGISWNSGSIGYADSVKGRFTISRDNKNSLYLQMNSLRAEDTALYYC SVHSFLAYWGQGTLLTVSS
139105- aa VL	393	DIVMTQTPLSLPVTGPGEPAISCRSSQSLLHSNGYNYLDWYLQKPGQSP QLLIYLGSNRASGVDPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQ TPYTFGQGTKEIK
139111		
139111- aa ScFv domain	394	EVQLLESGGGLVQPGGSLRLSCAVSGFALSNGHMSWVRRAPGKGLEW VSGIVYSGSTYYAASVKGRFTISRDNRSNTLYLQMNSLRPEDTAIYYCSA HGGESDVWGQGTITVTVSSASGGGGSGGRASGGGGSDIVMTQTPLSL VTPGQPASISCKSSQSLLRNDGKTPLYWYLQKAGQPPQLLIYEVS NRFS GVDPDRFSGSGSGTDFTLKISRVEAEDVGAAYYCMQNIQFSPFGGGTKLEI K
139111- nt ScFv domain	395	GAAGTGCAATTGTTGGAATCTGGAGGAGGACTTGTGCAGCCTGGAG GATCACTGAGACTTTCGTGTGCGGTGTCAGGCTTCGCCCTGAGCAAC CACGGCATGAGCTGGGTGCGGAGAGCCCCGGGAAGGGTCTGGAA TGGGTGTCCGGGATCGTCTACTCCGGTTCACTTACTACGCCGCAAG CGTGAAGGGTTCGCTTACCATTTCCTCGCGATAACTCCCGGAACACCC TGTACCTCAAATGAACTCCCTGCGGCCGAGGACACCGCCATCTAC TACTGTTCCGCGCATGGAGGAGAGTCCGATGTCTGGGGACAGGGCA CTACCGTGACCGTGTGAGCGCCTCGGGGGGAGGAGGCTCCGGCG GTCGCGCCTCCGGGGGGGGTGGCAGCGACATTGTGATGACGCAGA CTCCACTCTCGCTGTCCGTGACCCCGGGACAGCCCGCGTCCATCTC GTGCAAGAGCTCCAGAGCCTGCTGAGGAACGACGGAAGACTCCT CTGTATTGGTACCTCCAGAAGGCTGGACAGCCCCCGCAACTGCTCAT CTACGAAGTGTCAAATCGCTTCTCCGGGGTGCCGGATCGGTTTTCCG GCTCGGGATCGGGCACCGACTTCACCCTGAAAATCTCCAGGGTCGA GGCCGAGGACGTGGGAGCCTACTACTGCATGCAAAACATCCAGTTCC CTTCCTTCGGCGGCGGCACAAAGCTGGAGATTAAG
139111- aa VH	396	EVQLLESGGGLVQPGGSLRLSCAVSGFALSNGHMSWVRRAPGKGLEW VSGIVYSGSTYYAASVKGRFTISRDNRSNTLYLQMNSLRPEDTAIYYCSA HGGESDVWGQGTITVTVSS
139111- aa VL	397	DIVMTQTPLSLSVTPGQPASISCKSSQSLLRNDGKTPLYWYLQKAGQPP QLLIYEVS NRFS GVDPDRFSGSGSGTDFTLKISRVEAEDVGAAYYCMQNIQF PSFGGGTKLEIK
139100		
139100- aa ScFv domain	398	QVQLVQSGAEVRKTGASVKVSCASGYIFDNFGINWVRQAPGQGLEWM GWINPKNNNTNYAQKFQGRVTITADESTNTAYMEVSSLRSEDTAVYYCA RGPYYYQSYMVDVWGQGTMTVTVSSASGGGGSGGRASGGGGSDIVMTQ TPLSLPVTGPGEPAISCRSSQSLLHSNGYNYLNWYLQKPGQSPQLLIYLG SKRASGVDPDRFSGSGSGTDFTLHITRVGAEDVGVYYCMQALQTPYTFG QGTKEIK
139100- nt ScFv domain	399	CAAGTCCAACCTCGTCCAGTCCGGCGCAGAAGTCAGAAAAACCGGTG CTAGCGTGAAAGTGTCTGCAAGGCCTCCGGCTACATTTTCGATAAC

		TTCGGAATCAACTGGGTCAGACAGGCCCGGGCCAGGGGCTGGAAT GGATGGGATGGATCAACCCCAAGAACAACAACCAACTACGCACAG AAGTTCCAGGGCCGCGTGACTATCACCGCCGATGAATCGACCAATAC CGCCTACATGGAGGTGTCCTCCCTGCGGTCCGAGGACACTGCCGTG TATTACTGCGCGAGGGGCCCATACTACTACCAAAGCTACATGGACGT CTGGGGACAGGGAACCATGGTGACCGTGTCTATCCGCCTCCGGTGGT GGAGGCTCCGGGGGGCGGGCTTCAGGAGGCGGAGGAAGCGATATT GTGATGACCCAGACTCCGCTTAGCCTGCCCGTGAATCCTGGAGAACC GGCCTCCATTTCTGCGCGTCTCGCAATCACTCCTGCATTCCAACG GTTACAACTACCTGAATTGGTACCTCCAGAAGCCTGGCCAGTCGCCC CAGTTGCTGATCTATCTGGGCTCGAAGCGCGCCTCCGGGGTGCCTG ACCGGTTTAGCGGATCTGGGAGCGGCACGGACTTCACTCTCCACATC ACCCGCGTGGGAGCGGAGGACGTGGGAGTGTACTACTGTATGCAGG CGCTGCAGACTCCGTACACATTCGGACAGGGCACCAAGCTGGAGAT CAAG
139100- aa VH	400	QVQLVQSGAEVRKTGASVKVSCKASGYIFDNFGINWVRQAPGQGLEWM GWINPKNNNTNYAQKFQGRVTITADESTNTAYMEVSSLRSEDVAVYYCA RGPYYYQSYMVDVWGQGTMTVSS
139100- aa VL	401	DIVMTQTPLSLPVTPEPASISCRSSQSLLHSNGYNYLNWYLQKPGQSP QLLIYLGSKRASGVPDFRSGSGSGTDFTLHITRVGAEDVGVYYCMQALQ TPYTFGQGTKEIK
139101		
139101- aa ScFv domain	402	QVQLQESGGGLVQPGGSLRLSCAASGFTFSSDAMTWVRQAPGKGLEW VSVISGSGGTTYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYC AKLDSSGYYYARGPRYWGGTGLTVTVSSASGGGGSGGRASGGGGSDIQ LTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYGAST LASGVPARFSGSGSGTHFTLTINSLQSEDSATYYCQQSYKRASFGQGTK VEIK
139101- nt ScFv domain	403	CAAGTGCAACTTCAAGAATCAGGCGGAGGACTCGTGCAGCCCGGAG GATCATTGCGGCTCTCGTGCGCCGCCTCGGGCTTACCTTCTCGAGC GACGCCATGACCTGGGTCCGCCAGGCCCGGGGAAGGGGCTGGAA TGGGTGTCTGTGATTTCCGGCTCCGGGGGAACACTACGTACTACGCCGA TTCCGTGAAAGGTCGCTTCACTATCTCCCGGGACAACAGCAAGAACA CCCTTTATCTGCAAATGAATTCCCTCCGCGCCGAGGACACCGCCGTG TACTACTGCGCCAAGCTGGACTCCTCGGGCTACTACTATGCCCGGGG TCCGAGATACTGGGGACAGGGAACCCTCGTGACCGTGTCTCCGCG TCCGGCGGAGGAGGGTCGGGAGGGCGGGCCTCCGGCGGCGGCGG TTCGGACATCCAGCTGACCCAGTCCCCATCCTCACTGAGCGCAAGCG TGGGCGACAGAGTCACCATTACATGCAGGGCGTCCAGAGCATCAG CTCCTACCTGAACTGGTACCAACAGAAGCCTGGAAAGGCTCCTAAGC TGTTGATCTACGGGGCTTCGACCCTGGCATCCGGGGTGCCCGCGAG GTTTAGCGGAAGCGGTAGCGGCACTCACTTCACTCTGACCATTAAACA GCCTCCAGTCCGAGGATTAGCCACTTACTACTGTGAGCAGTCCTAC AAGCGGGCCAGCTTCGGACAGGGCACTAAGGTGAGATCAAG
139101- aa VH	404	QVQLQESGGGLVQPGGSLRLSCAASGFTFSSDAMTWVRQAPGKGLEW VSVISGSGGTTYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYC AKLDSSGYYYARGPRYWGGTGLTVTVSS
139101- aa VL	405	DIQLTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYG ASTLASGVPARFSGSGSGTHFTLTINSLQSEDSATYYCQQSYKRASFGQ GTKVEIK
139102		
139102- aa ScFv domain	406	QVQLVQSGAEVKKPGASVKVSCKASGYTFSNYGITWVRQAPGQGLEW MGWISAYNGNTNYAQKFQGRVTMTNRNTSISTAYMELSSLRSEDVAVYYC ARGPYYYYMDVWGKGTMTVTVSSASGGGGSGGRASGGGGSEIVMTQS PLSLPVTPEPASISCRSSQSLLYSNGYNYVDWYLQKPGQSPQLLIYLG

		NRASGVDPDRFSGSGSGTDFKLQISRVEAEDVGIYYCMQGRQFPYSFGQ GTKVEIK
139102- nt ScFv domain	407	CAAGTCCAAGTGGTCCAGAGCGGTGCAGAAGTGAAGAAGCCCGGAG CGAGCGTGAAAGTGTCTGCAAGGCTTCCGGGTACACCTTCTCCAAC TACGGCATCACTTGGGTGCGCCAGGCCCGGGACAGGGCCTGGAAT GGATGGGGTGGATTTCCGCGTACAACGGCAATACGAACTACGCTCAG AAGTTCCAGGGTAGAGTGACCATGACTAGGAACACCTCCATTTCCAC CGCCTACATGGAAGTGTCTTCCCTGCGGAGCGAGGACACCGCCGTG TACTATTGCGCCCGGGGACCATACTACTACTACATGGATGTCTGGGG GAAGGGGACTATGGTCACCGTGTATCCGCCTCGGGAGGCGGCGGA TCAGGAGGACGCGCCTCTGGTGGTGGAGGATCGGAGATCGTGATGA CCCAGAGCCCTCTCTCCTTGCCCGTGAAGTCTGGGGAGCCCGCATC CATTTTCATGCCGGAGCTCCAGTCACTTCTCTACTCCAACGGCTATAA CTACGTGGATTGGTACCTCCAAAAGCCGGGCCAGAGCCCGCAGCTG CTGATCTACCTGGGCTCGAACAGGGGCCAGCGGAGTGCCTGACCGGT TCTCCGGGTGCGGAAGCGGGACCGACTTCAAGCTGCAAATCTCGAG AGTGGAGGCCGAGGACGTGGGAATCTACTACTGTATGCAGGGCCGC CAGTTTCCGTACTCGTTCCGACAGGGCACCAAGTGGAAATCAAG
139102- aa VH	408	QVQLVQSGAEVKKPGASVKVSKASGYTFSNYGITWVRQAPGQGLEW MGWISAYNGNTNYAQKFQGRVTMTRNTSISTAYMELSSLRSEDVAVYYC ARGPYYYMDVWGKGMTVTVSS
139102- aa VL	409	EIVMTQSPLSLPVTPGEPASISCRSSQSLLYSNGYNYVDWYLQKPGQSP QLLIYLGSNRASGVDPDRFSGSGSGTDFKLQISRVEAEDVGIYYCMQGRQ FPYSFGQGGTKVEIK
139104		
139104- aa ScFv domain	410	EVQLLETGGGLVQPGGSLRLSCAVSGFALSNHGMSWVRRAPGKGLEW VSGIVYSGSTYYAASVKGRFTISRDNRSRNTLYLQMNSLRPEDTAIYYCSA HGGESDVWGQGTITVTVSSASGGGGSGGRASGGGGSEIVLTQSPATLS VSPGESATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASTRASGIPDR FSGSGSGTDFLTITSLQAEDVAVYYCQQYGSSTLTFGGGGTKVEIK
139104- nt ScFv domain	411	GAAGTGCAATTGCTCGAAACTGGAGGAGGTCTGGTGAACCTGGAG GATCACTTCGCTGTCTGCGCCGTGTCTGGGCTTTGCCCTGTCCAAC CATGGAATGAGCTGGGTCCGCCGCGCGCCGGGAAGGGCCTCGAA TGGGTGTCCGGCATCGTCTACTCCGGCTCCACCTACTACGCCGCGTC CGTGAAGGGCCGGTTCACGATTTACGGGACAACCTCGCGGAACACC CTGTACCTCCAAATGAATTCCCTTCGGCCGGAGGATACTGCCATCTA CTACTGCTCCGCCACCGGTGGCGAATCCGACGTCTGGGGCCAGGGA ACCACCGTGACCGTGTCCAGCGCGTCCGGGGGAGGAGGAAGCGGG GGTAGAGCATCGGGTGGAGGCGGATCAGAGATCGTGCTGACCCAGT CCCCCGCCACCTTGAGCGTGTCAACAGGAGAGTCCGCCACCCTGTC ATGCCGCGCCAGCCAGTCCGTGTCTCCAACCTGGCTTGGTACCAG CAGAAGCCGGGGCAGGCCCTAGACTCCTGATCTATGGGGCGTCA CCCGGGCATCTGGAATTCCCGATAGGTTTCAGCGGATCGGGCTCGGG CACTGACTTCACTCTGACCATCTCCTCGCTGCAAGCCGAGGACGTGG CTGTGTACTACTGTGACGAGTACGGAAGCTCCCTGACTTTCCGTGGC GGGACCAAAGTCGAGATTAAG
139104- aa VH	412	EVQLLETGGGLVQPGGSLRLSCAVSGFALSNHGMSWVRRAPGKGLEW VSGIVYSGSTYYAASVKGRFTISRDNRSRNTLYLQMNSLRPEDTAIYYCSA HGGESDVWGQGTITVTVSS
139104- aa VL	413	EIVLTQSPATLSVSPGESATLSCRASQSVSSNLAWYQQKPGQAPRLLIY GASTRASGIPDRFSGSGSGTDFLTITSLQAEDVAVYYCQQYGSSTLTFG GGTKVEIK
139106		
139106- aa ScFv domain	414	EVQLVETGGGLVQPGGSLRLSCAVSGFALSNHGMSWVRRAPGKGLEW VSGIVYSGSTYYAASVKGRFTISRDNRSRNTLYLQMNSLRPEDTAIYYCSA

		HGGESDVWGQGTTVTVSSASGGGGSGGRASGGGGSEIVMTQSPATLS VSPGERATLSCRASQSVSSKLAWYQQKPGQAPRLLMYGASIRATGIPDR FSGSGSGTEFTLTISLEPEDFAVYYCQQYGSSSWTFGQGTKVEIK
139106- nt ScFv domain	415	GAAGTGCAATTGGTGGAACTGGAGGAGGACTTGTGCAACCTGGAG GATCATTGAGACTGAGCTGCGCAGTGTCTGGGATTGCGCCTGAGCAAC CATGGAATGTCCTGGGTGAGAAGGGCCCTGGAAAAGGCCTCGAAT GGGTGTCAGGGATCGTGTACTCCGGTTCCTTACTACGCCGCTCC GTGAAGGGGCGCTTCACTATCTCACGGGATAACTCCCGCAATACCCT GTACCTCCAAATGAACAGCCTGCGGCCGGAGGATACCGCCATCTACT ACTGTTCCGCCACGGTGGAGAGTCTGACGTCTGGGGCCAGGGAAC TACCGTGACCGTGTCTCTCCGCGTCCGGCGGTGGAGGGAGCGGCGG CCGCGCCAGCGGCGGCGGAGGCTCCGAGATCGTGATGACCCAGAG CCCCGCTACTCTGTCTGGTGTCTGCCCGGAGAAAGGGCGACCCTGTCC TGCCGGGCGTCTGCAGTCCGTGAGCAGCAAGCTGGCTTGGTACCAGC AGAAGCCGGGCCAGGCACCACGCCTGCTTATGTACGGTGCCTCCAT TCGGGCCACCGGAATCCCGGACCGGTTCTCGGGGTCTGGGGTCCGG TACCGAGTTACACTGACCATTTCTCGCTCGAGCCCGAGGACTTTG CCGTCTATTACTGCCAGCAGTACGGCTCCTCCTCATGGACGTTCCGC CAGGGGACCAAGGTCGAAATCAAG
139106- aa VH	416	EVQLVETGGGLVQPGGSLRLSCAVSGFALSNHGMSWVRRAPGKGLEW VSGIVYSGSTYYAASVKGRFTISRDNRSRNTLYLQMNSLRPEDTAIYYCSA HGGESDVWGQGTTVTVSS
139106- aa VL	417	EIVMTQSPATLSVSPGERATLSCRASQSVSSKLAWYQQKPGQAPRLLM YGASIRATGIPDRFSGSGSGTEFTLTISLEPEDFAVYYCQQYGSSSWTF GQGTKVEIK
139107		
139107- aa ScFv domain	418	EVQLVETGGGVVQPGGSLRLSCAVSGFALSNHGMSWVRRAPGKGLEW VSGIVYSGSTYYAASVKGRFTISRDNRSRNTLYLQMNSLRPEDTAIYYCSA HGGESDVWGQGTTVTVSSASGGGGSGGRASGGGGSEIVLTQSPGTLT LSPGERATLSCRASQSVGSTNLAWYQQKPGQAPRLLIYDASNRATGIPD RFSGGGSGTDFTLTISRLEPEDFAVYYCQQYGSSPPWTFGQGTKVEIK
139107- nt ScFv domain	419	GAAGTGCAATTGGTGGAGACTGGAGGAGGAGTGGTGAACCTGGAG GAAGCCTGAGACTGTCATGCGCGGTGTCTGGGCTTCGCCCTCTCCAA CCACGGAATGTCCTGGGTCCGCCGGGCCCTGGGAAAGGACTTGAA TGGGTGTCCGGCATCGTGTACTCGGGTTCACCTACTACGCGGCCTC AGTGAAGGGCCGGTTTACTATTAGCCGCGACAACCTCCAGAAACACAC TGTACCTCCAAATGAACTCGCTGCGGCCGGAAGATACCGCTATCTAC TACTGCTCCGCCCATGGGGGAGAGTCCGACGTCTGGGGACAGGGCA CCTGTCACTGTGTCCAGCGCTTCCGGCGGTGGTGAAGCGGGGG ACGGGCCTCAGGAGGCGGTGGCAGCGAGATTGTGCTGACCCAGTCC CCCGGGACCCTGAGCCTGTCCCCGGGAGAAAGGGGCCACCCTCTCCT GTCTGGGCATCCCAGTCCGTGGGGTCTACTAACCTTGATGGTACCAG CAGAAGCCCGGCCAGGCCCTCGCCTGCTGATCTACGACGCGTCCA ATAGAGCCACCGGCATCCCGGATCGCTTCAGCGGAGGCGGATCGGG CACCGACTTCACCCTCACCATTTCAAGGCTGGAACCGGAGGACTTCG CCGTGTACTACTGCCAGCAGTATGGTTCTGTCCTCCACCTGGACGTT GGCCAGGGGACTAAGGTCGAGATCAAG
139107- aa VH	420	EVQLVETGGGVVQPGGSLRLSCAVSGFALSNHGMSWVRRAPGKGLEW VSGIVYSGSTYYAASVKGRFTISRDNRSRNTLYLQMNSLRPEDTAIYYCSA HGGESDVWGQGTTVTVSS
139107- aa VL	421	EIVLTQSPGTLTLSPGERATLSCRASQSVGSTNLAWYQQKPGQAPRLLI YDASNRATGIPDRFSGGGSGTDFTLTISRLEPEDFAVYYCQQYGSSPPW TFGQGTKVEIK
139108		
139108- aa	422	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWV

ScFv domain		SYISSSGSTIYYADSVKGRFTISRDNKNSLYLQMNSLRAEDTAVYYCAR ESGDGMDVWVGQGTTVTVSSASGGGGSGGRASGGGGSDIQMTQSPSS LSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPS RFGSGSGTDFTLTISLQPEDFATYYCQQSYTLAFGQGTKVDIK
139108- nt ScFv domain	423	CAAGTGCAACTCGTGGAATCTGGTGGAGGACTCGTGAAACCTGGAG GATCATTGAGACTGTCATGCGCGGCCTCGGGATTACGTTCTCCGAT TACTACATGAGCTGGATTGCGCAGGCTCCGGGGAAGGGACTGGAAT GGGTGTCCTACATTTCTCATCCGGCTCCACCATCTACTACGCGGAC TCCGTGAAGGGGAGATTCAACCATTAGCCGCGATAACGCCAAGAACAG CCTGTACCTTCAGATGAACTCCCTGCGGGCTGAAGATACTGCCGTCT ACTACTGCGCAAGGGAGAGCGGAGATGGGATGGACGTCTGGGGACA GGGTACCACTGTGACCGTGTCTGTCGGCCTCCGGCGGAGGGGGTTCTG GGTGAAGGGCCAGCGCGCGGCGGAGGCAGCGACATCCAGATGACC CAGTCCCCCTCATCGCTGTCCGCCTCCGTGGGCGACCGCGTCACCA TCACATGCCGGGCTCACAGTCGATCTCCTCCTACCTCAATTGGTAT CAGCAGAAGCCCGGAAAGGCCCTAAGCTTCTGATCTACGCAGCGT CCTCCCTGCAATCCGGGGTCCCATCTCGGTTCTCCGGCTCGGGCAG CGGTACCGACTTCACTCTGACCATCTCGAGCCTGCAGCCGGAGGACT TCGCCACTTACTACTGTGAGCAAAGCTACACCCTCGCGTTTGGCCAG GGCACCAAAGTGGACATCAAG
139108- aa VH	424	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWV SYISSSGSTIYYADSVKGRFTISRDNKNSLYLQMNSLRAEDTAVYYCAR ESGDGMDVWVGQGTTVTVSS
139108- aa VL	425	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYA ASSLQSGVPSRFGSGSGTDFTLTISLQPEDFATYYCQQSYTLAFGQG TKVDIK
139110		
139110- aa ScFv domain	426	QVQLVQSGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEW VSYISSSGNTIYYADSVKGRFTISRDNKNSLYLQMNSLRAEDTAVYYCA RSTMVREDYWVGQGLTVTVSSASGGGGSGGRASGGGGSDIVLTQSPLS LPVTLGQPASISCKSSESLVHNSGKTYLNWFHQRPGQSPRRLIYEVS NRDSGVPDRFTGSGSGTDFTLKISRVEAEDVGVYYCMQGTHTWPGTFGQGT KLEIK
139110- nt ScFv domain	427	CAAGTGCAACTGGTGCAAAGCGGAGGAGGATTGGTCAAACCCGGAG GAAGCCTGAGACTGTCATGCGCGGCCTCTGGATTACCTTCTCCGAT TACTACATGTCATGGATCAGACAGGCCCGGGGAAGGGCCTCGAAT GGGTGTCCTACATCTCGTCTCCGGGAACACCATCTACTACGCCGAC AGCGTGAAGGGCCGCTTTACCATTTCCCGCGACAACGCCAAGAAGCTC GCTGTACCTTCAGATGAATTCCTGCGGGCTGAAGATACCGCGGTGT ACTATTGCGCCCGGTCCACTATGGTCCGGGAGGACTACTGGGGACA GGGCACACTCGTGACCGTGTCCAGCGCGAGCGGGGGTGGAGGCAG CGGTGGACGCGCCTCCGGCGGCGGCGGTTGAGACATCGTGCTGACT CAGTCGCCCCTGTGCTGCCGGTCAACCCTGGGCCAACCGGCCTCAA TTAGCTGCAAGTCCTCGGAGAGCCTGGTGCACAACTCAGGAAAGACT TACCTGAACTGGTTCCATCAGCGGCCTGGACAGTCCCCACGGAGGC TCATCTATGAAGTGTCCAACAGGGATTCCGGGGTGCCCGACCGCTTC ACTGGCTCCGGGTCCGGCACCGACTTACCTTGAAATCTCCAGAGT GGAAGCCGAGGACGTGGGCGTGTACTACTGTATGCAGGGTACCCAC TGGCCTGGAACCTTTGGACAAGGAACTAAGCTCGAGATTAAG
139110- aa VH	428	QVQLVQSGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEW VSYISSSGNTIYYADSVKGRFTISRDNKNSLYLQMNSLRAEDTAVYYCA RSTMVREDYWVGQGLTVTVSS
139110- aa VL	429	DIVLTQSPLSLPVTLGQPASISCKSSESLVHNSGKTYLNWFHQRPGQSP RRLIYEVSNRDSGVPDRFTGSGSGTDFTLKISRVEAEDVGVYYCMQGT HTWPGTFGQGTKLEIK

139112		
139112- aa ScFv domain	430	QVQLVESGGGLVQPGGSLRLSCAVSGFALSNHGMSWVRRAPGKGLEW VSGIVYSGSTYYAASVKGRFTISRDNRSRNTLYLQMNSLRPEDTAIYYCSA HGGESDVWGQGTITVTVSSASGGGGSGGRASGGGGSDIRLTQSPSPLS ASVGDRVITTCQASEDINKFLNWHYQTPGKAPKLLIYDASTLQTVPSRF SGSGSGTDFTLTINSLQPEDIGTYQCQYESLPLTFGGGTKVEIK
139112- nt ScFv domain	431	CAAGTGCAACTCGTGGAATCTGGTGGAGGACTCGTGCAACCCGGTG GAAGCCTTAGGCTGTCTGTGCGCCGTCAGCGGGTTTGCTCTGAGCAA CCATGGAATGTCCTGGGTCCGCCGGGCACCGGGAAAAGGGCTGGAA TGGGTGTCCGGCATCGTGTACAGCGGGTCAACCTATTACGCCGCGT CCGTGAAGGGCAGATTCATCTCAAGAGACAACAGCCGGAACACC CTGTACTTGCAAATGAATTCCTGCGCCCCGAGGACACCGCCATCTA CTACTGCTCCGCCACCGAGGAGAGTCGGACGTGTGGGGCCAGGG AACGACTGTGACTGTGTCCAGCGCATCAGGAGGGGGTGGTTCGGGC GGCCGGGCCTCGGGGGGAGGAGGTTCCGACATTCGGCTGACCCAG TCCCGTCCCCACTGTGCGCCTCCGTGCGCGACCGCGTGACCATCA CTTGTCAGGCGTCCGAGGACATTAACAAGTTCCTGAACTGGTACCAC CAGACCCCTGGAAGGCCCCCAAGCTGCTGATCTACGATGCCTCGA CCCTTCAAACCTGGAGTGCCTAGCCGGTTCTCCGGGTCCGGCTCCGG CACTGATTTCACTCTGACCATCAACTCATTGCAGCCGGAAGATATCGG GACCTACTATTGCCAGCAGTACGAATCCCTCCCGCTCACATTCCGGC GGGAACCAAGGTCGAGATTAAG
139112- aa VH	432	QVQLVESGGGLVQPGGSLRLSCAVSGFALSNHGMSWVRRAPGKGLEW VSGIVYSGSTYYAASVKGRFTISRDNRSRNTLYLQMNSLRPEDTAIYYCSA HGGESDVWGQGTITVTVSS
139112- aa VL	433	DIRLTQSPSPLSASVGDRVITTCQASEDINKFLNWHYQTPGKAPKLLIYDA STLQTVPSRFSGSGSGTDFTLTINSLQPEDIGTYQCQYESLPLTFGGG TKVEIK
139113		
139113- aa ScFv domain	434	EVQLVETGGGLVQPGGSLRLSCAVSGFALSNHGMSWVRRAPGKGLEW VSGIVYSGSTYYAASVKGRFTISRDNRSRNTLYLQMNSLRPEDTAIYYCSA HGGESDVWGQGTITVTVSSASGGGGSGGRASGGGGSETTLTQSPATLS VSPGERATLSCRASQSVGSNLAWYQQKPGQGPRLLIYGASTRATGIPAR FSGSGSGTEFTLTISLQPEDFAVYYCQQYNDWLPVTFGQGTKEIK
139113- nt ScFv domain	435	GAAGTGCAATTGGTGGAACTGGAGGAGGACTTGTGCAACCTGGAG GATCATTGCGGCTCTCATGCGCTGTCTCCGGCTTCGCCCTGTCAAAT CACGGGATGTCTGTGGGTGAGACGGGCCCCGGGAAAAGGGTCTGGAAT GGGTGTCCGGGATTGTGTACAGCGGCTCCACCTACTACGCCGCTTC GGTCAAGGGCCGCTTCACTATTTACGGGACAACAGCCGCAACACCC TCTATCTGCAAATGAACTCTCTCCGCCCGGAGGATACCGCCATCTAC TACTGCTCCGCACACGGCGGCGAATCCGACGTGTGGGGACAGGGAA CCACTGTCACCGTGTCTCGTCGCATCCGGTGGCGGAGGATCGGGTGG CCGGGCCTCCGGGGGCGGCGGCAGCGAGACTACCCTGACCCAGTC CCCTGCCACTCTGTCCGTGAGCCCGGGAGAGAGAGCCACCCTTAGC TGCCGGGCGCAGCCAGAGCGTGGGCTCCAACCTGGCCTGGTACCAGC AGAAGCCAGGACAGGGTCCCAGGCTGCTGATCTACGGAGCCTCCAC TCGCGCGACCGGCATCCCCGCGAGGTTCTCCGGGTCCGGTTCGGG GACCGAGTTCACCCTGACCATCTCCTCCCTCCAACCGGAGGACTTCG CGGTGTACTACTGTGAGCAGTACAACGATTGGCTGCCCGTGACATTT GGACAGGGGACGAAGGTGGAAATCAAA
139113- aa VH	436	EVQLVETGGGLVQPGGSLRLSCAVSGFALSNHGMSWVRRAPGKGLEW VSGIVYSGSTYYAASVKGRFTISRDNRSRNTLYLQMNSLRPEDTAIYYCSA HGGESDVWGQGTITVTVSS
139113- aa VL	437	ETTLTQSPATLSVSPGERATLSCRASQSVGSNLAWYQQKPGQGPRLLIY GASTRATGIPARFSGSGSGTEFTLTISLQPEDFAVYYCQQYNDWLPVT

		FGQGTKVEIK
139114		
139114- aa ScFv domain	438	EVQLVESGGGLVQPGGSLRLSCAVSGFALSNHGMSWVRRAPGKGLEW VSGIVYSGSTYYAASVKGRFTISRDNRSNTLYLQMNSLRPEDTAIYYCSA HGGESDVWGQGTITVTVSSASGGGGSGGRASGGGGSEIVLTQSPGTLT LSPGERATLSCRASQSIGSSSLAWYQQKPGQAPRLLMYGASSRASGIPD RFGSGSGTDFLTISRLEPEDFAVYYCQQYAGSPPTFGQGTKVEIK
139114- nt ScFv domain	439	GAAGTGCAATTGGTGAATCTGGTGGAGGACTTGTGCAACCTGGAG GATCACTGAGACTGTCATGCGCGGTGTCCGGTTTTGCCCTGAGCAAT CATGGGATGTCGTGGGTCCGGCGCGCCCCCGAAAGGGTCTGGAAT GGGTGTCCGGTATCGTCTACTCCGGGAGCACTTACTACGCCGCGAG CGTGAAGGGCCGCTTACCATTTCGCCGATAACTCCCGCAACACCC TGACTTGCAATGAACTCGCTCCGGCCTGAGGAGACTGCCATCTAC TACTGCTCCGCACACGGAGGAGAATCCGACGTGTGGGGCCAGGGAA CTACCGTGACCGTCAGCAGCGCCTCCGGCGGGGGGGCTCAGGCG GACGGGCTAGCGGGCGCGGTGGCTCCGAGATCGTGCTGACCCAGT CGCCTGGCACTCTCTCGCTGAGCCCCGGGGAAAGGGCAACCCTGTC CTGTCCGGGCCAGCCAGTCCATTGGATCATCTCCCTCGCCTGGTATC AGCAGAAACCGGGACAGGCTCCGCGGCTGCTTATGTATGGGGCCAG CTCAAGAGCCTCCGGCATTCCCGACCGGTTCTCCGGGTCCGGTTCC GGCACCGATTTCACCTGACTATCTCGAGGCTGGAGCCAGAGGACTT CGCCGTGTACTACTGCCAGCAGTACGCGGGGTCCCCGCCGTTACG TTCGGACAGGGAACCAAGGTCGAGATCAAG
139114- aa VH	440	EVQLVESGGGLVQPGGSLRLSCAVSGFALSNHGMSWVRRAPGKGLEW VSGIVYSGSTYYAASVKGRFTISRDNRSNTLYLQMNSLRPEDTAIYYCSA HGGESDVWGQGTITVTVSS
139114- aa VL	441	EIVLTQSPGTLTLSPGERATLSCRASQSIGSSSLAWYQQKPGQAPRLLM YGASSRASGIPDRFSGSGSGTDFLTISRLEPEDFAVYYCQQYAGSPPT TFGQGTKVEIK
149362		
149362-aa ScFv domain	442	Qvqlqesgpglvkpsetlsltctvsggsissssyyywgrppgkglewigsiyygsayynpslksrv tisvdtksnqfslrlssvtaadtavyycarhwqewpdafdiwgqgtmvtvssggggsgggsgggsgs ettltqspafmsatpgdkviiscasqdiddamnwyqqkpggeaplfiiqsatpvpigpprfsgsgfgt dfsltinniesedaayyfcldhndfpltfgggkgleik
149362-nt ScFv domain	443	caagtgcagcttcaggaaagcggaccggcctgggtcaagccatccgaaactctctccctgacttgca ctgtgtctggcgttcctctcatctgctgactactactggggtggattaggcagccgcccggaaagg gactggagtggatcggaagcatctactattccggctcggcgtactacaaccttagctcaagtcgaga gtgacctctccgtggatacctccaagaaccagtttccctgcgcctgagctccgtgaccgcccgtgac accgcccgtgactactgtgctcggcattggcaggaatggcccgatgcctcgacatttggggccagggc actatggtcactgtgtcatccgggggtggaggcagcggggaggagggtccggggggggagggtca gagacaacctgacctagtcacccgattcatgtccgccactccgggagacaaggatcatctctgtg caaagcgtcccaggatctgacgatgccatgaattggtaccagcagaagcctggcgaagcggcgt gttcattatccaatccgcaacctcgccgctgctggaatcccaccgcggttcagcggcagcgggttcgg aacggactttccctgaccattaacaacattgagtcaggagcggcggcctactactctgctgcaacac gacaacttccctctcagcttcggccagggaaccaagctggaaatcaag
149362-aa VH	444	QVQLQESGPGVLKPSSETLSLTCTVSGGSISSSSYYYWGWIRQPPGKGLE WIGSIYSGSAYYNPSLKSRTISVDTSKNQFSLRLSSVTAADTAVYYCA RHWQEWPDADFIDWGQGTMTVSS
149362-aa VL	445	ETTLTQSPAFMSATPGDKVIISCKASQDIDDAMNWyQQKPGEAPLFIIQS ATSPVPGIPPRFSGSGFGTDFSLTINNIESEDAAYYFCLQHDNFPLTFGQ GTKLEIK
149363		
149363-aa ScFv domain	446	QVNLRESGPALVKPTQTLTLTCTFSGFSLRTSGMCSVSWIRQPPGKALEW LARIDWDEDKFYSTSLKTRTLISKDTSDNQVFLRMTNMDPADTATYYCA RSGAGGTSATAFDIWGPMTMTVSSGGGGSGGGSGGGSGGGSDIQMTQS

		PSSLSASVGDRTVITCRASQDIYNNLAWFQLKPGSAPRSLMYAANKSQS GVPSRFSGSASGTDFTLTISSLQPEDFATYYCQHYRFPYSFGQGTKLEI K
149363-nt ScFv domain	447	caagtcaatctgcgcgaatccggccccgccttggtcaagcctaccagaccctcactctgacctgtact ttctccggcttctccctgcggactccgggatgtgcgtgtcctggatcagacagcctccgggaaaggcc ctggagtggtctgcctgcattgactgggatgaggacaagtctactccacctcactcaagaccaggctg accatcagcaaagatacctctgacaaccaagtgtgctccgcacatgaccaacatggaccagccgac actgccacttactactgcgcgaggagcggagcggggcggaacctccgccaccgccttcgatatttggg gccccgggtaccatggtcaccgtgtcaagcggaggaggggggtccggggcgggcggttccggggga ggcggatcggacattcagatgactcagtcaccatcgtccctgagcgttagcgtggcgacagagtga caatcacttgcggggcatcccaggacatctataacaaccttgcgtggttcagctgaagcctggttccg caccgcggtcacttatgtacgccccaacaagagccagtcgggagtcggttccgggttccgggttcg gcctcgggaactgactcaccctgacgatctccagcctgcaacccgaggatttccacactactactgc cagcactactaccgcttccctactcgttcggacagggaaaccaagctggaaatcaag
149363-aa VH	448	QVNLRESGPALVKPTQTLTLCTFSGFSLRTSGMCVSWIRQPPGKALEW LARIDWDEDKFYSTSLKTRLTISKDTSNQQVVLMTNMDPADTATYYCA RSGAGGTSATAFDIWGPMTMTVSS
149363-aa VL	449	DIQMTQSPSSLSASVGDRTVITCRASQDIYNNLAWFQLKPGSAPRSLMY AANKSQSGVPSRFSGSASGTDFTLTISSLQPEDFATYYCQHYRFPYSF GQGTKLEIK
149364		
149364-aa ScFv domain	450	evqlvesggglvkpggslrlscaasgftfssysmnwvrqapgkglewvssisssssiyyadsvkgrft isrdnaknsllylqmnsiraedtavyycaktiaavyafdiwgqgtvtvssggggsgggsggggseivl tqspislpvtpeepasiscrssqslhsngynylwdwylqkpgqspqlliylgsnrsgvpdrfsgsgsgtd ftlkisrveaedvgvvyymqalqtpytfgggkileik
149364-nt ScFv domain	451	gaagtgcagctgtgcgaatccggggggggactggtcaagccgggcgggatcactgagactgtcctgcg ccgcgagcggcttcacgttctcctcactccatgaactgggtccgccaagccccgggaagggaactg gaatgggtgtcctctatctcctcgtcgtcgtcctacatctactacgccgactccgtgaagggaagattcac catttcccgcgacaacgcaaagaactcactgtacttgcgaatgaactcactccggggccgaagatactg ctgtgtactattgcgccaagactattgcgcgcgtctacgcttgcacatctggggccagggaaccaccgt gactgtgtcgtccggtggtggtgcgcggcgaggaggaagcggcgcggggggtccgagattgt gctgaccagtcgccactgagcctccctgtgacccccgaggaaccgcgcagcatcagctccgggtcc agccagtcctgtcctcactccaacggatacaattacctcgattgttacctcagaagcctggacaaag cccgagctgtcctacttgggatcaaaccgcgcgtcaggagtgctgaccggttctccggctcgg gcagcggtagcgaattcaccctgaaaatctccagggtggaggcagaggacgtgggagtgattactgt atgcaggcgctgcagactccgtacacatttgggcagggcaccaagctggagatcaag
149364-aa VH	452	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKLEW VSSISSSSSIYYADSVKGRFTISRDNKNSLYLQMNSLRAEDTAVYYCA KTIAAVYAFDIWGQGTITVTVSS
149364-aa VL	453	EIVLTQSPSLSPVTPEEPASISCRSSQSLLSNGYNLWDWYLQKPGQSPQ LLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVVYCMQALQT PYTFGQGTKLEIK
149365		
149365-aa ScFv domain	454	evqlvesggglvkpggslrlscaasgftfssysmnwvrqapgkglewvssissssgiyyadsvkgrfti srdnaknsllylqmnsiraedtavyycardlrgafdiwgqgtmtvssggggsgggsgggsgssyvt qspvsaaapgytatiscggnnigtksvhwyqqkpgqapllvirdsvrpskipgrfsgnsngmatlti sgvqagdeadfyqvwdsdsehvvfgggtklvl
149365-nt ScFv domain	455	gaagtcagctcgtggagtcggcgaggccttgtaagcctggaggttcgctgagactgtcctgcgc cgctccgggttcaccttctccgactactacatgtcctggatcagacaggccccgggaaaggcgctg aatgggtgtcctacatctcgtcgcggcagcactatctactacgcggactcagtgaaggggcggttca ccatttccgggataacgcgaagaactcgtgtatctgcaaatgaactcactgagggccgaggacac cgccgtgtactactgcgcgcgcgtatccgcggggcatttgacatctgggacaggggaaccatggtca cagtgccagcggagggggaggatcgggtggcggagggtccgggggtggaggctcctcctacgtgt gactcagagcccaagcgtcagcgtcgcgcgggttacagggaaccatctcctgtggcggaacaa cattgggaccaagctgtgctcactggtatcagcagaagccggggccaagctccctgttgggtatccgcg

		atgactccgtgcggcctagcaaaattccgggacggttctccggtccaacagcggcaatatggccact ctcaccatctcgggagtgaggccggagatgaagccgacttctactgccaagtctgggactcagactc cgagcatgtggtgttcggggggcggaaccaagctgactgtgctc
149365-aa VH	456	EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWV SYISSSGSTIYYADSVKGRFTISRDNKNSLYLQMNSLRAEDTAVYYCAR DLRGAFDIWGQGTMTVTVSS
149365-aa VL	457	SYVLTQSPSVSAAPGYTATISCGNNIGTKSVHWYQQKPGQAPLLVIRD DSVRPSKIPGRFSGSNSGNMATLTISGVQAGDEADFYCQVWDSSEHV VFGGGTKLTVL
149366		
149366-aa ScFv domain	458	qvqlvqsgaevkpgasvkvsckpsgyvtvshyihwvrrapggglewmgmnpssgvtaysqtlqg rvtmtsdtssstvymelsslrstedtamyycaregsgsgwyfdwgrgtlvvssggggsgggsggg gssyvltppsvsvspgqtasitcsdglskkyvswyqqkagqspvvlisrdkerpsgipdrfsgsns adtatltsgtqamdeadyycqawddttvfgggtklvl
149366-nt ScFv domain	459	caagtgcagctggtgcagagcggggccgaagtcaagaagccgggagcctccgtgaaagtgtcctg caagccttcgggatacaccgtgacctcccactacattcattgggtccgcccgcggccccaagga ctcgagtggatgggcatgatcaaccctagcggcggagtgaccgcgtacagccagacgctgcaggg acgcgtgactatgacctcggatacctcctcctccaccgtctatatggaactgtccagcctcgggtccgag gataccgccatgtactactgcgcccgggaaggatcaggctccgggtggtatttcgacttctggggaag aggcacctcgtgactgtgtcatctggggagggggttcgggtggtggcggatcgggaggaggcgggt tcctctacgtgtgaccagccaccctccgtgtccgtgagccccggccagactgcatcgattacatgt agcggcgacggcctctcaagaaatacgtgtcgtgtgaccagcagaaggccggacagagcccgggt gggtgctgatctcaagagataaggagcggcctagcggaaatcccgacaggttctcgggtccaactcc gcggaactgtactctgacctctcggggaccagggtatggacgaagccgattactactgccaag cctgggacgacactactgtcgtgtttggagggggacccaagttagccgtcctt
149366-aa VH	460	QVQLVQSGAEVKKPGASVKVSCKPSGYTVTSHYIHWVRRAPGQGLEW MGMINPSGGVTAYSQTLQGRVTMTSDTSSSTVYMESSLRSEDAMYY CAREGSGSGWYFDWGRGTLTVTVSS
149366-aa VL	461	SYVLTQPPSVSVSPGQTASITCSGDGLSKKYVSWYQQKAGQSPVVLISR DKERPSGIPDRFSGSNSADTATLTISGTQAMDEADYYCQAWDDTTVFVFG GGTKLTVL
149367		
149367-aa ScFv domain	462	QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYYWSWIRQHPGKGLE WIGYIYYSGSTYYNPSLKSRTISVDTSKNQFSLKLSSVTAADTAVYYCA RAGIAARLRGAFDIWGQGTMTVTVSSGGGGSGGGGSGGGGSDIVMTQS PSSVSASVGDRIITCRASQGIRNWLAWYQQKPGKAPNLLIYAASNLQS GVPSRFSGSGSGADFTLTISLQPEDVATYYCQKYNAPFTFGPGTKVDI K
149367-nt ScFv domain	463	caagtgcagcttcaggagagcggcccgggactcgtgaagccgtcccagaccctgtccctgacttga ccgtgtcgggaggaagcatctcgagcggaggctactattggtcgtggattcggcagcacctggaaa gggcctggaatggatcggtactactactcggctcgacctactacaacccatcgctgaagtcca gagtgaatctcagtggacacgtccaagaatcagttcagcctgaagctctcttcggtgactgcggccg acaccgctgtactactgcgcacgcgtggaattgccgcccgggtgaggggtgccttcgacattgg ggacagggcaccatggtcaccgtgtcctcggcggcggagggtccgggggtggaggctcaggagg aggggggtccgacatcgatgactcagtcgcccgaagcgtcagcgcgtccgtcggggacagagtg atcatcacctgtcggggtcccagggaattcgcaactggctggcctggatcagcagaagcccggaa aggcccccaacctgttgatctacgcgcctcaaacctccaatccggggtgcgagccgctcagcgg ctccggttcgggtgcgatttactctgacctctcctcctgcaacctgaagatgtggctacctactactg ccaaaagtacaactccgcaccttttactttcggaccggggaccaaagtggacattaag
149367-aa VH	464	QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYYWSWIRQHPGKGLE WIGYIYYSGSTYYNPSLKSRTISVDTSKNQFSLKLSSVTAADTAVYYCA RAGIAARLRGAFDIWGQGTMTVTVSS
149367-aa VL	465	DIVMTQSPSSVSASVGDRIITCRASQGIRNWLAWYQQKPGKAPNLLIYA ASNLQSGVPSRFSGSGSGADFTLTISLQPEDVATYYCQKYNAPFTFG PGTKVDIK

149368		
149368-aa ScFv domain	466	qvqlvqsgaevkpkpgssvkvsckasggtfssyaiswvrqapggglewmggiipifgtanyaqkfqgr vtitadeststaymelsslrsestavyyccarrggyqlrwdvllrsafdiwgggtmvtvssggggsggg gsggggssyvltppsvsvapggqtaritcggnnigsksvhwyqqkpgqapvlvlygknnrpsgvpdr fsgsrsgttasltitgaqaedeaddyccsrdsdssgdhrlvfgtgtkvtvl
149368-nt ScFv domain	467	caagtgcagctgggtccagtcgggcccggaggtcaagaagccgggagctctgtgaaagtgtcctgc aaggcctccgggggacacattagctcctacgccatctcctgggtccgccaagcaccgggtcaaggcct ggagtggatgggggaattatccctatcttcggcactgccaactacgcccagaagtccaggagcgc gtgaccattaccgcggaatccacccaccgcttatatggagctgtccagcttgcgtcgggaagat accgcccgtgtactactgcgcccggaggggtggataccagctgtgagatgggacgtgggctcctgc ggctggcgttcgacatctggggccagggcactatggtcactgtgtccagcggagaggcggatcggg aggcggcgatcagggggaggcgggtccagctacgtgcttactcaacccctcgggtgtcgtggccc cgggacagaccgccagaatcacttgcggaggaaacaacattgggtccaagagcgtgcattggtacc agcagaagccaggacaggccctgtgtggtgtctacgggaagaacaatcgcccagcggagtg ccggacaggttctcgggttcacgctccggtacaacccgcttactgactatcaccggggcccaggcag aggatgaagcggactactactgttctcccgggattcatccggcgaccacctccgggtgttcggaacc ggaacgaaggtcacctgtctg
149368-aa VH	468	QVQLVQSGAEVKKPGSSVKVSKASGGTFSSYAISWVRQAPGQGLEW MGGIIPFGTANYAQKFQGRVTITADESTAYMELSSLRSEDTAVYYCA RRGGYQLLRWDVGLLRSAFDIWGGGTMTVSS
149368-aa VL	469	SYVLTQPPSVSVAPGQTARITCGGNNIGSKSVHWYQQKPGQAPVLVLY GKNNRPSGVPDRFSGSRSGTTASLTITGAQAEDADYYCNSRDSSGDH LRVFGTGTKVTVL
149369		
149369-aa ScFv domain	470	evqlqqsgpglvkpsqtlsltcaisgdsvsnsaawnwirqspgrglewlgtrtyrskwysfyaislksrri inpdtsknqfslqlksvtpedtavyyccarsspegfllywfdpwgggtltvssggdsgsgggsgggss seltqdpavsvallgqitrtcggdsglgnyyatwyqqkpgqapvlviygttnrpsgipdrfsasssgntasl titgaqaedeaddyccnsrdssghllfvtggtkvvl
149369-nt ScFv domain	471	gaagtgcagctccaacagtcaggaccgggctcgtgaagccatcccagaccctgtccctgactgtg ccatctcgggagatagcgtgtcatcgaactccgcccgtggaactggattcggcagagcccgctccg cggactggagtggttgaaggacactactaccggtccaagtgttactcttctacgcgatctcgtgaa gtcccgcatatcattaaccctgatacctccaagaatcagtttccctccaactgaaatccgtcaccccc gaggacacagcagtgattactgcgcacggagcagccccgaaggactgttctgtattggtttgaccc ctggggccaggggactcttgaccgtgtcgagcggcgagatgggtccgggtggcgggtgttcgggg ggcggcgatcatcatcgaactgacccaggaccggcgtgtgtccgtggcgctgggacaaaccatc cgcattacgtgccaggagactccctgggcaactactacgccacttggtaccagcagaagccgggc caagcccctgtgttggtcatctacgggaccaacaacagacctccggcatccccgaccggttcagcgc ttcgtctccggcaacactgccagcctgaccatcactggagcgcaggccgaagatgaggccgacta ctactgaacagcagagactcctcgggtcatcacctctgttcggaactggaaccaaggtcacctgtctg
149369-aa VH	472	EVQLQQSGPGLVKPSQTLSTCAISGDSVSSNSAAWNWIRQSPSRGLE WLGRTYYRSKWYSFYAISLKSRIINPDTSKNQFSLQLKSVTPEDTAVYYC ARSSPEGLFLYWFDPWGQGLTVTVSS
149369-aa VL	473	SSELTQDPAVSVALGQTIRITCQGDLSLGNYYATWYQQKPGQAPVLVIYG TNNRPSGIPDRFSASSSGNTASLTITGAQAEDADYYCNSRDSSGHLL FGTGTKVTVL
BCMA_EBB-C1978-A4		
BCMA_EBB-C1978-A4 - aa ScFv domain	474	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEW VSAISGSGGSTYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYC AKVEGSGSLDYWGQGLTVTVSSGGGGSGGGGSGGGGSEIVMTQSPGT LSLSPGERATLSCRASQSVSSAYLAWYQQKPGQPPRLLISGASTRATGI PDRFGSGSGTDFTLTISRLEPEDFAVYYCQHYGSSFNSSLTFTFGQGT RLEIK
BCMA_EBB-C1978-A4 - nt	475	GAAGTGCAGCTCGTGGAGTCAGGAGGCGGCCTGGTCCAGCCGGA GGGTCCCTTAGACTGTCATGCGCCGCAAGCGGATTCACTTTCTCCTC

ScFv domain		CTATGCCATGAGCTGGGTCCGCCAAGCCCCCGGAAAGGGACTGGAA TGGGTGTCCGCCATCTCGGGGTCTGGAGGCTCAACTTACTACGCTGA CTCCGTGAAGGGACGGTTCACCATTAGCCGCGACAACCTCAAGAACA CCCTCTACCTCCAAATGAACTCCCTGCGGGCCGAGGATACCGCCGTC TACTACTGCGCCAAAGTGGAAGGTTTCAGGATCGCTGGACTACTGGGG ACAGGGTACTCTCGTGACCGTGTTCATCGGGCGGAGGAGGTTCCGGC GGTGGCGGCTCCGGCGGCGGAGGGTCCGAGATCGTGATGACCCAG AGCCCTGGTACTCTGAGCCTTTTCGCCGGGAGAAAGGGCCACCCTGT CCTGCCGCGCTTCCCAATCCGTGTCTCCGCGTACTTGGCGTGGTAC CAGCAGAAGCCGGGACAGCCCCCTCGGCTGCTGATCAGCGGGGCC AGCACC CGGGCAACCGGAATCCCAGACAGATTCCGGGGGTTCCGGCA GCGGCACAGATTTACCCTGACTATTTTCGAGGTTGGAGCCCGAGGAC TTTGCGGTGTATTACTGTCAGCACTACGGGTCGTCTTTAATGGCTCC AGCCTGTTACGTTCCGACAGGGGACCCGCCTGGAAATCAAG
BCMA_EBB- C1978-A4 - aa VH	476	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEW VSAISGSGGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYC AKVEGSGSLDYWGQGT LTVSS
BCMA_EBB- C1978-A4 - aa VL	477	EIVMTQSPGTLSPGERATLSCRASQSVSSAYLAWYQQKPGQPRLLI SGASTRATGIPDRFGSGSGTDFTLTISRLEPEDFAVYYCQHYGSSFN SSLFTFGQGT RLEIK
BCMA_EBB-C1978-G1		
BCMA_EBB- C1978-G1 - aa ScFv domain	478	EVQLVETGGGLVQPGGSLRLSCAASGITFSRYPMWSVRQAPGKGLEWV SGISDSGVSTYYADSAKGRFTISRDN SKNTLFLQMSSLRDEDTAVYYCVT RAGSEASDIWGQGTMTVTVSSGGGGSGGGGSGGGGSEIVLTQSPATLSL SPGERATLSCRASQSVSNLAWYQQKPGQAPRLLIYDASSRATGIPDRF SGSGSGTDFTLTISRLEPEDFAIYYCQQFGTSSGLT FGGG TKLEIK
BCMA_EBB- C1978-G1 - nt ScFv domain	479	GAAGTGCAACTGGTGGAACCGGTGGCGGCCTGGTGAGCCTGGAG GATCATTGAGGCTGTTCATGCGCGGCCAGCGGTATTACCTTCTCCCGG TACCCCATGTCTGGGTGAGACAGGCCCGGGGAAAGGGCTTGAAT GGGTGTCCGGGATCTCGGACTCCGGTGTGAGCACTTACTACGCCGA CTCCGCCAAGGGACGCTTCACCATTTCCCGGGACAACCTCGAAGAACA CCCTGTTCTCCAAATGAGCTCCCTCCGGGACGAGGATACTGCAGTG TACTACTGCGTGACCCGCGCCGGGTCCGAGGCGTCTGACATTTGGG GACAGGGCACTATGGTCACCGTGTCTGTCGGCGGAGGGGGCTCGG GAGGCGGTGGCAGCGGAGGAGGAGGGTCCGAGATCGTGCTGACCC AATCCCCGGCCACCCTCTCGCTGAGCCCTGGAGAAAGGGCAACCTT GTCCTGTGCGCGGAGCCAGTCCGTGAGCAACTCCCTGGCCTGGTAC CAGCAGAAGCCCGGACAGGCTCCGAGACTTCTGATCTACGACGCTTC GAGCCGGGCCACTGGAATCCCCGACCGCTTTTCGGGGTCCGGCTCA GGAACCGATTTACCCCTGACAATCTCACGGCTGGAGCCAGAGGATTT CGCCATCTATTACTGCCAGCAGTTCGGTACTTCTCCGGCCTGACTTT CGGAGGCGGCACGAAGCTCGAAATCAAG
BCMA_EBB- C1978-G1 - aa VH	480	EVQLVETGGGLVQPGGSLRLSCAASGITFSRYPMWSVRQAPGKGLEWV SGISDSGVSTYYADSAKGRFTISRDN SKNTLFLQMSSLRDEDTAVYYCVT RAGSEASDIWGQGTMTVTVSS
BCMA_EBB- C1978-G1 - aa VL	481	EIVLTQSPATLSLSPGERATLSCRASQSVSNLAWYQQKPGQAPRLLIYD ASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAIYYCQQFGTSSGLTFG GGTKLEIK
BCMA_EBB-C1979-C1		
BCMA_EBB- C1979-C1 - aa ScFv domain	482	QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEW VSAISGSGGSTYYADSVKGRFTISRDN AKNSLYLQMNSLRAEDTAIYYCA RATYKRELRYYYGMDVWGQGTMTVTVSSGGGGSGGGGSGGGGSEIVM TQSPGTVSLSPGERATLSCRASQSVSSSFLAWYQQKPGQAPRLLIYGAS SRATGIPDRFSGSGSGTDFTLTISRLEPEDSAVYYCQQYHSSPSWTFGQ

		GTRLEIK
BCMA_EBB-C1979-C1 - nt ScFv domain	483	CAAGTGCAGCTCGTGGAATCGGGTGGCGGACTGGTGCAGCCGGGG GGCTCACTTAGACTGTCCTGCGCGGCCAGCGGATTCACCTTCTCCTC CTACGCCATGTCCTGGGTGAGACAGGCCCTGGAAAGGGCCTGGAA TGGGTGTCCGCAATCAGCGGCAGCGGCGGCTCGACCTATTACGCGG ATTCAGTGAAGGGCAGATTACCATTTCCCGGGACAACGCCAAGAAC TCCTTGTACCTTCAAATGAACCTCCCTCCGCGCGGAAGATACCGCAAT CTACTACTGCGCTCGGGCCACTTACAAGAGGGGAAGTGCCTACTACT ACGGGATGGACGTCTGGGGCCAGGGAACCATGGTCACCGTGTCCAG CGGAGGAGGAGGATCGGGAGGAGGCGGTAGCGGGGGTGGAGGGT CGGAGATCGTGATGACCCAGTCCCCCGGCACTGTGTGCTGTCCCC CGGCGAACGGGCCACCCTGTCATGTGCGGGCCAGCCAGTCAGTGTG TCAAGCTTCCTCGCCTGGTACCAGCAGAAACCGGGACAAGCTCCCC GCCTGCTGATCTACGGAGCCAGCAGCCGGGCCACCGGTATTCTGA CCGGTTCTCCGGTTCGGGGTCCGGGACCGACTTTACTCTGACTATCT CTCGCCTCGAGCCAGAGGACTCCGCCGTGTATTACTGCCAGCAGTAC CACTCCTCCCCGTCTGGACGTTTCGGACAGGGCACAAGGCTGGAGA TTAAG
BCMA_EBB-C1979-C1 - aa VH	484	QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEW VSAISGSGGSTYYADSVKGRFTISRDNKNSLYLQMNSLRAEDTAIYYCA RATYKRELRYYYGMDVWGQGTMTVTVSS
BCMA_EBB-C1979-C1 - aa VL	485	EIVMTQSPGTVSLSPGERATLSCRASQSVSSSLAWYQQKPGQAPRLLI YGASSRATGIPDRFSGSGSDFTLTISRLEPEDSAVYYCQQYHSSPSW TFGQGTGTRLEIK
BCMA_EBB-C1978-C7		
BCMA_EBB-C1978-C7 - aa ScFv domain	486	EVQLVETGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEW VSAISGSGGSTYYADSVKGRFTISRDNKNTLYLQMNTLKAEDTAVYYCA RATYKRELRYYYGMDVWGQGTMTVTVSSGGGGSGGGSGGGGSEIVLT QSPSTLSLSPGESATLSCRASQSVSTTFLAWYQQKPGQAPRLLIYGSSN RATGIPDRFSGSGSDFTLTIRLEPEDFAVYYCQQYHSSPSWTFGQG TKVEIK
BCMA_EBB-C1978-C7 - nt ScFv domain	487	GAGGTGCAGCTTGTGGAACCGGTGGCGGACTGGTGCAGCCCGGA GGAAGCCTCAGGCTGTCCTGCGCCGCGTCCGGCTTACCTTCTCCT CGTACGCCATGTCCTGGGTCCGCCAGGCCCGGAAAGGGCCTGGA ATGGGTGTCCGCCATCTCTGGAAGCGGAGGTTCCACGTACTACGCG GACAGCGTCAAGGGAAGGTTACAATCTCCCGCGATAATTGGAAGAA CACTCTGTACCTTCAAATGAACACCCTGAAGGCCGAGGACACTGCTG TGTAATACTGCGCACGGGCCACCTACAAGAGAGAGCTCCGGTACTAC TACGGAATGGACGTCTGGGGCCAGGGAAGTACTGTGACCGTGTCTCT CGGGAGGGGGTGGCTCCGGGGGGGGCGGCTCCGGCGGAGGCGGT TCCGAGATTGTGCTGACCCAGTCACCTTCAACTCTGTGCTGTCCCC GGGAGAGAGCGCTACTCTGAGCTGCCGGGCCAGCCAGTCCGTGTCC ACCACCTTCCTCGCCTGGTATCAGCAGAAGCCGGGGCAGGCACCAC GGCTCTTGATCTACGGGTCAAGCAACAGAGCGACCGGAATTCCTGAC CGCTTCTCGGGGAGCGGTTCAAGCACCGACTTCACCCTGACTATCC GGCGCCTGGAACCCGAAGATTTCCCGGTGTATTACTGTCAACAGTAC CACTCCTCGCCGTCTCTGGACCTTTGGCCAAGGAACCAAAGTGGAAT CAAG
BCMA_EBB-C1978-C7 - aa VH	488	EVQLVETGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEW VSAISGSGGSTYYADSVKGRFTISRDNKNTLYLQMNTLKAEDTAVYYCA RATYKRELRYYYGMDVWGQGTMTVTVSS
BCMA_EBB-C1978-C7 - aa VL	489	EIVLTQSPSTLSLSPGESATLSCRASQSVSTTFLAWYQQKPGQAPRLLIY GSSNRATGIPDRFSGSGSDFTLTIRLEPEDFAVYYCQQYHSSPSWT FGQGTKVEIK
BCMA_EBB-C1978-D10		

BCMA_EBB-C1978-D10 - aa ScFv domain	490	EVQLVETGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEW VSGISWNSGSIGYADSVKGRFTISRDNKNSLYLQMNSLRDEDTAVYYC ARVGKAVPDVWGQGTITVTVSSGGGGSGGGGSGGGGSDIVMTQTPSSL SASVGDRVITICRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSR FSGSGSGTDFTLTISLQPEDFATYYCQQSYSTPYSFQGQTRLEIK
BCMA_EBB-C1978-D10- nt ScFv domain	491	GAAGTGCAGCTCGTGGAAGCTGGAGGTGGACTCGTGAGCCTGGAC GGTCGCTGCGGCTGAGCTGCGCTGCATCCGGCTTCACCTTCGACGA TTATGCCATGCACTGGGTCAGACAGGCGCCAGGGAAGGGACTTGAG TGGGTGTCCGGTATCAGCTGGAATAGCGGCTCAATCGGATACGCGG ACTCCGTGAAGGGAAGGTTACCATTTCCCGCGACAACGCCAAGAAC TCCCTGTACTTGCAAATGAACAGCCTCCGGGATGAGGACACTGCCGT GTACTACTGCGCCCCGCTCGGAAAAGCTGTGCCCCGACGTCTGGGGC CAGGGAACCACTGTGACCGTGTCCAGCGGCGGGGGTGGATCGGGC GGTGGAGGGTCCGGTGGAGGGGGCTCAGATATTGTGATGACCCAGA CCCCCTCGTCCCTGTCCGCCTCGGTCCGCGACCGCGTGAATATCAC ATGTAGAGCCTCGCAGAGCATCTCCAGCTACCTGAACTGGTATCAGC AGAAGCCGGGGAAGGCCCGAAGCTCCTGATCTACGCGGCATCATC ACTGCAATCGGGAGTGCCGAGCCGGTTTTCCGGGTCCGGCTCCGGC ACCGACTTCACGCTGACCATTTCTTCCCTGCAACCCGAGGACTTCGC CACTTACTACTGCCAGAGTCTTACTCCACCCCTTACTCCTTCGGCCA AGGAACCAGGCTGGAATCAAG
BCMA_EBB-C1978-D10 - aa VH	492	EVQLVETGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEW VSGISWNSGSIGYADSVKGRFTISRDNKNSLYLQMNSLRDEDTAVYYC ARVGKAVPDVWGQGTITVTVSS
BCMA_EBB-C1978-D10- aa VL	493	DIVMTQTPSSLSASVGDRVITICRASQSISSYLNWYQQKPGKAPKLLIYA ASSLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYSTPYSFG QGTRLEIK
BCMA_EBB-C1979-C12		
BCMA_EBB-C1979-C12- aa ScFv domain	494	EVQLVESGGGLVQPGRSLRLSCTASGFTFDDYAMHWVRQRPKGKLEW VASINWKGNLAYGDSVKGRFAISRDNKNTVFLQMNSLRTEDTAVYYC ASHQGVAYYNYAMDVWGRGTLTVSSGGGGSGGGGSGGGGSEIVLTQ SPGTLSPGERATLSCRATQSIGSSFLAWYQQRPGQAPRLLIYGASQR ATGIPDRFSGRSGTDFTLTISRVEPEDSAVYYCQHYESSPSWTFGQGT KVEIK
BCMA_EBB-C1979-C12 - nt ScFv domain	495	GAAGTGCAGCTCGTGAGAGCGGGGGAGGATTGGTGCAGCCCGGA AGGTCCCTGCGGCTCTCCTGCACTGCGTCTGGCTTCACCTTCGACGA CTACGCGATGCACTGGGTGAGACAGCGCCCGGGAAGGGCCTGGAA TGGGTGCGCTCAATCAACTGGAAGGGAACTCCCTGGCCTATGGCGA CAGCGTGAAGGGCCGCTTCGCCATTTGCGCGGACAACGCCAAGAAC ACCGTGTCTTGCAAATGAATCCCTGCGGACCGAGGATACCGCTGT GTACTACTGCGCCAGCCAGGGCGTGGCATACTATACTACGCCA TGGACGTGTGGGGAAGAGGGACGCTCGTCACCGTGTCTCCGGGG GCGGTGGATCGGGTGGAGGAGGAAGCGGTGGCGGGGGGACGCAAA TCGTGCTGACTCAGAGCCCGGGAACCTTTCACTGTCCCCGGGAGAA CGGGCCACTCTCTCGTGCCGGGCCACCCAGTCCATCGGCTCCTCCT TCCTTGCTGGTACCAGCAGAGGCCAGGACAGGCGCCCGCCTGCT GATCTACGGTGCTTCCCAACGCGCCACTGGCATTCTGACCGGTTCA GCGGCAGAGGGTGGGAACCGATTTCACTGACCATTTCCCGGGT GGAGCCCGAAGATTGCGCAGTCTACTACTGTCAGCATTACGAGTCCT CCCCTTCATGGACCTTCGGTCAAGGGACCAAGTGGAGATCAAG
BCMA_EBB-C1979-C12 - aa	496	EVQLVESGGGLVQPGRSLRLSCTASGFTFDDYAMHWVRQRPKGKLEW VASINWKGNLAYGDSVKGRFAISRDNKNTVFLQMNSLRTEDTAVYYC ASHQGVAYYNYAMDVWGRGTLTVSS

VH		
BCMA_EBB-C1979-C12 - aa VL	497	EIVLTQSPGTLISLSPGERATLSCRATQSIGSSFLAWYQQRPGQAPRLLIY GASQRATGIPDRFSGRSGTDFTLTISRVEPEDSAVYYCQHYESSPSWT FGQGTKVEIK
BCMA_EBB-C1980-G4		
BCMA_EBB-C1980-G4- aa ScFv domain	498	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEW VSAISGSGGSTYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYC AKVVRDGMVDVWGQGTITVTVSSGGGGSGGGGSGGGGSEIVLTQSPATL SLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP DRFSGNGSGTDFTLTISRLEPEDFAVYYCQQYGSPPRFTFGPGTKVDIK
BCMA_EBB-C1980-G4- nt ScFv domain	499	GAGGTGCAGTTGGTGCAGAAAGCGGGGGCGGGCTTGTGCAGCCTGGC GGATCACTGCGGCTGTCTGCGCGGCATCAGGCTTCACGTTTTCTTC CTACGCCATGTCTGCGGTGCGCCAGGCCCTGGAAAGGGACTGGAA TGGGTGTCCGCGATTTCCGGGGTCCGGCGGGAGCACCTACTACGCCG ATTCGGTGAAGGGCCGCTTCACTATCTCGCGGGACAACCTCCAAGAAC ACCCTCTACCTCCAAATGAATAGCCTGCGGGCCGAGGATACCGCCGT CTACTATTGCGCTAAGGTGCTGCGCGACGGAATGGACGTGTGGGGA CAGGGTACCACCGTGACAGTGTCTCGGGGGGAGGCGGTAGCGGC GGAGGAGGAAGCGGTGGTGGAGGTTCCGAGATTGTGCTGACTCAAT CACCCGCGACCTGAGCCTGTCCCCCGGCGAAAGGGCCACTCTGTC CTGTGCGGGCCAGCAATCAGTCTCCTCCTGCTACCTGGCCTGGTACC AGCAGAAGCCAGGACAGGCTCCGAGACTCCTTATCTATGGCGCATCC TCCCGCGCCACCGGAATCCCGGATAGGTTCTCGGGAAACGGATCGG GGACCGACTTCACTCTCACCATCTCCCGGCTGGAACCGGAGGACTTC GCCGTGTACTACTGCCAGCAGTACGGCAGCCCGCCTAGATTCATTT CGGCCCCGGGCACCAAAGTGGACATCAAG
BCMA_EBB-C1980-G4- aa VH	500	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEW VSAISGSGGSTYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYC AKVVRDGMVDVWGQGTITVTVSS
BCMA_EBB-C1980-G4- aa VL	501	EIVLTQSPATLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIY GASSRATGIPDRFSGNGSGTDFTLTISRLEPEDFAVYYCQQYGSPPRFT FGPGTKVDIK
BCMA_EBB-C1980-D2		
BCMA_EBB-C1980-D2- aa ScFv domain	502	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEW VSAISGSGGSTYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYC AKIPQTGTFDYWGQGLTVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTL SLSPGERATLSCRASQSVSSSYLAWYQQRPGQAPRLLIYGASSRATGIP DRFSGSGSGTDFTLTISRLEPEDFAVYYCQHYGSSPSWTFGQGRLEIK
BCMA_EBB-C1980-D2- nt ScFv domain	503	GAAGTGCAGCTGCTGGAGTCCGGCGGTGGATTGGTGAACCGGGG GGATCGCTCAGACTGTCTGTGCGGCGTCAGGCTTCACCTTCTCGAG CTACGCCATGTCATGGGTGAGACAGGCCCTGGAAAGGGTCTGGAA TGGGTGTCCGCCATTTCCGGGAGCGGGGGATCTACATACTACGCCG ATAGCGTGAAGGGCCGCTTCACTATTTCCCGGGACAACCTCCAAGAAC ACTCTCTATCTGCAAAATGAATCCCTCCGCGCTGAGGACACTGCCGT GTACTACTGCGCCAAAATCCCTCAGACCGGCACCTTCGACTACTGGG GACAGGGGACTCTGGTCACCGTCAGCAGCGGTGGCGGAGGTTCCG GGGGAGGAGGAAGCGGCGGCGGAGGGTCCGAGATTGTGCTGACCC AGTCACCCGGCACTTTGTCCCTGTGCGCTGGAGAAAGGGCCACCCTT TCCTGCCGGGCATCCCAATCCGTGTCTCCTCCTGCTACCTGGCCTGGTA CCAGCAGAGGCCCGGACAGGCCCCACGGCTTCTGATCTACGGAGCA AGCAGCCGCGCGACCGGTATCCCGGACCGGTTTTTCGGGCTCGGGCT CAGGAACTGACTTCAACCTCACCATCTCCCGCCTGGAACCCGAAGAT TTCGCTGTGTATTACTGCCAGCACTACGGCAGCTCCCCGTCCTGGAC GTTCGGCCAGGGAACCTCGGCTGGAGATCAAG

BCMA_EBB-C1980-D2- aa VH	504	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEW VSAISGSGGSTYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYC AKIPQTGTFDYWGQGTLLTVSS
BCMA_EBB-C1980-D2- aa VL	505	EIVLTQSPGTLSSLSPGERATLSCRASQSVSSSYLAWYQQRPGQAPRLLIY GASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQHYGSSPSWT FGQGTREIK
BCMA_EBB-C1978-A10		
BCMA_EBB-C1978-A10- aa ScFv domain	506	EVQLVETGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEW VSAISGSGGSTYYADSVKGRFTMSRENDKNSVFLQMNSLRVEDTGYYY CARANYKRELRYYYGMDVWGQGTMTVSSGGGGSGGGGSGGGGSEI VMTQSPGTLSSLSPGESATLSCRASQRVASNYLAWYQHKPGQAPSLISG ASSRATGVPDRFSGSGSGTDFTLAISRLEPEDSAVYYCQHYDSSPSWTF GQGTKVEIK
BCMA_EBB-C1978-A10- nt ScFv domain	507	GAAGTGCAACTGGTGGAACCGGTGGAGGACTCGTGCAGCCTGGCG GCAGCCTCCGGCTGAGCTGCGCCGCTTCGGGATTACCTTTCTCTCC TACGCGATGTCTTGGGTCAGACAGGCCCGGAAAGGGGCTGGAAT GGGTGTCAGCCATCTCCGGCTCCGGCGGATCAACGTACTACGCCGA CTCCGTGAAAGGCCGGTTCACCATGTGCGCGGAGAATGACAAGAACT CCGTGTTCTGCAAATGAACTCCCTGAGGGTGGAGGACACCGGAGT GTACTATTGTGCGCGCGCCAACTACAAGAGAGAGCTGCGGTACTACT ACGGAATGGACGTCTGGGGACAGGGAAGTATGGTGACCGTGTCTC CGGTGGAGGGGGAAGCGGCGGTGGAGGCAGCGGGGCGGGGTT CAGAAATTGTCATGACCCAGTCCCCGGGAAGTCTTTCCCTCTCCCC GGGGAATCCGCGACTTTGTCTGCGGGCCAGCCAGCGCGTGGCCT CGAACTACCTCGCATGGTACCAGCATAAGCCAGGCCAAGCCCCTTCC CTGCTGATTTCCGGGGCTAGCAGCCGCGCCACTGGCGTGCCGGATA GGTTCTCGGGAAGCGGCTCGGGTACCGATTTACCCCTGGCAATCTC GCGGCTGGAACCGGAGGATTGCGCCGTGTACTACTGCCAGCACTAT GACTCATCCCCCTCTGGACATTGCGACAGGGCACCAAGGTCGAGAT CAAG
BCMA_EBB-C1978-A10- aa VH	508	EVQLVETGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEW VSAISGSGGSTYYADSVKGRFTMSRENDKNSVFLQMNSLRVEDTGYYY CARANYKRELRYYYGMDVWGQGTMTVSS
BCMA_EBB-C1978-A10- aa VL	509	EIVMTQSPGTLSSLSPGESATLSCRASQRVASNYLAWYQHKPGQAPSLLI SGASSRATGVPDRFSGSGSGTDFTLAISRLEPEDSAVYYCQHYDSSPS WTFGQGTKVEIK
BCMA_EBB-C1978-D4		
BCMA_EBB-C1978-D4- aa ScFv domain	510	EVQLLETGGGLVQPGGSLRLSCAASGFSFSSYAMSWVRQAPGKGLEW VSAISGSGGSTYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYC AKALVGATGAFDIWGQGTLLTVSSGGGGSGGGGSGGGGSEIVLTQSPG TLSSLSPGERATLSCRASQSLSSNFLAWYQQKPGQAPGLLIYGASNWAT GTPDRFSGSGSGTDFTLTITRLEPEDFAVYYCQYYGTSPMYTFGQGTKV EIK
BCMA_EBB-C1978-D4- nt ScFv domain	511	GAAGTGCAGCTGCTCGAAACCGGTGGAGGGCTGGTGCAGCCAGGG GGCTCCCTGAGGCTTTCATGCGCCGCTAGCGGATTCTCCTTCTCCTC TTACGCCATGTCTGTTGGTCCGCCAAGCCCCTGGAAAAGGCCTGGAA TGGGTGTCCGCGATTTCCGGGAGCGGAGGTTTCGACCTATTACGCCG ACTCCGTGAAGGGCCGCTTTACCATCTCCCGGGATAACTCCAAGAAC ACTCTGTACCTCCAAATGAACTCGCTGAGAGCCGAGGACACCCCGT GTATTACTGCGCGAAGGCGCTGGTCCGCGCGAAGTGGGGCATTGAC ATCTGGGGACAGGGAAGTCTTGTGACCGTGTGAGCGGAGGCGGCG GCTCCGGCGGAGGAGGAGCGGGGGCGGTGGTTCCGAAATCGTGT TGACTCAGTCCCCGGGAACCCTGAGCTTGTACCCGGGGAGCGGGC

		CACTCTCTCCTGTGCGGCCTCCCAATCGCTCTCATCCAATTTCTGGC CTGGTACCAGCAGAAGCCCGGACAGGCCCGGGCCTGCTCATCTAC GGCGCTTCAAACCTGGGCAACGGGAACCCCTGATCGGTTGAGCGGAA GCGGATCGGGTACTGACTTTACCCTGACCATCACCAGACTGGAACCG GAGGACTTCGCCGTGTACTACTGCCAGTACTACGGCACCTCCCCAT GTACACATTTCGGACAGGGTACCAAGGTCGAGATTAAG
BCMA_EBB- C1978-D4- aa VH	512	EVQLLETGGGLVQPGGSLRLSCAASGFSFSSYAMSWVRQAPGKGLEW VSAISGSGGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYC AKALVGATGAFDIWQGQTLTVSS
BCMA_EBB- C1978-D4- aa VL	513	EIVLTQSPGTLSLSPGERATLSCRASQSLSSNFLAWYQQKPGQAPGLLIY GASNWATGTPDRFSGSGSGTDFTLTITRLEPEDFAVYYCQYYGTSPMYT FGQGTKVEIK
BCMA_EBB-C1980-A2		
BCMA_EBB- C1980-A2- aa ScFv domain	514	EVQLLES GGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEW VSAISGSGGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYC VLWFGEGFDPWGQGT LTVSSGGGGSGGGSGGGGSDIVLTQSP LSL PVTGPGEPA SISRSSQSL LHSNGYNYLDWYLQKPGQSPQLLIY LGSNRA SGVPDRFSGSGSGTDFTL KISRVEAEDVGVYYCMQALQ TPLTFGGG TKV DIK
BCMA_EBB- C1980-A2- nt ScFv domain	515	GAAGTGCAGCTGCTTGAGAGCGGTGGAGGTCTGGTGCAGCCCGGG GGATCACTGCGCCTGTCTGTGCCGCGTCCGGTTTCACTTTCTCCTC GTACGCCATGTGCTGGGTGAGACAGGCACCGGGAAAGGACTGGAA TGGGTGTGAGCCATTTTCGGGTTTCGGGGGGCAGCACCTACTACGCTG ACTCCGTGAAGGGCCGGTTCACCATTTCCCGCGACAACCTCCAAGAAC ACCTTGACCTCCAAATGAACTCCCTGCGGGCCGAAGATACCGCCGT GTATTACTGCGTGCTGTGGTTCGGAGAGGGATTGACCCGTGGGGA CAAGGAACACTCGTGACTGTGTCATCCGGCGGAGGCGGCAGCGGTG GCGGCGGTTCCGGCGGCGGCGGATCTGACATCGTGTTGACCCAGTC CCCTCTGAGCCTGCCGGTCACTCCTGGCGAACCAGCCAGCATCTCCT GCCGGTCGAGCCAGTCCCTCCTGCACTCCAATGGGTACAACCTACCTC GATTGGTATCTGCAAAGCCGGGCCAGAGCCCCAGCTGCTGATCTA CCTTGGGTCAAACCGCGCTTCCGGGGTGCTGATAGATTCTCCGGGT CCGGGAGCGGAACCGACTTTACCCTGAAAATCTCGAGGGTGGAGGC CGAGGACGTGCGAGTGTACTACTGCATGCAGGCGCTCCAGACTCCC CTGACCTTCGGAGGAGGAACGAAGGTGACATCAAGA
BCMA_EBB- C1980-A2- aa VH	516	EVQLLES GGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEW VSAISGSGGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYC VLWFGEGFDPWGQGT LTVSS
BCMA_EBB- C1980-A2- aa VL	517	DIVLTQSP LSLPVTGPGEPA SISRSSQSL LHSNGYNYLDWYLQKPGQSP QLLIY LGSNRA SGVPDRFSGSGSGTDFTL KISRVEAEDVGVYYCMQALQ TPLTFGGG TKVDIK
BCMA_EBB-C1981-C3		
BCMA_EBB- C1981-C3- aa ScFv domain	518	QVQLVES GGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEW VSAISGSGGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYC AKVGYDSSGYRDYYGMDVWGQGT TVTVSSGGGGSGGGSGGGGS EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLIY GTSSRATGISDRFSGSGSGTDFTLTISRLEPEDFAVYYCQHYGNSPPKFT FGPGTKLEIK
BCMA_EBB- C1981-C3- nt ScFv domain	519	CAAGTGCAGCTCGTGAGTCAGGCGGAGGACTGGTGCAGCCCGGG GGCTCCCTGAGACTTTCTGCGCGGCATCGGGTTTTACCTTCTCCTC CTATGCTATGCTCCTGGGTGCGCCAGGCCCGGGAAAGGACTGGAA TGGGTGTCCGCAATCAGCGGTAGCGGGGGCTCAACATACTACGCGG ACTCCGTCAAGGGTGCCTTCACTATTTCCCGGGACAACCTCCAAGAAT ACCCTGTACCTCCAAATGAACAGCCTCAGGGCCGAGGATACTGCCGT GTACTACTGCGCCAAAGTCGGATACGATAGCTCCGGTTACTACCGGG

		ACTACTACGGAATGGACGTGTGGGGACAGGGCACCACCGTGACCGT GTCAAGCGGCGGAGGCGGTTTCAGGAGGGGGAGGCTCCGGCGGTGG AGGGTCCGAAATCGTCCTGACTCAGTCGCCTGGCACTCTGTCGTTGT CCCCGGGGGAGCGCGCTACCCTGTCGTGTCGGGCGTCGCAGTCCG TGTCGAGCTCCTACCTCGCGTGGTACCAGCAGAAGCCCGGACAGGC CCCTAGACTTCTGATCTACGGCACTTCTTCACGCGCCACCGGGATCA GCGACAGGTTTACGCGGCTCCGGCTCCGGGACCGACTTCACCCTGAC CATTAGCCGGCTGGAGCCTGAAGATTTCCCGGTGTATTACTGCCAAC ACTACGGAAACTCGCCGCCAAAGTTCACGTTCCGACCCGGAACCAAG CTGGAAATCAAG
BCMA_EBB- C1981-C3- aa VH	520	QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEW VSAISGSGGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYC AKVGYDSSGYRDYYGMDVWGQGTITVTVSS
BCMA_EBB- C1981-C3- aa VL	521	EIVLTQSPGTL SLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIY GTSSRATGISDRFSGSGSGTDFTLTISRLEPEDFAVYYCQHYGNSPPKFT FGPGTKLEIK
BCMA_EBB-C1978-G4		
BCMA_EBB- C1978-G4- aa ScFv domain	522	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEW VSAISGSGGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYC AKMGWSSGYLGAFDIWGQGTITVTVSSGGGGSGGGGSGGGGSEIVLTQ SPGTL SLSPGERATLSCRASQSVASSFLAWYQQKPGQAPRLLIYGASGR ATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQHYGGSPRLTFGGGT KVDIK
BCMA_EBB- C1978-G4- nt ScFv domain	523	GAAGTCCAAC TGGTGGAGTCCGGGGGAGGGCTCGTGCAGCCCGGA GGCAGCCTTCGGCTGTCGTGCGCCGCCTCCGGGTTACGTTCTCAT CCTACGCGATGTCGTGGGT CAGACAGGCACCAGGAAAGGACTGGA ATGGGTGTCCGCCATTAGCGGCTCCGGCGGTAGCACCTACTATGCC GACTCAGTGAAGGGAAGGTTCACTATCTCCCGCGACAACAGCAAGAA CACCTGTACCTCCAAATGAACTCTCTGCGGGCCGAGGATACCGCG GTGTACTATTGCGCCAAGATGGGTTGGTCCAGCGGATACTTGGGAGC CTTCGACATTTGGGGACAGGGCACTACTGTGACCGTGTCTCCGGG GGTGGCGGATCGGGAGGCGGCGGCTCGGGTGGAGGGGGTTCCGAA ATCGTGTTGACCCAGTCACCGGGAACCCTCTCGCTGTCCCCGGGAG AACGGGCTACACTGTCATGTAGAGCGTCCCAGTCCGTGGCTTCCTCG TTCCTGGCCTGGTACCAGCAGAAGCCGGGACAGGCACCCCGCCTGC TCATCTACGGAGCCAGCGGCCGGGCGACCGGCATCCCTGACCGCTT CTCCGGTTCGGGCTCGGGCACCGACTTTACTCTGACCATTAGCAGGC TTGAGCCCCGAGGATTTTGCCGTGTACTACTGCCAACACTACGGGGGG AGCCCTCGCCTGACCTTCGGAGGCGGAAC TAAGGTCGATATCAAAA
BCMA_EBB- C1978-G4- aa VH	524	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEW VSAISGSGGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYC AKMGWSSGYLGAFDIWGQGTITVTVSS
BCMA_EBB- C1978-G4- aa VL	525	EIVLTQSPGTL SLSPGERATLSCRASQSVASSFLAWYQQKPGQAPRLLIY GASGRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQHYGGSPRLT FGGGTKVDIK

In some embodiments, additional exemplary CAR constructs are generated using the VH and VL sequences from PCT Publication WO2012/0163805 (the contents of which are hereby incorporated by reference in its entirety). In some embodiments, additional exemplary CAR constructs are generated using the VH and VL sequences from PCT Publication WO2016/014565 (the contents of which are hereby incorporated by reference in its entirety). In some embodiments, additional exemplary CAR constructs are generated using the VH and VL sequences from PCT Publication WO2014/122144 (the

contents of which are hereby incorporated by reference in its entirety). In some embodiments, additional exemplary CAR constructs are generated using the CAR molecules, and/or the VH and VL sequences from PCT Publication WO2016/014789 (the contents of which are hereby incorporated by reference in its entirety). In some embodiments, additional exemplary CAR constructs are generated using the CAR molecules, and/or the VH and VL sequences from PCT Publication WO2014/089335 (the contents of which are hereby incorporated by reference in its entirety). In some embodiments, additional exemplary CAR constructs are generated using the CAR molecules, and/or the VH and VL sequences from PCT Publication WO2014/140248 (the contents of which are hereby incorporated by reference in its entirety).

In some embodiments, additional exemplary CAR constructs can also be generated using the VH and VL sequences found in Table 12. The amino acid sequences of exemplary scFv domains comprising the VH and VL domains and a linker sequence, and full-length CARs are also found in Table 12.

Table 12. Additional exemplary BCMA binding domain sequences

Name	Sequence	SEQ ID NO:
A7D12.2 VH	QIQLVQSGPDLKKPGETVKLSCKASGYFTNFGMNWVKQAPGKGFKWMMAWIN TYTGESYFADDFKGRFAFSVETSATTAYLQINNLTEDTATYFCARGEIYYGYDG GFAYWGQGTLLTVSA	526
A7D12.2 VL	DVVMQTQSHRFMSTSVGDRVSITCRASQDVNTAVSWYQQKPGQSPKLLIFSASY RYTGVPDRFTGSGSGADFTLTISVQAEDLAVYYCQQHYSTPWTFGGGTKLDIK	527
A7D12.2 scFv domain	QIQLVQSGPDLKKPGETVKLSCKASGYFTNFGMNWVKQAPGKGFKWMMAWIN TYTGESYFADDFKGRFAFSVETSATTAYLQINNLTEDTATYFCARGEIYYGYDG GFAYWGQGTLLTVSAGGGGSGGGGSGGGGSDVVMQTQSHRFMSTSVGDRVSI TCRASQDVNTAVSWYQQKPGQSPKLLIFSASYRYTGVPDRFTGSGSGADFTLT SSVQAEDLAVYYCQQHYSTPWTFGGGTKLDIK	528
C11D5.3 VH	QIQLVQSGPELKKPGETVKISCKASGYFTDYSINWVKRAPGKGLKWMGWINTE TREPAYAYDFRGRFAFSLETSASTAYLQINNLTEDTATYFCALDYSYAMDYWG QGTSTVTVSS	529
C11D5.3 VL	DIVLTQSPASLMSLGKRATISCRASESVSVIGAHLIHWYQQKPGQPPLLIYLAS NLETGVPARFSGSGSGTDFTLTIDPVEEDDAVYISCLQSRIPTFGGGTKLEIK	530
C11D5.3 scFv domain	QIQLVQSGPELKKPGETVKISCKASGYFTDYSINWVKRAPGKGLKWMGWINTE TREPAYAYDFRGRFAFSLETSASTAYLQINNLTEDTATYFCALDYSYAMDYWG QGTSTVTVSSGGGGSGGGGSGGGGSGIQLVQSGPELKKPGETVKISCKASGYT FTDYSINWVKRAPGKGLKWMGWINTETREPAYAYDFRGRFAFSLETSASTAYL QINNLTEDTATYFCALDYSYAMDYWGQGTSTVTVSS	531
C12A3.2 VH	QIQLVQSGPELKKPGETVKISCKASGYTFRHYSMNWVKQAPGKGLKWMGRINT ESGVPIYADDFKGRFAFSVETSASTAYLVINNLKDEDTASYFCSNDYLYSLDFWG QGTALTIVSS	532
C12A3.2 VL	DIVLTQSPPSLMSLGKRATISCRASESVTILGSHLIYWYQQKPGQPPTLLIQLAS NVQTGVPARFSGSGSRTDFTLTIDPVEEDDAVYYCLQSRTIPTFGGGTKLEIK	533
C12A3.2 scFv domain	QIQLVQSGPELKKPGETVKISCKASGYTFRHYSMNWVKQAPGKGLKWMGRINT ESGVPIYADDFKGRFAFSVETSASTAYLVINNLKDEDTASYFCSNDYLYSLDFWG QGTALTIVSSGGGGSGGGGSGGGGSDIVLTQSPPSLMSLGKRATISCRASESV TILGSHLIYWYQQKPGQPPTLLIQLASNVQTGVPARFSGSGSRTDFTLTIDPVEE DDVAVYYCLQSRTIPTFGGGTKLEIK	534
C13F12.1	QIQLVQSGPELKKPGETVKISCKASGYTFTHYSMNWVKQAPGKGLKWMGRINT	535

VH	ETGEPLYADDFKGRFAFSLETSASTAYLVINNLKNEDTATFFCSNDYLYSCDYW GQGTTLTVSS	
C13F12.1 VL	DIVLTQSPPSLAMSLGKRATISCRASESVTILGSHLIYWYQQKPGQPPTLLIQLAS NVQTGVPARFSGSGSRTDFTLTIDPVEEDDVAVYYCLQSRTIPRTFGGGTKLEIK	536
C13F12.1 scFv domain	QIQLVQSGPELKKPGETVKISCKASGYTFTTHYSMNWVKQAPGKGLKWMGRINT ETGEPLYADDFKGRFAFSLETSASTAYLVINNLKNEDTATFFCSNDYLYSCDYW GQGTTLTVSSGGGGSGGGGSGGGGSDIVLTQSPPSLAMSLGKRATISCRASES VTILGSHLIYWYQQKPGQPPTLLIQLASNVQTGVPARFSGSGSRTDFTLTIDPVE EDDVAVYYCLQSRTIPRTFGGGTKLEIK	537

The human CDR sequences of the scFv domains are shown in Table 13 for the heavy chain variable domains and in Table 14 for the light chain variable domains. "ID" stands for the respective SEQ ID NO for each CDR. The CDRs are shown according to the Kabat definition, however, the CDRs under other convention, for example, Chothia or the combined Kabat/Chothia definitions may be readily deduced based on the VH and VL sequences above.

Table 13. Heavy Chain Variable Domain CDRs according to the Kabat numbering scheme (Kabat et al. (1991), "Sequences of Proteins of Immunological Interest," 5th Ed. Public Health Service, National Institutes of Health, Bethesda, MD)

Candidate	HCDR1	ID	HCDR2	ID	HCDR3	ID
139109	NHGMS	538	GIVYSGSTYYAASV KG	539	HGGESDV	540
139103	NYAMS	541	GISRSGENTYYADS VKG	542	SPAHHYGGMDV	543
139105	DYAMH	544	GISWNSGSIGYADS VKG	545	HSFLAY	546
139111	NHGMS	538	GIVYSGSTYYAASV KG	539	HGGESDV	540
139100	NFGIN	547	WINPKNNNTNYAQK FQG	548	GPYYYQSYMDV	549
139101	SDAMT	550	VISGSGGTTYADS VKG	551	LDSSGYYYARGPRY	552
139102	NYGIT	553	WISAYNGNTNYAQK FQG	554	GPYYYYMDV	555
139104	NHGMS	538	GIVYSGSTYYAASV KG	539	HGGESDV	540
139106	NHGMS	538	GIVYSGSTYYAASV KG	539	HGGESDV	540
139107	NHGMS	538	GIVYSGSTYYAASV KG	539	HGGESDV	540
139108	DYYMS	556	YISSSGSTIYYADSV KG	557	ESGDGMDV	558
139110	DYYMS	556	YISSSGNTIYYADSV KG	559	STMVREDY	560
139112	NHGMS	538	GIVYSGSTYYAASV KG	539	HGGESDV	540
139113	NHGMS	538	GIVYSGSTYYAASV KG	539	HGGESDV	540

139114	NHGMS	538	GIVYSGSTYYAASV KG	539	HGGESDV	540
149362	SSYYYWG	561	SIYYSGSAYYNPSL KS	562	HWQEWPAFDI	563
149363	TSGMCVS	564	RIDWDEDKFYSTSL KT	565	SGAGGTSATAFDI	566
149364	SYSMN	567	SISSSSYIYYADSV KG	568	TIAAVYAFDI	569
149365	DYYMS	556	YISSSGSTIYYADSV KG	557	DLRGAFDI	570
149366	SHYIH	571	MINPSGGVTAYSQT LQG	572	EGSGSGWYFDF	573
149367	SGGYWS	574	YIYYSGSTYYNPSLK S	575	AGIAARLRGAFDI	576
149368	SYAIS	577	GIPIFGTANYAQKF QG	578	RGGYQLLRWDVGLL RSAFDI	579
149369	SNSAAWN	580	RTYYRSKWYSFYAI SLKS	581	SSPEGLFLYWFDP	582
BCMA_EBB -C1978-A4	SYAMS	583	AISGSGGSTYYADS VKG	584	VEGSGSLDY	585
BCMA_EBB -C1978-G1	RYPMS	586	GISDSGVSTYYADS AKG	587	RAGSEASDI	588
BCMA_EBB -C1979-C1	SYAMS	583	AISGSGGSTYYADS VKG	584	ATYKRELRYYYGMD V	589
BCMA_EBB -C1978-C7	SYAMS	583	AISGSGGSTYYADS VKG	584	ATYKRELRYYYGMD V	589
BCMA_EBB -C1978-D10	DYAMH	544	GISWNSGSIGYADS VKG	545	VGKAVPDV	590
BCMA_EBB -C1979-C12	DYAMH	544	SINWKGNLAYGDS VKG	591	HQGVAYYNYAMDV	592
BCMA_EBB -C1980-G4	SYAMS	583	AISGSGGSTYYADS VKG	584	VVRDGMDV	593
BCMA_EBB -C1980-D2	SYAMS	583	AISGSGGSTYYADS VKG	584	IPQTGTFDY	594
BCMA_EBB -C1978-A10	SYAMS	583	AISGSGGSTYYADS VKG	584	ANYKRELRYYYGMD V	595
BCMA_EBB -C1978-D4	SYAMS	583	AISGSGGSTYYADS VKG	584	ALVGATGAFDI	596
BCMA_EBB -C1980-A2	SYAMS	583	AISGSGGSTYYADS VKG	584	WFGEGFDP	597
BCMA_EBB -C1981-C3	SYAMS	583	AISGSGGSTYYADS VKG	584	VGYDSSGYRDYY GMDV	598
BCMA_EBB -C1978-G4	SYAMS	583	AISGSGGSTYYADS VKG	584	MGWSSGYLGAFDI	599
A7D12.2	NFGMN	600	WINTYTGESYFADD FKG	601	GEIYYGYDGGFAY	602
C11D5.3	DYSIN	603	WINTETREPAYAYD FRG	604	DYSYAMDY	605
C12A3.2	HYSMN	606	RINTESGVPIYADDF KG	607	DYLYSLDF	608
C13F12.1	HYSMN	606	RINTETGEPLYADD FKG	609	DYLYSCDY	610

Table 14. Light Chain Variable Domain CDRs according to the Kabat numbering scheme (Kabat et al. (1991), "Sequences of Proteins of Immunological Interest," 5th Ed. Public Health Service, National Institutes of Health, Bethesda, MD)

Candidate	LCDR1	ID	LCDR2	ID	LCDR3	ID
139109	RASQSISSYLN	611	AASSLQS	612	QQSYSTPYT	613
139103	RASQSISSSFLA	614	GASRRAT	615	QQYHSSPSWT	616
139105	RSSQSLHLSNGYNYL D	617	LGSNRAS	618	MQALQTPYT	619
139111	KSSQSLLRNDGKTPL Y	620	EVSNRFS	621	MQNIQFPS	622
139100	RSSQSLHLSNGYNYL N	623	LGSKRAS	624	MQALQTPYT	619
139101	RASQSISSYLN	611	GASTLAS	625	QQSYKRAS	626
139102	RSSQSLLYSNGYNYV D	627	LGSNRAS	618	MQGRQFPYS	628
139104	RASQSVSSNLA	629	GASTRAS	630	QQYGSSLT	631
139106	RASQSVSSKLA	632	GASIRAT	636	QQYGSSSWT	637
139107	RASQSVGSTNLA	638	DASNRAT	639	QQYGSSPPWT	640
139108	RASQSISSYLN	611	AASSLQS	612	QQSYTLA	641
139110	KSSESLVHNSGKTYL N	642	EVSNRDS	643	MQGTHWPGT	644
139112	QASEDINKFLN	645	DASTLQT	646	QQYESLPLT	647
139113	RASQSVGSNLA	648	GASTRAT	649	QQYNDWLPVT	650
139114	RASQSIGSSSLA	651	GASSRAS	652	QQYAGSPFFT	653
149362	KASQDIDDAMN	654	SATSPVP	655	LQHDNFPLT	656
149363	RASQDIYNNLA	657	AANKSQS	658	QHYYRFPYS	659
149364	RSSQSLHLSNGYNYL D	617	LGSNRAS	618	MQALQTPYT	619
149365	GGNNIGTKSVH	660	DDSVRPS	661	QVWDSDSEHV V	662
149366	SGDGLSKKYVS	663	RDKERPS	664	QAWDDTTVV	665
149367	RASQGIRNWLA	666	AASNLQS	667	QKYNAPFT	668
149368	GGNNIGSKSVH	669	GKNNRPS	670	SSRDSSGDHL RV	671
149369	QGDSLGNYYAT	672	GTNNRPS	673	NSRDSSGHHL L	674
BCMA_EBB- C1978-A4	RASQSVSSAYLA	675	GASTRAT	649	QHYGSSFNGLS SLFT	676
BCMA_EBB- C1978-G1	RASQSVSNSLA	677	DASSRAT	678	QQFGTSSGLT	679
BCMA_EBB- C1979-C1	RASQSVSSSFLA	680	GASSRAT	681	QQYHSSPSWT	616
BCMA_EBB- C1978-C7	RASQSVSTTFLA	682	GSSNRAT	683	QQYHSSPSWT	616
BCMA_EBB- C1978-D10	RASQSISSYLN	611	AASSLQS	612	QQSYSTPYS	684
BCMA_EBB- C1979-C12	RATQSIGSSFLA	685	GASQRAT	686	QHYESSPSWT	687

BCMA_EBB-C1980-G4	RASQSVSSSYLA	688	GASSRAT	681	QQYGSPPRFT	689
BCMA_EBB-C1980-D2	RASQSVSSSYLA	688	GASSRAT	681	QHYGSSPSWT	690
BCMA_EBB-C1978-A10	RASQRVASNYLA	691	GASSRAT	681	QHYDSSPSWT	692
BCMA_EBB-C1978-D4	RASQSLSSNFLA	693	GASNWAT	694	QYYGTSPMYT	695
BCMA_EBB-C1980-A2	RSSQSLLSNGYNYL D	617	LGSNRAS	618	MQALQTPLT	696
BCMA_EBB-C1981-C3	RASQSVSSSYLA	688	GTSSRAT	697	QHYGNSPPKF T	698
BCMA_EBB-C1978-G4	RASQSVASSFLA	699	GASGRAT	700	QHYGGSPRLT	701
A7D12.2	RASQDVNTAVS	702	SASYRYT	703	QQHYSTPWT	704
C11D5.3	RASESVSIGAHLIH	705	LASNLET	706	LQSRIFPRT	707
C12A3.2	RASESVTILGSHLIY	708	LASNVQT	709	LQSRTIPRT	710
C13F12.1	RASESVTILGSHLIY	708	LASNVQT	709	LQSRTIPRT	710

In one embodiment, the BCMA binding domain comprises one or more (e.g., all three) light chain complementary determining region 1 (LC CDR1), light chain complementary determining region 2 (LC CDR2), and light chain complementary determining region 3 (LC CDR3) of a BCMA binding domain described herein, e.g., provided in Table 11, 12 or 14, and/or one or more (e.g., all three) heavy chain complementary determining region 1 (HC CDR1), heavy chain complementary determining region 2 (HC CDR2), and heavy chain complementary determining region 3 (HC CDR3) of a BCMA binding domain described herein, e.g., provided in Table 11, 12 or 13. In one embodiment, the BCMA binding domain comprises one, two, or all of LC CDR1, LC CDR2, and LC CDR3 of any amino acid sequences as provided in Table 11, incorporated herein by reference; and one, two or all of HC CDR1, HC CDR2, and HC CDR3 of any amino acid sequences as provided in Table 11.

In one embodiment, the BCMA binding domain comprises a light chain variable region described herein (e.g., in Table 11 or 12) and/or a heavy chain variable region described herein (e.g., in Table 11 or 12). In one embodiment, the BCMA binding domain is a scFv comprising a light chain and a heavy chain of an amino acid sequence listed in Table 11 or 12. In an embodiment, the BCMA binding domain (e.g., an scFv) comprises: a light chain variable region comprising an amino acid sequence having at least one, two or three modifications (e.g., substitutions, e.g., conservative substitutions) but not more than 30, 20 or 10 modifications (e.g., substitutions, e.g., conservative substitutions) of an amino acid sequence of a light chain variable region provided in Table 11 or 12, or a sequence with 95-99% identity with an amino acid sequence provided in Table 11 or 12; and/or a heavy chain variable region comprising an amino acid sequence having at least one, two or three modifications (e.g., substitutions, e.g., conservative substitutions) but not more than 30, 20 or 10 modifications (e.g., substitutions, e.g., conservative

substitutions) of an amino acid sequence of a heavy chain variable region provided in Table 11 or 12, or a sequence with 95-99% identity to an amino acid sequence provided in Table 11 or 12.

In one embodiment, the BCMA binding domain comprises an amino acid sequence selected from any one of SEQ ID NOs: 382, 386, 390, 394, 398, 402, 406, 410, 414, 418, 422, 426, 430, 434, 438, 442, 446, 450, 454, 458, 462, 466, 470, 474, 478, 482, 486, 490, 494, 498, 502, 506, 510, 514, 518, 522, 528, 531, 534, or 537; or an amino acid sequence having at least one, two or three modifications (e.g., substitutions, e.g., conservative substitutions) but not more than 30, 20 or 10 modifications (e.g., substitutions, e.g., conservative substitutions) to any of the aforesaid sequences; or a sequence with 95-99% identity to any of the aforesaid sequences. In one embodiment, the BCMA binding domain is a scFv, and a light chain variable region comprising an amino acid sequence described herein, e.g., in Table 11 or 12, is attached to a heavy chain variable region comprising an amino acid sequence described herein, e.g., in Table 11 or 12, via a linker, e.g., a linker described herein. In one embodiment, the BCMA binding domain includes a (Gly4-Ser)*n* linker, wherein *n* is 1, 2, 3, 4, 5, or 6, preferably 4 (SEQ ID NO: 967). The light chain variable region and heavy chain variable region of a scFv can be, e.g., in any of the following orientations: light chain variable region-linker-heavy chain variable region or heavy chain variable region-linker-light chain variable region.

Any known CAR, e.g., the BCMA antigen binding domain of any known CAR, in the art can be used in accordance with the instant invention to construct a CAR. For example, those described herein.

In one embodiment, an antigen binding domain against ROR1 is an antigen binding portion, e.g., CDRs, of an antibody described in, e.g., Hudecek et al., Clin Cancer Res 19(12):3153-3164 (2013); WO 2011159847; and US20130101607.

In one embodiment, an antigen binding domain against CD22 is an antigen binding portion, e.g., CDRs, of an antibody described in, e.g., Haso et al., Blood, 121(7): 1165-1174 (2013); Wayne et al., Clin Cancer Res 16(6): 1894-1903 (2010); Kato et al., Leuk Res 37(1):83-88 (2013); Creative BioMart (creativebiomart.net): MOM-18047-S(P).

In one embodiment, an antigen binding domain against CD20 is an antigen binding portion, e.g., CDRs, of the antibody Rituximab, Ofatumumab, Ocrelizumab, Veltuzumab, or GA101, or derivatives thereof. In one embodiment, an antigen binding domain against CD20 is an antigen binding portion as described in WO2016/164731, hereby incorporated by reference in its entirety.

In one embodiment, the antigen binding domain comprises one, two three (e.g., all three) heavy chain CDRs, HC CDR1, HC CDR2 and HC CDR3, from an antibody listed above, and/or one, two, three (e.g., all three) light chain CDRs, LC CDR1, LC CDR2 and LC CDR3, from an antibody that binds a tumor antigen listed above. In one embodiment, the antigen binding domain comprises a heavy chain variable region and/or a variable light chain region of an antibody that binds a tumor antigen listed above.

In one embodiment, the antigen binding domain of a CAR described herein is a scFv antibody fragment. In one aspect, such antibody fragments are functional in that they retain the equivalent binding affinity, e.g., they bind the same antigen with comparable efficacy, as the IgG antibody from which it is derived. In other embodiments, the antibody fragment has a lower binding affinity, e.g., it binds the same antigen with a lower binding affinity than the antibody from which it is derived, but is functional in that it provides a biological response described herein. In one embodiment, the CAR molecule comprises an antibody fragment that has a binding affinity K_D of 10^{-4} M to 10^{-8} M, e.g., 10^{-5} M to 10^{-7} M, e.g., 10^{-6} M or 10^{-7} M, for the target antigen. In one embodiment, the antibody fragment has a binding affinity that is at least five-fold, 10-fold, 20-fold, 30-fold, 50-fold, 100-fold or 1,000-fold less than a reference antibody, e.g., an antibody described herein.

In one embodiment, the antigen binding domain comprises a non-human antibody or antibody fragment, e.g., a mouse antibody or antibody fragment.

In another embodiment, the antigen binding domain comprises a humanized antibody or an antibody fragment. In some aspects, a non-human antibody is humanized, where specific sequences or regions of the antibody are modified to increase similarity to an antibody naturally produced in a human or fragment thereof. In one aspect, the antigen binding domain is humanized compared to the murine sequence of the antibody or antibody fragment, e.g., scFv, from which it is derived.

A humanized antibody can be produced using a variety of techniques known in the art, including but not limited to, CDR-grafting (see, e.g., European Patent No. EP 239,400; International Publication No. WO 91/09967; and U.S. Pat. Nos. 5,225,539, 5,530,101, and 5,585,089, each of which is incorporated herein in its entirety by reference), veneering or resurfacing (see, e.g., European Patent Nos. EP 592,106 and EP 519,596; Padlan, 1991, Molecular Immunology, 28(4/5):489-498; Studnicka et al., 1994, Protein Engineering, 7(6):805-814; and Roguska et al., 1994, PNAS, 91:969-973, each of which is incorporated herein by its entirety by reference), chain shuffling (see, e.g., U.S. Pat. No. 5,565,332, which is incorporated herein in its entirety by reference), and techniques disclosed in, e.g., U.S. Patent Application Publication No. US2005/0042664, U.S. Patent Application Publication No. US2005/0048617, U.S. Pat. No. 6,407,213, U.S. Pat. No. 5,766,886, International Publication No. WO 93/17105, Tan et al., J. Immunol., 169:1119-25 (2002), Caldas et al., Protein Eng., 13(5):353-60 (2000), Morea et al., Methods, 20(3):267-79 (2000), Baca et al., J. Biol. Chem., 272(16):10678-84 (1997), Roguska et al., Protein Eng., 9(10):895-904 (1996), Couto et al., Cancer Res., 55 (23 Supp):5973s-5977s (1995), Couto et al., Cancer Res., 55(8):1717-22 (1995), Sandhu J S, Gene, 150(2):409-10 (1994), and Pedersen et al., J. Mol. Biol., 235(3):959-73 (1994), each of which is incorporated herein in its entirety by reference. Often, framework residues in the framework regions will be substituted with the corresponding residue from the CDR donor antibody to alter, for example improve, antigen binding. These framework substitutions are identified by methods well-known in the art, e.g., by modeling of the interactions of the CDR and framework residues to identify framework residues important for antigen binding and sequence comparison to identify unusual

framework residues at particular positions. (See, e.g., Queen et al., U.S. Pat. No. 5,585,089; and Riechmann et al., 1988, *Nature*, 332:323, which are incorporated herein by reference in their entireties.)

A humanized antibody or antibody fragment has one or more amino acid residues remaining in it from a source which is nonhuman. These nonhuman amino acid residues are often referred to as "import" residues, which are typically taken from an "import" variable domain. As provided herein, humanized antibodies or antibody fragments comprise one or more CDRs from nonhuman immunoglobulin molecules and framework regions wherein the amino acid residues comprising the framework are derived completely or mostly from human germline. Multiple techniques for humanization of antibodies or antibody fragments are well-known in the art and can essentially be performed following the method of Winter and co-workers (Jones et al., *Nature*, 321:522-525 (1986); Riechmann et al., *Nature*, 332:323-327 (1988); Verhoeven et al., *Science*, 239:1534-1536 (1988)), by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody, i.e., CDR-grafting (EP 239,400; PCT Publication No. WO 91/09967; and U.S. Pat. Nos. 4,816,567; 6,331,415; 5,225,539; 5,530,101; 5,585,089; 6,548,640, the contents of which are incorporated herein by reference herein in their entirety).

In such humanized antibodies and antibody fragments, substantially less than an intact human variable domain has been substituted by the corresponding sequence from a nonhuman species. Humanized antibodies are often human antibodies in which some CDR residues and possibly some framework (FR) residues are substituted by residues from analogous sites in rodent antibodies. Humanization of antibodies and antibody fragments can also be achieved by veneering or resurfacing (EP 592,106; EP 519,596; Padlan, 1991, *Molecular Immunology*, 28(4/5):489-498; Studnicka et al., *Protein Engineering*, 7(6):805-814 (1994); and Roguska et al., *PNAS*, 91:969-973 (1994)) or chain shuffling (U.S. Pat. No. 5,565,332), the contents of which are incorporated herein by reference herein in their entirety.

The choice of human variable domains, both light and heavy, to be used in making the humanized antibodies is to reduce antigenicity. According to the so-called "best-fit" method, the sequence of the variable domain of a rodent antibody is screened against the entire library of known human variable-domain sequences. The human sequence which is closest to that of the rodent is then accepted as the human framework (FR) for the humanized antibody (Sims et al., *J. Immunol.*, 151:2296 (1993); Chothia et al., *J. Mol. Biol.*, 196:901 (1987), the contents of which are incorporated herein by reference herein in their entirety). Another method uses a particular framework derived from the consensus sequence of all human antibodies of a particular subgroup of light or heavy chains. The same framework may be used for several different humanized antibodies (see, e.g., Nicholson et al. *Mol. Immun.* 34 (16-17): 1157-1165 (1997); Carter et al., *Proc. Natl. Acad. Sci. USA*, 89:4285 (1992); Presta et al., *J. Immunol.*, 151:2623 (1993), the contents of which are incorporated herein by reference herein in their entirety). In some embodiments, the framework region, e.g., all four framework regions, of the heavy chain variable region are derived from a VH4_4-59 germline sequence. In one embodiment, the framework region can comprise, one, two, three, four or five modifications, e.g., substitutions, e.g., from the amino acid at the

corresponding murine sequence. In one embodiment, the framework region, e.g., all four framework regions of the light chain variable region are derived from a VK3_1.25 germline sequence. In one embodiment, the framework region can comprise, one, two, three, four or five modifications, e.g., substitutions, e.g., from the amino acid at the corresponding murine sequence.

5 In some aspects, the antibody fragment of a CAR is humanized with retention of high affinity for the target antigen and other favorable biological properties. According to one aspect of the invention, humanized antibodies and antibody fragments are prepared by a process of analysis of the parental sequences and various conceptual humanized products using three-dimensional models of the parental and humanized sequences. Three-dimensional immunoglobulin models are commonly available and are familiar to those
10 skilled in the art. Computer programs are available which illustrate and display probable three-dimensional conformational structures of selected candidate immunoglobulin sequences. Inspection of these displays permits analysis of the likely role of the residues in the functioning of the candidate immunoglobulin sequence, e.g., the analysis of residues that influence the ability of the candidate immunoglobulin to bind the target antigen. In this way, FR residues can be selected and combined from
15 the recipient and import sequences so that the desired antibody or antibody fragment characteristic, such as increased affinity for the target antigen, is achieved. In general, the CDR residues are directly and most substantially involved in influencing antigen binding.

A humanized antibody or antibody fragment may retain a similar antigenic specificity as the original antibody, e.g., in the present disclosure, the ability to bind human a tumor antigen as described herein. In
20 some embodiments, a humanized antibody or antibody fragment may have improved affinity and/or specificity of binding to a tumor antigen as described herein. In some embodiments, a humanized antibody or antibody fragment may have lower affinity and/or specificity of a tumor antigen as described herein or a B cell antigen as described herein.

In one aspect, the antigen binding domain of the invention is characterized by particular functional
25 features or properties of an antibody or antibody fragment. For example, in one aspect, the portion of a CAR of the invention that comprises an antigen binding domain specifically binds a tumor antigen as described herein.

In one aspect, the antigen binding domain is a fragment, e.g., a single chain variable fragment (scFv). In one aspect, the anti- tumor antigen as described herein binding domain is a Fv, a Fab, a (Fab')₂, or a bi-
30 functional (e.g. bi-specific) hybrid antibody (e.g., Lanzavecchia et al., Eur. J. Immunol. 17, 105 (1987)). In one aspect, the antibodies and fragments thereof of the invention binds a tumor antigen as described herein protein with wild-type or enhanced affinity.

In some instances, scFvs can be prepared according to method known in the art (see, for example, Bird et al., (1988) Science 242:423-426 and Huston et al., (1988) Proc. Natl. Acad. Sci. USA 85:5879-5883).
35 ScFv molecules can be produced by linking VH and VL regions together using flexible polypeptide linkers.

The scFv molecules comprise a linker (e.g., a Ser-Gly linker) with an optimized length and/or amino acid composition. The linker length can greatly affect how the variable regions of a scFv fold and interact. In fact, if a short polypeptide linker is employed (e.g., between 5-10 amino acids) intrachain folding is prevented. Interchain folding is also required to bring the two variable regions together to form a functional epitope binding site. For examples of linker orientation and size see, e.g., Hollinger et al. 1993 Proc Natl Acad. Sci. U.S.A. 90:6444-6448, U.S. Patent Application Publication Nos. 2005/0100543, 2005/0175606, 2007/0014794, and PCT publication Nos. WO2006/020258 and WO2007/024715, is incorporated herein by reference.

An scFv can comprise a linker of at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 25, 30, 35, 40, 45, 50, or more amino acid residues between its VL and VH regions. The linker sequence may comprise any naturally occurring amino acid. In some embodiments, the linker sequence comprises amino acids glycine and serine. In another embodiment, the linker sequence comprises sets of glycine and serine repeats such as (Gly₄Ser)_n, where n is a positive integer equal to or greater than 1 (SEQ ID NO:22). In one embodiment, the linker can be (Gly₄Ser)₄ (SEQ ID NO:29) or (Gly₄Ser)₃ (SEQ ID NO:30). Variation in the linker length may retain or enhance activity, giving rise to superior efficacy in activity studies.

In another aspect, the antigen binding domain is a T cell receptor ("TCR"), an engineered TCR, or a fragment thereof, for example, a single chain TCR (scTCR). Methods to make such TCRs are known in the art. See, e.g., Willemsen RA et al, Gene Therapy 7: 1369–1377 (2000); Zhang T et al, Cancer Gene Ther 11: 487–496 (2004); Aggen et al, Gene Ther. 19(4):365-74 (2012) (references are incorporated herein by its entirety). For example, scTCR can be engineered that contains the V α and V β genes from a T cell clone linked by a linker (e.g., a flexible peptide). This approach is very useful to cancer associated target that itself is intracellular, however, a fragment of such antigen (peptide) is presented on the surface of the cancer cells by MHC.

In one aspect, the antigen binding domain of the CAR comprises an amino acid sequence that is homologous to an antigen binding domain amino acid sequence described herein, and the antigen binding domain retains the desired functional properties of the antigen binding domain described herein.

In one specific aspect, the antigen binding domain of the CAR comprises an antibody fragment. In a further aspect, the antibody fragment comprises a scFv. In a further aspect, the antibody fragment comprises a variable heavy chain (VH) only.

In various aspects, the antigen binding domain of the CAR is engineered by modifying one or more amino acids within one or both variable regions (e.g., VH and/or VL), for example within one or more CDR regions and/or within one or more framework regions. In one specific aspect, the CAR composition of the invention comprises an antibody fragment. In a further aspect, the antibody fragment comprises an scFv.

It will be understood by one of ordinary skill in the art that the antibody or antibody fragment of the invention may further be modified such that they vary in amino acid sequence (e.g., from wild-type), but not in desired activity. For example, additional nucleotide substitutions leading to amino acid substitutions at "non-essential" amino acid residues may be made to the protein. For example, a nonessential amino acid residue in a molecule may be replaced with another amino acid residue from the same side chain family. In another embodiment, a string of amino acids can be replaced with a structurally similar string that differs in order and/or composition of side chain family members, e.g., a conservative substitution, in which an amino acid residue is replaced with an amino acid residue having a similar side chain, may be made.

Families of amino acid residues having similar side chains have been defined in the art, including basic side chains (e.g., lysine, arginine, histidine), acidic side chains (e.g., aspartic acid, glutamic acid), uncharged polar side chains (e.g., glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (e.g., alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (e.g., threonine, valine, isoleucine) and aromatic side chains (e.g., tyrosine, phenylalanine, tryptophan, histidine).

Percent identity in the context of two or more nucleic acids or polypeptide sequences, refers to two or more sequences that are the same. Two sequences are "substantially identical" if two sequences have a specified percentage of amino acid residues or nucleotides that are the same (e.g., 60% identity, optionally 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% identity over a specified region, or, when not specified, over the entire sequence), when compared and aligned for maximum correspondence over a comparison window, or designated region as measured using one of the following sequence comparison algorithms or by manual alignment and visual inspection. Optionally, the identity exists over a region that is at least about 50 nucleotides (or 10 amino acids) in length, or more preferably over a region that is 100 to 500 or 1000 or more nucleotides (or 20, 50, 200 or more amino acids) in length.

For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. Default program parameters can be used, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters. Methods of alignment of sequences for comparison are well known in the art. Optimal alignment of sequences for comparison can be conducted, e.g., by the local homology algorithm of Smith and Waterman, (1970) Adv. Appl. Math. 2:482c, by the homology alignment algorithm of Needleman and Wunsch, (1970) J. Mol. Biol. 48:443, by the search for similarity method of Pearson and Lipman, (1988)

Proc. Nat'l. Acad. Sci. USA 85:2444, by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI), or by manual alignment and visual inspection (see, e.g., Brent et al., (2003) Current Protocols in Molecular Biology).

- 5 Two examples of algorithms that are suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul et al., (1977) Nuc. Acids Res. 25:3389-3402; and Altschul et al., (1990) J. Mol. Biol. 215:403-410, respectively. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information.
- 10 The percent identity between two amino acid sequences can also be determined using the algorithm of E. Meyers and W. Miller, (1988) Comput. Appl. Biosci. 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. In addition, the percent identity between two amino acid sequences can be determined using the Needleman and Wunsch (1970) J. Mol. Biol. 48:444-453) algorithm which has been incorporated into
- 15 the GAP program in the GCG software package (available at www.gcg.com), using either a Blossom 62 matrix or a PAM250 matrix, and a gap weight of 16, 14, 12, 10, 8, 6, or 4 and a length weight of 1, 2, 3, 4, 5, or 6.

- In one aspect, the present disclosure contemplates modifications of the starting antibody or fragment (e.g., scFv) amino acid sequence that generate functionally equivalent molecules. For example, the VH
- 20 or VL of an antigen binding domain to a tumor antigen described herein, e.g., scFv, comprised in the CAR can be modified to retain at least about 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% identity of the starting VH or VL framework region of the antigen binding domain to the tumor antigen described herein, e.g., scFv. The present disclosure contemplates modifications of the entire
 - 25 CAR construct, e.g., modifications in one or more amino acid sequences of the various domains of the CAR construct in order to generate functionally equivalent molecules. The CAR construct can be modified to retain at least about 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% identity of the starting CAR construct.

30 ***Bispecific CARs***

- In an embodiment a multispecific antibody molecule is a bispecific antibody molecule. A bispecific antibody has specificity for no more than two antigens. A bispecific antibody molecule is characterized by a first immunoglobulin variable domain sequence which has binding specificity for a first epitope and a second immunoglobulin variable domain sequence that has binding specificity for a second epitope. In
- 35 an embodiment the first and second epitopes are on the same antigen, e.g., the same protein (or subunit

of a multimeric protein). In an embodiment the first and second epitopes overlap. In an embodiment the first and second epitopes do not overlap. In an embodiment the first and second epitopes are on different antigens, e.g., different proteins (or different subunits of a multimeric protein). In an embodiment a bispecific antibody molecule comprises a heavy chain variable domain sequence and a light chain variable domain sequence which have binding specificity for a first epitope and a heavy chain variable domain sequence and a light chain variable domain sequence which have binding specificity for a second epitope. In an embodiment a bispecific antibody molecule comprises a half antibody having binding specificity for a first epitope and a half antibody having binding specificity for a second epitope. In an embodiment a bispecific antibody molecule comprises a half antibody, or fragment thereof, having binding specificity for a first epitope and a half antibody, or fragment thereof, having binding specificity for a second epitope. In an embodiment a bispecific antibody molecule comprises a scFv, or fragment thereof, have binding specificity for a first epitope and a scFv, or fragment thereof, have binding specificity for a second epitope.

In certain embodiments, the antibody molecule is a multi-specific (e.g., a bispecific or a trispecific) antibody molecule. Protocols for generating bispecific or heterodimeric antibody molecules are known in the art; including but not limited to, for example, the "knob in a hole" approach described in, e.g., US 5731168; the electrostatic steering Fc pairing as described in, e.g., WO 09/089004, WO 06/106905 and WO 2010/129304; Strand Exchange Engineered Domains (SEED) heterodimer formation as described in, e.g., WO 07/110205; Fab arm exchange as described in, e.g., WO 08/119353, WO 2011/131746, and WO 2013/060867; double antibody conjugate, e.g., by antibody cross-linking to generate a bi-specific structure using a heterobifunctional reagent having an amine-reactive group and a sulfhydryl reactive group as described in, e.g., US 4433059; bispecific antibody determinants generated by recombining half antibodies (heavy-light chain pairs or Fabs) from different antibodies through cycle of reduction and oxidation of disulfide bonds between the two heavy chains, as described in, e.g., US 4444878; trifunctional antibodies, e.g., three Fab' fragments cross-linked through sulfhydryl reactive groups, as described in, e.g., US5273743; biosynthetic binding proteins, e.g., pair of scFvs cross-linked through C-terminal tails preferably through disulfide or amine-reactive chemical cross-linking, as described in, e.g., US5534254; bifunctional antibodies, e.g., Fab fragments with different binding specificities dimerized through leucine zippers (e.g., c-fos and c-jun) that have replaced the constant domain, as described in, e.g., US5582996; bispecific and oligospecific mono- and oligovalent receptors, e.g., VH-CH1 regions of two antibodies (two Fab fragments) linked through a polypeptide spacer between the CH1 region of one antibody and the VH region of the other antibody typically with associated light chains, as described in, e.g., US5591828; bispecific DNA-antibody conjugates, e.g., crosslinking of antibodies or Fab fragments through a double stranded piece of DNA, as described in, e.g., US5635602; bispecific fusion proteins, e.g., an expression construct containing two scFvs with a hydrophilic helical peptide linker between them and a full constant region, as described in, e.g., US5637481; multivalent and multispecific binding proteins, e.g., dimer of polypeptides having first domain with binding region of Ig heavy chain variable

region, and second domain with binding region of Ig light chain variable region, generally termed diabodies (higher order structures are also encompassed creating for bispecific, trispecific, or tetraspecific molecules, as described in, *e.g.*, US5837242; minibody constructs with linked VL and VH chains further connected with peptide spacers to an antibody hinge region and CH3 region, which can be dimerized to form bispecific/multivalent molecules, as described in, *e.g.*, US5837821; VH and VL domains linked with a short peptide linker (*e.g.*, 5 or 10 amino acids) or no linker at all in either orientation, which can form dimers to form bispecific diabodies; trimers and tetramers, as described in, *e.g.*, US5844094; String of VH domains (or VL domains in family members) connected by peptide linkages with crosslinkable groups at the C-terminus further associated with VL domains to form a series of FVs (or scFVs), as described in, *e.g.*, US5864019; and single chain binding polypeptides with both a VH and a VL domain linked through a peptide linker are combined into multivalent structures through non-covalent or chemical crosslinking to form, *e.g.*, homobivalent, heterobivalent, trivalent, and tetravalent structures using both scFV or diabody type format, as described in, *e.g.*, US5869620. Additional exemplary multispecific and bispecific molecules and methods of making the same are found, for example, in US5910573, US5932448, US5959083, US5989830, US6005079, US6239259, US6294353, US6333396, US6476198, US6511663, US6670453, US6743896, US6809185, US6833441, US7129330, US7183076, US7521056, US7527787, US7534866, US7612181, US2002004587A1, US2002076406A1, US2002103345A1, US2003207346A1, US2003211078A1, US2004219643A1, US2004220388A1, US2004242847A1, US2005003403A1, US2005004352A1, US2005069552A1, US2005079170A1, US2005100543A1, US2005136049A1, US2005136051A1, US2005163782A1, US2005266425A1, US2006083747A1, US2006120960A1, US2006204493A1, US2006263367A1, US2007004909A1, US2007087381A1, US2007128150A1, US2007141049A1, US2007154901A1, US2007274985A1, US2008050370A1, US2008069820A1, US2008152645A1, US2008171855A1, US2008241884A1, US2008254512A1, US2008260738A1, US2009130106A1, US2009148905A1, US2009155275A1, US2009162359A1, US2009162360A1, US2009175851A1, US2009175867A1, US2009232811A1, US2009234105A1, US2009263392A1, US2009274649A1, EP346087A2, WO0006605A2, WO02072635A2, WO04081051A1, WO06020258A2, WO2007044887A2, WO2007095338A2, WO2007137760A2, WO2008119353A1, WO2009021754A2, WO2009068630A1, WO9103493A1, WO9323537A1, WO9409131A1, WO9412625A2, WO9509917A1, WO9637621A2, WO9964460A1. The contents of the above-referenced applications are incorporated herein by reference in their entireties.

Within each antibody or antibody fragment (*e.g.*, scFv) of a bispecific antibody molecule, the VH can be upstream or downstream of the VL. In some embodiments, the upstream antibody or antibody fragment (*e.g.*, scFv) is arranged with its VH (VH₁) upstream of its VL (VL₁) and the downstream antibody or antibody fragment (*e.g.*, scFv) is arranged with its VL (VL₂) upstream of its VH (VH₂), such that the overall bispecific antibody molecule has the arrangement VH₁-VL₁-VL₂-VH₂. In other embodiments, the upstream antibody or antibody fragment (*e.g.*, scFv) is arranged with its VL (VL₁) upstream of its VH (VH₁) and the downstream antibody or antibody fragment (*e.g.*, scFv) is arranged with its VH (VH₂) upstream of

its VL (VL₂), such that the overall bispecific antibody molecule has the arrangement VL₁-VH₁-VH₂-VL₂.

Optionally, a linker is disposed between the two antibodies or antibody fragments (e.g., scFvs), e.g.,

between VL₁ and VL₂ if the construct is arranged as VH₁-VL₁-VL₂-VH₂, or between VH₁ and VH₂ if the

construct is arranged as VL₁-VH₁-VH₂-VL₂. The linker may be a linker as described herein, e.g., a (Gly₄-

5 Ser)_n linker, wherein n is 1, 2, 3, 4, 5, or 6, preferably 4 (SEQ ID NO: 967). In general, the linker between the two scFvs should be long enough to avoid mispairing between the domains of the two scFvs.

Optionally, a linker is disposed between the VL and VH of the first scFv. Optionally, a linker is disposed

between the VL and VH of the second scFv. In constructs that have multiple linkers, any two or more of

the linkers can be the same or different. Accordingly, in some embodiments, a bispecific CAR comprises

10 VLs, VHs, and optionally one or more linkers in an arrangement as described herein.

In one aspect, the chimeric antigen receptor comprises a bispecific antigen binding domain, a

transmembrane domain (e.g., as described herein), and an intracellular signaling domain (e.g., as

described herein). In embodiments, the bispecific antigen binding domain comprises a first

immunoglobulin variable domain sequence, e.g., an scFv (or comprises the light chain CDRs and/or

15 heavy chain CDRs from a scFv described herein), which binds an antigen, e.g., as described herein, e.g.,

(a CD19 binding domain or BCMA binding domain described herein, e.g., in Table 6 or Table 12), and a

second immunoglobulin variable domain sequence, e.g., a scFv (or comprises the light chain CDRs

and/or heavy chain CDRs from a scFv described herein), which has binding specificity for one or more

antigens described herein, e.g., comprises a scFv as described herein, e.g., comprising a mesothelin

20 binding domain or EGFRvIII binding domain (e.g., as described in Table 2 or Table 5). In embodiments,

the bispecific antigen binding domain comprises a CD19 binding domain described herein and a

mesothelin binding domain described herein. In embodiments, the bispecific antigen binding domain

comprises a BCMA binding domain described herein and a mesothelin binding domain described herein.

In embodiments, the bispecific antigen binding domain comprises a CD19 binding domain described

25 herein and a EGFRvIII binding domain described herein. In embodiments, the bispecific antigen binding

domain comprises a BCMA binding domain described herein and a EGFRvIII binding domain described

herein. In another aspect, the invention provides a cell (e.g., a population of cells), e.g., an immune

effector cell, e.g., a T cell or NK cell, e.g., as described herein, which is engineered to express (e.g.,

comprises) a bispecific CAR as described herein, e.g., a bispecific CAR comprising two antigen binding

30 domains described herein. Without being bound by any theory, it is believed that cells expressing such

bispecific CARs (e.g., comprising a two antigen binding domains, e.g., as described herein) are useful in

the methods and compositions described herein.

Chimeric TCR

In one aspect, the antigen binding domains described herein, e.g., the antibodies and antibody fragments,

35 e.g., provided in the Tables herein, can be grafted to one or more constant domain of a T cell receptor

("TCR") chain, for example, a TCR alpha or TCR beta chain, to create a chimeric TCR that binds

specificity to a tumor antigen described herein. Without being bound by theory, it is believed that chimeric TCRs will signal through the TCR complex upon antigen binding. For example, a mesothelin or CD19 scFv or a fragment thereof, e.g., a VL domain, or VH domain, as disclosed herein, can be grafted to the constant domain, e.g., at least a portion of the extracellular constant domain, the transmembrane domain and the cytoplasmic domain, of a TCR chain, for example, the TCR alpha chain and/or the TCR beta chain. As another example, the CDRs of an antibody or antibody fragment, e.g., the CDRs of any antibody or antibody fragment as described in Tables provided herein may be grafted into a TCR alpha and/or beta chain to create a chimeric TCR that binds specifically to a tumor antigen described herein. For example, the LCDRs disclosed herein may be grafted into the variable domain of a TCR alpha chain and the HCDRs disclosed herein may be grafted to the variable domain of a TCR beta chain, or vice versa. Such chimeric TCRs may be produced by methods known in the art (For example, Willemsen RA et al, Gene Therapy 2000; 7: 1369–1377; Zhang T et al, Cancer Gene Ther 2004; 11: 487–496; Aggen et al, Gene Ther. 2012 Apr;19(4):365-74).

Transmembrane Domain

With respect to the transmembrane domain, in various embodiments, a CAR can be designed to comprise a transmembrane domain that is attached to the extracellular domain of the CAR, e.g., the antigen binding domain. A transmembrane domain can include one or more additional amino acids adjacent to the transmembrane region, e.g., one or more amino acid associated with the extracellular region of the protein from which the transmembrane was derived (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 up to 15 amino acids of the extracellular region) and/or one or more additional amino acids associated with the intracellular region of the protein from which the transmembrane protein is derived (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 up to 15 amino acids of the intracellular region). In one aspect, the transmembrane domain is one that is associated with one of the other domains of the CAR, for example, the transmembrane domain is from the same protein as the intracellular signalling domain, e.g., the costimulatory domain. In some instances, the transmembrane domain can be selected or modified by amino acid substitution to avoid binding of such domains to the transmembrane domains of the same or different surface membrane proteins, e.g., to minimize interactions with other members of the receptor complex. In one aspect, the transmembrane domain is capable of homodimerization with another CAR on the cell surface of a CAR-expressing cell. In a different aspect, the amino acid sequence of the transmembrane domain may be modified or substituted so as to minimize interactions with the binding domains of the native binding partner present in the same CAR-expressing cell.

The transmembrane domain may be derived either from a natural or from a recombinant source. Where the source is natural, the domain may be derived from any membrane-bound or transmembrane protein. In one aspect the transmembrane domain is capable of signaling to the intracellular domain(s) whenever the CAR has bound to a target. A transmembrane domain of particular use in this invention may include at least the transmembrane region(s) of e.g., the alpha, beta or zeta chain of the T-cell receptor, CD28,

CD27, CD3 epsilon, CD45, CD4, CD5, CD8, CD9, CD16, CD22, CD33, CD37, CD64, CD80, CD86, CD134, CD137, CD154. In some embodiments, a transmembrane domain may include at least the transmembrane region(s) of, e.g., KIRDS2, OX40, CD2, CD27, LFA-1 (CD11a, CD18), ICOS (CD278), 4-1BB (CD137), GITR, CD40, BAFFR, HVEM (LIGHTR), SLAMF7, NKp80 (KLRF1), NKp44, NKp30, NKp46, CD160, CD19, IL2R beta, IL2R gamma, IL7R α , ITGA1, VLA1, CD49a, ITGA4, IA4, CD49D, ITGA6, VLA-6, CD49f, ITGAD, CD11d, ITGAE, CD103, ITGAL, CD11a, LFA-1, ITGAM, CD11b, ITGAX, CD11c, ITGB1, CD29, ITGB2, CD18, LFA-1, ITGB7, TNFR2, DNAM1 (CD226), SLAMF4 (CD244, 2B4), CD84, CD96 (Tactile), CEACAM1, CRTAM, Ly9 (CD229), CD160 (BY55), PSGL1, CD100 (SEMA4D), SLAMF6 (NTB-A, Ly108), SLAM (SLAMF1, CD150, IPO-3), BLAME (SLAMF8), SELPLG (CD162), LTBR, PAG/Cbp, NKG2D, NKG2C.

In some instances, the transmembrane domain can be attached to the extracellular region of the CAR, e.g., the antigen binding domain of the CAR, via a hinge, e.g., a hinge from a human protein. For example, in one embodiment, the hinge can be a human Ig (immunoglobulin) hinge, e.g., an IgG4 hinge, or a CD8a hinge. In one embodiment, the hinge or spacer comprises (e.g., consists of) the amino acid sequence of SEQ ID NO:4. In one aspect, the transmembrane domain comprises (e.g., consists of) a transmembrane domain of SEQ ID NO: 12.

In one aspect, the hinge or spacer comprises an IgG4 hinge. For example, in one embodiment, the hinge or spacer comprises a hinge of the amino acid sequence SEQ ID NO: 6. In some embodiments, the hinge or spacer comprises a hinge encoded by a nucleotide sequence of SEQ ID NO: 7. In one aspect, the hinge or spacer comprises an IgD hinge. For example, in one embodiment, the hinge or spacer comprises a hinge of the amino acid sequence SEQ ID NO: 8. In some embodiments, the hinge or spacer comprises a hinge encoded by a nucleotide sequence of SEQ ID NO: 9.

In one aspect, the transmembrane domain may be recombinant, in which case it will comprise predominantly hydrophobic residues such as leucine and valine. In one aspect a triplet of phenylalanine, tryptophan and valine can be found at each end of a recombinant transmembrane domain.

Optionally, a short oligo- or polypeptide linker, between 2 and 10 amino acids in length may form the linkage between the transmembrane domain and the cytoplasmic region of the CAR. A glycine-serine doublet provides a particularly suitable linker. For example, in one aspect, the linker comprises the amino acid sequence of GGGGSGGGGS (SEQ ID NO:10). In some embodiments, the linker is encoded by a nucleotide sequence of GGTGGCGGAGGTTCTGGAGGTGGAGGTTCC (SEQ ID NO:11).

In one aspect, the hinge or spacer comprises a KIR2DS2 hinge.

Cytoplasmic Domain

The cytoplasmic domain or region of the CAR includes an intracellular signaling domain. An intracellular signaling domain is generally responsible for activation of at least one of the normal effector functions of the immune cell in which the CAR has been introduced. The term “effector function” refers to a specialized function of a cell. Effector function of a T cell, for example, may be cytolytic activity or helper activity including the secretion of cytokines. Thus the term “intracellular signaling domain” refers to the portion of a protein which transduces the effector function signal and directs the cell to perform a specialized function. While usually the entire intracellular signaling domain can be employed, in many cases it is not necessary to use the entire chain. To the extent that a truncated portion of the intracellular signaling domain is used, such truncated portion may be used in place of the intact chain as long as it transduces the effector function signal. The term intracellular signaling domain is thus meant to include any truncated portion of the intracellular signaling domain sufficient to transduce the effector function signal.

Examples of intracellular signaling domains for use in the CAR of the invention include the cytoplasmic sequences of the T cell receptor (TCR) and co-receptors that act in concert to initiate signal transduction following antigen receptor engagement, as well as any derivative or variant of these sequences and any recombinant sequence that has the same functional capability.

It is known that signals generated through the TCR alone are insufficient for full activation of the T cell and that a secondary and/or costimulatory signal is also required. Thus, T cell activation can be said to be mediated by two distinct classes of cytoplasmic signaling sequences: those that initiate antigen-dependent primary activation through the TCR (primary intracellular signaling domains) and those that act in an antigen-independent manner to provide a secondary or costimulatory signal (secondary cytoplasmic domain, e.g., a costimulatory domain).

A primary signaling domain regulates primary activation of the TCR complex either in a stimulatory way, or in an inhibitory way. Primary intracellular signaling domains that act in a stimulatory manner may contain signaling motifs which are known as immunoreceptor tyrosine-based activation motifs or ITAMs.

Examples of ITAM containing primary intracellular signaling domains that are of particular use in the invention include those of TCR zeta, FcR gamma, FcR beta, CD3 gamma, CD3 delta, CD3 epsilon, CD5, CD22, CD79a, CD79b, CD278 (also known as “ICOS”), FcεRI, DAP10, DAP12, and CD66d. In one embodiment, a CAR of the invention comprises an intracellular signaling domain, e.g., a primary signaling domain of CD3-zeta, e.g., a CD3-zeta sequence described herein.

In one embodiment, a primary signaling domain comprises a modified ITAM domain, e.g., a mutated ITAM domain which has altered (e.g., increased or decreased) activity as compared to the native ITAM domain. In one embodiment, a primary signaling domain comprises a modified ITAM-containing primary

intracellular signaling domain, e.g., an optimized and/or truncated ITAM-containing primary intracellular signaling domain. In an embodiment, a primary signaling domain comprises one, two, three, four or more ITAM motifs.

The intracellular signaling domain of the CAR can comprise the CD3-zeta signaling domain by itself or it
 5 can be combined with any other desired intracellular signaling domain(s) useful in the context of a CAR of the invention. For example, the intracellular signaling domain of the CAR can comprise a CD3 zeta chain portion and a costimulatory signaling domain. The costimulatory signaling domain refers to a portion of the CAR comprising the intracellular domain of a costimulatory molecule. A costimulatory molecule is a
 10 cell surface molecule other than an antigen receptor or its ligands that is required for an efficient response of lymphocytes to an antigen. Examples of such molecules include CD27, CD28, 4-1BB (CD137), OX40, CD30, CD40, PD-1, ICOS, lymphocyte function-associated antigen-1 (LFA-1), CD2, CD7, LIGHT, NKG2C, B7-H3, and a ligand that specifically binds with CD83, and the like. For example, CD27
 costimulation has been demonstrated to enhance expansion, effector function, and survival of human
 CART cells in vitro and augments human T cell persistence and antitumor activity in vivo (Song et al.
 15 Blood. 2012; 119(3):696-706). Further examples of such costimulatory molecules include an MHC class I molecule, a TNF receptor protein, an Immunoglobulin-like protein, a cytokine receptor, an integrin, a signaling lymphocytic activation molecule (SLAM protein), an activating NK cell receptor, BTLA, a Toll
 ligand receptor, OX40, CD2, CD7, CD27, CD28, CD30, CD40, CDS, ICAM-1, LFA-1 (CD11a/CD18), 4-
 1BB (CD137), B7-H3, CDS, ICAM-1, ICOS (CD278), GITR, BAFFR, LIGHT, HVEM (LIGHTR), KIRDS2,
 20 SLAMF7, NKp80 (KLRP1), NKp44, NKp30, NKp46, CD19, CD4, CD8alpha, CD8beta, IL2R beta, IL2R
 gamma, IL7R alpha, ITGA4, VLA1, CD49a, ITGA4, IA4, CD49D, ITGA6, VLA-6, CD49f, ITGAD, CD11d,
 ITGAE, CD103, ITGAL, CD11a, LFA-1, ITGAM, CD11b, ITGAX, CD11c, ITGB1, CD29, ITGB2, CD18,
 LFA-1, ITGB7, NKG2D, NKG2C, TNFR2, TRANCE/RANKL, DNAM1 (CD226), SLAMF4 (CD244, 2B4),
 CD84, CD96 (Tactile), CEACAM1, CRTAM, Ly9 (CD229), CD160 (BY55), PSGL1, CD100 (SEMA4D),
 25 CD69, SLAMF6 (NTB-A, Ly108), SLAM (SLAMF1, CD150, IPO-3), BLAME (SLAMF8), SELPLG (CD162),
 LTBR, LAT, GADS, SLP-76, PAG/Cbp, CD19a, and a ligand that specifically binds with CD83.

The intracellular signaling sequences within the cytoplasmic portion of the CAR of the invention may be
 linked to each other in a random or specified order. Optionally, a short oligo- or polypeptide linker, for
 example, between 2 and 10 amino acids (e.g., 2, 3, 4, 5, 6, 7, 8, 9, or 10 amino acids) in length may form
 30 the linkage between intracellular signaling sequence. In one embodiment, a glycine-serine doublet can
 be used as a suitable linker. In one embodiment, a single amino acid, e.g., an alanine, a glycine, can be
 used as a suitable linker.

In one aspect, the intracellular signaling domain is designed to comprise two or more, e.g., 2, 3, 4, 5, or
 more, costimulatory signaling domains. In an embodiment, the two or more, e.g., 2, 3, 4, 5, or more,
 35 costimulatory signaling domains, are separated by a linker molecule, e.g., a linker molecule described
 herein. In one embodiment, the intracellular signaling domain comprises two costimulatory signaling

domains. In some embodiments, the linker molecule is a glycine residue. In some embodiments, the linker is an alanine residue.

In one aspect, the intracellular signaling domain is designed to comprise the signaling domain of CD3-zeta and the signaling domain of CD28. In one aspect, the intracellular signaling domain is designed to comprise the signaling domain of CD3-zeta and the signaling domain of 4-1BB. In one aspect, the signaling domain of 4-1BB is a signaling domain of SEQ ID NO: 14. In one aspect, the signaling domain of CD3-zeta is a signaling domain of SEQ ID NO: 18.

In one aspect, the intracellular signaling domain is designed to comprise the signaling domain of CD3-zeta and the signaling domain of CD27. In one aspect, the signaling domain of CD27 comprises an amino acid sequence of SEQ ID NO:16. In one aspect, the signalling domain of CD27 is encoded by a nucleic acid sequence of SEQ ID NO:17.

In one aspect, the intracellular is designed to comprise the signaling domain of CD3-zeta and the signaling domain of CD28. In one aspect, the signaling domain of CD28 comprises an amino acid sequence of SEQ ID NO: 124. In one aspect, the signaling domain of CD28 is encoded by a nucleic acid sequence of SEQ ID NO: 1113.

In one aspect, the intracellular is designed to comprise the signaling domain of CD3-zeta and the signaling domain of ICOS. In one aspect, the signaling domain of ICOS comprises an amino acid sequence of SEQ ID NO: 120. In one aspect, the signaling domain of ICOS is encoded by a nucleic acid sequence of SEQ ID NO: 1111.

In one aspect, the cell of the invention, e.g., described herein, e.g., a cell expressing two different CARs, includes CARs that each include an antigen binding domain that binds a target antigen described herein, a transmembrane domain, a primary signaling domain, and a costimulatory signaling domain. In embodiments of the aforementioned aspect, the costimulatory domain of the two different CARs may be the same or different. In embodiments, one or more of the two different CARs comprise more than one costimulatory signalling domains. In other aspects, the cell of the invention, e.g., described herein, e.g., a cell expressing two different CARs, includes a first CAR that includes an antigen binding domain that binds a target antigen described herein, a transmembrane domain, a primary signaling domain, but does not include a costimulatory signaling domain, and a second CAR that includes an antigen binding domain that binds a target antigen described herein, a transmembrane domain, and a costimulatory signaling domain, but does not include a primary signaling domain.

In one aspect, the CAR-expressing cell described herein, e.g. a cell expressing two different CARs can further comprise another, e.g., a third, CAR, e.g., another CAR that includes a different antigen binding domain, e.g., to the same target or a different target (e.g., a target other than a tumor antigen described herein or a different tumor antigen described herein). For example, in an embodiment where the cell of

the invention expresses a third CAR comprising an antigen binding domain that binds a second target tumor antigen, the third CAR includes an antigen binding domain to a target expressed the same cancer cell type as the tumor antigen targeted by the first or second CAR. In one embodiment, the CAR-expressing cell comprises a first CAR that targets a first tumor antigen and includes an intracellular signaling domain having a costimulatory signaling domain but not a primary signaling domain, and a third CAR that targets a second, different, tumor antigen and includes an intracellular signaling domain having a primary signaling domain but not a costimulatory signaling domain. While not wishing to be bound by theory, placement of a costimulatory signaling domain, e.g., 4-1BB, CD28, CD27 or OX-40, onto the first CAR, and the primary signaling domain, e.g., CD3 zeta, on the third CAR can limit the CAR activity to cells where both targets are expressed. In one embodiment, the cell of the invention comprises a first CAR that includes an antigen binding domain that binds a target antigen described herein, a transmembrane domain and a costimulatory domain and a second CAR that targets a different target antigen (e.g., an antigen expressed on that same cancer cell type as the first target antigen) and includes an antigen binding domain, a transmembrane domain and a primary signaling domain. In another embodiment, the cell of the invention comprises (i.e., is genetically engineered to express) a first CAR that includes an antigen binding domain that binds a target antigen described herein, a transmembrane domain and a primary signaling domain and a second CAR that targets a tumor antigen other than the first target antigen (e.g., an antigen expressed on the same cancer cell type as the first target antigen) and includes an antigen binding domain to the antigen, a transmembrane domain and a costimulatory signaling domain. In another embodiment, the cell of the invention comprises (i.e., is genetically engineered to express) a first CAR that includes an antigen binding domain that binds a target antigen described herein, a transmembrane domain, a costimulatory signaling domain and a primary signaling domain, and a second CAR that targets a tumor antigen other than the first target antigen (e.g., an antigen expressed on the same cancer cell type as the first target antigen) and includes an antigen binding domain to the antigen, a transmembrane domain, a costimulatory signaling domain and a primary signaling domain. In embodiments where both the first and second CAR include a costimulatory signaling domain, the costimulatory signaling domain of the first CAR and the second CAR may be derived from the same protein, e.g., from a costimulatory protein described herein, e.g., 4-1BB, CD28, or ICOS. In other embodiments, the costimulatory signaling domain of the first CAR and the second CAR may be derived from the different proteins, e.g., the first CAR includes a costimulatory signaling domain described herein, e.g., of 4-1BB, and the second CAR includes a different costimulatory signaling domain described herein, e.g., of CD28.

In one embodiment, the CAR-expressing cell comprises a CAR comprising antigen binding domain that bind target antigens described herein and an inhibitory CAR. In one embodiment, the inhibitory CAR comprises an antigen binding domain that binds an antigen found on normal cells but not cancer cells, e.g., normal cells that also express the tumor antigens targeted by the CAR comprising an antigen binding domain that binds a target antigen. In one embodiment, the inhibitory CAR comprises the antigen

binding domain, a transmembrane domain and an intracellular domain of an inhibitory molecule. For example, the intracellular domain of the inhibitory CAR can be an intracellular domain of PD1, PD-L1, CTLA4, TIM3, LAG3, VISTA, BTLA, TIGIT, LAIR1, CD160, 2B4, CD80, CD86, B7-H3 (CD276), B7-H4 (VTCN1), HVEM (TNFRSF14 or CD270), KIR, A2aR, MHC class I, MHC class II, GAL9, adenosine, or
 5 TGFR beta.

In one embodiment, the antigen binding domains of the different CARs can be such that the antigen binding domains do not interact with one another. For example, a cell expressing a first and second CAR can have an antigen binding domain of the first CAR, e.g., as a fragment, e.g., an scFv, that does not form an association with the antigen binding domain of the second CAR, e.g., the antigen binding domain
 10 of the second CAR is a VHH.

In some embodiments, the antigen binding domain comprises a single domain antigen binding (SDAB) molecules include molecules whose complementary determining regions are part of a single domain polypeptide. Examples include, but are not limited to, heavy chain variable domains, binding molecules naturally devoid of light chains, single domains derived from conventional 4-chain antibodies, engineered
 15 domains and single domain scaffolds other than those derived from antibodies. SDAB molecules may be any of the art, or any future single domain molecules. SDAB molecules may be derived from any species including, but not limited to mouse, human, camel, llama, lamprey, fish, shark, goat, rabbit, and bovine. This term also includes naturally occurring single domain antibody molecules from species other than Camelidae and sharks.

In one aspect, an SDAB molecule can be derived from a variable region of the immunoglobulin found in fish, such as, for example, that which is derived from the immunoglobulin isotype known as Novel Antigen Receptor (NAR) found in the serum of shark. Methods of producing single domain molecules derived from a variable region of NAR ("IgNARs") are described in WO 03/014161 and Streltsov (2005) Protein Sci.
 20 14:2901-2909.

According to another aspect, an SDAB molecule is a naturally occurring single domain antigen binding molecule known as heavy chain devoid of light chains. Such single domain molecules are disclosed in WO 9404678 and Hamers-Casterman, C. et al. (1993) Nature 363:446-448, for example. For clarity reasons, this variable domain derived from a heavy chain molecule naturally devoid of light chain is known herein as a VHH or nanobody to distinguish it from the conventional VH of four chain
 25 immunoglobulins. Such a VHH molecule can be derived from Camelidae species, for example in camel, llama, dromedary, alpaca and guanaco. Other species besides Camelidae may produce heavy chain molecules naturally devoid of light chain; such VHHs are within the scope of the invention.

The SDAB molecules can be recombinant, CDR-grafted, humanized, camelized, de-immunized and/or in vitro generated (e.g., selected by phage display).

It has also been discovered, that cells having a plurality of chimeric membrane embedded receptors comprising an antigen binding domain that interactions between the antigen binding domain of the receptors can be undesirable, e.g., because it inhibits the ability of one or more of the antigen binding domains to bind its cognate antigen. Accordingly, disclosed herein are cells having a first and a second non-naturally occurring chimeric membrane embedded receptor comprising antigen binding domains that minimize such interactions. Also disclosed herein are nucleic acids encoding a first and a second non-naturally occurring chimeric membrane embedded receptor comprising a antigen binding domains that minimize such interactions, as well as methods of making and using such cells and nucleic acids. In an embodiment the antigen binding domain of one of said first said second non-naturally occurring chimeric membrane embedded receptor, comprises an scFv, and the other comprises a single VH domain, e.g., a camelid, shark, or lamprey single VH domain, or a single VH domain derived from a human or mouse sequence.

In another aspect, the CAR-expressing cell described herein can further express another agent, e.g., an agent which enhances the activity of a CAR-expressing cell. For example, in one embodiment, the agent can be an agent which inhibits an inhibitory molecule. Inhibitory molecules, e.g., PD1, can, in some embodiments, decrease the ability of a CAR-expressing cell to mount an immune effector response. Examples of inhibitory molecules include PD1, PD-L1, CTLA4, TIM3, CEACAM (e.g., CEACAM-1, CEACAM-3 and/or CEACAM-5), LAG3, VISTA, BTLA, TIGIT, LAIR1, CD160, 2B4, CD80, CD86, B7-H3 (CD276), B7-H4 (VTCN1), HVEM (TNFRSF14 or CD270), KIR, A2aR, MHC class I, MHC class II, GAL9, adenosine, and TGFR beta.

In one embodiment, the agent which inhibits an inhibitory molecule, e.g., is a molecule described herein, e.g., an agent that comprises a first polypeptide, e.g., an inhibitory molecule, associated with a second polypeptide that provides a positive signal to the cell, e.g., an intracellular signaling domain described herein. In one embodiment, the agent comprises a first polypeptide, e.g., of an inhibitory molecule such as PD1, PD-L1, CTLA4, TIM3, CEACAM (e.g., CEACAM-1, CEACAM-3 and/or CEACAM-5), LAG3, VISTA, BTLA, TIGIT, LAIR1, CD160, 2B4, CD80, CD86, B7-H3 (CD276), B7-H4 (VTCN1), HVEM (TNFRSF14 or CD270), KIR, A2aR, MHC class I, MHC class II, GAL9, adenosine, and TGFR beta, or a fragment of any of these (e.g., at least a portion of an extracellular domain of any of these), and a second polypeptide which is an intracellular signaling domain described herein (e.g., comprising a costimulatory domain (e.g., 41BB, CD27 or CD28, e.g., as described herein) and/or a primary signaling domain (e.g., a CD3 zeta signaling domain described herein). In one embodiment, the agent comprises a first polypeptide of PD1 or a fragment thereof (e.g., at least a portion of an extracellular domain of PD1), and a second polypeptide of an intracellular signaling domain described herein (e.g., a CD28 signaling domain described herein and/or a CD3 zeta signaling domain described herein). PD1 is an inhibitory member of the CD28 family of receptors that also includes CD28, CTLA-4, ICOS, and BTLA. PD-1 is expressed on activated B cells, T cells and myeloid cells (Agata et al. 1996 Int. Immunol 8:765-75). Two ligands for

PD1, PD-L1 and PD-L2 have been shown to downregulate T cell activation upon binding to PD1 (Freeman et al. 2000 J Exp Med 192:1027-34; Latchman et al. 2001 Nat Immunol 2:261-8; Carter et al. 2002 Eur J Immunol 32:634-43). PD-L1 is abundant in human cancers (Dong et al. 2003 J Mol Med 81:281-7; Blank et al. 2005 Cancer Immunol. Immunother 54:307-314; Konishi et al. 2004 Clin Cancer Res 10:5094). Immune suppression can be reversed by inhibiting the local interaction of PD1 with PD-L1.

In one embodiment, the agent comprises the extracellular domain (ECD) of an inhibitory molecule, e.g., Programmed Death 1 (PD1), fused to a transmembrane domain and intracellular signaling domains such as 41BB and CD3 zeta (also referred to herein as a PD1 CAR). In one embodiment, the PD1 CAR, when used in combinations with a XCAR described herein, improves the persistence of the T cell. In one embodiment, the CAR is a PD1 CAR comprising the extracellular domain of PD1 indicated as underlined in SEQ ID NO: 26. In one embodiment, the PD1 CAR comprises the amino acid sequence of SEQ ID NO:26. In one embodiment, the PD1 CAR comprises the amino acid sequence of SEQ ID NO:39).

In one embodiment, the agent comprises a nucleic acid sequence encoding the PD1 CAR, e.g., the PD1 CAR described herein. In one embodiment, the nucleic acid sequence for the PD1 CAR is shown as SEQ ID NO: 27 in Table 1, with the sequence for PD1 ECD underlined.

In another aspect, the present disclosure provides a population of CAR-expressing cells. In some embodiments, the population of CAR-expressing cells comprises a mixture of cells expressing different CARs. For example, in one embodiment, the population of CART cells can include a first cell expressing a CAR having an antigen binding domain to a antigen described herein, and a second cell expressing a CAR having a different antigen binding domain, e.g., an antigen binding domain to a different antigen described herein, e.g., an antigen binding domain to a tumor antigen described herein that differs from the tumor antigen bound by the antigen binding domain of the CAR expressed by the first cell. As another example, the population of CAR-expressing cells can include a first cell expressing a CAR that includes an antigen binding domain to a tumor antigen described herein, and a second cell expressing a CAR that includes an antigen binding domain to a target other than a tumor antigen as described herein. In one embodiment, the population of CAR-expressing cells includes, e.g., a first cell expressing a CAR that includes a primary intracellular signaling domain, and a second cell expressing a CAR that includes a secondary signaling domain.

In another aspect, the present disclosure provides a population of cells wherein at least one cell in the population expresses a CAR having an antigen binding domain to a tumor antigen described herein, and a second cell expressing another agent, e.g., an agent which enhances the activity of a CAR-expressing cell. For example, in one embodiment, the agent can be an agent which inhibits an inhibitory molecule. Inhibitory molecules, e.g., PD-1, can, in some embodiments, decrease the ability of a CAR-expressing cell to mount an immune effector response. Examples of inhibitory molecules include PD-1, PD-L1,

CTLA4, TIM3, CEACAM (e.g., CEACAM-1, CEACAM-3 and/or CEACAM-5), LAG3, VISTA, BTLA, TIGIT, LAIR1, CD160, 2B4, CD80, CD86, B7-H3 (CD276), B7-H4 (VTCN1), HVEM (TNFRSF14 or CD270), KIR, A2aR, MHC class I, MHC class II, GAL9, adenosine, and TGFR beta. In one embodiment, the agent which inhibits an inhibitory molecule, e.g., is a molecule described herein, e.g., an agent that comprises a first polypeptide, e.g., an inhibitory molecule, associated with a second polypeptide that provides a positive signal to the cell, e.g., an intracellular signaling domain described herein. In one embodiment, the agent comprises a first polypeptide, e.g., of an inhibitory molecule such as PD-1, PD-L1, CTLA4, TIM3, CEACAM (e.g., CEACAM-1, CEACAM-3 and/or CEACAM-5), LAG3, VISTA, BTLA, TIGIT, LAIR1, CD160, 2B4, CD80, CD86, B7-H3 (CD276), B7-H4 (VTCN1), HVEM (TNFRSF14 or CD270), KIR, A2aR, MHC class I, MHC class II, GAL9, adenosine, and TGFR beta, or a fragment of any of these, and a second polypeptide which is an intracellular signaling domain described herein (e.g., comprising a costimulatory domain (e.g., 41BB, CD27, OX40 or CD28, e.g., as described herein) and/or a primary signaling domain (e.g., a CD3 zeta signaling domain described herein). In one embodiment, the agent comprises a first polypeptide of PD-1 or a fragment thereof, and a second polypeptide of an intracellular signaling domain described herein (e.g., a CD28 signaling domain described herein and/or a CD3 zeta signaling domain described herein).

In one aspect, the present disclosure provides methods comprising administering a population of CAR-expressing cells, e.g., a mixture of cells expressing different CARs, in combination with another agent, e.g., a kinase inhibitor, such as a kinase inhibitor described herein. In another aspect, the present disclosure provides methods comprising administering a population of cells wherein at least one cell in the population expresses a CAR having an antigen binding domain of a tumor antigen described herein, and a second cell expressing another agent, e.g., an agent which enhances the activity of a CAR-expressing cell, in combination with another agent, e.g., a kinase inhibitor, such as a kinase inhibitor described herein.

Exemplary CAR Molecules

The CAR molecules disclosed herein can comprise a binding domain that binds to a target, e.g., a target as described herein; a transmembrane domain, e.g., a transmembrane domain as described herein; and an intracellular signaling domain, e.g., an intracellular domain as described herein. In embodiments, the binding domain comprises a heavy chain complementary determining region 1 (HC CDR1), a heavy chain complementary determining region 2 (HC CDR2), and a heavy chain complementary determining region 3 (HC CDR3) of a heavy chain binding domain described herein, and/or a light chain complementary determining region 1 (LC CDR1), a light chain complementary determining region 2 (LC CDR2), and a light chain complementary determining region 3 (LC CDR3) of a light chain binding domain described herein.

In other embodiments, the CAR molecule comprises a CD19 CAR molecule described herein, e.g., a CD19 CAR molecule described in US-2015-0283178-A1, e.g., CTL019. In embodiments, the CD19 CAR comprises an amino acid, or has a nucleotide sequence shown in US-2015-0283178-A1, incorporated herein by reference, or a sequence substantially identical thereto (e.g., at least 85%, 90%, 95% or more identical thereto).

In one embodiment, the CAR T cell that specifically binds to CD19 has the USAN designation TISAGENLECLEUCET. CTL019 is made by a gene modification of T cells is mediated by stable insertion via transduction with a self-inactivating, replication deficient Lentiviral (LV) vector containing the CTL019 transgene under the control of the EF-1 alpha promoter. CTL019 can be a mixture of transgene positive and negative T cells that are delivered to the subject on the basis of percent transgene positive T cells.

In one embodiment, the CAR19 molecule comprises (e.g., consists of) an amino acid sequence as provided in Table 15A, or in Table 3 of International Publication No. WO2014/153270, filed March 15, 2014; incorporated herein by reference. The amino acid and nucleotide sequences encoding the CD19 CAR molecules and antigen binding domains (e.g., including one, two, three VH CDRs; and one, two, three VL CDRs according to Kabat or Chothia), are specified in WO2014/153270. In embodiments, the CD19 CAR comprises an amino acid, or has a nucleotide sequence shown in WO2014/153270 incorporated herein by reference, or a sequence substantially identical to any of the aforesaid sequences (e.g., at least 85%, 90%, 95% or more identical to any of the aforesaid CD19 CAR sequences). In one embodiment, the CAR molecule comprises (e.g., consists of) an amino acid sequence selected from any one of SEQ ID NOs: 897, 902, 907, 912, 917, 922, 927, 932, 937, 942, 947, 952, 956; or an amino acid sequence having at least one, two, three, four, five, 10, 15, 20 or 30 modifications (e.g., substitutions, e.g., conservative substitutions) but not more than 60, 50, or 40 modifications (e.g., substitutions, e.g., conservative substitutions) of an amino acid sequence selected from any one of SEQ ID NOs: 897, 902, 907, 912, 917, 922, 927, 932, 937, 942, 947, 952, 956; or an amino acid sequence having 85%, 90%, 95%, 96%, 97%, 98%, 99% identity to an amino acid sequence selected from any one of SEQ ID NOs: 897, 902, 907, 912, 917, 922, 927, 932, 937, 942, 947, 952, 956.

In one embodiment, the parental murine scFv sequence is the CAR19 construct provided in PCT publication WO2012/079000 (incorporated herein by reference) and provided herein in Table 15A. In one embodiment, the anti-CD19 binding domain is a scFv described in WO2012/079000 and provided herein in Table 15A.

In one embodiment, the CD19 CAR comprises an amino acid sequence provided as SEQ ID NO: 12 in PCT publication WO2012/079000. In embodiment, the amino acid sequence is:

MALPVTALLLPLALLLHAARPdiqmtqtsslsaslgdrvtiscrasqdiskylnwyqqkpdgtvklliyhtsrhsgvpsrfsqsgsgtdyslti
snleqediatyfcqqngntlpytfggggtkleitggggsgggsggggsevkqlqesgpglvapsqslsvtctvsgvslpdygvswirqprrkglewlgvi

wgsettyynsalksrliikdnksqvfikmnsqtdddaiyycahyyyggsyamydwggtsvtvssttpaprpptpaptiasqplslrpeacrpa
aggavhtrgldfacdiyiwaplagtcgvllslvitlyckrgrkklyifkqpfmrpvqttqeedgcscrpfpeeeeggcelrvkfsrsadapaykqggnqly
nelnlgrreedydvldkrgrdpemggkprknpqeglynelqkdmaeayseigmkgerrrgkghdglyqglstatkdydalhmqalppr
(SEQ ID NO: 891), or a sequence substantially identical thereto (e.g., at least 85%, 90% or 95% or higher
5 identical thereto), with or without the signal peptide sequence indicated in capital letters.

In embodiment, the amino acid sequence is:

dqmtqtsslsaslgdrvtiscrasqdiskylwyyqqkpdgtvkliihtsrhsgvpsrfsqsgsgtdysltisnleqediayfcqqgntlpytfgggtkle
itggggsgggsggggsevkqesgpglvapsqslsvtctvsgvslpdygvswirqpprkglewlgviwgsettyynsalksrliikdnksqvfikm
nslqtdddaiyycahyyyggsyamydwggtsvtvssttpaprpptpaptiasqplslrpeacrpaaggavhtrgldfacdiyiwaplagtcgvlls
10 lvitlyckrgrkklyifkqpfmrpvqttqeedgcscrpfpeeeeggcelrvkfsrsadapaykqggnqlynelnlgrreedydvldkrgrdpemggkprk
npqeglynelqkdmaeayseigmkgerrrgkghdglyqglstatkdydalhmqalppr (SEQ ID NO: 892), or a sequence
substantially homologous thereto (e.g., at least 85%, 90% or 95% or higher identical thereto).

In embodiments, the CAR molecule is a CD19 CAR molecule described herein, e.g., a
humanized CAR molecule described herein, e.g., a humanized CD19 CAR molecule of Table 15A or
15 having CDRs as set out in Tables 15B and 15C.

In embodiments, the CAR molecule is a CD19 CAR molecule described herein, e.g., a murine CAR
molecule described herein, e.g., a murine CD19 CAR molecule of Table 15A or having CDRs as set out
in Tables 15B and 15C.

In some embodiments, the CAR molecule comprises one, two, and/or three CDRs from the heavy
20 chain variable region and/or one, two, and/or three CDRs from the light chain variable region of the
murine or humanized CD19 CAR of Tables 15B and 15C.

In one embodiment, the antigen binding domain comprises one, two three (e.g., all three) heavy
chain CDRs, HC CDR1, HC CDR2 and HC CDR3, from an antibody listed herein, and/or one, two, three
(e.g., all three) light chain CDRs, LC CDR1, LC CDR2 and LC CDR3, from an antibody listed herein. In
25 one embodiment, the antigen binding domain comprises a heavy chain variable region and/or a variable
light chain region of an antibody listed or described herein.

Exemplary CD19 CARs include any of the CD19 CARs or anti-CD19 binding domains described herein,
e.g., in one or more tables (e.g., Table 15A) described herein (e.g., , or an anti-CD19 CAR described in
Xu et al. Blood 123.24(2014):3750-9; Kochenderfer et al. Blood 122.25(2013):4129-39, Cruz et al. Blood
30 122.17(2013):2965-73, NCT00586391, NCT01087294, NCT02456350, NCT00840853, NCT02659943,
NCT02650999, NCT02640209, NCT01747486, NCT02546739, NCT02656147, NCT02772198,
NCT00709033, NCT02081937, NCT00924326, NCT02735083, NCT02794246, NCT02746952,
NCT01593696, NCT02134262, NCT01853631, NCT02443831, NCT02277522, NCT02348216,

NCT02614066, NCT02030834, NCT02624258, NCT02625480, NCT02030847, NCT02644655, NCT02349698, NCT02813837, NCT02050347, NCT01683279, NCT02529813, NCT02537977, NCT02799550, NCT02672501, NCT02819583, NCT02028455, NCT01840566, NCT01318317, NCT01864889, NCT02706405, NCT01475058, NCT01430390, NCT02146924, NCT02051257, NCT02431988, NCT01815749, NCT02153580, NCT01865617, NCT02208362, NCT02685670, NCT02535364, NCT02631044, NCT02728882, NCT02735291, NCT01860937, NCT02822326, NCT02737085, NCT02465983, NCT02132624, NCT02782351, NCT01493453, NCT02652910, NCT02247609, NCT01029366, NCT01626495, NCT02721407, NCT01044069, NCT00422383, NCT01680991, NCT02794961, or NCT02456207, each of which is incorporated herein by reference in its entirety.

Exemplary CD19 CAR and antigen binding domain constructs that can be used in the methods described herein are shown in Table 15A. The light and heavy chain CDR sequences according to Kabat are shown by the bold and underlined text, and are also summarized in Tables 15A-C. The location of the signal sequence and histidine tag are also underlined. In embodiments, the CD19 CAR sequences and antigen binding fragments thereof do not include the signal sequence and/or histidine tag sequences.

In embodiments, the CD19 CAR comprises an anti- CD19 binding domain (e.g., murine or humanized anti- CD19 binding domain), a transmembrane domain, and an intracellular signaling domain, and wherein said anti- CD19 binding domain comprises a heavy chain complementary determining region 1 (HC CDR1), a heavy chain complementary determining region 2 (HC CDR2), and a heavy chain complementary determining region 3 (HC CDR3) of any anti- CD19 heavy chain binding domain amino acid sequences listed in Table 15A-C, or a sequence at least 85%, 90%, 95% or more identical thereto (e.g., having less than 5, 4, 3, 2 or 1 amino acid substitutions, e.g., conservative substitutions).

In one embodiment, the anti- CD19 binding domain comprises a light chain variable region described herein (e.g., in Table 15A) and/or a heavy chain variable region described herein (e.g., in Table 15A), or a sequence at least 85%, 90%, 95% or more identical thereto.

In one embodiment, the encoded anti- CD19 binding domain is a scFv comprising a light chain and a heavy chain of an amino acid sequence of Tables 5, or a sequence at least 85%, 90%, 95% or more identical thereto.

In an embodiment, the human or humanized anti- CD19 binding domain (e.g., an scFv) comprises: a light chain variable region comprising an amino acid sequence having at least one, two or three modifications (e.g., substitutions, e.g., conservative substitutions) but not more than 30, 20 or 10 modifications (e.g., substitutions, e.g., conservative substitutions) of an amino acid sequence of a light chain variable region provided in Table 15A, or a sequence at least 85%, 90%, 95% or more identical thereto; and/or a heavy chain variable region comprising an amino acid sequence having at least one, two or three modifications (e.g., substitutions, e.g., conservative substitutions) but not more than 30, 20 or 10 modifications (e.g.,

substitutions, e.g., conservative substitutions) of an amino acid sequence of a heavy chain variable region provided in Table 15A, or a sequence at least 85%, 90%, 95% or more identical thereto.

In one embodiment, the CAR molecule comprises a CD19 antigen binding domain (e.g., a murine, human or humanized antibody or antibody fragment that specifically binds to CD19), a transmembrane domain, and an intracellular signaling domain (e.g., an intracellular signaling domain comprising a costimulatory domain and/or a primary signaling domain).

Exemplary CAR19 molecules are provided in Table 15A (and also Table 7). The CAR molecules in Table 15A comprise a CD19 antigen binding domain, e.g., an amino acid sequence of any CD19 antigen binding domain provided in Table 7 or 10.

Table 15A. Exemplary CD19 CAR molecules

Name	SEQ ID NO:	Sequence
CAR 1		
CAR1 scFv domain	893	EIVMTQSPATLSLSPGERATLSCRASQDISKYLNWYQQKPGQAPRLLIYH TSRLHSGIPARFSGSGSGTDYTLTISSLQPEDFAVYFCQQGNTLPYTFGQ GTKLEIKGGGSGGGGSGGGGSGVQLQESGPGLVKPSSETLSLTCTVSGVS LPDYGVSWIRQPPGKGLEWIGVIWGSETTYSSSLKSRVTISKDNSKNQV SLKLSSVTAADTAVYYCAKHYYYGGSYAMDYWGQGT LTVSS
103101 CAR1 Soluble scFv - nt	894	atggccctccctgtcaccgccctgctgcttccgctggctcttctgctccacgcg ctcgccccgaaattgtgatgaccagtcacccgccactcttagcctttcaccgg tgagcgcgcaaccctgtcttgagagcctcccaagacatctcaaaatacctta tggtatcaacagaagcccgacaggctcctcgcttctgactctaccacaccagcc ggctccattctggaatccctgccaggttcagcggtagcggatctgggaccgacta caccctcactatcagctcactgcagccagaggacttcgctgtctatttctgtcag caagggaacacccctgcctacacctttggacagggcaccaagctcgagattaaag gtggaggtggcagcggaggaggtgggtccggcgggtggaggaagccaggtccaact ccaagaaagcggaccgggtcttgtgaagccatcagaaactctttcactgacttgt actgtgagcggagtgtctctccccgattacgggggtgtcttgatcagacagccac cggggaagggtctggaatggattggagtgtttggggctctgagactacttacta ctcttcatccctcaagtcacgcgtcaccatctcaaaggacaactctaagaatcag gtgtcactgaaactgtcatctgtgaccgcagccgacaccgccgtgtactattgcg ctaagcattactattatggcgggagctacgcaatggattactggggacaggggtac tctggtcaccgtgtccagccaccaccatcatcaccatcaccat
103101 CAR1 Soluble scFv	895	<u>MALPVTALLPLALLHAARP</u> eivmtqspatls slspgeratlscrasqdiskyl nwqqkpgqaprllyhtsrhlhsgiparfsgsgsgtdytltlisslqpedfavyfcq qgntlpytfgqgtkleikggggsgggsgggsgvqlqesgpglvkpsetlsltc tvsgvslpdygvswirpppgkglewigviwgsettyyssslksrvtiskdnsknq vslklssvtaadtavyycahyyyggsyamydywgqgtltvtvss <u>hhhhhhhh</u>

- aa		
104875 CAR 1 – Full - nt	896	atggccctccctgtcaccgccctgctgcttccgctggctcttctgctccacgccg ctcgccccgaaattgtgatgaccagtcacccgccactcttagcctttcacccg tgagcgcgcaacctgtcttgagagcctcccaagacatctcaaaatacctta tggatcaacagaagcccgacaggctcctcgcttctgatctaccacaccagcc ggctccattctggaatccctgccaggttcagcggtagcggatctgggaccgacta cacctcactatcagctcactgcagccagaggacttcgctgtctatcttctgtcag caagggaacacctgccctacacctttggacagggcaccaagctcgagattaaag gtggaggtggcagcggaggaggtgggtccggcgggtggaggaagccaggtccaact ccaagaaagcggaccgggtcttgtgaagccatcagaaactctttcactgacttgt actgtgagcggagtgtctctccccgattacgggggtgtcttggatcagacagccac cggggaaggggtctggaatggattggagtgatttggggctctgagactacttacta ctcttcatccctcaagtcacgcgtcaccatctcaaaggacaactctaagaatcag gtgtcactgaaactgtcatctgtgaccgcagccgacaccgccgtgtactattgcg ctaagcattactattatggcgggagctacgcaatggattactggggacaggggtac tctggtcaccgtgtccagcaccactacccagcaccgaggccacccacccggct cctaccatcgctcccagcctctgtccctgcgtccggaggcatgtagaccgcag ctggtggggccgtgcatacccggggtcttgacttcgctgcgatctacatttg ggccctctggctggtacttgccgggtcctgctgctttcactcgtgatcactctt tactgtaagcgcggctcggaagaagctgctgtacatctttaagcaacccttcatga ggcctgtgcagactactcaagaggaggacggctgttcatgccggttccagagga ggaggaaggcggctgcgaactgcgcgtgaaattcagccgcagcgcagatgtcca gcctacaagcaggggcagaaccagctctacaacgaactcaatcttggtcggagag aggagtacgacgtgctggacaagcggagaggacgggaccagaaatggcgggaa gccgcgcagaaagaatccccaagaggcctgtacaacgagctccaaaaggataag atggcagaagcctatagcgagattggatgaaaggggaacgcagaagaggcaaag gccacgacggactgtaccagggactcagcaccgccaccaaggacacctatgacgc tcttcacatgcaggccctgccgctcgg
104875 CAR 1 – Full - aa	897	MALPVTALLPLALLLHAARPeivmtqspatlslspgeratlsc <u>rasqdiskyl</u> <u>nyqqkpgqaprllyhtsr</u> lhsgiparfsgsgsgtdytlitisslqpedfavyfcg <u>qgntlpyt</u> fgqgtkleikgggsgggsgggsgqvlqesgpglvkpsetlsltc tvsgvslpdygvswirpppgkglewigviwgsettyysslsksrvtiskdnsk nqvslklssvtaadtavyycahhyyyggsyamydwgqgtltvtvsssttpaprpptpa ptiasqplslrpeacrpaaggavhtrglfacdiyiwaplagtcgvlllslvitl yckrgrklllyifkqpfmrpvqttqeedgcscrfeeeeeggcclrvkfrrsadap aykqqnqlynelnlgrreeydvldkrrgrdpemggkprkrnpqeglynelqkdk maeayseigmkgerrrgkghdglyqglstatkdydalhmqalppr
CAR 2		
CAR2 scFv domain	898	eivmtqspatlslspgeratlscrasqdiskylnyqqkpgqaprllyhtsr lhsgiparfsgsgsgtdytlitisslqpedfavyfcqgntlpytfgqgtkleikggg gsgggsgggsgqvlqesgpglvkpsetlsltcvsgvslpdygvswirpppgk glewigviwgsettyyqsslsksrvtiskdnskqnqvslklssvtaadtavyycah yyyggsyamydwgqgtltvtvss
103102	899	atggccctccctgtcaccgccctgctgcttccgctggctcttctgctccacgccg ctcgccccgaaattgtgatgaccagtcacccgccactcttagcctttcacccg

CAR2 - Soluble scFv - nt		tgagcgcgcaaccctgtcttgcagagcctcccaagacatctcaaaataccttaat tggtatcaacagaagcccgacaggtcctcgccttctgatctaccacaccagcc ggctccattctggaatccctgccaggttcagcggtagcggatctgggaccgacta caccctcactatcagctcactgcagccagaggacttcgctgtctatcttctgtcag caagggaacaccctgccctacacctttggacagggcaccaagctcgagattaaag gtggaggtggcagcggaggaggtgggtccggcgggtggaggaagccaggtccaact ccaagaaagcggaccgggtcttgtgaagccatcagaaactctttcactgacttgt actgtgagcggagtgtctctccccgattacgggggtgtcttggatcagacagccac cggggaagggctctggaatggattggagtgatttggggctctgagactacttacta ccaatcatccctcaagtcacgcgtcaccatctcaaaggacaactctaagaatcag gtgtcactgaaactgtcatctgtgaccgcagccgacaccgccgtgtactattgcg ctaagcattactattatggcgggagctacgcaatggattactggggacaggggtac tctggtcaccgtgtccagccaccaccatcatcaccatcaccat
103102 CAR2 - Soluble scFv - aa	900	<u>MALPVTALLPLALLHAARP</u>eiivmtqspatlslspgeratlscrasqdiskyl nyqqkpgqaprrlliyhtsrhsgiparfsgsgsgtdytltlisslqpedfavyfcq qgntlpytfqggtkleikgggsgggsgggsgqvlqesgpglvkpsetlsltc tvsgvslpdygvswirpppgkglewigviwgsettyyqsslksrvtiskdnskq vslklssvttaadtavyycakhyyyggsyamdywgqgtlvtvss<u>hhhhhhh</u>
104876 CAR 2 - Full - nt	901	atggccctccctgtcaccgccctgctgcttccgctggctcttctgctccacgcg ctcgccccgaaatttgtgatgaccagtcacccgccactcttagcctttcaccgg tgagcgcgcaaccctgtcttgcagagcctcccaagacatctcaaaataccttaat tggtatcaacagaagcccgacaggtcctcgccttctgatctaccacaccagcc ggctccattctggaatccctgccaggttcagcggtagcggatctgggaccgacta caccctcactatcagctcactgcagccagaggacttcgctgtctatcttctgtcag caagggaacaccctgccctacacctttggacagggcaccaagctcgagattaaag gtggaggtggcagcggaggaggtgggtccggcgggtggaggaagccaggtccaact ccaagaaagcggaccgggtcttgtgaagccatcagaaactctttcactgacttgt actgtgagcggagtgtctctccccgattacgggggtgtcttggatcagacagccac cggggaagggctctggaatggattggagtgatttggggctctgagactacttacta ccaatcatccctcaagtcacgcgtcaccatctcaaaggacaactctaagaatcag gtgtcactgaaactgtcatctgtgaccgcagccgacaccgccgtgtactattgcg ctaagcattactattatggcgggagctacgcaatggattactggggacaggggtac tctggtcaccgtgtccagcaccactacccagcaccgaggccaccaccccggt cctaccatcgctcccagcctctgtccctgcgtccggaggcatgtagaccgcgag ctggtggggccgtgcataaccggggtcttgacttcgcctgcgatatctacatttg ggccctctggctggtacttgccgggtcctgctgctttcactcgtgatcactctt tactgtaagcgcggtcggaagaagctgctgtacatctttaagcaacccttcatga ggcctgtgcagactactcaagaggaggacggctgttcatgccggttcccagagga ggaggaaggcggctgcgaactgcgcgtgaaattcagccgcagcgcagatgtcca gcctacaagcaggggcagaaccagctctacaacgaactcaatcttggtcggagag aggagtacgacgtgctggacaagcggagaggacgggaccagaaatggcggggaa gccgcgcagaaagaatccccaagaggcctgtacaacgagctccaaaaggataag atggcagaagcctatagcgagatttggtatgaaaggggaacgcagaagaggcaaag gccacgacggactgtaccagggaactcagcaccgccaccaaggacacctatgacgc tcttcacatgcaggccctgccgcctcgg

104876 CAR 2 - Full - aa	902	MALPVTALLLPLALLLHAARPeivmtqspatlsispgeratlsc <u>rasqdiskyln</u> wyqqkpgqaprrlliy <u>htsrhsg</u> giparfsgsgsgtdytlitisslqpedfavyfcg <u>ggntlpyt</u> fgqgtkleikgggsgggsgggsgggsgvqlqesgpglvkpsetlsltc tvsgvslp <u>dygvs</u> wirpppgkglewig <u>viwgsettyyqsslks</u> rvtiskdnskq vslklssvtaadtavyycak <u>hyyyggsyamyd</u> wgggtlvtvsssttppaprpptpa ptiasqplslrpeacrpaaggavhtrgldfacdiyiwaplagtcgvlllslvitl yckrgrklllyifkqpfmrpvqttqeedgcscrfpееееggcelrvkfrsadap aykqqnqlynelnlgrreeydvldkrrgrdpemggkprrknpqeglynelqkdk maeayseigmkgerrrgkghdglyqglstatkdydalhmqalppr
CAR 3		
CAR3 scFv domain	903	qvqlqesgpglvkpsetlsltctvsgvslpdygvswirpppgkglewigviwgse ttyyssslksrvtiskdnskqvslklssvtaadtavyycakhyyyggsyamydw gggtlvtvssggggsgggsggggseivmtqspatlsispgeratlscrasqdis kylnwyqqkpgqaprrlliyhtsrhsgiparfsgsgsgtdytlitisslqpedfav yfcqqgntlpytfgqgtkleik
103104 CAR 3 - Soluble scFv - nt	904	atggctctgcccgtagccgcactcctcctgccactggctctgctgcttcacgccg ctcgcccacaagtcagcttcaagaatcagggcctggctctggtgaagccatctga gactctgtccctcacttgaccgtgagcggagtgtccctcccagactacggagt agctggattagacagcctcccggaaaggactggagtggatcggagtgatttggg gtagcgaaaccacttactattcatcttccctgaagtcacgggtcaccatttcaaa ggataactcaaagaatcaagtgagcctcaagctctcatcagtcaccgccgctgac accgccgtgtattactgtgccaaagcattactactatggaggggtcctacgccatgg actactggggccagggaactctggctcactgtgtcatctggtggaggaggtagcgg aggaggcgggagcgggtggaggtggctccgaaatcgtgatgaccagagccctgca accctgtccctttctcccggggaacgggctaccctttctgtcgggcatcacaag atatctcaaaatacctcaattggatcaacagaagccgggacaggcccttaggct tcttatctaccacacctctcgctgcatagcgggattcccgacgcttttagcggg tctggaagcgggaccgactacactctgaccatctcatctctccagcccgaggact tcgccgtctacttctgccagcagggtaacaccctgccgtacaccttcggccaggg caccaagcttgagatcaaacatcaccaccatcatcaccatcac
103104 CAR 3 - Soluble scFv - aa	905	<u>MALPVTALLLPLALLLHAARP</u> qvqlqesgpglvkpsetlsltctvsgvslpdygv swirpppgkglewigviwgsettyyssslksrvtiskdnskqvslklssvtaad tavyycakhyyyggsyamydwgggtlvtvssggggsgggsggggseivmtqspa tislspgeratlscrasqdiskylnwyqqkpgqaprrlliyhtsrhsgiparfsg sgsgtdytlitisslqpedfavyfcqqgntlpytfgqgtkleik <u>hhhhhhh</u>
104877 CAR 3 – Full - nt	906	atggctctgcccgtagccgcactcctcctgccactggctctgctgcttcacgccg ctcgcccacaagtcagcttcaagaatcagggcctggctctggtgaagccatctga gactctgtccctcacttgaccgtgagcggagtgtccctcccagactacggagt agctggattagacagcctcccggaaaggactggagtggatcggagtgatttggg gtagcgaaaccacttactattcatcttccctgaagtcacgggtcaccatttcaaa ggataactcaaagaatcaagtgagcctcaagctctcatcagtcaccgccgctgac accgccgtgtattactgtgccaaagcattactactatggaggggtcctacgccatgg actactggggccagggaactctggctcactgtgtcatctggtggaggaggtagcgg aggaggcgggagcgggtggaggtggctccgaaatcgtgatgaccagagccctgca

		accctgtccctttctcccggggaacgggctaccctttcttgtcgggcatcacaag atatctcaaaatacctcaattggtatcaacagaagccgggacaggccctaggct tcttatctaccacacctctcgctgcatagcgggattcccgcacgcttttagcggg tctggaagcgggaccgactacactctgaccatctcatctctccagcccaggact tcgccgtctacttctgccagcagggtaacaccctgccgtacaccttcggccaggg caccaagcttgagatcaaaaccactactcccgtccaaggccacccacccctgcc ccgaccatcgctctcagccgctttccctgccgtccggaggcatgtagaccgcag ctggtggggccgtgcataaccggggtcttgacttcgctgcatatctacatttg ggccctctggtggtacttgcggggtcctgctgctttcactcgtgatcactctt tactgtaagcgcggtcggaagaagctgctgtacatctttaagcaacccttcatga ggcctgtgcagactactcaagaggaggacggctgttcatgccggttcccagagga ggaggaaggcggctgcgaactgcgctgaaattcagccgcagcgcagatgctcca gcctacaagcaggggcagaaccagctctacaacgaactcaatcttggtcggagag aggagtacgacgtgctggacaagcggagaggacgggacccagaaatggcgggaa gccgcgcagaaagaatccccaaagaggcctgtacaacgagctccaaaaggataag atggcagaagcctatagcgagattggtatgaaaggggaacgcagaagaggcaaag gccacgacggactgtaccagggactcagcaccgccaccaaggacacctatgacgc tcttcacatgcaggccctgccgctcgg
104877 CAR 3 – Full - aa	907	MALPVTALLLPLALLLHAARPqvqlqesgpglvkpsetlsltctvsgvslpdygv <u>swir</u> qppgkglewigviwgsettyysslksrvtiskdnskqvslklssvtaad tavyyca <hy< h="">yyggsyamywgqgtlvtvssgggsgggsggggseivmtqspa tislspgeratlscrasqdiskylnwyyqqkpgqaprllyhtsrlhsgiparfsg sgsgtdytltlisslqpedfavyfcqggntlpytfgggtkleiktttpprptpa ptiasqplslrpeacrpaaggavhtrgldfacdiyiwaplagtcgvllslvitl yckrgrklllyifkqpfmrpvqttqeedgcscrpfpeeeeggcelrvkfrrsadap aykqqnqlynelnlgrreeydvldkrrgrdpemggkprkrnpqeglynelqkdk maeyseigmkgerrrgkghdglyqglstatkdydalhmqalppr</hy<>
CAR 4		
CAR4 scFv domain	908	qvqlqesgpglvkpsetlsltctvsgvslpdygvswirqppgkglewigviwgse ttyyqsslksrvtiskdnskqvslklssvtaadtavyycahyyyggsyamyw gqgtlvtvssgggsgggsggggseivmtqspatlslspgeratlscrasqdis kylnwyyqqkpgqaprllyhtsrlhsgiparfsgsgsgtdytltlisslqpedfav yfcqggntlpytfgggtkleik
103106 CAR4 – Soluble scFv - nt	909	atggctctgcccgtgaccgcactcctcctgccactggctctgctgcttcacgcg ctcgcccacaagtccagcttcaagaatcagggcctggtctggtgaagccatctga gactctgtccctcacttgaccgtgagcggagtgtccctcccagactacggagtg agctggattagacagcctcccggaaaggactggagtggatcgagtgatttggg gtagcgaaaccacttactatcaatcttcctgaagtacgggtcaccatttcaa ggataactcaaagaatcaagtgagcctcaagctctcatcagtcaccgcgctgac accgccgtgtattactgtgccaagcattactactatggagggctctacgccatgg actactggggccagggaactctggtcactgtgtcatctggtggaggaggtagcgg aggaggcgggagcgggtggaggtggctccgaaatcgtgatgaccagagccctgca accctgtccctttctcccggggaacgggctaccctttcttgtcgggcatcacaag atatctcaaaatacctcaattggtatcaacagaagccgggacaggccctaggct tcttatctaccacacctctcgctgcatagcgggattcccgcacgcttttagcggg tctggaagcgggaccgactacactctgaccatctcatctctccagcccaggact

		tcgccgtctactttctgccagcagggtaacaccctgccgtacaccttcggccaggg caccaagcttgagatcaaacatcaccaccatcatcaccatcac
103106 CAR4 – Soluble scFv -aa	910	<u>MALPVTALLPLALLHAARP</u> qvqlqesgpglvkpsetlsltctvsgvslpdygv swirqppgkglewigviwgsettyyqsslksrvtiskdnskqvslklssvtaad tavyycahyyyggsyamydwgggtlvtvssgggsgggsggggseivmtqspa tllslspgeratlscrasqdiskylnwyqqkpgqaprlliyhtsrhsgiparfsg sgsgtdytlitisslqpedfavyfcqqgntlpytfgggtkleik <u>hhhhhhh</u>
104878 CAR 4 – Full - nt	911	atggctctgcccgtagccgcactcctcctgccactggctctgctgcttcacgcg ctcgcccacaagtcagcttcaagaatcagggcctggctctgggaagccatctga gactctgtccctcacttgaccgtgagcggagtgtccctcccagactacggagt agctggattagacagcctcccggaaaggactggagtggatcggagtgatttggg gtagcgaaccacttactatcaatcttccctgaagtcacgggtcaccatttcaaa ggataactcaaagaatcaagtgagcctcaagctctcatcagtcaccgccgctgac accgccgtgtattactgtgccaagcattactactatggagggctctacgccatgg actactggggccagggaaactctggctcactgtgtcatctgggtggaggaggtagcgg aggaggcgggagcgggtggaggtggctccgaaatcgtgatgaccagagccctgca accctgtccctttctcccggggaacgggctaccctttcttctgctgggcatcacaag atatctcaaaatacctcaattgggtatcaacagaagccgggacagggccctaggct tcttatctaccacacctctcgctgcatagcgggattcccgcacgctttagcggg tctggaagcgggaccgactacactctgaccatctcatctctccagcccaggact tcgccgtctactttctgccagcagggtaacaccctgccgtacaccttcggccaggg caccaagcttgagatcaaaaccactactcccgctccaaggccaccacccctgcc ccgaccatcgctctcagccgctttccctgctccggaggcatgtagaccgcag ctgggtggggccgtgcatacccggggtcttgacttcgctgcatatctacatttg ggccctctggctggtaacttgccgggtcctgctgctttcactcgtgatcactctt tactgtaagcgcggctcggaagaagctgctgtacatctttaagcaacccttcatga ggcctgtgcagactactcaagaggaggacggctgttcatgccggttcccagagga ggaggaaggcggctgcgaactgcgctgaaattcagccgcagcgcagatgctcca gcctacaagcaggggcagaaccagctctacaacgaactcaatcttggtcggagag aggagtacgacgtgctggacaagcggagaggacgggaccagaaatggcgggaa gccgcgcagaaagaatccccagaggcctgtacaacgagctccaaaaggataag atggcagaagcctatagcgagattggatgaaaggggaacgcagaagaggcaaag gccacgacggactgtaccagggactcagcaccgccaccaaggacacctatgacgc tcttcacatgcaggccctgccgcctcgg
104878 CAR 4 – Full - aa	912	<u>MALPVTALLPLALLHAARP</u> qvqlqesgpglvkpsetlsltctvsgvslp <u>dygv</u> <u>swirqppgkglewigviwgsettyyqsslks</u> rvtiskdnskqvslklssvtaad tavyycah <u>yyyggsyamydwgggtlvtvssgggsgggsggggseivmtqspa</u> tllslspgeratlsc <u>rasqdiskylnwyqqkpgqaprlliyhtsrhsg</u> iparfsg sgsgtdytlitisslqpedfavyfc <u>qqgntlpyt</u> fgggtkleiktttpprpptpa ptiasqplslrpeacrpaaggavhtrgldfacdiyiwaplagtcgvlllslvitl yckgrkkllyifkqpfmrpvqttqeedgcscrfpeeeeggcclrvkfsrsadap aykqqnqlynelnlgrreeydvldkrrrdpemggkprkrnpqeglynelqkdk maeyseigmkgerrrgkghdglyqglstatkdydalhmqalppr
CAR 5		

CAR5 scFv domain	913	eivmtqspatlslspgeratlscrasqdiskylnwyyqqkpgqaprrlliyhtsrh sgiparfsgsgsgtdytlitisslqpedfavyfcqqgntlpytfqggtkleikggg gsgggsgggsgggsgggsgvqlqesgpglvkpsetlsltctvsgvslpdygvswir qppgkglewigviwgsettyysssllksrvtiskdnsknqvsllkssvtaadtavy ycakhyyyggsyamydwgggtlvtvss
99789 CAR5 - Soluble scFv - nt	914	atggccctcccagtgaccgctctgctgctgctgctcctctcgacttcttctccatgccg ctcgccctgagatcgatcatgacccaaagccccgctaccctgtccctgtcaccggg cgagagggcaaccctttcatgcagggccagccaggacatttctaagtacctcaac tggtatcagcagaagccagggcaggctcctcgccctgctgatctaccacaccagcc gcctccacagcggatccccgccagattttccgggagcgggtctggaaccgacta caccctcaccatctcttctctgcagcccaggatttccgcgtctatttctgccag caggggaatactctgccgtacaccttcgggtcaaggtagcaagctggaaatcaagg gaggcggaggatcaggcgggtggcgggaagcggaggagggtggctccggaggaggagg ttcccaagtgcagcttcaagaatcaggaccggacttgtgaagccatcagaaacc ctctccctgacttgtaccgtgtccgggtgtgagcctccccgactacggagtctctt ggattcgccagcctccggggaagggtcttgatggattgggggtgatttggggatc agagactacttactactcttcatcacttaagtacgggtcaccatcagcaaagat aatagcaagaaccaagtgtcacttaagtgtcatctgtgaccgccgctgacaccg ccgtgtactattgtgccaaacattactattacggagggtcttatgctatggacta ctggggacaggggaccctgggtgactgtctctagccatcaccatcaccaccatcat cac
99789 CAR5 - Soluble scFv -aa	915	<u>MALPVTALLPLALLHAARP</u> eivmtqspatlslspgeratlscrasqdiskyln wyqqkpgqaprrlliyhtsrhsgiparfsgsgsgtdytlitisslqpedfavyfcq qgntlpytfqggtkleikggggsgggsgggsgggsgvqlqesgpglvkpset lsltctvsgvslpdygvswirqppgkglewigviwgsettyysssllksrvtiskd nsknqvsllkssvtaadtavyycakhyyyggsyamydwgggtlvtvss <u>hhhhhhh</u> <u>h</u>
104879 CAR 5 – Full - nt	916	atggccctccctgtcaccgccctgctgcttccgctggctcttctgctccacgccg ctcgccccgaaattgtgatgaccagtcacccgccactcttagcctttcaccggg tgagcgcgcaaccctgtcttgagagcctcccaagacatctcaaaataccttaat tggtatcaacagaagcccgacagggctcctcgcccttctgatctaccacaccagcc ggctccattctggaatccctgccaggttcagcggtagcggatctgggaccgacta caccctcactatcagctcactgcagccagaggacttcgctgtctatttctgtcag caagggaacaccctgccctacaccttggacagggcaccaagctcgagattaaag gtggagggtggcagcggaggagggtgggtccggcgggtggaggaagcggcggaggcgg gagccagggtccaactccaagaaagcggaccgggtcttgtgaagccatcagaaact ctttcactgacttgtactgtgagcggagtgtctctccccgattacggggtgtctt ggatcagacagccaccggggaagggtctggaatggattggagtgatttggggctc tgagactacttactactcttcatccctcaagtacgcgtcaccatctcaaaggac aactctaagaatcagggtgtcactgaaactgtcatctgtgaccgcagccgacaccg ccgtgtactattgcgctaagcattactattatggcgggagctacgcaatggatta ctggggacaggggtactctgggtcaccgtgtccagcaccactaccccagcaccgagg ccaccacccccggctcctaccatcgccctccagcctctgtccctgcgtccggagg catgtagaccgcagctgggtggggccgtgcatacccggggtcttgacttcgctg cgatatctacatttgggccccctctggctggtagcttgcgggggtcctgctgcttca ctcgatgactcttactgtgaagcgggtcggaagaagctgctgtacatcttta agcaacccttcatgaggcctgtgcagactactcaagaggaggacgggtgttcatg

		ccggttcccagaggaggaggaaggcggctgcgaactgcgcgtgaaattcagccgc agcgcagatgctccagcctacaagcaggggcagaaccagctctacaacgaactca atcttggtcggagagaggagtacgacgtgctggacaagcggagaggacgggaccc agaaatgggcggaagccgcgcagaaagaatccccaagagggcctgtacaacgag ctccaaaaggataagatggcagaagcctatagcgagattgggtatgaaaggggaac gcagaagaggcaaaggccacgacggactgtaccagggactcagcaccgccacca ggacacctatgacgctcttcacatgcaggccctgccgcctcgg
104879 CAR 5 – Full - aa	917	<u>MALPVTALLLPLALLLHAARP</u> eivmtqspatlsispgeratlsc <u>rasqdiskyln</u> wyqqkpgqaprrlliy <u>htsrh</u> sgiparfsgsgsgtdytlitisslqpedfavyfcg <u>qgntlpyt</u> fgqgtkleikgggsgggsgggsgggsgggsgvqlqesgpglvkps setlsltctvsgvslpdygvswirppgkglewigviwgsettyysslksrvtiskd nshkqvslklssvtaadtavyycakhyyyggsyamydwgqgtlvtvsssttpap paptiasqplslrpeacrpaaggavhtrglfacdiyiwaplagtcgvllls lvitlyckrgrklllyifkqpfmrpvqttqeedgcscrfeeeggcclrvkfsr sadapaykqqnqllynelnlgrreeydvldkrrgrdpemggkprkrnpqeglyne lqkdmaeyseigmkgerrrgkghdglyqglstatkdydalhmqalppr
CAR 6		
CAR6 scFv domain	918	eivmtqspatlsispgeratlscrasqdiskylnwyqqkpgqaprrlliyhtsrh sgiparfsgsgsgtdytlitisslqpedfavyfcqgntlpytfgqgtkleikggg sgggsgggsgggsgggsgvqlqesgpglvkpssetlsltctvsgvslpdygvswir ppgkglewigviwgsettyyqsslskrvtiskdnshkqvslklssvtaadtavy ycakhyyyggsyamydwgqgtlvtvss
99790 CAR6 - Soluble scFv - nt	919	atggccctcccagtgaccgctctgctgctgcctctcgcaacttcttctccatgccg ctcggcctgagatcgatgacccaaagccccgctaccctgtccctgtcaccgg cgagagggcaaccctttcatgcagggccagccaggacatttctaagtacctcaac tggtatcagcagaagccagggcaggctcctcgctgctgatctaccacaccagcc gcctccacagcggatccccgccagattttccgggagcgggtctggaaccgacta caccctcaccatctcttctctgcagcccgaggatttcgccgtctatttctgccag caggggaataactctgccgtacaccttcggtcaaggtaccaagctggaaatcaagg gagcgaggagatcaggcgtggcggaagcggaggaggtggctccggaggaggagg ttcccaagtgcagcttcaagaatcaggaccggacttgtgaagccatcagaaacc ctctccctgacttgaccgtgtccggtgtgagcctccccgactacggagtctctt ggattcgccagcctccggggaagggtcttgatggattgggggtgatttggggatc agagactacttactaccagtcacacttaagtcacgggtcaccatcagcaaagat aatagcaagaaccaagtgacacttaagctgtcatctgtgaccgccgctgacaccg ccgtgtactattgtgccaacattactattacggagggtcttatgctatggacta ctggggacaggggaccctgggtgactgtcttagccatcaccatcaccaccatcat cac
99790 CAR6 - Soluble scFv - aa	920	<u>MALPVTALLLPLALLLHAARP</u> eivmtqspatlsispgeratlscrasqdiskyln wyqqkpgqaprrlliyhtsrhsgiparfsgsgsgtdytlitisslqpedfavyfcq qgntlpytfgqgtkleikgggsgggsgggsgggsgggsgvqlqesgpglvkps setlsltctvsgvslpdygvswirppgkglewigviwgsettyyqsslskrvtiskd nshkqvslklssvtaadtavyycakhyyyggsyamydwgqgtlvtvss <u>hhhhhhh</u> <u>h</u>

104880 CAR6 – Full - nt	921	atggccctccctgtcacgcctgctgcttccgctggctcttctgtccacgcg ctcgccccgaaattgtgatgaccagtcacccgccactcttagcctttcaccg tgagcgcgcaaccctgtcttgagagcctcccaagacatctcaaaatacctaat tggtatcaacagaagcccgacaggtcctcgcttctgatctaccacaccagcc ggctccattctggaatccctgccaggttcagcggtagcggatctgggaccgacta caccctcactatcagctcactgcagccagaggacttcgctgtctatcttctgtcag caagggaacacccctgccctacacctttggacagggcaccaagctcgagattaaag gtggaggtggcagcggaggaggtgggtccggcgggtggaggaagcggaggcggagg gagccaggtccaactccaagaaagcggaccgggtcttgtgaagccatcagaaact ctttcactgacttgtactgtgagcggagtgtctctccccgattacggggtgtctt ggatcagacagccaccggggaagggctctggaatggattggagtgtttggggctc tgagactacttactaccaatcatccctcaagtcacgcgtcaccatctcaaaggac aactctaagaatcaggtgtcactgaaactgtcatctgtgaccgcagccgacaccg ccgtgtactattgcgctaagcattactattatggcgggagctacgcaatggatta ctggggacaggggtactctgggtcacctgtccagcaccactacccagcaccgagg ccaccaccccggtcctaccatcgctcccagcctctgtccctgcgtccggagg catgtagaccgcagctggtggggccgtgcatacccggggtcttgacttcgctg cgatatctacatttgggccccctctggctgggtacttgccgggtcctgctgcttca ctcgtgatcactctttactgtaagcgcggtcggaagaagctgctgtacatcttta agcaacccttcatgaggcctgtgcagactactcaagaggaggacggctgttcatg ccggttcccagaggaggaggaaggcggctgcgaactgcgcgtgaaattcagccgc agcgcagatgtccagcctacaagcaggggcagaaccagctctacaacgaactca atcttggtcggagagaggagtacgacgtgctggacaagcggagaggacgggaccc agaaatgggcgggaagccgcgcagaaagaatccccaagagggtctgtacaacgag ctccaaaaggataagatggcagaagcctatagcgagattgggtatgaaaggggaac gcagaagaggcaaaggccacgacggactgtaccagggtactcagcaccgccacca ggacacctatgacgctcttcacatgcaggccctgccgcctcgg
104880 CAR6 – Full – aa	922	MALPVTALLLPLALLLHAARPeivmtqspatlslspgeratlsc <u>rasqdiskyl</u> nwyqqkpgqaprlliy <u>htsr</u> lhsgiparfsgsgsgtdytltlisslqpedfavyfcg <u>ggntlpyt</u> fgqgtkleikggggsgggsgggsgggsgggsgvqlqesgpglvkpset lsltctvsgvslpdygvswirppgkglewigviwgsettyyqssllksrvtiskd nsknqvsllkssvtaadtavyycakhyyyggsyamydwgggtlvtvssttppap pptpaptiasqplslrpeacrpaaggavhtrglfacdiyiwaplagtcgvllls lvitlyckrgrklllyifkqpfmrpvqttqeedgcscrfpееееggcelrvkfsr sadapaykqqnqlynelnlgrreeydvldkrrgrdpemggkprkrnpqeglyne lqdkmaeayseigmkgerrrgkghdglyqglstatkdydalhmqalppr
CAR 7		
CAR7 scFv domain	923	qvqlqesgpglvkpsetlsltctvsgvslpdygvswirppgkglewigviwgse ttyysssllksrvtiskdnsknqvsllkssvtaadtavyycakhyyyggsyamydw gggtlvtvssggggsgggsgggsgggsgggseivmtqspatlslspgeratlscra sqdiskylnwyqqkpgqaprlliyhtsrhsgiparfsgsgsgtdytltlisslq edfavyfcqqgntlpytfgqgtkleik
100796 CAR7 -	924	atggcactgcctgtcactgcctcctgctgcctctggccctccttctgcatgccg ccaggccccaagtccagctgcaagagtcaggaccggactggtgaagcgtctga gactctctcactgacttgtaccgtcagcggcgtgtccctccccgactacggagt tcatggatccgccaacctccgggaaagggcttgaatggattggtgtcatctggg

Soluble scFv - nt		gttctgaaaccacctactactcatcttccctgaagtcacgggtgaccatcagcaa ggataattccaagaaccaggtcagccttaagctgtcatctgtgaccgctgctgac accgccgtgtattactgcgccaagcactactattacggaggaagctacgctatgg actattggggacagggcactctcgtgactgtgagcagcggcggtggagggtctgg aggtggaggatccggtggtggtgggtcaggcggaggaggagcagattgtgatg actcagtaccagccaccctttctctttcaccggcgagagagcaaccctgagct gtagagccagccaggacatttctaagtacctaactggatcagcaaaaaccggg gcaggccctcgccctcctgatctaccatacctcacgccttactctggtatcccc gctcggttagcggatcaggatctggtaccgactacactctgaccatttccagcc tgcagccagaagatttgcagtgatttctgccagcagggcaatacccttctta caccttcggtcagggaaccaagctcgaaatcaagcaccatcaccatcatcaccac cat
100796 CAR7 - Soluble scFv - aa	925	<u>MALPVTALLLPLALLLHAARP</u> qvqlqesgpglvkpsetlsltctvsgvslpdygv swirqppegkglewigviwgsettyyssslksrvtiskdsknqvsllssvtaad tavyycahyyyggsyamdywgqgtlvtvssgggsgggsgggsggggseivm tqspatlsispgeratlscrasqdiskylnwyqqkpgqaprllyhtsrhsgip arfsgsgsgtdytlitisslqpedfavyfcqqgntlpytfgqgtkleik <u>hhhhhhh</u> <u>h</u>
104881 CAR 7 Full - nt	926	atggctctgcccgtgaccgcactcctcctgccactggctctgctgcttcacgcg ctcgcccaacaagtcacgttcaagaatcagggcctggtctggtgaagccatctga gactctgtccctcacttgacccgtgagcggagtgtccctcccagactacggagt agctggattagacagcctcccgaaaggactggagtggatcggagtgatttggg gtagcgaaaccacttactattcatcttccctgaagtcacgggtcaccatttcaaa ggataactcaaagaatcaagtgagcctcaagctctcatcagtcaccgccgctgac accgccgtgtattactgtgccaagcattactactatggagggtcctacgccatgg actactggggccagggaactctggtcactgtgtcatctggtggaggaggtagcgg aggaggcgggagcgggtggaggtggctccggagggtggcggaagcgaaatcgtgatg accagagccctgcaaccctgtccctttctccggggaacgggctaccctttctt gtcgggcatcacaagatatctcaaaatacctcaattggtatcaacagaagccggg acaggccctaggtcttcttctaccacacctctcgccctgcatagcgggattccc gcacgcttagcgggtctggaagcgggaccgactacactctgaccatctcatctc tccagcccagaggacttcgccgtctacttctgccagcagggtaacacctgcccga caccttcggccagggcaccaagcttgagatcaaaaccactactccgctccaagg ccaccacccctgccccgaccatcgccctctcagccgctttccctgcgtccggagg catgtagaccgcagctggtggggccgtgcatacccggggtcttgacttcgcctg cgatatctacatttggggccctctggctggtagcttgccgggtcctgctgcttca ctcgtgatcactctttactgtaagcgggtcggaagaagctgctgtacatcttta agcaacccttcatgaggcctgtgcagactactcaagaggaggacggctgttcatg ccggttcccagaggaggaggaaggcgggtgcgaactgcgcgtgaaattcagccgc agcgcagatgctccagcctacaagcaggggcagaaccagctctacaacgaactca atcttggtcggagagaggagtacgacgtgctggacaagcggagaggacgggaccc agaaatgggcgggaagccgcgcagaaagaatcccaagagggcctgtacaacgag ctccaaaaggataagatggcagaagcctatagcgagattggtatgaaaggggaac gcagaagaggcaaaggccacgacggactgtaccagggactcagcaccgccacca ggacacctatgacgctcttcacatgcaggccctgccgcctcgg
104881	927	<u>MALPVTALLLPLALLLHAARP</u> qvqlqesgpglvkpsetlsltctvsgvslpdygv <u>swirqppegkglewigviwgsettyyssslks</u> rvtiskdsknqvsllssvtaad

CAR 7		tavyyca khyyyggsyandy wgqgtlvtvssggggsgggsgggsgggsggggseivm tqspatlslspgeratlsc rasqdiskyl nwyqqkpgqaprrlliy htsrlhsgip arfgsgsgsgtdytl ti sslqpedfavyfc qqgntlpyt fgqgtkleiktttppapr pptpaptiasqplslrpeacrpaaggavhtrgldfacdiyiwaplagtcgvllls lvitlyckrgrklllyifkqpfmrpvqttqeedgcscrfeeeeegggcelrvkfsr sadapaykqqgnqlynelnlgrreeydvldkrrgrdpemggkprkrnpqeglyne lqkdkmaeayseigmkgerrrgkghdglyqqglstatkdttydalhmqalppr
CAR 8		
CAR8 scFv domain	928	qvqlqesgpglvkpsetlsltctvsgvslpdygvswirppgkglewigviwgse ttyyqsslskrvtiskdnsknqvsiklssvtaadtavyyca khyyyggsyandy w gggtlvtvssggggsgggsgggsgggsggggseivmtqspatlslspgeratlscra sqdiskyl nwyqqkpgqaprrlliyhtsrlhsgip arfgsgsgsgtdytl ti sslq edfavyfc qqgntlpyt fgqgtkleik
100798 CAR8 - Soluble scFv - nt	929	atggcactgcctgtcactgccctcctgctgcctctggccctccttctgcatgccg ccaggccccaagtccagctgcaagagtcaggaccggactggatgaagccgtctga gactctctcactgacttgtaccgtcagcggcgtgtccctccccgactacggagt tcatggatccgccaacctcccggaagggcttgaatggattggtgtcatctggg gttctgaaaccacctactaccagctcttccctgaagtcagggtgaccatcagcaa ggataattccaagaaccaggtcagccttaagctgtcatctgtgaccgctgtgac accgccgtgtattactgcgccaagcactactattacggaggaagctacgctatgg actattggggacagggcactctcgtgactgtgagcagcggcggtggagggtctgg agggtggaggatccggtggtggtgggtcaggcggaggaggaggagcgagattgtgatg actcagtcaccagccaccctttctctttcaccggcgagagagcaaccctgagct gtagagccagccaggacatttctaagtacctcaactggtatcagcaaaaaccggg gcaggccctcgctcctgatctaccataacctcagccttcaactctggtatcccc gctcggttagcggatcaggatctggtaccgactacactctgaccattttccagcc tgcagccagaagatttcgcagtgattttctgccagcagggaataacccttcctta caccttcggtcagggaaccaagctcgaaatcaagcaccatcaccatcatcatcac cac
100798 CAR8 - Soluble scFv - aa	930	<u>MALPVTALLPLALLLHAARP</u> qvqlqesgpglvkpsetlsltctvsgvslpdygv swirppgkglewigviwgsettyyqsslskrvtiskdnsknqvsiklssvtaad tavyyca khyyyggsyandy wgqgtlvtvssggggsgggsgggsgggsggggseivm tqspatlslspgeratlscrasqdiskyl nwyqqkpgqaprrlliyhtsrlhsgip arfgsgsgsgtdytl ti sslqpedfavyfc qqgntlpyt fgqgtkleik hhhhhhh <u>h</u>
104882 CAR 8 – Full - nt	931	atggctctgcccgtgaccgcactcctcctgccactggctctgctgcttcacgcg ctcgcccacaagtccagcttcaagaatcagggcctggtctggtgaagccatctga gactctgtccctcacttgaccgtgagcggagtgtccctcccagactacggagt agctggattagacagcctcccggaagggactggagtggatcgaggtgatttggg gtagcgaaaccacttactatcaatcttccctgaagtcacgggtcaccattttcaaa ggataactcaaagaatcaagtgagcctcaagctctcatcagtcaccgccgctgac accgccgtgtattactgtgccaagcattactactatggagggtcctacgccatgg actactggggccagggaactctggtcactgtgtcatctggtggaggaggtagcgg aggaggcgggagcgggtggaggtggctccggaggcggtgggtcagaaatcgtgatg accagagccctgcaaccctgtccctttctcccggggaacgggctaccctttctt

		gtcgggcatcacagaatctctcaaaatacctcaattggtatcaacagaagccggg acaggccccctaggcttcttctaccacacctctcgccctgcatagcgggattccc gcacgcttttagcgggtctggaagcgggaccgactacactctgaccatctcatctc tccagcccaggacttcgccgtctacttctgccagcagggtaacaccctgccgta caccttcggccagggcaccaagcttgagatcaaaaccactactcccgtccaagg ccaccacccctgccccgaccatcgccctctcagccgctttccctgcgtccggagg catgtagaccgcagctggtggggccgtgcatacccggggtcttgacttcgctg cgatatctacatttgggccccctctggctggtacttgccgggtcctgctgctttca ctcgtgatcactctttactgtaagcgcggtcggaagaagctgctgtacatcttta agcaacccttcatgaggcctgtgcagactactcaagaggaggacggctgttcatg ccggttcccagaggaggaggaaggcggctgcgaactgcgcgtgaaattcagccgc agcgcagatgctccagcctacaagcaggggcagaaccagctctacaacgaactca atcttggtcggagagaggagtacgacgtgctggacaagcggagaggacgggaccc agaaatgggcgggaagccgcgcagaaagaatccccaagagggcctgtacaacgag ctccaaaaggataagatggcagaagcctatagcgagattggtatgaaaggggaac gcagaagaggcaaaggccacgacggactgtaccagggactcagcaccgccacca ggacacctatgacgctcttcacatgcaggccctgccgcctcgg
104882 CAR 8 – Full - aa	932	MALPVTALLPLALLHAARPqvqlqesgpglvkpsetlsltctvsgvslpdygv <u>swir</u> qppgkglewigviwgsettyyqsslksrvtiskdnknqvsllkssvtaad tavyycakhyyyggsyamydwgggtlvtvssggggsgggsgggsggggseivm tqspatlsispgeratlscrasqdiskylnwyqqkpgqaprllyhtsrhsgip arfsgsgsgtdytlitisslqpedfavyfcqggntlpytfqggtkleiktttppr pptpaptiasqplslrpeacrpaaggavhtrglfacdiyiwaplagtcgvllls lvitlyckrgrklllyifkqpfmrpvqttqeedgcsrfpeeeeggcelrvkfser sadapaykqqnqllynelnlgrreeydvldkrrgrdpemggkprkrnpqeglyne lqkdkmaeyseigmkgerrrgkghdglyqglstatkdydalhmqalppr
CAR 9		
CAR9 scFv domain	933	eivmtqspatlsispgeratlscrasqdiskylnwyqqkpgqaprllyhtsrh sgiparfsgsgsgtdytlitisslqpedfavyfcqggntlpytfqggtkleikggg gsgggsgggsgggsgggsgvqlqesgpglvkpsetlsltctvsgvslpdygvswir qppgkglewigviwgsettyynsslksrvtiskdnknqvsllkssvtaadtavy ycakhyyyggsyamydwgggtlvtvss
99789 CAR9 - Soluble scFv - nt	934	atggccctcccagtgaccgctctgctgctgctcctctcgcaacttcttctccatgcg ctcggcctgagatcgatgacccaaagccccgctaccctgtccctgtcaccgg cgagagggcaacccttcatgcagggccagccaggacatttctaagtacctcaac tggtatcagcagaagccagggcaggctcctcgccctgctgatctaccacaccagcc gcctccacagcggatccccgccagattttccgggagcgggtctggaaccgacta caccctcaccatctcttctctgcagcccaggatttcgccgtctatttctgccag caggggaatactctgccgtacaccttcgggtcaaggtagcaagctggaaatcaagg gaggcggaggatcaggcgggtggcgggaagcggaggagggtggctccggaggaggagg ttcccaagtgcagcttcaagaatcaggaccggacttgtagaagccatcagaaacc ctctccctgacttgtagcgtgtccgggtgtgagcctccccgactacggagtctctt ggattcgccagcctccggggaagggtcttgatggattgggggtgatttggggatc agagactacttactacaattcatcacttaagtacgggtcaccatcagcaaagat aatagcaagaaccaagtgtcacttaagtgtcatctgtgaccgccgctgacaccg ccgtgtactattgtgccaaacattactattacggagggtcttatgctatggacta

		ctggggacaggggaccctggtgactgtctctagccatcaccatcaccaccatcat cac
99789 CAR9 - Soluble scFv - aa	935	<u>MALPVTALLLPLALLLHAARP</u> eiivmtqspatlslspgeratlscrasqdiskyln wyqqkpgqaprrlliyhtsrhsgiparfsgsgsgtdytltlisslqpedfavyfcq qgntlpytfgqgtkleikggggsgggsgggsgggsgvqlqesgpglvkpset lsltctvsgvslpdygvswirpppgkglewigviwgsettyynsslksrvtiskd nsknqvsllkssvtaadtavyycahyyyggsyamydgqgtlvtvss <u>hhhhhhh</u> <u>h</u>
105974 CAR 9 – Full - nt	936	atggccctccctgtcaccgcctgctgcttccgctggctcttctgctccacgcg ctcgcccgaaattgtgatgaccagtcacccgccactcttagcctttcaccgcg tgagcgcgcaaccctgtcttgagagcctcccaagacatctcaaaataccttaat tggtatcaacagaagcccgacaggctcctcgcttctgatctaccacaccagcc ggctccattctggaatccctgccaggttcagcggtagcggatctgggaccgacta caccctcactatcagctcactgcagccagaggacttcgctgtctatttctgtcag caagggaacaccctgccctacacctttggacagggcaccaagctcgagattaaag gtggaggtggcagcggaggaggtgggtccggcgggtggaggaagcggaggcgggtg gagccaggtccaactccaagaaagcggaccgggtcttgtgaagccatcagaaact ctttcactgacttgtactgtgagcggagtgtctctccccgattacggggtgtctt ggatcagacagccaccggggaagggtctggaatggattggagtgtttggggctc tgagactacttactacaactcaccctcaagtacgcgtcaccatctcaaaggac aactctaagaatcaggtgtcactgaaactgtcatctgtgaccgcagccgacaccg ccgtgtactattgcgctaagcattactattatggcgggagctacgcaatggatta ctggggacagggtagctctgggtcaccgtgtccagcaccactaccccagcaccgagg ccaccaccccggtcctaccatcgctccagcctctgtccctgcgtccggagg catgtagaccgcagctggtggggccgtgcatacccggggtcttgacttcgctg cgatatctacatttgggccccctctggctggtacttgcggggtcctgctgcttca ctcgatgactctttactgtaagcgcggtcggaagaagctgctgtacatcttta agcaacccttcatgaggcctgtgcagactactcaagaggaggacggctgttcatg ccggttcccagaggaggaggaaggcggctgcgaactgcgcgtgaaattcagccgc agcgcagatgtccagcctacaagcaggggcagaaccagctctacaacgaactca atcttggtcggagagaggagtacgacgtgctggacaagcggagaggacgggacc agaaatgggcgggaagccgcgcagaaagaatcccaagagggctgtacaacgag ctccaaaaggataagatggcagaagcctatagcgagattggtatgaaaggggaac gcagaagaggcaaaggccacgacggactgtaccagggactcagcaccgccacca ggacacctatgacgctcttcacatgcaggccctgccgcctcgg
105974 CAR 9 – Full - aa	937	<u>MALPVTALLLPLALLLHAARPe</u> ivmtqspatlslspgeratlsc <u>rasqdiskyln</u> wyqqkpgqaprrlliy <u>htsrhsg</u> iparfsgsgsgtdytltlisslqpedfavyfc <u>g</u> <u>qgntlpyt</u> fgqgtkleikggggsgggsgggsgggsgvqlqesgpglvkpset lsltctvsgvslp <u>dygvs</u> wirpppgkglewig <u>viwgsettyynsslks</u> rvtiskd nsknqvsllkssvtaadtavyycah <u>yyyggsyamyd</u> wgqgtlvtvss <u>ttt</u> papr pptpaptiasqplslrpeacrpaaggavhtrglldfacdiyiwaplagtcgvllls lvitlyckrgrklllyifkqpfmrpvqttqeedgcscrfeeeggcelrvkfsr sadapaykqqnqlynelnlgrreeydvldkrrgrdpemggkprkrnpqeglyne lqdkmaeayseigmkgerrrgkghdglyqglstatkdydalhmqalppr
CAR10		

CAR10 scFv domain	938	qvqlqesgpglvkpsetlsltctvsgvslpdygvswirppgkglewigviwgsettyynsslksrvtiskdnskqnqslklssvtaadtavyycakhyyyggsyamdywgggtlvtvssgggsgggsgggsgggsgggseivmtqspatlsispgeratlscrasqdiskylnwyqqkpgqaprlliyhtsrhsgiparfsgsgsgtdytlitisslqp edfavyfcqqgntlpytfgggtkleik
100796 CAR10 - Soluble scFv - nt	939	atggcactgcctgtcactgccctcctgctgcctctggccctccttctgcatgccg ccaggccccaagtccagctgcaagagtcaggaccggactggatgaagccgtctga gactctctcactgacttgtaccgtcagcggcgtgtccctccccgactacggagtgtcatggatccgccaacctccgggaaagggcttgaaatggattgggtgtcatctggg gttctgaaaccacctaactacaactcttccctgaagtccagggtgacctacagcaa ggataattccaagaaccaggtcagccttaagctgtcatctgtgaccgctgctgac accgccgtgtattactgcgccaagcactactattacggaggaagctacgctatgg actattggggacagggcactctcgtgactgtgagcagcggcgggtggaggggtctgg aggtggaggatccgggtgggtgggtcaggcggaggaggagcagagattgtgatg actcagtcaccagccaccctttctctttcaccggcgagagagcaaccctgagct gtagagccagccaggacatttctaagtaacctcaactggatcagcaaaaaccggg gcaggccctcgctcctgatctaccataacctcagccttctactctggatcccc gctcggttagcggatcaggatctggtagcactacactctgaccatttccagcc tgcagccagaagatttgcagtgatttctgccagcagggcaatacccttctta caccttcggtcagggaaccaagctcgaaatcaagcaccatcaccatcatcaccac cat
100796 CAR10 - Soluble scFv - aa	940	<u>MALPVTALLPLALLHAARP</u> qvqlqesgpglvkpsetlsltctvsgvslpdygvswirppgkglewigviwgsettyynsslksrvtiskdnskqnqslklssvtaadtavyycakhyyyggsyamdywgggtlvtvssgggsgggsgggsgggsgggseivmtqspatlsispgeratlscrasqdiskylnwyqqkpgqaprlliyhtsrhsgiparfsgsgsgtdytlitisslqp edfavyfcqqgntlpytfgggtkleik <u>hhhhhhh</u> <u>h</u>
105975 CAR 10 Full - nt	941	atggccctccctgtcaccgccctgctgcttccgctggctcttctgctccacgcg ctcggcccgaaattgtgatgacctcagtcaccgccactcttagcctttcaccgg tgagcgcgcaaccctgtcttgagagcctcccaagacatctcaaaataccttaat tggatcaacagaagcccgacagggctcctcgcttctgatctaccacaccagcc ggctccattctggaatccctgccaggttcagcggtagcggatctgggaccgacta caccctcactatcagctcactgcagccagaggacttcgctgtctatttctgtcag caagggaacacccctgccctacaccttggacagggcaccaagctcgagattaaag gtggaggtggcagcggaggaggtgggtccggcgggtggaggaagcggaggggtgg gagccaggtccaactccaagaaagcggaccgggtcttgtgaagccatcagaaact ctttactgacttgtactgtgagcggagtgtctctccccgattacggggtgtctt ggatcagacagccaccggggaagggtctggaatggattggagtgatttggggctc tgagactacttactacaactcatccctcaagtcacgcgtcaccatctcaaggac aactctaagaatcaggtgtcactgaaactgtcatctgtgaccgcagccgacaccg ccgtgtactattgcgctaagcattactattatggcgggagctacgcaatggatta ctggggacaggggtactctgggtcaccgtgtccagcaccactacccagcaccgagg ccaccaccccggtcctaccatcgctcccagcctctgtccctcgctccggagg catgtagaccgcagctgggtggggccgtgcatacccggggtcttgacttcgctg cgatatctacatttgggccccctctggctggtagcttgcgggggtcctgctgcttca ctcgatgactcttactgtgaagcgggtcggaagaagctgctgtacatcttta agcaacccttcatgaggcctgtgcagactactcaagaggaggacgggtgttcatg

		ccggttcccagaggaggaggaaggcggctgcgaactgcgcgtgaaattcagccgc agcgcagatgctccagcctacaagcaggggcagaaccagctctacaacgaactca atcttggtcggagagaggagtacgacgtgctggacaagcggagaggacgggaccc agaaatgggcggaagccgcgcagaaagaatccccaagagggcctgtacaacgag ctccaaaaggataagatggcagaagcctatagcgagattggtatgaaaggggaac gcagaagaggcaaaggccacgacggactgtaccagggactcagcaccgccacca ggacacctatgacgctcttcacatgcaggccctgccgcctcgg
105975 CAR 10 Full - aa	942	MALPVTALLLPLALLLHAARPEIVMTQSPATLSLSPGERATLS C <u>RASQDISKYL</u> N WYQQKPGQAPRLLIY HTSRLHS GIPARFSGSGSGTDYTLTISSLPEDFAVYFCQ <u>QGN</u> TLPYT FGGQTKLEIKGGGSGGGGSGGGGSGGGGSGVQLQESGPGLVKPS SETLSLTCTVSGVSLP DYGV SWIRQPPGKGLEWIG VIWGSETTYNSSLKS SRVTISKD NSKNQVSLKLSSVTAADTAVYYCAK HYYYGGSYAMDY WGQGLVTVSSTTTPAPR PPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLS LVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFEEEEGGCELRVKFSR SADAPAYKQQQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNE LQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
CAR11		
CAR11 scFv domain	943	eivmtqspatlsislspgeratlscrasqdiskylnwyqqkpgqaprllyi htsrlh sgiparfsgsgsgtdytltiisslpedfavyfcqqgntlpytfggqtkleikggg gsgggsgggsgvqlqesgpglvkpsetlsltctvsgvslpdygvswirppgk glewigviwgsettyynsslksrvtiskdnskqvslklssvtaadtavyyca h yyyggsyamydwgqglvtvss
103101 CAR11 - Soluble scFv - nt	944	Atggccctccctgtcaccgcctgctgcttccgctggtctcttctgctccacgcg ctcgccccgaaattgtgatgaccagtcacccgccactcttagcctttcaccgg tgagcgcgcaaccctgtcttgagagcctcccaagacatctcaaaataccttaat tggtatcaacagaagcccgacaggtcctcgcttctgatctaccacaccagcc ggctccattctggaatccctgccaggttcagcggtagcggatctgggaccgacta caccctcactatcagctcactgcagccagaggacttcgctgtctatttctgtcag caagggaacaccctgccctacacctttggacagggcaccaagctcgagattaaag gtggaggtggcagcggaggaggtgggtccggcgggtggaggaagccaggtccaact ccaagaaagcggaccgggtcttgtgaagccatcagaaactctttcactgacttgt actgtgagcggagtgtctctccccgattacgggggtgtcttgatcagacagccac cggggaagggtctggaatggattggagtgatttggggctctgagactacttacta caattcatccctcaagtcacgcgtcaccatctcaaaggacaactctaagaatcag gtgtcactgaaactgtcatctgtgaccgcagccgacaccgccgtgtactattgcg ctaagcattactattatggcgggagctacgcaatggattactggggacaggggtac tctggtcaccgtgtccagccaccaccatcatcaccatcaccat
103101 CAR11 - Soluble scFv	945	<u>MALPVTALLLPLALLLHAAR</u> eivmtqspatlsislspgeratlscrasqdiskyln wyqqkpgqaprllyi htsrlh sgiparfsgsgsgtdytltiisslpedfavyfcq qgntlpytfggqtkleikgggsgggsgggsgvqlqesgpglvkpsetlsltc tvsgvslpdygvswirppgkglewigviwgsettyynsslksrvtiskdnskq

- aa		vs1klssvtaadtavyycakhyyyggsyamdywgqgtlvtvss <u>hhhhhhh</u>
105976 CAR 11 Full - nt	946	atggctctgcccgtgaccgcactcctcctgccactggctctgctgcttcacgccg ctcgcccacaagtccagcttcaagaatcagggcctggctctggtgaagccatctga gactctgtccctcacttgaccgtgagcggagtgtccctcccagactacggagt agctggattagacagcctcccgaaagggactggagtggatcggagtgatttggg gtagcgaaccacttactataactcttccctgaagtcacgggtcaccatttcaaa ggataactcaaagaatcaagtgagcctcaagctctcatcagtcaccgccgctgac accgccgtgtattactgtgccaagcattactactatggagggctctacgccatgg actactggggccagggaactctggctcactgtgtcatctggtggaggaggtagcgg aggaggcgggagcgggtggaggtggctccggaggtggcgaagcgaaatcgtgatg accagagccctgcaaccctgtccctttctccggggaacgggctaccctttctt gtcgggcatcacaagatatctcaaaatacctcaattggtatcaacagaagccggg acaggcccttaggcttcttctaccacacctctgcctgcatagcgggattccc gcacgcttagcgggtctggaagcgggaccgactacactctgaccatctcatctc tccagcccaggacttcgccgtctacttctgccagcagggtaacaccctgccgta caccttcggccagggcaccaagcttgagatcaaaaccactactccgctccaagg ccaccacccctgcccagaccatgcctctcagccgctttccctgcgtccggagg catgtagaccgcagctggtggggccgtgcataccgggggtcttgacttcgctg cgatatctacatttgggcccctctggctggtacttgccgggtcctgctgctttca ctcgtgatcactcttactgtgaagcgggtcggaagaagctgctgtacatcttta agcaacccttcatgaggcctgtgcagactactcaagaggaggacggctgttcatg ccggttcccagaggaggaggaaggcggctgcgaactgcgcgtgaaattcagccgc agcgcagatgctccagcctacaagcaggggcagaaccagctctacaacgaactca atcttggtcggagagaggagtacgacgtgctggacaagcggagaggacgggaccc agaaatggcggggaagccgcgcagaaagaatccccaagagggcctgtacaacgag ctccaaaaggataagatggcagaagcctatagcgagattggtatgaaaggggaac gcagaagaggcaaaggccacgacggactgtaccagggactcagcaccgccacca ggacacctatgacgctcttcacatgcaggccctgccgctcgg
105976 CAR 11 Full - aa	947	MALPVTALLPLALLLHAARPQVQLQESGPGLVKPSSETLSLTCTVSGVSLP <u>DYGV</u> <u>SWIRQPPGKGLEWIGVIWGSETTYYNSSLKS</u> RVTIISKDNSKNQVSLKLSSVTAAD TAVYYCAK <u>HYYYGGSYAMDY</u> WGQGTlvtvssggggsgggsgggsgggsgggseivm TQSPATLSLSPGERATLSC <u>RASQDISKYL</u> NWYQQKPGQAPRLLIY <u>HTSRLHSG</u> IP ARFSGSGSGTDYTLTISSLQPEDFAVYFC <u>QQGNTLPYT</u> FGQGTKLEIKTTTPAPR PPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLS LVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSR SADAPAYKQGQNQLYNELNLGRREEYDVLDRRGRDPEMGGKPRRKNPQEGLYNE LQDKMAEAYSEIGMKGERRRGKGDGLYQGLSTATKDTYDALHMQALPPR
CAR12		
CAR12 scFv domain	948	qvqlqesgpglvkpsetlsltctvsgvslpdygvswirqppgkglewigviwgse tтынsslkrsvtiskdnsknqvs1klssvtaadtavyycakhyyyggsyamdyw gggtlvtvssggggsgggsgggsgggseivmtqspatls1spgeratlsrasqdis kylnwqqkpgqaprllyhtsrlhsgiparfsgsgsgtdytltiisslqpedfav

		yfcqqgntlpytfqggtkleik
103104 CAR12 - Soluble scFv - nt	949	atggctctgcccgtgaccgcactcctcctgccactggctctgctgcttcacgcg ctcgcccacaagtcacagcttcaagaatcagggcctggctctggtgaagccatctga gactctgtccctcacttgaccgtgagcggagtgtccctcccagactacggagtg agctggattagacagcctcccggaaaggactggagtggatcggagtgatttggg gtagcgaaaccacttactataactcttcctgaagtcacgggtcaccatttcaaa ggataactcaaagaatcaagtgaacctcaagctctcatcagtcaccgcgcgtgac accgcgctgtattactgtgccaaagcattactactatggagggctcctacgccatgg actactggggccagggaactctggctcactgtgtcatctggtggaggaggtagcgg aggaggcgggagcgggtggaggtggctccgaaatcgtgatgaccagagccctgca accctgtccctttctcccggggaacgggctaccctttcttgcgggcatcacaag atatctcaaaatacctcaattgggtatcaacagaagccgggacaggccctaggct tcttatctaccacacctctcgctgcatagcgggattcccgacgcttttagcggg tctggaagcgggaccgactacactctgaccatctcatctctccagcccgaggact tcgccgtctacttctgccagcagggtaacaccctgcggtacaccttcggccaggg caccaagcttgagatcaaacatcaccaccatcatcaccatcac
103104 CAR12 - Soluble scFv -aa	950	<u>MALPVTALLPLALLHAARP</u> qvqlqesgpglvkpsetlsltctvsgvslpdygv swlrqppgkglewigviwgsettyynsslksrvtiskdsknqvsllkssvtaad tavyycahyyyggsyamdywgqgtlvtvssggggsgggsgggseivmtqspa tllslspgeratlscrasqdiskylnwyqqkpgqaprlliyhtsrllhsgiparfsg sgsgtdytltiisslqpedfavyfcqqgntlpytfqggtkleik <u>hhhhhhhh</u>
105977 CAR 12 - Full - nt	951	atggccctccctgtcacgcacctgctgcttccgctggctcttctgctccacgcg ctcgggcccgaaattgtgatgaccagtcacccgccactcttagcctttcacccgg tgagcgcgcgaacctgtcttgcagagcctcccaagacatctcaaaataccttaat tgggtatcaacagaagcccgacaggctcctcgcttctgatctaccacaccagcc ggctccattctggaatccctgccaggttcagcggtagcggatctgggaccgacta caccctcactatcagctcactgcagccagaggacttcgctgtctatttctgtcag caagggaacacctgcctacacctttggacagggcaccaagctcgagattaaag gtggaggtggcagcggaggaggtgggtccggcgggtggaggaagccaggtccaact ccaagaaagcggaccgggtcttgtgaagccatcagaaactctttcactgacttgt actgtgagcggagtgtctctccccgattacgggggtgtcttggatcagacagccac cggggaagggtctggaatggattggagtgatttggggctctgagactacttacta caactcatccctcaagtcacgcgtcaccatctcaaaggacaactctaagaatcag gtgtcactgaaactgtcatctgtgaccgcagccgacaccgcggtgtactattgcg ctaagcattactattatggcgggagctacgcaatggattactggggacagggtac tctggtcacctgtccagcaccactacccagcaccgaggccacccaccccggt cctaccatcgctcccagcctctgtccctgcgtccggaggcatgtagaccgcag ctggtggggccgtgcatacccggggtcttgacttcgctgcgatctacatttg ggccctctggctggtacttgcggggctcctgctgctttcactcgtgatcactctt tactgtaagcgcggctcggaagaagctgctgtacatctttaagcaacccttcatga ggcctgtgcagactactcaagaggaggacggctgttcatgccggttcccagagga ggaggaaggcggctgcgaactgcgcgtgaaattcagccgcagcgcagatgctcca gcctacaagcaggggcagaaccagctctacaacgaactcaatcttggtcggagag aggagtacgacgtgctggacaagcggagaggacgggaccagaaatggcggggaa gccgcgcagaaagaatccccaagaggcctgtacaacgagctccaaaaggataag atggcagaagcctatagcgagatttggtatgaaaggggaacgcagaagaggcaaag

		gccacgacggactgtaccagggaactcagcaccgccaccaaggacacctatgaagcgtcttcacatgcaggccctgccgcctcgg
105977 CAR 12 – Full - aa	952	MALPVTALLLPLALLLHAARPEIVMTQSPATLSLSPGERATLS C <u>RASQDISKYL</u> N WYQQKPGQAPRLLIY HTSRLHS GIPARFSGSGSGTDYTLTISSLPEDFAVYFCQ <u>QGNLTLPYT</u> FGQGTKLEIKGGGGSGGGGSGGGGSQVQLQESGPGLVKPSSETLSLTC TVSGVSLP DYGVS WIRQPPGKGLEWIG VIWGSETTYNSSLKS RVTISKDNSKNQ VSLKLSSVTAADTAVYYCAK HYYYGGSYAMDY WGQGLTVTSSTTTPAPRPPTPA PTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITL YCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAP AYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDK MAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
CTL019		
CTL019 – Soluble scFv-Histag - nt	953	atggccctgcccgtcaccgctctgctgctgccccttgctctgcttcttcacatgcag caaggccggacatccagatgacccaaaccacctcatccctctctgctctcttg agacaggggtgaccatttcttgctgcgcgcagccaggacatcagcaagtatctgaac tggtatcagcagaagccggacggaaccgtgaagctcctgatctaccatacctctc gctgcatagcggcgtgccctcacgcttctctggaagcggatcaggaaccgatta ttctctcactatttcaaattcttgagcaggaagatattgccacctatttctgccag cagggtataaccctgccctacaccttcggaggaggagaccaagctcgaaatcaccg gtggaggaggcagcggcgggtggagggtctggtggagggtggttctgaggtgaagct gcaagaatcaggccctggacttggtggccccttcacagtccttgagcgtgacttgc accgtgtccggagtctccctgcccgactacggagtgatcatggatcagacaacctc cacggaaaggactggaatggctcgggtgtcatctggggtagcgaaactacttacta caattcagccctcaaaagcagggtgactattatcaaggacaacagcaagtcccaa gtctttcttaagatgaactcactccagactgacgacaccgcaatctactattgtg ctaagcactactactacggaggatcctacgctatggattactggggacaaggtac ttccgtcactgtctcttcacaccatcatcaccatcaccatcac
CTL019 – Soluble scFv-Histag - aa	954	<u>MALPVTALLLPLALLLHAARP</u> diqmtqttsslsaslgdrvtiscrasqdiskyl wyqqkpdgtvkllyhtsrhlsgvpsrfsrgsgsgtdysltisnleqediatyf qgntlpytfgggtkleitggggsgggsggggsevklqesgpglvapsqslsvtc tvsgvslpdygvswirqpprkglewlgviwgsettyynsalksrltiikdnksq vflkmnslqtddtaiyycahyyyggsyamydgqgtsvtvss <u>hhhhhhh</u>
CTL019 Full - nt	955	atggccttaccagtgaaccgcttgctcctgccgctggccttgctgctccacgcg ccaggccggacatccagatgacacagactacatccctcctgtctgctctctggg agacagagtcaccatcagttgcagggaagtcaggacattagtaaatatttaaat tggtatcagcagaaccagatggaactgttaaactcctgatctaccatacatcaa gattacactcaggagtcccatcaaggttcagtggcagtggggtctggaacagatta ttctctcaccattagcaacctggagcaagaagatattgccacttacttttgcaa cagggtataacgcttcggtacacgttcggaggggggaccaagctggagatcacag gtggcgggtggctcgggcgggtgggtgggtcgggtggcggcggatctgaggtgaaact

		gcaggagtcaggacctggcctggtggcgccctcacagagcctgtccgtcacatgc actgtctcaggggtctcattaccgcactatggtgtaagctggattcgccagcctc cacgaaaggggtctggagtggtgggagtaatatggggtagtgaaaccacatacta taattcagctctcaaattccagactgaccatcatcaaggacaactccaagagccaa gttttcttaaaaatgaacagtctgcaaactgatgacacagccatttactactgtg ccaaacattattactacggtggtagctatgctatggactactggggccaaggaac ctcagtcaccgtctcctcaaccacgacgccagcgccgagaccaccaacaccggcg cccaccatcgctcgagccccctgtccctgcgcccagaggcgtgccggccagcgg cgggggcgcgagtgacacgagggggctggacttcgcctgtgatatctacatctg ggcgcccttggcgggacttgtggggctccttctcctgtcactggttatcaccctt tactgcaaacggggcagaaagaaactcctgtatatattcaaacaaccatttatga gaccagtacaaactactcaagaggaagatggctgtagctgccgatttccagaaga agaagaaggaggatgtgaactgagagtgaagttcagcaggagcgcagacgcccc gcgtacaagcagggccagaaccagctctataacgagctcaatctaggacgaagag aggagtacgatgttttgacaagagacgtggcgggaccctgagatggggggaaa gccgagaaggaagaaccctcaggaaggcctgtacaatgaactgcagaaagataag atggcggaggcctacagtgaattgggatgaaaggcgagcgccggaggggcaagg ggcacgatggccttaccaggggtctcagtacagccaccaaggacacctacgacgc ccttcacatgcaggccctgccccctgc
CTL019 Full - aa	956	MALPVTALLLPLALLLHAARPdiqmtqttsslsaslgdrvtiscrasqdiskyl nwyqqkpdgtvkllyhtsrhsgvpsrfsrgsgtdysltisnleqediatyfcq qgntlpytfgggtkleitggggsgggsggggsevglqesgpglvapsqslsvtc tvsgvslpdygvswirqprrkglewlgviwgsettyynsalksrhtiikdnksq vflkmnslqtddtaiyycahyyyggsyamywgqgtsvtvssttppaprpptpa ptiasqplslrpeacrpaaggavhtrglfdacdiyiwaplagtcgvllslvitl yckrgkrklllyifkqpfmrpvqttqeedgcscrpfpeeeeggcclrvkfsrsadap aykqqgnqlynelnlgrreeydvldkrrgrdpemggkprkrnpqeglynelqkdk maeyseigmkgerrrgkghdglyqglstatkdydalhmqalppr
CTL019 scFv domain	957	diqmtqttsslsaslgdrvtiscrasqdiskylnwyqqkpdgtvkllyhtsrh sgvpsrfsrgsgtdysltisnleqediatyfcqgntlpytfgggtkleitggg gsgggsggggsevglqesgpglvapsqslsvtcvsgvslpdygvswirqprrk glewlgviwgsettyynsalksrhtiikdnksqvflkmnslqtddtaiyycah yyyggsyamywgqgtsvtvss
mCAR1 scFv	983	QVQLLES GAELVRPGSSVKISCKASGYAFSSYWMNWVKQRPGQGLEWIGQIYPGD GDTNNGKFKGQATLTADKSSSTAYMQLSGLTSEDSAVYSCARKTISSVDFYFD YWGQGTTVTGGSGGGSGGGSGGGSELVLTQSPKFMSTSVGDRVSVTCKASQNVG TNVAWYQQKPGQSPKPLIYSATYRNSGVPRFTGSGSGTDFTLTITNVQSKDLAD YFCQYNRYPYTSFFFTKLEIKRRS
mCAR1 Full - aa	984	QVQLLES GAELVRPGSSVKISCKASGYAFSSYWMNWVKQRPGQGLEWIGQIYPGD GDTNNGKFKGQATLTADKSSSTAYMQLSGLTSEDSAVYSCARKTISSVDFYFD YWGQGTTVTGGSGGGSGGGSGGGSELVLTQSPKFMSTSVGDRVSVTCKASQNVG TNVAWYQQKPGQSPKPLIYSATYRNSGVPRFTGSGSGTDFTLTITNVQSKDLAD YFCQYNRYPYTSFFFTKLEIKRRSKIIEVMYPPPYLDNEKSNGTIIHVKGKHLCP SPLFPGPSKPFWLVVVGVLACYLLVTVAFIIFWVRSKRSRLHSDYMMTPRR PGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYD VLDKRRGRDPGEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHG

		LYQGLSTATKDTYDALHMQALPPR
mCAR2 scFv	985	DIQMTQTTSSLSASLGDRVTISCRASQDISKYLNWYQQKPDGTVKLLIYHSTRLH SGVPSRFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPYTFGGGKLEITGST SGSGKPGSGEGSTKGEVKLQESGPGLVAPSQSLSVTCTVSGVSLPDYGVSWIRQP PRKGLEWLGVIWGSETTYYNALKSRLTIKDNSKSQVFLKMNSLQTDDETAIYYC AKHYYYGGSYAMDYWGQGTSTVTSSE
mCAR2 CAR - aa	986	DIQMTQTTSSLSASLGDRVTISCRASQDISKYLNWYQQKPDGTVKLLIYHSTRLH SGVPSRFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPYTFGGGKLEITGST SGSGKPGSGEGSTKGEVKLQESGPGLVAPSQSLSVTCTVSGVSLPDYGVSWIRQP PRKGLEWLGVIWGSETTYYNALKSRLTIKDNSKSQVFLKMNSLQTDDETAIY YCAKHYYYGGSYAMDYWGQGTSTVTSSESKEYGPPCPPCPMFVLLVVVGGVLACYS LLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFEEEEGGCELRV KFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDRRGRDPEMGGKPRRKNPQEG LYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR L
mCAR2 Full - aa	987	DIQMTQTTSSLSASLGDRVTISCRASQDISKYLNWYQQKPDGTVKLLI YHSTRLHSGVPSRFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPYTF GGGKLEITGSTSGSGKPGSGEGSTKGEVKLQESGPGLVAPSQSLSVTCT VSGVSLPDYGVSWIRQPPRKGLEWLGVIWGSETTYYNALKSRLTIKDN SKSQVFLKMNSLQTDDETAIYYCAKHYYYGGSYAMDYWGQGTSTVTSSES KEYGPPCPPCPMFVLLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIF KQPFMRPVQTTQEEDGCSCRFEEEEGGCELRVKFSRSADAPAYQQGQNQL YNELNLGRREEYDVLDRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAY SEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPRLEGGGEGRGS LLTCGDVEENPGPRMLLLVTSLLLCELPHFAFLIPRKVCNGIGIGEFKD SLSINATNIKHFKNCTSIGDLHILPVAFRGDSFTHTPPLDPQELDILKT VKEITGFLLIQAWPENRTDLHAFENLEIIRGRKQHGQFSLAVVSLNITS LGLRSLKEISDGDVVISGNKNLCYANTINWKKLFGTSGQKTKIISNRGEN SCKATGQVCHALCSPEGCWGPEPRDCVSCRNVSRGRECDKCNLLEGEPR EFVENSECIQCHPECLPQAMNITCTGRGPDNCIQCAHYIDGPHCVKTCPA GVMGENNTLVWKYADAGHVC HLCHPNCTYGCTGPGLEGCP TNGPKIP SIA TGMVGALLLL LVVALGIGLF M
mCAR3 scFv	988	DIQMTQTTSSLSASLGDRVTISCRASQDISKYLNWYQQKPDGTVKLLIYHSTRLH SGVPSRFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPYTFGGGKLEITGST SGSGKPGSGEGSTKGEVKLQESGPGLVAPSQSLSVTCTVSGVSLPDYGVSWIRQP PRKGLEWLGVIWGSETTYYNALKSRLTIKDNSKSQVFLKMNSLQTDDETAIYYC AKHYYYGGSYAMDYWGQGTSTVTSSE
mCAR3 Full - aa	989	DIQMTQTTSSLSASLGDRVTISCRASQDISKYLNWYQQKPDGTVKLLIYHSTRLH SGVPSRFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPYTFGGGKLEITGST SGSGKPGSGEGSTKGEVKLQESGPGLVAPSQSLSVTCTVSGVSLPDYGVSWIRQP PRKGLEWLGVIWGSETTYYNALKSRLTIKDNSKSQVFLKMNSLQTDDETAIYYC AKHYYYGGSYAMDYWGQGTSTVTSSEAAIEVMYPPPYLDNEKSNGTIIHVKGKHL CPSPFLFPGPSKPFVLLVVVGGVLACYSLLVTVAFIIFWVRSKRSLRLHSDYMNMT PRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRRE EYDVLDRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKG

		HDGLYQGLSTATKDTYDALHMQALPPR
SSJ25-C1 VH sequence	379	QVQLLESGLVLRPGSSVKISCKASGYAFSSYWMNWVKQRPGQGLEWIGQIYPGD GDTNNGKFKGQATLTADKSSSTAYMQLSGLTSEDSAVYSCARKTISVVDYFD YWGQGTITV
SSJ25-C1 VL sequence	380	ELVLTQSPKFMSTSVGDRVSVTCKASQNVGTNVAWYQQKPGQSPKPLIYSATYRN SGVPDRFTGSGSGTDFTLTITNVQSKDLADYFYFCQYNRYPYTSGGGTKLEIKRR S

In some embodiments, the CD19 CAR or binding domain includes the amino acid sequence of CTL019, or is encoded by the nucleotide sequence of CTL019 according to Table 5 with or without the leader sequence or the his tag, or a sequence substantially identical thereto (e.g., at least 85%, 90%, 95% or higher identity).

In some embodiments, the CDRs are defined according to the Kabat numbering scheme, the Chothia numbering scheme, or a combination thereof.

The sequences of humanized CDR sequences of the scFv domains are shown in Table 15B for the heavy chain variable domains and in Table 15C for the light chain variable domains. "ID" stands for the respective SEQ ID NO for each CDR.

Table 15B. Heavy Chain Variable Domain CDRs (according to Kabat)

Candidate	FW	HCDR1	SEQ		HCDR2	SEQ		HCDR3	SEQ	
			ID			ID			ID	
murine_CART19		DYGVS	958		VIWGSETTYNSALKS	959		HYYYGGSYAMDY	960	
humanized_CART19 a	VH4	DYGVS	958		VIWGSETTYYS SS SLKS	961		HYYYGGSYAMDY	960	
humanized_CART19 b	VH4	DYGVS	958		VIWGSETTYYQ SS SLKS	962		HYYYGGSYAMDY	960	
humanized_CART19 c	VH4	DYGVS	958		VIWGSETTYYNS SS SLKS	963		HYYYGGSYAMDY	960	

Table 15C Light Chain Variable Domain CDRs (according to Kabat)

Candidate	FW	LCDR1	SEQ		LCDR2	SEQ		LCDR3	SEQ	
			ID			ID			ID	

			ID		ID		ID
murine_CART19		RASQDISKYLN	964	HTSRLHS	965	QQGNTLPYT	966
humanized_CART19 a	VK3	RASQDISKYLN	964	HTSRLHS	965	QQGNTLPYT	966
humanized_CART19 b	VK3	RASQDISKYLN	964	HTSRLHS	965	QQGNTLPYT	966
humanized_CART19 c	VK3	RASQDISKYLN	964	HTSRLHS	965	QQGNTLPYT	966

In one embodiment, the CAR comprises a CAR molecule comprising a BCMA antigen binding domain (e.g., a murine, human or humanized antibody or antibody fragment that specifically binds to BCMA, e.g., human BCMA), a transmembrane domain, and an intracellular signaling domain (e.g., an intracellular signaling domain comprising a costimulatory domain and/or a primary signaling domain).

Exemplary CAR molecules are provided in Table 16, or Table 1 of WO2016/014565, or as otherwise described herein. The CAR molecules in Table 16 comprise a BCMA antigen binding domain, e.g., an amino acid sequence of any BCMA antigen binding domain provided in Table 11 or 12.

Table 16. Exemplary CAR molecules. Sequences are provided with a leader sequence.

Name/ Description	SEQ ID NO:	Sequence
139109		
139109- aa Full CAR	789	MALPVTALLLPLALLLHAARPEVQLVESGGGLVQPGGSLRLSCAVSGFALS NHGMSWVRRAPGKGLEWVSGIVYSGSTYYAASVKGRFTISRDNSTNTLYL QMNSLRPEDTAIYYCSAHGGESDVWGQGTITVTVSSASGGGGSGGRASG GGGSDIQLTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPKAPKLL IYAASSLQSGVPSRFSGSGSGTDFLTISLQPEDFATYYCQSYSTPYTF GQGTKVEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDF ACDIYWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEE DGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEY DVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGER RRGKGHDGLYQGLSTATKDTYDALHMQALPPR
139109- nt Full CAR	790	ATGGCCCTCCCTGTACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTC CACGCCGCTCGGCCCGAAGTGCAATTGGTGGAATCAGGGGGAGGACT TGTGCAGCCTGGAGGATCGCTGAGACTGTCATGTGCCGTGTCCGGCTT TGCCCTGTCCAACCACGGGATGTCCTGGGTCCGCCGCGCGCCTGGAA AGGGCCTCGAATGGGTGTCTGGGTATTGTGTACAGCGGTAGCACCTACT ATGCCGCATCCGTGAAGGGGAGATTCACCATCAGCCGGGACAACCTCCA GGAACACTCTGTACCTCCAAATGAATTCGCTGAGGCCAGAGGACACTG CCATCTACTACTGCTCCGCGCATGGCGGAGAGTCCGACGTCTGGGGA CAGGGGACCAACCGTGACCGTGTCTAGCGCGTCCGGCGGAGGCGGCA GCGGGGGTCCGGCATCAGGGGGCGGCGGATCGGACATCCAGCTCAC CCAGTCCCCGAGCTCGCTGTCCGCTCCGTGGGAGATCGGGTCACCA TCACGTGCCGCGCCAGCCAGTCGATTCCTCCTACCTGAACTGGTACC

		AACAGAAGCCCGGAAAAAGCCCCGAAGCTTCTCATCTACGCCGCCTCGA GCCTGCAGTCAGGAGTGCCCTCACGGTTCTCCGGCTCCGGTTCCGGTA CTGATTTACCCTGACCATTTCTCCCTGCAACCGGAGGACTTCGCTAC TTACTACTGCCAGCAGTCGTACTCCACCCCTACACTTTCGGACAAGGC ACCAAGGTCGAAATCAAGACCACTACCCAGCACCGAGGCCACCCACC CCGGCTCCTACCATCGCCTCCCAGCCTCTGTCCCTGCGTCCGGAGGCA TGTAGACCCGCAGCTGGTGGGGCCGTGCATACCCGGGGTCTTGACTT CGCCTGCGATATCTACATTTGGGCCCCCTCTGGCTGGTACTTGCGGGGT CCTGCTGCTTTCACTCGTGATCACTCTTTACTGTAAGCGCGGTGCGAAG AAGCTGCTGTACATCTTTAAGCAACCCTTCATGAGGCCTGTGCAGACTA CTCAAGAGGAGGACGGCTGTTTCATGCCGGTTCCAGAGGAGGAGGAA GGCGGCTGCGAACTGCGCGTGAAATTCAGCCGCAGCGCAGATGCTCC AGCCTACAAGCAGGGGCAGAACAGCTCTACAACGAACTCAATCTTG TCGGAGAGAGGAGTACGACGTGCTGGACAAGCGGAGAGGACGGGACC CAGAAATGGGCGGGAAGCCGCGCAGAAAGAATCCCCAAGAGGGCCTG TACAACGAGCTCCAAAAGGATAAGATGGCAGAAGCCTATAGCGAGATT GGTATGAAAGGGGAACGCAGAAAGAGGCAAAGGCCACGACGGACTGTA CCAGGGACTCAGCACCGCCACCAAGGACACCTATGACGCTCTTCACAT GCAGGCCCTGCCGCCTCGG
139103		
139103- aa Full CAR	791	MALPVTALLPLALLHAARPQVQLVESGGGLVQPGRSLRLSCAASGFTFS NYAMSWVRQAPGKGLGWVSGISRSGENTYYADSVKGRFTISRDN SKNTL YLQMNSLRDEDTAVYYCARSPAHYYGMDVWGQGTTVTVSSASGGGGS GGRASGGGGS DIVLTQSPGTLSPGERATLSCRASQSISSSFLAWYQQK PGQAPRLLIYGASRRATGIPDRFSGSGSGTDFTLTISRLEPEDSAVYYCQQ YHSSPSWTFGQGTKLEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGG AVHTRGLDFACDIYWAPLAGTCGVLLSLVITLYCKRGRKKLLYIFKQPFMR PVQTTQEEDGCSRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNEL NLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYS EIGMKGERRRRGKGDGLYQGLSTATKDTYDALHMQALPPR
139103- nt Full CAR	792	ATGGCCCTCCCTGTCAACGCCCTGCTGCTTCCGCTGGCTCTTCTGCTC CACGCCGCTCGGCCCAAGTGCAACTCGTGGAATCTGGTGGAGGACT CGTGCAACCCGGAAGATCGCTTAGACTGTCTGTGCCGCCAGCGGGTT CACTTTCTCGAACTACGCGATGTCTGCGGTCCGCCAGGCACCCGAAAA GGGACTCGGTTGGGTGTCCGGCATTTCCCGGTCCGGCGAAAAATACCTA CTACGCCGACTCCGTGAAGGGCCGCTTACCATCTCAAGGGACAACAG CAAAAACACCCTGTACTTGCAAATGAACTCCCTGCGGGATGAAGATACA GCCGTGTACTATTGCGCCCGGTGCGCTGCCATTACTACGGCGGAATG GACGTCTGGGGACAGGGAACCACTGTGACTGTCAGCAGCGCGTCCGG TGGCGGCGGCTCAGGGGGTCCGGCCTCCGGGGGGGGAGGGTCCGAC ATCGTGCTGACCCAGTCCCCGGGAACCCTGAGCCTGAGCCCGGGAGA GCGCGCGACCCTGTCATGCCGGGCATCCAGAGCATTAGCTCCTCCTT TCTCGCCTGGTATCAGCAGAAGCCCCGACAGGCCCCGAGGCTGCTGA TCTACGGCGCTAGCAGAAGGGCTACCGGAATCCAGACCGGTTCTCCG GCTCCGGTTCCGGGACCGATTTACCCCTTACTATCTCGCGCCTGGAAC CTGAGGACTCCGCCGTCTACTACTGCCAGCAGTACCACTCATCCCCGT CGTGGACGTTCCGACAGGGCACCAAGCTGGAGATTAAGACCACTACCC CAGCACCGAGGCCACCCACCCCGGCTCCTACCATCGCCTCCCAGCCT CTGTCCCTGCGTCCGGAGGCATGTAGACCCGCAGCTGGTGGGGCCGT GCATACCCGGGGTCTTGACTTGCCTGCGATATCTACATTTGGGCCCC TCTGGCTGGTACTTGCGGGGTCTGCTGCTTTCACTCGTGATCACTCTT TACTGTAAGCGCGGTGCGGAAGAAGCTGCTGTACATCTTTAAGCAACCCT TCATGAGGCCTGTGCAGACTACTCAAGAGGAGGACGGCTGTTTCATGCC GGTTCCCAGAGGAGGAGGAAGGCGGCTGCGAACTGCGCGTGAAATTC AGCCGCAGCGCAGATGCTCCAGCCTACAAGCAGGGGCAGAACCAAGCT

		CTACAACGAACTCAATCTTGGTCGGAGAGAGGAGTACGACGTGCTGGA CAAGCGGAGAGGACGGGACCCAGAAATGGGCGGGAAGCCGCGCAGA AAGAATCCCCAAGAGGGCCTGTACAACGAGCTCCAAAAGGATAAGATG GCAGAAGCCTATAGCGAGATTGGTATGAAAGGGGAACGCAGAAGAGG CAAAGGCCACGACGACTGTACCAGGGACTCAGCACCGCCACCAAGG ACACCTATGACGCTCTTCACATGCAGGCCCTGCCGCTCGG
139105		
139105- aa Full CAR	793	MALPVTALLLPLALLLHAARPQVQLVESGGGLVQPGRSLRLSCAASGFTFD DYAMHWVRQAPGKGLEWVSGISWNSGSGYADSVKGRFTISRDNKNSL YLQMNSLR AEDTALYYCSVHSLAYWGQGLTVTVSSASGGGGSGGRASG GGGSDIVMTQTPLSLPVTGPGEPAISCRSSQSLLHSNGYNYLDWYLQKPG QSPQLLIYLGSNRASGVDPDRFSGSGSDFTLTKISRVEAEDVGYYCMQA LQTPYTFGQGTKVEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAV HTRGLDFACDIYWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPV QTTQEEDGCSCRFPEEEEGGCEL RVKFSRSADAPAYKQGQNQLYNELNL GRREEYDVLDKRRGRDPENMGKPRRKNPQEGLYNELQKDKMAEAYSEIG MKGERRRGKHGHDGLYQGLSTATKDTYDALHMQALPPR
139105- nt Full CAR	794	ATGGCCCTCCCTGTACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTC CACGCCGCTCGGCCCAAGTCAACTCGTCAATCCGGTGGAGGTCT GGTCCAACCTGGTAGAAGCCTGAGACTGTCGTGTGCGGCCAGCGGATT CACCTTTGATGACTATGCTATGCACTGGGTGCGGCAGGCCAGGAAA GGGCCTGGAATGGGTGTCGGGAATTAGCTGGAACCTCGGGTCCATTG GCTACGCCGACTCCGTGAAGGGCCGCTTCACCATCTCCCGCACAAC GCAAAGAACTCCCTGTACTTGCAAATGAACTCGCTCAGGGCTGAGGAT ACCGCGCTGTACTACTGCTCCGTGCATTCTTCTGCGCTACTGGGGA CAGGGAACCTCTGGTCACCGTGTGAGCGCCTCCGGCGGCGGGGGCTC GGGTGGACGGGCCTCGGGCGGAGGGGGGTCCGACATCGTGATGACC CAGACCCCGCTGAGCTTGCCCGTGA CTCCCGGAGAGCCTGCATCCATC TCCTGCCGGTCATCCAGTCCCTTCTCCACTCCAACGGATACTACTACC TCGACTGGTACCTCCAGAAGCCGGGACAGAGCCCTCAGCTTCTGATCT ACCTGGGGTCAAATAGAGCCTCAGGAGTGCCGGATCGGTTACGCGGAT CTGGTTCGGGAAC TGATTTCACTCTGAAGATTTCCCGCGTGGAAGCCG AGGACGTGGGCGTCTACTACTGTATGCAGGCGCTGCAGACCCCTATA CCTTCGGCCAAGGGACGAAAGTGAGATCAAGACCACTACCCAGCAC CGAGGCCACCCACCCCGGCTCCTACCATCGCCTCCAGCCTCTGTCCC TGCGTCCGGAGGCATGTAGACCCGCAGCTGGTGGGGCCGTGCATACC CGGGGTCTTGACTTCGCCTGCGATATCTACATTTGGGCCCTCTGGCT GGTACTTGCGGGGTCTGCTGCTTTCACTCGTGATCACTCTTTACTGTA AGCGCGGTGCGGAAGAAGCTGCTGTACATCTTTAAGCAACCTTCATGA GGCCTGTGCAGACTACTCAAGAGGAGGACGGCTGTTTCATGCCGTTCC CAGAGGAGGAGGAAGGCGGCTGCGAACTGCGCGTGAAATTCAGCCGC AGCGCAGATGCTCCAGCCTACAAGCAGGGGCAGAACCAAGCTCTACAAC GAACTCAATCTTGGTCGGAGAGAGGAGTACGACGTGCTGGACAAGCG GAGAGGACGGGACCCAGAAATGGGCGGGAAGCCGCGCAGAAAGAATC CCCAAGAGGGCCTGTACAACGAGCTCCAAAAGGATAAGATGGCAGAAG CCTATAGCGAGATTGGTATGAAAGGGGAACGCAGAAGAGGCAAAGGCC ACGACGGA CTGTACCAGGGACTCAGCACCGCCACCAAGGACACCTATG ACGCTCTTCACATGCAGGCCCTGCCGCTCGG
139111		
139111- aa Full CAR	795	MALPVTALLLPLALLLHAARPEVQLLESGGGLVQPGSLRLSCAVSGFALS NHGMSWVRRAPGKGLEWVSGIVYSGSTYYAASVKGRFTISRDNARNLTL QMNSLRPEDTAIYYCSAHGGESDVWGQGTTVTVSSASGGGGSGGRASG GGGSDIVMTQTPLSLSVTPGQPASISCKSSQSLLRNDGKTPLYWYLQKAG QPPQLLIYEVSNRFSGVDPDRFSGSGSDFTLTKISRVEAEDVGAYYCMQNI QFPSFGGGTKLEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHT RGLDFACDIYWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQ

		TTQEEDGCSCRFPEEEEEGGCELRVKFSRSADAPAYKQGQNLQLYNELNLGRREEYDVLDRRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHGDLQGLSTATKDTYDALHMQALPPR
139111- nt Full CAR	796	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTC CACGCCGCTCGGCCCGAAGTGCAATTGTTGGAATCTGGAGGAGGACTT GTGCAGCCTGGAGGATCACTGAGACTTTCGTGTGCGGTGTCAGGCTTC GCCCTGAGCAACCACGGCATGAGCTGGGTGCGGAGAGCCCCGGGGAA GGGTCTGGAATGGGTGTCCGGGATCGTCTACTCCGGTTCAACTTACTA CGCCGCAAGCGTGAAGGGTCGCTTACCATTTCGCCGATAACTCCCG GAACACCCTGTACCTCCAAATGAACTCCCTGCGGCCCGAGGACACCGC CATCTACTACTGTTCCGCGCATGGAGGAGAGTCCGATGTCTGGGGACA GGGCACTACCGTGACCGTGTGAGCGCCTCGGGGGGAGGAGGCTCC GGCGGTGCGGCCTCCGGGGGGGGTGGCAGCGACATTGTGATGACGC AGACTCCACTCTCGCTGTCCGTGACCCCGGGACAGCCCGCGTCCATCT CGTGCAAGAGCTCCCAGAGCCTGCTGAGGAACGACGGAAAGACTCCT CTGTATTGGTACCTCCAGAAGGCTGGACAGCCCCCGCAACTGCTCATC TACGAAGTGTCAAATCGCTTCTCCGGGGTGC GGATCGGTTTTCCGGC TCGGGATCGGGCACCGACTTCACCCTGAAAATCTCCAGGGTCGAGGCC GAGGACGTGGGAGCCTACTACTGCATGCAAAACATCCAGTTCCCTTCC TTCGGCGGGCGGCACAAAGCTGGAGATTAAGACCACTACCCAGCACCG AGGCCACCCACCCCGGCTCCTACCATCGCCTCCAGCCTCTGTCCCTG CGTCCGGAGGCATGTAGACCCGCAGCTGGTGGGGCGGTGCATACCCG GGGTCTTGACTTCGCCTGCGATATCTACATTTGGGCCCTCTGGCTGG TACTTGCGGGTCTGCTGCTTTCACTCGTGATCACTCTTTACTGTAAG CGCGGTGCGGAAGAAGCTGCTGTACATCTTTAAGCAACCCTTCATGAGG CCTGTGCAGACTACTCAAGAGGAGGACGGCTGTTTCATGCCGGTTCCCA GAGGAGGAGGAAGGCGGTGCGAACTGCGCGTGAAATTCAGCCGCAG CGCAGATGCTCCAGCCTACAAGCAGGGGCAGAACCAGCTCTACAACGA ACTCAATCTTGGTCGGAGAGAGGAGTACGACGTGCTGGACAAGCGGA GAGGACGGGACCCAGAAATGGGCGGGAAGCCGCGCAGAAAGAATCCC CAAGAGGGCCTGTACAACGAGCTCCAAAAGGATAAGATGGCAGAAGCC TATAGCGAGATTGGTATGAAAGGGGAACGCAGAAGAGGCAAAGGCCAC GACGGACTGTACCAGGGAAGTACGACCCGCCACCAAGGACACCTATGAC GCTCTTCACATGCAGGCCCTGCCGCCTCGG
139100		
139100- aa Full CAR	797	MALPVTALLPLALLHAARPQVQLVQSGAEVRKTGASVKVSKASGYIFD NFGINWVRQAPGQGLEWMGWINPKNNNTNYAQKFQGRVTITADESTNTA YMEVSSLRSED TAVYYCARGPYYYQSYMDVWGQGTMTVSSASGGGGS GGRASGGGSDIVMTQTPLSLPVTPEPASISCRSSQSLLHSNGYNLW YLQKPGQSPQLLIYLGSKRASGVPDRFSGSGSGTDFTLHITRVGAEDGVY YCMQALQTPYTFGQGTKLEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPA AGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKLLYIFKQ PFMRPVQTTQEEDGCSCRFPEEEEEGGCELRVKFSRSADAPAYKQGQNLQ LYNELNLGRREEYDVLDRRRGRDPEMGGKPRRKNPQEGLYNELQKDKMA EAYSEIGMKGERRRGKGHGDLQGLSTATKDTYDALHMQALPPR
139100- nt Full CAR	798	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTC CACGCCGCTCGGCCCGAAGTCCAACCTCGTCCAGTCCGGCGCAGAAGT CAGAAAAACCGGTGCTAGCGTGAAAGTGTCTGCAAGGCCTCCGGCTA CATTTTCGATAACTTCGGAATCAACTGGGTGAGACAGGCCCGGGCCA GGGGCTGGAATGGATGGGATGGATCAACCCCAAGAACAACAACACCAA CTACGCACAGAAGTTCCAGGGCCGCGTGACTATCACCGCCGATGAATC GACCAATACCGCCTACATGGAGGTGTCCTCCCTGCGGTGCGAGGACAC TGCCGTGTATTACTGCGCGAGGGGGCCCATACTACTACCAAAGCTACAT GGACGTCTGGGGACAGGGAACCATGGTGACCGTGTGATCCGCCTCCG GTGGTGGAGGCTCCGGGGGGCGGGCTTCAGGAGGCGGAGGAAGCGA TATTGTGATGACCCAGACTCCGCTTAGCCTGCCCGTGACTCCTGGAGA

		ACCGGCCTCCATTTCTGCCGGTCTCGCAATCACTCCTGCATTCCAAC GGTTACAACTACCTGAATTGGTACCTCCAGAAGCCTGGCCAGTCGCCC CAGTTGCTGATCTATCTGGGCTCGAAGCGCGCCTCCGGGGTGCCTGAC CGGTTTAGCGGATCTGGGAGCGGCACGGACTTCACTCTCCACATCACC CGCGTGGGAGCGGAGGACGTGGGAGTGTACTACTGTATGCAGGCGCT GCAGACTCCGTACACATTCGGACAGGGCACCAAGCTGGAGATCAAGAC CACTACCCAGCACCAGAGGCCACCCACCCCGGCTCCTACCATCGCCTC CCAGCCTCTGTCCCTGCGTCCGGAGGCATGTAGACCCGCAGCTGGTG GGGCCGTGCATAACCCGGGGTCTTGACTTCGCCTGCGATATCTACATTT GGGCCCCCTCTGGCTGGTACTTGCGGGGTCTGCTGCTTTCACTCGTGA TCACTCTTTACTGTAAGCGCGGTTCGGAAGAAGCTGCTGTACATCTTAA GCAACCCTTCATGAGGCCTGTGCAGACTACTCAAGAGGAGGACGGCTG TTCATGCCGGTTCCAGAGGAGGAGGAAGGCGGCTGCGAACTGCGCG TGAAATTCAGCCGCAGCGCAGATGCTCCAGCCTACAAGCAGGGGCAGA ACCAGCTCTACAACGAACCTCAATCTTGGTTCGGAGAGAGGAGTACGACG TGCTGGACAAGCGGAGAGGACGGGACCCAGAAATGGGCGGGAAGCC GCGCAGAAAGAATCCCCAAGAGGGCCTGTACAACGAGCTCCAAAAGGA TAAGATGGCAGAAGCCTATAGCGAGATTGGTATGAAAGGGGAACGCAG AAGAGGCAAAGGCCACGACGACTGTACCAGGGACTCAGCACCGCCA CCAAGGACACCTATGACGCTCTTCACATGCAGGCCCTGCCGCTCGG
139101		
139101- aa Full CAR	799	MALPVTALLPLALLHAARPQVQLQESGGGLVQPGGSLRLSCAASGFTFS SDAMTWVRQAPGKLEWVSVISGSGGTTYADSVKGRFTISRDN SKNTLY LQMNSLRAEDTAVYYCAKLDSSGYYYARGPRYWQGTLTVSSASGGGG SGGRASGGGSDIQLTQSPSSLSASVGDRTITCRASQSISSYLNWYQQK PGKAPKLLIYGASTLASGVPARFSGSGSHTFTLTINSLQSEDSATYYCQQ SYKRASFGQGTKEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAV HTRGLDFACDIYWAPLAGTCGVLLLSLVITLYCKRGRKLLYIFKQPFMRPV QTTQEEDGCSCRFPEEEEGGCEL RVKFSRSADAPAYKQGQNQLYNELNL GRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIG MKGERRRRGKGHDLGYQLSTATKDTYDALHMQALPPR
139101- nt Full CAR	800	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTC CACGCCGCTCGGCCCAAGTGCAACTTCAAGAATCAGGCGGAGGACT CGTGCAGCCCGGAGGATCATTGCGGCTCTCGTGCGCCGCTCGGGCT TCACCTTCTCGAGCGACGCCATGACCTGGGTCCGCCAGGCCCGGGG AAGGGGCTGGAATGGGTGTCTGTGATTTCCGGCTCCGGGGGAACCTAC GTACTACGCCGATTCCGTGAAAGGTGCGCTTCACTATCTCCCGGGACAA CAGCAAGAACACCCCTTATCTGCAAAATGAATCCCTCCGCGCCGAGGA CACCGCCGTGTACTACTGCGCCAAGCTGGACTCCTCGGGCTACTACTA TGCCCGGGGTCCGAGATACTGGGGACAGGGAACCTCGTGACCGTGT CCTCCGCGTCCGGCGGAGGAGGGTCCGGAGGGCGGGCCTCCGGCGG CGGCGGTTCCGACATCCAGCTGACCCAGTCCCACCTCACTGAGCGC AAGCGTGGGCGACAGAGTCACCATTACATGCAGGGCGTCCCAGAGCAT CAGCTCCTACCTGAACTGGTACCAACAGAAGCCTGGAAGGCTCCTAA GCTGTTGATCTACGGGGCTTCGACCCCTGGCATCCGGGGTGCCCGCGA GGTTTAGCGGAAGCGGTAGCGGCACTCACTTCACTCTGACCATTAAACA GCCTCCAGTCCGAGGATTCAGCCACTTACTACTGTCAGCAGTCCTACAA GCGGGCCAGCTTCGGACAGGGCACTAAGGTGAGATCAAGACCACTA CCCCAGCACCGAGGCCACCCACCCCGGCTCCTACCATCGCCTCCAG CCTCTGTCCCTGCGTCCGGAGGCATGTAGACCCGCAGCTGGTGGGGC CGTGCATACCCGGGGTCTTGACTTCGCCTGCGATATCTACATTTGGGC CCCTCTGGCTGGTACTTGCGGGGTCTGCTGCTTTCACTCGTGATCAC TCTTTACTGTAAGCGCGGTTCGGAAGAAGCTGCTGTACATCTTTAAGCAA CCCTTCATGAGGCCTGTGCAGACTACTCAAGAGGAGGACGGCTGTTCA TGCCGGTTCCAGAGGAGGAGGAAGGCGGCTGCGAACTGCGCGTGAA ATTCAGCCGCAGCGCAGATGCTCCAGCCTACAAGCAGGGGCAGAACC

		AGCTCTACAACGAACCTCAATCTTGGTCCGAGAGAGGAGTACGACGTGC TGGACAAGCGGAGAGGACGGGACCCAGAAATGGGCGGGAAGCCGCG CAGAAAGAATCCCCAAGAGGGCCTGTACAACGAGCTCCAAAAGGATAA GATGGCAGAAGCCTATAGCGAGATTGGTATGAAAGGGGAACGCAGAAG AGGCAAAGGCCACGACGGACTGTACCAGGGACTCAGCACCGCCACCA AGGACACCTATGACGCTCTTCACATGCAGGCCCTGCCGCCTCGG
139102		
139102- aa Full CAR	801	MALPVTALLLPLALLLHAARPQVQLVQSGAEVKKPGASVKVSCKASGYTFS NYGITWVRQAPGQGLEWMGWISAYNGNTNYAQKFQGRVTMTRNTSISTA YMESSLRSEDYAVYYCARGPYYYMDVWVGKGTMTVSSASGGGGSGG RASGGGGSEIVMTQSPLSLPVTPEPASISCRSSQSLLYSNGYNYVDWYL QKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKQISRVEAEDVGIYYC MQGRQFPYSFGQGTKEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAG GAVHTRGLDFACDIYWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPF MRPVQTTQEEDGCSRFPEEEEEGGCELRVKFSRSADAPAYKQGQNQLYN ELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAY SEIGMKGERRRRGKHDGLYQGLSTATKDTYDALHMQALPPR
139102- nt Full CAR	802	ATGGCCCTCCCTGTACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTC CACGCCGCTCGGCCCAAGTCCAAGTGGTCCAGAGCGGTGCAGAAGT GAAGAAGCCCCGAGCGAGCGTGAAAGTGTCTGCAAGGCTTCCGGGT ACACCTTCTCCAAGTACGGCATCACTTGGGTGCGCCAGGCCCGGGAC AGGGCCTGGAATGGATGGGGTGGATTTCGCGGTACAACGGCAATACGA ACTACGCTCAGAAGTTCCAGGGTAGAGTGACCATGACTAGGAACACCT CCATTTCCACCGCCTACATGGAAGTGTCTCCCTGCGGAGCGAGGACA CCGCCGTGTACTATTGCGCCCGGGACCATACTACTACTACATGGATG TCTGGGGGAAGGGGACTATGGTCACCGTGTATCCGCTCGGGAGGC GGCGGATCAGGAGGACGCGCCTCTGGTGGTGGAGGATCGGAGATCGT GATGACCCAGAGCCCTCTCTCCTTGCCCGTGACTCCTGGGGAGCCCG CATCCATTTATGCGGAGCTCCAGTCACTTCTCTACTCCAACGGCTA TAACTACGTGGATTGGTACCTCCAAAAGCCGGGCCAGAGCCCGCAGCT GCTGATCTACCTGGGCTCGAACAGGGGCCAGCGGAGTGCTGACCGGT TCTCCGGGTGCGGAAGCGGGACCGACTTCAAGCTGCAAATCTCGAGA GTGGAGGCCGAGGACGTGGGAATCTACTACTGTATGCAGGGCCGCCA GTTTCCGTACTCGTTCGGACAGGGCACCAAAGTGGAATCAAGACCAC TACCCAGCACCGAGGCCACCCACCCCGGCTCCTACCATCGCCTCCCA GCCTCTGTCCCTGCGTCCGGAGGCATGTAGACCCGCAGCTGGTGGGG CCGTGCATACCCGGGGTCTTGACTTCGCCTGCGATATCTACATTTGGG CCCCTCTGGCTGGTACTTGCGGGGTCTGCTGCTTTCACTCGTGATCA CTCTTTACTGTAAGCGCGGTGCGAAGAAGCTGCTGTACATCTTTAAGCA ACCCTTCATGAGGCCTGTGCAGACTACTCAAGAGGAGGACGGCTGTTC ATGCCGTTCCAGAGGAGGAGGAAGGCGGCTGCGAACTGCGCGTGA AATTCAGCCGCAGCGCAGATGCTCCAGCCTACAAGCAGGGGGCAGAAC CAGCTCTACAACGAACCTCAATCTTGGTCCGAGAGAGGAGTACGACGTG CTGGACAAGCGGAGAGGACGGGACCCAGAAATGGGCGGGGAAGCCGC GCAGAAAGAATCCCCAAGAGGGCCTGTACAACGAGCTCCAAAAGGATA AGATGGCAGAAGCCTATAGCGAGATTGGTATGAAAGGGGAACGCAGAA GAGGCAAAGGCCACGACGGACTGTACCAGGGACTCAGCACCGCCACC AAGGACACCTATGACGCTCTTCACATGCAGGCCCTGCCGCCTCGG
139104		
139104- aa Full CAR	803	MALPVTALLLPLALLLHAARPEVQLLETGGGLVQPGGSLRLSCAVSGFALS NHGMSWVRRAPGKGLEWVSGIVYSGSTYYAASVKGRFTISRDNSRNTLYL QMNSLRPEDTAIYYCSAHGGESDVWQGTTVTVSSASGGGGSGGRASG GGGSEIVLTQSPATLSVSPGESATLSCRASQSVSSNLAWYQKPGQAPRL LIYGASTRASGIPDRFSGSGSGTDFTLTISLQAEDVAVYYCQYQYSSSLTF GGGKVEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDF ACDIYWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEE

		DGCSCRFPEEEEEGGCEL RVKFSRSADAPAYKQGQNQLYNELNLGRREEY DVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGER RRGKGHDGLYQGLSTATKDTYDALHMQALPPR
139104- nt Full CAR	804	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTC CACGCCGCTCGGCCCGAAGTGCAATTGCTCGAACTGGAGGAGGTCT GGTGCAACCTGGAGGATCACTTCGCCTGTCCTGCGCCGTGTCGGGCTT TGCCCTGTCCAACCATGGAATGAGCTGGGTCCGCCGCGCGCCGGGGA AGGGCCTCGAATGGGTGTCCGGCATCGTCTACTCCGGCTCCACCTACT ACGCCGCGTCCGTGAAGGGCCGGTTCACGATTTACAGGGACAACCTCG CGGAACACCCTGTACCTCCAAATGAATTCCCTTCGGCCGGAGGATACT GCCATCTACTACTGCTCCGCCACGGTGGCGAATCCGACGTCTGGGG CCAGGGAACCACCGTGACCGTGTCCAGCGCGTCCGGGGGAGGAGGAA GCGGGGGTAGAGCATCGGGTGGAGGCGGATCAGAGATCGTGCTGACC CAGTCCCCCGCCACCTTGAGCGTGTACCAGGAGAGTCCGCCACCCT GTCATGCCGCGCCAGCCAGTCCGTGTCCTCCAACCTGGCTTGGTACCA GCAGAAGCCGGGGCAGGCCCCCTAGACTCCTGATCTATGGGGCGTCA CCCGGGCATCTGGAATTCCCGATAGGTTACAGCGGATCGGGCTCGGGC ACTGACTTCACTCTGACCATCTCCTCGCTGCAAGCCGAGGACGTGGCT GTGTACTACTGTCAGCAGTACGGAAGCTCCCTGACTTTCCGTGGCGGG ACCAAAGTCGAGATTAAGACCACTACCCAGCACCGAGGCCACCCACC CCGGCTCCTACCATCGCCTCCAGCCTCTGTCCCTGCGTCCGGAGGCA TGTAGACCCGCGAGCTGGTGGGGCCGTGCATACCCGGGGTCTTGACTT CGCCTGCGATATCTACATTTGGGCCCTCTGGCTGGTACTTGCGGGGT CCTGCTGCTTTCACTCGTGATCACTCTTTACTGTAAGCGCGGTGCGAAG AAGCTGCTGTACATCTTTAAGCAACCCTTCATGAGGCCTGTGCAGACTA CTCAAGAGGAGGACGGCTGTTTCATGCCGTTCCAGAGGAGGAGGAA GGCGGCTGCGAACTGCGCGTGAAATTCAGCCGCGAGCGCAGATGCTCC AGCCTACAAGCAGGGGCAGAACCAGCTCTACAACGAACTCAATCTTGG TCGGAGAGAGGAGTACGACGTGCTGGACAAGCGGAGAGGACGGGACC CAGAAATGGGCGGGAAGCCGCGCAGAAAGAATCCCCAAGAGGGCCTG TACAACGAGCTCCAAAAGGATAAGATGGCAGAAGCCTATAGCGAGATT GGTATGAAAGGGGAACGCAGAAGAGGCAAAGGCCACGACGGACTGTA CCAGGGACTCAGCACCGCCACCAAGGACACCTATGACGCTCTTCACAT GCAGGCCCTGCCGCCTCGG
139106		
139106- aa Full CAR	805	MALPVTALLPLALLHAARPEVQLVETGGGLVQPGGSLRLSCAVSGFALS NHGMSWVRRAPGKGLEWVSGIVYSGSTYYAASVKGRFTISRDNSENTRYL QMNSLRPEDTAIYYCSAHGGESDVWGQGTTVTVSSASGGGGSGGRASG GGGSEIVMTQSPATLSVSPGERATLSCRASQSVSSKLAWYQQKPGQAPR LLMYGASIRATGIPDRFSGSGSGTEFTLTISLEPEDFAVYYCQQYSSSW TFGQGTKVEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGL DFACDIYIWAPLAGTCGVLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQ EEDGDCSCRFPEEEEEGGCEL RVKFSRSADAPAYKQGQNQLYNELNLGRRE EYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGE RRRKGHDGLYQGLSTATKDTYDALHMQALPPR
139106- nt Full CAR	806	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTC CACGCCGCTCGGCCCGAAGTGCAATTGGTGGAACCTGGAGGAGGACT TGTGCAACCTGGAGGATCATTGAGACTGAGCTGCGCAGTGTCCGGATT CGCCCTGAGCAACCATGGAATGTCCTGGGTGAGAAGGGCCCTGGAA AAGGCCTCGAATGGGTGTACGGGATCGTGTACTCCGGTTCCACTTACT ACGCCGCTCCGTGAAGGGGCGCTTCACTATCTACAGGGATAACTCCC GCAATACCCTGTACCTCCAAATGAACAGCCTGCGGCCGGAGGATACCG CCATCTACTACTGTTCCGCCACGGTGGAGAGTCTGACGTCTGGGGCC AGGGAACCTACCGTGACCGTGTCTCCGCGTCCGGCGGTGGAGGGAGC GGCGGCCGCGCCAGCGGCGGCGGAGGCTCCGAGATCGTGATGACCC AGAGCCCCGCTACTCTGTCGGTGTGCGCCGGAGAAAGGGCGACCTG

		TCCTGCCGGGCGTTCGCAGTCCGTGAGCAGCAAGCTGGCTTGGTACCA GCAGAAGCCGGGCCAGGCACCACGCCTGCTTATGTACGGTGCCTCCA TTCGGGCCACCGGAATCCCGGACCGGTTCTCGGGGTCTGGGTCCGGT ACCGAGTTCACACTGACCATTTCCTCGCTCGAGCCCCGAGGACTTTGCC GTCTATTACTGCCAGCAGTACGGCTCCTCCTCATGGACGTTTCGGCCAG GGGACCAAGGTCGAAATCAAGACCACTACCCCAGCACCGAGGCCACC CACCCCGGCTCCTACCATCGCCTCCAGCCTCTGTCCCTGCGTCCGGA GGCATGTAGACCCGCAGCTGGTGGGGCCGTGCATACCCGGGGTCTTG ACTTCGCCTGCGATATCTACATTTGGGCCCTCTGGCTGGTACTTGCG GGGTCTGCTGCTTTCACTCGTGATCACTCTTACTGTAAGCGCGGTGCG GAAGAAGCTGCTGTACATCTTTAAGCAACCCTTCATGAGGCCTGTGCAG ACTACTCAAGAGGAGGACGGCTGTTTCATGCCGGTTCACAGAGGAGGA GGAAGGCGGCTGCGAACTGCGCGTGAAATTCAGCCGCAGCGCAGATG CTCCAGCCTACAAGCAGGGGCAGAACCAAGCTCTACAACGAACTCAATC TTGGTCGGAGAGAGGAGTACGACGTGCTGGACAAGCGGAGAGGACGG GACCCAGAAATGGGCGGGAAGCCGCGCAGAAAGAATCCCCAAGAGGG CCTGTACAACGAGCTCCAAAAGGATAAGATGGCAGAAGCCTATAGCGA GATTGGTATGAAAGGGGAACGCAGAAAGAGGCAAGGCCACGACGGAC TGTACCAGGGACTCAGCACCGCCACCAAGGACACCTATGACGCTCTTC ACATGCAGGCCCTGCCGCCTCGG
139107		
139107- aa Full CAR	807	MALPVTALLPLALLHAARPEVQLVETGGGVVQPGGSLRLSCAVSGFALS NHGMSWVRRAPGKGLEWVSGIVYSGSTYYAASVKGRFTISRDNSTNTLYL QMNSLRPEDTAIYYCSAHGGESDVWGQGTTVTVSSASGGGGSGGRASG GGGSEIVLTQSPGTLSPGERATLSCRASQSVGSTNLAWYQQKPGQAP RLLIYDASNRTGIPDRFSGGSGTDFTLTISRLEPEDFAVYYCQQYGSSP PWTFGQGTKVEIKTTTPAPRPPTPAPTASQPLSLRPEACRPAAGGAVHTR GLDFACDIYWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTT QEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRR EEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKG ERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
139107- nt Full CAR	808	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTC CACGCCGCTCGGCCCGAAGTGCAATTGGTGGAGACTGGAGGAGGAGT GGTGCAACCTGGAGGAAGCCTGAGACTGTCATGCGCGGTGTCGGGCT TCGCCCTCTCCAACCACGAATGTCCTGGGTCCGCCGGGCCCTGGG AAAGGACTTGAATGGGTGTCCGGCATCGTGTACTCGGGTTCACCTAC TACGCGGCCTCAGTGAAGGGCCGGTTTACTATTAGCCGCGACAACCTCC AGAAACACACTGTACCTCCAAATGAACTCGCTGCGGCCGGAAGATACC GCTATCTACTACTGCTCCGCCCATGGGGGAGAGTTCGGACGTCTGGGG ACAGGGCACCACTGTCACTGTGTCCAGCGCTTCCGGCGGTGGTGGAA GCGGGGGACGGGCCTCAGGAGGCGGTGGCAGCGAGATTGTGCTGAC CCAGTCCCCCGGGACCTGAGCCTGTCCCCGGGAGAAAGGGGCCACCC TCTCCTGTGCGGCATCCCAGTCCGTGGGGTCTACTAACCTTGCATGGT ACCAGCAGAAGCCCGGCCAGGCCCTCGCCTGCTGATCTACGACGCG TCCAATAGAGCCACCGGCATCCCGGATCGCTTCAGCGGAGGCGGATC GGGCACCGACTTCACCCTCACCATTTCAGGCTGGAACCGGAGGACTT CGCCGTGTACTACTGCCAGCAGTATGGTTCGTCCCCACCCTGGACGTT CGGCCAGGGGACTAAGGTGAGATCAAGACCACTACCCAGCACCGA GGCACCCACCCCGGCTCCTACCATCGCCTCCAGCCTCTGTCCCTGC GTCCGGAGGCATGTAGACCCGCAGCTGGTGGGGCCGTGCATACCCGG GGTCTTGACTTCGCCTGCGATATCTACATTTGGGCCCTCTGGCTGGTA CTTGCGGGGTCTGCTGCTTTCACTCGTGATCACTCTTACTGTAAGCG CGGTGCGAAGAAGCTGCTGTACATCTTTAAGCAACCCTTCATGAGGCC TGTGCAGACTACTCAAGAGGAGGACGGCTGTTTCATGCCGGTTCACAGA GGAGGAGGAAGGCGGCTGCGAACTGCGCGTGAAATTCAGCCGCAGCG CAGATGCTCCAGCCTACAAGCAGGGGCAGAACCAAGCTCTACAACGAAC

		TCAATCTTGGTCGGAGAGAGGAGTACGACGTGCTGGACAAGCGGAGA GGACGGGACCCAGAAATGGGCGGGAAGCCGCGCAGAAAGAATCCCCA AGAGGGCCTGTACAACGAGCTCCAAAAGGATAAGATGGCAGAAGCCTA TAGCGAGATTGGTATGAAAGGGGAACGCAGAAGAGGCCAAAGGCCACG ACGGACTGTACCAGGGACTCAGCACCGCCACCAAGGACACCTATGACG CTCTTCACATGCAGGCCCTGCCGCTCGG
139108		
139108- aa Full CAR	809	MALPVTALLLPLALLLHAARPQVQLVESGGGLVKPGGSLRLSCAASGFTFS DYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRFTISRDNKNSLYL QMNSLRAEDTAVYYCARESGDGMVWVGQTTVTVSSASGGGGSGGRA SGGGGSDIQMTQSPSSLSASVGDRTITCRASQSISSYLNWYQQKPGKAP KLLIYAASSLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYTLAF GQGTKVDIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDF ACDIYWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEE DGCSCRFPEEEEEGGCELRVKFSRSADAPAYKQGQNLYNELNLGRREEY DVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGER RRGKGHDGLYQGLSTATKDTYDALHMQALPPR
139108- nt Full CAR	810	ATGGCCCTCCCTGTACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTC CACGCCGCTCGGCCCAAGTGCAACTCGTGGAATCTGGTGGAGGACT CGTGAAACCTGGAGGATCATTGAGACTGTCATGCGCGGCCTCGGGATT CACGTTCTCCGATTACTACATGAGCTGGATTCCGAGGCTCCGGGGAA GGGACTGGAATGGGTGTCTCTACATTTCTCATCCGCTCCACCATCTA CTACGCGGACTCCGTGAAGGGGAGATTACCATTAGCCGCGATAACGC CAAGAACAGCCTGTACCTTCAGATGAACTCCCTGCGGGCTGAAGATAC TGCCGTCTACTACTGCGCAAGGGAGAGCGGAGATGGGATGGACGTCT GGGGACAGGGTACCACTGTGACCGTGTCTGTCGGCCTCCGGCGGAGGG GGTTCGGGTGGAAGGGGCCAGCGGCGGCGGAGGCAGCGACATCCAGA TGACCCAGTCCCCCTCATCGCTGTCCGCTCCGTGGGCGACCGCGTC ACCATCACATGCCGGGCCTCACAGTCGATCTCCTCCTACCTCAATTGGT ATCAGCAGAAGCCCGGAAAGGCCCTAAGCTTCTGATCTACGCAGCGT CCTCCCTGCAATCCGGGGTCCCATCTCGGTTCTCCGGCTCGGGCAGC GGTACCGACTTCACTCTGACCATCTCGAGCCTGCAGCCGGAGGACTTC GCCACTTACTACTGTGAGCAAAGCTACACCCTCGCGTTTGGCCAGGGC ACCAAAGTGGACATCAAGACCACTACCCAGCACCGAGGCCACCCACC CCGGCTCCTACCATCGCCTCCCAGCCTCTGTCCCTGCGTCCGGAGGCA TGTAGACCCCGCAGCTGGTGGGGCCGTGCATACCCGGGGTCTTGACTT CGCCTGCGATATCTACATTTGGGCCCTCTGGCTGGTACTTGCGGGGT CCTGCTGCTTTCACTCGTGATCACTCTTTACTGTAAGCGCGGTGCGAAG AAGCTGCTGTACATCTTTAAGCAACCCTTCATGAGGCCTGTGCAGACTA CTCAAGAGGAGGACGGCTGTTTCATGCCGTTCCAGAGGAGGAGGAA GGCGGCTGCGAACTGCGCGTGAAATTCAGCCGCAGCGCAGATGCTCC AGCCTACAAGCAGGGGCAGAACCAGCTCTACAACGAACTCAATCTTGG TCGGAGAGAGGAGTACGACGTGCTGGACAAGCGGAGGACGGGACC CAGAAATGGGCGGGAAGCCGCGCAGAAAGAATCCCCAAGAGGGCCTG TACAACGAGCTCCAAAAGGATAAGATGGCAGAAGCCTATAGCGAGATT GGTATGAAAGGGGAACGCAGAAGAGGCAAAGGCCACGACGACTGTA CCAGGGAATCAGCACCGCCACCAAGGACACCTATGACGCTCTTCACAT GCAGGCCCTGCCGCTCGG
139110		
139110- aa Full CAR	811	MALPVTALLLPLALLLHAARPQVQLVQSGGGLVKPGGSLRLSCAASGFTFS DYMSWIRQAPGKGLEWVSYISSSGNTIYYADSVKGRFTISRDNKNSLYL QMNSLRAEDTAVYYCARSTMVREDYWGQGLTVTVSSASGGGGSGGRAS GGGGSDIVLTQSPLSLPVTLGQPASISCKSSESLVHNSGKTYLNWFHQR GQSPRRLIYEVSNRDSGVPDRFTGSGSGTDFTLKISRVEAEDVGVYYCMQ GTHWPGTFGQGTKLEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGA VHTRGLDFACDIYWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRP

		VQTTQEEDGCSCRFPEEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELN LGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEI GMKGERRRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
139110- nt Full CAR	812	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTC CACGCCGCTCGGCCCAAGTGCAACTGGTGCAAAGCGGAGGAGGATT GGTCAAACCCGGAGGAAGCCTGAGACTGTCATGCGCGGCCTCTGGATT CACCTTCTCCGATTACTACATGTCATGGATCAGACAGGCCCCGGGGAA GGGCCTCGAATGGGTGTCTACATCTCGTCCTCCGGGAACACCATCTA CTACGCCGACAGCGTGAAGGGCCGCTTTACCATTTCGCCGACAACGC AAAGAACTCGCTGTACCTTCAGATGAATTCCTGCGGGCTGAAGATACC GCGGTGTACTATTGCGCCCGGTCCACTATGGTCCGGGAGGACTACTGG GGACAGGGCACACTCGTGACCGTGTCCAGCGCGAGCGGGGGTGGAG GCAGCGGTGGACGCGCCTCCGGCGGGCGGCGGTTTCAGACATCGTGCTG ACTCAGTCGCCCCCTGTCGCTGCCGGTCACCCTGGGCCAACCGGCCTC AATTAGCTGCAAGTCCTCGGAGAGCCTGGTGCACAACTCAGGAAAGAC TTACCTGAACTGGTTCATCAGCGGCCTGGACAGTCCCCACGGAGGCT CATCTATGAAGTGTCCAACAGGGATTCCGGGGGTGCCGACCGCTTCAC TGGCTCCGGGTCCGGCACCGACTTCACCTTGAAAATCTCCAGAGTGA AGCCGAGGACGTGGGCGTGTACTACTGTATGCAGGGTACCCACTGGC CTGGAACCTTTGGACAAGGAACCTAAGCTCGAGATTAAGACCACTACCC CAGCACCGAGGCCACCCACCCCGGCTCCTACCATCGCCTCCAGCCT CTGTCCCTGCGTCCGGAGGCATGTAGACCCGCAGCTGGTGGGGCCGT GCATACCCGGGGTCTTGACTTCGCCTGCGATATCTACATTTGGGCCCC TCTGGCTGGTACTTGCGGGGTCTGCTGCTTTCACTCGTGATCACTCTT TACTGTAAGCGCGGTGCGGAAGAAGCTGCTGTACATCTTTAAGCAACCT TCATGAGGCCTGTGCAGACTACTCAAGAGGAGGACGGCTGTTTCATGCC GGTTCCAGAGGAGGAGGAAGGCGGCTGCGAACTGCGCGTGAAATTC AGCCGCAGCGCAGATGCTCCAGCCTACAAGCAGGGGCAGAACCAGCT CTACAACGAACTCAATCTTGTCGGAGAGAGGAGTACGACGTGCTGGA CAAGCGGAGAGGACGGGACCCAGAAATGGGCGGGAAGCCGCGCAGA AAGAATCCCCAAGAGGGCCTGTACAACGAGCTCCAAAAGGATAAGATG GCAGAAGCCTATAGCGAGATTGGTATGAAAGGGGAACGCAGAAGAGG CAAAGGCCACGACGGACTGTACCAGGGACTCAGCACCGCCACCAAGG ACACCTATGACGCTCTTCACATGCAGGCCCTGCCGCTCGG
139112		
139112- aa Full CAR	813	MALPVTALLPLALLHAARPQVQLVESGGGLVQPGGSLRLSCAVSGFALS NHGMSWVRRAPGKGLEWVSGIVYSGSTYYAASVKGRFTISRDNSTNTLYL QMNSLRPEDTAIYYCSAHGGESDVWGQGTITVTVSSASGGGGSGGRASG GGGSDIRLTQSPSPLSASVGDRTITCQASEDINKFLNWHQTPGKAPKLLI YDASTLQTGVPSRFSGSGSGTDFTLINSLQPEDIGTYCQYQYESLPLTFG GGTKVEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFA CDIYIWAPLAGTCGVLLLSLVITLYCKRGRKLLYIFKQPFMRPVQTTQEED GCSCRFPEEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLRREEYD VLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERR RGKGHDGLYQGLSTATKDTYDALHMQALPPR
139112- nt Full CAR	814	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTC CACGCCGCTCGGCCCAAGTGCAACTCGTGGAATCTGGTGGAGGACT CGTGCAACCCGGTGGAAGCCTTAGGCTGTCGTGCGCCGTCAGCGGGT TTGCTCTGAGCAACCATGGAATGTCTGGGTCCGCCGGGCACCGGGA AAAGGGCTGGAATGGGTGTCCGGCATCGTGACAGCGGGTCAACCTAT TACGCCGCGTCCGTGAAGGGCAGATTCACTATCTCAAGAGACAACAGC CGGAACACCCTGTACTTGCAATGAATTCCTGCGCCCCGAGGACACC GCCATCTACTACTGCTCCGCCACGGAGGAGAGTCCGACGTGTGGGG CCAGGGAACGACTGTGACTGTGTCCAGCGCATCAGGAGGGGGTGGTT CGGGCGGCCGGGCTCGGGGGGAGGAGGTTCCGACATTCCGCTGAC CCAGTCCCCGTCCCCACTGTCCGGCTCCGTCCGGCAGCCGCTGACCA

		TCACTTGT CAGGCGTCCGAGGACATTAACAAGTTCCTGAACTGGTACCA CCAGACCCCTGGAAAGGCCCCCAAGCTGCTGATCTACGATGCCTCGAC CCTTCAAACCTGGAGTGCCTAGCCGTTCTCCGGGTCCGGCTCCGGCAC TGATTTCACTCTGACCATCAACTCATTGCAGCCGGAAGATATCGGGACC TACTATTGCCAGCAGTACGAATCCCTCCCGCTCACATTCCGGCGGGGA ACCAAGGTCGAGATTAAGACCACTACCCAGCACCAGAGGCCACCCACC CCGGCTCCTACCATCGCCTCCCAGCCTCTGTCCCTGCGTCCGGAGGCA TGTAGACCCGCAGCTGGTGGGGCCGTGCATACCCGGGGTCTTGAATT CGCCTGCGATATCTACATTTGGGCCCTCTGGCTGGTACTTGCGGGGT CCTGCTGCTTTCACTCGTGATCACTCTTTACTGTAAGCGCGGTGCGAAG AAGCTGCTGTACATCTTTAAGCAACCCTTCATGAGGCCTGTGCAGACTA CTCAAGAGGAGGACGGCTGTTTCATGCCGGTTCAGAGAGGAGGAGGAA GGCGGCTGCCAACTGCGCGTGAAATTCAGCCGCAGCGCAGATGCTCC AGCCTACAAGCAGGGGCAGAACAGCTCTACAACGAACTCAATCTTGG TCGGAGAGAGGAGTACGACGTGCTGGACAAGCGGAGAGGACGGGACC CAGAAATGGGCGGGAAGCCGCGCAGAAAGAATCCCCAAGAGGGCCTG TACAACGAGCTCCAAAAGGATAAGATGGCAGAAGCCTATAGCGAGATT GGTATGAAAGGGGAACGCAGAAAGGCAAAGGCCACGACGGACTGTA CCAGGACTCAGCACCGCCACCAAGGACACCTATGACGCTCTTACAT GCAGGCCCTGCCGCTCGG
139113		
139113- aa Full CAR	815	MALPVTALLPLALLHAARPEVQLVETGGGLVQPGGSLRLSCAVSGFALS NHGMSWVRRAPGKGLEWVSGIVYSGSTYYAASVKGRFTISRDNSTNTLYL QMNSLRPEDTAIYYCSAHGGESDVWGQGTTVTVSSASGGGGSGGRASG GGGSETTLTQSPATLSVSPGERATLSCRASQSVGSNLAWYQKPGQGPR LLIYGASTRATGIPARFSGSGSTEFTLTISLQPEDFAVYYCQQYNDWLPV TFGQGTKVEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGL DFACDIYWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQ EEDGCSCRFPEEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRRE EYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGE RRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
139113- nt Full CAR	816	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTC CACGCCGCTCGGCCCGAAGTGCAATTGGTGGAACCTGGAGGAGGACT TGTGCAACCTGGAGGATCATTGCGGCTCTCATGCGCTGTCTCCGGCTT CGCCCTGTCAAATCACGGGATGTCGTGGGTGACAGCGGGCCCCGGGAA AGGGTCTGGAATGGGTGTCGGGGATTGTGTACAGCGGCTCCACCTACT ACGCCGCTTCGGTCAAGGGCCGCTTCACTATTTACGGGACAACAGCC GCAACACCCTCTATCTGCAAATGAACTCTCTCCGCCCGGAGGATACCG CCATCTACTACTGCTCCGCACACGGCGGCGAATCCGACGTGTGGGGA CAGGGAACCACTGTCACCGTGTCTGTCGCGCATCCGGTGGCGGAGGATC GGGTGGCCGGGCTCCGGGGGCGGCGGCAGCGAGACTACCCTGACC CAGTCCCCTGCCACTCTGTCCGTGAGCCCGGGAGAGAGAGCCACCCT TAGCTGCCGGGCCAGCCAGAGCGTGGGCTCCAACCTGGCCTGGTACC AGCAGAAGCCAGGACAGGGTCCCAGGCTGCTGATCTACGGAGCCTCC ACTCGCGCGACCGGCATCCCCGCGAGGTTCTCCGGGTCCGGTTCCGG GACCGAGTTCACCCTGACCATCTCCTCCCTCCAACCGGAGGACTTCGC GGTGTACTACTGTGACAGTACAACGATTGGCTGCCCGTGACATTTGG ACAGGGGACGAAGGTGGAAATCAAAACCACTACCCAGCACCGAGGC CACCCACCCCGGCTCCTACCATCGCCTCCCAGCCTCTGTCCCTGCGTC CGGAGGCATGTAGACCCGCAGCTGGTGGGGCCGTGCATACCCGGGGT CTTGACTTCGCTGCGATATCTACATTTGGGCCCTCTGGCTGGTACTT GCGGGGTCCTGCTGCTTTCACTCGTGATCACTCTTTACTGTAAGCGCG GTCGGAAGAAGCTGCTGTACATCTTTAAGCAACCCTTCATGAGGCCTGT GCAGACTACTCAAGAGGAGGACGGCTGTTTCATGCCGGTTCAGAGGA GGAGGAAGGCGGCTGCGAACTGCGCGTGAAATTCAGCCGCAGCGCAG ATGCTCCAGCCTACAAGCAGGGGCAGAACCAAGCTCTACAACGAACTCA

		ATCTTGGTCGGAGAGAGGAGTACGACGTGCTGGACAAGCGGAGAGGA CGGGACCCAGAAATGGGCGGGAAGCCGCGCAGAAAGAATCCCCAAGA GGGCCTGTACAACGAGCTCCAAAAGGATAAGATGGCAGAAGCCTATAG CGAGATTGGTATGAAAGGGGAACGCAGAAGAGGCCAAAGGCCACGACG GACTGTACCAGGGACTCAGCACCGCCACCAAGGACACCTATGACGCTC TTCACATGCAGGCCCTGCCGCCTCGG
139114		
139114- aa Full CAR	817	MALPVTALLLPLALLHAARPEVQLVESGGGLVQPGGSLRLSCAVSGFALS NHGMSWVRRAPGKGLEWVSGIVYSGSTYYAASVKGRFTISRDNRSNTLYL QMNSLRPEDTAIYYCSAHGGESDVWQQGTTVTVSSASGGGGSGGRASG GGGSEIVLTQSPGTLSPGERATLSCRASQSIGSSSLAWYQQKPGQAPR LLMYGASSRASGIPDRFSGSGSDFTLTISRLEPEDFAVYYCQQYAGSPP FTFGQGTKEIKTTTPAPRPPTPAPTASQPLSLRPEACRPAAGGAVHTRG LDFACDIYWAPLAGTCGVLLLSLVITLYCKRGRKLLYIFKQPFMRPVQTTQ EEDGCSCRFPEEEEEGGCELRVKFSRSADAPAYKQGQNLYNELNLGRRE EYDVLDKRRGRDPENGGKPRRKNPQEGLYNELQDKMAEAYSEIGMKGE RRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
139114- nt Full CAR	818	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTC CACGCCGCTCGGCCCGAAGTGCAATTGGTGGAATCTGGTGAGGACTT GTGCAACCTGGAGGATCACTGAGACTGTCATGCGCGGTGTCCGGTTTT GCCCTGAGCAATCATGGGATGTCGTGGGTCCGGCGGCCCGCCGAA GGGTCTGGAATGGGTGTCGGGTATCGTCTACTCCGGGAGCACTTACTA CGCCGCGAGCGTGAAGGGCCGCTTACCATTTCGCCGATAACTCCC GCAACACCCTGTACTTGCAAATGAACTCGCTCCGGCCTGAGGACACTG CCATCTACTACTGCTCCGCACACGGAGGAGAATCCGACGTGTGGGGCC AGGGAACCTACCGTGACCGTCAGCAGCGCCTCCGGCGGGCGGGGCTCA GGCGGACGGGCTAGCGGCGGCGGTGGCTCCGAGATCGTGCTGACCC AGTCGCCTGGCACTCTCTCGCTGAGCCCCGGGGAAGGGCAACCCTG TCCTGTCGGGCCAGCCAGTCCATTGGATCATCCTCCCTCGCCTGGTAT CAGCAGAAACCGGGACAGGCTCCGCGGCTGCTTATGTATGGGGCCAG CTCAAGAGCCTCCGGCATTCCCGACCGGTTCTCCGGGTCCGGTTCCG GCACCGATTTACCCCTGACTATCTCGAGGCTGGAGCCAGAGGACTTCG CCGTGTACTACTGCCAGCAGTACGCGGGGTCCCCGCCGTTACGTTTCG GACAGGGAACCAAGGTCGAGATCAAGACCACTACCCAGCACCGAGG CCACCCACCCCGGCTCCTACCATCGCCTCCAGCCTCTGTCCCTGCGT CCGGAGGCATGTAGACCCGCAGCTGGTGGGGCCGTGCATACCCGGGG TCTTGACTTCGCCTGCGATATCTACATTTGGGCCCTCTGGCTGGTACT TGCGGGGTCTGCTGCTTTCACTCGTGATCACTCTTTACTGTAAGCGCG GTCCGAAGAAGCTGCTGTACATCTTTAAGCAACCCTTCATGAGGCCTGT GCAGACTACTCAAGAGGAGGACGGCTGTTTCATGCCGTTCCCAGAGGA GGAGGAAGGCGGCTGCGAACTGCGCGTGAAATTCAGCCGCAGCGCAG ATGCTCCAGCCTACAAGCAGGGGCAGAACCAGCTCTACAACGAACCTCA ATCTTGGTCGGAGAGAGGAGTACGACGTGCTGGACAAGCGGAGAGGA CGGGACCCAGAAATGGGCGGGAAGCCGCGCAGAAAGAAATCCCCAAGA GGGCCTGTACAACGAGCTCCAAAAGGATAAGATGGCAGAAGCCTATAG CGAGATTGGTATGAAAGGGGAACGCAGAAGAGGCCAAAGGCCACGACG GACTGTACCAGGGACTCAGCACCGCCACCAAGGACACCTATGACGCTC TTCACATGCAGGCCCTGCCGCCTCGG
149362		
149362-aa Full CAR	819	malpvtalllplallhaarqvqlqesgpglvkpsetlsltctvsggsissyywgywirpppgklewigsi yygsayynpslksrvtsivdtsknqfslrsvtaadtavyycarhwqewpdafdiwgqgmvvtvssgg ggsgggsgggsggsetltqspafmsatpgdkviiskasqdiddamnwyqqkpgeaplfiiqsatpvp gipprfsgsgfgtdfsltinnesedaayyfcldhndfpltfqggtkleikttppaprpptpaptiasqplslrpea crpaaggavhtrglfacdiywaplagtcgvllslvitlyckrgrklllyifkqpfmrpvqtteedgcscrfpe eeeggcelrvkfsrsadapaykqgqnllynlnlgrreeydvldkrrgrdpemggkprrrknppqeglynel qkdkmaeayseigmkgerrrgkghdglyqglstatkdydalhmqalppr

149362-nt Full CAR	820	atggccctccctgtaccgcccctgctgcttccgctggctcttctgctccacgcccgtcggccccaagtgcag cttcaggaaagcggaccgggctgtgtaagccatccgaaactcttccctgacttgactgtgtctggcg gttccatctcatgctgtactactactgggctggattaggcagccgcccggaaagggactggagtggat cggaagcatctactattccggctcggcgtactacaaccctagcctcaagtcgagagtaccatctccgtg gatacctccaagaaccagtttccctgcgctgagctccgtgaccgcccgtgacaccgcccgtgtactactg tgctcggcattggcaggaatggcccgatgcttcgacatttggggccagggcactatggtcactgtgtcatc cgggggtggaggcagcgggggaggagggtccggggggggagggtcagagacaaccttgaccaggt caccgcattcatgtccgcccactccgggagacaaggatcatctctgtgcaaacggtcccaggatatcga cgatgccatgaattggtaccagcagaagcctggcgaagcgccgctgttcattatccaatccgcaacctcg cccgtgcctggaatccaccgcggttcagcggcagcggttcggaaccgacttttccctgaccattaacaa cattgagtcaggagcggcctactacttctgctgcaacacgacaacttccctctacggttcggccagg gaaccaagctggaaatcaagaccactaccccagcaccgaggccaccaccccggctctaccatcgc ctcccagcctctgctcctgctcggaggcatgtagaccgcagctgggtggggccgtgcatacccgggggt cttgacttcgctgcgatactacatttggggccctctgctggttacttgccgggtctgtctgttctactcgtga tactctttactgtaagcgggtcggagaagctgtgtacatctttaagcaaccttcatgaggcctgtgca gactactcaagaggaggacggctgttcatgcccgttcccagaggaggaggaaggcggctgcgaactg cgcgtaaatcagccgcagcgcagatgtccagcctacaagcaggggcagaaccagctctacaacg aactcaatcttgctcggagagaggagtacgacgtgctggacaagcggagaggacgggaccagaaa tgggcgggaagccgcgagaaagaatcccaagaggcctgtacaacgagctccaaaaggataag atggcagaagcctatagcgagattggtatgaaaggggaacgcagaagaggcaaaaggccacgacgg actgtaccagggactcagcaccgcccaccaaggacacctatgacgctcttcacatgcaggccctgcgcgc tcgg
149363		
149363-aa Full CAR	821	malpvtallplallhaarqvnlresgpalkvptqtlitctfsgfslrtsgmcvswirppgkalewlaridwd edkfystslktrltiskdtsdnqvvlrmtndpadtatyycarsgaggsatafdiwwpgtmvvtssggggs ggggsggggsdiqmtqspsslsasvgrvritcrasqdiynnlawfqlkpgsaprslymaanksqsgvp srfsgsasgtdftltisslqpedfatyyqhyrpfysfgggtkleiktttpprptpaptiasqpslrpeacrp aaggavhtrgldfacdiyiwaplagtcgvllslvitlyckrgrklliyifkqpfmrpvqtteedgcsrfpeee eggcelrvkfsrsadapaykqqnqllynelnlgrreeydvldkrgrdpemggkprkrnpqeglynelqk dkmaeayseigmkgerrrgkghdglyqglstatkdydalhmqalppr
149363-nt Full CAR	822	atggccctccctgtaccgcccctgctgcttccgctggctcttctgctccacgcccgtcggccccaagtcaatc tgcggaatccggcccccgctgtgtaagcctaccagaccctactctgacctgtacttctccggcttctc cctcgggacttccgggatgtgctgtcctggatcagacagcctccgggaaaggccctggagtggctcgtc cgattgactgggatgaggacaagttctactccactcactcaagaccaggctgaccatcagcaaagat acctctgacaaccaagtgggtgctccgcatgaccaacatggaccagccgacactgccacttactactgc gcgaggagcggagcgggcggaacctccgccaccgcttcgatattggggcccggtaccatggtcac cgtgtcaagcggaggaggggggtccggggcgcggttccgggggaggcggatcggacattcagat gactcagtcaccatcgtccctgagcgttagcgtgggcgacagagtgaacatcacttgcgggcatccca ggacatctataacaaccttgcgtggtccagctgaagcctggttccgcaccgcggtcacttatgtacgccg ccaacaagagccagtcgggagtgccgtcccgggttttccgggtcggcctcgggaactgacttaccctgac gatctccagcctgaacccgaggatttgcgcacctactactgccagcactactaccgcttccctactcgttc ggacagggaaccaagctggaaatcaagaccactaccccagcaccgaggccaccaccccggctcct accatcgctcccagcctctgtccctgctcggaggcatgtagaccgcagctggtggggccgtgcata cccggggtcttgacttcgctgcgatactacatttggggccctctggtggttacttgccgggtcctgtgcttt cactcgtgatcactcttactgtaagcgcgggtcggaagaagctgctgtacatctttaagcaaccttcatgag gctgtgcagactactcaagaggaggacggctgttcatgcccgttccagaggaggaggaaggcggct cggaactgcgctgaaattcagccgcagcgcagatgctccagcctacaagcaggggcagaaccagct ctacaacgaactcaatcttggtcggagagaggagtacgacgtgctggacaagcggagaggacgggac ccagaaatgggcggaagcgcgcagaaagaatcccaagaggcctgtacaacgagctccaaaa ggataagatggcagaagcctatagcgagattggtatgaaaggggaacgcagaagaggcaaaaggcca cgacggactgtaccagggactcagcaccgcccaccaaggacacctatgacgctcttcacatgcaggccc tgccgctcgg
149364		
149364-aa Full CAR	823	malpvtallplallhaarpevqlvesggglvkpggsrlscaasgftfssysmnwvrqapgkglewvssis ssssyiyadvkgrftisrdnaknsllylqmnsiraedtavyycaktiaavyafdiwgggttvvtssggggs ggggsggggseivltqspslpvtpeepasiscrssqslhsngynyldwylkpggspqlllylgsnrsg

		vpdrfsgsgsgtdftlkisrveaedvgvyycmqalqtpytfqggtkleikttppaprpptpaptiasqplslrpe acrpaaggavhtrglfacdiyiwaplagtcgvllslvitlyckrgrkillyifkqpfmrpvqtteedgcsrpf eeeeggcelrvkfsrsadapaykqggnqlynelnlgrreeydvldkrrrdpemmkgprknpqeglyn elqdkmaeayseigmkgerrrgkghdglyqglstatkdydalhmqalppr
149364-nt Full CAR	824	atggccctccctgtcaccgcccgtgcttccgctggctcttctgctccacgcccgtcgccccaagtgcag ctgtcgaatccgggggggactggtaagccgggaggatcactgagactgtcctgcgcccgcagcgg cttcacgttctcctactccatgaactgggtccgccaagccccgggaagggaactggaatgggtgtcct ctatctcctcgtcgtcctacatctactacgcccactccgtgaagggaagattcaccatttcccgcgaca acgcaaagaactactgtacttgcaaatgaactcactccggggccgaagatactgctgtgtactattgcgcc aagactattgccgcccgtactcgttccgacatctggggccagggaaccaccgtgactgtgtcgtccgggtg tgggtggctcgggaggagggaagcggcgccggggggtccgagattgtgctgaccagtcgccactg agcctccctgtgaccccgagggaaccgcccagcatcagctgccggtccagccagtccttctcactcc aacggatacaattacctcgattggtaccttcagaagcctggacaaagcccgcagctgctcatctacttggg atcaaaccgcgctcaggagtgcctgaccggttctccggctcgggcagcgggtaccgatttaccctgaa aatctccagggtggaggcagaggacgtgggagtgtattactgtatgcaggcgctgcagactccgtacac atttgggcagggcaccaagctggagatcaagaccactaccccagaccgaggccaccaccccggt cctaccatcgctcccagcctctgtccctcgtccggaggcatgtagaccgcagctggtggggcgtgc atacccggggtctgacttgcctgcgatatctacatttggggccctctggctggtacttgcggggtcctgtc ctttactcgtgatcactcttactgtaagcgcggctcggaagaagctgctgtacatcttaagcaaccctcat gaggcctgtgcagactactcaagaggaggacgggtgttcagccggttccagaggaggaggaagggc ggctgcgaactgcgctgaaattcagccgcagcgcagatgtccagcctacaagcaggggcagaacc agctctacaacgaactcaatcttggtcggaagaggagtagacgtgtggaacaggcgagaggacg ggaccagaaaatgggagggaagccgcgagaaagaatccccaagaggggcctgtacaacgagctcc aaaaggataagatggcagaagcctatagcgagattggtatgaaaggggaacgcagaagaggcaaa ggccacgacggactgtaccagggactcagcaccgcccaccaaggacacctatgacgctcttcacatgca ggccctgccgctcgg
149365		
149365-aa Full CAR	825	malpvtallplalllhaarpevqlvesggglvkpggsrlscaasgftfsdymswirqapgkglewvsyis ssgstiyadsvkgrftisrdnaknslylqmnsiraedtavyycardlrgafdiwgggtmvtvssggggsg ggsggggssyvltspsvsaaapgytatiscggnnigtksvhwyqqkpgqapllvirdsvrpskipgrfs gsnsgnmatltsigvqagdeadfycqvwsdsehvvfgggtklvlttppaprpptpaptiasqplslrpea crpaaggavhtrglfacdiyiwaplagtcgvllslvitlyckrgrkillyifkqpfmrpvqtteedgcsrpf eeeggcelrvkfsrsadapaykqggnqlynelnlgrreeydvldkrrrdpemmkgprknpqeglyn elqdkmaeayseigmkgerrrgkghdglyqglstatkdydalhmqalppr
149365-nt Full CAR	826	atggccctccctgtcaccgcccgtgcttccgctggctcttctgctccacgcccgtcgccccaagtccag ctcgtggagtccggcggaggccttgtgaagcctggagggtcgtgagactgtcctgcgcccgtccggctt caccttctccgactactacatgtcctggatcagacaggccccgggaaggcctggaatgggtgtcctac atctcgtcatcgggcagcactatctactacgcccactcagtgaaagggcggttaccatttcccgggataa cggaagaactcgtgtatctgcaaatgaactcactgagggccgaggacaccgcccgtgtactactgcgc ccgcatctccgcccggcatttgacatctggggacagggaaccatggtacagtgtccagcggagggg gaggatcgggtggcggagggttccgggggtggaggctcctcctacgtgctgactcagagcccaagcgtc agcgtgcgcccgttacacggcaaccatctcctgtggcggaacaacattgggaccaagtctgtgcac tggatcagcagaagccgggccaagctcccctgttggatcccgatgactccgtgcggcctagcaaa attccgggacggttctccggtccaacagcggcaatatggcactctcaccatctcgggagtgcaggccg gagatgaagccgacttctactgccaagtctgggactcagactccgagcatgtggtgttcggggcgga ccaagctgactgtgtcaccactacccagcaccgaggccaccaccccggtcctaccatcgctccc agcctctgcccgtcgtccggaggcatgtagaccgcagctgggtggggcgtgcatacccggggtctga cttcgctgcgatatctacatttggggccctctggctggtacttgcgggggtcctgtgttctactcgtgatcact ctttactgtaagcgcggctcggaagaagctgctgtacatcttaagcaaccctcatgaggcctgtgcagact actcaagaggaggacggctgttcatgccggttccagaggagggaaggcggtgcgaactgcgcg tgaaattcagccgcagcgcagatgtccagcctacaagcaggggcagaaccagctctacaacgaact caatcttggtcggagagaggagtacgacgtgtggacaagcggagaggacgggaccagaaatggg cggaagccgcgcagaaagaatccccaagaggcctgtacaacgagctccaaaaggataagatgg cagaagcctatagcgagattggtatgaaaggggaacgcagaagaggcaaggccacgacggactgt accagggactcagcaccgcccaccaaggacacctatgacgctcttcacatgcaggccctgccgctcgg
149366		

149366-aa Full CAR	827	malpvtallplalllhaarqvqlvqsgaevkpgasvkvscpsgytvtshyihwvrrapggglewmg minpssgvtaysqtlqgrvmtsdtsstvmelssrsedtamyycaregsgsgwyfdwgrgtltvss ggggsgggsgggssyvtqppsvsvpgqtasitcsgdglskkyvswyqqkagqspvvlisrder psgipdrfsgnsadatltsigtqamdeadyycqawddttvfgggtkltvlttppaprpptpaptiasqpls lrpeacrpaaggavhtrglfacdiyiwaplagtcgvllslvitlyckrgrklllyfkqpfmrpvqttqeedgcs crfpeeeeggcelrvkfsrsadapaykqqnqlynelnlgrreeydvldkrrgrdpemggkprkrnpqeg lynelqkdkmaeayseigmkgerrrrgkghdglyqglstatkdydalhmqalppr
149366-nt Full CAR	828	atggccctccctgtcaccgcccgtgcttccgctggctcttctgctccacgcccgtcggcccaagtgcag ctgggtcagagcggggccgaagtcaagaagccgggagcctccgtgaaagtgtcctgcaagcctcgg gatacccgtagctcccactacattcattgggtccgcccggcccaaggactcagtggtatgg gcatgatcaaccctagcggcgagtgaccgcgtacagccagacgctgcagggacgctgactatgac ctcggatacctcctcctcaccgtctatatggaactgtccagcctcgggtccgaggataccgcatgtacta ctgccccgggaaggatcaggctccgggtggtatttcgacttctggggaagaggcaccctcgtgactgtg tcatctgggggaggggggttccgggtggtggcggtatcgggagggcggttcatcctacgtgctgaccag ccaccctccgtgtccgtgagccccggccagactgcacgtacattatgtagcggcgacggcctctccaag aaatacgtgtcgtgtaccagcagaaggccggacagagcccggtggtgctgtatcgaagagataagg gcgccctagcggaaatccgggacaggttctcgggttccaactccgggacactgtactctgaccatctcg gggaccaggtatggacgaagccgattactactgccaagcctgggacgacactactgtcgtgtttgga gggggcaccaagttgaccgtccttaccactacccagcaccgaggccaccaccccggtcctaccat cgctcccagcctctgtccctgcgtccggaggcatgtagaccgcagctggtggggcggtgcatacccg gggtcttgacttcgctgcgatatctacatttggccctctggctggtacttgcggggctcgtcgtcttactc gtgatcactcttactgaagcgcggtcggaagaagctgctgtacatcttaagcaaccctcatgaggcct gtgcagactactcaagaggaggacggctgttcagccggttccagaggagggaaggcggtgcg aactgcgctgaaattcagccgcagcgcatgtctccagcctacaagcaggggcagaaccagctcta caacgaactcaatcttggtcggagagaggagtacgacgtgtcggacaagcggagaggacgggaccc agaaatggcggggaagccgcgcagaaagaatcccaagagggctgtacaacgagctccaaaagg ataagatggcagaagcctatagcgagattggtatgaaaggggaacgcagaagaggcaaaggccacg acggactgtaccagggactcagcaccgccaccaaggacacctatgacgtcttcacatgcaggccctg ccgcctcgg
149367		
149367-aa Full CAR	829	malpvtallplalllhaarqvqlqesgpglvkpsqtlstctvsggsissggyywswirhpgkglewigyi yysgstyynpslksrvtsivdtsknqfslkssvtaadtavyycaragiaarlgafdiwggtmtvssggg gsgggsgggsgdivmtqspssvasvgdrviitcrasqgirnwlawyqqkpgkapnlliyaasnlgsg vpsrfsgsgadftltisslqpedvatyyccqkynsapftfpgtkvdiktppaprpptpaptiasqpls acrpaaggavhtrglfacdiyiwaplagtcgvllslvitlyckrgrklllyfkqpfmrpvqttqeedgcs crfpeeeeggcelrvkfsrsadapaykqqnqlynelnlgrreeydvldkrrgrdpemggkprkrnpqeg lynelqkdkmaeayseigmkgerrrrgkghdglyqglstatkdydalhmqalppr
149367-nt Full CAR	830	atggccctccctgtcaccgcccgtgcttccgctggctcttctgctccacgcccgtcggcccaagtgcag cttcaggagagcggcccggtactcgtgaagccgtcccagaccctgtccctgactgcaccgtgtcggga ggaagcatctcagcggaggctactattgggtcgtgattcggcagcaccctggaaaggcctggaatgg atcggctacatctactactcggctcgcactactacaacccatcgctgaagtccagagtacaatctcagt ggacacgtccaagaatcagttcagcctgaagctctctccgtgactgcggccgacacccggctgtactact gcgcacgcgctggaattgccgcccggctgaggggtgcttcgacatttggggacagggcaccatggtca ccgtgtcctccggcgggagggttccgggggtggaggctcaggaggaggggggtccgacatcgtcatg actcagtcgcccctcaagcgtcagcgcgtccgtcggggacagagtgtatcatcactgtcggcgctccag ggaattcgcaactggctggcctggtatcagcagaagcccggaaggcccccacactgttgatctacgcc gcctcaaaccctccaatccgggtgcccagccgctcagcggctccgggtcgggtgccgatttcaacttgac catctcctccctgcaacctgaagatgttggtactactactactgccaagaagtaacactccgacactttacttc ggaccggggaccaaagtggacattaagaccactacccagcaccgaggccaccaccccggtcct accatcgctcccagcctctgtccctgcgtccggaggcatgtagaccgcagctggtggggcggtgcata cccggtgttgacttcgctgcgatatctacatttggccctctggctggtacttgcggggctcgtgcttt cactcgtgatcactcttactgaagcgcggtcggaagaagctgctgtacatcttaagcaaccctcatgag gcctgtgcagactactcaagaggaggacggctgtcatgccgttcccagaggaggaggaaggcggt gcgaactgcgctgaaattcagccgcagcgcagatgtccagcctacaagcaggggcagaaccagct ctacaacgaactcaatcttggtcggagagaggagtacgacgtgtggacaagcggagaggacgggac ccagaaatggcggggaagccgcgcagaaagaatcccaagagggctgtacaacgagctccaaa

		ggataagatggcagaagcctatagcgagattggatgaaaggggaacgcagaagaggcaaaggcca cgacggactgtaccagggactcagcaccgccaccaaggacacctatgacgctcttcacatgcaggccc tgccgctcgg
149368		
149368-aa Full CAR	831	malpvtalllplalllhaarpqvlvqsgaevkpkpgssvkvskasggtfssyaiswvrqapggglewmg giipifgtanyaqkfgrvitadeststaymelsslrstedtavyyccarrggyqllrwdvllrsafdiwggqtm vtvssggggsgggsgggssyvtqppsvsvapggqtaritcggnnigsksvhwyqqkpgqapvlvly gknnrpsgvpdrfsgsrsgttasltitgaqaedeaddyccsrdsdghlrvfgtgktvlttpprptpap tiasqplslrpeacrpaaggavhtrglfacdiyiwaplagtcgvllslvitlyckrgrklllyifkqpfmrpvqt qeedgcscrfeeeeeggcelrvkfsrsadapaykqgnqlynelnlgrrreydvlkrrrdpemmggkp rrknpqeglynelqkdkmaeayseigmkgerrrgkghdglyqglstatkdydalhmqlppr
149368-nt Full CAR	832	atggccctccctgtcaccgcccctgtcgtccgctggtcttctgtccacgcccgtcggccccaagtgcag ctggtccagtcggggcgccgaggtcaagaagcccgaggctctgtgaaagtgtcctgcaaggcctccgg gggcaccttagctcctacgcatctcctgggtccgccaagcaccgggtcaaggcctggagtgatggg gggaattatccctatcttcggcactgccaaactacgcccagaagtccagggaacgctgaccattaccgcg gacgaatccacctccaccgcttatatggagctgtccagcttgcgtcgggaagataccgcccgtgtactactg cgcccgagggggtgataccagctgtgagatgggacgtgggctcctgcggctcggcgttcgacatctg gggccagggcactatggctactgtgtccagcggaggaggcggatcgggaggcggcgatcaggggg aggcgggtccagctactgtctactcaaccccttcgggtccgtggccccgggacagaccgccagaatc actgctggaggaaacaacattgggtccaagagcgtgcattggtaccagcagaagccaggacaggccc ctgtgctgggtgtctacgggaagaacaatcgcccagcggagtgccggacagggttcgggttcacgctc cggtaacacgcttactgactatcaccggggcccaggcagaggatgaagcggactactactgttcctc ccgggattcatccggcgaccacctccgggtgttcgggaaccggaacgaaggtcaccgtgtgaccactac ccagcaccgaggccaccaccccggtcctaccatcgctccagcctgtccctgcgtccggaggc atgtagaccgcagctggtggggcggtgcataaccgggggtcttgacttcgctcgcatactacatttgggc ccctctggctgttacttgcgggtctctgtcgttctactcgtgatcactcttactgtaagcgggtcggaa agctgctgtacatcttaagcaaccctcatgaggcctgtgcagactactcaagaggaggacggctgttca tgccggttccagaggaggagggaaggcggctgcgaactgcgcgtgaaattcagccgcagcgcagatg ctccagcctacaagcaggggcagaaccagctctacaacgaactcaatcttggtcggagagaggagtac gacgtgctggacaagcggagaggacgggaccagaaatgggcgggaagccgcgcagaaagaatc ccaagagggcctgtacaacgagctccaaaaggataagatggcagaagcctatagcgagattggtatg aaaggggaacgcagaagaggcaaaggccacgacggactgtaccagggactcagaccgccacca aggacacctatgacgctcttcacatgcaggccctgcgcctcgg
149369		
149369-aa Full CAR	833	malpvtalllplalllhaarpevqlqqsgpglvkpsqtlslcaisgdsvsnsaawnwirqsparglewlg yyskwyfyaiksriinpdtsknqfslqlksvtpedtavyyccarrspegflywfdpwwggtlvvssgg dsgggggsgggsseltqdpavsvlqgtitrcqgdslnyyatwyqqkpgqapvlviygnnrpsgi pdrfsasssgntasltitgaqaedeaddyccnsrdssghllfgtgktvlttpprptpapptiasqplslr eacrpaaggavhtrglfacdiyiwaplagtcgvllslvitlyckrgrklllyifkqpfmrpvqtqeedgcscr peeeeeggcelrvkfsrsadapaykqgnqlynelnlgrrreydvlkrrrdpemmggkprknpqegly nelqkdkmaeayseigmkgerrrgkghdglyqglstatkdydalhmqlppr
149369-nt Full CAR	834	atggccctccctgtcaccgcccctgtcgtccgctggtcttctgtccacgcccgtcggccccaagtgcag ctccaacagtcaggaccggggtcgtgaagccatccagaccctgtccctgacttgcctatcgggag atagcgtgtcatcgaactccgcccgtggaactggatcggcagagcccgtcccgggactggagtggtc ttggaaggacctactaccggtccaagtgttactcttctacgcgatctcgtgaagtcccgcatatcattaa ccctgatactccaagaatcagttctccctccaactgaaatccgtcacccccaggacacagcagtgatt actgcgacggagcagccccgaaggactgttctgtattggttgaccctggggccaggggactctgtg accgtgtcagcggcgagatgggtccggtggcgtggttcggggggcgcgatcatcatccgaact gaccaggaaccggctgtgtcgtggcgctgggacaaaccatccgcattacgtgccaggagactccct gggcaactactacgccacttggtagcagcagaagcgggccaagccctgtgttgggtcatctacgggac caacaacagaccctccggcatcccgaccgggtcagcgtctcgtcccgcaacactgcagcctgac catcactggagcgcaggccgaagatgaggccgactactactgcaacagcagagactcctcgggtcatc acctctgttcggaactggaaccaagggtaccgtgctgaccactacccagcaccgaggccacccacc cggtcctaccatcgctccagcctctgtccctgcgtccggaggcatgtagaccgcagctggtggggc cgtgcataccggggtcttacttcgctcgtatctacatttggccctctggtggtacttgcgggtcc tgctgttctactcgtgatcactcttactgtaagcgggtcgggaagaagctgctgtacatcttaagcaacc

		ttcatgaggcctgtgcagactactcaagaggaggacggctgttcacgccggttcccagaggaggaggaa ggcggctgcgaactgcgcgtgaaattcagccgcagcgcagatgtccagcctacaagcaggggcaga accagctctacaacgaactcaatcttggcggagagaggagtacgacgtgctggacaagcggagagg acgggaccagaaatggcgggaagccgcgcagaaagaatccccaagagggcctgtacaacgag ctccaaaaggataagatggcagaagcctatagcgagattggtatgaaagggaacgcagaagaggc aaaggccacgacggactgtaccagggactcagcaccgccaccaaggacacctatgacgtcttcacat gcaggccctgccgcctcgg
BCMA_EBB-C1978-A4		
BCMA_EBB- C1978-A4 - aa Full CART	835	MALPVTALLPLALLHAARPEVQLVESGGGLVQPGGSLRLSCAASGFTFS SYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDN SKNTLY LQMNSLRAEDTAVYYCAKVEGSGSLDYWGQGLTVTVSSGGGGSGGGGS GGGGSEIVMTQSPGTLSPGERATLSCRASQSVSSAYLAWYQQKPGQP PRLLISGASTRATGIPDRFGSGSGTDFTLTISRLEPEDFAVYYCQHYGSSF NGSSLFTFGQGRLEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGA VHTRGLDFACDIYWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRP VQTTQEEDGCSCRFPEEEEEGGCEL RVKFSRSADAPAYKQGQNQLYNELN LGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQDKMAEAYSEI GMKGERRRGKGH DGLYQGLSTATKDTYDALHMQALPPR
BCMA_EBB- C1978-A4 - nt Full CART	836	ATGGCCCTCCCTGTACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTC CACGCCGCTCGGCCCGAAGTGCAGCTCGTGGAGTCAGGAGGCGGCCT GGTCCAGCCGGGAGGGTCCCTTAGACTGT CATGCGCCGCAAGCGGAT TCACTTTCTCCTCCTATGCCATGAGCTGGGTCCGCCAAGCCCCCGAA AGGGACTGGAATGGGTGTCCGCCATCTCGGGGTCTGGAGGCTCAACTT ACTACGCTGACTCCGTGAAGGGACGGTTCACCATTAGCCGCGACAAC CCAAGAACACCTCTACCTCCAAATGAACTCCCTGCGGGCCGAGGATA CCGCCGTCTACTACTGCGCCAAAGTGGAAGGTT CAGGATCGCTGGACT ACTGGGGACAGGGTACTCTCGTGACCGTGT CATCGGGCGGAGGAGGT TCCGGCGGTGGCGGCTCCGGCGGCGGAGGGT CCGGAGATCGTGATGA CCCAGAGCCCTGGTACTCTGAGCCTTTCGCCGGGAGAAAGGGCCACC CTGTCTGCGCGCTTCCCAATCCGTGTCTCCTCCGCGTACTTGGCGTGG TACCAGCAGAAGCCGGGACAGCCCCCTCGGCTGCTGATCAGCGGGGC CAGCACCCGGGCAACCGGAATCCAGACAGATTCGGGGGTTCGGGCA GCGGCACAGATTTACCCTGACTATTTGAGGTTGAGCCCCGAGGACT TTGCGGTGTATTACTGT CAGCACTACGGGTCTGCTCTTAATGGCTCCAG CCTGTTACGTTCCGACAGGGGACCCGCCTGGAAATCAAGACCACTAC CCCAGCACCGAGGCCACCCACCCCGGCTCCTACCATCGCTCCCAGC CTCTGTCCCTGCGTCCGGAaggcatgtagaccgcagctggtggggccgtgcatacccg gtcttgacttcgctgcgatatctacattgggcccctctggctggtacttgcggggtcctgctgttctactcgt gatcactcttactgtaagcgcggtcggaagaagctgctgtacatcttaagcaaccttcatgaggcctgt gcagactactcaagaggaggacggctgttcacgccggttcccagaggaggagggaaggcggctgcgaa ctgcgcgtgaaattcagccgcagcgcagatgtccagcctacaagcaggggcagaaccagctctaca acgaactcaatcttggcggagagaggagtacgacgtgctggacaagcggagaggacgggaccag aatggcgggaagccgcgcagaaagaatccccaagagggcctgtacaacgagctccaaaaggat aagatggcagaagcctatagcgagattggtatgaaagggaacgcagaagaggcgaaggccacga cggactgtaccagggactcagcaccgccaccaaggacacctatgacgtcttcacatgcaggccctgc cgctcgg
BCMA_EBB-C1978-G1		
BCMA_EBB- C1978-G1 - aa Full CART	837	MALPVTALLPLALLHAARPEVQLVETGGGLVQPGGSLRLSCAASGITFS RYPMSWVRQAPGKGLEWVSGISDSGVSTYYADSAKGRFTISRDN SKNTLF LQMSSLRDEDTAVYYCVTRAGSEASDIWGQGMVTVSSGGGGSGGGGS GGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSNLAWYQQKPGQAPR LLIYDASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAIYYCQQFGTSSGLT FGGGTKLEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLD FACDIYWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEE DGCSCRFPEEEEEGGCEL RVKFSRSADAPAYKQGQNQLYNELNLGRREEY DVL DKRRGRDPEMGGKPRRKNPQEGLYNELQDKMAEAYSEIGMKG

		RRGKGHDGLYQGLSTATKDTYDALHMQALPPR
BCMA_EBB-C1978-G1 - nt Full CART	838	ATGGCCCTCCCTGTACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTC CACGCCGCTCGGCCCAAGTGCAACTGGTGGAACCGGTGGCGGCCT GGTGCAGCCTGGAGGATCATTGAGGCTGTCATGCGCGGCCAGCGGTA TTACCTTCTCCCGGTACCCCATGTCCTGGGTGAGACAGGCCCGGGGA AAGGGCTTGAATGGGTGTCCGGGATCTCGGACTCCGGTGTGAGCACTT ACTACGCCGACTCCGCCAAGGGACGCTTCACCATTTCGCGGGACAAC CGAAGAACACCCTGTTCTCCTCAAATGAGCTCCCTCCGGGACGAGGATA CTGCAGTGTACTACTGCGTGACCCGCGCCGGGTCCGAGGCGTCTGAC ATTTGGGGACAGGGCACTATGGTCAACGTGTGCTCCGGCGGAGGGGG CTCGGGAGGCGGTGGCAGCGGAGGAGGAGGGTCCGAGATCGTGCTG ACCCAATCCCCGGCCACCCTCTCGCTGAGCCCTGGAGAAAGGGCAAC CTTGCTCTGTGCGCGGAGCCAGTCCGTGAGCAACTCCCTGGCCTGGTA CCAGCAGAAGCCCGGACAGGCTCCGAGACTTCTGATCTACGACGCTTC GAGCCGGGCCACTGGAATCCCCGACCGCTTTTCGGGGTCCGGCTCAG GAACCGATTTACCCTGACAATCTCACGGCTGGAGCCAGAGGATTTTCG CCATCTATTACTGCCAGCAGTTCGGTACTTCTCCGGCCTGACTTTTCGG AGGCGGCACGAAGCTCGAAATCAAGACCACTACCCAGACCCGAGGC CACCCACCCCGGCTCCTACCATCGCCTCCAGCCTCTGTCCCTGCGTC CGGAggcatgtagaccgcagctggtggggccgtgcataccggggtcttgacttcgctcgatctct acattggccctctgctggtacttgccgggtcctgctgcttctactcgtgatcactcttactgaagcgcg gtcggaagaagctgctgtacatctttaagcaaccctcatgaggcctgtgcagactactcaagaggagga cggctgtcatgccggtcccagaggaggaaggcggctgcgaactgcgctgaaattcagccgca gcgcatgtctccagcctacaagcaggggcagaaaccagctctacaacgaactcaatcttgctcgga gaggagtacgagctgctggacaagcggagaggacgggacccagaaatggcggggaagccgcgca gaaagaatcccaagaggcctgtacaacgagctccaaaaggataagatggcagaagcctatagcg agattggtatgaaaggggaacgcagaagaggcaaaaggccacgagcgactgtaccagggactcagc accgccaccaaggacacctatgacgctcttcacatgcaggccctgccgctcgg
BCMA_EBB-C1979-C1		
BCMA_EBB-C1979-C1 - aa Full CART	839	MALPVTALLLPLALLHAARPQVQLVESGGGLVQPGGSLRLSCAASGFTFS SYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDNKNSL YLQMNSLR AEDTAIYYCARATYKRELRYYYGMDVWGQGTMTVTVSSGGGG SGGGSGGGGSEIVMTQSPGTVSLSPGERATLSCRASQSVSSSFLAWYQ QKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDSAVYYC QQYHSSPSWTFGQGT RLEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAA GGAVHTRGLDFACDIYWAPLAGTCGVLLLSLVITLYCKRGRKLLYIFKQPF MRPVQTTQEEDGCSCRFPEEEEEGGCEL RVKFSRSADAPAYKQGQNQLYN ELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAY SEIGMKGERRRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
BCMA_EBB-C1979-C1 - nt Full CART	840	ATGGCCCTCCCTGTACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTC CACGCCGCTCGGCCCAAGTGCACTCGTGGAATCGGGTGGCGGACT GGTGCAGCCGGGGGGGCTCACTTAGACTGTCCTGCGCGGCCAGCGGAT TCACTTTCTCCTCCTACGCCATGTCCTGGGTGAGACAGGCCCTGGAA AGGGCCTGGAATGGGTGTCCGCAATCAGCGGCAGCGGCGGCTCGACC TATTACGCGGATTCAGTGAAGGGCAGATTACCATTTCCCGGGACAAC GCCAAGAACTCCTTGACCTTCAAATGAACTCCCTCCGCGCGGAAGATA CCGCAATCTACTACTGCGCTCGGGCCACTTACAAGAGGGAAGTGGCT ACTACTACGGGATGGACGTCTGGGGCCAGGGAACCATGGTCACCGTG TCCAGCGGAGGAGGAGGATCGGGAGGAGGCGGTAGCGGGGGTGGAG GGTCGGAGATCGTGATGACCCAGTCCCCCGGCACTGTGTGCTGTCC CCCGGCGAACGGGCCACCCTGTCATGTGCGGGCCAGCCAGTCAGTGTC GTCAAGCTTCTCGCCTGGTACCAGCAGAAACCGGGACAAGCTCCCCG CCTGCTGATCTACGGAGCCAGCAGCCGGGCCACCGGTATTCTGACC GGTTCTCCGGTTCGGGGTCCGGGACCGACTTTACTCTGACTATCTCTC GCCTCGAGCCAGAGGACTCCGCCGTGTATTACTGCCAGCAGTACCACT CCTCCCGTCTCTGGACGTTCCGACAGGGGCACAAGGCTGGAGATTAAGA

		CCACTACCCCAGCACCGAGGCCACCCACCCCGGCTCCTACCATCGCCT CCCAGCCTCTGTCCCTGCGTCCGGAaggcatgtagaccgcagctggtggggcgtgc ataccggggtcttgacttcgctgcgatatctacattgggcccctctggtggtacttgcggggtcctgctg cttctactcgtgatcactcttactgtaagcgcggtcggaagaagctgctgtacatcttaagcaaccctcat gaggcctgtgcagactactcaagaggaggacggctgttcagccggtcccagaggaggaggaaggc ggctgcgaactgcgctgaaattcagccgcagcgcagatgtccagcctacaagcaggggcagaacc agctctacaacgaactcaatcttggcggagagaggagtacgacgtgctggacaagcggagaggacg ggaccagaaatgggcggaagccgcgcagaaagaatccccaagaggcctgtacaacgagctcc aaaaggataagatggcagaagcctatagcgagattggtatgaaaggggaacgcagaagaggcaaa ggccacgacggactgtaccagggactcagcaccgccaccaaggacacctatgacgtcttcacatgca ggccctgccgcctcgg
BCMA_EBB-C1978-C7		
BCMA_EBB- C1978-C7 - aa Full CART	841	MALPVTALLLPLALLHAARPEVQLVETGGGLVQPGGSLRLSCAASGFTFS SYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDNKNTLY LQMNTLKAEDTAVYYCARATYKRELRYYYGMDVWVGQTTVTVSSGGGGS GGGSGGGGSEIVLTQSPSTLSLSPGESATLSCRASQSVSTTFLAWYQQK PGQAPRLLIYGSSNRATGIPDRFSGSGSGTDFTLTIRLEPEDFAVYYCQQ YHSSPSWTFGQGTKVEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGG AVHTRGLDFACDIYWAPLAGTCGVLLSLVITLYCKRGRKLLYIFKQPFMR PVQTTQEEDGCSRFPEEEEGGCELRVKFSRSADAPAYKQGNQLYNEL NLGRREYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYS EIGMKGERRRRGKHDGLYQGLSTATKDTYDALHMQALPPR
BCMA_EBB- C1978-C7 - nt Full CART	842	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTC CACGCCGCTCGGCCCGAGGTGCAGCTTGTGGAACCGGTGGCGGACT GGTGCAGCCCGGAGGAAGCCTCAGGCTGTCCTGCGCCGCGTCCGGCT TCACCTTCTCCTCGTACGCCATGTCTGGGTCCGCCAGGCCCGCGAA AGGGCCTGGAATGGGTGTCCGCCATCTCTGGAAGCGGAGGTTCCACG TACTACGCGGACAGCGTCAAGGGAAGGTTCAATCTCCCGCGATAAT TCGAAGAACACTCTGTACCTTCAAATGAACACCCTGAAGGCCGAGGAC ACTGCTGTGTACTACTGCGCACGGGCCACCTACAAGAGAGAGCTCCGG TACTACTACGGAATGGACGTCTGGGGCCAGGGAAGTACTGTGACCGTG TCCTCGGGAGGGGGTGGCTCCGGGGGGGGCGGCTCCGGCGGAGGC GGTTCCGAGATTGTGCTGACCCAGTCACCTTCAACTCTGTGCTGTCC CCGGGAGAGAGCGCTACTCTGAGCTGCCGGGCCAGCCAGTCCGTGTC CACCACCTTCTCCTCGCCTGGTATCAGCAGAAGCCGGGGCAGGCACCAC GGCTCTTGATCTACGGGTCAAGCAACAGAGCGACCGGAATTCTTGACC GCTTCTCGGGGAGCGGTTCAAGCACCGACTTCACCCTGACTATCCGGC GCCTGGAACCCGAAGATTTGCGCGTGTATTACTGTCAACAGTACCACTC CTCGCGGTCTTGACCTTTGGCCAAGGAACCAAGTGGAATCAAGAC CACTACCCCAGCACCGAGGCCACCCACCCCGGCTCCTACCATCGCCTC CCAGCCTCTGTCCCTGCGTCCGGAaggcatgtagaccgcagctggtggggcgtgcat accgggggtcttgacttcgctgcgatatctacattgggcccctctggtggtacttgcggggtcctgctgctt tactcgtgatcactcttactgtaagcgcggtcggaagaagctgctgtacatcttaagcaaccctcatga ggcctgtgcagactactcaagaggaggacggctgttcagccggtcccagaggaggaggaaggcgg ctgcgaactgcgctgaaattcagccgcagcgcagatgtccagcctacaagcaggggcagaaccag ctctacaacgaactcaatcttggcggagagaggagtacgacgtgctggacaagcggagaggacggg accagaaatgggcggaagccgcgcagaaagaatccccaagaggcctgtacaacgagctccaa aaggataagatggcagaagcctatagcgagattggtatgaaaggggaacgcagaagaggcaagg ccacgacggactgtaccagggactcagcaccgccaccaaggacacctatgacgtcttcacatgcagg ccctgccgcctcgg
BCMA_EBB-C1978-D10		
BCMA_EBB- C1978-D10 - aa Full CART	843	MALPVTALLLPLALLHAARPEVQLVETGGGLVQGRSLRLSCAASGFTFD DYAMHWVRQAPGKGLEWVSGISWNSGSIGYADSVKGRFTISRDNKNSL YLQMNSLRDEDTAVYYCARVGKAVPDVWGQTTVTVSSGGGGSGGGGS GGGSDIVMTQTPSSLSASVGDRVITICRASQSISSYLNWYQQKPKGKAPK LLIYAASSLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQSYSTPYS

		FGQGTRLEIKTTTTAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLD FACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEE DGCSCRFPEEEEEGGCEL RVKFSRSADAPAYKQGQNQLYNELNLGRREEY DVLDKRRGRDPPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGER RRGKGHDGLYQGLSTATKDTYDALHMQALPPR
BCMA_EBB- C1978-D10 - nt Full CART	844	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTC CACGCCGCTCGGCCCGAAGTGCAGCTCGTGGAACTGGAGGTGGACT CGTGCAGCCTGGACGGTGCCTGCGGCTGAGCTGCGCTGCATCCGGCT TCACCTTCGACGATTATGCCATGCACTGGGTGAGACAGGCGCCAGGGA AGGGACTTGAGTGGGTGTCCGGTATCAGCTGGAATAGCGGCTCAATCG GATACGCGGACTCCGTGAAGGGAAGGTTACCATTTCCCGCGACAACG CCAAGAACTCCCTGTACTTGCAAATGAACAGCCTCCGGGATGAGGACA CTGCCGTGTACTACTGCGCCCGCTCGGAAAAGCTGTGCCCGACGTCT GGGGCCAGGGAACCACTGTGACCGTGTCCAGCGGCGGGGGTGGATC GGGCGGTGGAGGGTCCGGTGGAGGGGGCTCAGATATTGTGATGACCC AGACCCCTCGTCCCTGTCCGCCTCGGTGCGCGACCGCGTGACTATCA CATGTAGAGCCTCGCAGAGCATCTCCAGCTACCTGAACTGGTATCAGC AGAAGCCGGGGAAGGCCCGGAAGCTCCTGATCTACGCGGCATCATCA CTGCAATCGGGAGTGGCGAGCCGGTTTTCCGGGTCCGGCTCCGGCAC CGACTTCACGCTGACCATTTCTTCCCTGCAACCCGAGGACTTCGCCACT TACTACTGCCAGCAGTCCTACTCCACCCCTTACTCCTTCGGCCAAGGAA CCAGGCTGGAATCAAGACCACTACCCAGCACCGAGGCCACCCACC CCGGCTCCTACCATCGCCTCCAGCCTCTGTCCCTGCGTCCGGAaggcat gtagaccgcagctggtggggcgtgcataccggggtctgactcgctcgatattacattgggcc cctctggtggtacttgccgggtcctgctgcttactcgtgatcactcttactgaagcgcggtcggaagaa gctgctgtacatcttaagcaaccctcatgaggcctgtgcagactactcaagaggaggacggctgtcat gccggttccagaggaggaggaaggcggtgcgaactgcgctgaaattcagccgcagcgagatg ctccagcctacaagcaggggcagaaccagctctacaacgaactcaatcttggtcggagagaggagtac gacgtgctggacaagcggagaggacgggaccagaaatggcggggaagccgcgagaaagaatc cccaagagggcctgtacaacgagctccaaaaggataagatggcagaagcctatagcgagattggtatg aaaggggaacgcagaagaggcaaggccacgacggactgtaccagggactcagaccgcccacca aggacacctatgacgctctcatatgcaggccctgccgctcgg
BCMA_EBB-C1979-C12		
BCMA_EBB- C1979-C12 - aa Full CART	845	MALPVTALLPLALLHAARPEVQLVESGGGLVQPGRSLRLSCTASGFTFD DYAMHWVRQRPGKLEWVASINWKGNSLAYGDSVKGRFAISRDNANTV FLQMNSLRTEDEVYYCASHQGVAYYNYAMDVWGRGTLTVTVSSGGGGS GGGSGGGGSEIVLTQSPGTLSPGERATLSCRATQSIGSSFLAWYQQR PGQAPRLLIYGASQRATGIPDRFSGRSGTDFTLTISRVEPEDSAVYYCQH YESSPSWTFGQGTKEIKTTTTAPRPPTPAPTIASQPLSLRPEACRPAAGG AVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMR PVQTTQEEDGCSCRFPEEEEEGGCEL RVKFSRSADAPAYKQGQNQLYNEL NLGRREEYDVLDKRRGRDPPEMGGKPRRKNPQEGLYNELQKDKMAEAYS EIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
BCMA_EBB- C1979-C12 - nt Full CART	846	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTC CACGCCGCTCGGCCCGAAGTGCAGCTCGTGGAGAGCGGGGGAGGATT GGTGCAGCCCCGAAGGTCCCTGCGGCTCTCCTGCACTGCGTCTGGCT TCACCTTCGACGACTACGCGATGCACTGGGTGAGACAGCGCCCGGGA AAGGGCCTGGAATGGGTGCGCTCAATCAACTGGAAGGGAACTCCCTG GCCTATGGCGACAGCGTGAAGGGCCGCTTCGCCATTTGCGCGACAA CGCCAAGAACACCGTGTCTTGCAAATGAATTCCTGCGGACCGAGGA TACCGCTGTGTACTACTGCGCCAGCCACCAGGGCGTGGCATACTATAA CTACGCCATGGACGTGTGGGGAAGAGGGACGCTCGTACCGTGTCTCT CCGGGGGCGGTGGATCGGGTGGAGGAGGAAGCGGTGGCGGGGGCA GCGAAATCGTGCTGACTCAGAGCCCGGGAACCTTTCACTGTCCCCGG GAGAACGGGCCACTCTCTCGTGCCGGGCCACCCAGTCCATCGGCTCC TCCTTCCTTGCTGGTACCAGCAGAGGCCAGGACAGGCGCCCCGCCT

		GCTGATCTACGGTGCTTCCCAACGCGCCACTGGCATTCTGACCGGTT CAGCGGCAGAGGGTCGGGAACCGATTTCACTGACCATTTCCCGGT GGAGCCCGAAGATTTCGGCAGTCTACTACTGTCAGCATTACGAGTCCTC CCCTTCATGGACCTTCGGTCAAGGGACCAAAGTGGAGATCAAGACCAC TACCCAGCACCGAGGCCACCCACCCCGGCTCCTACCATCGCCTCCCA GCCTCTGTCCCTGCGTCCGGAaggcatgtagaccgcagctggtggggccgtgcataccc ggggtcttgacttcgcctgcgatatctacatttggccctctggctggtacttgcggggtcctgctgcttcac tcgtgatactcttactgtaagcgcggtcggaagaagctgctgtacatcttaagcaaccctcatgaggcc tgtgcagactactcaagaggaggacggctgtcatgcccgttccagaggaggaggaaggcggtgcg aactgcggtgaaattcagccgcagcgagatgctccagcctacaagcaggggcagaaccagctcta caacgaactcaatcttggtcggagagaggagtacgacgtgctggacaagcggagaggacgggaccc agaaatggcggggaagccgcgagaaagaatccccaagagggctgtacaacgagctccaaaagg ataagatggcagaagcctatagcgagattggtatgaaaggggaacgcagaagaggcaaaggccacg acggactgtaccagggactcagcaccgccaccaaggacacctatgacgtcttcacatgcaggccctg ccgcctcgg
BCMA_EBB-C1980-G4		
BCMA_EBB- C1980-G4- aa Full CART	847	MALPVTALLLPLALLLHAARPEVQLVESGGGLVQPGGSLRLSCAASGFTFS SYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDN SKNTLY LQMNSLRAEDTAVYYCAKVVRDGM DVWGQGT VTVSSGGGSGGGGS GGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAP RLLIYGASSRATGIPDRFSGNGSGTDFTLTISRLEPEDFAVYYCQQYGSPP RFTFGPGTKVDIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTR GLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKLLYIFKQPFMRPVQTT QEEDGCSCRFPEEEEGGCEL RVKFSRSADAPAYKQGQNQLYNELNLGRR EEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKG ERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
BCMA_EBB- C1980-G4- nt Full CART	848	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTC CAGCCGCTCGGCCCGAGGTGCAGTTGGTCGAAAGCGGGGGCGGGC TTGTGCAGCCTGGCGGATCACTGCGGCTGTCCTGCGCGGCATCAGGC TTCACGTTTTCTTCTACGCCATGTCCTGGGTGCGCCAGGCCCTGGA AAGGGACTGGAATGGGTGTCCGCGATTTCCGGGTCCGGCGGGAGCAC CTACTACGCCGATTCCGTGAAGGGCCGCTTCACTATCTCGCGGGACAA CTCCAAGAACACCCTCTACCTCCAAATGAATAGCCTGCGGGCCGAGGA TACCGCCGTCTACTATTGCGCTAAGGTGCTGCGCGACGGAATGGACGT GTGGGGACAGGGTACCACCGTGACAGTGTCTCCTCGGGGGGAGGCGGTA GCGGCGGAGGAGGAAGCGGTGGTGGAGGTTCCGAGATTGTGCTGACT CAATCACCCGCGACCCTGAGCCTGTCCCCCGGCGAAAGGGCCACTCT GTCCTGTGCGGGCCAGCCAATCAGTCTCCTCCTCGTACCTGGCCTGGTA CCAGCAGAAGCCAGGACAGGCTCCGAGACTCCTTATCTATGGCGCATC CTCCCGCGCCACCGGAATCCCGGATAGGTTCTCGGGAACGGATCGG GGACCGACTTCACTCTCACCATCTCCCGGCTGGAACCGGAGGACTTCG CCGTGTACTACTGCCAGCAGTACGGCAGCCCGCCTAGATTCACTTTCG GCCCCGGCACCAAAGTGGACATCAAGACCACTACCCAGCACCGAGG CCACCCACCCCGGCTCCTACCATCGCCTCCAGCCTCTGTCCCTGCGT CCGGAaggcatgtagaccgcagctggtggggccgtgcataccggggtcttgacttcgcctgcgatat ctacatttggccctctggctggtacttgcggggtcctgctgcttctactcgtgatactcttactgtaagcgc ggtcggaagaagctgctgtacatcttaagcaaccctcatgaggcctgtgcagactactcaagaggagg acggctgtcatgcccgttcccagaggaggaggaaggcggtgcgaactgcgctgaaattcagccgc agcgagatgctccagcctacaagcaggggcagaaccagctctacaacgaactcaatcttggtcggag agaggagtacgacgtgctggacaagcggagaggacgggacccagaaatggcggggaagccgcgc agaaagaatccccaagagggctgtacaacgagctccaaaaggataagatggcagaagcctatagc gagattggtatgaaaggggaacgcagaagaggcaaaggccacgacggactgtaccagggactcag caccgccaccaaggacacctatgacgtcttcacatgcaggccctgccgcctcgg
BCMA_EBB-C1980-D2		
BCMA_EBB- C1980-D2- aa	849	MALPVTALLLPLALLLHAARPEVQLLES GGGLVQPGGSLRLSCAASGFTFS SYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDN SKNTLY

Full CART		LQMNSLRAEDTAVYYCAKIPQTGTDFDYWGQGLVTVSSGGGGSGGGGSG GGGSEIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQRPGQAPR LLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQHYGSSPS WTFGQGTREIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRG LDFACDIYWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQ EEDGCSCRFPEEEEEGGCELRVKFSRSADAPAYKQGGQNQLYNELNLGRRE EYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQDKDMAEAYSEIGMKGE RRRGKGHGDLGYQGLSTATKDTYDALHMQALPPR
BCMA_EBB- C1980-D2- nt Full CART	850	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTC CACGCCGCTCGGCCCGAAGTGACAGCTGCTGGAGTCCGGCGGTGGATT GGTGCAACCGGGGGGATCGCTCAGACTGTCCTGTGCGGCGTCAGGCT TCACCTTCTCGAGCTACGCCATGTCATGGGTGACACAGGCCCTGGAA AGGGTCTGGAATGGGTGTCCGCCATTTCCGGGAGCGGGGGATCTACA TACTACGCCGATAGCGTGAAGGGCCGCTTACCATTTCCTGGGACAAC TCCAAGAACTCTCTATCTGCAAATGAACTCCCTCCGCGCTGAGGACA CTGCCGTGTACTACTGCGCCAAAATCCCTCAGACCGGCACCTTCGACT ACTGGGGACAGGGGACTCTGGTCACCGTCAGCAGCGGTGGCGGAGGT TCGGGGGGAGGAGGAAGCGCGCGGAGGGTCCGAGATTGGCTGA CCCAGTCACCCGGCACTTTGTCCCTGTGCGCTGGAGAAAGTGCCACCC TTTCCTGCCGGCATCCCAATCCGTGTCTCCTCGTACCTGGCCTGGT ACCAGCAGAGGCCCGGACAGGCCCCACGGCTTCTGATCTACGGAGCA AGCAGCCGCGCGACCGGTATCCCGGACCGGTTTTCGGGCTCGGGCTC AGGAACTGACTTCACCTCACCATCTCCCGCCTGGAACCCGAAGATTT CGCTGTGTATTACTGCCAGCACTACGGCAGCTCCCCGTCTGGACGTT CGGCCAGGGAACCTCGGCTGGAGATCAAGACCACTACCCAGCACCGA GGCCACCCACCCCGGCTCCTACCATCGCCTCCAGCCTCTGTCCCTGC GTCCGGAaggcatgtagaccgcagctggtggggccgtgcataccggggtcttgacttcgctgcg atatctacattgggccccctctgctggtactgcggggtctctgctgttactcgtgatcactcttactgtaa gcgcggtcggaagaagctgctgtacatcttaagcaaccctcatgaggcctgtgcagactactcaagag gaggacggtggtcatgccggtccagaggaggaggaaggcggctgcgaactgcgcgtgaaattcag ccgcagcgcagatgctccagcctacaagcaggggcagaaccagctctacaacgaactcaatcttggtc ggagagaggagtacgacgtgctggacaagcggagaggacgggaccagaaatgggcgggaagcc gcgcagaaagaatcccaagagggcctgtacaacgagctccaaaaggataagatggcagaaagccta tagcgagattggtatgaaaggggaacgcagaagaggcaaaggccacgagcgtgtaccaggagact cagcaccgcaccaaggacacatgacgctcttcacatgcaggccctgcccgcctcg
BCMA_EBB-C1978-A10		
BCMA_EBB- C1978-A10- aa Full CART	851	MALPVTALLPLALLLHAARPEVQLVETGGGLVQPGGSLRLSCAASGFTFS SYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTMSRENDKNS VFLQMNSLRVEDTGVIYCARANYKRELRYYYGMDVWGQTMVTVSSGG GGSGGGGGSGGGGSEIVMTQSPGTLSPGESATLSCRASQVRASNYLAW YQHKPGQAPSLISGASSRATGVPDRFSGSGSGTDFTLAISRLEPEDSAVY YCQHYDSSPSWTFGQGTKEIKTTTPAPRPPTPAPTIASQPLSLRPEACRP AAGGAVHTRGLDFACDIYWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFK QPFMRPVQTTQEEDGCSCRFPEEEEEGGCELRVKFSRSADAPAYKQGGQN QLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQDK MAEAYSEIGMKGERRRRGKGHGDLGYQGLSTATKDTYDALHMQALPPR
BCMA_EBB- C1978-A10- nt Full CART	852	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTC CACGCCGCTCGGCCCGAAGTGCAACTGGTGGAACCGGTGGAGGACT CGTGACAGCCTGGCGGCAGCCTCCGGCTGAGCTGCGCCGCTTCCGGAT TCACCTTTTCTCTCTACGCGATGTCTTGGGTGACACAGGCCCCCGGAA AGGGGCTGGAATGGGTGTGAGCCATCTCCGGCTCCGGCGGATCAACG TACTACGCCGACTCCGTGAAAGGCCGTTACCATTGTCGCGCGAGAAT GACAAGAACTCCGTGTTCTGCAAATGAACTCCCTGAGGGTGGAGGAC ACCGGAGTGTACTATTGTGCGCGCGCCAACATAAGAGAGAGCTGCGG TACTACTACGGAATGGACGTCTGGGGACAGGGAACATATGGTGACCGTG TCATCCGGTGGAGGGGGAAGCGCGCGGTGGAGGCAGCGGGGGCGGGG

		GTTCAGAAATTGTCATGACCCAGTCCCCGGGAACCTTTCCCTCTCCCC CGGGGAATCCGCGACTTTGTCCTGCCGGGCCAGCCAGCGCGTGGCCT CGAACTACCTCGCATGGTACCAGCATAAGCCAGGCCAAGCCCCCTTCCC TGCTGATTTCCGGGGGCTAGCAGCCGCGCCACTGGCGTGCCGGATAGG TTCTCGGGAAGCGGCTCGGGTACCGATTTACCCCTGGCAATCTCGCGG CTGGAACCGGAGGATTCGGCCGTGTACTACTGCCAGCACTATGACTCA TCCCCCTCCTGGACATTTCGGACAGGGCACCAAGGTTCGAGATCAAGACC ACTACCCAGCACCGAGGCCACCCACCCCGGCTCCTACCATCGCCTCC CAGCCTCTGTCCCTGCGTCCGGAaggcatgtagaccgcagctgggtggggccgtgcata cccggggctgtgacttcgcctgcgatatctacatttggggccctctggctgttgcggggctctgtgcttt cactcgtgatcactcttactgtaagcgcggtcggaagaagctgctgtacattttaagcaaccctcatgag gcctgtgcagactactcaagaggaggacggctgtcatgccggttcccagaggaggaggaaggcggt gcgaactgcgctgaaattcagccgcagcgcagatgctccagcctacaagcaggggcagaaccagct ctacaacgaactcaatcttggtcggagagaggagtacgacgtgctggacaagcggagaggacggggac ccagaaatgggcggaagccgcgcagaaagaatcccaagaggcctgtacaacgagctccaaaa ggataagatggcagaagcctatagcgagattggtatgaaaggggaacgcagaagaggcaaaggcca cgacggactgtaccagggactcagcaccgccaccaaggacacctatgacgtcttcacatgcaggccc tgccgcctcgg
BCMA_EBB-C1978-D4		
BCMA_EBB-C1978-D4- aa Full CART	853	MALPVTALLPLALLHAARPEVQLLETGGGLVQPGGSLRLSCAASGFSFS SYAMSWVRQAPGKLEWVSAISGSGGSTYYADSVKGRFTISRDN SKNTLY LQMNSLRAEDTAVYYCAKALVGATGAFDIWGQGLTVTVSSGGGGSGGGG SGGGGSEIVLTQSPGTLSPGERATLSCRASQSLSSNFLAWYQQKPGQA PGLLIYGASNWATGTPDRFSGSGSGTDFTLTITRLEPEDFAVYYCQYYGTS PMYTFGQGTKVEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHT RGLDFACDIYWAPLAGTCGVLLLSLVITLYCKRGRKLLYIFKQPFMRPVQ TTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLG RREEYDVLDRRRGRDPEMGGKPRRKNPQEGLYNELQDKMAEAYSEIGM KGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
BCMA_EBB-C1978-D4- nt Full CART	854	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTC CACGCCGCTCGGCCGAAGTGCAGCTGCTCGAAACCGGTGGAGGGCT GGTGCAGCCAGGGGGCTCCCTGAGGCTTTCATGCGCCGCTAGCGGAT TCTCCTTCTCCTCTTACGCCATGTCGTGGGTCCGCCAAGCCCCTGGAA AAGGCCTGGAATGGGTGTCCGCGATTTCGGGAGCGGAGGTTTCGACC TATTACGCCGACTCCGTGAAGGGCCGCTTTACCATCTCCCGGGATAAC TCCAAGAACA CTCTGTACCTCCAAATGAACTCGCTGAGAGCCGAGGAC ACCGCCGTGTATTACTGCGCGAAGGCGCTGGTCGGCGCGACTGGGGC ATTCGACATCTGGGGACAGGGAACCTTTGTGACCGTGTGAGCGGAGG CGGCGGCTCCGGCGGAGGAGGGAGCGGGGGCGGTGGTTCCGAAATC GTGTTGACTCAGTCCCCGGGAACCCTGAGCTTGTACCCGGGGAGCG GGCCACTCTCTCTGTGCGCGCTCCCAATCGCTCTCATCCAATTTCTGT GCCTGGTACCAGCAGAAGCCCGGACAGGCCCGGGCCTGCTCATCTA CGGCGCTTCAAAC TGGGCAACGGGAACCCCTGATCGGTTTCAGCGGAA GCGGATCGGGTACTGACTTTACCTGACCATCACCAGACTGGAACCGG AGGACTTCGCCGTGTACTACTGCCAGTACTACGGCACCTCCCCCATGT ACACATTCGGACAGGGTACCAAGGTTCGAGATTAAGACCACTACCCAG CACCGAGGCCACCCACCCCGGCTCCTACCATCGCCTCCAGCCTCTGT CCTGCGTCCGGAaggcatgtagaccgcagctgggtggggccgtgcataaccggggctgtgactt cgctgcgatatctacatttggggccctctggctgttgcggggctctgtgctttcactcgtgatcactctt tactgtaagcgcggtcggaagaagctgctgtacattttaagcaaccctcatgaggcctgtgcagactac tcaagaggaggacggctgtcatgccggttcccagaggaggaggaaggcggtgcgaactgcgctg aaattcagccgcagcgcagatgctccagcctacaagcaggggcagaaccagctctacaacgaactca atcttggtcggagagaggagtacgacgtgctggacaagcggagaggacgggaccagaaatgggcg ggaagccgcgcagaaagaatcccaagaggcctgtacaacgagctccaaaaggataagatggca gaagcctatagcgagattggtatgaaaggggaacgcagaagaggcaaaggccacgacggactgtac cagggactcagcaccgccaccaaggacacctatgacgtcttcacatgcaggccctgcgcctcgg

BCMA_EBB-C1980-A2		
BCMA_EBB-C1980-A2- aa Full CART	855	MALPVTALLLPLALLLHAARPEVQLLESGGGLVQPGGSLRLSCAASGFTFS SYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDN SKNTLY LQMNSLRAEDTAVYYCVLWFGEGFDPWGQGT LVTVSSGGGGSGGGGSG GGGSDIVLTQSPLSLPVTGPGEPA SISRSSQSLLSNGYNYLDWYLQKPG QSPQLLIYLGSNRASGV PDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQA LQTPLTFGGGT KVDIKTTTPAPRPPTPAPT IASQPLSLRPEACRPAAGGAV HTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPV QTTQEEDGCSCRFPEEEEGGCEL RVKFSRSADAPAYKQGQNQLYNELNL GRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIG MKGERRRRGKGHDLGYQGLSTATKDTYDALHMQALPPR
BCMA_EBB-C1980-A2- nt Full CART	856	ATGGCCCTCCCTGTACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTC CACGCCGCTCGGCCCGAAGTGCAGCTGCTTGAGAGCGGTGGAGGTCT GGTGCAGCCCGGGGGATCACTGCGCCTGTCCTGTGCCGCGTCCGGTT TCACTTTCTCCTCGTACGCCATGTCGTGGGT CAGACAGGCACCGGGAA AGGGACTGGAATGGGTGT CAGCCATTTCCGGTTCGGGGGGCAGCACC TACTACGCTGACTCCGTGAAGGGCCGGTTCACCATTTCCCGCGACAAC TCCAAGAACACCTTGACCTCCAAATGAACTCCCTGCGGGCCGAAGAT ACCGCCGTGTATTACTGCGTGCTGTGGTTCGGAGAGGGATTTCGACCCG TGGGGACAAGGAACACTCGTGACTGTGT CATCCGGCGGAGCGGCAG CGGTGGCGCGGTTCCGGCGGCGGATCTGACATCGTGTGGTACCC AGTCCCCTCTGAGCCTGCCGGTCACTCCTGGCGAACCAGCCAGCATCT CCTGCCGGTTCGAGCCAGTCCCTCCTGCACTCCAATGGGTACAAC TACC TCGATTGGTATCTGCAAAGCCGGGCCAGAGCCCCAGCTGCTGATCT ACCTTGGGTCAAACCGCGCTTCCGGGGTGCCTGATAGATTCTCCGGGT CCGGGAGCGGAACCGACTTTACCCTGAAAATCTCGAGGGTGGAGGCC GAGGACGTCGGAGTGTACTACTGCATGCAGGCGCTCCAGACTCCCCTG ACCTTCGGAGGAGGAACGAAGGTGACATCAAGACCACTACCCAGCA CCGAGGCCACCCACCCCGGCTCCTACCATCGCCTCCAGCCTCTGTCC CTGCGTCCGGA ggcagtagaccgcagctggggggcgtgcataccggggcttgacttgc ctgcgatactacattggggccctctggctgtacttgcggggtcctgtgcttactcgtgacactcttact gtaagcgcggtcgaagaagctgctgtacatcttaagcaaccctcatgaggcctgtgcagactactca agaggaggacggctgtcatgccggttccagaggaggaggaaggcggtgcgaactgcgctgaaa ttcagccgcagcgagatgctccagcctacaagcaggggcagaaccagctctacaacgaactcaatct tggtcggagagaggagtacgagctgtggacaagcggagaggacgggaccagaaatgggcgga agccgcgcagaaagaatcccaagaggcctgtacaacgagctcaaaaggataagatggcagaa gcctatagcgagattggtatgaaaggggaacgcagaaagggcagcagcgtgtaccag ggactcagcaccgccaccaaggacacctatgacgctcttcacatgcaggccctgccgcctcgg
BCMA_EBB-C1981-C3		
BCMA_EBB-C1981-C3- aa Full CART	857	MALPVTALLLPLALLLHAARPQVQLVESGGGLVQPGGSLRLSCAASGFTFS SYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDN SKNTLY LQMNSLRAEDTAVYYCAKVGYDSSGYRDYYGMDVWGQGT TTVTVSSGG GGSGGGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVSSYLAW YQQKPGQAPRLLIYGTSSRATGISDRFSGSGSGTDFTLTISRLEPEDFAVYY CQHYGNSPPKFTFGPGTKLEIKTTTPAPRPPTPAPT IASQPLSLRPEACRPA AGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQ PFMRPVQTTQEEDGCSCRFPEEEEGGCEL RVKFSRSADAPAYKQGQNQL YNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMA EAYSEIGMKGERRRRGKGHDLGYQGLSTATKDTYDALHMQALPPR
BCMA_EBB-C1981-C3- nt Full CART	858	ATGGCCCTCCCTGTACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTC CACGCCGCTCGGCCCGAAGTGCAGCTCGTGGAGTCAGGCGGAGGACT GGTGCAGCCCGGGGGCTCCCTGAGACTTTCTGCGCGGCATCGGGTT TTACCTTCTCCTCCTATGCTATGTCCTGGGTGCGCCAGGCCCGGGAA AGGGACTGGAATGGGTGTCCGCAATCAGCGGTAGCGGGGGCTCAACA TACTACGCCGACTCCGTCAAGGGTGCCTTCACTATTTCCCGGGACAAC TCCAAGAATACCCTGTACCTCCAAATGAACAGCCTCAGGGCCGAGGAT

		ACTGCCGTGTACTACTGCGCCAAAGTCGGATACGATAGCTCCGGTTAC TACCGGGACTACTACGGAATGGACGTGTGGGGACAGGGCACCACCGT GACCGTGTCAAGCGGCGGAGGCGGTTGAGGAGGGGGAGGCTCCGGC GGTGGAGGGTCCGAAATCGTCCTGACTCAGTCGCCTGGCACTCTGTGC TTGTCCCCGGGGGAGCGCGCTACCCTGTCGTGTGGGGCGTCGCAGTC CGTGTGAGCTCCTACCTCGCGTGGTACCAGCAGAAGCCCGGACAGG CCCCTAGACTTCTGATCTACGGCACTTCTTCACGCGCCACCGGGATCA GCGACAGGTTGAGCGGCTCCGGCTCCGGGACCGACTTCACCCTGACC ATTAGCCGGCTGGAGCCTGAAGATTTGCGCGTGTATTACTGCCAACACT ACGGAAACTCGCCGCCAAAGTTCACGTTCCGGACCCGGAACCAAGCTGG AAATCAAGACCACTACCCCAGCACCGAGGCCACCCACCCCGGCTCCTA CCATCGCCTCCCAGCCTCTGTCCCTGCGTCCGGAGgcatgtagaccgcagctg gtggggccgtgcatacccggtcttgacttcgctgcgatatctacattgggcccctctggtggtacttg cggggtcgtgctttactcgtgatcactctttactgtaagcgcggtcggaagaagctgctgtacatctta agcaacctcatgaggcctgtgcagactactcaagaggaggacggctgttcagccggttccagagg aggaggaaggcgctgcgaactgcgctgaaattcagccgcagcgcagatgtccagcctacaagca ggggcagaaccagctctacaacgaactcaatcttgctcgagagaggagtacgacgtgtggacaag cggagaggacgggacccagaaatggcggggaagccgcgcagaaagaatccccaagaggcctgt acaacgagctccaaaaggataagatggcagaagcctatagcgagattggtatgaaaggggaacgca gaagaggcaaaggccacgacggactgtaccagggactcagaccgccaaccaaggacacatgac gctctcacatgcaggccctgcccgcctcg
BCMA_EBB-C1978-G4		
BCMA_EBB- C1978-G4- aa Full CART	859	MALPVTALLPLALLHARPEVQLVESGGGLVQPGGSLRLSCAASGFTFS SYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDNKNTLY LQMNSLRAEDTAVYYCAKMGWSSGYLGAFDIWGGTTVTVSSGGGGSG GGGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVASSFLAWYQQK PGQAPRLLIYGASGRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQH YGGSPRLTFGGGTKVDIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGG AVHTRGLDFACDIYWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMR PVQTTQEEDGCSRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNEL NLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYS EIGMKGERRRRGKHDGLYQGLSTATKDTYDALHMQALPPR
BCMA_EBB- C1978-G4- nt Full CART	860	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTC CACGCCGCTCGGCCCGAAGTCCAACCTGGTGGAGTCCGGGGGAGGGCT CGTGCAGCCCGGAGGCAGCCTTCGGCTGTCGTGCGCCGCCTCCGGGT TCACGTTCTCATCTACGCGATGTCGTGGGTGAGACAGGCACCAGGAA AGGGACTGGAATGGGTGTCCGCCATTAGCGGCTCCGGCGGTAGCACC TACTATGCCGACTCAGTGAAGGGAAGGTTCACTATCTCCCGCGACAAC AGCAAGAACACCCTGTACCTCCAAATGAACTCTCTGCGGGCCGAGGAT ACCGCGGTGTACTATTGCGCCAAGATGGGTTGGTCCAGCGGATACTTG GGAGCCTTCGACATTTGGGGACAGGGCACTACTGTGACCGTGTCTCC GGGGGTGGCGGATCGGGAGGCGCGGCTCGGGTGGAGGGGGTTCCG AAATCGTGTTGACCCAGTCACCGGGAACCCTCTCGTGTCCCCGGGAG AACGGGCTACACTGTATGTAGAGCGTCCAGTCCGTGCCCTTCTCTCT TCCTGGCCTGGTACCAGCAGAAGCCGGGACAGGCACCCCGCTGCTC ATCTACGGAGCCAGCGGCCGGGCGACCGGCATCCCTGACCGCTTCTC CGGTTCCGGCTCGGGCACCGACTTTACTCTGACCATTAGCAGGCTTGA GCCCGAGGATTTTGCGGTGTACTACTGCCAACACTACGGGGGGAGCCC TCGCCTGACCTTCGGAGGCGGAACCTAAGGTCGATATCAAAACCACTAC CCCAGCACCGAGGCCACCCACCCCGGCTCCTACCATCGCCTCCAGC CTCTGTCCCTGCGTCCGGAGgcatgtagaccgcagctggtggggccgtgcatacccggtg gtcttgacttcgctgcgatatctacattgggcccctctggtggtacttgcggggtcctgctgctttactcgt gatcactctttactgtaagcgcggtcggaagaagctgctgtacatcttaagcaaccttcatgaggcctgt gcagactactcaagaggaggacggctgttcagccggttccagaggaggaggaaggcggtgcgaa ctgcgctgaaattcagccgcagcgcagatgtccagcctacaagcaggggcagaaccagctctaca acgaactcaatcttggtcgagagaggagtacgacgtgtggacaagcggagaggacgggacccag

		aaatgggcggaagccgcgcagaaagaatccccaagagggcctgtacaacgagctccaaaaggat aagatggcagaagcctatagcgagattggtatgaaaggggaacgcagaagaggcaaaggccacga cggactgtaccagggactcagcaccgccaccaaggacacctatgacgctctcacatgcaggccctgc cgctcgg
--	--	---

In one embodiment, the CAR comprises (e.g., consists of) an amino acid sequence provided in Table 16, or Table 1 of WO2016/014565, or as otherwise described herein. In one embodiment, the CAR comprises (e.g., consists of) an amino acid sequence selected from any one of SEQ ID NOs: 789, 791, 793, 795, 797, 799, 801, 803, 805, 807, 809, 811, 813, 815, 817, 819, 821, 823, 825, 827, 829, 831, 833, 835, 837, 839, 841, 843, 845, 847, 849, 851, 853, 855, 857, 859; or an amino acid sequence having at least one, two, three, four, five, 10, 15, 20 or 30 modifications (e.g., substitutions, e.g., conservative substitutions) but not more than 60, 50, or 40 modifications (e.g., substitutions, e.g., conservative substitutions) of an amino acid sequence selected from any one of SEQ ID NOs: 789, 791, 793, 795, 797, 799, 801, 803, 805, 807, 809, 811, 813, 815, 817, 819, 821, 823, 825, 827, 829, 831, 833, 835, 837, 839, 841, 843, 845, 847, 849, 851, 853, 855, 857, 859; or an amino acid sequence having 85%, 90%, 95%, 96%, 97%, 98%, 99% identity to an amino acid sequence selected from any one of SEQ ID NOs: 789, 791, 793, 795, 797, 799, 801, 803, 805, 807, 809, 811, 813, 815, 817, 819, 821, 823, 825, 827, 829, 831, 833, 835, 837, 839, 841, 843, 845, 847, 849, 851, 853, 855, 857, 859.

In one embodiment, the CAR molecule comprises a mesothelin antigen binding domain (e.g., a murine, human or humanized antibody or antibody fragment that specifically binds to mesothelin), a transmembrane domain, and an intracellular signaling domain (e.g., an intracellular signaling domain comprising a costimulatory domain and/or a primary signaling domain).

Exemplary CAR molecules that target mesothelin are described herein, and are provided in Table 17.

The CAR molecules in Table 17 comprise a mesothelin antigen binding domain, e.g., an amino acid sequence of any mesothelin antigen binding domain provided in Table 3. The leader sequence is in bold and underlined, CDRs are underlined, and the linker sequence between the heavy and light chain of the antigen binding region is shaded in grey.

Table 17. Exemplary CAR molecules

Name	Amino Acid Sequence	SEQ ID NO:
M5 CAR	<u>MALPVTALLPLALLHAARP</u> QVQLVQSGAEVEKPGASVKVSCKASGYTFTDYY MHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQGRVTMTRDTSISTAYMELSRL RSDDTAVYYCASGWDYWGQGTLLTVSSGGGGSGGGGSGGGGSGGGGSDIV MTQSPSSLSASVGDRVTITCRASQSIRYYLSWYQQKPGKAPKLLIYTASILQNGVP SRFSGSGSGTDFTLTISSLQPEDFATYYCLQTYTTPDFGPGTKVEIKTTTPAPRPPT PAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYWAPLAGTCGVLLLSLVITL YCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAP AYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQK DKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR	724

M11 CAR	<u>MALPVTALLPLALLHAARP</u> QVQLQQSGAEVKKPGASVKVSCKASGYTFTGYY MHWVRQAPGQGLEWMGWNPNSGGTNYAQNFQGRVTMTRDTSISTAYMELRRL RSDDTAVYYCASGWDYWGQGLTVTVSSGGGGSGGGGSGGGGSGGGGSDIR MTQSPSSLSASVGDRVTITCRASQSIRYYLSWYQQKPGKAPKLLIYTASILQNGVP SRFSGSGSGTDFTLTISLQPEDFATYYCLQTYTTPDFGPGTKVEIKTTTPAPRPPT PAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYWAPLAGTCGVLLLSLVITL YCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCEL RVKFSRSADAP AYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQK DKMAEAYSEIGMKGERRRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR	725
SS1 CAR	<u>MALPVTALLPLALLHAARP</u> QVQLQQSGPELEKPGASVKISCKASGYSFTGYTM NWKVQSHGKSLEWIGLITPYNGASSYNQKFRGKATLTVDKSSSTAYMDLLSLTSE DSAVYFCARGGYDGRGFDYWGQGTITVTVSSGGGGSGGGGSGGGGSDIELTQS PAIMSASPGKVTMTCSASSSVSYMHWWYQQKSGTSPKRWIYDTSKLASGVPGRF SGSGSGNSYSLTISSVEAEDDATYYCQWWSGYPLTFGAGTKLEITTPAPRPPTPA PTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYWAPLAGTCGVLLLSLVITLYC KRGKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCEL RVKFSRSADAPA	726
M1 CAR	<u>MALPVTALLPLALLHAARP</u> QVQLQQSGAEVKKPGASVKVSCKASGYTFTGYY MHWVRQAPGQGLEWMGRINPNSGGTNYAQKFQGRVTMTRDTSISTAYMELSR RSEDATVYYCARGRYYGMDVWGQGTMTVTVSSGGGGSGGGGSGGGGSGGGG EIVLTQSPATLSLSPGERATISCRASQSVSSNFAWYQQRPGQAPRLIYDASNRAT GIPPRFSGSGTDFTLTISLQPEDFAAAYYCHQRSNWLYTFGQGTQVDIKTTTPA PRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYWAPLAGTCGVLL SLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCEL RVKFSR SADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLY NELQDKMAEAYSEIGMKGERRRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR	727
M2 CAR	<u>MALPVTALLPLALLHAARP</u> QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYY MHWVRQAPGQGLEWMGWNPNSGGTNYAQKFQGRVTMTRDTSISTAYMELSR RSDDTAVYYCARDLRRTVTPRAYYGMDVWGQGTITVTVSSGGGGSGGGGSGG GGSGGGGSDIQLTQSPSTLSASVGDRVTITCQASQDISNSLNWYQQKAGKAPKLLI YDASTLETGVPSRFSGSGSGTDFSTISLQPEDFATYYCQQHDNLPLTFGQGTQV EIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYWAPLAG TCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCE LRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRK NPQEGLYNELQDKMAEAYSEIGMKGERRRRGKGGHDGLYQGLSTATKDTYDALHM QALPPR	728
M3 CAR	<u>MALPVTALLPLALLHAARP</u> QVQLVQSGAEVKKPGAPVKVSCKASGYTFTGYY MHWVRQAPGQGLEWMGWNPNSGGTNYAQKFQGRVTMTRDTSISTAYMELSR RSDDTAVYYCARGWDGSSYYDYWGQGLTVTVSSGGGGSGGGGSGGGGSGG GGSDIVLTQTPSSLSASVGDRVTITCRASQSINTYLNWYQHKPGKAPKLLIYAASSL QSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSFSPFTFGGKLEIKTTTP APRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYWAPLAGTCGVLL LSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCEL RVKFS RSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLY NELQDKMAEAYSEIGMKGERRRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR	729
M4 CAR	<u>MALPVTALLPLALLHAARP</u> QVQLVESGGGLVQPGGSLRLSCAASGFTFSYW MHWVRQVPKGKGLVWVSRINTDGSSTTYADSVGRFTISRDNKNTLYLQMNSLR DDDTAVYYCVGGHWAVWGQGTITVTVSSGGGGSGGGGSGGGGSGGGGSDIQM TQSPSTLSASVGDRVTITCRASQISDRLAWYQQKPGKAPKLLIYKASSLESVPS RFSGSGSGTEFTLTISLQPDFAVYYCQQYGHLPMTYFGQGTQVEIKTTTPAPRP PTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYWAPLAGTCGVLLLSLV ITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCEL RVKFSRSAD APAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNEL QDKMAEAYSEIGMKGERRRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR	730
M6 CAR	<u>MALPVTALLPLALLHAARP</u> QVQLVQSGAEVKKPGASVKVSCKASGYTFTSY MHWVRQAPGQGLEWMGIINPSSGGSTSYAQKFQGRVTMTRDTSTSTVYMESSLR	731

	SEDTAVYYCARYRLIAVAGDYYYYGMDVWGQGTMTVSSGGGGSGGGGSGGGGSGGGGSDIQMTQSPSSVSASVGDRVTITCRASQGVGRWLAWYQQKPGTAPKLIYAASLTQSGVPSRFSGSGSGTDFTLTINNLPEDFATYYCQQANSFPLTFGGGTREIKTTTTAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR	
M7 CAR	<u>MALPVTALLPLALLHAARP</u> QVQLVQSGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQMNSLR AEDTAVYYCARWVKVSSSSPAFDYWGGGTLTVTVSSGGGGSGGGGSGGGGSGGGGSGSEIVLTQSPATLSLSPGERAILSCRASQSVYTKYLGWYQQKPGQAPRLLIYDAST RATGIPDRFSGSGSGTDFTLTINRLEPEDFAVYYCQHYGGSPLITFGQGTREIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYWAPLAGTCGV LLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR	732
M8 CAR	<u>MALPVTALLPLALLHAARP</u> QVQLQQSGAEVKKPGASVKVSCKTSGYPFTGYS LHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQGRVTMTTRDTSISTAYMELSR LRSDDTAVYYCARDHYGGNSLFYWGGGTLTVTVSSGGGGSGGGGSGGGGSGGGGSGSDIQLTQSPSSISASVGDTVSTICRASQDSGTWLAWYQQKPGKAPNLLMYDAST LEDGVPSRFSGSASGTEFTLTNRLQPEDSATYYCQQYNSYPLTFGGGTKVDIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYWAPLAGTCGV LLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR	733
M9 CAR	<u>MALPVTALLPLALLHAARP</u> QVQLVQSGAEVKKPGASVEVSCKASGYTFTSYI MHWVRQAPGQGLEWMGIINPSSGGSTGYAQKFQGRVTMTTRDTSSTVHMESSL RSEDTAVYYCARGGYSSSSDAFDIWGGGTMVTVSSGGGGSGGGGSGGGGSGGGGSGSDIQLTQSPSLASVGDRVTITCRASQDISSALAWYQQKPGTPPKLLIYDASS LESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQFSSYPLTFGGGTRLEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYWAPLAGTCGV LLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR	734
M10 CAR	<u>MALPVTALLPLALLHAARP</u> QVQLVQSGAEVKKPGASVKVSCASGYTFTSYGI SWVRQAPGQGLEWMGWISAYNGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLR SDDTAVYYCARVAGGIYYYYGMDVWGQGTITVTVSSGGGGSGGGGSGGGGSGGGGSGGGSDIVMTQTPDSLAVSLGERATISCKSSHSVLNRRNNKNYLAWYQQKPGQPPKLLFYWASTRKSGVPDRFSGSGSGTDFTLTISSLQPEDFATYFCQQQTQTFPLTFGGGTRLEINTTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR	735
M12 CAR	<u>MALPVTALLPLALLHAARP</u> QVQLVQSGAEVKKPGASVKVSCASGYTFTGYI MHWVRQAPGQGLEWMGRINPNSGGTNYAQKFQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARTTTTSYAFDIWGQGTMTVTVSSGGGGSGGGGSGGGGSGGGGSGGGSDIQLTQSPSTLSASVGDRVTITCRASQSISTWLAWYQQKPGKAPNLLIYKASTLES GVPSRFSGSGSGTEFTLTISLQPDDFATYYCQQYNTYSPYTFGGGTKLEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR	736

	NELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR	
M13 CAR	<u>MALPVTALLPLALLHAARP</u> QVQLVQSGGGLVKPGGSLRLSCEASGFIFSDYYM GWIRQAPGKGLEWVSYIGRSGSSMYADSVKGRFTFSRDNAKNSLYLQMNSLRA EDTAVYYCAASPVAATEDFQHWGQGLTLTVSSGGGGSGGGGSGGGGSGGGG SDIVMTQTPTLSLSPGERATLSCRASQSVTSNYLAWYQQKPGQAPRLLLF <u>GAST</u> <u>RAT</u> GIPDRFSGSGSGTDFTLTINRLEPEDFAMYYCQQYGSAPVTFGQGTKEIKTT TPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYWAPLAGTCGV LLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVK FSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQE GLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALP PR	737
M14 CAR	<u>MALPVTALLPLALLHAARP</u> QVQLVQSGAEVRAPGASVKISCKASGFTFRGYYI HWVRQAPGQGLEWMGIINPSGGSRAYAQKFQGRVTMTTRDTSTSTVYMESSSLRS DDTAMYYCARTASCGGDCYYLDYWGQGLTLTVSSGGGGSGGGGSGGGGSGG GGSDIQMTQSPPTLSASVGDRVTITCRASENVNIWLAWYQQKPGKAPKLLIYKSSS <u>LASGVPSRFSGSGSGAEFTLTISSLQPD</u> FATYYCQQYQSYPLTFGGGTKVDIKTT TPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYWAPLAGTCGV LLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVK FSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQE GLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALP PR	738
M15 CAR	<u>MALPVTALLPLALLHAARP</u> QVQLVQSGGGLVQPGRSLRLSCAASGFTFDDYA MHWVRQAPGKGLEWVSGISWNSGSGIYADSVKGRFTISRDNANKNSLYLQMNSLR AEDTAVYYCAKDGSSSWSWGYFDYWGQGLTLTVSSGGGGSGGGGSGGGGSS SELTQDPAVSVALGQTVRTTCQGDALRSYYASWYQQKPGQAPMLVIYKNNRPS GIPDRFSGSDSGDTASLTITGAQAEDEADYYCNSRDSSGYPVFGTGKTVLTTTP APRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYWAPLAGTCGVLL LSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFS RSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEG LYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR	739
M16 CAR	<u>MALPVTALLPLALLHAARP</u> EVQLVESGGGLVQPGRSLRLSCAASGFTFDDYA MHWVRQAPGKGLEWVSGISWNSGSTGYADSVKGRFTISRDNANKNSLYLQMNSL RAEDTALYYCAKDSSSWYGGGSAFDIWGQGTMTVTVSSGGGGSGGGGSGGGGS SSELTQEPAVSVALGQTVRITCQGDLSRSYYASWYQQKPGQAPVLVIFGRSRRPS GIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDNTANHYVFGTGKTLVLT PAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYWAPLAGTCGV LLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVK SRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEG LYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPP R	740
M17 CAR	<u>MALPVTALLPLALLHAARP</u> EVQLVESGGGLVQPGRSLRLSCAASGFTFDDYA MHWVRQAPGKGLEWVSGISWNSGSTGYADSVKGRFTISRDNANKNSLYLQMNSL RAEDTALYYCAKDSSSWYGGGSAFDIWGQGTMTVTVSSGGGGSGGGGSGGGGS SSELTQDPAVSVALGQTVRITCQGDLSRSYYASWYQQKPGQAPVLVIYKNNRPS GIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRGSSGNHYVFGTGKTVLTT TPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYWAPLAGTCGV LLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVK FSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQE GLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALP PR	741
M18 CAR	<u>MALPVTALLPLALLHAARP</u> QVQLVQSGGGLVQPGGSLRLSCAASGFTFSSYW MHWVRQAPGKGLVWVSRINSDGSSTSYADSVKGRFTISRDNANKNTLYLQMNSLR AEDTAVYYCVRTGWVGSYYYMDVWGKTTTVTVSSGGGGSGGGGSGGGGSGG GGGSEIVLTQSPGTLSPGERATLSCRASQSVSSNYLAWYQQKPGQPRLIYD <u>VSTRAT</u> GIPARFSGGGSGTDFTLTISLEPEDFAVYYCQQRSNWPPWTFGQGT EIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYWAPLAG	742

	TCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEEGGCE LRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPGEMGGKPRRK NPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGGHDGLYQGLSTATKDTYDALHM QALPPR	
M19 CAR	<u>MALPVTALLPLALLHAARP</u> QVQLVQSGGGVQPGRSLRLSCAASGFTFSSYG MHWVRQAPGKGLEWVAVISYDGSNKYYADSVKGRFTISRDN SKNTLYLQMNSLR AEDTAVYYCAK <u>GYSRYYYGMDVW</u> QGTTVTVSSGGGGSGGGGSGGGGSGG GGSEIVMTQSPATLSLSPGERAILSCRASQSVYTKYLGWYQQKPGQAPRLLIYDAS TRATGIPDRFSGSGSGTDFTLTINRLEPEDFAVYYCQHYYGGSPLITFGQGTKVDIKT TTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYWAPLAGTCG VLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEEGGCELRV KFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPGEMGGKPRRKNPQ EGLYNELQKDKMAEAYSEIGMKGERRRRGKGGHDGLYQGLSTATKDTYDALHMQUAL PPR	743
M20 CAR	<u>MALPVTALLPLALLHAARP</u> QVQLVQSGGGLVQPGGSLRLSCAASGFTFSSYA MSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDN SKNTLYLQMNSLR AEDTAVYYCAKREAAAGHDWYFDLWGRGTLVTVSSGGGGSGGGGSGGGGSGG GGSDIRVTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASS LQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYSIPLTFGQGTKVEIKTTT PAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYWAPLAGTCGVL LLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEEGGCELRVKF SRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPGEMGGKPRRKNPQEG LYNELQKDKMAEAYSEIGMKGERRRRGKGGHDGLYQGLSTATKDTYDALHMQUALPP R	744
M21 CAR	<u>MALPVTALLPLALLHAARP</u> QVQLVQSWAEVKKPGASVKVSCKASGYTFTSY MHWVRQAPGQGLEWMGIINPSGGSTSYAQKFQGRVTMTRDTSTSTVYMELSNL RSEDTAVYYCARSPRVTTGYFDYWGGQTLVTVSSGGGGSGGGGSGGGGSGGG GSDIQLTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYKASSL ESGVPSRFSGSGSGTEFTLTISLQPDDEFATYYCQQYSSYPLTFGGGTRLEIKTTT PAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYWAPLAGTCGVL LLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEEGGCELRVKF SRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPGEMGGKPRRKNPQEG LYNELQKDKMAEAYSEIGMKGERRRRGKGGHDGLYQGLSTATKDTYDALHMQUALPP R	745
M22 CAR	<u>MALPVTALLPLALLHAARP</u> QVQLVQSGAEVRRPGASVKISCRASGDTSTRHYI HWLRQAPGQGPWGMVINPTTGPATGSPAYAQMLQGRVTMTRDTSTRTVYMEL RSLRFEDTAVYYCARSVVGSRAPYYFDYWGGQTLVTVSSGGGGSGGGGSGGG GSGGGGSDIQTQSPSSLSASVGDRVTITCRASQGISDYSAWYQQKPGKAPKLLI YAASTLQSGVPSRFSGSGSGTDFTLTISYLSQSEDFATYYCQQYSSYPLTFGGGK VDIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYWAPLA GTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEEGGC ELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPGEMGGKPRRK NPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGGHDGLYQGLSTATKDTYDALH MQALPPR	746
M23 CAR	<u>MALPVTALLPLALLHAARP</u> QVQLQQSGAEVKKPGASVKVSCKASGYTFTNYY MHWVRQAPGQGLEWMGIINPSGGYTYYAQKFQGRVTMTRDTSTSTVYMELSSLR SEDTAVYYCARIRSCGGDCYYFDNWGGQTLVTVSSGGGGSGGGGSGGGGSGG GGSDIQLTQSPSTLSASVGDRVTITCRASENVNIWLAWYQQKPGKAPKLLIYKSSS LASGVPSRFSGSGSGAEFTLTISLQPDDEFATYYCQQYQSYPLTFGGGKVDIKTT TPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYWAPLAGTCGV LLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEEGGCELRVK FSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPGEMGGKPRRKNPQE GLYNELQKDKMAEAYSEIGMKGERRRRGKGGHDGLYQGLSTATKDTYDALHMQUALP PR	747
M24 CAR	<u>MALPVTALLPLALLHAARP</u> QITLKESGPALVKPTQTLTCTFSGFSLSLAGVH VGWIRQPPGKALEWLALISWADDKRYRPSLRSLDITRVTSKDQVVL SMTNMQPE	748

DTATYYCALQGFDGYEANWGPGLTVTVSSGGGGSGGGGSGGGGSGGGGSDIV MTQSPSSLSASAGDRVTITCRASRGISSALAWYQQKPGKPPKLLIYDASSLESGVP SRFSGSGSGTDFLTIDSLPEDFATYYCQQSYSTPWTFGQGTKVDIKTTTPAPRP PTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYWAPLAGTCGVLLLSLVI TLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFEEEEEGGCELRVKFSRSAD APAYKQQGNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNEL QKDKMAEAYSEIGMKGERRRGKGHDLGLYQGLSTATKDTYDALHMQALPPR	
---	--

In one embodiment, a CAR molecule that binds mesothelin, comprises (e.g., consists of) an amino acid sequence as provided in Table 17, or Table 2 of International Publication No. WO2015/090230, filed December 19, 2014; incorporated herein by reference. In one embodiment, the CAR molecule comprises (e.g., consists of) an amino acid sequence selected from any one of SEQ ID NOs: 724-748; or an amino acid sequence having at least one, two, three, four, five, 10, 15, 20 or 30 modifications (e.g., substitutions, e.g., conservative substitutions) but not more than 60, 50, or 40 modifications (e.g., substitutions, e.g., conservative substitutions) of an amino acid sequence selected from any one of SEQ ID NOs: 724-748; or an amino acid sequence having 85%, 90%, 95%, 96%, 97%, 98%, 99% identity to an amino acid sequence selected from any one of SEQ ID NOs: 724-748.

In one embodiment, the CAR molecule comprises an EGFRvIII antigen binding domain (e.g., a murine, human or humanized antibody or antibody fragment that specifically binds to EGFRvIII), a transmembrane domain, and an intracellular signaling domain (e.g., an intracellular signaling domain comprising a costimulatory domain and/or a primary signaling domain).

Exemplary CAR molecules that target EGFRvIII are described herein, and are provided in Table 18, or in Table 2 of WO/2014/130657 or as described in WO2016/014789.

Table 18. Exemplary Humanized CAR Constructs. Sequences are provided with a leader, and the CDRs are underlined. Nt stands for nucleic acid and aa stands for amino acid

Name	SEQ ID NO:	Sequence
CAR 1		
CAR 1 – Full – nt	769	atggccctccctgtcaccgcctgtgcttccgtggctcttctgtctccacgcgcgtcgcccgagatc cagctggtgcagtcgggagctgaagtcacaaagcctggcgcaaccgtcaagatcctgtgcaaag gatcaggggtcaacatcgaggactactacatccattgggtgcaacaggcaccggaaaaggcctg gagtggatggggaggattgaccagaaaatgacgaaaccaagtacggaccgatctccaagga cgggtgaccatcacggctgacactccactaacaccgtctacatggaactctcgagcctcgctcgg aagataccgcggtgtactactgcgccttagagggtgagtgactctgaggacaagggaactaccgtca ccgtgtcgtcaggtggcggaggatcaggcggaggcggctccggtggaggaggaagcggagga ggtggctccgacgtggtgatgacgcagtcaccggactccttggcgggtgagcctgggtgaacgcgcc actatcaactgcaagagctccagagcttgcctggactccgatggaagacttatctcaattggctgca acagaagcctggccagcgcgcaaaagagactcatctactgggtgagcaagctggatagcggagtg ccagatcgggtttcgggatcgggctcaggcaccgacttcaccctgactatttccctccaagccga ggatgtggcgtctactactgttggcaggggactcactcccggggacctcgggtggaggcactaag gtggagatcaaaaccactacccagcaccgaggccaccaccccggtcctaccatgcctccc agcctctgtccctgcgtccggaggcatgtagaccgcagctgggtggggcgtgcataccgggggtc ttgactcgcctgcgatatctacattgggccctctggctggtactgcggggctcgtgctttactcg tgatcactcttactgtaagcgggtcggagaagctgctgtacatcttaagcaaccctcatgaggc

		ctgtgcagactactcaagaggaggacggctgtcatgccggttcccagaggaggaggaaggcgg ctgcgaactgcgctgaaattcagccgcagcgcagatgtccagcctacaagcaggggcagaac cagctctacaacgaactcaatcttggtcggagagaggagtacgacgtgtggacaagcggagag gacgggaccagaaatgggagggaagccgcgcagaaagaatcccaagaggcctgtacaa cgagctccaaaaggataagatggcagaagcctatagcgagattggtatgaagggaacgcag aagaggcaaaggccacgacggactgtaccagggactcagcaccgccaccaaggacacctatg acgctcttcacatgcaggccctgccgctcgg
CAR 1 – Full - aa	770	malpvtalllplalllhaarpeiqvlvqsgaevkkpgatvkisckgsgfniedvyyihwvqqapgkglew mgridpendetkyqpfqgrvtitadtstntvymelsslrstedavyycafragvywgggtvtvss ggggsgggsgggsgggsgggsvmtqspdslavslgeratinckssqslldsdgktylnwlqq kpgqpkrllslvskldsgvdpdrfsgsgsgtdftlisslqaedvavyywqgthfpatfgggtkveik ttppaprpptpaptiasqplslrpeacrpaaggavhtrglfacdiyiwaplagtcgvllslvitlyckrgrk klyifkqpfmrpvqttqeedgcscrpfpeeeeggcelrvkfsrsadapaykqgnqlynelnlgree ydvldkrrgrdpemggkprkrnpqeglynelqkdkmaeayseigmkgerrrgkghdglyqglsta tkdtydalhmqalppr
CAR 2		
CAR 2 - Full - nt	771	atggccctccctgtcaccgcctgtgcttccgctggctcttctgtctccacgcgcgtcggcccgacgtg gtcatgactcaaagcccagattccttggtgtctccctggagaaaagagcaacgatcaattgcaaaa gtctgcagtcctgttgactccgatggaaaaacctacctaactggctgcagcagaagccggga caaccaccaaagcggctgatttccctcgtgtccaagctggacagcggcgtgccggtatcgttctcg gcagcggctcgggaaccgatttactctcactatttctgactgcaagcggaggacgtggcgggtgat tactgtggcagggcactcacttcccgggtacttttggagggtaccaaagtcgaaatcaagggtg gaggcgggagcggaggaggcgggtcggaggaggaggatcgggtggcggagggtcagaaat ccagctgggtcagtcaggtgccgaagtgaagaagcctggggccacgggtgaagatctcgtgcaag gggagcggattcaacatcgaggattactacatccattgggtgcaacagggccctggcaagggt ggaatggatgggaaggatcgaccccgagaatgacgagactaagtacggcccgtatctccaaggga cgggtgaccatcactgcagacacttcaaccaacaccgtctacatggaactctcctcgtcgtcgtccg aggacaccgcgtgtactactgtgttctcagaggaggagtctactggggacagggaacgaccgtg accgtcagctcaaccactacccagcaccgaggccaccaccccggtctaccatcgctccca gcctctgtccctcgtcggaggcatgttagaccgcagctggtggggcgtgcataccgggggtctt gactcgcctcgtgatactacattggggccctctggctggtacttgcgggtctcgtcttactcgt gatcacttctactgtaagcgcgtcggagaagaagctgtgtacatcttaagcaacccttcatgaggcc tgtcagactactcaagaggaggacggctgttcatgccggttcccagaggaggagggaaggcggct gcgaactgcgctgaaattcagccgcagcgcagatgtccagcctacaagcaggggcagaacc agctctacaacgaactcaatcttggtcggagagaggagtacgacgtgtggacaagcggagagg acgggaccagaaatgggagggaagccgcgcagaaagaatcccaagaggcctgtacaac gagctccaaaaggataagatggcagaagcctatagcgagattggtatgaagggggaacgcaga agaggcaaaggccacgacggactgtaccagggactcagcaccgccaccaaggacacatga cgctcttcacatgcaggccctgccgctcgg
CAR 2 - Full - aa	772	malpvtalllplalllhaarpdvmtqspdslavslgeratinckssqslldsdgktylnwlqqkpgq ppkrllslvskldsgvdpdrfsgsgsgtdftlisslqaedvavyywqgthfpatfgggtkveikggg gsgggsgggsgggsgggseiqlvqsgaevkkpgatvkisckgsgfniedvyyihwvqqapgkgle wmgridpendetkyqpfqgrvtitadtstntvymelsslrstedavyycafragvywgggtvtv ssttpaprpptpaptiasqplslrpeacrpaaggavhtrglfacdiyiwaplagtcgvllslvitlyckr grkklyifkqpfmrpvqttqeedgcscrpfpeeeeggcelrvkfsrsadapaykqgnqlynelnlgrr eeydvldkrrgrdpemggkprkrnpqeglynelqkdkmaeayseigmkgerrrgkghdglyqgl statkdydalhmqalppr
CAR 3		
CAR 3 – Full - nt	773	atggccctccctgtcaccgcctgtgcttccgctggctcttctgtctccacgcgcgtcggcccgaaatc cagctgggtgcaaagcggagccgagggtgaagaagcccgagaatccctgcgcattctgtgtaagg gttccggctttaacatcgaggattactacatccactgggtgagacagatgccgggcaaggctctgga atggatgggcccgcacgcgggagaacgcagcaaaacaaatcaggaccaaacttccaaggaca tgtactatttccgggatacctcatcaacactgtctacttgcagtggagctcgtcaaggcgtcga taccgccatgtactactgcgcattcagaggagggtgtgtactggggccagggcactacggtcaccgtg tctcgggagggtggagggtcaggaggcggaggctcggcggtggaggatcaggcggaggagg aagcgtatgtgtcatgactcaatccctcactgtcactgctcactctgggcaaccggcttccatctc

		atgcaagtcaagccaatcgctgctcgactccgacggaaaaacctaactcaattggcttcagcagcg cccaggccagtcgcctcggaggctgatctactcgtgctgaagcttgactccgggtgcccgatcg gttagcgggaagcggatcggggaccgacttcacgttgagattagccgggtggaagccgaggac gtgggagtctattactgctggcaggggacccacttcccgggactttcggaggaggaccaaagtc gagattaagaccactaccccagcaccgaggccaccaccccggtcctaccatgcctcccagc ctctgtccctgctccgaggcatgtagaccgcagctggtggggccgtgcataccggggtctga cttcgctgcatatctacattgggcccctctggctggtactgctgggtcctgctgttactcgtgat cactcttactgtaagcgcggtcgggaagaagctgctgtacatcttaagcaaccctcatgaggcctgt gcagactactcaagaggaggacggctgtcatgccgttcccagaggaggaggaaggcggctgc gaactgcgctgaaattcagccgcagcgcagatgtccagcctacaagcaggggcagaaccag ctctacaacgaactcaatcttggtcggagagaggagtacgacgtgctggacaagcggagaggac gggaccagaaatggcggggaagccgcgcagaaagaatccccaagaggggcctgtacaacga gctccaaaaggataagatggcagaagcctatagcgagattggtatgaaaggggaacgcagaag aggcaaaggccacgacggactgtaccagggactcagcaccgccaccaaggacacatgacg ctctcacatgcaggccctgcccctcgg
CAR 3 – Full - aa	774	malpvtallplallhaarpeiqvlvqsgaevkkgpeslrisksgsfnie dyvih wvrqmpgkglew m gridpendetkyqpfqg hvtisadtsintvylqwsslkasdtamyyca rggv wgqgtvtv ssgggsgggsgggsgggsggsvmtqspislpvtlqgpasis ckssqslldsdgktyln wlq qrpgqsprrlis lvsklds gvprdfsgsgsgtdftlkisrveadvgyyc wqgthfpq tfgggtkvei kttpprptpaptiasqplsrpeacrpaaggavhtrgldfacdiywaplagtcgvllslvitlyckrgr kkilyifkqpfmrpvqtteedgcscrfeeeeeggcelrvkfsrsadapaykqgnqlynelnlgrr eydvldkrrrdpemggkprknpqeglynelqkdkmaeayseigmkgerrrgkghdglyqglst atkdtydalhmqalppr
CAR 4		
CAR 4 – Full - nt	775	atggccctccctgtcaccgcccgtgctgctccgctggctcttctgctccacgcccgtcggcccagcgc gtcatgacccaatcccctctctccctgcccgtcaccctgggtcagccggcgtcgatctcatgaaaa gtcacagtcctgctggattcggacggaaaaacctaactgaactggctccaacagaggccgggtc agtccctcgcagactgatctcgtggtgagcaagctcgactcgggtgtgcccgatcgggttccgg gtcaggatcgggcaccgactttacgctcaagatttcgagagtggaggccgaggatgtgggagtga ctattgtggcagggcacgcatttcccgggaccttggaggcgggactaagggtggaatcaaggg agggtggcggatcaggcggaggaggcagcggcggagggtgatcaggaggcggagggtcagag atccagctggtcaaagcggagcagaggtaagaagccaggcagctccctcgcatttcgtgcaa agggagcggctcaacattgaagattactacatccactgggtgcccgaatccaggaaagggtct ggaatggatgggacggatcgaccagaaaatgatgaaactaagtagcggaccgatctccaagga cacgtcactatctccgcgacacttcgatcaacaccgtgtacctccagtgaggacgctgaaagcct ccgacaccgctatgtactactgtgccttccgaggagggtctactgggacaggggactactgtgac cgtgtcgtccaccactacccagcaccgaggccaccaccccggtcctaccatgcctcccagc ctctgtccctgctccgaggcatgtagaccgcagctggtggggccgtgcataccggggtcttga cttcgctgcatatctacattgggcccctctggctggtactgctgggtcctgctgttactcgtgat cactcttactgtaagcgcggtcgggaagaagctgctgtacatcttaagcaaccctcatgaggcctgt gcagactactcaagaggaggacggctgtcatgccgttcccagaggaggaggaaggcggctgc gaactgcgctgaaattcagccgcagcgcagatgtccagcctacaagcaggggcagaaccag ctctacaacgaactcaatcttggtcggagagaggagtacgacgtgctggacaagcggagaggac gggaccagaaatggcggggaagccgcgcagaaagaatccccaagaggggcctgtacaacga gctccaaaaggataagatggcagaagcctatagcgagattggtatgaaaggggaacgcagaag aggcaaaggccacgacggactgtaccagggactcagcaccgccaccaaggacacatgacg ctctcacatgcaggccctgcccctcgg
CAR 4 – Full - aa	776	malpvtallplallhaarpdvmtqspislpvtlqgpasis ckssqslldsdgktyln wlqqrpgqs prrlis lvsklds gvprdfsgsgsgtdftlkisrveadvgyyc wqgthfpq tfgggtkveikggg sgggsgggsgggsgggseiqvlvqsgaevkkgpeslrisksgsfnie dyvih wvrqmpgkglew m gridpendetkyqpfqg hvtisadtsintvylqwsslkasdtamyyca rggv wgqgtvtv ssttpaprptpaptiasqplsrpeacrpaaggavhtrgldfacdiywaplagtcgvllslvitlyckr grkilyifkqpfmrpvqtteedgcscrfeeeeeggcelrvkfsrsadapaykqgnqlynelnlgrr eeydvldkrrrdpemggkprknpqeglynelqkdkmaeayseigmkgerrrgkghdglyqgl statkdydalhmqalppr
CAR 5		

CAR 5 – Full - nt	777	atggccctccctgtcaccgccctgctgcttccgctggctcttctgctccacgccgctcgcccgaaatc cagctcgtgcagagcggagccgaggtcaagaaaccgggtgctaccgtgaagattcatgaagg gatcgggcttcaacatcgaggattactacatccactgggtgcagcaggcaccaggaaaaggactt gaatggatggccggatcgacccggaaaatgacgagactaagtacggccctatctccaaggac gggtgacgatcaccgcagacactagcaccacaccgtctatatgaaactctcgctccctgaggtccg aagatactgccgtgtactactgtgctttcgcgagggtgtgtactggggacaggggtaccaccgtcac cgtgtcatcggcggtggaggtccggtggaggggtcaggaggcggtggaagcggaggagg cggcagcgacgtggtcatgactcaatcgccgctgtcgctgccgctactctgggacaacccgcgtc catcagctgcaaactcctcgagctactgcttgactccgatgaaagacctacctaactggctgcag caacgccaggccaatcccaagacgcctgatctcgttgggtgcaagctggactcaggggtgcc ggaccggttctccgggagcgggtcgggcacggatttcaactctcaagatctccagagtgaagccg aggatgtgggagtctactactgctggcagggaacccatttccctggaacttttggcggaggaaactaa ggctcgagattaaaaccactaccccagcaccgaggccacccaccccggtcctaccatcgctccc agcctctgtccctgctcggagggatgtagaccgcagctgggtggggcggtgcatacccggggtc ttgactcgcctgcgatatctacatttgggcccctctggctgggtactcgggggtcctgctgcttactcg tgatcactcttactgtaagcgggtcggaagaagctgctgtacatcttaagcaacccctcatgaggc ctgtgcagactactcaagaggaggacggctgttcatgcccgttccagaggaggaggaaggcgg ctgcgaactgcgctgaaattcagccgcagcgcagatgtccagcctacaagcaggggacagaac cagctctacaacgaactcaatcttggtcggagagaggagtacgactgtggacaagcggagag gacgggaccagaaaatggcggggaagccgcgcagaaagaatcccaagagggcctgtacaac cgagctccaaaaggataagatggcagaagcctatagcgagattggtatgaaaggggaacgcag aagaggcaaaaggccacgacggactgtaccagggactcagcaccgccaccaaggacacctaig acgctcttcacatgcaggccctgccgctcgg
CAR 5 – Full - aa	778	malpvtalllplalllhaarpeiqlvqsgaevkkpgatvkiscksgsfnie dyvih wvqqapgkglew m gridpendetkyqpfqg rvitadtstntvymelssrsedavvycafr gqvvy wgqgtvtvss ggggsgggsgggsgggsgggsgdvmtqspislpvtlgqpasis ckssqslldsdktyln wlqqr pgqsprrlis lvskldsg vprdfsgsgsgtdftlkisrveadvgyyc wqathfpgt fgggtkveikt ttpaprpptpaptiasqplslrpeacrpaaggavhtrglfdacdiyiwaplagtcgvllslvitlyckgrk kilyifkqpfmrpvqtqeedgcscrfeeeggcelrvkfsrsadapaykqgnqlynelnlgree ydvldkrrgrdpemggkprknpqeglynelqkdkmaeyseigmkgerrrgkghdglyqglsta tkdtydalhmqalppr
CAR 6		
CAR6 – Full - nt	779	atggccctccctgtcaccgccctgctgcttccgctggctcttctgctccacgccgctcgcccgagatt cagctcgtgcaatcgggagcgggaagtcaagaagccaggagagtccttgcggatctcatgaagg gtagcggctttaacatcgaggattactacatccactgggtgaggcagatcgccggggaagggactcg aatggatgggacggatcgacccagaaaacgacgaaactaagtacgggtccgatcttccaaggcca tgtactattagcggcgtacttcaatcaataccgtgtatctgcaatgggtcctcattgaaagcctcagat accgcgatgtactactgtgcttccagaggaggggtctactggggacagggaaactaccgtgactgtct cgtccggcgaggcgggtcaggaggtggcggcagcggaggaggaggggtccggcgagggtgg gtccgacgtcgtgatgacccagagccctgacagcctggcagtgagcctggcgaaagagctacc attaactgcaaatcgtcgagagcctgctggactcggacggaaaacgtacctcaattggctgcag caaaagcctggccagccaccgaagcgccttatctcactgggtgtcgaagctggattcgggagtgccc gatcgttctcgggtcgggatcgggtactgacttaccctcactatctcctcgcttcaagcagaggac gtggcgtctactactgtggtcagggaacccacttccgggaaccttcggcgaggaggacgaaagt ggagatcaagaccactacccagcaccgaggccacccaccccggtcctaccatcgctcccag cctctgtccctgctcggaggcatgtagaccgcagctgggtggggcggtgcatacccggggtcttg actcgcctgcgatatctacatttggcccctctggctgggtacttgcgggtcctgctgcttccactcgtg atcactcttactgtaagcgggtcggaagaagctgctgtacatcttlaagcaaccctcatgaggcct gtgcagactactcaagaggaggacggctgttcatgcccgttccagaggaggaggaaggcgggt gcaactgcgcgtgaaattcagccgcagcgcagatgtccagcctacaagcaggggcagaacc agctctacaacgaactcaatcttggtcggagagaggagtacgactgtctggacaagcggagagg acgggaccagaaaatggcggggaagccgcgcagaaagaatcccaagagggcctgtacaac gagctccaaaaggataagatggcagaagcctatagcgagattggtatgaaaggggaacgcaga agaggcaaaaggccacgacggactgtaccagggactcagcaccgccaccaaggacacctaiga cgctcttcacatgcaggccctgccgctcgg
CAR6 –	780	malpvtalllplalllhaarpeiqlvqsgaevkkpgeslrisksgsfnie dyvih wvrqmpgkglew

Full – aa		mgridpendetkyqpfqg hvtisadtsintvylqwsslkasdtamyycaf rggvywgggtvtv ssggsgsgsgsgsgsgsgsgsdvmtqspdslavslgeratinc kssqslldsdqktylnwl qqkpgppkrlis lvskldsgvpdfrfsgsgsgtdftltisslqaedvavyyc wqgthfpqtfgggtkv eikttppaprpptpaptiasqplslrpeacrpaaggavhtrglfacdiyiwaplagtcgvllslvitlyckr grkklyifkqpfmrpvqttqeedgcsrfpeeeeggcelrvkfsrsadapaykqggnqlynelnlgr eeydvldkrrrdpemggkprknpqeglynelqkdkmaeayseigmkgerrrgkghdglyqgl statkdydalhmqalppr
CAR 7		
CAR 7 Full - nt	781	atggccctccctgtcaccgccctgtctctccgtctgtctcttctgtctccacgccgtcggcccgacgtg gtgatgactcagtcgcctgactcgtctgtctccctggagagcgggccactatcaattgcaagtc atcccagtcgtctgtgattccgacgggaaaacctacctaattggctgcagcaaaacccgggac agcctccaaagcggctcatcagcctggtgtccaagtggacagcggcgtgccagaccgcttctccg gttcgggaagcgggtactgtattcacgctgaccatctcatccctcaagcggaggatgtggcagctac tactgttggcagggcacgcatttccgggacatttggaggaggaccgaaggtcgaaatcaaggga ggagggtggctcgggaggagggtcgggaggaggaggatcaggaggcgggtggaagcgaga ttcaactgttcagagcggcgagaaagcaagaagccgggtgaatcgtcagaatctcgtgcaaa ggatcgggattcaacatcgaggactactacattcactgggtcagacaaatgccgggcaaagggt ggaatggatgggaggatcgaccccgaaaacgatgaaccaagtacggaccaatcttcaagg gcacgtgaccatttccggcggacacctcaatcaacactgtgtacctccagtgaggctcacttaaggcc agcgataccgccatgtactattgcgttccggcggagggtgtactggggacagggcactactgtga ccgtgtcatccaccactacccagaccgaggccaccacccggctcctaccatcgctctccag cctctgctcctgctcggaggcatgtagaccgcagctgggtggggcgtgcataccgggggtcttg acttgcctgcatatctacatttggccctctgtgtgtacttgcgggtcgtcttctcactgtg atcactcttactgttaagcgcggctcggaagaagctgtgtacatcttaagcaaccctcatgaggct gtgcagactactcaagaggaggacggctgttcatgccggtcccagaggaggagggaagggcgt gcgaactgcgcgtgaaattcagccgcagcgagatgtccagcctacaagcaggggcagaacc agctctacaacgaactcaatcttggcggagagaggagtacgacgtgtggacaagcggagagg acgggacccagaaatgggagggaagccgcgagaaagaatcccaagagggcctgtacaac gagctccaaaaggataagatggcagaagcctatagcgagattggtatgaaaggggaacgcaga agaggcaaaggccacgacggactgtaccagggactcagcaccgccaccaaggacacatga cgctctcacatgcaggccctgccgctcgg
CAR 7 Full - aa	782	malpvtallplallhaarpdvmtqspdslavslgeratinc kssqslldsdqktylnwlqqkpgg ppkrlis lvskldsgvpdfrfsgsgsgtdftltisslqaedvavyyc wqgthfpqtfgggtkveikggg gsgggsgsgsgsgsgsgsgseiqlvqsgaevkkpgeslriscgsgfnie dyvihwvrmpgkgle wmgridpendetkyqpfqg hvtisadtsintvylqwsslkasdtamyycaf rggvywgggtvtv vssttpaprpptpaptiasqplslrpeacrpaaggavhtrglfacdiyiwaplagtcgvllslvitlyck rgrkklyifkqpfmrpvqttqeedgcsrfpeeeeggcelrvkfsrsadapaykqggnqlynelnlgr reeydvldkrrrdpemggkprknpqeglynelqkdkmaeayseigmkgerrrgkghdglyqgl statkdydalhmqalppr
CAR 8		
CAR 8 – Full - nt	783	atggccctccctgtcaccgccctgtctctccgtctgtctcttctgtctccacgccgtcggcccgatgtg gtcatgacgcagtcaccactgtccctccccgtgacccttgacagccagcgtcgattagctgcaagt catcccaatccctgtcgtatcggtggaaagacctatctcaactggctgcagcaaaagaccgggtc agagccctaggagactcatctcgttgggtgtcaaaagctggacagcggagtgccggaccgggttccg gttcgggatcggggacggacttactctgaagatttcacgggtggaagctgaggatgtgggagtgt ctactgtggcagggaacccatttccctggcacttttggcggagggaactaaggctgaaatcaaggg aggagggtggctcgggaggaggcggatcggcggaggcgggagcggcggaggagggtccgaa atccaactgtccagtcaggagccgaagtgaagaaacccgggagccaccgtcaaaatcagctgt agggatcgggattcaatcagaggactactacatccactgggtgcagcaagctccgggcaaggga ctggagtggatggggcgcacgcagccagagaacgcagcaaaacaaatcggcccgatcttcaa gggagggtgaccatcaccgcggacacctcaactaactgtgtacatggagctgagctccctgcg ctccgaagatactgcagctactactgcgccttccgggtgtgtactggggacagggcaccact gtgactgtcagctcgaccactacccagcaccgaggccaccacccggctcctaccatcgctcc cagcctctgtccctgcgtcggaggcatgttagaccgcagctgggtggggcgtgcataccgggggt cttgacttgcctgcgatactacatttggccctctgtgtgtacttgcgggtcgtcttctcactc gtgatcactcttactgttaagcgcggctcggaagaagctgtgtacatcttaagcaaccctcatgagg

		cctgtgcagactactcaagaggaggacggctgttcatgccgggtcccagaggaggaggaaggcg gctgcgaactgcgcgtgaaattcagccgcagcgcagatgtccagcctacaagcaggggcagaa ccagctctacaacgaactcaatcttggcggagagaggagtacgacgtgctggacaagcggaga ggacgggaccagaaatggcggggaagccgcgcagaaagaatcccaagaggcctgtaca acgagctccaaaaggataagatggcagaagcctatagcgagattggtatgaaaggggaacgca gaagaggcaaaggccacgacggactgtaccagggactcagcaccgccaccaaggacacctat gacgctcttcacatgcaggccctgccgcctcgg
CAR 8 – Full - aa	784	malpvtalllplalllhaarpdvmtqspislrvltlqgpasisc <u>kssqsllds dqktyln</u> wlqrrpgqs prrlis <u>lvsklds</u> gvprdfsgsgsgtdftlkisrveaedvgvyyc <u>wqgthfpqt</u> fgggkveikgggg sgggsgggsgggsgggseqlvqsgaevkkpgatvkisksgsfnie <u>dyviah</u> wvqqapgkglew mg <u>ridpendetkyqpfqg</u> rvtitadtstntvymelssrsedtavyycafr <u>qgvv</u> wgqgtvtvss ttpaprpptpaptiasqplslrpeacrpaaggavhtrglfacdiyiwaplagtcgvllslvitlyckrgrk klyifkqpfmrpvqttqeedgcscrfeeeeeggcelrvkfsrsadapaykqgnqlynelnlgree ydldkrrgrdpemggkprknpqeglynelqkdkmaeayseigmkgerrrgkghdglyqglsta tkdtydalhmqalppr
CAR 9 Mouse anti-EGFRvIII clone 3C10		
CAR 9 – Full - nt	785	atggccctccctgtcaccgcctgtcgtctccgtggctcttctgctccacgcgcgtcggcccgagatc cagctccaacagagcggagccgaactggtcaaaccgggagcgtcggtagaagtgtcatgactg gatcgggcttcaacatcgaggattactacatccactgggtcaagcaacgcaccgagcaggggctg gaatggatcggacggatcgaccccgaaaacgatgaaaccaagtacgggcctatcttcaaggac gggccaccattacggctgacacgtcaagcaataccgtctacctccagctttccagcctgacctcca ggacactgccgtgtactactgcgcctcagaggaggcgtgtactggggaccaggaaccactttgac cgtgtccagcggaggcgggtggatcaggaggaggaggctcaggcgggtggcggctcgcacatgga cgtggtcatgactcagtcgcccgctgacccgtcgggtggcaattggacagagcgcacatctcgtgc aagagctcacagtcgctgctggattccgacggaagacttatctgaactggctgctccaaagacca gggcaatcaccgaaacgccttatctccctgggtgctgaaactcgactcgggtgctccggatcgggttac cggtagcgggtccggcacggactcactctccgcatttcgagggtggaagcggaggatcctgggat ctactactgttggcagggaaccacttccctgggacttttggaggcggaaactaagctgaaatcaag accactacccagcaccgaggccacccacccggctcctaccatcgctcccagcctctgtccctg cgtccggaggcatgtagaccgcagctggtggggcgggtgcatacccggggtcttgacttcgctgc gatatctacatttgggccctctggctggtacttgcggggtcctgctgcttactcgtgatcactttact gtaagcgggtcggagaagctgctgtacatcttaagcaacccttcagaggcctgtgcagactac tcaagaggaggacggctgtcatgccggtcccagaggaggagggaaggcggctgcgaactgcgc gtgaaattcagccgcagcgcagatgtccagcctacaagcaggggcagaaccagctctacaacg aactcaatcttggtcggagagaggagtacgacgtgtggacaagcggagaggacgggaccag aaatgggcggaagccgcgcagaaagaatcccaagagggcctgtacaacgagctccaaag gataagatggcagaagcctatagcgagattggtatgaaaggggaacgcagaagaggcaagg ccacgacggactgtaccagggactcagcaccgccaccaaggacacctatgacgctcttcacatgc aggccctgccgcctcgg
CAR 9 – Full - aa	786	malpvtalllplalllhaarpeiqlqsgaelvkpgasvklscgtsgsfnie <u>dyviah</u> wvkqrteqglewig <u>ridpendetkyqpfqg</u> ratitadtssntvylqlssltedavyycafr <u>qgvv</u> wpgtltvssgggg sgggsgggshmdvmtqspitlsvaigqsasisc <u>kssqsllds dqktyln</u> wlqrrpgqspkrli <u>lvsklds</u> gvprdfsgsgtdftlrisrveaedlgiiyc <u>wqgthfpqt</u> fgggkveiktttppaprpptpa ptiasqplslrpeacrpaaggavhtrglfacdiyiwaplagtcgvllslvitlyckrgrkklyifkqpfmr pvqttqeedgcscrfeeeeeggcelrvkfsrsadapaykqgnqlynelnlgreeydldkrrgrd pemggkprknpqeglynelqkdkmaeayseigmkgerrrgkghdglyqglstatkdtydalhm qalppr
CAR10 Anti-EGFRvIII clone 139		
CAR 10 Full - nt	787	atggccctccctgtcaccgcctgtcgtctccgtggctcttctgctccacgcgcgtcggcccgatattc aaatgactcagagcccttcatccctgagcgcagcgtcggagacagggtagcatcacgtgccgg gcatoccaaaggcattagaaataacttggcgtggtatcagcaaaaaccaggaaaggccccgaagc gcctgatctacgcggcctccaacctcagtcaggagtgcctcgcgttcaccgggagcggtagcg gaactgagttacccttatcgtgtcgtccctgcagccagaggacttcgcgacctactactgctccagc atcactcgtaccgcgttgcgttcgggaggcgggaaccaaggctgaaatcaaacgcactggctgcagct caggggtccggtaaaccgggatcgggagaaggatcgggaagtccaagtctggagagcggaggc ggactcgtgcaacctggcgggtcgtcgggtcagctgtgccgcgtcgggttttacttccagctcgtac

		gctatgtcatgggtgcggcaggctccgggaaaggggctggaatgggtgtccgctatttccggctcgg gtggaagcaccaattacgcgactccgtgaagggacgcttcacatctcacgggataactccaag aatactctgtacctccagatgaactcgtgagagccgaggacaccgcagtgtactactgcgcaggg tcaagcggctgttccgaatactggggacagggcacccctgctactgtcagctccaccactaccca gcaccgaggccacccacccggctcctaccatcgctccagcctgtccctgcgtccggaggga ttagacccgcagctggtggggccgtgcataccggggtcttgacttcgctgcgatactacatttg gcccctctggctggtacttgcggggctctgctgtttactcgtgatcactcttactgtaagcggctg gaagaagctgctgtacatctttaagcaaccctcatgaggcctgtgcagactactcaagaggagga cggctgttcatgccggtcccagaggaggaggaaggcggctgcgaactgcgctgaaattcagcc gcagcgagatgtccagcctacaagcaggggcagaaccagctctacaacgaactcaatcttgg cggagagaggagtacgacgtgctggacaagcggagaggacgggacccagaaatggcgggga agccgcgcagaaagaatccccagagggcctgtacaacgagctccaaaaggataagatggca gaagcctatagcgagattggtatgaaaggggaacgcagaagaggcaaaggccacgacggact gtaccagggaactcagcaccgccaccaaggacacctatgacgctcttcacatgcaggccctgccg ctcgg
CAR 10 Full - aa	788	malpvtallplallhaarpdiqmtqspsslsasvgdrvtitcrasqgirnnlawyqqkpgkapkriya asnlqsgvpsrftgsgsgteftlivsslpqdfatyyclqhhsypltsgggtkveikrtgstsgskpgsg egsevqlesggglvqpggsrlscaasgftssyamswwrqapgkglewvsaisgsggstnyad svkgrftisrdnskntlylqmnsraedtavyycagssgswseywgqgtlvtssttpaprpptpapti asqplslrpeacrpaaggavhtrgldfacdiyiwaplagtcgvllslvitlyckgrkkllyfifkqpfmrpv qttqeedgcscrfeeeeeggcelrvkfsrsadapaykqqnqlynelnlgreeydvldkrrgrdpe mggkprkrnpqeglynelqkdkmaeayseigmkgerrrgkghdglyqglstatkdydalhmql ppr

In one embodiment, a CAR molecule that binds EGFRvIII comprises (e.g., consists of) an amino acid sequence as provided in Table 18. In one embodiment, the CAR that binds EGFRvIII comprises (e.g., consists of) an amino acid sequence selected from any one of SEQ ID NOs: 770, 772, 774, 776, 778, 780, 782, 784, 786, 788; or an amino acid sequence having at least one, two, three, four, five, 10, 15, 20 or 30 modifications (e.g., substitutions, e.g., conservative substitutions) but not more than 60, 50, or 40 modifications (e.g., substitutions, e.g., conservative substitutions) of an amino acid sequence selected from any one of SEQ ID NOs: 770, 772, 774, 776, 778, 780, 782, 784, 786, 788; or an amino acid sequence having 85%, 90%, 95%, 96%, 97%, 98%, 99% identity to an amino acid sequence selected from any one of SEQ ID NOs: 770, 772, 774, 776, 778, 780, 782, 784, 786, 788.

In one embodiment, a CAR molecule comprises a CD123 antigen binding domain (e.g., a murine, human or humanized antibody or antibody fragment that specifically binds to CD123), a transmembrane domain, and an intracellular signaling domain (e.g., an intracellular signaling domain comprising a costimulatory domain and/or a primary signaling domain). Exemplary CAR molecules that target CD123 include those provided in Table 19, and those provided in Tables 2, 6 and 9 of WO2016/028896. Other exemplary CAR molecules that target CD123 are described in WO/2014/130635 (e.g., Table 1 of WO/2014/130635). Other exemplary CAR molecules that target CD123 are described in WO/2014/144622.

In one embodiment, a CAR molecule that binds CD123 comprises (e.g., consists of) an amino acid sequence as provided in Table 19. In one embodiment, the CAR that binds CD123 comprises (e.g., consists of) an amino acid sequence selected from any one of SEQ ID NOs: 750, 755, 760, 765; or an

amino acid sequence having at least one, two, three, four, five, 10, 15, 20 or 30 modifications (e.g., substitutions, e.g., conservative substitutions) but not more than 60, 50, or 40 modifications (e.g., substitutions, e.g., conservative substitutions) of an amino acid sequence selected from any one of SEQ ID NOs: 750, 755, 760, 765; or an amino acid sequence having 85%, 90%, 95%, 96%, 97%, 98%, 99% identity to an amino acid sequence selected from any one of SEQ ID NOs: 750, 755, 760, 765.

Table 19. Exemplary CAR sequences

Name	SEQ ID	Sequence
CAR123-2 NT	749	atggccctccctgtcaccgcccgtgcttccgctggctcttctgtccacgcccgtcggccccaagtgcaa ctcgtccaaagcggagcgggaagtcaagaaccggagcagcgtgaaagtgtcctgcaaagcctccg gctacacctttacgggctactacatgcactgggtgcgcagggcaccaggacagggcttgaatgatgg gatgatcaaccctaattcgggcggaactaactacgcacagaagttccaggggagagtactgtactc gggatacctccatctcaactgtctacatggaactctcccgcttgcggtcagatgatacggcagtgactact gcgcccgcgacatgaatactcgtgctaccgtgccgttcgacatctggggacaggggactatggttactgtc tcatcgggctggaggtcaggaggaggcggctcgggaggcggaggtcggacattcagatgaccca gtcccatctctctgtcggccagcgtcggagataggggtaccattacgtcgggcctcgcaaagcatct cctcgtacctcaactggtatcagcaaaagccgggaaaggcgcctaagctgctgatctacgccgcttcga gcttgcaaagcggggtgccatccagattctcgggatcaggctcaggaaccgacttcacctgaccgtga acagcctccagccggaggactttgccacttactactgccagcaggagactccgtgccgcttactttcggg gggggtaccgcctggagatcaagaccactacccagcaccgaggccacccaccccgctcctacca tcgctccagcctctgtccctgcgtccggaggcatgtagaccgcagctggtggggccgtgcatacccg gggtcttgacttcgctgcgatatctacatttgggccctctggctggtacttgcggggtcctgtgctttactc gtgatcactcttactgtaagcgcggtcgggaagaagctgctgtacatcttaagcaaccctcatgaggcct gtgcagactactcaagaggaggacggctgttcatgccggtcccagaggaggaggaaggcggctgcg aactgcgctgaaatcagccgcagcgcagatgtccagcctacaagcaggggcagaaccagctcta caacgaactcaatcttggctcggagagaggagtacgacgtgctggacaagcggagaggacgggaccc agaaatggcggggaagccgcgagaaagaatcccaagagggctgtacaacgagctccaaagg ataagatggcagaagcctatagcgagattggtatgaaaggggaacgcagaagaggcacaaggccacg acggactgtaccagggactcagcaccgcaccaaggacacatgacgctcttcacatgcaggccctg ccgcctcgg
CAR123-2 AA	750	malpvtallplallhaarpqvlvqsgaevkkgasvkvscasgytftgyymhwvrqapggglewm gwinpnsggttnyaqkfqgrvlttrdsistvymelsrlrddtavyyccardmnilatvpfdiwgggtmvtvss ggggsgggsgggsgdiqmtqspsslsasvgrvritcrasqsisssylnwyyqqkpgkapklliyaasslq sgvpsrfsrgsgsgtdftltvnslqpedfatyyccqgdsvglftgggtrleiktttpprptpaptiasqplslrp eacrpaaggavhtrglfacdiyiwaplagtcgvllslvitlyckrgrklllyifkqpfmrpvqtteedgcsrf peeeeggcelrvkfsrsadapaykqgnqlynelnlgrrreydvldkrrrdpemmkgprknpqegly nelqkdkmaeyseigmkgerrrgkghdglyggstatkdydalhmqalppr
CAR123-2 scFv	751	malpvtallplallhaarpqvlvqsgaevkkgasvkvscasgytftgyymhwvrqapggglewm gwinpnsggttnyaqkfqgrvlttrdsistvymelsrlrddtavyyccardmnilatvpfdiwgggtmvtvss ggggsgggsgggsgdiqmtqspsslsasvgrvritcrasqsisssylnwyyqqkpgkapklliyaasslq sgvpsrfsrgsgsgtdftltvnslqpedfatyyccqgdsvglftgggtrleik
CAR123-2 VH	752	QVQLVQSGAEVKKPGASVKVSCASGYTFTGYMHWVRQAPGQGLEWM GWINPNSSGTTNYAQKFQGRVLTTRDTSISTVYMELSRLRSDDTAVYYCAR DMNILATVPFDIWGQGTMTVSS
CAR123-2 VL	753	DIQMTQSPSSLSASVGRVITCRASQSISSYLNWYQQKPGKAPKLLIYAA SSLQSGVPSRFSGSGSGTDFTLTVNLSLPEDFATYYCQQGDSVPLTFGG GTRLEIK
CAR123-3 NT	754	atggccctccctgtcaccgcccgtgcttccgctggctcttctgtccacgcccgtcggccccaagtccaa ctcgttcaatccggcgcagaaagtcaagaagccaggagcatcagtgaagtgtcctgcaaagcctcagg ctacatcttcacgggatactacatccactgggtgcgccaggctccgggcccaggcccttgagtggatgggc tgatcaaccctaactctgggggaaccaactacgctcagaagttccaggggagggtcactatgactcgc gatacctccatctccactgcgtacatggaactctcgggactgagatccgacgatcctgcggtgtactactgc

		gccccgggacatgaacatcttggcgaccgtgccgtttgacatttggggacagggcaccctcgtcactgtgtc gagcgggtgaggaggctcgggggtggcgatcaggagggggaggaagcgacatccagctgactc agagcccatcgtcgtgtccgcgtcgggtgggggtagagtaccattacttgcgcgccagccagagcat ctcatcatatctgaattggtaccagcagaagccccgaaaggcccaaaaactgctgatctacgtgcaag cagcctccaatcgggagtgccgtcacgggtctccgggtccgggttcgggaactgactttaccctgaccgtga attcgtgcaaccggaggatttcgccactactactgtcagcaaggagactccgtgccgtgaccttcggg ggaggcaccaaggtcgaaatcaagaccactacccagcaccgaggccaccaccccggtcctacc atcgctcccagcctctgtccctgcgtccggaggcatgtagaccgcagctggtggggccgtgcataccc ggggtctgacttcgcctgcgatatctacatttggggccctctggctggtacttgcggggctcgtgctttcac tcgtgatcactcttactgtaagcgcggtcggaagaagctgctgtacatcttaagcaaccctcatgaggcc tgtgcagactactcaagaggaggacggctgtcatgccggtcccagaggaggaggaaggcggtgcg aactgcgcgtgaaattcagccgcagcgcagatgctccagcctacaagcaggggcagaaccagctcta caacgaactcaatcttggtcggagagaggagtacgacgtgctggacaagcggagaggacgggaccc agaaatggcggggaagccgcgcagaaagaatccccaagagggcctgtacaacgagctccaaaagg ataagatggcagaagcctatagcgagattggtatgaaaggggaacgcagaagaggcaaaggccacg acggactgtaccagggactcagcaccgccaccaaggacacctatgacgctcttcacatgcaggccctg ccgcctcgg
CAR123-3 AA	755	malpvtallplallhaarpqvqlvqsgaevkpgasvkvscasgyiftgyiihwwrqapggglewmg winpnsnggtnyaqkfqgrvtmtrdtsistaymelsglrddpavyycardmnilatvpfdiwgggtltvss ggggsgggsggggsdiqltqspsslsasvgdrvtitcrasqsissylhwyqqkpgkapklliyaasslqs gvpsrfsgsgsgtdftltvnsllqpedfatyyccqgdsvppltfgggtkveiktpprptpaptiasqplslrp eacrpaaggavhtrglfdacdiyiwaplagtcgvllslvitlyckrgrklliyfkapfmrpvqtqeedgcscrfl peeeeggcelrvkfsrsadapaykqggnqlynelnlgrreeydvldkrrgrdpemggkprkrnpqegly nelqkdkmaeayseigmkgerrrgkghdglyqglstatkdydalhmqalppr
CAR123-3 scFv	756	malpvtallplallhaarpqvqlvqsgaevkpgasvkvscasgyiftgyiihwwrqapggglewmg winpnsnggtnyaqkfqgrvtmtrdtsistaymelsglrddpavyycardmnilatvpfdiwgggtltvss ggggsgggsggggsdiqltqspsslsasvgdrvtitcrasqsissylhwyqqkpgkapklliyaasslqs gvpsrfsgsgsgtdftltvnsllqpedfatyyccqgdsvppltfgggtkveik
CAR123-3 VH	757	QVQLVQSGAEVKKPGASVKVSCASGYIFTGYIIHWWVRQAPGQGLEWMG WINPNSGGTNYAQKFQGRVTMTRDTSISTAYMELSGLRDDPAVYYCARD MNILATVPFDIWGQGTLTVSS
CAR123-3 VL	758	DIQLTQSPSSLSASVGDRVTITCRASQSISYLNWYQQKPGKAPKLLIYAAS SLQSGVPSRFSGSGSGTDFTLTVNSLQPEDFATYYCQQGDSVPLTFGGGT KVEIK
CAR123-4 NT	759	atggccctccctgtcaccgacctgctgcttcgctggtcttctgtccacgccgctcggccccaagtccaa ctccaacagtcaggcgcagaagtgaaaaagagcgggtcatcggtgaaagtgtcatgcaaagcctcgg gctacaccttactgactactatgactggtcgcgcaggcaccgggacagggacttgagtggatgg gatggatcaaccgaattcaggggacactaactacgcgcagaagtccaggggagagtacacctgac gagggacacctcaatttcgaccttcatatggaattgtcgcgcctgagatcggacgatactgctgtgact actgtgccgcgcagacatgaacatctcgcgactgtgccttttgatatctggggacaggggactatgggtacc gtttctccgcttcgggtggcggagggtcgggaggccgggctccggtggaggaggcagcgacatcca gatgactcagagcccttctcgtgagcgcctcagtgaggagatcgcgtgaccatcacttgcggggccagc cagtcatttctgcttacctcaattgtaccagcagaagccgggaaaggcgcccaagcttctgtatcag ctgcgagctccctgcaaagcggggtgcgagccgattctcgggttcgggtcgggaaccgacttactct gacctctcatccctgcaaccagaggactttgccacctactactgccaacaaggagattctgtccactga cggtcggcggaggaaaccaaggtcgaaatcaagaccactacccagcaccgaggccaccaccccg ctctaccatcgctcccagcctctgtccctgcgtccggaggcatgtagaccgcagctggtggggccgtg cataccgggggtcttgacttcgctgcgatatctacatttggggccctctggctggtacttgcgggtcgtg gctttactcgtgatcactcttactgtaagcgcggtcggaagaagctgctgtacatcttaagcaaccctca tgaggcctgtgcagactactcaagaggaggacggctgtcatgccggttccagaggaggaggaaggc ggctgcgaactgcgcgtgaaattcagccgcagcgcagatgctccagcctacaagcaggggcagaaacc agctctacaacgaactcaatcttggtcggagagaggagtacgacgtgctggacaagcggagaggacg ggaccagaaatggcggggaagccgcgcagaaagaatccccaagaggcctgtacaacgagctcc aaaaggataagatggcagaagcctatagcgagattggtatgaaaggggaacgcagaagaggcaaa ggccacgacggactgtaccagggactcagcaccgccaccaaggacacctatgacgctcttcacatgca ggccctgccgcctcgg

CAR123-4 AA	760	malpvtalllplalllhaarqvqlqqsgaevkksgasvkvskasgytftdyymhwlrqapggglewm winpnsgdtnyaqkfqgrvlttrdtsistvymelsrlrsddtavyyccardmnilatvpfdiwgggtmvtvssa sgggsggrasggggsdiqmtqspsslsasvgdrvtitcrasqsissylnwyqqkpgkapklliyaassl qsgvpsrfsgsgsgtdftltisslqpedfatyyccqgdsvppltfgggkveikttppaprpptaptiasqplslr peacrpaaggavhtrglfacdiyiwaplagtcgvllslvitlyck
CAR123-4 scFv	761	MALPVTALLLPLALLLHAARPQVQLQQSGAEVKKSGASVKVSKASGYTFT DYMHVLRQAPGQGLEWMGWINPNSGDNTYAQKFQGRVLTTRDTSISTV YMELSLRSDDTAVYYCARDMNILATVPFDIWGQGTMTVSSASGGGGS GGRASGGGGSDIQMTQSPSSLSASVGDRVTITCRASQSISYLNWYQQKPG KAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQG DSVPLTFGGGKVEIK
CAR123-4 VH	762	QVQLQQSGAEVKKSGASVKVSKASGYTFTDYMHVLRQAPGQGLEWM GWINPNSGDNTYAQKFQGRVLTTRDTSISTVYMELSLRSDDTAVYYCAR DMNILATVPFDIWGQGTMTVSS
CAR123-4 VL	763	DIQMTQSPSSLSASVGDRVTITCRASQSISYLNWYQQKPGKAPKLLIYAA SSLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQGDSVPLTFGGG TKVEIK
CAR123-1 NT	764	atggccctccctgtcaccgcccgtctgctccgctggtctcttctgctccacgcccgtcggccccaagtccaa ctcgtccagtcaggagcgaagtaagaagcccgagcgtcagtaaaagtgcatgcaaagcctcgg gctacactttcactgggtactacatgcactgggtgcgcaggctccaggacaggactggaatggtg gatgatcaaccgaactccggtggcaccattacgcccagaagtccaggggagggtagcatgact cgcgacacgtcgatcagcaccgcatacatggagctgtcaagactccggtccgacgatactgcccgtgtac tactgcgacgggacatgaacattctggccaccgtgcttttgacatctggggtagggaaactatggttacc gtgtcctctggtggaggcggctccggcggggggggaagcggaggcgggtggaagcagacattcagatga cccagtcgcttcaccccttcggcgagcgtgggagatcgcgctactatcactgtcgggcctcgagtcga tctccacctacccaattggtaccagcagaagccaggaaaagcaccgaatctgctgatctacgcccgtt ttccttgcaatcgggagtgccaagcagattcagcggatcgggacaggcactgattccacctaccatca actcgtcgaaccggaggatttcgtactactattgccaacaaggagacagcgtgccgctcaccttcgg cggagggactaagctggaaatcaagaccactacccagcaccgaggccaccaccccggtcctac catcgctcccagcctctgtccctgcgtccggaggcatgtagaccgcagctggtggggccgtgcatacc cggggtcttgacttcgctgcgatatctacattgggcccctctggtggtacttgccgggtcctgctgttca ctcgtgatcactcttactgtaagcgcggtcgggaagaagctgctgtacatcttaagcaaccctcatgaggc ctgtgcagactactcaagaggaggacggctgttcagccggtcccagaggaggaggaaggcggctgc gaactgcgctgaaattcagccgcagcgcagatgctccagcctacaagcaggggcagaaccagctct acaacgaactcaatcttggtcggagagaggagtacgacgtgctggacaagcggagaggacgggacc cagaaatggcggggaagccgcgagaaagaatcccaagagggctgtacaacgagctccaaaag gataagatggcagaagcctatagcgagattggtatgaaaggggaacgcagaagaggcaaaggccac gacggactgtaccagggactcagcaccgccaccaaggacacatgatcgtcttcacatgcaggccct gccgcctcgg
CAR123-1 AA	765	malpvtalllplalllhaarqvqlvqsgaevkkpgasvkvskasgytftgyymhwvrqapggglewm gwinpnsggtnyaqkfqgrvlttrdtsistaymelsrlrsddtavyyccardmnilatvpfdiwgggtmvtvs sgggsgggsgggsggggsdiqmtqspsslsasvgdrvtitcrasqsistylnwyqqkpgkapnlliyaafslq sgvpsrfsgsgsgtdftltinslqpedfatyyccqgdsvppltfgggkveikttppaprpptaptiasqplslr eacrpaaggavhtrglfacdiyiwaplagtcgvllslvitlyckrgrklliyikqpfmrpvqtteedgcscr peeeeggcelrvkfsrsadapaykqgnqlynelnlgrreeydvldkrrgrdpemggkprknpqegly nelqkdkmaeyseigmkgerrrgkghdglyggllstatkdydalhmqalppr
CAR123-1 scFv	766	malpvtalllplalllhaarqvqlvqsgaevkkpgasvkvskasgytftgyymhwvrqapggglewm gwinpnsggtnyaqkfqgrvlttrdtsistaymelsrlrsddtavyyccardmnilatvpfdiwgggtmvtvs sgggsgggsgggsggggsdiqmtqspsslsasvgdrvtitcrasqsistylnwyqqkpgkapnlliyaafslq sgvpsrfsgsgsgtdftltinslqpedfatyyccqgdsvppltfgggkveik
CAR123-1 VH	767	QVQLVQSGAEVKKPGASVKVSKASGYTFTGYMHVLRQAPGQGLEWM GWINPNSGGNTYAQKFQGRVTMTRDTSISTAYMELSLRSDDTAVYYCAR DMNILATVPFDIWGQGTMTVSS
CAR123-1 VL	768	DIQMTQSPSSLSASVGDRVTITCRASQSISTYLNWYQQKPGKAPNLLIYAAF SLQSGVPSRFSGSGSGTDFTLTINSLQPEDFATYYCQQGDSVPLTFGGGT

		KLEIK
--	--	-------

In one embodiment, the CAR molecule comprises a CD33 antigen binding domain (e.g., a murine, human or humanized antibody or antibody fragment that specifically binds to CD33), a transmembrane domain, and an intracellular signaling domain (e.g., an intracellular signaling domain comprising a costimulatory domain and/or a primary signaling domain). Exemplary CAR molecules that target CD33 are described herein, and are provided in WO2016/014576, e.g., in Table 2 of WO2016/014576.

In one embodiment, the CAR molecule comprises a CLL-1 antigen binding domain (e.g., a murine, human or humanized antibody or antibody fragment that specifically binds to CLL-1), a transmembrane domain, and an intracellular signaling domain (e.g., an intracellular signaling domain comprising a costimulatory domain and/or a primary signaling domain). Exemplary CAR molecules that target CLL-1 are described herein, and are provided in WO/2016/014535, e.g., in Table 2 of WO2016/014535.

Natural Killer Cell Receptor (NKR) CARs

In an embodiment, the CAR molecule described herein comprises one or more components of a natural killer cell receptor (NKR). The NKR component can be a transmembrane domain, a hinge domain, or a cytoplasmic domain from any of the following natural killer cell receptors: killer cell immunoglobulin-like receptor (KIR), e.g., KIR2DL1, KIR2DL2/L3, KIR2DL4, KIR2DL5A, KIR2DL5B, KIR2DS1, KIR2DS2, KIR2DS3, KIR2DS4, KIR2DS5, KIR3DL1/S1, KIR3DL2, KIR3DL3, KIR2DP1, and KIR3DP1; natural cytotoxicity receptor (NCR), e.g., NKp30, NKp44, NKp46; signaling lymphocyte activation molecule (SLAM) family of immune cell receptors, e.g., CD48, CD229, 2B4, CD84, NTB-A, CRACC, BLAME, and CD2F-10; Fc receptor (FcR), e.g., CD16, and CD64; and Ly49 receptors, e.g., LY49A, LY49C. The CAR molecules comprising components of NKRs described herein may interact with an adaptor molecule or intracellular signaling domain, e.g., DAP12. Exemplary configurations and sequences of CAR molecules comprising NKR components are described in International Publication No. WO2014/145252, the contents of which are hereby incorporated by reference.

Split CAR

In some embodiments, a CAR-expressing cell described herein uses a split CAR. The split CAR approach is described in more detail in publications WO2014/055442 and WO2014/055657, incorporated herein by reference. Briefly, a split CAR system comprises a cell expressing a first CAR having a first antigen binding domain and a costimulatory domain (e.g., 41BB), and the cell also expresses a second CAR having a second antigen binding domain and an intracellular signaling domain (e.g., CD3 zeta). When the cell encounters the first antigen, the costimulatory domain is activated, and the cell proliferates. When the cell encounters the second antigen, the intracellular signaling domain is activated and cell-killing activity begins. Thus, the CAR-expressing cell is only fully activated in the presence of both

antigens. In embodiments the first antigen binding domain recognizes an antigen described herein, e.g., comprises an antigen binding domain described herein, and the second antigen binding domain recognizes a second antigen described herein.

Exemplary characteristics of the temporally expressed CARs of the invention

- 5 In some embodiments, it is beneficial that the antigen binding domain is operably linked to another domain of the CAR, such as the transmembrane domain or the intracellular domain, both described elsewhere herein, for expression in the cell. In one embodiment, a nucleic acid encoding the antigen binding domain is operably linked to a nucleic acid encoding a transmembrane domain and a nucleic acid encoding an intracellular domain.
- 10 Between the antigen binding domain and the transmembrane domain of the CAR, or between the intracellular domain and the transmembrane domain of the CAR, a spacer domain may be incorporated. As used herein, the term “spacer domain” generally means any oligo- or polypeptide that functions to link the transmembrane domain to, either the antigen binding domain or, the intracellular domain in the polypeptide chain. In one embodiment, the spacer domain may comprise up to 300 amino acids,
- 15 preferably 10 to 100 amino acids and most preferably 25 to 50 amino acids. In another embodiment, a short oligo- or polypeptide linker, preferably between 2 and 10 amino acids in length may form the linkage between the transmembrane domain and the intracellular domain of the CAR. An example of a linker includes a glycine-serine doublet.

In some embodiments, the CAR further comprises a signal peptide. In one embodiment, the signal peptide comprises a nucleic acid sequence comprising

20 ATGGCCTTACCAAGTGACCGCCTTGCTCCTGCCGCTGGCCTTGCTGCTCCACGCCGCCAGGCCG or SEQ ID NO: 3034. In another embodiment, the signal peptide comprises the amino acid sequence comprising MALPVTALLPLALLHAARP or SEQ ID NO: 3035.

In some embodiments, the CAR further comprises a dimerization domain, such a dimerization domain from FKBP or similar molecule. In such an embodiment, the presence of CAR molecules on the surface of the modified T cell is prevented by spontaneous aggregation of the CAR molecules in the cytoplasm or other internal location in the cell.

25

In yet another embodiment, the dimerization domain comprises the nucleic acid sequence comprising

30 CGGGGCGTGACAGGTTGAGACAATTTCCCCAGGAGATGGGCGAACGTTCCCCAAGCGCGGACAGAC
 ATGCGTTGTGCACTACACAGGAATGTTGGAGGACGGAAAGAAAATGGACAGTTCAAGAGATCGGAA
 CAAACCATTCAAATTCATGTTGGGAAAACAGGAAGTGATACGGGGCTGGGAAGAGGGTGTAGCGCA
 AATGTCCGTTGGTCAACGAGCAAACTCACGATAAGTCCCGATTATGCTTACGGCGCAACCGGTCAC
 CCGGGCATCATACCGCCTCATGCGACTTTGGTCTTTGATGTGGAGCTGTTGAAACTTGAACTCGCG
 GAGTACAGGTTGAAACAATATCACCCGGGGACGGGCGGACTTTTCCGAAGAGAGGTCAGACCTGCG

TCGTCCATTATACCGGTATGCTGGAGGACGGAAAGAAAATGGACAGCTCACGGGACCGAAATAAAC
 CATTCAAATTTATGTTGGGGAAACAAGAGGTTATCAGGGGCTGGGAGGAGGGTGTGGCCCAGATGT
 CTGTCCGTCAGCGCGCGAAACTCACAATCTCTCCGATTATGCGTATGGGGCGACAGGGCATCCGG
 GAATTATCCCTCCCCACGCTACCTTGGTTTTTCGATGTTGAGCTTCTGAAGTTGGAGACCAGAGGAGT
 5 TCAAGTGGAGACAATATCTCCTGGGGATGGACGGACGTTCCCCAAGCGCGGCCAGACCTGTGTAGT
 CCACTACACAGGGATGCTTGAAGACGGAAAAAAGATGGATAGCAGTAGAGATCGCAACAAACCATT
 AAGTTCATGCTGGGGAAAGCAGGAAGTAATACGCGGCTGGGAGGAAGGCGTGGCACAGATGAGTGT
 TGGTCAACGGGCCAAACTTACTATTTCTCCGATTATGCGTATGGAGCCACCGGGCACCTGGCATT
 ATCCCACCCCATGCCACATTGGTTTTTGACGTTGAATTGCTTAAATTGGAGACCAGGGGAGTCCAAG
 10 TGGAAACAATATCACCGGGGGATGGTCGGACTTTTCCTAAAAGGGGGCCAAACCTGTGTAGTCCATTA
 TACCGGAATGCTCGAAGACGGAAAGAAAATGGACTCTTCTAGAGACCGCAATAAGCCCTTCAAGTTC
 ATGTTGGGTAAGCAAGAGGTGATCCGGGGCTGGGAAGAGGGGGTGGCTCAAATGTCCGTCGGTCA
 GCGAGCTAACTGACTATTTCCCAGACTACGCATATGGAGCGACTGGCCACCCCGGTATTATTCT
 CCCCATGCGACTCTCGTGTTCGACGTAGAACTCTTGAAATTGGAACG or SEQ ID NO: 3015.

15 In another such embodiment, the dimerization domain comprises the amino acid sequence comprising
 RGVQVETISPGDGRTPFKRGQTCVVHYTGMLEDGKKMDSSRDRNKPFFKMLGKQEVIRGWEEGVAQM
 SVGQRAKLTISPDYAYGATGHPGIIPPHATLVFDVELLKLETRGVQVETISPGDGRTPFKRGQTCVVHYTG
 MLEDGKKMDSSRDRNKPFFKMLGKQEVIRGWEEGVAQMSVGQRAKLTISPDYAYGATGHPGIIPPHATL
 VFDVELLKLETRGVQVETISPGDGRTPFKRGQTCVVHYTGMLEDGKKMDSSRDRNKPFFKMLGKQEVIR
 20 GWEEGVAQMSVGQRAKLTISPDYAYGATGHPGIIPPHATLVFDVELLKLETRGVQVETISPGDGRTPFKR
 GQTCVVHYTGMLEDGKKMDSSRDRNKPFFKMLGKQEVIRGWEEGVAQMSVGQRAKLTISPDYAYGAT
 GHPGIIPPHATLVFDVELLKLET or SEQ ID NO: 980 (described elsewhere herein).

Solubilization of the dimerization domains with a solubilizing agent, administered to the cell or to a
 mammal comprising the cell, prevents dimerization and allows the construct to egress through the
 25 secretory system, where it is processed via furin cleavage to express a functional cell surface CAR.

In the presence of a solubilizing agent, the CAR molecules are separated and aggregation is prevented.
 Administration of a solubilizing agent would prevent dimerization or aggregation of the CAR molecules
 and allow the CAR molecules to be presented on the surface of the T cell. In one embodiment, the furin
 cleavage site comprises the nucleic acid sequence comprising TCAGCCCGGAACAGGCGGAAGAGA or
 30 SEQ ID NO:3016. In another embodiment, the furin cleavage site comprises the amino acid sequence
 SARNRRKR or SEQ ID NO: 3017.

Composition

In one embodiment, the invention includes an isolated nucleic acid sequence comprising a nucleic acid
 sequence comprising a suicide gene comprising a nucleic acid sequence selected from the group
 consisting of SEQ ID NOs: 3001-3004; and a nucleic acid sequence encoding a CAR comprising an anti-

B cell binding domain, a transmembrane domain, a costimulatory domain and an intracellular signaling domain. In some embodiments, the isolated nucleic acid sequence comprises SEQ ID NO: 3018, 3020, 3024, 3026, 3028 or 3030.

In one embodiment, the invention includes an isolated polypeptide comprising an amino acid sequence encoded by a suicide gene wherein the amino acid sequence is selected from the group consisting of SEQ ID NOs: 3005-3007; and a CAR comprising an anti-B cell binding domain, a transmembrane domain, a costimulatory domain and an intracellular signaling domain. In some embodiments, the isolated polypeptide comprises an amino acid sequence of SEQ ID NO: 3019, 3021, 3026, 3028, 3030 or 3034.

In another embodiment, the invention includes an isolated nucleic acid sequence comprising a nucleic acid encoding a dimerization domain; and a CAR comprising an anti-B cell binding domain, a transmembrane domain, a costimulatory domain and an intracellular signaling domain. In some embodiments, the dimerization domain comprises the amino acid sequence of SEQ ID NO: 980. In other embodiments, the isolated nucleic acid sequence comprises SEQ ID NO: 977 or 3032.

In yet another embodiment, the invention includes an isolated polypeptide comprising a dimerization domain; and a CAR comprising an anti-B cell binding domain, a transmembrane domain, a costimulatory domain and an intracellular signaling domain. In some embodiments, the isolated polypeptide comprises an amino acid sequence of SEQ ID NO: 978 or 3033.

5 SIGNAL PEPTIDE

In certain preferred embodiments, the fusion proteins of the invention further include a signal peptide. Signal peptides are useful if it is desirable to have the protein follow the secretory pathway. In preferred embodiments, this signal peptide will be engineered to be present at the very N-terminus of the fusion protein. Exemplary signal peptides are set forth below:

- | | |
|----|--|
| 10 | CD8: MALPVTALLPLALLHAARP (SEQ ID NO: 2) |
| | GMCSFR: MLLLVTSLLLCELPHPAFLIP (SEQ ID NO: 43) |
| | IL2: MYRMQLLSIALSLALVTNS (SEQ ID NO: 44) |
| | IgK chain: MAQVKLQESGTELAKPGAAYK (SEQ ID NO: 45) |
| | NPC2: MRFLAATFLLLALSTAAQA (SEQ ID NO: 46) |
| 15 | LAMB1: MGLLQLLAFSFLALCRARVRA (SEQ ID NO: 1114) |
| | P3IP1: MLLAWVQAFLVSNMLLAEAYG (SEQ ID NO: 1115) |
| | DMKN: MKFQGPLACLLLALCLGSGEA (SEQ ID NO: 1116) |

TPA: MDAMKRGLCCVLLLCGAVFVSP (SEQ ID NO: 1117)

PCSK9: MGTVSSRRSWWPLLLLLLLLLLGPAGARAQEDD (SEQ ID NO: 1118)

KDEL (SEQ ID NO: 47) or KKXX and derivatives at the very C-terminus of the protein of interest can be engineered if the protein of interest is an ER-resident protein. These sequences must be inserted
5 together with the signal peptide.

Proteins of interest can be engineered to include glycosylation patterns for internalization via mannose-6-phosphate receptor and targeting to the endosomal/ lysosomal system. These should be included in the protein of interest itself, if this is a protein resident in that compartment. Consensus for N-glycosylation is Asn-X-Ser/Thr, where X is any aminoacid except proline (Pro), serine (Ser), and threonine (Thr).

10 In embodiments where it is desirable to have proteins of interested targeted at the peroxisome, the fusion protein can be engineered to include a C-terminal peroxisomal targeting signal (e.g., PTS1: -SKL).

CLEAVAGE SITES

Each fusion protein of the invention includes a cleavage site. The cleavage site can either be self-cleavage sites and/or protease cleavage sites. The cleavage site can be designed to be cleaved by any
15 site-specific protease that is expressed in a cell of interest (either through recombinant expression or endogenous expression) at adequate levels to cleave off the conditional expression domain, e.g., a degradation domain or an aggregation domain. In important aspects of the invention, the protease cleavage site is chosen to correspond to a protease natively (or by virtue of cell engineering) to be present in a cellular compartment relevant to the expression of the protein of interest. I.e., the
20 intracellular trafficking of the protease should overlap or partially overlap with the intracellular trafficking of the protein of interest that contains the conditional expression domain, e.g., a degradation domain or an aggregation domain employed. For example, if the protein of interest is located at the cell surface, the enzyme to cleave it can be added exogenous to the cell.

If the protein of interest resides in the endosomal/lysosomal system a protease cleavage site for an
25 enzyme resident in those compartments can be used. Such protease/consensus motifs include, e.g.,

Furin: RX(K/R)R consensus motif

PCSK1: RX(K/R)R consensus motif

PCSK5: RX(K/R)R consensus motif

PCSK6: RX(K/R)R consensus motif

30 PCSK7: RXXX[KR]R consensus motif

Cathepsin B : RRX

Granzyme B : I-E-P-D-X (SEQ ID NO: 35)

Factor XA: Ile – Glu/Asp-Gly-Arg

Enterokinase: Asp-Asp-Asp-Asp-Lys (SEQ ID NO: 36)

5 Genenase: Pro-Gly-Ala-Ala-His-Tyr (SEQ ID NO: 37)

Sortase: LPXTG/A

PreScission protease: Leu-Glu-Val-Phe-Gln-Gly-Pro (SEQ ID NO: 38)

Thrombin: Leu-Val-Pro-Arg-Gly-Ser (SEQ ID NO: 40)

TEV protease: E-N-L-Y-F-Q-G (SEQ ID NO: 41)

10 Elastase 1 [AGSV]-x (SEQ ID NO: 42)

In some embodiments, the fusion protein described herein includes a furin cleavage site. In some embodiments, the fusion proteins described herein include any one of furin cleavage sites listed in Table 20.

In some embodiments, the fusion proteins described herein include a furin cleavage site selected from
 15 RTKR (SEQ ID NO: 123) or a sequence having at least 90%, 95%, 97%, 98%, or 99% identity thereto;
 GTGAEDPRPSRKRRSLGDVG (SEQ ID NO: 125) or a sequence having at least 90%, 95%, 97%, 98%,
 or 99% identity thereto; GTGAEDPRPSRKRR (SEQ ID NO: 127) or a sequence having at least 90%,
 95%, 97%, 98%, or 99% identity thereto; LQWLEQQVAKRRTKR (SEQ ID NO: 129) or a sequence
 having at least 90%, 95%, 97%, 98%, or 99% identity thereto; GTGAEDPRPSRKRRSLGG (SEQ ID NO:
 20 131) or a sequence having at least 90%, 95%, 97%, 98%, or 99% identity thereto;
 GTGAEDPRPSRKRRSLG (SEQ ID NO: 133) or a sequence having at least 90%, 95%, 97%, 98%, or
 99% identity thereto; SLNLTESHNSRKRR (SEQ ID NO: 135) or a sequence having at least 90%, 95%,
 97%, 98%, or 99% identity thereto; or CKINGYPKRGRKRR (SEQ ID NO: 137) or a sequence having at
 least 90%, 95%, 97%, 98%, or 99% identity thereto.

25 In some embodiments, the fusion proteins described herein include a furin cleavage site selected from
 RTKR (SEQ ID NO: 123); GTGAEDPRPSRKRRSLGDVG (SEQ ID NO: 125); GTGAEDPRPSRKRR
 (SEQ ID NO: 127); LQWLEQQVAKRRTKR (SEQ ID NO: 129); GTGAEDPRPSRKRRSLGG (SEQ ID NO:
 131); GTGAEDPRPSRKRRSLG (SEQ ID NO: 133); SLNLTESHNSRKRR (SEQ ID NO: 135); or
 CKINGYPKRGRKRR (SEQ ID NO: 137).

In some embodiments, the fusion proteins described herein include a furin cleavage site selected from GTGAEDPRPSRKRRSLGDVG (SEQ ID NO: 125) or a sequence having at least 90%, 95%, 97%, 98%, or 99% identity thereto, or GTGAEDPRPSRKRR (SEQ ID NO: 127) or a sequence having at least 90%, 95%, 97%, 98%, or 99% identity thereto.

- 5 In some embodiments, the fusion proteins described herein include a furin cleavage site selected from GTGAEDPRPSRKRRSLGDVG (SEQ ID NO: 125) or GTGAEDPRPSRKRR (SEQ ID NO: 127).

In some embodiments, the fusion proteins described herein include the furin cleavage site of GTGAEDPRPSRKRRSLGDVG (SEQ ID NO: 125).

Table 20. Exemplary furin cleavage site

	Amino acid sequence	Nucleic acid sequence
Furin cleavage site1	RTKR (SEQ ID NO: 123)	cgtactaaaaga (SEQ ID NO: 1112)
Furin cleavage site2	GTGAEDPRPSRKRRSLGDVG (SEQ ID NO: 125)	ggaaccggcgcggaagacccccggccctccaggaag cgaaggctccctcgagacgtgggt (SEQ ID NO: 126)
Furin cleavage site3	GTGAEDPRPSRKRR (SEQ ID NO: 127)	ggaaccggcgcggaagacccccggccctccaggaag cgaagg (SEQ ID NO: 128)
Furin cleavage site4	LQWLEQQVAKRRTKR (SEQ ID NO: 129)	ctgcaatggctggagcagcaggtggcgaagcggagaa ctaagcgg (SEQ ID NO: 130)
Furin cleavage site5	GTGAEDPRPSRKRRSLGG (SEQ ID NO: 131)	ggcacaggtgccgaggaccctcgccaagccgcaaaa ggaggtcactggcggc (SEQ ID NO: 132)
Furin cleavage site6	GTGAEDPRPSRKRRSLG (SEQ ID NO: 133)	ggaaccggagcagaagatccagaccaagccggaag aggcggctccctgggt (SEQ ID NO: 134)
Furin cleavage site7	SLNLTESHNSRKRR (SEQ ID NO: 135)	agtctcaattgactgagtcacacaattccaggaagaaaa gg (SEQ ID NO: 136)
Furin cleavage site8	CKINGYPKRGRKRR (SEQ ID NO: 137)	tgcaagatcaacggctaccctaagaggggcagaaagc ggcgg (SEQ ID NO: 138)

10

CONDITIONAL EXPRESSION DOMAINS

- The fusion protein of the invention can include a conditional expression domain. In some embodiments a conditional expression domain has a first state and a second state, e.g., states of aggregation or conformational states, e.g., states of stabilization/destabilization, or states of folding/misfolding. The first state is associated with, causes, or mediates cell surface expression or extracellular expression of one or more (e.g., all) portions of the fusion protein at a first rate or level and the second state is associated with, causes, or mediates cell surface expression or extracellular expression of one or more (e.g., all) portions of the fusion protein at a second rate or level. In an embodiment, the second state has a level or rate that is greater, e.g., 2, 3, 4, 5, 6, 7, 8, 9, 10, 20, or 30 fold greater, than the rate or level of the first state. In an embodiment one of the states, e.g., the second state, is associated with, maintained by, or caused by the presence of an expression compound. In an embodiment, the presence of the expression compound can

20

be associated with, cause, or mediate a change in a physical property, e.g., the second state is associated with an altered level of the physical property, e.g., presence of the expression compound is associated with, causes, or mediates the transformation of a first state with first value for a physical property to a second state with a second value for a physical property, e.g., wherein the property can

5 comprise molecular weight, stability, absorbance at a preselected wavelength, the ability to interact with another molecule, or solubility. In an embodiment, the presence of the expression compound can be associated with, cause, or mediate the transformation of a first folding state to a second folding state, e.g., from misfolded to more properly folded state, e.g., a first state susceptible to degradation to a second state less susceptible to degradation than the first state; or from a first folding state that has a

10 first level of degradation to a second folding state that has a second, lessor, level of degradation, e.g., in a cell of interest. In an embodiment, the presence of the expression compound can be associated with, cause, or mediate disassociation or disaggregation of a first and a second conditional expression domains, e.g., from a higher order association to a lower order association, e.g., from a dimer to monomers, or from tetramers to lower order structures, e.g., dimers or monomers. In an embodiment, the

15 presence of the expression compound can be associated with, cause, or mediate a change in solubility, e.g., the second state is associated with a higher level of solubility, e.g., presence of the expression compound is associated with, causes, or mediates the transformation of a first state with lower solubility to a second state with higher solubility. In an embodiment, the presence of the expression compound can be associated with, cause, or mediate the transformation of a first state of localization or

20 compartmentalization of one or more or all portions of the fusion protein to a second state of localization or compartmentalization of one or more or all portions of the fusion protein, e.g., from the golgi or ER to another compartment or localization, e.g., the cytosol, a membrane, the cell surface, or extracellular space.

In an embodiment, the presence of the expression compound can be associated with, cause, or mediate,

25 the transformation from or of a first folding state to a second folding state, e.g., from a misfolded state to a more properly folded state, e.g., a first state susceptible to degradation to a second state less susceptible to degradation than the first state; or from a first folding state that has a first level of degradation to a second folding state that has a second, lessor, level of degradation, e.g., in a cell of interest.

30 In an embodiment, one of the states, e.g., the second state, is associated with, causes, or mediates cleavage at the cleavage site. While not wishing to be bound by theory, it is believed, that in some embodiments, cleavage results or is associated with cell surface expression or extracellular expression of one or more (e.g., all) portions of the fusion protein. In an embodiment, absent an expression compound, when expressed in a cell of interest, fusion protein, e.g., a first level, e.g., a large fraction, of

35 the fusion protein, comprising a conditional expression domain is not detectable either on the cell surface or extracellularly, e.g., by steric hinderance of the cleavage by the another entity, e.g., the conditional

expression domain. Conversely, in the presence of an expression compound, surface expression and/or extracellular expression of one or more (e.g., all) domains of the fusion protein is transformed to a second level which is higher than the first level, e.g., substantially increased, e.g., by 2, 3, 4, 5, or 10 fold over the first level or increased, e.g., by at least 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 150, 200, 300, 400, 500, 600, 700, 800, 900, or 1000% over the first level. Thus, in an embodiment, a conditional expression domain is identifiable or characterized by the following characteristics: (1) it is not naturally occurring in the context of the fusion protein, e.g., it is recombinant or engineered; (2) surface expression and/or extracellular expression is regulated co-translationally or post-translationally; (3) the rate of surface expression and/or extracellular expression is substantially increased in the presence of an expression compound.

In an embodiment, addition of expression compound, e.g., deaggregation compound or stabilization compound, to a plurality of cells, e.g., host cells or cells comprising fusion proteins described herein, causes a transformation of a sub-plurality of cells from the first state to the second state, e.g., states of aggregation or conformational states, e.g., states of stabilization/destabilization, or states of folding/misfolding as described herein. In an embodiment, in the absence of expression compound, e.g., deaggregation compound or stabilization compound, less than 10, 9, 8, 7, 6, 5, 4, 3, 2, or 1% of the cells in the plurality comprise the second state, and greater than or equal to 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% of the cells in the plurality comprise the first state. In an embodiment, in the presence of expression compound, e.g., deaggregation compound or stabilization compound, greater than or equal to 20, 30, 40, 50, 60, 70, 80, 90, or 95% of the cells in the plurality comprise the second state, and less than 20, 15, 10, 9, 8, 7, 6, 5, 4, 3, 2, or 1% of the cells in the plurality comprise the first state. Determination of the percentages of cells in a plurality comprising a state can be made using methods described throughout the specification, for example, as used in Figure 4.

In embodiments, a conditional expression domain is a degradation domain, for example, as described herein. In other embodiments, a conditional expression domain is an aggregation domain, for example as described herein. In an embodiment, a conditional expression domain does not comprise a degradation domain. In an embodiment, a conditional expression domain does not comprise an aggregation domain. In embodiments, the fusion protein comprising the conditional expression domain comprises a transmembrane protein, e.g., a chimeric antigen receptor (CAR), e.g., as described herein. In some embodiments, the conditional expression domain is a degradation domain. In some embodiments, the conditional expression domain is an aggregation domain.

AGGREGATION DOMAINS

In some embodiments, the conditional expression domain is an aggregation domain. Methods of generating aggregation domains that cause intracellular aggregation in the absence of an expression compound, e.g., a deaggregation compound, are known in the art and discussed further below.

5 The present disclosure encompasses aggregation domains derived from any naturally occurring protein. Preferably, fusion proteins of the invention will include an aggregation domain for which no deaggregation compound is natively expressed or provided in the cell compartments of interest. For example, if the fusion protein is designed for expression in T-cells, it is preferable to select an aggregation domain which is paired with a deaggregation compound that is not naturally present in T-cells. Thus, the aggregation
 10 domain, when expressed in the cell of interest, will only be deaggregated in the presence of deaggregation compound. Notably, this property can be engineered by either engineering the aggregation domain to no longer bind a natively expressed/present deaggregation compound (in which case the aggregation domain will only deaggregate in the presence of a synthetic compound) or by expressing the aggregation domain in a compartment where the natively expressed/present ligand does
 15 not occur (e.g., the aggregation domain can be derived from a species other than the species in which the fusion protein will be expressed).

Aggregation domain –deaggregation compound pairs can be derived from any naturally occurring or synthetically developed protein. Deaggregation compounds can be any naturally occurring or synthetic compounds. In certain embodiments, the deaggregation compounds will be existing prescription or over-
 20 the-counter medicines. Examples of proteins that can be engineered to possess the properties of an aggregation domain are set forth below along with a corresponding deaggregation compound.

In one embodiment, the aggregation domain is a dimerization domain, e.g., is derived from an FKBP protein (FKBP). In some embodiments, the aggregation domain comprises an amino acid sequence selected from SEQ ID NO: 975 or a sequence having at least 90%, 95%, 97%, 98%, or 99% identity
 25 thereto, or SEQ ID NO: 976 or a sequence having at least 90%, 95%, 97%, 98%, or 99% identity thereto. In some embodiments, the aggregation domain comprises an amino acid sequence selected from SEQ ID NO: 979 or a sequence having at least 90%, 95%, 97%, 98%, or 99% identity thereto, or SEQ ID NO: 980 or a sequence having at least 90%, 95%, 97%, 98%, or 99% identity thereto. When the aggregation domain is derived from an FKBP, the deaggregation compound can be selected from AP21998 or
 30 AP22542, known in the art and described in Rollins et al 2000 PNAS vol. 97 no. 13, 7096-7101, WO/2000/023600, and Rivera, V. M., et al. (2000) *Regulation of protein secretion through controlled aggregation in the endoplasmic reticulum*. Science 287: 826-30. Each of these references is incorporated by reference in its entirety. While not wishing to be bound by theory, FKBP domains comprising F36M substitutions associate into dimers. The FKBP F36M dimers can be disassociated, e.g., deaggregated,
 35 by addition of ligand, e.g., FK506, rapamycin, AP22542, AP21998, or Shield-1.

GVQVETISPGDGRTFPPKRGQTCVVHYTGMLEDGKKFDSSSRDRNKPFFKMLGKQEVIRGWEEGVAQMSV
GQRAKLTISPDYAYGATGHPGIIPPHATLVFDVELLKLE (SEQ ID NO: 975)

GVQVETISPGDGRTFPPKRGQTCVVHYTGMLEDGKKMDSSSRDRNKPFFKMLGKQEVIRGWEEGVAQMS
VGQRAKLTISPDYAYGATGHPGIIPPHATLVFDVELLKLE (SEQ ID NO: 976)

5 RGVQVETISPGDGRTFPPKRGQTCVVHYTGMLEDGKKFDSSSRDRNKPFFKMLGKQEVIRGWEEGVAQM
SVGQRAKLTISPDYAYGATGHPGIIPPHATLVFDVELLKLETRGVQVETISPGDGRTFPPKRGQTCVVHYTG
MLEDGKKMDSSSRDRNKPFFKMLGKQEVIRGWEEGVAQMSVGQRAKLTISPDYAYGATGHPGIIPPHATL
VFDVELLKLETRGVQVETISPGDGRTFPPKRGQTCVVHYTGMLEDGKKMDSSSRDRNKPFFKMLGKQEVIR
GWEEGVAQMSVGQRAKLTISPDYAYGATGHPGIIPPHATLVFDVELLKLETRGVQVETISPGDGRTFPPK
10 GQTCVVHYTGMLEDGKKMDSSSRDRNKPFFKMLGKQEVIRGWEEGVAQMSVGQRAKLTISPDYAYGAT
GHPGIIPPHATLVFDVELLKLET (SEQ ID NO: 979)

RGVQVETISPGDGRTFPPKRGQTCVVHYTGMLEDGKKMDSSSRDRNKPFFKMLGKQEVIRGWEEGVAQM
SVGQRAKLTISPDYAYGATGHPGIIPPHATLVFDVELLKLETRGVQVETISPGDGRTFPPKRGQTCVVHYTG
MLEDGKKMDSSSRDRNKPFFKMLGKQEVIRGWEEGVAQMSVGQRAKLTISPDYAYGATGHPGIIPPHATL
15 VFDVELLKLETRGVQVETISPGDGRTFPPKRGQTCVVHYTGMLEDGKKMDSSSRDRNKPFFKMLGKQEVIR
GWEEGVAQMSVGQRAKLTISPDYAYGATGHPGIIPPHATLVFDVELLKLETRGVQVETISPGDGRTFPPK
GQTCVVHYTGMLEDGKKMDSSSRDRNKPFFKMLGKQEVIRGWEEGVAQMSVGQRAKLTISPDYAYGAT
GHPGIIPPHATLVFDVELLKLET (SEQ ID NO: 980)

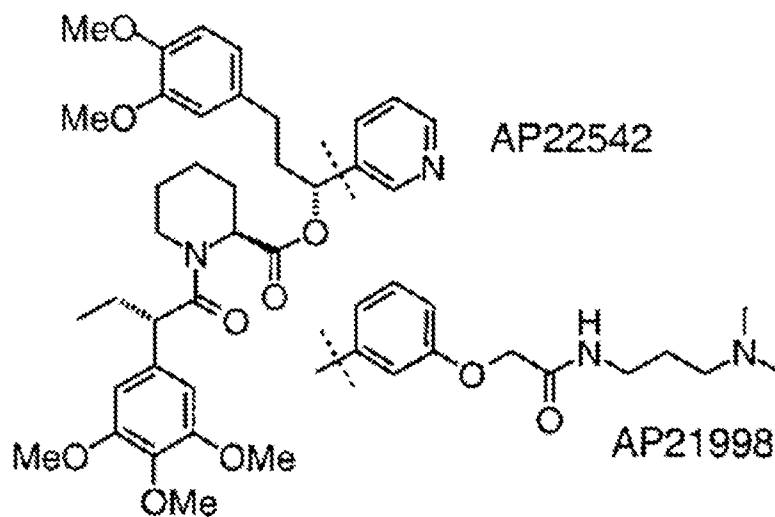
In another embodiment, the aggregation domain is derived from a UVR8 protein. UVR8 is a plant
20 photoreceptor protein (Chen et al. 2013. J. Cell. Biol. v201 no. 4: 631-640; Rizzini, L., et al. 2011.
Science. 332:103–106; Christie, J.M., et al. 2012. Science. 335:1492–1496; Wu, D., et al. 2012. Nature.
484:214–219). Each of these references is incorporated by reference in its entirety. UVR8 constitutively
forms photolabile homodimers which dissociate upon absorption of ultraviolet B (UVB) radiation (280-320
nm). In an embodiment, the aggregation domain is derived from a UVR8 domain, and the deaggregation
25 compound is a suitable dose of UVB radiation. In an embodiment, the suitable dose of UVB radiation is
sufficient to dissociate at least 25, 50, 75, or 100% of the UVR8 homodimers. In an embodiment, the
suitable dose of UVB is minimally toxic to a cell comprising the fusion protein.

In some embodiments, a fusion protein of the present invention comprises multiple, e.g., 2, 3, 4, 5, 6, 7, 8,
9, 10, or more, copies of a conditional expression domain, e.g., an aggregation domain or degradation
30 domain. In some embodiments, a fusion protein of the present invention comprises multiple, e.g., 2, 3, 4,
5, 6, 7, 8, 9, 10, or more, aggregation domains.

In some embodiments, each of the multiple aggregation domains is a copy of the same aggregation
domain. Such aggregation domains would bind to each other to form homooligomers, e.g., homodimers,

In some embodiments, a fusion protein of the present invention comprises a plurality, e.g., more than one, of aggregation domains, wherein the plurality comprises more than one type, e.g., a first type and a second type, of aggregation domain. In some embodiments, the first type of aggregation domain associates, e.g., binds to and promotes oligomerization or aggregation, with the second type of aggregation domain; such association represents heteromeric association or heterooligomerization of aggregation domains, e.g., into heterodimers. In some embodiments, a fusion protein of the present invention comprises two, four, six, or eight aggregation domains, wherein the fusion protein comprises at least one of each type, e.g., a first type and a second type, of aggregation domain. In one embodiment, a fusion protein comprising a plurality of aggregation domains, wherein the plurality comprises more than one type, e.g., a first type and a second type, of aggregation domain, comprises equal numbers of each type of aggregation domain. In some embodiments, wherein a fusion protein comprises four or more (e.g., six, eight, ten, or more) aggregation domains, the aggregation domains are disposed in an alternating pattern in the fusion protein, e.g., type 1, type 2, type 1, type 2. In some embodiments, wherein a fusion protein comprises four or more (e.g., six, eight, ten, or more) aggregation domains, the aggregation domains are disposed in a block pattern in the fusion protein, e.g., type 1, type 1, type 2, type 2. In some embodiments, the first type of aggregation domain does not appreciably associate with other copies of the first type of aggregation domain and the second type of aggregation domain does not appreciably associate with other copies of the second type of aggregation domain. In some embodiments, the first type of aggregation domain only appreciably associates with other copies of the first type of aggregation domain and the second type of aggregation domain only appreciably associates with other copies of the second type of aggregation domain.

In some embodiments, the expression compound, e.g., deaggregation compound, is AP21998 or AP22542 (chemical structure shown here; AP21998 and AP22542 are the same in the portion left of the dashed line and differ in the portion right of the dashed line). Preparation and use of AP21998 and AP22542 can be found in the art and in Rollins et al. 2000, Amara, J. F., et al. (1997) Proc. Natl. Acad. Sci. USA 94, 10618–10623, Clackson, T., et al. (1998) Proc. Natl. Acad. Sci. USA 95, 10437–10442, and Yang, W., et al. (2000) J. Med. Chem. 43, 1135–1142. Each of these references is incorporated by reference in its entirety.



In some embodiments, the expression compound, e.g., deaggregation compound, is FK506 (tacrolimus) or rapamycin (sirolimus). In some embodiments, the conditional expression domain, e.g., aggregation domain, is derived from FKBP and the expression compound, e.g., deaggregation compound, is FK506 (tacrolimus) or rapamycin (sirolimus). Preparation and use of FK506 and rapamycin can be found in the art.

In some embodiments, the expression compound, e.g., deaggregation compound, inhibits interaction between aggregation domains. In some embodiments, wherein the deaggregation compound is FK506, rapamycin, AP22542, or AP21998, the deaggregation compound inhibits interaction between fusion proteins comprising an aggregation domain derived from FKBP F36M.

An exemplary aggregation domain-deaggregation compound pair has been generated and is featured in the present invention (SEQ ID NOs: 977 (nucleic acid) and 978 (amino acid)). This aggregation domain comprises an FKBP F36M domain as described in: "A ligand-reversible dimerization system for controlling protein-protein interactions." Rollins et al. PNAS vol. 97 no. 13, 7096-7101, and WO/2000/023600. Each of these references is incorporated by reference in its entirety.

CD19bbz on-CAR nucleotide sequence, CD19 on-CAR (SEQ ID NO:977)

Signal peptide-conditional aggregation domains (4 repeats)- Furin site-FMC63bbz

ATGGCCTTACCACTGACCGCCTTGCTCCTGCCGCTGGCCTTGCTGCTCCACGCCGCCAGGCCGGGATCCCGGGGCG
TGCAGGTTGAGACAATTTCCCCAGGAGATGGGCGAACGTTCCCCAAGCGCGGACAGACATGCGTTGTGCACTACA
CAGGAATGTTGGAGGACGGAAAGAAAATGGACAGTTCAAGAGATCGGAACAAACCATTCAAATTCATGTTGGGA
AAACAGGAAGTGATACGGGGCTGGGAAGAGGGTGTAGCGCAAATGTCCGTTGGTCAACGAGCAAACTCACGAT

AAGTCCCGATTATGCTTACGGCGCAACCGGTCACCCGGGCATCATACCGCCTCATGCGACTTTGGTCTTTGATGTG
 GAGCTGTTGAACTTGAACTCGCGGAGTACAGGTTGAAACAATATCACCCGGGGACGGGCGGACTTTTCCGAAG
 AGAGGTCAGACCTGCGTCGTCCATTATACCGGTATGCTGGAGGACGGAAAGAAAATGGACAGCTCACGGGACCG
 AAATAAACCATTCAAATTTATGTTGGGGAAACAAGAGGTTATCAGGGGCTGGGAGGAGGGTGTGGCCAGATGT
 5 CTGTCCGGTCAGCGCGCGAACTCACAATCTCTCCGGATTATGCGTATGGGGCGACAGGGCATCCGGGAATTATCC
 CTCCCCACGCTACCTTGTTTTGATGTTGAGCTTCTGAAGTTGGAGACCAGAGGAGTTCAAGTGGAGACAATATC
 TCCTGGGGATGGACGGACGTTCCCCAAGCGCGGCCAGACCTGTGTAGTCCACTACACAGGGATGCTTGAAGACG
 GAAAAAAGATGGATAGCAGTAGAGATCGCAACAAACATTTAAGTTCATGCTGGGGAAGCAGGAAGTAATACGC
 GGCTGGGAGGAAGGCGTGGCACAGATGAGTGTGGTCAACGGGCCAACTTACTATTTCTCCCGATTATGCGTAT
 10 GGAGCCACCGGGCACCTGGCATTATCCACCCCATGCCACATTGGTTTTGACGTTGAATTGCTTAAATTGGAGA
 CCAGGGGAGTCCAAGTGGAAACAATATCACCGGGGGATGGTCGGACTTTTCTAAAAGGGGCCAAACCTGTGTA
 GTCCATTATACCGGAATGCTCGAAGACGGAAAGAAAATGGACTCTTCTAGAGACCGCAATAAGCCCTTCAAGTTCA
 TGTGGGTAAAGCAAGAGGTGATCCGGGGCTGGGAAGAGGGGGTGCCTCAAATGTCCGTCGGTCAGCGAGCTAAA
 CTGACTATTTCCCAGACTACGCATATGGAGCGACTGGCCACCCCGGTATTATTCCTCCCATGCGACTCTCGTGTT
 15 CGACGTAGAATCTTGAAATTGGAAACGTCAGCCGGAACAGGCGGAAGAGAGGATCCGACATCCAGATGACAC
 AGACTACATCCTCCCTGTCTGCCTCTCTGGGAGACAGAGTCACCATCAGTTGCAGGGCAAGTCAGGACATTAGTAA
 ATATTTAAATTGGTATCAGCAGAAACCAGATGGAAGTGTAACTCCTGATCTACCATACATCAAGATTACACTCAG
 GAGTCCCATCAAGGTTCAAGTGGCAGTGGGTCTGGAACAGATTATTCTCTACCATTAGCAACCTGGAGCAAGAAG
 ATATTGCCACTTACTTTTGCCAACAGGGTAATACGCTTCCGTACACGTTCCGAGGGGGGACTAAGTTGGAAATAAC
 20 AGGTGGCGGTGGCTCGGGCGGTGGTGGGTGGGTGGCGCGGATCTGAGGTGAACTGCAGGAGTCAGGACCT
 GGCCTGGTGGCGCCCTCACAGAGCCTGTCCGTACATGCACTGTCTCAGGGGTCTCATTACCCGACTATGGTGTA
 GCTGGATTGCGCAGCCTCCACGAAAGGTCTGGAGTGGCTGGGAGTAATATGGGGTAGTGAAACCACATACTATA
 ATTCAGCTCTCAAATCCAGACTGACCATCATCAAGGACAACTCCAAGAGCCAAGTTTTCTTAAAAATGAACAGTCT
 GCAAACCTGATGACACAGCCATTTACTACTGTGCCAAACATTATTACTACGGTGGTAGCTATGCTATGGACTACTGG
 25 GGTCAAGGAACCTCAGTACCGTCTCCTCAGCTAGCACCACGACGCCAGCGCCGCGACCACCAACACCGGCGCCC
 ACCATCGCGTCGCAGCCCCTGTCCCTGCGCCCAGAGGCGTGCCGGCCAGCGGCGGGGGGCGCAGTGACACGAG
 GGGGCTGGACTTCGCTGTGATTCCGGAATCTACATCTGGGCGCCCTTGGCCGGGACTTGTGGGGTCTTCTCTG
 TCACTGGTTATCACCTTTACTGCAAACGGGGCAGAAAGAACTCCTGTATATATTCAAACAACCATTTATGAGACC
 AGTACAACTACTCAAGAGGAAGATGGCTGTAGCTGCCGATTTCCAGAAGAAGAAGAAGGAGGATGTGAAGTGA
 30 GAGTGAAGTTCAGCAGGAGCGCAGACGCCCCGCGTACCAGCAGGGCCAGAACCAGCTCTATAACGAGCTCAAT
 CTAGGACGAAGAGAGGAGTACGATGTTTTGGACAAGAGACGTGGCCGGGACCCTGAGATGGGGGGAAAGCCGA
 GAAGGAAGAACCCTCAGGAAGGCCTGTACAATGAAGTGCAGAAAGATAAGATGGCGGAGGCCTACAGTGAAGT
 GGGATGAAAGGCGAGCGCCGAGGGGCAAGGGGCACGATGGCCTTACCAGGGTCTCAGTACAGCCACCAAGG
 ACACCTACGACGCCCTTACATGCAGGCCCTGCCCCCTCGCTAA
 35

CD19bbz on-CAR amino acid sequence (SEQ ID NO:978)

Signal peptide-conditional aggregation domains (4 repeats)-Furin site-FMC63bbz

MALPVTALLPLALLHAARPGSRGVQVETISPGDGRTFPRGQTCVVHYTGMLEDGKKMDSSRDRNKPFFKMLGKQ
EVIRGWEEGVAQMSVGQRAKLTISPDIYAGATGHPGIIPPHATLVFDVELLKLETRGVQVETISPGDGRTFPRGQTCV

VHYTGMLEDGKKMDSSDRNKPFFKMLGKQEVIRGWEEGVAQMSVGQRAKLTISPDYAYGATGHPGIIPPHATLVFD
 VELLKLETRGVQVETISPGDGRTFPRGQTCVVHYTGMLEDGKKMDSSDRNKPFFKMLGKQEVIRGWEEGVAQMS
 VGQRAKLTISPDYAYGATGHPGIIPPHATLVFDVELLKLETRGVQVETISPGDGRTFPRGQTCVVHYTGMLEDGKKMD
 SSRDRNKPFFKMLGKQEVIRGWEEGVAQMSVGQRAKLTISPDYAYGATGHPGIIPPHATLVFDVELLKLETSARNRRKR
 5 GSDIQMTQTSSLSASLGDRVTISCRASQDISKYNWYQQKPDGTVKLLIYHTSRLHSGVPSRFSGSGSGTDYSLTISNLE
 QEDIATYFCQQGNTLPYTFGGGKLEITGGGGSGGGGSGGGGSEVKLQESGPGLVAPSQSLSVTCTVSGVSLPDYGVS
 WIRQPPRKGLEWLGVWGETTYNSALKSRLTIKDNSKSQVFLKMNSLQTDDTAIYYCAKHYYYGGSYAMDYWGQG
 TSVTVSSASTTTPAPRPPTPAPTASQPLSLRPEACRPAAGGAVHTRGLDFACDSGIYWAPLAGTCGVLLLSLVITLYCKR
 GRKKLLYIFKQPFMRPVQTTQEEDGCSCRFEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDR
 10 RGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPRZ

DEGRADATION DOMAINS

In some embodiments, the conditional expression domain is a degradation domain. Methods of
 15 generating degradation domains that are selectively stable in the presence of a stabilization compound
 are well known in the art and discussed further below. Several such domain-stabilization compound pairs
 have been generated to date and are featured in the present invention. These include degradation
 domains based on FKBP (e.g., using a "Shield" stabilization compound) as described in: A Rapid,
 Reversible, and Tunable Method to Regulate Protein Function in Living Cells Using Synthetic Small
 20 Molecules." Banaszynski, L. A.; Chen, L.-C.; Maynard-Smith, L. A.; Ooi, A. G. L.; Wandless, T. J. Cell,
 2006, 126, 995-1004; domains based on DHFR (e.g., using trimethoprim as a stabilization compound) as
 described in A general chemical method to regulate protein stability in the mammalian central nervous
 system. Iwamoto, M.; Björklund, T.; Lundberg, C.; Kirik, D.; Wandless, T. J. Chemistry & Biology, 2010,
 17, 981-988; and domains based on estrogen receptor alpha (e.g., where 4OHT is used as a stabilization
 25 compound) as described in Destabilizing domains derived from the human estrogen receptor Y Miyazaki,
 H Imoto, L-c Chen, TJ Wandless J. Am. Chem. Soc. 2012, 134, 3942-3945. Each of these references is
 incorporated by reference in its entirety.

The present disclosure encompasses degradation domains derived from any naturally occurring protein.
 Preferably, fusion proteins of the invention will include a degradation domain for which there is no ligand
 30 natively expressed in the cell compartments of interest. For example, if the fusion protein is designed for
 expression in T-cells, it is preferable to select a degradation domain for which there is no naturally
 occurring ligand present in T cells. Thus, the degradation domain, when expressed in the cell of interest,
 will only be stabilized in the presence of an exogenously added compound. Notably, this property can be
 engineered by either engineering the degradation domain to no longer bind a natively expressed ligand
 35 (in which case the degradation domain will only be stable in the presence of a synthetic compound) or by
 expressing the degradation domain in a compartment where the natively expressed ligand does not occur

(e.g., the degradation domain can be derived from a species other than the species in which the fusion protein will be expressed).

Degradation domain –stabilization compound pairs can be derived from any naturally occurring or synthetically developed protein. Stabilization compounds can be any naturally occurring or synthetic compounds. In certain embodiments, the stabilization compounds will be existing prescription or over-the-counter medicines. Examples of proteins that can be engineered to possess the properties of a degradation domain are set forth in Table 21 below along with a corresponding stabilization compound.

In some embodiments, the degradation domain is derived from a protein listed in Table 21.

In some embodiments, the degradation domain is derived from an estrogen receptor (ER). In some embodiments, the degradation domain comprises an amino acid sequence selected from SEQ ID NO: 58 or a sequence having at least 90%, 95%, 97%, 98%, or 99% identity thereto, or SEQ ID NO: 121 or a sequence having at least 90%, 95%, 97%, 98%, or 99% identity thereto. In some embodiments, the degradation domain comprises an amino acid sequence selected from SEQ ID NO: 58, or SEQ ID NO: 121. When the degradation domain is derived from an estrogen receptor, the stabilization compound can be selected from Bazedoxifene or 4-hydroxy tamoxifen (4-OHT). In some embodiments, the stabilization compound is Bazedoxifene. Tamoxifen and Bazedoxifene are FDA approved drugs, and thus are safe to use in human.

In some embodiments, the degradation domain is derived from an FKB protein (FKBP). In some embodiments, the degradation domain comprises an amino acid sequence of SEQ ID NO: 56 or a sequence having at least 90%, 95%, 97%, 98%, or 99% identity thereto. In some embodiments, the degradation domain comprises an amino acid sequence of SEQ ID NO: 56. When the degradation domain is derived from a FKBP, the stabilization compound can be Shield-1.

In some embodiments, the degradation domain is derived from dihydrofolate reductase (DHFR). In some embodiments, the degradation domain comprises an amino acid sequence selected from SEQ ID NO: 57 or a sequence having at least 90%, 95%, 97%, 98%, or 99% identity thereto. In some embodiments, the degradation domain comprises an amino acid sequence selected from SEQ ID NO: 57. When the degradation domain is derived from a DHFR, the stabilization compound can be Trimethoprim.

In some embodiments, the degradation domain is not derived from an FKB protein, estrogen receptor, or DHFR.

Table 21. Exemplary proteins for generating degradation domains

Type	Activity of drug	Drug examples
<i>Oxidoreductases</i>		

Aldehyde dehydrogenase	Inhibitor	Disulfiram
Monoamine oxidases (MAOs)	MAO-A inhibitor	Tranylcypromine, moclobemide
	MAO-B inhibitor	Tranylcypromine
Cyclooxygenases (COXs)	COX1 inhibitor	Acetylsalicylic acid, profens, acetaminophen and dipyron (as arachidonylamides)
	COX2 inhibitor	Acetylsalicylic acid, profens, acetaminophen and dipyron (as arachidonylamides)
Vitamin K epoxide reductase	Inhibitor	Warfarin, phenprocoumon
Aromatase	Inhibitor	Exemestane
Lanosterol demethylase (fungal)	Inhibitor	Azole antifungals
Lipoxygenases	Inhibitor	Mesalazine
	5-lipoxygenase inhibitor	Zileuton
Thyroidal peroxidase	Inhibitor	Thiouracils
Iodothyronine-5' deiodinase	Inhibitor	Propylthiouracil
Inosine monophosphate dehydrogenase	Inhibitor	Mycophenolate mofetil
HMG-CoA reductase	Inhibitor	Statins

α -5-Testosterone reductase	Inhibitor	Finasteride, dutasteride
Dihydrofolate reductase (bacterial)	Inhibitor	Trimethoprim
Dihydrofolate reductase (human)	Inhibitor	Methotrexate, pemetrexed
Dihydrofolate reductase (parasitic)	Inhibitor	Proguanil
Dihydroorotate reductase	Inhibitor	Leflunomide
Enoyl reductase (mycobacterial)	Inhibitor	Isoniazid
Squalene epoxidase (fungal)	Inhibitor	Terbinafin
Δ -14 reductase (fungal)	Inhibitor	Amorolfine
Xanthine oxidase	Inhibitor	Allopurinol
4-Hydroxyphenylpyruvate dioxygenase	Inhibitor	Nitisinone
Ribonucleoside diphosphate reductase	Inhibitor	Hydroxycarbamide
Transferases		
Protein kinase C	Inhibitor	Miltefosine
Bacterial peptidyl transferase	Inhibitor	Chloramphenicol
Catecholamine-O-methyltransferase	Inhibitor	Entacapone
RNA polymerase (bacterial)	Inhibitor	Ansamycins
Reverse transcriptases (viral)	Competitive inhibitors	Zidovudine

	Allosteric inhibitors	Efavirenz
DNA polymerases	Inhibitor	Acyclovir, suramin
GABA transaminase	Inhibitor	Valproic acid, vigabatrin
Tyrosine kinases	PDGFR/ABL/KIT inhibitor	Imatinib
	EGFR inhibitor	Erlotinib
	β -VEGFR2/PDGFR/KIT/FLT3	Sunitinib
	β -VEGFR2/PDGFR/RAF	Sorafenib
Glycinamide ribonucleotide formyl transferase	Inhibitor	Pemetrexed
Phosphoenolpyruvate transferase (MurA, bacterial)	Inhibitor	Fosfomycin
Human cytosolic branched-chain aminotransferase (hBCATc)	Inhibitor	Gabapentin
<i>Hydrolases (proteases)</i>		
Aspartyl proteases (viral)	HIV protease inhibitor	Saquinavir, indinavir
<i>Hydrolases (serine proteases)</i>		
Unspecific	Unspecific inhibitors	Aprotinine
Bacterial serine protease	Direct inhibitor	β -lactams
Bacterial serine protease	Indirect inhibitor	Glycopeptides
Bacterial lactamases	Direct inhibitor	Sulbactam
Human antithrombin	Activator	Heparins
Human plasminogen	Activator	Streptokinase

Human coagulation factor	Activator	Factor IX complex, Factor VIII
Human factor Xa	Inhibitor	Fondaparinux
<i>Hydrolases (metalloproteases)</i>		
Human ACE	Inhibitor	Captopril
Human HRD	Inhibitor	Cilastatin
Human carboxypeptidase A (Zn)	Inhibitor	Penicillamine
Human enkephalinase	Inhibitor	Racecadotril
<i>Hydrolases (other)</i>		
26S proteasome	Inhibitor	Bortezomib
Esterases	AChE inhibitor	Physostigmine
	AChE reactivators	Obidoxime
	PDE inhibitor	Caffeine
	PDE3 inhibitor	Amrinon, milrinone
	PDE4 inhibitor	Papaverine
	PDE5 inhibitor	Sildenafil
	HDAC inhibitor	Valproic acid
	HDAC3/HDAC7 inhibitor	Carbamezepine
Glycosidases (viral)	α -glycosidase inhibitor	Zanamivir, oseltamivir
Glycosidases (human)	a-glycosidase inhibitor	Acarbose

Lipases	Gastrointestinal lipases inhibitor	Orlistat
Phosphatases	Calcineurin inhibitor	Cyclosporin
	Inositol polyphosphate phosphatase inhibitor	Lithium ions
GTPases	Rac1 inhibitor	6-Thio-GTP (azathioprine metabolite)
Phosphorylases	Bacterial C55-lipid phosphate dephosphorylase inhibitor	Bacitracin
Lyases		
DOPA decarboxylase	Inhibitor	Carbidopa
Carbonic anhydrase	Inhibitor	Acetazolamide
Histidine decarboxylase	Inhibitor	Tritoqualine
Ornithine decarboxylase	Inhibitor	Eflornithine
Soluble guanylyl cyclase	Activator	Nitric acid esters, molsidomine
Isomerases		
Alanine racemase	Inhibitor	D-Cycloserine
DNA gyrases (bacterial)	Inhibitor	Fluoroquinolones
Topoisomerases	Topoisomerase I inhibitor	Irinotecan
	Topoisomerase II inhibitor	Etoposide
8,7 isomerase (fungal)	Inhibitor	Amorolfine
Ligases (also known as synthases)		

Dihydropteroate synthase	Inhibitor	Sulphonamides
Thymidylate synthase (fungal and human)	Inhibitor	Fluorouracil
Thymidylate synthase (human)	Inhibitor	Methotrexate, pemetrexed
Phosphofructokinase	Inhibitor	Antimony compounds
mTOR	Inhibitor	Rapamycin
Haem polymerase (Plasmodium)	Inhibitor	Quinoline antimalarials
β -1,3--D-glucansynthase (fungi)	Inhibitor	Caspofungin
Glucosylceramide synthase	Inhibitor	Miglustat
Substrate	Drug substance	
Asparagine	Asparaginase	
Urate	Rasburicase (a urate oxidase)	
VAMP–synaptobrevin, SNAP25, Syntaxin	Light chain of the botulinum neurotoxin (Zn-endopeptidase)	
Type	Activity of drug	Drug examples
<i>Direct ligand-gated ion channel receptors</i>		
GABA _A receptors	Barbiturate binding site agonists	Barbiturate
	Benzodiazepine binding site agonists	Benzodiazepines
	Benzodiazepine binding site antagonists	Flumazenil
Acetylcholine receptors	Nicotinic receptor agonists	Pyrantel (of <i>Angiostrongylus</i>), levamisole
	Nicotinic receptor stabilizing antagonists	Alcuronium
	Nicotinic receptor depolarizing antagonists	Suxamethonium
	Nicotinic receptor allosteric modulators	Galantamine
Glutamate receptors (ionotropic)	NMDA subtype antagonists	Memantine
	NMDA subtype expression modulators	Acamprosate

	NMDA subtype phencyclidine binding site antagonists	Ketamine
<i>G-protein-coupled receptors</i>		
Acetylcholine receptors	Muscarinic receptor agonists	Pilocarpine
	Muscarinic receptor antagonists	Tropane derivatives
	Muscarinic receptor M ₃ antagonists	Darifenacine
Adenosine receptors	Agonists	Adenosine
	Adenosine A ₁ receptor agonists	Lignans from valerian
	Adenosine A ₁ receptor antagonists	Caffeine, theophylline
	Adenosine A _{2A} receptor antagonists	Caffeine, theophylline
Adrenoceptors	Agonists	Adrenaline, noradrenaline, ephedrine
	α_1 - and α_2 -receptors agonists	Xylometazoline
	α_1 -receptor antagonists	Ergotamine
	α_2 -receptor, central agonists	Methyldopa (as methylnoradrenaline)
	β -adrenoceptor antagonists	Isoprenaline
	β_1 -receptor antagonists	Propranolol, atenolol
	β_2 -receptor agonists	Salbutamol
	β_2 -receptor antagonists	Propranolol
Angiotensin receptors	AT ₁ -receptors antagonists	Sartans
Calcium-sensing receptor	Agonists	Strontium ions
	Allosteric activators	Cinacalcet
Cannabinoid receptors	CB ₁ - and CB ₂ -receptors agonists	Dronabinol
Cysteinyl-leukotriene receptors	Antagonists	Montelukast
Dopamine receptors	Dopamine receptor subtype direct agonists	Dopamine, levodopa
	D ₂ , D ₃ and D ₄ agonists	Apomorphine
	D ₂ , D ₃ and D ₄ antagonists	Chlorpromazine, fluphenazine, haloperidol, metoclopramide, ziprasidone
Endothelin receptors (ET _A , ET _B)	Antagonists	Bosentan
GABA _B receptors	Agonists	Baclofen
Glucagon receptors	Agonists	Glucagon
Glucagon-like peptide-1 receptor	Agonists	Exenatide
Histamine receptors	H ₁ -antagonists	Diphenhydramine
	H ₂ -antagonists	Cimetidine
Opioid receptors	μ -opioid agonists	Morphine, buprenorphine

	μ -, κ - and δ -opioid antagonists	Naltrexone
	κ -opioid antagonists	Buprenorphine
Neurokinin receptors	NK ₁ receptor antagonists	Aprepitant
Prostanoid receptors	Agonists	Misoprostol, sulprostone, iloprost
Prostamide receptors	Agonists	Bimatoprost
Purinergic receptors	P ₂ Y ₁₂ antagonists	Clopidogrel
Serotonin receptors	Subtype-specific (partial) agonists	Ergometrine, ergotamine
	5-HT _{1A} partial agonists	Buspirone
	5-HT _{1B/1D} agonists	Triptans
	5-HT _{2A} antagonists	Quetiapine, ziprasidone
	5-HT ₃ antagonists	Granisetron
	5-HT ₄ partial agonists	Tegaserode
Vasopressin receptors	Agonists	Vasopressin
	V ₁ agonists	Terlipressin
	V ₂ agonists	Desmopressin
	OT agonists	Oxytocin
	OT antagonists	Atosiban
Cytokine receptors		
Class I cytokine receptors	Growth hormone receptor antagonists	Pegvisomant
	Erythropoietin receptor agonists	Erythropoietin
	Granulocyte colony stimulating factor agonists	Filgrastim
	Granulocyte-macrophage colony stimulating factor agonists	Molgramostim
	Interleukin-1 receptor antagonists	Anakinra
	Interleukin-2 receptor agonists	Aldesleukin
TNF α receptors	Mimetics (soluble)	Etanercept
Integrin receptors		
Glycoprotein IIb/IIIa receptor	Antagonists	Tirofiban
Receptors associated with a tyrosine kinase		
Insulin receptor	Direct agonists	Insulin
Insulin receptor	Sensitizers	Biguanides
Nuclear receptors (steroid hormone receptors)		
Mineralocorticoid receptor	Agonists	Aldosterone
	Antagonists	Spironolactone
Glucocorticoid receptor	Agonists	Glucocorticoids
Progesterone receptor	Agonists	Gestagens
Estrogen receptor	Agonists	Oestrogens

	(Partial) antagonists	Clomifene
	Antagonists	Fulvestrant
	Modulators	Tamoxifen, raloxifene
	Androgen receptor Agonists	Testosterone
	Antagonists	Cyproterone acetate
Vitamin D receptor	Agonists	Retinoids
ACTH receptor agonists	Agonists	Tetracosactide (also known as cosyntropin)
Nuclear receptors (other)		
	α -Retinoic acid receptors RAR agonists	Isotretinoin
	β -RAR agonists	Adapalene, isotretinoin
	γ -RAR agonists	Adapalene, isotretinoin
Peroxisome proliferator-activated receptor (PPAR)	α -PPAR agonists	Fibrates
	γ -PPAR agonists	Glitazones
Thyroid hormone receptors	Agonists	L-Thyroxine
Voltage-gated Ca^{2+} channels		
General	Inhibitor	Oxcarbazepine
In <i>Schistosoma sp.</i>	Inhibitor	Praziquantel
L-type channels	Inhibitor	Dihydropyridines, diltiazem, lercanidipine, pregabalin, verapamil
T-type channels	Inhibitor	Succinimides
K ⁺ channels		
Epithelial K ⁺ channels	Opener Inhibitor	Diazoxide, minoxidil
		Nateglinide, sulphonylureas
Voltage-gated K ⁺ channels	Inhibitor	Amiodarone
Na⁺ channels		
Epithelial Na ⁺ channels (ENaC)	Inhibitor	Amiloride, bupivacaine, lidocaine, procainamide, quinidine
Voltage-gated Na ⁺ channels	Inhibitor	Carbamazepine, flecainide, lamotrigine, phenytoin, propafenone, topiramate, valproic acid
Ryanodine-inositol 1,4,5-triphosphate receptor Ca^{2+} channel (RIR-CaC) family		
Ryanodine receptors	Inhibitor	Dantrolene
Transient receptor potential Ca^{2+} channel (TRP-CC) family		
TRPV1 receptors	Inhibitor	Acetaminophen (as arachidonylamide)
Cl ⁻ channels		

Cl ⁻ channel	Inhibitor (mast cells) Opener (parasites)	Cromolyn sodium Ivermectin
Cation-chloride cotransporter (CCC) family	Thiazide-sensitive NaCl symporter, human inhibitor	Thiazide diuretics
	Bumetanide-sensitive NaCl/KCl symporters, human inhibitor	Furosemide
Na ⁺ /H ⁺ antiporters	Inhibitor	Amiloride, triamterene
Proton pumps	Ca ²⁺ -dependent ATPase (PfATP6; Plasmodia) inhibitor	Artemisinin and derivatives
H ⁺ /K ⁺ -ATPase	Inhibitor	Omeprazole
Na ⁺ /K ⁺ ATPase	Inhibitor	Cardiac glycosides
Eukaryotic (putative) sterol transporter (EST) family	Niemann-Pick C1 like 1 (NPC1L1) protein inhibitor	Ezetimibe
Neurotransmitter/Na ⁺ symporter (NSS) family	Serotonin/Na ⁺ symporter inhibitor	Cocaine, tricyclic antidepressants, paroxetine
	Noradrenaline/Na ⁺ symporter inhibitor	Bupropion, venlafaxine
	Dopamine/Na ⁺ symporter inhibitor	Tricyclic antidepressants, cocaine, amphetamines
	Vesicular monoamine transporter inhibitor	Reserpine
Nucleic acids		
DNA and RNA	Alkylation	Chlorambucil, cyclophosphamide, dacarbazine
	Complexation	Cisplatin
	Intercalation	Doxorubicin
	Oxidative degradation	Bleomycin
	Strand breaks	Nitroimidazoles
RNA	Interaction with 16S-rRNA	Aminoglycoside anti-infectives
	Interaction with 23S-rRNA	Macrolide anti-infectives
	23S-rRNA/tRNA/2-polypeptide complex	Oxazolidinone anti-infectives
Spindle	Inhibition of development	Vinca alkaloids
	Inhibition of desaggregation	Taxanes
Inhibition of mitosis	—	Colchicine
Ribosome		
30S subunit (bacterial)	Inhibitors	Tetracyclines
50S subunit (bacterial)	Inhibitors	Lincosamides, quinupristin–dalfopristin

Degradation domains can be engineered from known proteins (e.g., those proteins set forth in the above table) through any of a variety of routine methods known in the art. Generally, such methods employ first creating a library of interest including proteins derived from the, e.g., naturally occurring protein. Second, cells or cell populations expressing proteins from individual library constructs will be selected on the basis of whether the expression of the derived protein is dependent on the presence of the desired stabilization

compound. The process of derivation and selection can be repeated in as many cycles necessary to identify a suitable candidate.

For example, a library can be created through rational protein design based on sampling different structures and putative affinities of the protein domain to the selected compound. Alternatively, a library
5 can be generated by random mutagenesis of the target protein. In either case, e.g., Jurkat cells can be transduced with a lentiviral library generated from the constructs. Jurkat cells can then undergo a round of FACS sorting, to eliminate cells that constitutively express the protein of interest. In the next stage, the sorted cells are incubated with the compound of choice for 24 hrs and positive cells are FACS sorted. These are expanded through single cell cloning. From there, individual transduced clones will be
10 assessed for the ability to induce expression of the protein of interest in a compound-dependent manner.

SUICIDE GENES AND DOMAINS

The present invention, in part, utilizes CAR technology for methods of selectively ablating or activating modified T cells from a subject after adoptive transfer. In one embodiment, a modified CAR T
15 cell is selectively ablated in the subject by inducing activation of a suicide domain in the modified T cell. In another embodiment, a modified T cell is selectively activated in the subject by actively preventing the apoptosis of modified CAR T cell during therapy. In yet another embodiment, the modified T cell is selectively activated in the subject by allowing cell-surface expression of the CAR construct.

Some of the potential side effects of non-target cell recognition by CAR T cells can be overcome
20 by the co-expression of a suicide gene in the CAR T cell. In addition, the CAR T cells can be selectively ablated after targeting B cells for depletion to treat autoantibody or alloantibody diseases or conditions.

The invention includes an isolated nucleic acid comprising a suicide gene. Examples of suicide genes include, but are not limited to, herpes simplex virus thymidine kinase (HSV-TK), the cytoplasmic domain of Fas, a caspase such as caspase-8 or caspase-9, cytosine deaminase, E1A, FHIT, and other
25 known suicide or apoptosis-inducing genes (Straathof et al., 2005, Blood 105:4247-4254; Cohen et al., 1999, Leuk. Lymphoma 34:473-480; Thomis et al., 2001, Blood 97:1249-1257; Tey et al., 2007, Biol. Blood Marrow Transplant 13:913-924; and Di Stasi et al., 2011, N. Engl. J. Med. 365:1673-1683).

The suicide gene may be operably linked to a promoter, such as an inducible promoter sequence. Examples of inducible promoters include, but are not limited to, a heat shock promoter, a tetracycline-
30 regulated promoter, a steroid-regulated promoter, a metal-regulated promoter, an estrogen receptor-regulated promoter, and others known in the art. In one aspect, the invention includes an isolated nucleic acid sequence comprising a nucleic acid sequence comprising a suicide gene and a nucleic acid encoding a chimeric antigen receptor. In another aspect, the invention includes an isolated nucleic acid

sequence comprising a nucleic acid sequence comprising a suicide gene and a nucleic acid encoding a chimeric antigen receptor. In one embodiment, the suicide gene comprises the nucleic acid selected from the group consisting of

ATGCTCGAGGGGGTTCAGGTGGAGACTATCAGCCCGGGCGACGGACGGACATTCCCAAAGCGCGG
 5 GCAGACGTGTGTGGTGCATTACACCGGGATGCTTGAGGACGGAAAGAAAGTGGACTCTTCCCGAGA
 CCGAAATAAACCATTCAAGTTCATGTTGGGCAAGCAGGAGGTATCAGAGGGTGGGAGGAGGGCGT
 CGCTCAGATGAGTGTCTGGACAGAGGGCCAAGCTCACGATCTCCCCTGATTACGCCTACGGGGCAAC
 TGGTCACCCCGGAATCATCCCCCTCACGCAACCCTCGTGTTCGACGTCGAGCTGCTCAAACCTGGA
 ATCAGGCGGAGGCAGTGGCGCTAGCGGGTTTGGCGATGTCGGTGCCCTTGAAAGCTTGAGAGGAA
 10 ATGCCGATCTCGCTTACATCTTGAGCATGGAGCCCTGTGGGCACTGTCTGATCATCAACAATGTTAA
 CTTTTGCCGGGAGTCCGGCCTGCGCACACGCACAGGCTCCAACATTGACTGCGAAAACTTCGAAG
 GAGGTTTAGCTCTCTGCATTTTCATGGTAGAGGTGAAGGGGGATCTGACCGCCAAGAAAATGGTTCTC
 GCCCTTCTCGAGCTTGCGCAGCAGGACCATGGAGCGCTTGACTGTTGTGTGTTGTGATACTGAGC
 CATGGCTGTCAGGCTTCCCATCTCCAGTTTCCAGGGGCCGTGTACGGAACCGATGGATGCCCTGTG
 15 TCAGTTGAAAAGATCGTAAACATCTTTAACGGAACATCTTGCCCGAGCCTCGGCGGTAAACCGAAGC
 TTTTTTTTATCCAGGCCTGCGGCGGTGAACAGAAAGATCATGGCTTCGAGGTTGCCAGTACCAGCCC
 TGAAGACGAATCCCCCGGGTCAAATCCTGAACCAGATGCGACCCCTTTCCAGGAAGGACTCCGCAC
 TTTTGACCAGCTTGACGCCATTTCTCCCTGCCAACACCTTCCGACATATTTGTAAGCTACTCCACCT
 TTCCAGGATTCGTGAGCTGGCGCGACCCAAAATCCGGCAGTTGGTATGTTGAAACCCTGGACGATAT
 20 TTTGAAACAATGGGCCCACAGTGAGGACCTGCAGTCCCTTCTTCTGCGCGTAGCCAATGCCGTGTC
 AGTCAAAGGGATTTACAAGCAGATGCCAGGCTGCTTAATTTCTGCGCAAGAACTGTTTTTTAAGA
 CCAGT or SEQ ID NO: 3001;
 CGGACGGACATTCCCAAAGCGCGGGCAGACGTGTGTGGTGCATTACACCGGGATGCTTGAGGACG
 GAAAGAAAGTGGACTCTTCCCGAGACCGAAATAAACCATTCAAGTTCATGTTGGGCAAGCAGGAGGT
 25 TATCAGAGGGTGGGAGGAGGGCGTCGCTCAGATGAGTGTCTGGACAGAGGGCCAAGCTCACGATCT
 CCCCTGATTACGCCTACGGGGCAACTGGTCACCCCGGAATCATCCCCCTCACGCAACCCTCGTGT
 TCGACGTCGAGCTGCTCAAACCTGGAATCAGGCGGAGGCAGTGGCGGGTTTGGCGATGTCGGTGCC
 CTTGAAAGCTTGAGAGGAAATGCCGATCTCGCTTACATCTTGAGCATGGAGCCCTGTGGGCACTGTC
 TGATCATCAACAATGTTAACTTTTGCCGGGAGTCCGGCCTGCGCACACGCACAGGCTCCAACATTGA
 30 CTGCGAAAACTTCGAAGGAGGTTTAGCTCTCTGCATTTTCATGGTAGAGGTGAAGGGGGATCTGACC
 GCCAAGAAAAATGGTTCTCGCCCTTCTCGAGCTTGCGCAGCAGGACCATGGAGCGCTTGACTGTTGT
 GTCGTTGTGATACTGAGCCATGGCTGTCAGGCTTCCCATCTCCAGTTTCCAGGGGCCGTGTACGGA
 ACCGATGGATGCCCTGTGTGAGTTGAAAAGATCGTAAACATCTTTAACGGAACATCTTGCCCGAGCC
 TCGGCGGTAAACCGAAGCTTTTTTTTATCCAGGCCTGCGGCGGTGAACAGAAAGATCATGGCTTCGA
 35 GGTTGCCAGTACCAGCCCTGAAGACGAATCCCCCGGGTCAAATCCTGAACCAGATGCGACCCCTTT
 CCAGGAAGGACTCCGCACCTTTGACCAGCTTGACGCCATTTCTCCCTGCCAACACCTTCCGACATA
 TTTGTAAGCTACTCCACCTTTCCAGGATTCGTGAGCTGGCGCGACCCAAAATCCGGCAGTTGGTATG

TTGAAACCCTGGACGATATCTTCGAACAATGGGCCACAGTGAGGACCTGCAGTCCCTTCTTCTGCG
CGTAGCCAATGCCGTGTCAGTCAAAGGGATTTACAAGCAGATGCCAGGCTGCTTTAATTCCTGCGC
AAGAACTGTTTTTTAAGACCAGTTGAGTCGACGGAGGAGGAG or SEQ ID NO: 3002;
GGGGTTCAGGTGGAGACTATCAGCCCGGGCGACGGACGGACATTCCCAAAGCGCGGGCAGACGTG
5 TGTGGTGCATTACACCGGGATGCTTGAGGACGGAAAGAAAGTGGACTCTTCCCGAGACCGAAATAA
ACCATTCAAGTTCATGTTGGGCAAGCAGGAGGTTATCAGAGGGTGGGAGGAGGGCGTCGCTCAGAT
GAGTGTGCGACAGAGGGCCAAGCTCACGATCTCCCCTGATTACGCCTACGGGGCAACTGGTCACCC
CGGAATCATCCCCCTCACGCAACCCTCGTGTTTCGACGTGAGCTGCTCAAACCTGGAATCAGGCGG
AGGCAGTGGCGGGTTTGGCGATGTCGGTGCCCTTGAAAGCTTGAGAGGAAATGCCGATCTCGCTTA
10 CATCTTGAGCATGGAGCCCTGTGGGCACTGTCTGATCATCAACAATGTTAACTTTTGGCGGGAGTCC
GGCCTGCGCACACGCACAGGCTCCAACATTGACTGCGAAAACTTCGAAGGAGGTTTAGCTCTCTG
CATTTTCATGGTAGAGGTGAAGGGGGATCTGACCGCCAAGAAAATGGTTCTCGCCCTTCTCGAGCTTG
CGCAGCAGGACCATGGAGCGCTTGACTGTTGTGTGCTTGTGATACTGAGCCATGGCTGTCAGGCTT
CCCATCTCCAGTTTCCAGGGGCCGTGTACGGAACCGATGGATGCCCTGTGTGAGTTGAAAAGATCG
15 TAAACATCTTTAACGGAACATCTTGCCCGAGCCTCGGCGGTAAACCGAAGCTTTTTTTTATCCAGGCC
TGCGGCGGTGAACAGAAAGATCATGGCTTCGAGGTTGCCAGTACCAGCCCTGAAGACGAATCCCC
GGGTCAAATCCTGAACCAGATGCGACCCCTTTCCAGGAAGGACTCCGCACTTTTGACCAGCTTGAC
GCCATTTCTCCCTGCCAACACCTTCCGACATATTTGTAAGCTACTCCACCTTCCAGGATTCGTGAG
CTGGCGCGACCCAAAATCCGGCAGTTGGTATGTTGAAACCCTGGACGATATCTTCGAACAATGGGC
20 CCACAGTGAGGACCTGCAGTCCCTTCTTCTGCGCGTAGCCAATGCCGTGTCAGTCAAAGGGATTTAC
AAGCAGATGCCAGGCTGCTTTAATTTCTGCGCAAGAACTGTTTTTTAAGACCAGTTGA or SEQ ID
NO: 3003; and
AGAGGCGTGCAGGTGGAAACCATCTCTCCCGGCGACGGCAGAACCTTCCCTAAGAGGGGCCAGAC
CTGCGTGGTGCCTACACCGGCATGCTGGAAGATGGCAAGAAGATGGACAGCTCCCGGGACCGGA
25 ACAAGCCCTTCAAGTTCATGCTGGGCAAGCAGGAAGTGATCCGGGGCTGGGAAGAGGGCGTGGCA
CAGATGTCTGTGGGCCAGAGAGCCAAGCTGACCATCAGCCCCGATTACGCCTACGGCGCCACAGG
CCACCCTGGCATCATTCCTCCACACGCCACACTGGTGTTCGATGTGGAAGTCTGAAAGCTGAAAC
CCGGGGAGTGCAGGTGGAACAATCAGCCCTGGCGACGGCCGACCTTCCAAAACGGGGACAGA
CATGTGTGGTGCATTATACAGGGATGCTGGAAGATGGGAAAAAATGGATAGCAGCCGCGACCGCA
30 ACAAACCTTTAAGTTTATGCTGGGGAAACAGGAAGTGATTAGAGGCTGGGAAGAGGGGGTGGCAC
AGATGAGCGTGGGACAGCGGGCCAACTGACAATCTCCCCGACTATGCCTATGGGGCCACCGGA
CACCCCGGAATCATCCACCTCATGCTACCCTGGTGTGTTGACGTGGAAGTCTGAAACTGGAAACAA
GCGGCGGAGGCAGCGGCGGCTTTGGAGATGTGGGAGCCCTGGAAAGCCTGCGGGGCAATGCCGA
TCTGGCCTACATCCTGAGCATGGAACCCTGCGGCCACTGCCTGATTATCAACAACGTGAACTTCTGC
35 AGAGAGAGCGGCCTGCGGACCAGAACCGGCAGCAACATCGACTGCGAGAAGCTGCGGCGGAGATT
CAGCAGCCTGCACTTCATGGTGAAGTGAAGGGGGACCTGACCGCCAAGAAAATGGTGCTGGCTCT
GCTGGAAGTGGCCAGCAGGATCATGGCGCCCTGGAAGTGTGCGTGGTGTGATCCTGAGCCACG

GCTGCCAGGCCAGCCATCTGCAGTTTCCCGGCGCTGTGTATGGCACCGATGGCTGCCCTGTGTCCG
 TGGAAAAGATCGTGAATATCTTCAACGGCACCAGCTGCCCCAGCCTGGGCGGAAAGCCTAAGCTGT
 TCTTTATTCAAGCCTGTGGGGGCGAGCAGAAGGACCACGGATTTGAGGTGGCCAGCACCTCCCCCG
 AGGATGAGAGCCCTGGCAGCAACCCTGAGCCTGACGCCACCCCATTCAGGAAGGACTGCGGACC
 5 TTCCAGCAGCTGGACGCCATCTCTAGCCTGCCACCCCCAGCGACATCTTCGTGTCCTACAGCACC
 TTCCCTGGCTTTGTGTCCTGGCGGGACCCCAAGTCCGGCTCTTGGTACGTGGAAACCCTGGACGAC
 ATCTTTGAGCAGTGGGCCCCATAGCGAGGACCTGCAGAGCCTGCTGCTGAGGGTGGCCAATGCCGT
 GTCCGTGAAGGGCATCTACAAGCAGATGCCCGGCTGCTTCAACTTCCTGCGGAAGAAGCTGTTTTTC
 AAGACCAGC or SEQ ID NO: 3004.

10 In another embodiment, the suicide gene encodes an amino acid sequence selected from the
 group consisting of
 MLEGVQVETISPGDGRTFPPKRGQTCVVHYTGMLDGGKKVDSSRDRNKPFFKMLGKQEVIRGWEEGVAQ
 MSVGQRAKLTISPDYAYGATGHPGIIPPHATLVFDVELLKLESGGGSGASGFGDVGALESRLGNADLAYIL
 SMEPCGHCLIINNPNFCRESGLRTRTGSNIDCEKLRRRFSSLHFMVEVKGDLTAKKMLALLELAQQDHG
 15 ALDCCVVILSHGCQASHLQFPGAVYGTGCPVSVEKIVNIFNGTSCPSLGGKPKLFFIQACGGEQKDHG
 FEVASTSPEDESPGSNPEPDATPFQEGLRTFDQLDAISSLPTPSDIFVSYSTFPGFVSWRDPKSGSWYVE
 TLDDIFEQWAHSEDLSLLLVRANAVSVKGIYKQMPGCFNLRKKLFFKTS or SEQ ID NO: 3005;
 GVQVETISPGDGRTFPPKRGQTCVVHYTGMLDGGKKVDSSRDRNKPFFKMLGKQEVIRGWEEGVAQMS
 VGQRAKLTISPDYAYGATGHPGIIPPHATLVFDVELLKLESGGGSGGFGDVGALESRLGNADLAYILSMEP
 20 CGHCLIINNPNFCRESGLRTRTGSNIDCEKLRRRFSSLHFMVEVKGDLTAKKMLALLELAQQDHGALDC
 CVVVILSHGCQASHLQFPGAVYGTGCPVSVEKIVNIFNGTSCPSLGGKPKLFFIQACGGEQKDHGFEVA
 STSPEDESPGSNPEPDATPFQEGLRTFDQLDAISSLPTPSDIFVSYSTFPGFVSWRDPKSGSWYVETLDD
 IFEQWAHSEDLSLLLVRANAVSVKGIYKQMPGCFNLRKKLFFKTS or SEQ ID NO: 3006; and
 RGVQVETISPGDGRTFPPKRGQTCVVHYTGMLDGGKKMDSSRDRNKPFFKMLGKQEVIRGWEEGVAQM
 25 SVGQRAKLTISPDYAYGATGHPGIIPPHATLVFDVELLKLETRGVQVETISPGDGRTFPPKRGQTCVVHYTG
 MLEDGKKMDSSRDRNKPFFKMLGKQEVIRGWEEGVAQMSVGQRAKLTISPDYAYGATGHPGIIPPHATL
 VFDVELLKLETSGGGSGGFGDVGALESRLGNADLAYILSMEPCGHCLIINNPNFCRESGLRTRTGSNIDC
 EKLRRRFSSLHFMVEVKGDLTAKKMLALLELAQQDHGALDCCVVILSHGCQASHLQFPGAVYGTGDC
 PVSVEKIVNIFNGTSCPSLGGKPKLFFIQACGGEQKDHGFEVASTSPEDESPGSNPEPDATPFQEGLRTF
 30 DQLDAISSLPTPSDIFVSYSTFPGFVSWRDPKSGSWYVETLDDIFEQWAHSEDLSLLLVRANAVSVKGIY
 KQMPGCFNLRKKLFFKTS or SEQ ID NO: 3007. In yet another embodiment, the suicide gene has an
 inducible promoter.

In some embodiments, the suicide gene is in an expression vector. In an exemplary
 embodiment, the present invention includes a vector comprising a nucleic acid sequence comprising a
 35 suicide gene comprising SEQ ID NOs: 3001, 3002, 3003 or 3004. The expression vector may also

include other genes, such as a chimeric antigen receptor and/or CRISPR system disclosed elsewhere herein.

The invention also includes a cell comprising the suicide gene. In an exemplary aspect, the present invention includes a modified cell comprising a nucleic acid comprising a suicide gene encoding
5 an amino acid sequence selected from the group consisting of SEQ ID NO: 3005, 3006, and 3007 and a nucleic acid encoding a chimeric antigen receptor. In another aspect, the present invention includes a modified cell comprising a nucleic acid comprising a suicide gene selected from the group consisting of
10 SEQ ID NO: 3001, 3002, 3003 and 3004 and a nucleic acid encoding a chimeric antigen receptor. In one embodiment, the suicide gene encodes an amino acid sequence selected from the group consisting of SEQ ID NO: 3005, 3006, and 3007. In another embodiment, the suicide gene has an inducible promoter.

In one embodiment, the CAR modified T cell comprises nucleic acids encoding a suicide gene as a separate nucleic acid sequence from the CAR construct described elsewhere herein. For example, HSV-TK, i-Casp9, the cytoplasmic domain of Fas, or a caspase can be incorporated into genetically
15 engineered T cells separate from the CAR construct. In another embodiment, the CAR modified T cell comprises a suicide gene in the same construct as the nucleic acids encoding the CAR. In this embodiment, the nucleic acids comprising the suicide gene may be upstream or downstream of the nucleic acids encoding the CAR.

In one embodiment, expression of the suicide gene is activated in the cell by contacting the cell
20 with an inducing agent administered to the cell or to a mammal comprising the cell. The inducing agent then activates an inducible promoter to express the suicide gene. In such an embodiment, the inducing agent is administered to the subject to induce expression of the suicide gene.

In another embodiment, a suicide gene product that is expressed from the suicide gene is activated by an activating agent, such as a dimerization agent. For example, the dimerization agent, such
25 as AP20187, promotes dimerization and activation of caspase-9 molecules.

In some embodiments with constitutive expression of the suicide gene, expression of the suicide gene may be turned off in the cell by contacting the cell with an inhibiting agent administered to the cell or to a mammal comprising the cell. The inhibiting agent selectively turns off expression. For example, caspase-9 is constitutively expressed in the cell and the addition of an inhibiting agent represses
30 expression or activation of caspase-9. In one embodiment, the inhibiting agent is administered to the subject to repress expression of the suicide gene.

In some embodiments with constitutive expression of the suicide gene, activation of the suicide gene product may be repressed in the cell by contacting the cell with an inhibiting agent, such as a solubilizing agent, administered to the cell or to a mammal comprising the cell. The inhibiting agent

represses activation of the suicide gene product, such as by preventing dimerization of the caspase-9 molecules. In one embodiment, the solubilizing agent is administered to the subject to repress activation of the suicide gene product.

In some aspects, the suicide gene is not immunogenic to the cell comprising the suicide gene or host harboring the suicide gene. Although thymidine kinase (TK) may be employed, it can be immunogenic. Alternatively, examples of suicide genes that are not immunogenic to the host include caspase-9, caspase-8, and cytosine deaminase.

In yet another embodiment, suicide gene expression is linked in tandem to one or more dimerization domains, which cause aggregation of the fusion protein containing the suicide domain and the dimerization domain, preventing cell-surface expression and hence function of the suicide gene.

In yet another embodiment, the nucleic acid sequence encoding a dimerization domain, linked to a suicide gene, comprises the nucleic acid sequence selected from the group consisting of GGAAGCGGCGCCACCAATTTTCAGCCTGCTGAAACAGGCGGCGACGTGGAAGAGAACCCTGGCCC T or SEQ ID NO: 3008;

AGTGGCTCCGGCGCAACAAATTTCTCCTTGCTGAAACAGGCAGGCGACGTTGAGGAAAATCCCGGC CCA or SEQ ID NO: 3009;

GGCTCCGGCGCAACAAATTTCTCCTTGCTGAAACAGGCAGGCGACGTTGAGGAAAATCCCGGCCCA or SEQ ID NO: 3010; GGGGTTTCAGGTGGAGACTATCAGCCCGGGCGA or SEQ ID NO: 3011; and

GGCTCCGGCGCAACAAATTTCTCCTTGCTGAAACAGGCAGGCGACGTTGAGGAAAATCCCGGCCCA

or SEQ ID NO: 3012. In another such embodiment, the dimerization domain, linked to a suicide domain, comprises the amino acid sequence selected from the group consisting of

GSGATNFSLLKQAGDVEENPGP or SEQ ID NO: 3013; and RKRRGSGATNFSLLKQAGDVEENPGP or SEQ ID NO: 3014.

Solubilization of the dimerization domains, with a solubilizing agent, administered to the cell or to a mammal comprising the cell, prevents aggregation and allows the construct to egress through the secretory system.

As described herein, the present invention includes a method of modifying a T cell with a chimeric antigen receptor (CAR) and a suicide gene. Thus, the present invention encompasses a nucleic acid encoding a CAR or a modified T cell comprising a CAR, wherein the CAR includes an antigen binding domain, a transmembrane domain and an intracellular domain.

One or more domains or a fragment of a domain of the CAR may be human. In one embodiment, the present invention includes a fully human CAR. The nucleic acid sequences coding for the desired domains can be obtained using recombinant methods known in the art, such as, for example by screening libraries from cells expressing the gene, by deriving the gene from a vector known to include

the same, or by isolating directly from cells and tissues containing the same, using standard techniques. Alternatively, the gene of interest can be produced synthetically, rather than as a cloned molecule.

Example of CARs are described in U.S. Patent Nos.: 8,911,993, 8,906,682, 8,975,071, 8,916,381, 9,102,760, 9,101,584, and 9,102,761, all of which are incorporated herein by reference in their
5 entireties.

NUCLEIC ACID AND VECTORS

In another aspect, the invention pertains to a nucleic acid encoding any of the fusion proteins described herein, or a vector comprising such a nucleic acid. In one embodiment, the vector is chosen from a DNA
10 vector, an RNA vector, a plasmid, a lentivirus vector, adenoviral vector, or a retrovirus vector. In one embodiment, the vector is a lentivirus vector.

In some embodiments, the nucleic acids described herein include a sequence encoding a furin cleavage site. In some embodiments, the nucleic acids described herein include any one of SEQ ID NOs: 1112, 126, 128, 130, 132, 134, 136, or 138, or a sequence having at least 90%, 95%, 97%, 98%, or 99%
15 identity thereto. In some embodiments, the nucleic acids described herein include any one of SEQ ID NOs: 1112, 126, 128, 130, 132, 134, 136, or 138. In some embodiments, the nucleic acids described herein include SEQ ID NO: 126 or SEQ ID NO: 128. In some embodiments, the nucleic acids described herein include SEQ ID NO: 126.

In some embodiments, the nucleic acids described herein include a sequence encoding a conditional
20 expression domain, e.g., an aggregation domain or a degradation domain. In some embodiments, the nucleic acids described herein include a sequence encoding an aggregation domain derived from FKBP, e.g., FKBP F36M. In some embodiments, the nucleic acids described herein include a sequence encoding a degradation domain derived from an estrogen receptor (ER). In some embodiments, the nucleic acids described herein include SEQ ID NO: 1110 or SEQ ID NO: 122, or a sequence having at
25 least 90%, 95%, 97%, 98%, or 99% identity thereto. In some embodiments, the nucleic acids described herein include SEQ ID NO: 1110 or SEQ ID NO: 122. In some embodiments, the nucleic acids described herein include SEQ ID NO: 122.

The present disclosure also provides vectors in which a DNA of the present disclosure is inserted. Vectors derived from retroviruses such as the lentivirus are suitable tools to achieve long-term gene transfer since
30 they allow long-term, stable integration of a transgene and its propagation in daughter cells. Lentiviral vectors have the added advantage over vectors derived from onco-retroviruses such as murine leukemia viruses in that they can transduce non-proliferating cells, such as hepatocytes. They also have the added advantage of low immunogenicity. A retroviral vector may also be, e.g., a gammaretroviral vector. A

gammaretroviral vector may include, e.g., a promoter, a packaging signal (ψ), a primer binding site (PBS), one or more (e.g., two) long terminal repeats (LTR), and a transgene of interest, e.g., a gene encoding a CAR. A gammaretroviral vector may lack viral structural genes such as gag, pol, and env. Exemplary gammaretroviral vectors include Murine Leukemia Virus (MLV), Spleen-Focus Forming Virus (SFFV), and
 5 Myeloproliferative Sarcoma Virus (MPSV), and vectors derived therefrom. Other gammaretroviral vectors are described, e.g., in Tobias Maetzig et al., "Gammaretroviral Vectors: Biology, Technology and Application" *Viruses*. 2011 Jun; 3(6): 677–713.

In another embodiment, the vector comprising the nucleic acid encoding the desired fusion protein of the invention is an adenoviral vector (A5/35). In another embodiment, the expression of nucleic acids
 10 encoding chimeric molecules can be accomplished using of transposons such as sleeping beauty, crisper, CAS9, and zinc finger nucleases. See below June et al. 2009 *Nature Reviews Immunology* 9.10: 704-716, is incorporated herein by reference.

The nucleic acid can be cloned into a number of types of vectors. For example, the nucleic acid can be cloned into a vector including, but not limited to a plasmid, a phagemid, a phage derivative, an animal
 15 virus, and a cosmid. Vectors of particular interest include expression vectors, replication vectors, probe generation vectors, and sequencing vectors.

Disclosed herein are methods for producing an in vitro transcribed RNA chimeric molecule. The present disclosure also includes a chimeric molecule encoding RNA construct that can be directly transfected into a cell. A method for generating mRNA for use in transfection can involve in vitro transcription (IVT) of a
 20 template with specially designed primers, followed by polyA addition, to produce a construct containing 3' and 5' untranslated sequence ("UTR"), a 5' cap and/or Internal Ribosome Entry Site (IRES), the nucleic acid to be expressed, and a polyA tail, typically 50-5000 bases in length (SEQ ID NO:32). RNA so produced can efficiently transfect different kinds of cells. In one aspect, the template includes sequences for the CAR.

25 **Nucleic Acid Constructs Encoding a fusion protein comprising a CAR**

The present disclosure also provides nucleic acid molecules encoding a fusion protein, e.g., as described herein, comprising a domain that includes one or more of the CAR constructs targeting an antigen described herein. In one aspect, the nucleic acid molecule is provided as a messenger RNA transcript. In one aspect, the nucleic acid molecule is provided as a DNA construct.

30 Accordingly, in one aspect, the invention pertains to a nucleic acid molecule encoding a fusion protein, e.g., as described herein, comprising a chimeric antigen receptor (CAR), wherein the CAR comprises an antigen binding domain that binds to an antigen described herein, a transmembrane domain (e.g., a transmembrane domain described herein), and an intracellular signaling domain (e.g., an intracellular signaling domain described herein) comprising a stimulatory domain, e.g., a costimulatory signaling

- domain (e.g., a costimulatory signaling domain described herein) and/or a primary signaling domain (e.g., a primary signaling domain described herein, e.g., a zeta chain described herein). In one embodiment, the transmembrane domain is transmembrane domain of a protein selected from the group consisting of the alpha, beta or zeta chain of the T-cell receptor, CD28, CD3 epsilon, CD45, CD4, CD5, CD8, CD9, CD16, CD22, CD33, CD37, CD64, CD80, CD86, CD134, CD137 and CD154. In some embodiments, a transmembrane domain may include at least the transmembrane region(s) of, e.g., KIRDS2, OX40, CD2, CD27, LFA-1 (CD11a, CD18), ICOS (CD278), 4-1BB (CD137), GITR, CD40, BAFFR, HVEM (LIGHTR), SLAMF7, NKp80 (KLRF1), NKp44, NKp30, NKp46, CD160, CD19, IL2R beta, IL2R gamma, IL7R α , ITGA1, VLA1, CD49a, ITGA4, IA4, CD49D, ITGA6, VLA-6, CD49f, ITGAD, CD11d, ITGAE, CD103, ITGAL, CD11a, LFA-1, ITGAM, CD11b, ITGAX, CD11c, ITGB1, CD29, ITGB2, CD18, LFA-1, ITGB7, NKG2D, NKG2C, TNFR2, DNAM1 (CD226), SLAMF4 (CD244, 2B4), CD84, CD96 (Tactile), CEACAM1, CRTAM, Ly9 (CD229), CD160 (BY55), PSGL1, CD100 (SEMA4D), SLAMF6 (NTB-A, Ly108), SLAM (SLAMF1, CD150, IPO-3), BLAME (SLAMF8), SELPLG (CD162), LTBR, PAG/Cbp, NKG2D, and NKG2C.
- In one embodiment, the transmembrane domain comprises a sequence of SEQ ID NO: 12, or a sequence with 95-99% identity thereof. In one embodiment, the antigen binding domain is connected to the transmembrane domain by a hinge region, e.g., a hinge described herein. In one embodiment, the hinge region comprises SEQ ID NO:4 or SEQ ID NO:6 or SEQ ID NO:8 or SEQ ID NO:10, or a sequence with 95-99% identity thereof. In one embodiment, the isolated nucleic acid molecule further comprises a sequence encoding a costimulatory domain. In one embodiment, the costimulatory domain is a functional signaling domain of a protein selected from the group consisting of OX40, CD27, CD28, CDS, ICAM-1, LFA-1 (CD11a/CD18), ICOS (CD278), and 4-1BB (CD137). Further examples of such costimulatory molecules include CDS, ICAM-1, GITR, BAFFR, HVEM (LIGHTR), SLAMF7, NKp80 (KLRF1), NKp44, NKp30, NKp46, CD160, CD19, CD4, CD8alpha, CD8beta, IL2R beta, IL2R gamma, IL7R alpha, ITGA4, VLA1, CD49a, ITGA4, IA4, CD49D, ITGA6, VLA-6, CD49f, ITGAD, CD11d, ITGAE, CD103, ITGAL, CD11a, LFA-1, ITGAM, CD11b, ITGAX, CD11c, ITGB1, CD29, ITGB2, CD18, LFA-1, ITGB7, NKG2D, NKG2C, TNFR2, TRANCE/RANKL, DNAM1 (CD226), SLAMF4 (CD244, 2B4), CD84, CD96 (Tactile), CEACAM1, CRTAM, Ly9 (CD229), CD160 (BY55), PSGL1, CD100 (SEMA4D), CD69, SLAMF6 (NTB-A, Ly108), SLAM (SLAMF1, CD150, IPO-3), BLAME (SLAMF8), SELPLG (CD162), LTBR, LAT, GADS, SLP-76, PAG/Cbp, NKG2D, and NKG2C. In one embodiment, the intracellular signaling domain comprises a functional signaling domain of 4-1BB and a functional signaling domain of CD3 zeta. In one embodiment, the intracellular signaling domain comprises the sequence of SEQ ID NO: 14, 16, 120, or 124, or a sequence with 95-99% identity thereof, and the sequence of SEQ ID NO: 18 or SEQ ID NO:20, or a sequence with 95-99% identity thereof, wherein the sequences comprising the intracellular signaling domain are expressed in the same frame and as a single polypeptide chain.

In another aspect, the invention pertains to an isolated nucleic acid molecule encoding a fusion protein, e.g., as described herein, comprising a domain that includes a CAR construct comprising a leader sequence of SEQ ID NO: 2, a scFv domain as described herein, a hinge region of SEQ ID NO:4 or SEQ ID NO:6 or SEQ ID NO:8 or SEQ ID NO:10 (or a sequence with 95-99% identity thereof), a

5 transmembrane domain having a sequence of SEQ ID NO: 12 (or a sequence with 95-99% identity thereof), a 4-1BB costimulatory domain having a sequence of SEQ ID NO:14, a CD27 costimulatory domain having a sequence of SEQ ID NO:16 (or a sequence with 95-99% identity thereof), a ICOS costimulatory domain having a sequence of SEQ ID NO: 120 (or a sequence with 95-99% identity thereof) or a CD28 costimulatory domain having a sequence of SEQ ID NO:124, and a CD3 zeta
10 stimulatory domain having a sequence of SEQ ID NO:18 or SEQ ID NO:20 (or a sequence with 95-99% identity thereof).

The nucleic acid sequences coding for the desired molecules can be obtained using recombinant methods known in the art, such as, for example by screening libraries from cells expressing the gene, by deriving the gene from a vector known to include the same, or by isolating directly from cells and tissues
15 containing the same, using standard techniques. Alternatively, the gene of interest can be produced synthetically, rather than cloned.

The present disclosure also provides vectors in which a nucleic acid of the present disclosure is inserted. Vectors derived from retroviruses such as the lentivirus are suitable tools to achieve long-term gene transfer since they allow long-term, stable integration of a transgene and its propagation in daughter cells.
20 Lentiviral vectors have the added advantage over vectors derived from onco-retroviruses such as murine leukemia viruses in that they can transduce non-proliferating cells, such as hepatocytes. They also have the added advantage of low immunogenicity.

In another embodiment, the vector comprising the nucleic acid encoding a fusion protein, e.g., as described herein, comprising a domain that includes a CAR of the invention is an adenoviral vector
25 (A5/35). In another embodiment, the expression of nucleic acids encoding CARs can be accomplished using of transposons such as sleeping beauty, crispr/CAS9, and zinc finger nucleases. See below June et al. 2009*Nature Reviews Immunology* 9.10: 704-716, is incorporated herein by reference.

In brief summary, the expression of natural or synthetic nucleic acids encoding a fusion protein, e.g., as described herein, comprising a domain that includes CARs is typically achieved by operably linking a
30 nucleic acid encoding the CAR polypeptide or portions thereof to a promoter, and incorporating the construct into an expression vector. The vectors can be suitable for replication and integration in eukaryotes. Typical cloning vectors contain transcription and translation terminators, initiation sequences, and promoters useful for regulation of the expression of the desired nucleic acid sequence.

The expression constructs of the present disclosure may also be used for nucleic acid immunization and
35 gene therapy, using standard gene delivery protocols. Methods for gene delivery are known in the art.

See, e.g., U.S. Pat. Nos. 5,399,346, 5,580,859, 5,589,466, incorporated by reference herein in their entireties. In another embodiment, the invention provides a gene therapy vector.

The nucleic acid can be cloned into a number of types of vectors. For example, the nucleic acid can be cloned into a vector including, but not limited to a plasmid, a phagemid, a phage derivative, an animal virus, and a cosmid. Vectors of particular interest include expression vectors, replication vectors, probe generation vectors, and sequencing vectors.

Further, the expression vector may be provided to a cell in the form of a viral vector. Viral vector technology is well known in the art and is described, for example, in Sambrook et al., 2012, MOLECULAR CLONING: A LABORATORY MANUAL, volumes 1 -4, Cold Spring Harbor Press, NY), and in other virology and molecular biology manuals. Viruses, which are useful as vectors include, but are not limited to, retroviruses, adenoviruses, adeno- associated viruses, herpes viruses, and lentiviruses. In general, a suitable vector contains an origin of replication functional in at least one organism, a promoter sequence, convenient restriction endonuclease sites, and one or more selectable markers, (e.g., WO 01/96584; WO 01/29058; and U.S. Pat. No. 6,326,193).

A number of viral based systems have been developed for gene transfer into mammalian cells. For example, retroviruses provide a convenient platform for gene delivery systems. A selected gene can be inserted into a vector and packaged in retroviral particles using techniques known in the art. The recombinant virus can then be isolated and delivered to cells of the subject either in vivo or ex vivo. A number of retroviral systems are known in the art. In some embodiments, adenovirus vectors are used. A number of adenovirus vectors are known in the art. In one embodiment, lentivirus vectors are used.

Additional promoter elements, e.g., enhancers, regulate the frequency of transcriptional initiation. Typically, these are located in the region 30-110 bp upstream of the start site, although a number of promoters have been shown to contain functional elements downstream of the start site as well. The spacing between promoter elements frequently is flexible, so that promoter function is preserved when elements are inverted or moved relative to one another. In the thymidine kinase (tk) promoter, the spacing between promoter elements can be increased to 50 bp apart before activity begins to decline. Depending on the promoter, it appears that individual elements can function either cooperatively or independently to activate transcription. Exemplary promoters include the CMV IE gene, EF-1 α , ubiquitin C, or phosphoglycerokinase (PGK) promoters.

An example of a promoter that is capable of expressing a fusion protein, e.g., as described herein, comprising a domain that includes aCAR encoding nucleic acid molecule in a mammalian T cell is the EF1a promoter. The native EF1a promoter drives expression of the alpha subunit of the elongation factor-1 complex, which is responsible for the enzymatic delivery of aminoacyl tRNAs to the ribosome. The EF1a promoter has been extensively used in mammalian expression plasmids and has been shown to be effective in driving expression of a fusion protein, e.g., as described herein, a fusion protein

comprising a domain that includes a CAR, from nucleic acid molecules cloned into a lentiviral vector. See, e.g., Milone et al., Mol. Ther. 17(8): 1453–1464 (2009). In one aspect, the EF1a promoter comprises the sequence provided as SEQ ID NO:1.

Another example of a promoter is the immediate early cytomegalovirus (CMV) promoter sequence. This promoter sequence is a strong constitutive promoter sequence capable of driving high levels of expression of any polynucleotide sequence operatively linked thereto. However, other constitutive promoter sequences may also be used, including, but not limited to the simian virus 40 (SV40) early promoter, mouse mammary tumor virus (MMTV), human immunodeficiency virus (HIV) long terminal repeat (LTR) promoter, MoMuLV promoter, an avian leukemia virus promoter, an Epstein-Barr virus immediate early promoter, a Rous sarcoma virus promoter, as well as human gene promoters such as, but not limited to, the actin promoter, the myosin promoter, the elongation factor-1 α promoter, the hemoglobin promoter, and the creatine kinase promoter. Further, the invention should not be limited to the use of constitutive promoters. Inducible promoters are also contemplated as part of the invention. The use of an inducible promoter provides a molecular switch capable of turning on expression of the polynucleotide sequence which it is operatively linked when such expression is desired, or turning off the expression when expression is not desired. Examples of inducible promoters include, but are not limited to a metallothionein promoter, a glucocorticoid promoter, a progesterone promoter, and a tetracycline promoter.

Another example of a promoter is the phosphoglycerate kinase (PGK) promoter. In embodiments, a truncated PGK promoter (e.g., a PGK promoter with one or more, e.g., 1, 2, 5, 10, 100, 200, 300, or 400, nucleotide deletions when compared to the wild-type PGK promoter sequence) may be desired. The nucleotide sequences of exemplary PGK promoters are provided below.

WT PGK Promoter

ACCCCTCTCTCCAGCCACTAAGCCAGTTGCTCCCTCGGCTGACGGCTGCACGCGAGGCCTCCGAAC
 25 GTCTTACGCCTTGTGGCGCGCCCGTCCTTGTCCCGGGTGTGATGGCGGGGTGTGGGGCGGAGGGC
 GTGGCGGGGAAGGGCCGGCGACGAGAGCCGCGCGGGACGACTCGTCGGCGATAACCGGTGTCCG
 GTAGCGCCAGCCGCGCGACGGTAACGAGGGACCGCGACAGGCAGACGCTCCCATGATCACTCTGC
 ACGCCGAAGGCAAATAGTGCAGGCCGTGCGGCGCTTGCGCTTCCTTGGAAGGGCTGAATCCCCGC
 CTCGTCCTTCGCAGCGGCCCCCGGGTGTTCCTCATCGCCGCTTCTAGGCCCACTGCGACGCTTGCC
 30 TGCACTTCTTACACGCTCTGGGTCCCAGCCGCGGCGACGCAAAGGGCCTTGGTGCGGGTCTCGTC
 GGCGCAGGGACGCGTTTGGGTCCCGACGGAACCTTTCCGCGTTGGGGTTGGGGCACCATAAGCT(
 SEQ ID NO: 185)

Exemplary truncated PGK Promoters:

PGK100:

ACCCCTCTCTCCAGCCACTAAGCCAGTTGCTCCCTCGGCTGACGGCTGCACGCGAGGCCTCCGAAC
GTCTTACGCCTTGTGGCGCGCCCGTCCTTGTCCCGGGTGTGATGGCGGGGTG (SEQ ID NO: 186)

PGK200:

ACCCCTCTCTCCAGCCACTAAGCCAGTTGCTCCCTCGGCTGACGGCTGCACGCGAGGCCTCCGAAC
5 GTCTTACGCCTTGTGGCGCGCCCGTCCTTGTCCCGGGTGTGATGGCGGGGTGTGGGGCGGAGGGC
GTGGCGGGGAAGGGCCGGCGACGAGAGCCGCGCGGGACGACTCGTCGGCGATAACCGGTGTCGG
GTAGCGCCAGCCGCGCGACGGTAACG (SEQ ID NO: 187)

PGK300:

ACCCCTCTCTCCAGCCACTAAGCCAGTTGCTCCCTCGGCTGACGGCTGCACGCGAGGCCTCCGAAC
10 GTCTTACGCCTTGTGGCGCGCCCGTCCTTGTCCCGGGTGTGATGGCGGGGTGTGGGGCGGAGGGC
GTGGCGGGGAAGGGCCGGCGACGAGAGCCGCGCGGGACGACTCGTCGGCGATAACCGGTGTCGG
GTAGCGCCAGCCGCGCGACGGTAACGAGGGACCGCGACAGGCAGACGCTCCCATGATCACTCTGC
ACGCCGAAGGCAAATAGTGCAGGCCGTGCGGCGCTTGGCGTTCCTTGAAGGGCTGAATCCCCG
(SEQ ID NO: 188)

15 PGK400:

ACCCCTCTCTCCAGCCACTAAGCCAGTTGCTCCCTCGGCTGACGGCTGCACGCGAGGCCTCCGAAC
GTCTTACGCCTTGTGGCGCGCCCGTCCTTGTCCCGGGTGTGATGGCGGGGTGTGGGGCGGAGGGC
GTGGCGGGGAAGGGCCGGCGACGAGAGCCGCGCGGGACGACTCGTCGGCGATAACCGGTGTCGG
GTAGCGCCAGCCGCGCGACGGTAACGAGGGACCGCGACAGGCAGACGCTCCCATGATCACTCTGC
20 ACGCCGAAGGCAAATAGTGCAGGCCGTGCGGCGCTTGGCGTTCCTTGAAGGGCTGAATCCCCG
CTCGTCTTTCGAGCGGCCCGGGTGTTCATCGCCGCTTCTAGGCCCACTGCGACGCTTGCC
TGCACTTCTTACACGCTCTGGGTCCCAGCCG (SEQ ID NO: 189)

A vector may also include, e.g., a signal sequence to facilitate secretion, a polyadenylation signal and
transcription terminator (e.g., from Bovine Growth Hormone (BGH) gene), an element allowing episomal
25 replication and replication in prokaryotes (e.g. SV40 origin and ColE1 or others known in the art) and/or
elements to allow selection (e.g., ampicillin resistance gene and/or zeocin marker).

In order to assess the expression of a fusion protein, e.g., as described herein, comprising a domain that
includes a CAR polypeptide or portions thereof, the expression vector to be introduced into a cell can also
contain either a selectable marker gene or a reporter gene or both to facilitate identification and selection
30 of expressing cells from the population of cells sought to be transfected or infected through viral vectors.
In other aspects, the selectable marker may be carried on a separate piece of DNA and used in a co-
transfection procedure. Both selectable markers and reporter genes may be flanked with appropriate

regulatory sequences to enable expression in the host cells. Useful selectable markers include, for example, antibiotic-resistance genes, such as neo and the like.

Reporter genes are used for identifying potentially transfected cells and for evaluating the functionality of regulatory sequences. In general, a reporter gene is a gene that is not present in or expressed by the recipient organism or tissue and that encodes a polypeptide whose expression is manifested by some easily detectable property, e.g., enzymatic activity. Expression of the reporter gene is assayed at a suitable time after the DNA has been introduced into the recipient cells. Suitable reporter genes may include genes encoding luciferase, beta-galactosidase, chloramphenicol acetyl transferase, secreted alkaline phosphatase, or the green fluorescent protein gene (e.g., Ui-Tei et al., 2000 FEBS Letters 479: 79-82). Suitable expression systems are well known and may be prepared using known techniques or obtained commercially. In general, the construct with the minimal 5' flanking region showing the highest level of expression of reporter gene is identified as the promoter. Such promoter regions may be linked to a reporter gene and used to evaluate agents for the ability to modulate promoter-driven transcription.

In some embodiments, the a vector comprising a nucleic acid sequence encoding a fusion protein described herein, e.g., a fusion protein comprising a CAR molecule described herein, can further comprise a second nucleic acid sequence encoding a polypeptide, e.g., an agent that increases the activity of the fusion protein, e.g., as described herein, comprising a domain that includes CAR molecule. In some embodiments a single nucleic acid molecule, or vector comprising said nucleic acid molecule, encodes multiple fusion proteins, e.g., as described herein, each comprising domains that include a CAR, described herein. In some embodiments, the nucleic acid encoding the a first fusion protein is under separate regulatory control (e.g., by a promoter described herein) from the nucleic acid encoding a second fusion protein (e.g., by a promoter described herein). In other embodiments, the two or more nucleic acid sequences are encoded by a single nucleic molecule in the same frame and as a single polypeptide chain. In this aspect, the two or more fusion proteins, e.g., as described herein, each comprising a domain that includes a CAR, can, e.g., be separated by one or more peptide cleavage sites (e.g., an auto-cleavage site or a substrate for an intracellular protease). Examples of peptide cleavage sites include the following, wherein the GSG residues are optional:

T2A: (GSG) E G R G S L L T C G D V E E N P G P (SEQ ID NO: 190)

P2A: (GSG) A T N F S L L K Q A G D V E E N P G P (SEQ ID NO: 191)

E2A: (GSG) Q C T N Y A L L K L A G D V E S N P G P (SEQ ID NO: 192)

F2A: (GSG) V K Q T L N F D L L K L A G D V E S N P G P (SEQ ID NO: 193)

Methods of introducing and expressing genes into a cell are known in the art. In the context of an expression vector, the vector can be readily introduced into a host cell, e.g., mammalian, bacterial, yeast,

or insect cell by any method in the art. For example, the expression vector can be transferred into a host cell by physical, chemical, or biological means.

Physical methods for introducing a polynucleotide into a host cell include calcium phosphate precipitation, lipofection, particle bombardment, microinjection, electroporation, and the like. Methods for producing
5 cells comprising vectors and/or exogenous nucleic acids are well-known in the art. See, for example, Sambrook et al., 2012, MOLECULAR CLONING: A LABORATORY MANUAL, volumes 1 -4, Cold Spring Harbor Press, NY). A preferred method for the introduction of a polynucleotide into a host cell is calcium phosphate transfection or electroporation.

Biological methods for introducing a polynucleotide of interest into a host cell include the use of DNA and
10 RNA vectors. Viral vectors, and especially retroviral vectors, have become the most widely used method for inserting genes into mammalian, e.g., human cells. Other viral vectors can be derived from lentivirus, poxviruses, herpes simplex virus I, adenoviruses and adeno-associated viruses, and the like. See, for example, U.S. Pat. Nos. 5,350,674 and 5,585,362.

Chemical means for introducing a polynucleotide into a host cell include colloidal dispersion systems,
15 such as macromolecule complexes, nanocapsules, microspheres, beads, and lipid-based systems including oil-in-water emulsions, micelles, mixed micelles, and liposomes. An exemplary colloidal system for use as a delivery vehicle in vitro and in vivo is a liposome (e.g., an artificial membrane vesicle). Other methods of state-of-the-art targeted delivery of nucleic acids are available, such as delivery of polynucleotides with targeted nanoparticles or other suitable sub-micron sized delivery system.

In the case where a non-viral delivery system is utilized, an exemplary delivery vehicle is a liposome. The
20 use of lipid formulations is contemplated for the introduction of the nucleic acids into a host cell (in vitro, ex vivo or in vivo). In another aspect, the nucleic acid may be associated with a lipid. The nucleic acid associated with a lipid may be encapsulated in the aqueous interior of a liposome, interspersed within the lipid bilayer of a liposome, attached to a liposome via a linking molecule that is associated with both the
25 liposome and the oligonucleotide, entrapped in a liposome, complexed with a liposome, dispersed in a solution containing a lipid, mixed with a lipid, combined with a lipid, contained as a suspension in a lipid, contained or complexed with a micelle, or otherwise associated with a lipid. Lipid, lipid/DNA or lipid/expression vector associated compositions are not limited to any particular structure in solution. For example, they may be present in a bilayer structure, as micelles, or with a "collapsed" structure. They may
30 also simply be interspersed in a solution, possibly forming aggregates that are not uniform in size or shape. Lipids are fatty substances which may be naturally occurring or synthetic lipids. For example, lipids include the fatty droplets that naturally occur in the cytoplasm as well as the class of compounds which contain long-chain aliphatic hydrocarbons and their derivatives, such as fatty acids, alcohols, amines, amino alcohols, and aldehydes.

Lipids suitable for use can be obtained from commercial sources. For example, dimyristyl phosphatidylcholine ("DMPC") can be obtained from Sigma, St. Louis, MO; dicetyl phosphate ("DCP") can be obtained from K & K Laboratories (Plainview, NY); cholesterol ("Choi") can be obtained from Calbiochem-Behring; dimyristyl phosphatidylglycerol ("DMPG") and other lipids may be obtained from
5 Avanti Polar Lipids, Inc. (Birmingham, AL.). Stock solutions of lipids in chloroform or chloroform/methanol can be stored at about -20°C. Chloroform is used as the only solvent since it is more readily evaporated than methanol. "Liposome" is a generic term encompassing a variety of single and multilamellar lipid vehicles formed by the generation of enclosed lipid bilayers or aggregates. Liposomes can be characterized as having vesicular structures with a phospholipid bilayer membrane and an inner aqueous
10 medium. Multilamellar liposomes have multiple lipid layers separated by aqueous medium. They form spontaneously when phospholipids are suspended in an excess of aqueous solution. The lipid components undergo self-rearrangement before the formation of closed structures and entrap water and dissolved solutes between the lipid bilayers (Ghosh et al., 1991 Glycobiology 5: 505-10). However, compositions that have different structures in solution than the normal vesicular structure are also
15 encompassed. For example, the lipids may assume a micellar structure or merely exist as nonuniform aggregates of lipid molecules. Also contemplated are lipofectamine-nucleic acid complexes.

Regardless of the method used to introduce exogenous nucleic acids into a host cell or otherwise expose a cell to the inhibitor of the present disclosure, in order to confirm the presence of the recombinant DNA sequence in the host cell, a variety of assays may be performed. Such assays include, for example,
20 "molecular biological" assays well known to those of skill in the art, such as Southern and Northern blotting, RT-PCR and PCR; "biochemical" assays, such as detecting the presence or absence of a particular peptide, e.g., by immunological means (ELISAs and Western blots) or by assays described herein to identify agents falling within the scope of the invention.

The present disclosure further provides a vector comprising a fusion protein, e.g., as described herein, comprising a domain that includes a CAR, -encoding nucleic acid molecule. In one embodiment, the vector comprises a CAR encoding nucleic acid molecule, e.g., as described herein. In one embodiment, the vector comprises two CAR encoding nucleic acid molecules. In one aspect, the one or more CAR
25 vectors (e.g., the vector comprising a first CAR encoding nucleic acid molecule and the vector comprising a second CAR encoding nucleic acid molecule, or the vector comprising both a first and second CAR encoding nucleic acids) can be directly transduced into a cell, e.g., a T cell or a NK cell. In one aspect, the vector is a cloning or expression vector, e.g., a vector including, but not limited to, one or more plasmids (e.g., expression plasmids, cloning vectors, minicircles, minivectors, double minute
30 chromosomes), retroviral and lentiviral vector constructs. In one aspect, the vector is capable of expressing the CAR construct in mammalian immune effector cells (e.g., T cells, NK cells).

35 In one embodiment, where stable expression of one or more (e.g., one or two) fusion proteins, e.g., as described herein, each comprising a domain that includes a CAR, is desired, a vector comprising one or

more (e.g., one or two) CAR-encoding nucleic acid molecules is transduced into an immune effector cell. For example, immune effector cells with stable expression of two fusion proteins, e.g., as described herein, each comprising a domain that include a CAR, can be generated using lentiviral vectors. Cells that exhibit stable expression of a two fusion proteins, e.g., as described herein, each comprising a domain that includes a CAR, express the CARs for at least 1 week, 2 weeks, 3 weeks, 4 weeks, 5 weeks, 6 weeks, 7 weeks, 8 weeks, 3 months, 6 months, 9 months, or 12 months after transduction.

In one embodiment, where transient expression of one or more (e.g., one or two) fusion proteins, e.g., as described herein, comprising a domain that includes a CAR is desired, one or more (e.g., one or two) fusion protein -encoding nucleic acid molecules is transfected into an immune effector cell. The one or more (e.g., one or two) fusion proteins, e.g., as described herein, comprising a domain that includes a CAR, -encoding nucleic acid molecules may be a vector comprising a one or more (e.g., one or two) CAR encoding nucleic acid molecules, or an *in vitro* transcribed RNA one or more (e.g., one or two) CARs. *In vitro* transcribed RNA CARs and methods for transfection into immune effector cells are further described below. Cells that exhibit transient expression of a one or more (e.g., one or two) CAR express the one or more (e.g., one or two) CAR for 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15 days after transfection.

RNA Transfection

Disclosed herein are methods for producing an *in vitro* transcribed RNA encoding a fusion protein, e.g., as described herein, comprising a domain that includes a CAR. The present disclosure also includes a fusion protein, e.g., as described herein, comprising a domain that includes CAR, -encoding RNA construct that can be directly transfected into a cell. A method for generating mRNA for use in transfection can involve *in vitro* transcription (IVT) of a template with specially designed primers, followed by polyA addition, to produce a construct containing 3' and 5' untranslated sequence ("UTR"), a 5' cap and/or Internal Ribosome Entry Site (IRES), the nucleic acid to be expressed, and a polyA tail, typically 50-5000 bases in length (SEQ ID NO: 32). RNA so produced can efficiently transfect different kinds of cells. In one aspect, the template includes sequences for the CAR.

In one aspect, a fusion protein, e.g., as described herein, comprising a domain that includes a CAR, of the present disclosure is encoded by a messenger RNA (mRNA). In one aspect, the mRNA encoding a CAR described herein is introduced into a T cell or a NK cell.

In one embodiment, the *in vitro* transcribed RNA encoding a fusion protein, e.g., as described herein, comprising a domain that includes a CAR can be introduced to a cell as a form of transient transfection. The RNA is produced by *in vitro* transcription using a polymerase chain reaction (PCR)-generated template. DNA of interest from any source can be directly converted by PCR into a template for *in vitro* mRNA synthesis using appropriate primers and RNA polymerase. The source of the DNA can be, for example, genomic DNA, plasmid DNA, phage DNA, cDNA, synthetic DNA sequence or any other appropriate source of DNA. The desired template for *in vitro* transcription is a fusion protein, e.g., as

described herein, comprising a domain that includes a CAR, described herein. For example, the template for the RNA CAR comprises an extracellular region comprising a single chain variable domain of an antibody to an antigen described herein; a hinge region (e.g., a hinge region described herein), a transmembrane domain (e.g., a transmembrane domain described herein such as a transmembrane domain of CD8a); and a cytoplasmic region that includes an intracellular signaling domain, e.g., an intracellular signaling domain described herein, e.g., comprising the signaling domain of CD3-zeta and the signaling domain of 4-1BB.

In one embodiment, the DNA to be used for PCR contains an open reading frame. The DNA can be from a naturally occurring DNA sequence from the genome of an organism. In one embodiment, the nucleic acid can include some or all of the 5' and/or 3' untranslated regions (UTRs). The nucleic acid can include exons and introns. In one embodiment, the DNA to be used for PCR is a human nucleic acid sequence. In another embodiment, the DNA to be used for PCR is a human nucleic acid sequence including the 5' and 3' UTRs. The DNA can alternatively be an artificial DNA sequence that is not normally expressed in a naturally occurring organism. An exemplary artificial DNA sequence is one that contains portions of genes that are ligated together to form an open reading frame that encodes a fusion protein. The portions of DNA that are ligated together can be from a single organism or from more than one organism.

PCR is used to generate a template for in vitro transcription of mRNA which is used for transfection.

Methods for performing PCR are well known in the art. Primers for use in PCR are designed to have regions that are substantially complementary to regions of the DNA to be used as a template for the PCR.

"Substantially complementary," as used herein, refers to sequences of nucleotides where a majority or all of the bases in the primer sequence are complementary, or one or more bases are non-complementary, or mismatched. Substantially complementary sequences are able to anneal or hybridize with the intended DNA target under annealing conditions used for PCR. The primers can be designed to be substantially complementary to any portion of the DNA template. For example, the primers can be designed to amplify the portion of a nucleic acid that is normally transcribed in cells (the open reading frame), including 5' and 3' UTRs. The primers can also be designed to amplify a portion of a nucleic acid that encodes a particular domain of interest. In one embodiment, the primers are designed to amplify the coding region of a human cDNA, including all or portions of the 5' and 3' UTRs. Primers useful for PCR can be generated by synthetic methods that are well known in the art. "Forward primers" are primers that contain a region of nucleotides that are substantially complementary to nucleotides on the DNA template that are upstream of the DNA sequence that is to be amplified. "Upstream" is used herein to refer to a location 5' to the DNA sequence to be amplified relative to the coding strand. "Reverse primers" are primers that contain a region of nucleotides that are substantially complementary to a double-stranded DNA template that are downstream of the DNA sequence that is to be amplified. "Downstream" is used herein to refer to a location 3' to the DNA sequence to be amplified relative to the coding strand.

Any DNA polymerase useful for PCR can be used in the methods disclosed herein. The reagents and polymerase are commercially available from a number of sources.

Chemical structures with the ability to promote stability and/or translation efficiency may also be used. The RNA preferably has 5' and 3' UTRs. In one embodiment, the 5' UTR is between one and 3000
5 nucleotides in length. The length of 5' and 3' UTR sequences to be added to the coding region can be altered by different methods, including, but not limited to, designing primers for PCR that anneal to different regions of the UTRs. Using this approach, one of ordinary skill in the art can modify the 5' and 3' UTR lengths required to achieve optimal translation efficiency following transfection of the transcribed RNA.

10 The 5' and 3' UTRs can be the naturally occurring, endogenous 5' and 3' UTRs for the nucleic acid of interest. Alternatively, UTR sequences that are not endogenous to the nucleic acid of interest can be added by incorporating the UTR sequences into the forward and reverse primers or by any other modifications of the template. The use of UTR sequences that are not endogenous to the nucleic acid of interest can be useful for modifying the stability and/or translation efficiency of the RNA. For example, it is
15 known that AU-rich elements in 3' UTR sequences can decrease the stability of mRNA. Therefore, 3' UTRs can be selected or designed to increase the stability of the transcribed RNA based on properties of UTRs that are well known in the art.

In one embodiment, the 5' UTR can contain the Kozak sequence of the endogenous nucleic acid. Alternatively, when a 5' UTR that is not endogenous to the nucleic acid of interest is being added by PCR
20 as described above, a consensus Kozak sequence can be redesigned by adding the 5' UTR sequence. Kozak sequences can increase the efficiency of translation of some RNA transcripts, but does not appear to be required for all RNAs to enable efficient translation. The requirement for Kozak sequences for many mRNAs is known in the art. In other embodiments the 5' UTR can be 5'UTR of an RNA virus whose RNA genome is stable in cells. In other embodiments various nucleotide analogues can be used in the 3' or 5'
25 UTR to impede exonuclease degradation of the mRNA.

To enable synthesis of RNA from a DNA template without the need for gene cloning, a promoter of transcription should be attached to the DNA template upstream of the sequence to be transcribed. When a sequence that functions as a promoter for an RNA polymerase is added to the 5' end of the forward
30 primer, the RNA polymerase promoter becomes incorporated into the PCR product upstream of the open reading frame that is to be transcribed. In one preferred embodiment, the promoter is a T7 polymerase promoter, as described elsewhere herein. Other useful promoters include, but are not limited to, T3 and SP6 RNA polymerase promoters. Consensus nucleotide sequences for T7, T3 and SP6 promoters are known in the art.

In a preferred embodiment, the mRNA has both a cap on the 5' end and a 3' poly(A) tail which determine
35 ribosome binding, initiation of translation and stability mRNA in the cell. On a circular DNA template, for

instance, plasmid DNA, RNA polymerase produces a long concatameric product which is not suitable for expression in eukaryotic cells. The transcription of plasmid DNA linearized at the end of the 3' UTR results in normal sized mRNA which is not effective in eukaryotic transfection even if it is polyadenylated after transcription.

- 5 On a linear DNA template, phage T7 RNA polymerase can extend the 3' end of the transcript beyond the last base of the template (Schenborn and Mierendorf, *Nuc Acids Res.*, 13:6223-36 (1985); Nacheva and Berzal-Herranz, *Eur. J. Biochem.*, 270:1485-65 (2003).

The conventional method of integration of polyA/T stretches into a DNA template is molecular cloning. However polyA/T sequence integrated into plasmid DNA can cause plasmid instability, which is why
10 plasmid DNA templates obtained from bacterial cells are often highly contaminated with deletions and other aberrations. This makes cloning procedures not only laborious and time consuming but often not reliable. That is why a method which allows construction of DNA templates with polyA/T 3' stretch without cloning highly desirable.

The polyA/T segment of the transcriptional DNA template can be produced during PCR by using a
15 reverse primer containing a polyT tail, such as 100T tail (SEQ ID NO: 968) (size can be 50-5000 T (SEQ ID NO: 974)), or after PCR by any other method, including, but not limited to, DNA ligation or in vitro recombination. Poly(A) tails also provide stability to RNAs and reduce their degradation. Generally, the length of a poly(A) tail positively correlates with the stability of the transcribed RNA. In one embodiment, the poly(A) tail is between 100 and 5000 adenosines (SEQ ID NO: 82).

20 Poly(A) tails of RNAs can be further extended following in vitro transcription with the use of a poly(A) polymerase, such as E. coli polyA polymerase (E-PAP). In one embodiment, increasing the length of a poly(A) tail from 100 nucleotides to between 300 and 400 nucleotides (SEQ ID NO: 969) results in about a two-fold increase in the translation efficiency of the RNA. Additionally, the attachment of different chemical groups to the 3' end can increase mRNA stability. Such attachment can contain
25 modified/artificial nucleotides, aptamers and other compounds. For example, ATP analogs can be incorporated into the poly(A) tail using poly(A) polymerase. ATP analogs can further increase the stability of the RNA.

5' caps on also provide stability to RNA molecules. In a preferred embodiment, RNAs produced by the methods disclosed herein include a 5' cap. The 5' cap is provided using techniques known in the art and
30 described herein (Cougot, et al., *Trends in Biochem. Sci.*, 29:436-444 (2001); Stepinski, et al., *RNA*, 7:1468-95 (2001); Elango, et al., *Biochim. Biophys. Res. Commun.*, 330:958-966 (2005)).

The RNAs produced by the methods disclosed herein can also contain an internal ribosome entry site (IRES) sequence. The IRES sequence may be any viral, chromosomal or artificially designed sequence which initiates cap-independent ribosome binding to mRNA and facilitates the initiation of translation. Any

solutes suitable for cell electroporation, which can contain factors facilitating cellular permeability and viability such as sugars, peptides, lipids, proteins, antioxidants, and surfactants can be included.

RNA can be introduced into target cells using any of a number of different methods, for instance, commercially available methods which include, but are not limited to, electroporation (Amaxa Nucleofector-II (Amaxa Biosystems, Cologne, Germany)), (ECM 830 (BTX) (Harvard Instruments, Boston, Mass.) or the Gene Pulser II (BioRad, Denver, Colo.), Multiporator (Eppendorf, Hamburg Germany), cationic liposome mediated transfection using lipofection, polymer encapsulation, peptide mediated transfection, or biolistic particle delivery systems such as "gene guns" (see, for example, Nishikawa, et al. Hum Gene Ther., 12(8):861-70 (2001).

10

Non-viral delivery methods

In some aspects, non-viral methods can be used to deliver a nucleic acid encoding a chimeric molecule or fusion protein described herein into a cell or tissue or a subject.

In some embodiments, the non-viral method includes the use of a transposon (also called a transposable element). In some embodiments, a transposon is a piece of DNA that can insert itself at a location in a genome, for example, a piece of DNA that is capable of self-replicating and inserting its copy into a genome, or a piece of DNA that can be spliced out of a longer nucleic acid and inserted into another place in a genome. For example, a transposon comprises a DNA sequence made up of inverted repeats flanking genes for transposition.

In some embodiments, cells, e.g., T or NK cells, are generated that express a chimeric molecule or fusion protein, e.g., as described herein, by using a combination of gene insertion using the SBTS and genetic editing using a nuclease (e.g., Zinc finger nucleases (ZFNs), Transcription Activator-Like Effector Nucleases (TALENs), the CRISPR/Cas system, or engineered meganuclease re-engineered homing endonucleases).

In some embodiments, use of a non-viral method of delivery permits reprogramming of cells, e.g., T or NK cells, and direct infusion of the cells into a subject. Advantages of non-viral vectors include but are not limited to the ease and relatively low cost of producing sufficient amounts required to meet a patient population, stability during storage, and lack of immunogenicity.

HOST CELLS

Also provided herein are cells, e.g., immune effector cells (e.g., a population of cells, e.g., a population of immune effector cells) comprising a nucleic acid molecule, a fusion protein molecule, or a vector, e.g., as

described herein. In some embodiments, the provided cells comprise a fusion protein, e.g., as described herein, comprising a domain that includes a CAR, a nucleic acid molecule encoding a fusion protein comprising a domain that includes a CAR, or a vector comprising the same.

In certain aspects, immune effector cells, e.g., T cells or NK cells, can be obtained from a unit of blood collected from a subject using any number of techniques known to the skilled artisan, such as Ficoll™ separation. In one preferred aspect, cells from the circulating blood of an individual are obtained by apheresis. The apheresis product typically contains lymphocytes, including T cells, monocytes, granulocytes, B cells, other nucleated white blood cells, red blood cells, and platelets. In one aspect, the cells collected by apheresis may be washed to remove the plasma fraction and, optionally, to place the cells in an appropriate buffer or media for subsequent processing steps. In one embodiment, the cells are washed with phosphate buffered saline (PBS). In an alternative embodiment, the wash solution lacks calcium and may lack magnesium or may lack many if not all divalent cations.

Initial activation steps in the absence of calcium can lead to magnified activation. As those of ordinary skill in the art would readily appreciate a washing step may be accomplished by methods known to those in the art, such as by using a semi-automated “flow-through” centrifuge (for example, the Cobe 2991 cell processor, the Baxter CytoMate, or the Haemonetics Cell Saver 5) according to the manufacturer’s instructions. After washing, the cells may be resuspended in a variety of biocompatible buffers, such as, for example, Ca-free, Mg-free PBS, PlasmaLyte A, or other saline solution with or without buffer. Alternatively, the undesirable components of the apheresis sample may be removed and the cells directly resuspended in culture media.

It is recognized that the methods of the application can utilize culture media conditions comprising 5% or less, for example 2%, human AB serum, and employ known culture media conditions and compositions, for example those described in Smith *et al.*, “Ex vivo expansion of human T cells for adoptive immunotherapy using the novel Xeno-free CTS Immune Cell Serum Replacement” *Clinical & Translational Immunology* (2015) 4, e31; doi:10.1038/cti.2014.31.

In one aspect, T cells are isolated from peripheral blood lymphocytes by lysing the red blood cells and depleting the monocytes, for example, by centrifugation through a PERCOLL™ gradient or by counterflow centrifugal elutriation.

The methods described herein can include, e.g., selection of a specific subpopulation of immune effector cells, e.g., T cells, that are a T regulatory cell-depleted population, CD25+ depleted cells, using, e.g., a negative selection technique, e.g., described herein. Preferably, the population of T regulatory depleted cells contains less than 30%, 25%, 20%, 15%, 10%, 5%, 4%, 3%, 2%, 1% of CD25+ cells.

In one embodiment, T regulatory cells, e.g., CD25+ T cells, are removed from the population using an anti-CD25 antibody, or fragment thereof, or a CD25-binding ligand, IL-2. In one embodiment, the anti-

CD25 antibody, or fragment thereof, or CD25-binding ligand is conjugated to a substrate, e.g., a bead, or is otherwise coated on a substrate, e.g., a bead. In one embodiment, the anti-CD25 antibody, or fragment thereof, is conjugated to a substrate as described herein.

In one embodiment, the T regulatory cells, e.g., CD25+ T cells, are removed from the population using CD25 depletion reagent from Miltenyi™. In one embodiment, the ratio of cells to CD25 depletion reagent is 1e7 cells to 20 uL, or 1e7 cells to 15 uL, or 1e7 cells to 10 uL, or 1e7 cells to 5 uL, or 1e7 cells to 2.5 uL, or 1e7 cells to 1.25 uL. In one embodiment, e.g., for T regulatory cells, e.g., CD25+ depletion, greater than 500 million cells/ml is used. In a further aspect, a concentration of cells of 600, 700, 800, or 900 million cells/ml is used.

In one embodiment, the population of immune effector cells to be depleted includes about 6×10^9 CD25+ T cells. In other aspects, the population of immune effector cells to be depleted include about 1×10^9 to 1×10^{10} CD25+ T cell, and any integer value in between. In one embodiment, the resulting population T regulatory depleted cells has 2×10^9 T regulatory cells, e.g., CD25+ cells, or less (e.g., 1×10^9 , 5×10^8 , 1×10^8 , 5×10^7 , 1×10^7 , or less CD25+ cells).

In one embodiment, the T regulatory cells, e.g., CD25+ cells, are removed from the population using the CliniMAC system with a depletion tubing set, such as, e.g., tubing 162-01. In one embodiment, the CliniMAC system is run on a depletion setting such as, e.g., DEPLETION2.1.

Without wishing to be bound by a particular theory, decreasing the level of negative regulators of immune cells (e.g., decreasing the number of unwanted immune cells, e.g., T_{REG} cells), in a subject prior to apheresis or during manufacturing of a fusion protein, e.g., as described herein, comprising a domain that includes a CAR, -expressing cell product can reduce the risk of subject relapse. For example, methods of depleting T_{REG} cells are known in the art. Methods of decreasing T_{REG} cells include, but are not limited to, cyclophosphamide, anti-GITR antibody (an anti-GITR antibody described herein), CD25-depletion, and combinations thereof.

In some embodiments, the manufacturing methods comprise reducing the number of (e.g., depleting) T_{REG} cells prior to manufacturing of the fusion protein, e.g., as described herein, comprising a domain that includes a CAR, -expressing cell. For example, manufacturing methods comprise contacting the sample, e.g., the apheresis sample, with an anti-GITR antibody and/or an anti-CD25 antibody (or fragment thereof, or a CD25-binding ligand), e.g., to deplete T_{REG} cells prior to manufacturing of the CAR-expressing cell (e.g., T cell, NK cell) product.

In an embodiment, a subject is pre-treated with one or more therapies that reduce T_{REG} cells prior to collection of cells for fusion protein, e.g., as described herein, comprising a domain that includes a CAR, -expressing cell product manufacturing, thereby reducing the risk of subject relapse to fusion protein, e.g., as described herein, comprising a domain that includes a CAR, -expressing cell treatment. In an

embodiment, methods of decreasing T_{REG} cells include, but are not limited to, administration to the subject of one or more of cyclophosphamide, anti-GITR antibody, CD25-depletion, or a combination thereof. Administration of one or more of cyclophosphamide, anti-GITR antibody, CD25-depletion, or a combination thereof, can occur before, during or after an infusion of the CAR-expressing cell product.

5 In an embodiment, a subject is pre-treated with cyclophosphamide prior to collection of cells for CAR-expressing cell product manufacturing, thereby reducing the risk of subject relapse to fusion protein, e.g., as described herein, comprising a domain that includes a CAR, -expressing cell treatment. In an embodiment, a subject is pre-treated with an anti-GITR antibody prior to collection of cells for CAR-expressing cell product manufacturing, thereby reducing the risk of subject relapse to CAR-expressing
10 cell treatment.

In one embodiment, the population of cells to be removed are neither the regulatory T cells or tumor cells, but cells that otherwise negatively affect the expansion and/or function of CART cells, e.g. cells expressing CD14, CD11b, CD33, CD15, or other markers expressed by potentially immune suppressive cells. In one embodiment, such cells are envisioned to be removed concurrently with regulatory T cells
15 and/or tumor cells, or following said depletion, or in another order.

The methods described herein can include more than one selection step, e.g., more than one depletion step. Enrichment of a T cell population by negative selection can be accomplished, e.g., with a combination of antibodies directed to surface markers unique to the negatively selected cells. One method is cell sorting and/or selection via negative magnetic immunoadherence or flow cytometry that
20 uses a cocktail of monoclonal antibodies directed to cell surface markers present on the cells negatively selected. For example, to enrich for CD4+ cells by negative selection, a monoclonal antibody cocktail can include antibodies to CD14, CD20, CD11b, CD16, HLA-DR, and CD8.

The methods described herein can further include removing cells from the population which express a tumor antigen, e.g., a tumor antigen that does not comprise CD25, e.g., CD19, CD30, CD38, CD123, CD20, CD14 or CD11b, to thereby provide a population of T regulatory depleted, e.g., CD25+ depleted, and tumor antigen depleted cells that are suitable for expression of a fusion protein, e.g., as described
25 herein, comprising a domain that includes a CAR, e.g., a CAR described herein. In one embodiment, tumor antigen expressing cells are removed simultaneously with the T regulatory, e.g., CD25+ cells. For example, an anti-CD25 antibody, or fragment thereof, and an anti-tumor antigen antibody, or fragment
30 thereof, can be attached to the same substrate, e.g., bead, which can be used to remove the cells or an anti-CD25 antibody, or fragment thereof, or the anti-tumor antigen antibody, or fragment thereof, can be attached to separate beads, a mixture of which can be used to remove the cells. In other embodiments, the removal of T regulatory cells, e.g., CD25+ cells, and the removal of the tumor antigen expressing cells is sequential, and can occur, e.g., in either order.

Also provided are methods that include removing cells from the population which express a check point inhibitor, e.g., a check point inhibitor described herein, e.g., one or more of PD1+ cells, LAG3+ cells, and TIM3+ cells, to thereby provide a population of T regulatory depleted, e.g., CD25+ depleted cells, and check point inhibitor depleted cells, e.g., PD1+, LAG3+ and/or TIM3+ depleted cells. Exemplary check point inhibitors include B7-H1, B7-1, CD160, P1H, 2B4, PD1, TIM3, CEACAM (e.g., CEACAM-1, CEACAM-3 and/or CEACAM-5), LAG3, TIGIT, CTLA-4, BTLA and LAIR1. In one embodiment, check point inhibitor expressing cells are removed simultaneously with the T regulatory, e.g., CD25+ cells. For example, an anti-CD25 antibody, or fragment thereof, and an anti-check point inhibitor antibody, or fragment thereof, can be attached to the same bead which can be used to remove the cells, or an anti-CD25 antibody, or fragment thereof, and the anti-check point inhibitor antibody, or fragment thereof, can be attached to separate beads, a mixture of which can be used to remove the cells. In other embodiments, the removal of T regulatory cells, e.g., CD25+ cells, and the removal of the check point inhibitor expressing cells is sequential, and can occur, e.g., in either order.

Methods described herein can include a positive selection step. For example, T cells can be isolated by incubation with anti-CD3/anti-CD28 (e.g., 3x28)-conjugated beads, such as DYNABEADS® M-450 CD3/CD28 T, for a time period sufficient for positive selection of the desired T cells. In one embodiment, the time period is about 30 minutes. In a further embodiment, the time period ranges from 30 minutes to 36 hours or longer and all integer values there between. In a further embodiment, the time period is at least 1, 2, 3, 4, 5, or 6 hours. In yet another embodiment, the time period is 10 to 24 hours, e.g., 24 hours. Longer incubation times may be used to isolate T cells in any situation where there are few T cells as compared to other cell types, such as in isolating tumor infiltrating lymphocytes (TIL) from tumor tissue or from immunocompromised individuals. Further, use of longer incubation times can increase the efficiency of capture of CD8+ T cells. Thus, by simply shortening or lengthening the time T cells are allowed to bind to the CD3/CD28 beads and/or by increasing or decreasing the ratio of beads to T cells (as described further herein), subpopulations of T cells can be preferentially selected for or against at culture initiation or at other time points during the process. Additionally, by increasing or decreasing the ratio of anti-CD3 and/or anti-CD28 antibodies on the beads or other surface, subpopulations of T cells can be preferentially selected for or against at culture initiation or at other desired time points.

In one embodiment, a T cell population can be selected that expresses one or more of IFN- γ , TNF α , IL-17A, IL-2, IL-3, IL-4, GM-CSF, IL-10, IL-13, granzyme B, and perforin, or other appropriate molecules, e.g., other cytokines. Methods for screening for cell expression can be determined, e.g., by the methods described in PCT Publication No.: WO 2013/126712.

For isolation of a desired population of cells by positive or negative selection, the concentration of cells and surface (e.g., particles such as beads) can be varied. In certain aspects, it may be desirable to significantly decrease the volume in which beads and cells are mixed together (e.g., increase the concentration of cells), to ensure maximum contact of cells and beads. For example, in one aspect, a

concentration of 10 billion cells/ml, 9 billion/ml, 8 billion/ml, 7 billion/ml, 6 billion/ml, or 5 billion/ml is used. In one aspect, a concentration of 1 billion cells/ml is used. In yet one aspect, a concentration of cells from 75, 80, 85, 90, 95, or 100 million cells/ml is used. In further aspects, concentrations of 125 or 150 million cells/ml can be used.

- 5 Using high concentrations can result in increased cell yield, cell activation, and cell expansion. Further, use of high cell concentrations allows more efficient capture of cells that may weakly express target antigens of interest, such as CD28-negative T cells, or from samples where there are many tumor cells present (e.g., leukemic blood, tumor tissue, etc.). Such populations of cells may have therapeutic value and would be desirable to obtain. For example, using high concentration of cells allows more efficient
10 selection of CD8+ T cells that normally have weaker CD28 expression.

- In a related aspect, it may be desirable to use lower concentrations of cells. By significantly diluting the mixture of T cells and surface (e.g., particles such as beads), interactions between the particles and cells is minimized. This selects for cells that express high amounts of desired antigens to be bound to the particles. For example, CD4+ T cells express higher levels of CD28 and are more efficiently captured
15 than CD8+ T cells in dilute concentrations. In one aspect, the concentration of cells used is 5×10^6 /ml. In other aspects, the concentration used can be from about 1×10^5 /ml to 1×10^6 /ml, and any integer value in between.

In other aspects, the cells may be incubated on a rotator for varying lengths of time at varying speeds at either 2-10°C or at room temperature.

- 20 T cells for stimulation can also be frozen after a washing step. Wishing not to be bound by theory, the freeze and subsequent thaw step provides a more uniform product by removing granulocytes and to some extent monocytes in the cell population. After the washing step that removes plasma and platelets, the cells may be suspended in a freezing solution. While many freezing solutions and parameters are known in the art and will be useful in this context, one method involves using PBS containing 20% DMSO
25 and 8% human serum albumin, or culture media containing 10% Dextran 40 and 5% Dextrose, 20% Human Serum Albumin and 7.5% DMSO, or 31.25% Plasmalyte-A, 31.25% Dextrose 5%, 0.45% NaCl, 10% Dextran 40 and 5% Dextrose, 20% Human Serum Albumin, and 7.5% DMSO or other suitable cell freezing media containing for example, Hespan and PlasmaLyte A, the cells then are frozen to -80°C at a rate of 1° per minute and stored in the vapor phase of a liquid nitrogen storage tank. Other methods of
30 controlled freezing may be used as well as uncontrolled freezing immediately at -20° C or in liquid nitrogen.

In certain aspects, cryopreserved cells are thawed and washed as described herein and allowed to rest for one hour at room temperature prior to activation using the methods of the present invention.

Also contemplated in the context of the invention is the collection of blood samples or apheresis product from a subject at a time period prior to when the expanded cells as described herein might be needed. As such, the source of the cells to be expanded can be collected at any time point necessary, and desired cells, such as T cells, isolated and frozen for later use in immune effector cell therapy for any number of diseases or conditions that would benefit from immune effector cell therapy, such as those described herein. In one aspect a blood sample or an apheresis is taken from a generally healthy subject. In certain aspects, a blood sample or an apheresis is taken from a generally healthy subject who is at risk of developing a disease, but who has not yet developed a disease, and the cells of interest are isolated and frozen for later use. In certain aspects, the T cells may be expanded, frozen, and used at a later time. In certain aspects, samples are collected from a patient shortly after diagnosis of a particular disease as described herein but prior to any treatments. In a further aspect, the cells are isolated from a blood sample or an apheresis from a subject prior to any number of relevant treatment modalities, including but not limited to treatment with agents such as natalizumab, efalizumab, antiviral agents, chemotherapy, radiation, immunosuppressive agents, such as cyclosporin, azathioprine, methotrexate, mycophenolate, and FK506, antibodies, or other immunoablative agents such as CAMPATH, anti-CD3 antibodies, cytoxan, fludarabine, cyclosporin, FK506, rapamycin, mycophenolic acid, steroids, FR901228, and irradiation.

In a further aspect of the present invention, T cells are obtained from a patient directly following treatment that leaves the subject with functional T cells. In this regard, it has been observed that following certain cancer treatments, in particular treatments with drugs that damage the immune system, shortly after treatment during the period when patients would normally be recovering from the treatment, the quality of T cells obtained may be optimal or improved for their ability to expand ex vivo. Likewise, following ex vivo manipulation using the methods described herein, these cells may be in a preferred state for enhanced engraftment and in vivo expansion. Thus, it is contemplated within the context of the present disclosure to collect blood cells, including T cells, dendritic cells, or other cells of the hematopoietic lineage, during this recovery phase. Further, in certain aspects, mobilization (for example, mobilization with GM-CSF) and conditioning regimens can be used to create a condition in a subject wherein repopulation, recirculation, regeneration, and/or expansion of particular cell types is favored, especially during a defined window of time following therapy. Illustrative cell types include T cells, B cells, dendritic cells, and other cells of the immune system.

In one embodiment, the immune effector cells expressing a fusion protein, e.g., as described herein, comprising a domain that includes a CAR molecule, e.g., a CAR molecule described herein, are obtained from a subject that has received a low, immune enhancing dose of an mTOR inhibitor. In an embodiment, the population of immune effector cells, e.g., T cells, to be engineered to express a CAR, are harvested after a sufficient time, or after sufficient dosing of the low, immune enhancing, dose of an mTOR inhibitor, such that the level of PD1 negative immune effector cells, e.g., T cells, or the ratio of PD1

negative immune effector cells, e.g., T cells/ PD1 positive immune effector cells, e.g., T cells, in the subject or harvested from the subject has been, at least transiently, increased.

In other embodiments, population of immune effector cells, e.g., T cells, which have, or will be engineered to express a fusion protein, e.g., as described herein, comprising a domain that includes a CAR, can be treated ex vivo by contact with an amount of an mTOR inhibitor that increases the number of PD1 negative immune effector cells, e.g., T cells or increases the ratio of PD1 negative immune effector cells, e.g., T cells/ PD1 positive immune effector cells, e.g., T cells.

In one embodiment, a T cell population is diacylglycerol kinase (DGK)-deficient. DGK-deficient cells include cells that do not express DGK RNA or protein, or have reduced or inhibited DGK activity. DGK-deficient cells can be generated by genetic approaches, e.g., administering RNA-interfering agents, e.g., siRNA, shRNA, miRNA, to reduce or prevent DGK expression. Alternatively, DGK-deficient cells can be generated by treatment with DGK inhibitors described herein.

In one embodiment, a T cell population is Ikaros-deficient. Ikaros-deficient cells include cells that do not express Ikaros RNA or protein, or have reduced or inhibited Ikaros activity, Ikaros-deficient cells can be generated by genetic approaches, e.g., administering RNA-interfering agents, e.g., siRNA, shRNA, miRNA, to reduce or prevent Ikaros expression. Alternatively, Ikaros-deficient cells can be generated by treatment with Ikaros inhibitors, e.g., lenalidomide.

In embodiments, a T cell population is DGK-deficient and Ikaros-deficient, e.g., does not express DGK and Ikaros, or has reduced or inhibited DGK and Ikaros activity. Such DGK and Ikaros-deficient cells can be generated by any of the methods described herein.

In an embodiment, the NK cells are obtained from the subject. In another embodiment, the NK cells are an NK cell line, e.g., NK-92 cell line (Conkwest).

Additional Expressed Agents

In another embodiment, a fusion protein, e.g., as described herein, comprising a domain that includes a CAR, -expressing immune effector cell described herein can further express another agent, e.g., an agent which enhances the activity of a CAR-expressing cell. For example, in one embodiment, the agent can be an agent which inhibits an inhibitory molecule. Examples of inhibitory molecules include PD-1, PD-L1, CTLA-4, TIM-3, CEACAM (e.g., CEACAM-1, CEACAM-3 and/or CEACAM-5), LAG-3, VISTA, BTLA, TIGIT, LAIR1, CD160, 2B4 and TGFR beta, e.g., as described herein. In one embodiment, the agent that inhibits an inhibitory molecule comprises a first polypeptide, e.g., an inhibitory molecule, associated with a second polypeptide that provides a positive signal to the cell, e.g., an intracellular signaling domain described herein. In one embodiment, the agent comprises a first polypeptide, e.g., of an inhibitory

molecule such as PD-1, PD-L1, CTLA-4, TIM-3, CEACAM (e.g., CEACAM-1, CEACAM-3 and/or CEACAM-5), LAG-3, VISTA, BTLA, TIGIT, LAIR1, CD160, 2B4 or TGFR beta, or a fragment of any of these, and a second polypeptide which is an intracellular signaling domain described herein (e.g., comprising a costimulatory domain (e.g., 41BB, CD27 or CD28, e.g., as described herein) and/or a primary signaling domain (e.g., a CD3 zeta signaling domain described herein). In one embodiment, the agent comprises a first polypeptide of PD-1 or a fragment thereof, and a second polypeptide of an intracellular signaling domain described herein (e.g., a CD28, CD27, OX40 or 4-1BB signaling domain described herein and/or a CD3 zeta signaling domain described herein).

In one embodiment, the fusion protein, e.g., as described herein, comprising a domain that includes a CAR, -expressing immune effector cell described herein can further comprise a second fusion protein, e.g., as described herein, comprising a domain that includes a CAR, e.g., a second CAR that includes a different antigen binding domain, e.g., to the same target (e.g., a target described above) or a different target. In one embodiment, the second CAR includes an antigen binding domain to a target expressed on the same cancer cell type as the target of the first CAR. In one embodiment, the CAR-expressing immune effector cell comprises a first CAR that targets a first antigen and includes an intracellular signaling domain having a costimulatory signaling domain but not a primary signaling domain, and a second CAR that targets a second, different, antigen and includes an intracellular signaling domain having a primary signaling domain but not a costimulatory signaling domain.

While not wishing to be bound by theory, placement of a costimulatory signaling domain, e.g., 4-1BB, CD28, CD27 or OX-40, onto the first CAR, and the primary signaling domain, e.g., CD3 zeta, on the second CAR can limit the CAR activity to cells where both targets are expressed. In one embodiment, the CAR expressing immune effector cell comprises a first CAR that includes an antigen binding domain that targets, e.g., a target described above, a transmembrane domain and a costimulatory domain and a second CAR that targets an antigen other than antigen targeted by the first CAR (e.g., an antigen expressed on the same cancer cell type as the first target) and includes an antigen binding domain, a transmembrane domain and a primary signaling domain. In another embodiment, the CAR expressing immune effector cell comprises a first CAR that includes an antigen binding domain that targets, e.g., a target described above, a transmembrane domain and a primary signaling domain and a second CAR that targets an antigen other than antigen targeted by the first CAR (e.g., an antigen expressed on the same cancer cell type as the first target) and includes an antigen binding domain to the antigen, a transmembrane domain and a costimulatory signaling domain.

In one embodiment, the CAR-expressing immune effector cell comprises a CAR described herein, e.g., a CAR to a target described above, and an inhibitory CAR. In one embodiment, the inhibitory CAR comprises an antigen binding domain that binds an antigen found on normal cells but not cancer cells, e.g., normal cells that also express the target. In one embodiment, the inhibitory CAR comprises the antigen binding domain, a transmembrane domain and an intracellular domain of an inhibitory molecule.

For example, the intracellular domain of the inhibitory CAR can be an intracellular domain of PD1, PD-L1, CTLA-4, TIM-3, CEACAM (e.g., CEACAM-1, CEACAM-3 and/or CEACAM-5), LAG-3, VISTA, BTLA, TIGIT, LAIR1, CD160, 2B4 or TGFR beta.

5 In one embodiment, an immune effector cell (e.g., T cell, NK cell) comprises a first CAR comprising an antigen binding domain that binds to a tumor antigen as described herein, and a second CAR comprising a PD1 extracellular domain or a fragment thereof.

In one embodiment, the cell further comprises an inhibitory molecule as described above.

10 In one embodiment, the second CAR in the cell is an inhibitory CAR, wherein the inhibitory CAR comprises an antigen binding domain, a transmembrane domain, and an intracellular domain of an inhibitory molecule. The inhibitory molecule can be chosen from one or more of: PD1, PD-L1, CTLA-4, TIM-3, LAG-3, VISTA, BTLA, TIGIT, LAIR1, CD160, 2B4, TGFR beta, CEACAM-1, CEACAM-3, and CEACAM-5. In one embodiment, the second CAR molecule comprises the extracellular domain of PD1 or a fragment thereof.

15 In embodiments, the second CAR molecule in the cell further comprises an intracellular signaling domain comprising a primary signaling domain and/or an intracellular signaling domain.

In other embodiments, the intracellular signaling domain in the cell comprises a primary signaling domain comprising the functional domain of CD3 zeta and a costimulatory signaling domain comprising the functional domain of 4-1BB.

20 In one embodiment, the second CAR molecule in the cell comprises the amino acid sequence of SEQ ID NO: 26.

In certain embodiments, the antigen binding domain of the first CAR molecule comprises a scFv and the antigen binding domain of the second CAR molecule does not comprise a scFv. For example, the antigen binding domain of the first CAR molecule comprises a scFv and the antigen binding domain of the second CAR molecule comprises a camelid VHH domain.

25 Split CAR

In some embodiments, the CAR-expressing cell uses a split CAR. The split CAR approach is described in more detail in publications WO2014/055442 and WO2014/055657. Briefly, a split CAR system comprises a cell expressing a first CAR having a first antigen binding domain and a costimulatory domain (e.g., 41BB), and the cell also expresses a second CAR having a second antigen binding domain and an intracellular signaling domain (e.g., CD3 zeta). When the cell encounters the first antigen, the costimulatory domain is activated, and the cell proliferates. When the cell encounters the second antigen,

30

the intracellular signaling domain is activated and cell-killing activity begins. Thus, the CAR-expressing cell is only fully activated in the presence of both antigens.

Multiple CAR expression

In one aspect, the fusion protein, e.g., as described herein, comprising a domain that includes a CAR, -
5 expressing cell described herein can further comprise a second fusion protein, e.g., as described herein, comprising a domain that includes a CAR, e.g., a second CAR that includes a different antigen binding domain, e.g., to the same target or a different target (e.g., a target other than a cancer associated antigen described herein or a different cancer associated antigen described herein). In one embodiment, the second CAR includes an antigen binding domain to a target expressed the same cancer cell type as the
10 cancer associated antigen. In one embodiment, the CAR-expressing cell comprises a first CAR that targets a first antigen and includes an intracellular signaling domain having a costimulatory signaling domain but not a primary signaling domain, and a second CAR that targets a second, different, antigen and includes an intracellular signaling domain having a primary signaling domain but not a costimulatory signaling domain. While not wishing to be bound by theory, placement of a costimulatory signaling
15 domain, e.g., 4-1BB, CD28, CD27 or OX-40, onto the first CAR, and the primary signaling domain, e.g., CD3 zeta, on the second CAR can limit the CAR activity to cells where both targets are expressed. In one embodiment, the CAR expressing cell comprises a first cancer associated antigen CAR that includes an antigen binding domain that binds a target antigen described herein, a transmembrane domain and a costimulatory domain and a second CAR that targets a different target antigen (e.g., an
20 antigen expressed on that same cancer cell type as the first target antigen) and includes an antigen binding domain, a transmembrane domain and a primary signaling domain. In another embodiment, the CAR expressing cell comprises a first CAR that includes an antigen binding domain that binds a target antigen described herein, a transmembrane domain and a primary signaling domain and a second CAR that targets an antigen other than the first target antigen (e.g., an antigen expressed on the same cancer
25 cell type as the first target antigen) and includes an antigen binding domain to the antigen, a transmembrane domain and a costimulatory signaling domain.

In some embodiments, the claimed invention comprises a first and second CAR, wherein the antigen binding domain of one of said first CAR said second CAR does not comprise a variable light domain and a variable heavy domain. In some embodiments, the antigen binding domain of one of said first CAR said
30 second CAR is an scFv, and the other is not an scFv. In some embodiments, the antigen binding domain of one of said first CAR said second CAR comprises a single VH domain, e.g., a camelid, shark, or lamprey single VH domain, or a single VH domain derived from a human or mouse sequence. In some embodiments, the antigen binding domain of one of said first CAR said second CAR comprises a nanobody. In some embodiments, the antigen binding domain of one of said first CAR said second CAR
35 comprises a camelid VHH domain.

Allogeneic cells

In embodiments described herein, the immune effector cell can be an allogeneic immune effector cell, e.g., T cell or NK cell. For example, the cell can be an allogeneic T cell, e.g., an allogeneic T cell lacking expression of a functional T cell receptor (TCR) and/or human leukocyte antigen (HLA), e.g., HLA class I
 5 and/or HLA class II or beta 2 microglobulin (B2M).

A T cell lacking a functional TCR can be, e.g., engineered such that it does not express any functional TCR on its surface, engineered such that it does not express one or more subunits that comprise a functional TCR, e.g., TRAC, TRBC1, TRBC2, CD3E, CD3G, or CD3D, or engineered such that it produces very little functional TCR on its surface. Alternatively, the T cell can express a substantially
 10 impaired TCR, e.g., by expression of mutated or truncated forms of one or more of the subunits of the TCR. The term "substantially impaired TCR" means that this TCR will not elicit an adverse immune reaction in a host.

A T cell described herein can be, e.g., engineered such that it does not express a functional HLA on its surface. For example, a T cell described herein, can be engineered such that cell surface expression
 15 HLA, e.g., HLA class I and/or HLA class II, or subunit or regulator of HLA expression, e.g., B2M, is downregulated.

A T cell described herein can be, e.g., engineered such that it does not express a functional B2M on its surface. For example, a T cell described herein, can be engineered such that cell surface expression of B2M is downregulated.

20 In some embodiments, the T cell can lack a functional TCR and a functional HLA, e.g., HLA class I and/or HLA class II.

Modified T cells that lack expression of a functional TCR and/or HLA can be obtained by any suitable means, including a knock out or knock down of one or more subunit of TCR or HLA. For example, the T cell can include a knock down of TCR and/or HLA using siRNA, shRNA, clustered regularly interspaced
 25 short palindromic repeats (CRISPR) transcription-activator like effector nuclease (TALEN), or zinc finger endonuclease (ZFN).

In some embodiments, the allogeneic cell can be a cell which does not express or expresses at low levels an inhibitory molecule, e.g. by any method described herein. For example, the cell can be a cell that does not express or expresses at low levels an inhibitory molecule, e.g., that can decrease the ability of a CAR-
 30 expressing cell to mount an immune effector response. Examples of inhibitory molecules include PD1, PD-L1, CTLA4, TIM3, CEACAM (e.g., CEACAM-1, CEACAM-3 and/or CEACAM-5), LAG3, VISTA, BTLA, TIGIT, LAIR1, CD160, 2B4 and TGFR beta. Inhibition of an inhibitory molecule, e.g., by inhibition at the DNA, RNA or protein level, can optimize a CAR-expressing cell performance. In embodiments, an inhibitory nucleic acid, e.g., an inhibitory nucleic acid, e.g., a dsRNA, e.g., an siRNA or shRNA, a

clustered regularly interspaced short palindromic repeats (CRISPR), a transcription-activator like effector nuclease (TALEN), or a zinc finger endonuclease (ZFN), e.g., as described herein, can be used.

siRNA and shRNA

- 5 In some embodiments, TCR expression and/or HLA or B2M expression can be inhibited using siRNA or shRNA that targets a nucleic acid encoding a TCR and/or HLA in a T cell.

CRISPR

- 10 “CRISPR” or “CRISPR to TCR and/or HLA” or “CRISPR to inhibit TCR and/or HLA” as used herein refers to a set of clustered regularly interspaced short palindromic repeats, or a system comprising such a set of repeats. “Cas”, as used herein, refers to a CRISPR-associated protein. A “CRISPR/Cas” system refers to a system derived from CRISPR and Cas which can be used to silence or mutate a TCR and/or HLA or B2M gene.

- 15 Artificial CRISPR/Cas systems can be generated which inhibit TCR and/or HLA, using technology known in the art, e.g., that described in U.S. Publication No. 20140068797, and Cong (2013) *Science* 339: 819-823. Other artificial CRISPR/Cas systems that are known in the art may also be generated which inhibit TCR and/or HLA, e.g., that described in Tsai (2014) *Nature Biotechnol.*, 32:6 569-576, U.S. Patent No.: 8,871,445; 8,865,406; 8,795,965; 8,771,945; and 8,697,359.

TALEN

- 20 “TALEN” or “TALEN to HLA and/or TCR” or “TALEN to inhibit HLA and/or TCR” refers to a transcription activator-like effector nuclease, an artificial nuclease which can be used to edit the HLA or B2M and/or TCR gene.

- 25 TALENs are produced artificially by fusing a TAL effector DNA binding domain to a DNA cleavage domain. Transcription activator-like effects (TALEs) can be engineered to bind any desired DNA sequence, including a portion of the HLA or TCR gene. By combining an engineered TALE with a DNA cleavage domain, a restriction enzyme can be produced which is specific to any desired DNA sequence, including a HLA or TCR sequence. These can then be introduced into a cell, wherein they can be used for genome editing. Boch (2011) *Nature Biotech.* 29: 135-6; and Boch et al. (2009) *Science* 326: 1509-12; Moscou et al. (2009) *Science* 326: 3501.

- 30 TALENs specific to sequences in HLA or TCR can be constructed using any method known in the art, including various schemes using modular components. Zhang et al. (2011) *Nature Biotech.* 29: 149-53; Geibler et al. (2011) *PLoS ONE* 6: e19509.

Zinc finger nuclease to inhibit HLA and/or TCR

“ZFN” or “Zinc Finger Nuclease” or “ZFN to HLA and/or TCR” or “ZFN to inhibit HLA and/or TCR” refer to a zinc finger nuclease, an artificial nuclease which can be used to edit the HLA and/or TCR or B2M gene.

- 5 ZFNs specific to sequences in HLA AND/OR TCR can be constructed using any method known in the art. See, e.g., Provasi (2011) *Nature Med.* 18: 807-815; Torikai (2013) *Blood* 122: 1341-1349; Cathomen et al. (2008) *Mol. Ther.* 16: 1200-7; Guo et al. (2010) *J. Mol. Biol.* 400: 96; U.S. Patent Publication 2011/0158957; and U.S. Patent Publication 2012/0060230.

Telomerase expression

- 10 While not wishing to be bound by any particular theory, in some embodiments, a therapeutic T cell has short term persistence in a patient, due to shortened telomeres in the T cell; accordingly, transfection with a telomerase gene can lengthen the telomeres of the T cell and improve persistence of the T cell in the patient. See Carl June, “Adoptive T cell therapy for cancer in the clinic”, *Journal of Clinical Investigation*, 117:1466-1476 (2007). Thus, in an embodiment, an immune effector cell, e.g., a T cell, ectopically
 15 expresses a telomerase subunit, e.g., the catalytic subunit of telomerase, e.g., TERT, e.g., hTERT. In some aspects, this disclosure provides a method of producing a CAR-expressing cell, comprising contacting a cell with a nucleic acid encoding a telomerase subunit, e.g., the catalytic subunit of telomerase, e.g., TERT, e.g., hTERT. The cell may be contacted with the nucleic acid before, simultaneous with, or after being contacted with a construct encoding a CAR.

20 Expansion and Activation

- Immune effector cells such as T cells may be activated and expanded generally using methods as described, for example, in U.S. Patents 6,352,694; 6,534,055; 6,905,680; 6,692,964; 5,858,358; 6,887,466; 6,905,681; 7,144,575; 7,067,318; 7,172,869; 7,232,566; 7,175,843; 5,883,223; 6,905,874; 6,797,514; 6,867,041; and U.S. Patent Application Publication No. 20060121005, each of which is
 25 incorporated by reference in its entirety.

- Generally, a population of immune effector cells e.g., T regulatory cell depleted cells, may be expanded by contact with a surface having attached thereto an agent that stimulates a CD3/TCR complex associated signal and a ligand that stimulates a costimulatory molecule on the surface of the T cells. In particular, T cell populations may be stimulated as described herein, such as by contact with an anti-CD3
 30 antibody, or antigen-binding fragment thereof, or an anti-CD2 antibody immobilized on a surface, or by contact with a protein kinase C activator (e.g., bryostatin) in conjunction with a calcium ionophore. For co-stimulation of an accessory molecule on the surface of the T cells, a ligand that binds the accessory molecule is used. For example, a population of T cells can be contacted with an anti-CD3 antibody and

an anti-CD28 antibody, under conditions appropriate for stimulating proliferation of the T cells. To stimulate proliferation of either CD4+ T cells or CD8+ T cells, an anti-CD3 antibody and an anti-CD28 antibody can be used. Examples of an anti-CD28 antibody include 9.3, B-T3, XR-CD28 (Diacclone, Besançon, France) can be used as can other methods commonly known in the art (Berg et al., Transplant Proc. 30(8):3975-3977, 1998; Haanen et al., J. Exp. Med. 190(9):1319-1328, 1999; Garland et al., J. Immunol Meth. 227(1-2):53-63, 1999).

In certain aspects, the primary stimulatory signal and the costimulatory signal for the T cell may be provided by different protocols. For example, the agents providing each signal may be in solution or coupled to a surface. When coupled to a surface, the agents may be coupled to the same surface (i.e., in “cis” formation) or to separate surfaces (i.e., in “trans” formation). Alternatively, one agent may be coupled to a surface and the other agent in solution. In one aspect, the agent providing the costimulatory signal is bound to a cell surface and the agent providing the primary activation signal is in solution or coupled to a surface. In certain aspects, both agents can be in solution. In one aspect, the agents may be in soluble form, and then cross-linked to a surface, such as a cell expressing Fc receptors or an antibody or other binding agent which will bind to the agents. In this regard, see for example, U.S. Patent Application Publication Nos. 20040101519 and 20060034810 for artificial antigen presenting cells (aAPCs) that are contemplated for use in activating and expanding T cells in the present invention.

In one aspect, the two agents are immobilized on beads, either on the same bead, i.e., “cis,” or to separate beads, i.e., “trans.” By way of example, the agent providing the primary activation signal is an anti-CD3 antibody or an antigen-binding fragment thereof and the agent providing the costimulatory signal is an anti-CD28 antibody or antigen-binding fragment thereof; and both agents are co-immobilized to the same bead in equivalent molecular amounts. In one aspect, a 1:1 ratio of each antibody bound to the beads for CD4+ T cell expansion and T cell growth is used. In certain aspects of the present invention, a ratio of anti CD3:CD28 antibodies bound to the beads is used such that an increase in T cell expansion is observed as compared to the expansion observed using a ratio of 1:1. In one particular aspect an increase of from about 1 to about 3 fold is observed as compared to the expansion observed using a ratio of 1:1. In one aspect, the ratio of CD3:CD28 antibody bound to the beads ranges from 100:1 to 1:100 and all integer values there between. In one aspect, more anti-CD28 antibody is bound to the particles than anti-CD3 antibody, i.e., the ratio of CD3:CD28 is less than one. In certain aspects, the ratio of anti CD28 antibody to anti CD3 antibody bound to the beads is greater than 2:1. In one particular aspect, a 1:100 CD3:CD28 ratio of antibody bound to beads is used. In one aspect, a 1:75 CD3:CD28 ratio of antibody bound to beads is used. In a further aspect, a 1:50 CD3:CD28 ratio of antibody bound to beads is used. In one aspect, a 1:30 CD3:CD28 ratio of antibody bound to beads is used. In one preferred aspect, a 1:10 CD3:CD28 ratio of antibody bound to beads is used. In one aspect, a 1:3 CD3:CD28 ratio of antibody bound to the beads is used. In yet one aspect, a 3:1 CD3:CD28 ratio of antibody bound to the beads is used.

Ratios of particles to cells from 1:500 to 500:1 and any integer values in between may be used to stimulate T cells or other target cells. As those of ordinary skill in the art can readily appreciate, the ratio of particles to cells may depend on particle size relative to the target cell. For example, small sized beads could only bind a few cells, while larger beads could bind many. In certain aspects the ratio of cells to particles ranges from 1:100 to 100:1 and any integer values in-between and in further aspects the ratio comprises 1:9 to 9:1 and any integer values in between, can also be used to stimulate T cells. The ratio of anti-CD3- and anti-CD28-coupled particles to T cells that result in T cell stimulation can vary as noted above, however certain preferred values include 1:100, 1:50, 1:40, 1:30, 1:20, 1:10, 1:9, 1:8, 1:7, 1:6, 1:5, 1:4, 1:3, 1:2, 1:1, 2:1, 3:1, 4:1, 5:1, 6:1, 7:1, 8:1, 9:1, 10:1, and 15:1 with one preferred ratio being at least 1:1 particles per T cell. In one aspect, a ratio of particles to cells of 1:1 or less is used. In one particular aspect, a preferred particle: cell ratio is 1:5. In further aspects, the ratio of particles to cells can be varied depending on the day of stimulation. For example, in one aspect, the ratio of particles to cells is from 1:1 to 10:1 on the first day and additional particles are added to the cells every day or every other day thereafter for up to 10 days, at final ratios of from 1:1 to 1:10 (based on cell counts on the day of addition). In one particular aspect, the ratio of particles to cells is 1:1 on the first day of stimulation and adjusted to 1:5 on the third and fifth days of stimulation. In one aspect, particles are added on a daily or every other day basis to a final ratio of 1:1 on the first day, and 1:5 on the third and fifth days of stimulation. In one aspect, the ratio of particles to cells is 2:1 on the first day of stimulation and adjusted to 1:10 on the third and fifth days of stimulation. In one aspect, particles are added on a daily or every other day basis to a final ratio of 1:1 on the first day, and 1:10 on the third and fifth days of stimulation. One of skill in the art will appreciate that a variety of other ratios may be suitable for use in the present invention. In particular, ratios will vary depending on particle size and on cell size and type. In one aspect, the most typical ratios for use are in the neighborhood of 1:1, 2:1 and 3:1 on the first day.

In further aspects, the cells, such as T cells, are combined with agent-coated beads, the beads and the cells are subsequently separated, and then the cells are cultured. In an alternative aspect, prior to culture, the agent-coated beads and cells are not separated but are cultured together. In a further aspect, the beads and cells are first concentrated by application of a force, such as a magnetic force, resulting in increased ligation of cell surface markers, thereby inducing cell stimulation.

By way of example, cell surface proteins may be ligated by allowing paramagnetic beads to which anti-CD3 and anti-CD28 are attached (3x28 beads) to contact the T cells. In one aspect the cells (for example, 10^4 to 10^9 T cells) and beads (for example, DYNABEADS® M-450 CD3/CD28 T paramagnetic beads at a ratio of 1:1) are combined in a buffer, for example PBS (without divalent cations such as, calcium and magnesium). Again, those of ordinary skill in the art can readily appreciate any cell concentration may be used. For example, the target cell may be very rare in the sample and comprise only 0.01% of the sample or the entire sample (i.e., 100%) may comprise the target cell of interest. Accordingly, any cell number is within the context of the present invention. In certain aspects, it may be desirable to significantly decrease

the volume in which particles and cells are mixed together (i.e., increase the concentration of cells), to ensure maximum contact of cells and particles. For example, in one aspect, a concentration of about 10 billion cells/ml, 9 billion/ml, 8 billion/ml, 7 billion/ml, 6 billion/ml, 5 billion/ml, or 2 billion cells/ml is used. In one aspect, greater than 100 million cells/ml is used. In a further aspect, a concentration of cells of 10, 15, 20, 25, 30, 35, 40, 45, or 50 million cells/ml is used. In yet one aspect, a concentration of cells from 75, 80, 85, 90, 95, or 100 million cells/ml is used. In further aspects, concentrations of 125 or 150 million cells/ml can be used. Using high concentrations can result in increased cell yield, cell activation, and cell expansion. Further, use of high cell concentrations allows more efficient capture of cells that may weakly express target antigens of interest, such as CD28-negative T cells. Such populations of cells may have therapeutic value and would be desirable to obtain in certain aspects. For example, using high concentration of cells allows more efficient selection of CD8⁺ T cells that normally have weaker CD28 expression.

In one embodiment, cells transduced with a nucleic acid encoding a fusion protein, e.g., as described herein, comprising a domain that includes a CAR, e.g., a CAR described herein, are expanded, e.g., by a method described herein. In one embodiment, the cells are expanded in culture for a period of several hours (e.g., about 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 18, 21 hours) to about 14 days (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14 days). In one embodiment, the cells are expanded for a period of 4 to 9 days. In one embodiment, the cells are expanded for a period of 8 days or less, e.g., 7, 6 or 5 days. In one embodiment, the cells are expanded in culture for 5 days, and the resulting cells are more potent than the same cells expanded in culture for 9 days under the same culture conditions. Potency can be defined, e.g., by various T cell functions, e.g. proliferation, target cell killing, cytokine production, activation, migration, or combinations thereof. In one embodiment, the cells are expanded for 5 days show at least a one, two, three or four fold increase in cells doublings upon antigen stimulation as compared to the same cells expanded in culture for 9 days under the same culture conditions. In one embodiment, the cells are expanded in culture for 5 days, and the resulting cells exhibit higher proinflammatory cytokine production, e.g., IFN- γ and/or GM-CSF levels, as compared to the same cells expanded in culture for 9 days under the same culture conditions. In one embodiment, the cells expanded for 5 days show at least a one, two, three, four, five, ten fold or more increase in pg/ml of proinflammatory cytokine production, e.g., IFN- γ and/or GM-CSF levels, as compared to the same cells expanded in culture for 9 days under the same culture conditions.

Several cycles of stimulation may also be desired such that culture time of T cells can be 60 days or more. Conditions appropriate for T cell culture include an appropriate media (e.g., Minimal Essential Media or RPMI Media 1640 or, X-vivo 15, (Lonza)) that may contain factors necessary for proliferation and viability, including serum (e.g., fetal bovine or human serum), interleukin-2 (IL-2), insulin, IFN- γ , IL-4, IL-7, GM-CSF, IL-10, IL-12, IL-15, TGF β , and TNF- α or any other additives for the growth of cells known to the skilled artisan. Other additives for the growth of cells include, but are not limited to, surfactant,

plasmanate, and reducing agents such as N-acetyl-cysteine and 2-mercaptoethanol. Media can include RPMI 1640, AIM-V, DMEM, MEM, α -MEM, F-12, X-Vivo 15, and X-Vivo 20, Optimizer, with added amino acids, sodium pyruvate, and vitamins, either serum-free or supplemented with an appropriate amount of serum (or plasma) or a defined set of hormones, and/or an amount of cytokine(s) sufficient for the growth and expansion of T cells. Antibiotics, e.g., penicillin and streptomycin, are included only in experimental cultures, not in cultures of cells that are to be infused into a subject. The target cells are maintained under conditions necessary to support growth, for example, an appropriate temperature (e.g., 37° C) and atmosphere (e.g., air plus 5% CO₂).

In one embodiment, the cells are expanded in an appropriate media (e.g., media described herein) that includes one or more interleukin that result in at least a 200-fold (e.g., 200-fold, 250-fold, 300-fold, 350-fold) increase in cells over a 14 day expansion period, e.g., as measured by a method described herein such as flow cytometry. In one embodiment, the cells are expanded in the presence of IL-15 and/or IL-7 (e.g., IL-15 and IL-7).

In embodiments, methods described herein, e.g., fusion protein, e.g., as described herein, comprising a domain that includes a CAR, -expressing cell manufacturing methods, comprise removing T regulatory cells, e.g., CD25+ T cells, from a cell population, e.g., using an anti-CD25 antibody, or fragment thereof, or a CD25-binding ligand, IL-2. Methods of removing T regulatory cells, e.g., CD25+ T cells, from a cell population are described herein. In embodiments, the methods, e.g., manufacturing methods, further comprise contacting a cell population (e.g., a cell population in which T regulatory cells, such as CD25+ T cells, have been depleted; or a cell population that has previously contacted an anti-CD25 antibody, fragment thereof, or CD25-binding ligand) with IL-15 and/or IL-7. For example, the cell population (e.g., that has previously contacted an anti-CD25 antibody, fragment thereof, or CD25-binding ligand) is expanded in the presence of IL-15 and/or IL-7.

In some embodiments a fusion protein, e.g., as described herein, comprising a domain that includes a CAR, -expressing cell described herein is contacted with a composition comprising a interleukin-15 (IL-15) polypeptide, a interleukin-15 receptor alpha (IL-15Ra) polypeptide, or a combination of both a IL-15 polypeptide and a IL-15Ra polypeptide e.g., hetIL-15, during the manufacturing of the CAR-expressing cell, e.g., ex vivo. In embodiments, a CAR-expressing cell described herein is contacted with a composition comprising a IL-15 polypeptide during the manufacturing of the CAR-expressing cell, e.g., ex vivo. In embodiments, a CAR-expressing cell described herein is contacted with a composition comprising a combination of both a IL-15 polypeptide and a IL-15 Ra polypeptide during the manufacturing of the CAR-expressing cell, e.g., ex vivo. In embodiments, a CAR-expressing cell described herein is contacted with a composition comprising hetIL-15 during the manufacturing of the CAR-expressing cell, e.g., ex vivo.

In one embodiment the fusion protein, e.g., as described herein, comprising a domain that includes a CAR, -expressing cell described herein is contacted with a composition comprising hetIL-15 during ex vivo expansion. In an embodiment, the CAR-expressing cell described herein is contacted with a composition comprising an IL-15 polypeptide during ex vivo expansion. In an embodiment, the CAR-expressing cell described herein is contacted with a composition comprising both an IL-15 polypeptide and an IL-15Ra polypeptide during ex vivo expansion. In one embodiment the contacting results in the survival and proliferation of a lymphocyte subpopulation, e.g., CD8⁺ T cells.

T cells that have been exposed to varied stimulation times may exhibit different characteristics. For example, typical blood or apheresed peripheral blood mononuclear cell products have a helper T cell population (TH, CD4⁺) that is greater than the cytotoxic or suppressor T cell population (TC, CD8⁺). Ex vivo expansion of T cells by stimulating CD3 and CD28 receptors produces a population of T cells that prior to about days 8-9 consists predominately of TH cells, while after about days 8-9, the population of T cells comprises an increasingly greater population of TC cells. Accordingly, depending on the purpose of treatment, infusing a subject with a T cell population comprising predominately of TH cells may be advantageous. Similarly, if an antigen-specific subset of TC cells has been isolated it may be beneficial to expand this subset to a greater degree.

Further, in addition to CD4 and CD8 markers, other phenotypic markers vary significantly, but in large part, reproducibly during the course of the cell expansion process. Thus, such reproducibility enables the ability to tailor an activated T cell product for specific purposes.

Once a fusion protein, e.g., as described herein, comprising a domain that includes a CAR, described herein is constructed, various assays can be used to evaluate the activity of the molecule, such as but not limited to, the ability to expand T cells following antigen stimulation, sustain T cell expansion in the absence of re-stimulation, and anti-cancer activities in appropriate in vitro and animal models. Assays to evaluate the effects of a cars of the present disclosure are described in further detail below

Western blot analysis of fusion protein, e.g., as described herein, comprising a domain that includes a CAR, expression in primary T cells can be used to detect the presence of monomers and dimers. See, e.g., Milone *et al.*, Molecular Therapy 17(8): 1453-1464 (2009). Very briefly, T cells (1:1 mixture of CD4⁺ and CD8⁺ T cells) expressing the CARs are expanded *in vitro* for more than 10 days followed by lysis and SDS-PAGE under reducing conditions. CARs containing the full length TCR- ζ cytoplasmic domain and the endogenous TCR- ζ chain are detected by western blotting using an antibody to the TCR- ζ chain. The same T cell subsets are used for SDS-PAGE analysis under non-reducing conditions to permit evaluation of covalent dimer formation.

In vitro expansion of fusion protein⁺, e.g., as described herein, comprising a domain that includes a CAR, e.g., CAR⁺, T cells following antigen stimulation can be measured by flow cytometry. For example, a mixture of CD4⁺ and CD8⁺ T cells are stimulated with α CD3/ α CD28 aAPCs followed by transduction with

lentiviral vectors expressing GFP under the control of the promoters to be analyzed. Exemplary promoters include the CMV IE gene, EF-1 α , ubiquitin C, or phosphoglycerokinase (PGK) promoters. GFP fluorescence is evaluated on day 6 of culture in the CD4⁺ and/or CD8⁺ T cell subsets by flow cytometry. See, e.g., Milone *et al.*, Molecular Therapy 17(8): 1453-1464 (2009). Alternatively, a mixture of CD4⁺ and CD8⁺ T cells are stimulated with α CD3/ α CD28 coated magnetic beads on day 0, and transduced with CAR on day 1 using a bicistronic lentiviral vector expressing CAR along with eGFP using a 2A ribosomal skipping sequence. Cultures are re-stimulated with either a cancer associated antigen as described herein⁺ K562 cells (K562 expressing a cancer associated antigen as described herein), wild-type K562 cells (K562 wild type) or K562 cells expressing hCD32 and 4-1BBL in the presence of antiCD3 and anti-CD28 antibody (K562-BBL-3/28) following washing. Exogenous IL-2 is added to the cultures every other day at 100 IU/ml. GFP⁺ T cells are enumerated by flow cytometry using bead-based counting. See, e.g., Milone *et al.*, Molecular Therapy 17(8): 1453-1464 (2009).

Sustained fusion protein⁺, e.g., as described herein, comprising a domain that includes a CAR, e.g., CAR⁺, T cell expansion in the absence of re-stimulation can also be measured. See, e.g., Milone *et al.*, Molecular Therapy 17(8): 1453-1464 (2009). Briefly, mean T cell volume (fl) is measured on day 8 of culture using a Coulter Multisizer III particle counter, a Nexcelom Cellometer Vision or Millipore Scepter, following stimulation with α CD3/ α CD28 coated magnetic beads on day 0, and transduction with the indicated CAR on day 1.

Animal models can also be used to measure a CART activity. For example, xenograft model using human a cancer associated antigen described herein-specific CAR⁺ T cells to treat a primary human pre-B ALL in immunodeficient mice can be used. See, e.g., Milone *et al.*, Molecular Therapy 17(8): 1453-1464 (2009). Very briefly, after establishment of ALL, mice are randomized as to treatment groups. Different numbers of a cancer associated antigen -specific CARengineered T cells are coinjected at a 1:1 ratio into NOD-SCID- $\gamma^{-/-}$ mice bearing B-ALL. The number of copies of a cancer associated antigen -specific CAR vector in spleen DNA from mice is evaluated at various times following T cell injection. Animals are assessed for leukemia at weekly intervals. Peripheral blood a cancer associate antigen as described herein⁺ B-ALL blast cell counts are measured in mice that are injected with a cancer associated antigen described herein- ζ CAR⁺ T cells or mock-transduced T cells. Survival curves for the groups are compared using the log-rank test. In addition, absolute peripheral blood CD4⁺ and CD8⁺ T cell counts 4 weeks following T cell injection in NOD-SCID- $\gamma^{-/-}$ mice can also be analyzed. Mice are injected with leukemic cells and 3 weeks later are injected with T cells engineered to express CAR by a bicistronic lentiviral vector that encodes the CAR linked to eGFP. T cells are normalized to 45–50% input GFP⁺ T cells by mixing with mock-transduced cells prior to injection, and confirmed by flow cytometry. Animals are assessed for leukemia at 1-week intervals. Survival curves for the CAR⁺ T cell groups are compared using the log-rank test.

Dose dependent fusion protein, e.g., as described herein, comprising a domain that includes a CAR, treatment response can be evaluated. See, e.g., Milone *et al.*, Molecular Therapy 17(8): 1453-1464 (2009). For example, peripheral blood is obtained 35–70 days after establishing leukemia in mice injected on day 21 with CAR T cells, an equivalent number of mock-transduced T cells, or no T cells. Mice from each group are randomly bled for determination of peripheral blood a cancer associate antigen as described herein⁺ ALL blast counts and then killed on days 35 and 49. The remaining animals are evaluated on days 57 and 70.

Assessment of cell proliferation and cytokine production has been previously described, e.g., at Milone *et al.*, Molecular Therapy 17(8): 1453-1464 (2009). Briefly, assessment of CAR-mediated proliferation is performed in microtiter plates by mixing washed T cells with K562 cells expressing a cancer associated antigen described herein (K19) or CD32 and CD137 (KT32-BBL) for a final T-cell:K562 ratio of 2:1. K562 cells are irradiated with gamma-radiation prior to use. Anti-CD3 (clone OKT3) and anti- CD28 (clone 9.3) monoclonal antibodies are added to cultures with KT32-BBL cells to serve as a positive control for stimulating T-cell proliferation since these signals support long-term CD8⁺ T cell expansion *ex vivo*. T cells are enumerated in cultures using CountBright™ fluorescent beads (Invitrogen, Carlsbad, CA) and flow cytometry as described by the manufacturer. CAR⁺ T cells are identified by GFP expression using T cells that are engineered with eGFP-2A linked CAR-expressing lentiviral vectors. For CAR⁺ T cells not expressing GFP, the CAR⁺ T cells are detected with biotinylated recombinant a cancer associate antigen as described herein protein and a secondary avidin-PE conjugate. CD4⁺ and CD8⁺ expression on T cells are also simultaneously detected with specific monoclonal antibodies (BD Biosciences). Cytokine measurements are performed on supernatants collected 24 hours following re-stimulation using the human TH1/TH2 cytokine cytometric bead array kit (BD Biosciences, San Diego, CA) according the manufacturer's instructions. Fluorescence is assessed using a FACScalibur flow cytometer, and data is analyzed according to the manufacturer's instructions.

Cytotoxicity can be assessed by a standard ⁵¹Cr-release assay. See, e.g., Milone *et al.*, Molecular Therapy 17(8): 1453-1464 (2009). Briefly, target cells (K562 lines and primary pro-B-ALL cells) are loaded with ⁵¹Cr (as NaCrO₄, New England Nuclear, Boston, MA) at 37°C for 2 hours with frequent agitation, washed twice in complete RPMI and plated into microtiter plates. Effector T cells are mixed with target cells in the wells in complete RPMI at varying ratios of effector cell:target cell (E:T). Additional wells containing media only (spontaneous release, SR) or a 1% solution of triton-X 100 detergent (total release, TR) are also prepared. After 4 hours of incubation at 37°C, supernatant from each well is harvested. Released ⁵¹Cr is then measured using a gamma particle counter (Packard Instrument Co., Waltham, MA). Each condition is performed in at least triplicate, and the percentage of lysis is calculated using the formula: % Lysis = (ER– SR) / (TR – SR), where ER represents the average ⁵¹Cr released for each experimental condition.

Imaging technologies can be used to evaluate specific trafficking and proliferation of CARs in tumor-bearing animal models. Such assays have been described, for example, in Barrett *et al.*, Human Gene Therapy 22:1575-1586 (2011). Briefly, NOD/SCID/ $\gamma c^{-/-}$ (NSG) mice are injected IV with Nalm-6 cells followed 7 days later with T cells 4 hour after electroporation with the CAR constructs. The T cells are stably transfected with a lentiviral construct to express firefly luciferase, and mice are imaged for bioluminescence. Alternatively, therapeutic efficacy and specificity of a single injection of CAR⁺ T cells in Nalm-6 xenograft model can be measured as the following: NSG mice are injected with Nalm-6 transduced to stably express firefly luciferase, followed by a single tail-vein injection of T cells electroporated with cars of the present disclosure 7 days later. Animals are imaged at various time points post injection. For example, photon-density heat maps of firefly luciferase-positive leukemia in representative mice at day 5 (2 days before treatment) and day 8 (24 hr post CAR⁺ PBLs) can be generated.

Other assays, including those described in the Example section herein as well as those that are known in the art can also be used to evaluate the CARs described herein.

Methods of making CAR-expressing cells

In another aspect, the invention pertains to a method of making a cell (e.g., an immune effector cell or population thereof) comprising introducing into (e.g., transducing) a cell, e.g., a T cell or a NK cell described herein, with a vector of comprising a nucleic acid encoding a fusion protein, e.g., as described herein, comprising a domain that includes a CAR, e.g., a CAR described herein; or a nucleic acid encoding a CAR molecule e.g., a CAR described herein.

The cell in the methods is an immune effector cell (e.g., a T cell or a NK cell, or a combination thereof). In some embodiments, the cell in the methods is diacylglycerol kinase (DGK) and/or Ikaros deficient.

In some embodiment, the introducing the nucleic acid molecule encoding a CAR comprises transducing a vector comprising the nucleic acid molecule encoding a fusion protein, e.g., as described herein, comprising a domain that includes a CAR, or transfecting the nucleic acid molecule encoding a CAR, wherein the nucleic acid molecule is an in vitro transcribed RNA.

In some embodiments, the method further comprises:

providing a population of immune effector cells (e.g., T cells or NK cells); and

removing T regulatory cells from the population, thereby providing a population of T regulatory-depleted cells;

wherein steps a) and b) are performed prior to introducing the nucleic acid encoding the fusion protein, e.g., as described herein, comprising a domain that includes a CAR, to the population.

In embodiments of the methods, the T regulatory cells comprise CD25⁺ T cells, and are removed from the cell population using an anti-CD25 antibody, or fragment thereof. The anti-CD25 antibody, or
5 fragment thereof, can be conjugated to a substrate, e.g., a bead.

In other embodiments, the population of T regulatory-depleted cells provided from step (b) contains less than 30%, 25%, 20%, 15%, 10%, 5%, 4%, 3%, 2%, 1% of CD25⁺ cells.

In yet other embodiments, the method further comprises removing cells from the population which express a tumor antigen that does not comprise CD25 to provide a population of T regulatory-depleted
10 and tumor antigen depleted cells prior to introducing the nucleic acid encoding a fusion protein, e.g., as described herein, comprising a domain that includes a CAR, to the population. The tumor antigen can be selected from CD19, CD30, CD38, CD123, CD20, CD14 or CD11b, or a combination thereof.

In other embodiments, the method further comprises removing cells from the population which express a checkpoint inhibitor, to provide a population of T regulatory-depleted and inhibitory molecule depleted
15 cells prior to introducing the nucleic acid encoding a fusion protein, e.g., as described herein, comprising a domain that includes a CAR, to the population. The checkpoint inhibitor can be chosen from PD-1, LAG-3, TIM3, B7-H1, CD160, P1H, 2B4, CEACAM (e.g., CEACAM-1, CEACAM-3, and/or CEACAM-5), TIGIT, CTLA-4, BTLA, and LAIR1.

Further embodiments disclosed herein encompass providing a population of immune effector cells. The
20 population of immune effector cells provided can be selected based upon the expression of one or more of CD3, CD28, CD4, CD8, CD45RA, and/or CD45RO. In certain embodiments, the population of immune effector cells provided are CD3⁺ and/or CD28⁺.

In certain embodiments of the method, the method further comprises expanding the population of cells after the nucleic acid molecule encoding a fusion protein, e.g., as described herein, comprising a domain
25 that includes a CAR, has been introduced.

In embodiments, the population of cells is expanded for a period of 8 days or less.

In certain embodiments, the population of cells is expanded in culture for 5 days, and the resulting cells are more potent than the same cells expanded in culture for 9 days under the same culture conditions.

In other embodiments, the population of cells is expanded in culture for 5 days show at least a one, two,
30 three or four fold increase in cell doublings upon antigen stimulation as compared to the same cells expanded in culture for 9 days under the same culture conditions.

In yet other embodiments, the population of cells is expanded in culture for 5 days, and the resulting cells exhibit higher proinflammatory IFN- γ and/or GM-CSF levels, as compared to the same cells expanded in culture for 9 days under the same culture conditions.

In other embodiments, the population of cells is expanded by culturing the cells in the presence of an agent that stimulates a CD3/TCR complex associated signal and/or a ligand that stimulates a costimulatory molecule on the surface of the cells. The agent can be a bead conjugated with anti-CD3 antibody, or a fragment thereof, and/or anti-CD28 antibody, or a fragment thereof.

In other embodiments, the population of cells is expanded in an appropriate media that includes one or more interleukin that result in at least a 200-fold, 250-fold, 300-fold, or 350-fold increase in cells over a 14 day expansion period, as measured by flow cytometry.

In other embodiments, the population of cells is expanded in the presence IL-15 and/or IL-7.

In certain embodiments, the method further includes cryopreserving the population of the cells after the appropriate expansion period.

In yet other embodiments, the method of making disclosed herein further comprises contacting the population of immune effector cells with a nucleic acid encoding a telomerase subunit, e.g., hTERT. The nucleic acid encoding the telomerase subunit can be DNA.

The present disclosure also provides a method of generating a population of RNA-engineered cells, e.g., cells described herein, e.g., immune effector cells (e.g., T cells, NK cells), transiently expressing exogenous RNA. The method comprises introducing an *in vitro* transcribed RNA or synthetic RNA into a cell, where the RNA comprises a nucleic acid encoding a fusion protein, e.g., as described herein, comprising a domain that includes a CAR molecule, described herein.

In another aspect, the invention pertains to a method of providing an anti-tumor immunity in a subject comprising administering to the subject an effective amount of a cell comprising a fusion protein, e.g., as described herein, comprising a domain that includes a CAR molecule, e.g., a cell expressing a CAR molecule described herein. In one embodiment, the cell is an autologous T cell or NK cell. In one embodiment, the cell is an allogeneic T cell or NK cell. In one embodiment, the subject is a human.

In one aspect, the invention includes a population of autologous cells that are transfected or transduced with a vector comprising a nucleic acid molecule encoding a fusion protein, e.g., as described herein, comprising a domain that includes a CAR molecule, e.g., as described herein. In one embodiment, the vector is a retroviral vector. In one embodiment, the vector is a self-inactivating lentiviral vector as described elsewhere herein. In one embodiment, the vector is delivered (e.g., by transfecting or electroporating) to a cell, e.g., a T cell or a NK cell, wherein the vector comprises a nucleic acid molecule encoding a CAR of the present disclosure as described herein, which is transcribed as an mRNA

molecule, and the CARs of the present disclosure is translated from the RNA molecule and expressed on the surface of the cell.

In another aspect, the present disclosure provides a population of fusion protein, e.g., as described herein, comprising a domain that includes a CAR, -expressing cells, e.g., CAR-expressing immune effector cells (e.g., T cells or NK cells). In some embodiments, the population of CAR-expressing cells comprises a mixture of cells expressing different CARs. For example, in one embodiment, the population of CAR-expressing immune effector cells (e.g., T cells or NK cells) can include a first cell expressing a CAR having an antigen binding domain that binds to a first tumor antigen as described herein, and a second cell expressing a CAR having a different antigen binding domain that binds to a second tumor antigen as described herein. As another example, the population of CAR-expressing cells can include a first cell expressing a CAR that includes an antigen binding domain that binds to a tumor antigen as described herein, and a second cell expressing a CAR that includes an antigen binding domain to a target other than a tumor antigen as described herein. In one embodiment, the population of CAR-expressing cells includes, e.g., a first cell expressing a CAR that includes a primary intracellular signaling domain, and a second cell expressing a CAR that includes a secondary signaling domain, e.g., a costimulatory signaling domain.

In another aspect, the present disclosure provides a population of cells wherein at least one cell in the population expresses a fusion protein, e.g., as described herein, comprising a domain that includes a CAR having an antigen binding domain that binds to a tumor antigen as described herein, and a second cell expressing another agent, e.g., an agent which enhances the activity of a CAR-expressing cell. For example, in one embodiment, the agent can be an agent which inhibits an inhibitory molecule. Examples of inhibitory molecules include PD-1, PD-L1, CTLA-4, TIM-3, CEACAM (e.g., CEACAM-1, CEACAM-3 and/or CEACAM-5), LAG-3, VISTA, BTLA, TIGIT, LAIR1, CD160, 2B4 and TGFR beta. In one embodiment, the agent which inhibits an inhibitory molecule, e.g., is a molecule described herein, e.g., an agent that comprises a first polypeptide, e.g., an inhibitory molecule, associated with a second polypeptide that provides a positive signal to the cell, e.g., an intracellular signaling domain described herein. In one embodiment, the agent comprises a first polypeptide, e.g., of an inhibitory molecule such as PD-1, LAG-3, CTLA-4, CD160, BTLA, LAIR1, TIM-3, CEACAM (e.g., CEACAM-1, CEACAM-3 and/or CEACAM-5), 2B4 and TIGIT, or a fragment of any of these, and a second polypeptide which is an intracellular signaling domain described herein (e.g., comprising a costimulatory domain (e.g., 41BB, CD27 or CD28, e.g., as described herein) and/or a primary signaling domain (e.g., a CD3 zeta signaling domain described herein). In one embodiment, the agent comprises a first polypeptide of PD-1 or a fragment thereof, and a second polypeptide of an intracellular signaling domain described herein (e.g., a CD28, CD27, OX40 or 4-1BB signaling domain described herein and/or a CD3 zeta signaling domain described herein).

In one embodiment, the nucleic acid molecule encoding a fusion protein, e.g., as described herein, comprising a domain that includes a CAR of the present disclosure molecule, e.g., as described herein, is expressed as an mRNA molecule. In one embodiment, the genetically modified CAR of the present invention-expressing cells, e.g., immune effector cells (e.g., T cells, NK cells), can be generated by
5 transfecting or electroporating an RNA molecule encoding the desired CARs (e.g., without a vector sequence) into the cell. In one embodiment, a CAR of the present disclosure molecule is translated from the RNA molecule once it is incorporated and expressed on the surface of the recombinant cell.

A method for generating mRNA for use in transfection involves *in vitro* transcription (IVT) of a template with specially designed primers, followed by polyA addition, to produce a construct containing 3' and 5' untranslated sequence ("UTR") (e.g., a 3' and/or 5' UTR described herein), a 5' cap (e.g., a 5' cap
10 described herein) and/or Internal Ribosome Entry Site (IRES) (e.g., an IRES described herein), the nucleic acid to be expressed, and a polyA tail, typically 50-5000 bases in length (SEQ ID NO:32). RNA so produced can efficiently transfect different kinds of cells. In one embodiment, the template includes sequences for the fusion protein, e.g., as described herein, comprising a domain that includes a CAR. In
15 an embodiment, an RNA fusion protein, e.g., as described herein, comprising a domain that includes a CAR, vector is transduced into a cell, e.g., a T cell or a NK cell, by electroporation.

In one embodiment, the fusion protein, e.g., as described herein, comprising a domain that includes a CAR, is introduced into immune effector cells (e.g., T cells, NK cells), e.g., using *in vitro* transcription, and the subject (e.g., human) receives an initial administration of fusion protein, e.g., as described herein,
20 comprising a domain that includes a CAR, immune effector cells (e.g., T cells, NK cells) of the invention, and one or more subsequent administrations of the fusion protein, e.g., as described herein, comprising a domain that includes a CAR, immune effector cells (e.g., T cells, NK cells) of the invention, wherein the one or more subsequent administrations are administered less than 15 days, e.g., 14, 13, 12, 11, 10, 9, 8, 7, 6, 5, 4, 3, or 2 days after the previous administration. In one embodiment, more than one
25 administration of the CAR immune effector cells (e.g., T cells, NK cells) of the invention are administered to the subject (e.g., human) per week, e.g., 2, 3, or 4 administrations of the CAR immune effector cells (e.g., T cells, NK cells) of the invention are administered per week. In one embodiment, the subject (e.g., human subject) receives more than one administration of the CAR immune effector cells (e.g., T cells, NK cells) per week (e.g., 2, 3 or 4 administrations per week) (also referred to herein as a cycle), followed by a
30 week of no CAR immune effector cells (e.g., T cells, NK cells) administrations, and then one or more additional administration of the CAR immune effector cells (e.g., T cells, NK cells) (e.g., more than one administration of the CAR immune effector cells (e.g., T cells, NK cells) per week) is administered to the subject. In another embodiment, the subject (e.g., human subject) receives more than one cycle of CAR immune effector cells (e.g., T cells, NK cells), and the time between each cycle is less than 10, 9, 8, 7, 6,
35 5, 4, or 3 days. In one embodiment, the CAR immune effector cells (e.g., T cells, NK cells) are administered every other day for 3 administrations per week. In one embodiment, the CAR immune

effector cells (e.g., T cells, NK cells) of the invention are administered for at least two, three, four, five, six, seven, eight or more weeks.

In one aspect, CAR-expressing cells are generated using lentiviral viral vectors, such as lentivirus. Cells, e.g., CARTs, generated that way will have stable CAR expression.

- 5 In one aspect, CAR-expressing cells, e.g., CARTs, are generated using a viral vector such as a gammaretroviral vector, e.g., a gammaretroviral vector described herein. CARTs generated using these vectors can have stable CAR expression.

- 10 In one aspect, CARTs transiently express CAR vectors for 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15 days after transduction. Transient expression of CARs can be effected by RNA CAR vector delivery. In one aspect, the CAR RNA is transduced into the T cell by electroporation.

A potential issue that can arise in patients being treated using transiently expressing CAR immune effector cells (e.g., T cells, NK cells) (particularly with murine scFv bearing CARTs) is anaphylaxis after multiple treatments.

- 15 Without being bound by this theory, it is believed that such an anaphylactic response might be caused by a patient developing humoral anti-CAR response, i.e., anti-CAR antibodies having an anti-IgE isotype. It is thought that a patient's antibody producing cells undergo a class switch from IgG isotype (that does not cause anaphylaxis) to IgE isotype when there is a ten to fourteen day break in exposure to antigen. If a patient is at high risk of generating an anti-CAR antibody response during the course of transient CAR therapy (such as those generated by RNA transductions), CART infusion breaks should not last more
20 than ten to fourteen days.

METHODS OF CONDITIONALLY EXPRESSING A PROTEIN AND THERAPEUTIC APPLICATION

- 25 Provided herein are also methods of conditionally expressing a fusion protein (e.g., comprising a CAR polypeptide). Such methods can include contacting a host cell comprising any of the fusion proteins described herein or a nucleic acid encoding such a fusion protein with a expression compound, e.g., a deaggregation compound or stabilization compound.

- 30 In the presence of the stabilization compound, the degradation domain of the fusion protein assumes a conformation resistant to cellular degradation, and a protease cleaves the protease cleavage site within the fusion protein, thereby resulting in cleavage of the degradation domain from the desired protein and the expression of the desired protein. In the absence of the stabilization compound, the degradation domain of the fusion protein assumes a conformation permissive to cellular degradation, which results in degradation of the fusion protein. In some embodiments, the host cell is contacted with the stabilization

compound in vivo. In some embodiments, the host cell is contacted with the stabilization compound ex vivo.

In the presence of the deaggregation compound, the deaggregation domain of the fusion protein assumes a conformation resistant to oligomerization (e.g., dimerization), causing the fusion protein to enter a monomeric state accessible to a protease, and a protease cleaves the protease cleavage site within the fusion protein, thereby resulting in cleavage of the aggregation domain from the desired protein and the expression of the desired protein. In the absence of the deaggregation compound, the deaggregation domain of the fusion protein assumes a conformation permissive to dimerization, causing the fusion protein to enter into an oligomeric, e.g., dimeric, e.g., aggregated state. The oligomeric, e.g., dimeric, e.g., aggregated state prevents the fusion protein from moving between cellular compartments or from being secreted. The oligomeric, e.g., dimeric, e.g., aggregated state is inaccessible to protease. In some embodiments, the host cell is contacted with the deaggregation compound in vivo. In some embodiments, the host cell is contacted with the deaggregation compound ex vivo.

The stabilization compound can be selected based on the degradation domain. For example, when the degradation domain is derived from an estrogen receptor, the stabilization compound can be selected from Bazedoxifene or 4-hydroxy tamoxifen (4-OHT). Tamoxifen and Bazedoxifene are FDA approved drugs, and thus are safe to use in human. If the degradation domain is derived from an FKB protein, the stabilization compound can be Shield1.

The deaggregation compound can be selected based on the deaggregation domain. For example, when the deaggregation domain is derived from FKBP, the deaggregation compound can be selected from FK506, rapamycin, AP22542, or AP21998.

In another aspect, the present disclosure provides methods comprising administering a fusion protein of the invention as a therapy. Typically, such administration will be in the form of host cells (e.g., autologous or allogeneic host cells) expressing the fusion protein of invention to the subject. Accordingly, through administration of a corresponding stabilization compound (either in vivo or ex vivo), the expression of the therapeutic (i.e., the protein remaining after cleavage of the degradation domain) can be regulated. Accordingly, through administration of a corresponding deaggregation compound (either in vivo or ex vivo), the expression of the therapeutic (i.e., the protein remaining after cleavage of the aggregation domain) can be regulated. Thus, expression of known synthetic therapeutic proteins or transmembrane receptors (e.g., a fusion protein, e.g., as described herein, comprising a domain that includes a CAR molecule described herein) can be regulated. In one embodiment, the subject has a disorder described herein, e.g., the subject has cancer, e.g., the subject has a cancer which expresses a target antigen described herein. In one embodiment, the subject is a human.

Provided herein are methods of treating a subject having a disease associated with expression of a tumor antigen by administering to the subject an effective amount of a host cell comprising any of the fusion proteins described herein or a nucleic acid encoding such a fusion protein. In some embodiments, the fusion protein comprises a chimeric antigen receptor (CAR), which comprises, in an N-terminal to C-terminal direction, an antigen binding domain that specifically binds the tumor antigen, a transmembrane domain, and one or more intracellular signaling domains. In some embodiments, the host cell is autologous to the subject. In some embodiments, the host cell is allogenic to said subject. In some embodiments, the host cell is contacted with an expression compound, e.g., stabilization compound or deaggregation compound. In the presence of the stabilization compound, the degradation domain of the fusion protein assumes a conformation resistant to cellular degradation, and a protease cleaves the protease cleavage site within the fusion protein, thereby results in cleavage of the degradation domain from the desired protein and the expression of the desired protein. In the absence of the stabilization compound, the degradation domain of the fusion protein assumes a conformation permissive to cellular degradation, which results in degradation of the fusion protein. In the presence of the deaggregation compound, the aggregation domain of the fusion protein assumes a conformation resistant to oligomerization or aggregation, and a protease cleaves the protease cleavage site within the fusion protein, thereby resulting in cleavage of the aggregation domain from the desired protein and the expression of the desired protein. In the absence of the deaggregation compound, the aggregation domain of the fusion protein assumes a conformation permissive to oligomerization or aggregation, which results in aggregation of the fusion protein.

In another aspect, the invention pertains to a method of treating a subject having a disease associated with expression of a cancer associated antigen as described herein comprising administering to the subject an effective amount of a cell comprising a fusion protein comprising a CAR molecule, e.g., a fusion protein comprising a CAR molecule described herein.

In yet another aspect, the invention features a method of treating a subject having a disease associated with expression of a tumor antigen (e.g., an antigen described herein), comprising administering to the subject an effective amount of a cell, e.g., an immune effector cell (e.g., a population of immune effector cells) comprising a fusion protein comprising a CAR molecule, wherein the CAR molecule comprises an antigen binding domain, a transmembrane domain, and an intracellular domain, said intracellular domain comprises a costimulatory domain and/or a primary signaling domain, wherein said antigen binding domain binds to the tumor antigen associated with the disease, e.g. a tumor antigen as described herein.

In a related aspect, the invention features a method of treating a subject having a disease associated with expression of a tumor antigen. The method comprises administering to the subject an effective amount of a cell, e.g., an immune effector cell (e.g., a population of immune effector cells), comprising a fusion protein comprising a CAR molecule, in combination with an agent that increases the efficacy of the immune cell, wherein:

the agent that increases the efficacy of the immune cell is chosen from one or more of:

(i) a protein phosphatase inhibitor;

(ii) a kinase inhibitor;

(iii) a cytokine;

5 (iv) an inhibitor of an immune inhibitory molecule; or

(v) an agent that decreases the level or activity of a T_{REG} cell.

In another aspect, the invention features a composition comprising an immune effector cell (e.g., a population of immune effector cells) comprising a fusion protein comprising a CAR molecule (e.g., a fusion protein comprising a CAR molecule as described herein) for use in the treatment of a subject
10 having a disease associated with expression of a tumor antigen, e.g., a disorder as described herein.

In certain embodiments of any of the aforesaid methods or uses, the disease associated with a tumor antigen, e.g., a tumor antigen described herein, is selected from a proliferative disease such as a cancer or malignancy or a precancerous condition such as a myelodysplasia, a myelodysplastic syndrome or a preleukemia, or is a non-cancer related indication associated with expression of a tumor antigen
15 described herein. In one embodiment, the disease is a cancer described herein, e.g., a cancer described herein as being associated with a target described herein. In one embodiment, the disease is a hematologic cancer. In one embodiment, the hematologic cancer is leukemia. In one embodiment, the cancer is selected from the group consisting of one or more acute leukemias including but not limited to B-cell acute lymphoid leukemia ("BALL"), T-cell acute lymphoid leukemia ("TALL"), acute lymphoid
20 leukemia (ALL); one or more chronic leukemias including but not limited to chronic myelogenous leukemia (CML), chronic lymphocytic leukemia (CLL); additional hematologic cancers or hematologic conditions including, but not limited to B cell prolymphocytic leukemia, blastic plasmacytoid dendritic cell neoplasm, Burkitt's lymphoma, diffuse large B cell lymphoma, follicular lymphoma, hairy cell leukemia, small cell- or a large cell-follicular lymphoma, malignant lymphoproliferative conditions, MALT lymphoma, mantle cell lymphoma, Marginal zone lymphoma, multiple myeloma, myelodysplasia and myelodysplastic
25 syndrome, non-Hodgkin lymphoma, Hodgkin lymphoma, plasmablastic lymphoma, plasmacytoid dendritic cell neoplasm, Waldenstrom macroglobulinemia, and "preleukemia" which are a diverse collection of hematological conditions united by ineffective production (or dysplasia) of myeloid blood cells, and to disease associated with expression of a tumor antigen described herein include, but not limited to,
30 atypical and/or non-classical cancers, malignancies, precancerous conditions or proliferative diseases expressing a tumor antigen as described herein; and any combination thereof. In another embodiment, the disease associated with a tumor antigen described herein is a solid tumor.

In certain embodiments, the methods or uses are carried out in combination with an agent that increases the efficacy of the immune effector cell, e.g., an agent as described herein.

In any of the aforesaid methods or uses, the disease associated with expression of the tumor antigen is selected from the group consisting of a proliferative disease, a precancerous condition, a cancer, and a
5 non-cancer related indication associated with expression of the tumor antigen.

The cancer can be a hematologic cancer, e.g., a cancer chosen from one or more of chronic lymphocytic leukemia (CLL), acute leukemias, acute lymphoid leukemia (ALL), B-cell acute lymphoid leukemia (B-ALL), T-cell acute lymphoid leukemia (T-ALL), chronic myelogenous leukemia (CML), B cell
10 polymphocytic leukemia, blastic plasmacytoid dendritic cell neoplasm, Burkitt's lymphoma, diffuse large B cell lymphoma, follicular lymphoma, hairy cell leukemia, small cell- or a large cell-follicular lymphoma, malignant lymphoproliferative conditions, MALT lymphoma, mantle cell lymphoma, marginal zone lymphoma, multiple myeloma, myelodysplasia and myelodysplastic syndrome, non-Hodgkin's lymphoma, Hodgkin's lymphoma, plasmablastic lymphoma, plasmacytoid dendritic cell neoplasm, Waldenstrom macroglobulinemia, or pre-leukemia.

The cancer can also be chosen from colon cancer, rectal cancer, renal-cell carcinoma, liver cancer, non-small cell carcinoma of the lung, cancer of the small intestine, cancer of the esophagus, melanoma, bone
15 cancer, pancreatic cancer, skin cancer, cancer of the head or neck, cutaneous or intraocular malignant melanoma, uterine cancer, ovarian cancer, rectal cancer, cancer of the anal region, stomach cancer, testicular cancer, uterine cancer, carcinoma of the fallopian tubes, carcinoma of the endometrium, carcinoma of the cervix, carcinoma of the vagina, carcinoma of the vulva, Hodgkin's Disease, non-Hodgkin's lymphoma, cancer of the endocrine system, cancer of the thyroid gland, cancer of the parathyroid gland, cancer of the adrenal gland, sarcoma of soft tissue, cancer of the urethra, cancer of the penis, solid tumors of childhood, cancer of the bladder, cancer of the kidney or ureter, carcinoma of the renal pelvis, neoplasm of the central nervous system (CNS), primary CNS lymphoma, tumor
20 angiogenesis, spinal axis tumor, brain stem glioma, pituitary adenoma, Kaposi's sarcoma, epidermoid cancer, squamous cell cancer, T-cell lymphoma, environmentally induced cancers, combinations of said cancers, and metastatic lesions of said cancers.

In certain embodiments of the methods or uses described herein, the cell is administered in combination with an agent that increases the efficacy of the cell, e.g., one or more of a protein phosphatase inhibitor, a
30 kinase inhibitor, a cytokine, an inhibitor of an immune inhibitory molecule; or an agent that decreases the level or activity of a T_{REG} cell.

In certain embodiments of the methods or uses described herein, the protein phosphatase inhibitor is a SHP-1 inhibitor and/or an SHP-2 inhibitor.

In other embodiments of the methods or uses described herein, kinase inhibitor is chosen from one or more of a CDK4 inhibitor, a CDK4/6 inhibitor (e.g., palbociclib), a BTK inhibitor (e.g., ibrutinib or RN-486), an mTOR inhibitor (e.g., rapamycin or everolimus (RAD001)), an MNK inhibitor, or a dual P13K/mTOR inhibitor. In one embodiment, the BTK inhibitor does not reduce or inhibit the kinase activity of interleukin-2-inducible kinase (ITK).

In other embodiments of the methods or uses described herein, the agent that inhibits the immune inhibitory molecule comprises an antibody or antibody fragment, an inhibitory nucleic acid, a clustered regularly interspaced short palindromic repeats (CRISPR), a transcription-activator like effector nuclease (TALEN), or a zinc finger endonuclease (ZFN) that inhibits the expression of the inhibitory molecule.

In other embodiments of the methods or uses described herein, the agent that decreases the level or activity of the TREG cells is chosen from cyclophosphamide, anti-GITR antibody, CD25-depletion, or a combination thereof.

In certain embodiments of the methods or uses described herein, the immune inhibitory molecule is selected from the group consisting of PD1, PD-L1, CTLA-4, TIM-3, LAG-3, VISTA, BTLA, TIGIT, LAIR1, CD160, 2B4, TGFR beta, CEACAM-1, CEACAM-3, and CEACAM-5.

In other embodiments, the agent that inhibits the inhibitory molecule comprises a first polypeptide comprising an inhibitory molecule or a fragment thereof and a second polypeptide that provides a positive signal to the cell, and wherein the first and second polypeptides are expressed on the CAR-containing immune cells, wherein (i) the first polypeptide comprises PD1, PD-L1, CTLA-4, TIM-3, LAG3, VISTA, BTLA, TIGIT, LAIR1, CD160, 2B4, TGFR beta, CEACAM-1, CEACAM-3, and CEACAM-5 or a fragment thereof; and/or (ii) the second polypeptide comprises an intracellular signaling domain comprising a primary signaling domain and/or a costimulatory signaling domain. In one embodiment, the primary signaling domain comprises a functional domain of CD3 zeta; and/or the costimulatory signaling domain comprises a functional domain of a protein selected from 41BB, CD27 and CD28.

In other embodiments, the cytokine is chosen from IL-7, IL-15, IL-18, or IL-21, or a combination thereof.

In other embodiments, the immune effector cell comprising the fusion protein and a second, e.g., any of the combination therapies disclosed herein (e.g., the agent that that increases the efficacy of the immune effector cell) are administered substantially simultaneously or sequentially.

In other embodiments, the immune cell comprising the fusion protein is administered in combination with a molecule that targets GITR and/or modulates GITR function. In certain embodiments, the molecule targeting GITR and/or modulating GITR function is administered prior to the CAR-expressing cell or population of cells, or prior to apheresis.

In one embodiment, lymphocyte infusion, for example allogeneic lymphocyte infusion, is used in the treatment of the cancer, wherein the lymphocyte infusion comprises at least one CAR-expressing cell of the present invention. In one embodiment, autologous lymphocyte infusion is used in the treatment of the cancer, wherein the autologous lymphocyte infusion comprises at least one CAR-expressing cell

5 described herein.

In one embodiment, the cell is a T cell and the T cell is diacylglycerol kinase (DGK) deficient. In one embodiment, the cell is a T cell and the T cell is Ikaros deficient. In one embodiment, the cell is a T cell and the T cell is both DGK and Ikaros deficient.

10 In one embodiment, the method includes administering a cell expressing the fusion protein comprising a CAR molecule, as described herein, in combination with an agent which enhances the activity of a CAR-expressing cell, wherein the agent is a cytokine, e.g., IL-7, IL-15, IL-18, IL-21, or a combination thereof. The cytokine can be delivered in combination with, e.g., simultaneously or shortly after, administration of the CAR-expressing cell. Alternatively, the cytokine can be delivered after a prolonged period of time after administration of the CAR-expressing cell, e.g., after assessment of the subject's response to the

15 CAR-expressing cell. In one embodiment the cytokine is administered to the subject simultaneously (e.g., administered on the same day) with or shortly after administration (e.g., administered 1 day, 2 days, 3 days, 4 days, 5 days, 6 days, or 7 days after administration) of the cell or population of cells of any of claims 61-80. In other embodiments, the cytokine is administered to the subject after a prolonged period of time (e.g., e.g., at least 2 weeks, 3 weeks, 4 weeks, 6 weeks, 8 weeks, 10 weeks, or more) after

20 administration of the cell or population of cells of any of claims 61-80, or after assessment of the subject's response to the cell.

In other embodiments, the cells expressing a fusion protein comprising a CAR molecule are administered in combination with an agent that ameliorates one or more side effects associated with administration of a cell expressing a CAR molecule. Side effects associated with the CAR-expressing cell can be chosen

25 from cytokine release syndrome (CRS) or hemophagocytic lymphohistiocytosis (HLH).

In embodiments of any of the aforeseaid methods or uses, the cells expressing the CAR molecule are administered in combination with an agent that treats the disease associated with expression of the tumor antigen, e.g., any of the second or third therapies disclosed herein. Additional exemplary combinations include one or more of the following.

30 In another embodiment, the cell expressing the CAR molecule, e.g., as described herein, can be administered in combination with another agent, e.g., a kinase inhibitor and/or checkpoint inhibitor described herein. In an embodiment, a cell expressing the CAR molecule can further express another agent, e.g., an agent which enhances the activity of a CAR-expressing cell.

For example, in one embodiment, the agent that enhances the activity of a CAR-expressing cell can be an agent which inhibits an inhibitory molecule (e.g., an immune inhibitor molecule). Examples of inhibitory molecules include PD1, PD-L1, CTLA-4, TIM-3, CEACAM (e.g., CEACAM-1, CEACAM-3 and/or CEACAM-5), LAG-3, VISTA, BTLA, TIGIT, LAIR1, CD160, 2B4 and TGFR beta.

- 5 In one embodiment, the agent that inhibits the inhibitory molecule is an inhibitory nucleic acid is a dsRNA, a siRNA, or a shRNA. In embodiments, the inhibitory nucleic acid is linked to the nucleic acid that encodes a component of the CAR molecule. For example, the inhibitory molecule can be expressed on the CAR-expressing cell.

- 10 In another embodiment, the agent which inhibits an inhibitory molecule, e.g., is a molecule described herein, e.g., an agent that comprises a first polypeptide, e.g., an inhibitory molecule, associated with a second polypeptide that provides a positive signal to the cell, e.g., an intracellular signaling domain described herein. In one embodiment, the agent comprises a first polypeptide, e.g., of an inhibitory molecule such as PD-1, PD-L1, CTLA-4, TIM-3, CEACAM (e.g., CEACAM-1, CEACAM-3 and/or CEACAM-5), LAG-3, VISTA, BTLA, TIGIT, LAIR1, CD160, 2B4 or TGFR beta, or a fragment of any of
15 these (e.g., at least a portion of the extracellular domain of any of these), and a second polypeptide which is an intracellular signaling domain described herein (e.g., comprising a costimulatory domain (e.g., 41BB, CD27 or CD28, e.g., as described herein) and/or a primary signaling domain (e.g., a CD3 zeta signaling domain described herein). In one embodiment, the agent comprises a first polypeptide of PD1 or a fragment thereof (e.g., at least a portion of the extracellular domain of PD1), and a second polypeptide of
20 an intracellular signaling domain described herein (e.g., a CD28 signaling domain described herein and/or a CD3 zeta signaling domain described herein).

In one embodiment, the cell of the present invention, e.g., T cell or NK cell, is administered to a subject that has received a previous stem cell transplantation, e.g., autologous stem cell transplantation.

- 25 In one embodiment, the cell of the present invention, e.g., T cell or NK cells, is administered to a subject that has received a previous dose of melphalan.

In one embodiment, the cell expressing a fusion protein comprising a CAR molecule, e.g., a CAR molecule described herein, is administered in combination with an agent that increases the efficacy of a cell expressing a CAR molecule, e.g., an agent described herein.

- 30 In one embodiment, the cells expressing a fusion protein comprising a CAR molecule, e.g., a CAR molecule described herein, are administered in combination with a low, immune enhancing dose of an mTOR inhibitor. While not wishing to be bound by theory, it is believed that treatment with a low, immune enhancing, dose (e.g., a dose that is insufficient to completely suppress the immune system but sufficient to improve immune function) is accompanied by a decrease in PD-1 positive T cells or an increase in PD-

1 negative cells. PD-1 positive T cells, but not PD-1 negative T cells, can be exhausted by engagement with cells which express a PD-1 ligand, e.g., PD-L1 or PD-L2.

In an embodiment this approach can be used to optimize the performance of CAR cells described herein in the subject. While not wishing to be bound by theory, it is believed that, in an embodiment, the performance of endogenous, non-modified immune effector cells, e.g., T cells or NK cells, is improved. While not wishing to be bound by theory, it is believed that, in an embodiment, the performance of a target antigen CAR- expressing cell is improved. In other embodiments, cells, e.g., T cells or NK cells, which have, or will be engineered to express a CAR, can be treated ex vivo by contact with an amount of an mTOR inhibitor that increases the number of PD1 negative immune effector cells, e.g., T cells or increases the ratio of PD1 negative immune effector cells, e.g., T cells/ PD1 positive immune effector cells, e.g., T cells.

In an embodiment, administration of a low, immune enhancing, dose of an mTOR inhibitor, e.g., an allosteric inhibitor, e.g., RAD001, or a catalytic inhibitor, is initiated prior to administration of an CAR expressing cell described herein, e.g., T cells or NK cells. In an embodiment, the CAR cells are administered after a sufficient time, or sufficient dosing, of an mTOR inhibitor, such that the level of PD1 negative immune effector cells, e.g., T cells or NK cells, or the ratio of PD1 negative immune effector cells, e.g., T cells/ PD1 positive immune effector cells, e.g., T cells, has been, at least transiently, increased.

In an embodiment, the cell, e.g., T cell or NK cell, to be engineered to express a CAR, is harvested after a sufficient time, or after sufficient dosing of the low, immune enhancing, dose of an mTOR inhibitor, such that the level of PD1 negative immune effector cells, e.g., T cells, or the ratio of PD1 negative immune effector cells, e.g., T cells/ PD1 positive immune effector cells, e.g., T cells, in the subject or harvested from the subject has been, at least transiently, increased.

In one embodiment, the cell expressing a fusion protein comprising a CAR molecule, e.g., a CAR molecule described herein, is administered in combination with an agent that ameliorates one or more side effect associated with administration of a cell expressing a CAR molecule, e.g., an agent described herein.

In one embodiment, the cell expressing a fusion protein comprising a CAR molecule, e.g., a CAR molecule described herein, is administered in combination with an agent that treats the disease associated with a cancer associated antigen as described herein, e.g., an agent described herein.

In one embodiment, a cell expressing two or more fusion proteins comprising CAR molecules, e.g., as described herein, is administered to a subject in need thereof to treat cancer. In one embodiment, a population of cells including a fusion protein comprising a CAR expressing cell, e.g., as described herein, is administered to a subject in need thereof to treat cancer.

In one embodiment, the cell expressing a fusion protein comprising a CAR molecule, e.g., a CAR molecule described herein, is administered at a dose and/or dosing schedule described herein.

In one embodiment, the fusion protein comprising a CAR molecule is introduced into immune effector cells (e.g., T cells, NK cells), e.g., using *in vitro* transcription, and the subject (e.g., human) receives an initial administration of cells comprising a fusion protein comprising a CAR molecule, and one or more subsequent administrations of cells comprising a fusion protein comprising a CAR molecule, wherein the one or more subsequent administrations are administered less than 15 days, e.g., 14, 13, 12, 11, 10, 9, 8, 7, 6, 5, 4, 3, or 2 days after the previous administration. In one embodiment, more than one administration of cells comprising a fusion protein comprising a CAR molecule are administered to the subject (e.g., human) per week, e.g., 2, 3, or 4 administrations of cells comprising a fusion protein comprising a CAR molecule are administered per week. In one embodiment, the subject (e.g., human subject) receives more than one administration of cells comprising a fusion protein comprising a CAR molecule per week (e.g., 2, 3 or 4 administrations per week) (also referred to herein as a cycle), followed by a week of no administration of cells comprising a fusion protein comprising a CAR molecule, and then one or more additional administration of cells comprising a CAR molecule (e.g., more than one administration of the cells comprising a CAR molecule per week) is administered to the subject. In another embodiment, the subject (e.g., human subject) receives more than one cycle of cells comprising a fusion protein comprising a CAR molecule, and the time between each cycle is less than 10, 9, 8, 7, 6, 5, 4, or 3 days. In one embodiment, the cells comprising a fusion protein comprising a CAR molecule are administered every other day for 3 administrations per week. In one embodiment, the cells comprising a fusion protein comprising a CAR molecule are administered for at least two, three, four, five, six, seven, eight or more weeks.

In one embodiment, the cells expressing a fusion protein comprising a CAR molecule, e.g., a CAR molecule described herein, are administered as a first line treatment for the disease, e.g., the cancer, e.g., the cancer described herein. In another embodiment, the cells expressing a fusion protein comprising a CAR molecule, e.g., a CAR molecule described herein, are administered as a second, third, fourth line treatment for the disease, e.g., the cancer, e.g., the cancer described herein.

In one embodiment, a population of cells described herein is administered.

In another aspect, the invention pertains to a cell expressing a fusion protein comprising a CAR molecule described herein for use as a medicament in combination with a kinase inhibitor and/or a checkpoint inhibitor as described herein. In another aspect, the invention pertains to a kinase inhibitor and/or a checkpoint inhibitor described herein for use as a medicament in combination with a cell expressing a CAR molecule described herein.

In another aspect, the invention pertains to a cell expressing a fusion protein comprising a CAR molecule described herein for use in combination with a cytokine, e.g., IL-7, IL-15 and/or IL-21 as described herein,

in the treatment of a disease expressing a tumor antigen targeted by the CAR. In another aspect, the invention pertains to a cytokine described herein for use in combination with a cell expressing a fusion protein comprising a CAR molecule described herein, in the treatment of a disease expressing a tumor antigen targeted by the CAR.

5 In another aspect, the invention pertains to a cell expressing a fusion protein comprising a CAR molecule described herein for use in combination with a kinase inhibitor and/or a checkpoint inhibitor as described herein, in the treatment of a disease expressing a tumor antigen targeted by the CAR. In another aspect, the invention pertains to a kinase inhibitor and/or a checkpoint inhibitor described herein for use in combination with a cell expressing a fusion protein comprising a CAR molecule described herein, in the treatment of a disease expressing a tumor antigen targeted by the CAR.

In another aspect, the present disclosure provides a method comprising administering a fusion protein comprising a CAR molecule, e.g., a CAR molecule described herein, or a cell comprising a nucleic acid encoding a fusion protein comprising a CAR molecule, e.g., a CAR molecule described herein. In one embodiment, the subject has a disorder described herein, e.g., the subject has cancer, e.g., the subject has a cancer and has tumor-supporting cells which express a tumor-supporting antigen described herein. In one embodiment, the subject is a human.

In one embodiment of the methods or uses described herein, the fusion protein comprising CAR molecule is administered in combination with another agent. In one embodiment, the agent can be a kinase inhibitor, e.g., a CDK4/6 inhibitor, a BTK inhibitor, an mTOR inhibitor, a MNK inhibitor, or a dual PI3K/mTOR inhibitor, and combinations thereof. In one embodiment, the kinase inhibitor is a CDK4 inhibitor, e.g., a CDK4 inhibitor described herein, e.g., a CD4/6 inhibitor, such as, e.g., 6-Acetyl-8-cyclopentyl-5-methyl-2-(5-piperazin-1-yl-pyridin-2-ylamino)-8*H*-pyrido[2,3-*d*]pyrimidin-7-one, hydrochloride (also referred to as palbociclib or PD0332991). In one embodiment, the kinase inhibitor is a BTK inhibitor, e.g., a BTK inhibitor described herein, such as, e.g., ibrutinib. In one embodiment, the kinase inhibitor is an mTOR inhibitor, e.g., an mTOR inhibitor described herein, such as, e.g., rapamycin, a rapamycin analog, OSI-027. The mTOR inhibitor can be, e.g., an mTORC1 inhibitor and/or an mTORC2 inhibitor, e.g., an mTORC1 inhibitor and/or mTORC2 inhibitor described herein. In one embodiment, the kinase inhibitor is a MNK inhibitor, e.g., a MNK inhibitor described herein, such as, e.g., 4-amino-5-(4-fluoroanilino)-pyrazolo [3,4-*d*] pyrimidine. The MNK inhibitor can be, e.g., a MNK1a, MNK1b, MNK2a and/or MNK2b inhibitor. The dual PI3K/mTOR inhibitor can be, e.g., PF-04695102.

In one embodiment of the methods or uses described herein, the kinase inhibitor is a CDK4 inhibitor selected from aloisine A; flavopiridol or HMR-1275, 2-(2-chlorophenyl)-5,7-dihydroxy-8-[(3*S*,4*R*)-3-hydroxy-1-methyl-4-piperidinyl]-4-chromenone; crizotinib (PF-02341066; 2-(2-Chlorophenyl)-5,7-dihydroxy-8-[(2*R*,3*S*)-2-(hydroxymethyl)-1-methyl-3-pyrrolidinyl]-4*H*-1-benzopyran-4-one, hydrochloride (P276-00); 1-methyl-5-[[2-[5-(trifluoromethyl)-1*H*-imidazol-2-yl]-4-pyridinyl]oxy]-*N*-[4-

(trifluoromethyl)phenyl]-1*H*-benzimidazol-2-amine (RAF265); indisulam (E7070); roscovitine (CYC202); palbociclib (PD0332991); dinaciclib (SCH727965); N-[5-[(5-*tert*-butyloxazol-2-yl)methyl]thio]thiazol-2-yl]piperidine-4-carboxamide (BMS 387032); 4-[[9-chloro-7-(2,6-difluorophenyl)-5*H*-pyrimido[5,4-*d*][2]benzazepin-2-yl]amino]-benzoic acid (MLN8054); 5-[3-(4,6-difluoro-1*H*-benzimidazol-2-yl)-1*H*-indazol-5-yl]-*N*-ethyl-4-methyl-3-pyridinemethanamine (AG-024322); 4-(2,6-dichlorobenzoylamino)-1*H*-pyrazole-3-carboxylic acid *N*-(piperidin-4-yl)amide (AT7519); 4-[2-methyl-1-(1-methylethyl)-1*H*-imidazol-5-yl]-*N*-[4-(methylsulfonyl)phenyl]-2-pyrimidinamine (AZD5438); and XL281 (BMS908662).

In one embodiment of the methods or uses described herein, the kinase inhibitor is a CDK4 inhibitor, e.g., palbociclib (PD0332991), and the palbociclib is administered at a dose of about 50 mg, 60 mg, 70 mg, 75 mg, 80 mg, 90 mg, 100 mg, 105 mg, 110 mg, 115 mg, 120 mg, 125 mg, 130 mg, 135 mg (e.g., 75 mg, 100 mg or 125 mg) daily for a period of time, e.g., daily for 14-21 days of a 28 day cycle, or daily for 7-12 days of a 21 day cycle. In one embodiment, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12 or more cycles of palbociclib are administered.

In one embodiment of the methods or uses described herein, the kinase inhibitor is a BTK inhibitor selected from ibrutinib (PCI-32765); GDC-0834; RN-486; CGI-560; CGI-1764; HM-71224; CC-292; ONO-4059; CNX-774; and LFM-A13. In one embodiment, the BTK inhibitor does not reduce or inhibit the kinase activity of interleukin-2-inducible kinase (ITK), and is selected from GDC-0834; RN-486; CGI-560; CGI-1764; HM-71224; CC-292; ONO-4059; CNX-774; and LFM-A13.

In one embodiment of the methods or uses described herein, the kinase inhibitor is a BTK inhibitor, e.g., ibrutinib (PCI-32765), and the ibrutinib is administered at a dose of about 250 mg, 300 mg, 350 mg, 400 mg, 420 mg, 440 mg, 460 mg, 480 mg, 500 mg, 520 mg, 540 mg, 560 mg, 580 mg, 600 mg (e.g., 250 mg, 420 mg or 560 mg) daily for a period of time, e.g., daily for 21 day cycle, or daily for 28 day cycle. In one embodiment, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12 or more cycles of ibrutinib are administered.

In one embodiment of the methods or uses described herein, the kinase inhibitor is a BTK inhibitor that does not inhibit the kinase activity of ITK, e.g., RN-486, and RN-486 is administered at a dose of about 100 mg, 110 mg, 120 mg, 130 mg, 140 mg, 150 mg, 160 mg, 170 mg, 180 mg, 190 mg, 200 mg, 210 mg, 220 mg, 230 mg, 240 mg, 250 mg (e.g., 150 mg, 200 mg or 250 mg) daily for a period of time, e.g., daily a 28 day cycle. In one embodiment, 1, 2, 3, 4, 5, 6, 7, or more cycles of RN-486 are administered.

In one embodiment of the methods or uses described herein, the kinase inhibitor is an mTOR inhibitor selected from temsirolimus; ridaforolimus (1*R*,2*R*,4*S*)-4-[(2*R*)-2 [(1*R*,9*S*,12*S*,15*R*,16*E*,18*R*,19*R*,21*R*,23*S*,24*E*,26*E*,28*Z*,30*S*,32*S*,35*R*)-1,18-dihydroxy-19,30-dimethoxy-15,17,21,23, 29,35-hexamethyl-2,3,10,14,20-penta-oxo-11,36-dioxo-4-azatricyclo[30.3.1.0^{4,9}] hexatriaconta-16,24,26,28-tetraen-12-yl]propyl]-2-methoxycyclohexyl dimethylphosphinate, also known as AP23573 and MK8669; everolimus (RAD001); rapamycin (AY22989); simapimod; (5-{2,4-bis[(3*S*)-3-methylmorpholin-4-yl]pyrido[2,3-*d*]pyrimidin-7-yl}-2-methoxyphenyl)methanol (AZD8055); 2-amino-8-[*trans*-4-(2-

hydroxyethoxy)cyclohexyl]-6-(6-methoxy-3-pyridinyl)-4-methyl-pyrido[2,3-*d*]pyrimidin-7(8*H*)-one (PF04691502); and *N*²-[1,4-dioxo-4-[[4-(4-oxo-8-phenyl-4*H*-1-benzopyran-2-yl)morpholinium-4-yl]methoxy]butyl]-L-arginylglycyl-L- α -aspartyl-L-serine- (SEQ ID NO: 982), inner salt (SF1126); and XL765.

In one embodiment of the methods or uses described herein, the kinase inhibitor is an mTOR inhibitor, e.g., rapamycin, and the rapamycin is administered at a dose of about 3 mg, 4 mg, 5 mg, 6 mg, 7 mg, 8 mg, 9 mg, 10 mg (e.g., 6 mg) daily for a period of time, e.g., daily for 21 day cycle, or daily for 28 day cycle. In one embodiment, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12 or more cycles of rapamycin are administered. In one embodiment, the kinase inhibitor is an mTOR inhibitor, e.g., everolimus and the everolimus is administered at a dose of about 2 mg, 2.5 mg, 3 mg, 4 mg, 5 mg, 6 mg, 7 mg, 8 mg, 9 mg, 10 mg, 11 mg, 12 mg, 13 mg, 14 mg, 15 mg (e.g., 10 mg) daily for a period of time, e.g., daily for 28 day cycle. In one embodiment, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12 or more cycles of everolimus are administered.

In one embodiment of the methods or uses described herein, the kinase inhibitor is an MNK inhibitor selected from CGP052088; 4-amino-3-(p-fluorophenylamino)-pyrazolo [3,4-*d*] pyrimidine (CGP57380); cercosporamide; ETC-1780445-2; and 4-amino-5-(4-fluoroanilino)-pyrazolo [3,4-*d*] pyrimidine.

In one embodiment of the methods or uses described herein, the kinase inhibitor is a dual phosphatidylinositol 3-kinase (PI3K) and mTOR inhibitor selected from 2-Amino-8-[trans-4-(2-hydroxyethoxy)cyclohexyl]-6-(6-methoxy-3-pyridinyl)-4-methyl-pyrido[2,3-*d*]pyrimidin-7(8*H*)-one (PF-04691502); N-[4-[[4-(Dimethylamino)-1-piperidinyl]carbonyl]phenyl]-N'-[4-(4,6-di-4-morpholinyl-1,3,5-triazin-2-yl)phenyl]urea (PF-05212384, PKI-587); 2-Methyl-2-{4-[3-methyl-2-oxo-8-(quinolin-3-yl)-2,3-dihydro-1*H*-imidazo[4,5-*c*]quinolin-1-yl]phenyl}propanenitrile (BEZ-235); apitolisib (GDC-0980, RG7422); 2,4-Difluoro-N-[2-(methyloxy)-5-[4-(4-pyridazinyl)-6-quinolinyl]-3-pyridinyl]benzenesulfonamide (GSK2126458); 8-(6-methoxypyridin-3-yl)-3-methyl-1-(4-(piperazin-1-yl)-3-(trifluoromethyl)phenyl)-1*H*-imidazo[4,5-*c*]quinolin-2(3*H*)-one Maleic acid (NVP-BGT226); 3-[4-(4-Morpholinylpyrido[3',2':4,5]furo[3,2-*d*]pyrimidin-2-yl]phenol (PI-103); 5-(9-isopropyl-8-methyl-2-morpholino-9*H*-purin-6-yl)pyrimidin-2-amine (VS-5584, SB2343); and N-[2-[(3,5-Dimethoxyphenyl)amino]quinoxalin-3-yl]-4-[(4-methyl-3-methoxyphenyl)carbonyl]aminophenylsulfonamide (XL765).

In one embodiment of the methods or uses described herein, a cell comprising a fusion protein described herein is administered to a subject in combination with a protein tyrosine phosphatase inhibitor, e.g., a protein tyrosine phosphatase inhibitor described herein. In one embodiment, the protein tyrosine phosphatase inhibitor is an SHP-1 inhibitor, e.g., an SHP-1 inhibitor described herein, such as, e.g., sodium stibogluconate. In one embodiment, the protein tyrosine phosphatase inhibitor is an SHP-2 inhibitor.

In one embodiment of the methods or uses described herein, a cell comprising a fusion protein described herein is administered in combination with another agent, and the agent is a cytokine. The cytokine can

be, e.g., IL-7, IL-15, IL-21, or a combination thereof. In another embodiment, a cell comprising a fusion protein described herein is administered in combination with a checkpoint inhibitor, e.g., a checkpoint inhibitor described herein. For example, in one embodiment, the check point inhibitor inhibits an inhibitory molecule selected from PD-1, PD-L1, CTLA-4, TIM-3, CEACAM (e.g., CEACAM-1, CEACAM-3 and/or
5 CEACAM-5), LAG-3, VISTA, BTLA, TIGIT, LAIR1, CD160, 2B4 and TGFR beta.

In one aspect, the fusion protein described herein can be used to eradicate a normal cell that express a tumor antigen as described herein, thereby applicable for use as a cellular conditioning therapy prior to cell transplantation. In one aspect, the normal cell that expresses a tumor antigen as described herein is a normal stem cell and the cell transplantation is a stem cell transplantation.

10 METHODS OF TREATMENT OF AUTOANTIBODY OR ALLOANTIBODY CONDITIONS

The present invention includes methods for treating autoantibody or alloantibody diseases or conditions in a subject by targeting B cells, including the autoantibody or alloantibody producing B cells, with anti-B cell modified T cells. In one embodiment, after B cell depletion by the modified T cells, or following the onset of an adverse reaction to the modified T cells, the modified T cells are then selectively ablated in the
15 subject by activating a suicide gene that has been inserted into the modified T cells.

In one aspect, the invention includes a method for treating an autoantibody or alloantibody disease or condition in a subject in need thereof comprising administering an effective amount of a pharmaceutical composition comprising a modified T cell to the subject. The modified T cell comprises a nucleic acid comprising a suicide gene and a nucleic acid encoding a chimeric antigen receptor comprising an anti-B
20 cell binding domain, a transmembrane domain, a costimulatory domain and an intracellular signaling domain.

In one embodiment, the method further comprises inducing expression of the suicide gene to produce a suicide gene product that induces cell death of the modified T cell. In one such embodiment, administering an inducing agent induces expression of the suicide gene. In another embodiment,
25 inducing expression of the suicide gene occurs after the modified T cell exerts cytotoxic function against B cells or after an onset of an adverse reaction in the subject to the modified T cell.

In another embodiment, the method further comprises activating a suicide gene product of the suicide gene to induce cell death of the modified T cell. In one such embodiment, administering an activating agent to promote dimerization of the suicide gene product to activate the suicide gene product. In
30 another embodiment, activating the suicide gene product occurs after the modified T cell exerts cytotoxic function against B cells or after an onset of an adverse reaction in the subject to the modified T cell or after therapeutic effect is achieved.

In yet another embodiment, the method further comprises inhibiting expression of the suicide gene to inhibit cell death of the modified T cell. In one such embodiment, administering an inhibiting agent inhibits expression of the suicide gene. In another embodiment, administering the inhibiting agent occurs concurrently with administration of the modified T cell and continues as the modified T cell exerts cytotoxic function against B cells and may be ceased after an onset of an adverse reaction in the subject to the modified T cell.

In still another embodiment, the method comprises repressing activation of a suicide gene product of the suicide gene to repress cell death of the modified T cell. In one such embodiment, administering a solubilizing agent prevents dimerization of the suicide gene product to prevent activation the suicide gene product. In another embodiment, administering the solubilizing agent occurs concurrently with administration of the modified T cell and continues as the modified T cell exerts cytotoxic function against B cells and may be ceased after an onset of an adverse reaction in the subject to the modified T cell or after therapeutic effect is achieved.

In yet another embodiment, the method further comprises administering a solubilizing agent to prevent dimerization of the CAR, wherein the CAR is linked to a dimerization domain, such as a dimerization domain of FKBP or similar molecule. In such an embodiment, the CAR molecules spontaneously aggregate in the cytoplasm or other internal location, thereby preventing presentation of the CAR molecules on the surface of the modified T cell. In another embodiment, administering the solubilizing agent occurs concurrently with administration of the modified T cell and continues as the modified T cell exerts cytotoxic function against B cells and may be ceased after an onset of an adverse reaction in the subject to the modified T cell or after therapeutic effect is achieved.

The modified T cells can be administered to an animal, preferably a mammal, even more preferably a human, to suppress an immune reaction, such as those common to an autoimmune disease or condition or an alloantibody disease or condition.

In addition, the modified T cells of the present invention can be used for the treatment of any condition in which a diminished or otherwise inhibited immune response, especially a cell-mediated immune response, is desired in order to treat or alleviate the disease. In one aspect, the invention includes treating a condition, such as an autoantibody or alloantibody disease, in a subject, comprising administering to the subject a therapeutically effective amount of a pharmaceutical composition comprising the modified T cell described herein.

Examples of autoantibody diseases or conditions include, but are not limited to, bullous pemphigoid, epidermolysis bullosa acquisita, p200 pemphigoid, linear IgA bullous dermatosis, other pemphigoid group diseases, dermatitis herpetiformis, celiac disease, myasthenia gravis, Goodpasture's syndrome, granulomatosis with polyangiitis and other ANCA+ vasculitides, autoimmune limbic encephalitis, anti-N-methyl-D-aspartate receptor encephalitis, neuromyelitis optica, autoimmune hemolytic anemia,

autoantibody-associated end-organ damage in lupus and other connective tissue diseases (due to anti-dsDNA, anti-Ro, and other autoantibodies), Graves' and Hashimoto's thyroiditis, anti-insulin antibodies in diabetes, anti-insulin receptor antibodies in autoimmune hypoglycemia, cryoglobulinemia, rheumatoid arthritis, multiple sclerosis, Sjogren's syndrome, dermatomyositis, anti-Fc-epsilon receptor antibodies in chronic idiopathic urticaria, anti-folate receptor antibodies, anti-endothelial receptor or anti-adrenergic receptor antibodies in pulmonary arterial hypertension, refractory hypertension, dilated cardiomyopathy, and an autoinflammatory syndrome.

An example of alloantibody disease or condition, includes, but are not limited to, an immune reaction resulting from organ transplant, blood transfusion and production of donor-specific HLA and/or b2-microglobulin antibodies, pregnancy sensitization against blood group or Rh antigens or protein replacement therapy, such as with Factor VIII, α -L-iduronidase, type VII collagen, etc. including, but not limited to, the replacement proteins listed in Gorzelany, et al. (Sci. Transl. Med., 5(178):178s10, 2013).

In one embodiment, the disease or condition is pemphigus. Longitudinal analysis of B cell repertoires in pemphigus patients during treatment has shown that pemphigus patients relapse with the same anti-Dsg B cell clones observed in active disease. Collectively these data indicate that a single, but truly complete, B cell depletion eliminating all anti-Dsg B cell clones by targeting a pan-B cell marker, such as CD20 or alternatively CD19, may be curative in pemphigus patients. The pathologic clones will be eliminated, a healthy B cell repertoire will reform, and another rare break in tolerance is unlikely to recur.

By analogy, this same approach should also be effective for any B-cell or antibody-mediated disease; for example diseases caused by alloantibodies resulting from blood transfusion or sensitization during pregnancy, donor-specific HLA alloantibodies that complicate organ transplant, and alloantibodies resulting from protein replacement therapy for genetic diseases. Even if alloantibodies recur due to re-exposure to alloantigen, intermittent re-treatment to completely, but transiently, eliminate B cells (and consequently alloantibodies) will be beneficial in these diseases.

PHARMACEUTICAL COMPOSITIONS

Pharmaceutical compositions of the present disclosure may comprise any fusion protein, nucleic acid encoding such a fusion protein, as described herein, and one or more pharmaceutically or physiologically acceptable carriers, diluents or excipients. Such compositions may comprise buffers such as neutral buffered saline, phosphate buffered saline and the like; carbohydrates such as glucose, mannose, sucrose or dextrans, mannitol; proteins; polypeptides or amino acids such as glycine; antioxidants; chelating agents such as EDTA or glutathione; adjuvants (e.g., aluminum hydroxide); and preservatives. Compositions of the present disclosure are in one aspect formulated for intravenous administration.

Pharmaceutical compositions of the present disclosure may be administered in a manner appropriate to the disease to be treated (or prevented). The quantity and frequency of administration will be determined by such factors as the condition of the patient, and the type and severity of the patient's disease, although appropriate dosages may be determined by clinical trials.

5 In one aspect, the invention includes a pharmaceutical composition formulated for use in the method as described herein, the composition comprising a modified T cell comprising a nucleic acid encoding a suicide gene and a nucleic acid encoding a chimeric antigen receptor comprising an anti-B cell binding domain, a transmembrane domain, a costimulatory domain and an intracellular signaling domain.

10 In another aspect, the invention includes a pharmaceutical composition formulated for use in the method as described herein, the composition comprising a modified T cell comprising a nucleic acid encoding a dimerization domain and a chimeric antigen receptor (CAR) comprising an anti-B cell binding domain, a transmembrane domain, a costimulatory domain and an intracellular signaling domain

15 In one embodiment, the pharmaceutical composition is substantially free of, e.g., there are no detectable levels of a contaminant, e.g., selected from the group consisting of endotoxin, mycoplasma, replication competent lentivirus (RCL), p24, VSV-G nucleic acid, HIV gag, residual anti-CD3/anti-CD28 coated beads, mouse antibodies, pooled human serum, bovine serum albumin, bovine serum, culture media components, vector packaging cell or plasmid components, a bacterium and a fungus. In one embodiment, the bacterium is at least one selected from the group consisting of *Alcaligenes faecalis*, *Candida albicans*, *Escherichia coli*, *Haemophilus influenza*, *Neisseria meningitidis*, *Pseudomonas*
20 *aeruginosa*, *Staphylococcus aureus*, *Streptococcus pneumonia*, and *Streptococcus pyogenes* group A.

When "an immunologically effective amount," "an anti-tumor effective amount," "a tumor-inhibiting effective amount," or "therapeutic amount" is indicated, the precise amount of the compositions of the present disclosure to be administered can be determined by a physician with consideration of individual differences in age, weight, tumor size, extent of infection or metastasis, and condition of the patient
25 (subject). It can generally be stated that a pharmaceutical composition comprising the immune effector cells (e.g., T cells, NK cells) described herein may be administered at a dosage of 10^4 to 10^9 cells/kg body weight, in some instances 10^5 to 10^6 cells/kg body weight, including all integer values within those ranges. T cell compositions may also be administered multiple times at these dosages. The cells can be administered by using infusion techniques that are commonly known in immunotherapy (see, e.g.,
30 Rosenberg et al., New Eng. J. of Med. 319:1676, 1988).

In certain aspects, it may be desired to administer activated immune effector cells (e.g., T cells, NK cells) to a subject and then subsequently redraw blood (or have an apheresis performed), activate immune effector cells (e.g., T cells, NK cells) therefrom according to the present invention, and reinfuse the patient with these activated and expanded immune effector cells (e.g., T cells, NK cells). This process can be
35 carried out multiple times every few weeks. In certain aspects, immune effector cells (e.g., T cells, NK

cells) can be activated from blood draws of from 10cc to 400cc. In certain aspects, immune effector cells (e.g., T cells, NK cells) are activated from blood draws of 20cc, 30cc, 40cc, 50cc, 60cc, 70cc, 80cc, 90cc, or 100cc.

5 The administration of the subject compositions may be carried out in any convenient manner, including by aerosol inhalation, injection, ingestion, transfusion, implantation or transplantation. The compositions described herein may be administered to a patient transarterially, subcutaneously, intradermally, intratumorally, intranodally, intramedullary, intramuscularly, by intravenous (i.v.) injection, or intraperitoneally. In one aspect, the cell compositions of the present disclosure are administered to a patient by intradermal or subcutaneous injection. In one aspect, the cell compositions of the present
10 disclosure are administered by i.v. injection. The compositions of immune effector cells (e.g., T cells, NK cells) may be injected directly into a tumor, lymph node, or site of infection.

In a particular exemplary aspect, subjects may undergo leukapheresis, wherein leukocytes are collected, enriched, or depleted ex vivo to select and/or isolate the cells of interest, e.g., T cells. These T cell isolates may be expanded by methods known in the art and treated such that one or more CAR
15 constructs of the invention may be introduced, thereby creating a CAR T cell of the invention. Subjects in need thereof may subsequently undergo standard treatment with high dose chemotherapy followed by peripheral blood stem cell transplantation. In certain aspects, following or concurrent with the transplant, subjects receive an infusion of the expanded CAR T cells of the present invention. In an additional aspect, expanded cells are administered before or following surgery.

20 The dosage of the above treatments to be administered to a patient will vary with the precise nature of the condition being treated and the recipient of the treatment. The scaling of dosages for human administration can be performed according to art-accepted practices.

EXAMPLES

25 EXAMPLE 1: MATERIALS AND METHODS FOR EXAMPLES 1-13.

Constructs

The following constructs shown in Table 22 were used in Examples 1-13.

Note that the invention encompasses both orientations of heavy and light chain.

30 **Table 22.** Sequences of various constructs (in bold is the signal peptide used; underlined> are the furin cleavage sites.)

Construct	Protein Sequence	DNA sequence
-----------	------------------	--------------

ER _{mut} _Furin_ Flexi-12	MALPVTALLPLALLHAARPR SSLALSLTADQMVSALLDAEPP LYSEYDPTRPFSEASMMGLLTN LADRELVHMINWAKRVPGFVDL ALHDQVHLLLECAWMEILMIGLV WRSMEHPGKLLFAPNLLLDNRQ GKCVEGGVEIFDMLLATSSRFR MMNLQGEEFVCLKSIILLNSGVY TFLSSTLKSLEEKDHIHRVLDKIT DTLIHLMAGLTLQQQHQRRLA QLLLILSHIRHMSSSRMEHLYSM KCKNVVPLSDLLLEMLDAHRLR <u>TKRIWELKKDVVVVELDWYPDA</u> PGEMVVLTCDTPEEDGITWTLD QSSEVLGSGKTLTIQVKEFGDA GQYCHKGGEVLSHSLLLHKK EDGEWSTDILKDQKEPKNKTFLR CEAKNYSGRFTCWWLTISTDL TFSVKSSRGSSDPQGVTCGAAT LSAERVVRGDNKEYEYSVEQCED SACPAAEESLPIEVMVDAVHKLK YENYTSSFFIRDIKPDPPKNLQL KPLKNSRQVEVSWEYPDTWST PHSYFSLTFCVQVQGKSKREKK DRVFTDKTSATVICRKNASISVR AQDRYYSSSWSEWASVPCSGG GSGGGSGGGSRLNPVATPDGP MFPCLHHSQNLLRAVSNNMLQKA RQTLEFYPTSEEIDHEDITKDK TSTVEACLPLELTKNESCLNSRE TSFITNGSCLASRKTSFMMALCL SSIYEDLKMYQVEFKTMNAKLL MDPKRQIFLDQNMLAVIDELMQ ALNFNSETVPQKSSLEEPDFYK TKIKLCILLHAFRIRAVTIDRVMSY LNAS (SEQ ID NO: 48)	atggccctccctgtcaccgccctgtgcttccgtggctcttctgctc cacgccgctcggccccgggtcgtggtggcactttccctgactgccg accagatgggtgcgcccttctggacgccgagcctccaattctgta ctcggagtacgatccgactcgccttctccgaagccagcatgat gggcctgttgactaacctggcgaccgcgagtggtgcacatgatt aactgggctaagcgggtgccgggttcgtggacctggccctgca cgaccaagtgcacctcctggaatgcgcctggatggaaatcctcat gatcggcctcgtgtggagatccatggagcatcccggaagctcct gttgcacccaacctcctgcttgatcgcaaccaggggaaaatgctg ggaaggggggtgcgagatttcgacatgctgctgccacctctcc cggttccggatgatgaatctgcaggggagaagagtctgtgtctga agtcaatcatcctgctgaactccggggtctatacctctgagctcg acctcaagtactggaggaaaaagaccacatccatcgctgct cgataagatcacgcacaccttatccatctatggcgaaggctgg actgacctgcaacagcagcaccagaggctggcccagttgctgc tgattctgagccacatccggcacatgctgtccaagaggatggaac acctgtacagcatgaagtgaagaacgtcgtgcctctgtccgatct gctcctggaaatgctggacgcgcacagactccgtactaaaaga (SEQ ID NO: 49)
linker	GGGSGGGSGGGSRLNPV (SEQ ID NO: 52)	gtggtggcggtggaagcggcggtggcgaagcggcggtggcg gcagcagaaacctccccgtgg (SEQ ID NO: 53)
FKBP L106P	GVQVETISPGDGRTFPRKGQTC VVHYTGMLDGGKKVDSSRDNR KPFKFM LGKQEVIRGWEEGVAQ MSVGQRAKLTISPDYAYGATGH PGIIPPHATLVFDVELLKPE (SEQ ID NO: 56)	
DHFR R12Y/G27S/ Y100I	ISLIAALAVDYVIGMENAMPWNL PADLAWFKRNTLNKPVIMGRHT WESIGRPLPGRKNIILSSQPSTD DRVTWVKSVDIAAACGDVPEI MVIGGGRVIEQFLPKAQKLYLTH IDAEVEGDTHFPDYEPDDWESV FSEFHDADAQNHSYCFEILER R (SEQ ID NO: 57)	
ER	RSSLALSLTADQMVSALLDAEP	

T371A_L384 M_M421G_N 519S_G521R _Y537S	PILYSEYDPTRPFSEASMMGLLT NLADRELVHMINWAKRVPGFVD LALHDQVHLLCAWMEILMIGLV WRSMEHPGKLLFAPNLLDRNQ GKCVEGGVEIFDMLLATSSRFR MMNLQGEEFVCLKSIILLNSGVY TFLSSTLKSLEEKDHIHRVLDKIT DTLIHLMAGLTLQQQHQRRLA QLLLILSHIRHMSSKRMEHLYSM KCKNVVPLSDLLLEMLDAHRL (SEQ ID NO: 1119)	
CG#c43 FKBP _{mut} _HA_ Furin_CAR19	MALPVTALLPLALLLHAARPG VQVETISPGDGRTPFKRGQTCV VHYTGMLLEDGKKVDSSRDRNK PFKFM LGKQEVIRGWEEGVAQ MSVGQRAKL TISPDYAYGATGH PGIIPPHATLVFDVELLKPEYPYD VPDYAFPVDRTKREIVMTQSPA TSLSPGERATLSCRASQDISKY LNWYQQKPGQAPRLIYHTSRL HSGIPARFSGSGSGTDYTLTISS LQPEDFAVYFCQQGNTLPYTFG QGKLEIKGGGSGGGSGGGSGGG GSQVQLQESGPGLVKPSSETLSL TCTVSGVSLPDYGVSWIRQPPG KGLEWIGVIWGSETTYSSSLKS RVTISKDNSKNQVSLKLSSVTAA DTAVYYCAKHYYYGGSYAMDY WGQGT LVTVSSTTTPAPRPPTP APTIASQPLSLRPEACRPAAGG AVHTRGLDFACDIYIWAPLAGTC GVLLLSLVITLYCKRGRKKLLYIF KQPFMRPVQTTQEEDGCSCRF PEEEEGGCELRVKFSRSADAPA YKQGQNQLYNELNLGRREEYD VLDKRRGRDPEMGGKPRRKNP QEGLYNELQKDKMAEAYSEIGM KGERRRGKGHGDL YQGLSTAT KDTYDALHMQALPPR (SEQ ID NO: 59)	atggccctccctgtcaccgccctgtcgtctccgctggctcttctgctc cacgccgctcggcccgagtgaggtggaaccatctccccag gagacgggcgccaccttccccaaagcgcgccagacctgtgtgtg gcactacaccgggatgttgaagatggaagaaagtcgattcct cccggaacagaaacaagcccttaagttatgctaggcaagcag gaggtgatccgaggtcgggaagaaggggtgccagatgagtg tgggtcagagagccaaactgactatactccagattatgcctatgg tgccactgggcacccaggcatcatccaccacatgccactctcgt cttcgatgtggagcttctaaaaccggaatacccttatgatgttctg attatgcttccccgtggatcgtactaaaagagaaattgtgatgacc cagtcacccgccactcttagccttccaccggtagcgcgcaacc ctgtcttcagagcctccaagacatctcaaaatcccttaattggtgta tcaacagaagcccgacaggtcctcgccttctgatctaccacac cagccggtcctcattctggaatccctgccagggtcagcggtagcgg atctgggacgcactacaccctcactatcagctcactgcagccaga ggacttcgctgtctatttctgtcagcaagggaacaccctgccctac accttggacagggcaccaagctcgagattaaagggtggaggtgg cagcggaggaggtgggtccggcggtggaggaagccaggtcca actccaagaaagcggaccgggtcttgaagccatcagaaactc ttcactgactgtactgtgagcggagtgctctccccgattacgggg tgtcttgatcagacagccaccggggaaggggtctggaatggattg gagtgattggggctctgagactactactactcttcatccctcaagt cacgcgtcaccatctcaaaggacaactctaagaatcagggtgtca ctgaaactgtcatctgtgaccgcagccgacaccgcccgtgtactatt gcgctaagcattactattatggcgggagctacgcaatggattactg gggacaggggtactctggtcaccgtgtccagcaccactacccag caccgagggccacccaccccggtcctaccatcgctcccagcct ctgtccctgctccggaggtcatgtagaccgcagctgggtggggc cgtgcatacccggggtcttgactcgctgcgatctacatttggg cccctctggctggtacttgccgggtcctgtcgttctcactcgtgatca ctcttactgtaagcgcggtcggaagaagctgtgtacatcttaag caaccctcatgaggcctgtgcagactactcaagaggaggacgg ctgttcattgcgggtcccagaggaggaggaaggcggtcgcgaa ctgcgcgtgaaattcagccgcagcgcagatgtccagcctacaa gcaggggcagaaaccagctctacaacgaactcaatcttggtcgga gagaggagtacgacgtgctggacaagcggagaggacgggac ccagaaatggcggggaagccgcgcagaaagaatccccaaaga gggctctgtacaacgagctccaaaaggataagatggcagaagc ctatagcgagattggtatgaaaggggaacgcagaaagggcaa aggccacgacggactgtaccagggactcagcaccgccaccaa ggacacctatgacgctcttcacatgcaggccctgcgcctcgg (SEQ ID NO: 60)
CG#c44 FKBP _{mut} _HA_Furinmu	MALPVTALLPLALLLHAARPG VQVETISPGDGRTPFKRGQTCV VHYTGMLLEDGKKVDSSRDRNK	atggccctccctgtcaccgccctgtcgtctccgctggctcttctgctc cacgccgctcggcccgagtgaggtggaaccatctccccag gagacgggcgccaccttccccaaagcgcgccagacctgtgtgtg

t_CAR19	PFK FMLGKQEVIRGWEEGVAQ MSVGQRAKL TISPDYAYGATGH PGIIPPHATLVFDVELLKPEYPYD VPDYAFPVDATKREIVMTQSPA TSLSPGERATLSCRASQDISKY LNWYQQKPGQAPRLLIYHTSRL HSGIPARFSGSGSGTDYTLTISS LQPEDFAVYFCQQGNTPYTFG QGTKLEIKGGGSGGGSGGG GSQVQLQESGPGLVKPSSETLSL TCTVSGVSLPDYGVSWIRQPPG KGLEWIGVIWGSETTYSSSLKS RVTISKDNSKNQVSLKLSSVTAA DTAVYYCAKHYYGGSYAMDY WGQGLTVTSSTTTPAPRPPTP APTIASQPLSLRPEACRPAAGG AVHTRGLDFACDIYWAPLAGTC GVLLLSLVITLYCKRGRKKLLYIF KQPFMRPVQTTQEEDGCSCRF PEEEEGGCEL RVKFSRSADAPA YKQGQNQLYNELNLGRREEYD VLDKRRGRDPEMGGKPRRKNP QEGLYNELQKDKMAEAYSEIGM KGERRRGK GHDGLYQGLSTAT KDTYDALHMQALPPR (SEQ ID NO: 61)	gcactacaccgggatgctgaagatggaagaaagtcgattcct cccgggacagaaacaagcccttaagttatgctaggcaagcag gagggtgatccgaggctggaagaaggggtgccagatgagtg tgggtcagagagccaaactgactatatctccagattatgcctatgg tgccactgggcacccaggcatcatccaccacatgccactctcgt cttcgatgtggagcttctaaaaccggaatacccttatgatgttcctg attatgctttcccggtggatgtactaaaagagaaattgtgatgacc cagtcaccccgccactcttagccttcacccgggtgagcgcaacc ctgtcttcagagcctccaagacatctcaaaatacccttaattggtat caacagaagcccgacaggctcctgccttctgatctaccacac cagccggctccattctggaatccctgccagggtcagcggtagcgg atctgggaccgactacaccctcactatcagctcactgcagccaga ggacttcgctgtctatttctgtcagcaagggaacaccctgccctac accttggacagggcaccaagctcagattaaagggtggagggtg cagcggaggagggtgggtccggcggtggaggaagccagggtcca actccaagaaagcggaccgggtcttgaagccatcagaaactc ttcactgactgtactgtgagcggagtgctctcccgattacgggg tgcttgatcagacagccaccggggaagggtctggaatggattg gagtgatttgggctctgagactactactactcttccctcaagt cacgcgtcaccatctcaaaggacaactcaagaatcagggtgta ctgaaactgtcatctgtgaccgcagccgacccgctgtactatt gcgctaagcattactattatggcgaggctacgcaatggactactg gggacaggggtactctggtcaccgtgtccagcaccactacccag caccgaggccacccaccccggtcctaccatgcctcccagcct ctgtccctgcgtccggaggcatgtagaccgcagctgggtgggc cgtgcatacccggggtctgacttcgctgcgatactacatttggg cccctctggctggtacttgcggggctcgtgctttcactcgtgatca ctcttactgtaagcgcggtcgggaagaagctgctgtacatcttaag caaccctcatgaggcctgtgcagactactcaagaggaggacgg ctgttcacgtccggttccagaggaggaggaaggcggtcgcgaa ctgcgcgtgaaattcagccgcagcgcagatgtccagcctacaa gcaggggcagaaccagctctacaacgaactcaatcttggtcgga gagaggagtacgacgtgctggacaagcggagaggacgggac ccagaaatgggcggaagccgcgcagaaagaatccccaaga gggctctgtacaacgagctccaaaaggataagatggcagaagc ctatagcgagattggtatgaaaggggaacgcagaagaggcaa aggccacgacggactgtaccagggtactcagaccgccaccaa ggacacctatgacgctcttcacatgcaggccctgccgcctcgg (SEQ ID NO: 62)
CG#c45 DHFR _{mut} _HA _Furin_CAR1 9	MALPVTALLLPLALLLHAARPIS LIAALAVDYVIGMENAMPWNLP DLAWFKRNTLNKPVIMGRHTWE SIGRPLPGRKNILSSQPSTDDR VTWVKSVD EIAACGDVPEIMVI GGGRVIEQFLPKAQKLYLTHIDA EVEGDTHFPDYEPDDWESVFS EFHDADAQNSHSHSYCFEILERRY PYDVPDYAFPVDRTKREIVMTQ SPATLSLSPGERATLSCRASQDI SKYLNWYQQKPGQAPRLLIYHT SRLHSGIPARFSGSGSGTDYTL TISSLQPEDFAVYFCQQGNTPY TFGQGTKLEIKGGGSGGGGS GGGSGSQVQLQESGPGLVKPSE TSLTCTVSGVSLPDYGVSWIR QPPGKGLEWIGVIWGSETTYYS	atggccctccctgtcaccgcctgtgcttccgctggctcttctgctc cacgcgcgtcggccatctctctgattgccgctctggcgtggact acgtgatcgggatggaacacgctatgccatggaatctgcccgcc gatctggcttgggtcaagaggaaacacccctgaacaagccagtgtat catgggcagacacacttgggagtcattggccggccctgcctg gacgcaagaacatcattctgagctccagccctctaccgacgac agggtgacatgggtgaaaagtgtggacgaagccattgccgctg cggagatgtgccgagatcatggtatcggcggaggaggagagtg atcgagcagttcctgcctaaggccagaaactgtactgtactcac attgacgtgagggtgaaggggacacccatttctgattatgagc cagacgattgggaaagcgtgttctccgagtttcacgacgccgatg ctcagaactctcatagttattgcttgagatctggaaaggagatac ccttatgatgttctgattatgcttcccggtggatcgtactaaaaga gaaattgtgatgaccagtcacccgccactcttagccttcacccg gtgagcgcgcaaccctgtctgagagcctccaagacatctca aaataccttaattggtatcaacagaagcccgacaggctcctcgc cttctgatctaccacaccagccggctccattctggaatccctgcc

	SSLKSRVTISKDNSKNQVSLKLS SVTAADTAVYYCAKHYYYGGSY AMDYWGQGLTVTSSTTTPAP RPPTPAPTIASQPLSLRPEACRP AAGGAVHTRGLDFACDIYWAPL AGTCGVLLLSLVITLYCKRGRKK LLYIFKQPFMRPVQTTQEEDGC SCRFPEEEEEGGCEL RVKFSRSA DAPAYKQGQNQLYNELNLGRR EEYDVLDKRRGRDPEMGGKPR RKNPQEGLYNELQKDKMAEAY SEIGMKGERRRGKGHDGLYQG LSTATKDTYDALHMQALPPR (SEQ ID NO: 63)	ggttcagcggtagcggatctgggaccgactacacctcactatca gctcactgcagccagaggacttcgctgtctatttctgtcagcaagg gaacacctgccctacacctttggacagggcaccagctcgag attaaagggtggaggtggcagcggaggaggtgggtccggcgggtg gaggaagccaggtccaactccaagaaagcggaccgggtctgt gaagccatcagaaactcttctactgactgtactgtgagcggagtg tcttccccgattacgggggtcttggatcagacagccaccgggg aagggtctggaatggattggagtgattggggctctgagactact actactctcatccctcaagtcacgcgtcaccatctcaaaggacaa ctctaagaatcagggtgtcactgaaactgtcatctgtgaccgcagcc gacaccgccgtgtactattgcgctaagcattactattatggcggga gctacgcaatggattactggggacaggggtactctgtgtaccgtgt ccagcaccactaccccagcaccgaggccacccacccggctc ctaccatgcctcccagcctctgtccctgcgtccggaggcatgtag accgcgagctggtggggccgtgcataccgggggtctgtacttcgc ctgcgatactacatttggccccctctggtggtacttgcgggtcct gctgcttctactcgtgatcactcttactgtaagcgggtcggaaga agctgctgtacatcttaagcaaccttcatgaggcctgtgcagact actcaagaggaggacggctgttcatgcgggttcccagaggagg aggaaggcggctgcgaactgcgcgtgaaattcagccgcagcgc agatgctccagcctacaagcaggggcagaccagctctacaac gaactcaatcttggtcggagagaggtacgacgtgctggacaa gaggagaggacgggacccagaaatggcggggaagccgcgc agaaagaatccccaagagggtctgtacaacgagctccaaaag gataagatggcagaagcctatagcgagattggtatgaaagggg aacgcagaagaggcaaaggccacgacggactgtaccagggga ctcagcaccgccaccaaggacacctatgacgtcttcacatgca ggccctgcgcctcgg (SEQ ID NO: 64)
CG#c46 DHFR_{mut} _HA_Furinmu t_CAR19	MALPVTALLLPLALLLHAARPIS LIAALAVDYVIGMENAMPWNLP DLAWFKRNTLNKPVIMGRHTWE SIGRPLPGRKNILSSQPSTDDR VTWVKSVDEAIAACGDVPEIMVI GGGRVIEQFLPKAQKLYLTHIDA EVEGDTHFPDYEPDDWESVFS EFHDADAQNSHSYCFEILERRY PYDVPDYAFPVDATKREIVMTQ SPATLSLSPGERATLSRASQDI SKYLNWYQQKPGQAPRLLIYHT SRLHSGIPARFSGSGSGTDYTL TISSLQPEDFAVYFCQQGNTLPY TFGQGTKLEIKGGGSGSGGGS GGGSQVQLQESGPGLVKPSE TSLTCTVSGVSLPDYGVSWIR QPPGKGLEWIGVIWGSETTYYS SSLKSRVTISKDNSKNQVSLKLS SVTAADTAVYYCAKHYYYGGSY AMDYWGQGLTVTSSTTTPAP RPPTPAPTIASQPLSLRPEACRP AAGGAVHTRGLDFACDIYWAPL AGTCGVLLLSLVITLYCKRGRKK LLYIFKQPFMRPVQTTQEEDGC SCRFPEEEEEGGCEL RVKFSRSA DAPAYKQGQNQLYNELNLGRR EEYDVLDKRRGRDPEMGGKPR RKNPQEGLYNELQKDKMAEAY	atggccctccctgtcaccgccctgctgctccgctggctcttctgctc cacgccgctcggccatctctctgattgcgctctggcctggact acgtgatcgggatggaacacgtatgccatggaatctgcccgcc gatctggcttgggtcaagaggaaacacctgaacaagccagtgtat catgggcagacacacttgggagtcattggccggccctgctcctg gacgcaagaacatattctgagctccagccctctaccgacgac aggggtgacatgggtgaaaagtgtggacgaagccattgccgctt cggagatgtcccagagatcatggtatcggcggaggaggagatg atcgagcagttctgcctaaggccagaaactgtactgtactcac attgacgtgagggtggaaggggacacccatttctgattatgagc cagacgattgggaaagcgtgttctccgagtttcacgacgccgatg ctcagaactctcatagtattgcttggatctcggaaaggagatac ccttatgatgttctgattatgcttccccgtggatgctactaaaaga gaaattgtgatgaccagtcaccgccactcttagccttaccgg gtgagcgcgaacctgtcttgacagagcctcccaagacatctca aaataccttaattggtatcaacagaagccggacaggctcctgc cttctgactaccacaccagcggctccattctggaatccctgcca gggtcagcggtagcggatctgggaccgactacacctcactatca gctcactgcagccagaggacttcgctgtctatttctgtcagcaagg gaacacctgccctacacctttggacagggcaccagctcgag attaaagggtggaggtggcagcggaggaggtgggtccggcgggtg gaggaagccaggtccaactccaagaaagcggaccgggtctgt gaagccatcagaaactcttctactgactgtactgtgagcggagtg tcttccccgattacgggggtcttggatcagacagccaccgggg aagggtctggaatggattggagtgattggggctctgagactact actactctcatccctcaagtcacgcgtcaccatctcaaaggacaa ctctaagaatcagggtgtcactgaaactgtcatctgtgaccgcagcc gacaccgccgtgtactattgcgctaagcattactattatggcggga

	SEIGMKGERRRGKGHDGLYQG LSTATKDTYDALHMQALPPR (SEQ ID NO: 65)	gctacgcaatggattactggggacaggggtactctggtcaccgtg ccagcaccactaccccagcaccgagggccaccaccccggtc ctaccatgcctcccagcctctgtccctgcgtccgagggcatgtag accgcagctggtggggccgtgcataccggggtctgacttcgc ctcgatactacatttggccctctggctggtacttgcgggtcct gctgcttctactcgtgatcactcttactgtaagcgcggtcggaaga agctgctgtacatcttaagcaaccctcatgaggcctgtgcagact actcaagaggaggacggctgttcatgccggtccagaggagg aggaaggcggctgcgaactgcgctgaaattcagccgcagcgc agatgctccagcctacaagcaggggcagaaccagctctacaac gaactcaatcttggctcgagagaggagtacgacgtgtggacaa gctgagaggacgggacccagaaatggcggggaagccgcgc agaaagaatccccaagagggcctgtacaacgagctccaaaag gataagatggcagaagcctatagcgagattggtatgaaagggg aacgcagaagaggcaaaggccacgacggactgtaccagggg ctcagcaccgccaccaaggacacctatgacgtcttcacatgca ggccttgcgcctcgg (SEQ ID NO: 66)
CG#c47 ER _{mut} _HA_Fu rin-CAR19	MALPVTALLPLALLHAARPR SSLALSLTADQMVSALLDAEPI LYSEYDPTTRPFSEASMMGLLTN LADRELVHMINWAKRVPGFVDL ALHDQVHLLCAWMEILMIGLV WRSMEHPGKLLFAPNLLDRNQ GKCVEGGVEIFDMLLATSSRFR MMNLQGEEFVCLKSIILLNSGVY TFLSSTLKSLEEKDHIHRVLDKIT DTLIHLMAGLTLQQHQRLA QLLLILSHIRHMSSKRMEHLYSM KCKNVVPLSDLLLEMLDAHRLY PYDVPDYAFPVDRTKREIVMTQ SPATLSLSPGERATLSCRASQDI SKYLNWYQQKPGQAPRLIYHT SRLHSGIPARFSGSGSGTDYTL TISSLQPEDFAVYFCQQGNTLPY TFGQGTKLEIKGGGSGGGGS GGGGSQVQLQESGPGLVKPS E TLSLTCTVSGVSLPDYGVSWIR QPPGKGLEWIGVIWGSETTYYS SSLKSRVTISKDNSKNQVSLKLS SVTAADTAVYYCAKHYYYGGSY AMDYWGQGTLVTVSSTTPAP RPPTPAPTIASQPLSLRPEACRP AAGGAVHTRGLDFACDIYIWAPL AGTCGVLLLSLVITLYCKRGRKK LLYIFKQPFMRPVQTTQEEDGC SCRFPEEEEGGCELRVKFSRSA DAPAYKQGQNQLYNELNLGRR EEYDVLDKRRGRDPEMGKPR RKNPQEGLYNELQKDKMAEAY SEIGMKGERRRGKGHDGLYQG LSTATKDTYDALHMQALPPR (SEQ ID NO: 67)	atggccctccctgtcaccgcccgtgctgctccgctggctcttctgctc cacgcccgtcgcccccgtgctgctggcacttccctgactgccc accagatggtgtccgcccctctggacgcccagcctccaattctgta ctcggagtacgatccgactcgcccgttccgaagccagcatgat gggcctgttgactaacctggcggacccgagtggtgacatgat taactgggctaagcgggtgccgggctgctggacctggccctgca cgaccaagtgcacctcctggaatgcgctggatggaaatcctcat gatcgccctcgtgtggagatccatggagcatcccggaagactcct gtttgcacccaacctcctgctgatcgcaaccaggggaaaatgcgt ggaaggggggtgctgagatttgcacatgctgctcgccacctcttc cggttccggatgatgaatctgcaggagagaagagtctgtgtctga agtcaatcatcctgctgaactccgggtctataccttctgagctcg acctcaagtcactggaggaaaaagaccacatccatcgctgct cgataagatcaccgacaccttatccatctcatggcgaaggctgg actgacctgcaacagcagcaccagaggctggcccagttgctg ctgattctgagccacatccggcacatgctgccaagaggatggaa cacctgtacagcatgaagtgaagaacgtgctgctctgctcgat ctgctcctggaaatgctggacgcgcacagactctaccctatgatg ttcctgattatgctttcccgtggatcgtaaaaagagaaattgtga tgaccagtcacccgccactcttagccttccaccgggtgagcgcg caacctgtctgcagagcctccaagacatctcaaaataacctta attggtatcaacagaagcccgacagggtcctcgcttctgatcta ccacaccagccggctccattctggaatccctgccaggttcagcgg tagcggatctgggaccgactacacctcactatcagctcactgca gccagaggacttcgctgtctattctgtcagcaagggaacacctg cctacacctttggacagggcaccgaagctcgagattaaagggtg agggtggcagcggaggagggtgggtccggcgggtggagggaagcca gggtccaactccaagaaagcggacccgggtctgtgaagccatcag aaactcttactgactgtactgtgagcggagtgctctccccgatt acgggggtgtcttgatcagacagccaccggggaagggtctgga atgattggagtgattggggctctgagactactactactcttcac cctcaagtcacgcgtcacatctcaaaggacaactctaagaatc agggtgactgaaactgtcatctgtgaccgcagccgacaccgcc gtgtactattgcgctaagcattactattatggcgggagctacgcaat ggattactggggacaggggtactctgggtcaccgtgtccagaccac taccacagcaccgagggccaccaccccggtcctaccatcgctc cccagcctctgctcctgctcggtccggaggcatgtagaccgcagctg gtggggccgtgcatacccggggtcttgaactcgcctgcgatactta catttggggccctctggtggtacttgcggggctcgtgcttctact

		cgatgactcttactgtaagcgcggtcggaagaagctgctgtac atcttaagcaaccctcatgaggcctgtgcagactactcaagagg aggacggctgttcatgccggtcccagaggaggaggaaggcgg ctcgaactgcgctgaaattcagccgcagcgcagatgtccag cctacaagcaggggcagaaccagctctacaacgaactcaatctt ggtcggagagaggagtacgacgtgtggacaagcggagagg acgggaccagaaaatggcggaagccgcgcagaaagaatc cccaagaggcctgtacaacgagctccaaaaggataagatgg cagaagcctatagcgagattggtatgaaaggggaacgcagaa gaggcaaaaggccacgacggactgtaccagggactcagcaccg ccaccaaggacacctatgacgctcttcacatgcaggccctgccg cctcgg (SEQ ID NO: 68)
CG#c48 ER _{mut} _HA_Fu rinMmut_CA R19	MALPVTALLPLALLHAARPR SSLALSLTADQMVSALLDAEPP LYSEYDPTRPFSEASMMGLLTN LADRELVHMINWAKRVPGFVDL ALHDQVHLLCAWMEILMIGLV WRSMEHPGKLLFAPNLLDRNQ GKCVEGGVEIFDMLLATSSRFR MMNLQGEFVCLKSIILLNSGVY TFLSSTLKSLEEKDHIHRVLDKIT DTLIHLMKAGLTLQQQHQR LALLILSHIRHMSSKRMEHLYSM KCKNVVPLSDLLEMLDAHRLY PYDVPDYAFPVDATKREIVMTQ SPATLSLSPGERATLSCRASQDI SKYLNWYQQKPGQAPRLIYHT SRLHSGIPARFSGSGSGTDYTL TISSLQPEDFAVYFCQQGNTLPY TFGQGTKEIKGGGSGGGGS GGGGSQVQLQESGPGLVKPSE TSLTCTVSGVSLPDYGVSWIR QPPGKGLEWIGVIWGSETTYYS SSLKSRVTISKDNSKNQVSLKLS SVTAADTAVYYCAKHYYYGGSY AMDYWGQGLTVTVSSTTPAP RPPTPAPTIASQPLSLRPEACRP AAGGAVHTRGLDFACDIYWAPL AGTCGVLLSLVITLYCKRGRKK LLYIFKQPFMRPVQTTQEEDGC SCRFPETEEGGCELRVKFSRSA DAPAYKQGQNQLYNELNLGRR EEYDVLDRRRRDPPEMGGKPR RKNPQEGLYNELQKDKMAEAY SEIGMKGERRRGKGHDGLYQG LSTATKDTYDALHMQALPPR (SEQ ID NO: 69)	atggccctccctgtcaccgccctgtcgttccgctggctcttctgctc cacgccgctcggcccggtcgtcgttggcacttccctgactgcg accagatggtgtcggcccttctggacgcccagcctccaattctgta ctcggagtacgatccgactcggcgttccgaagccagcatgat gggctgttgactaacctggcgacccgaggttggtgcacatgat taactgggctaagcgggtgcgggctcgtggacctggccctgca cgaccaagtgcacctcctggaatgcgctggtggaatcctcat gatcggcctcgtgtggagatccatggagcatccgggaaagctcct gtttgcacccaacctcctgctgtatgcgaaccaggggaaatgcgt ggaagggggtgtcgagatttcgacatgtcgtcgcacacctctcc cgggtccggatgatgaatcgcaggagagaagagttcgtgtgtga agtcaatcatcctgtgaactccgggtctataccctcctgagctcg accctcaagtcactggaggaaaaagaccacatccatcgctgct cgataagatcaccgacaccctatccatctcatggcgaaggctgg actgacctgcaacagcagcaccagaggctggccagttgtcgt ctgattctgagccacatccggcacatgtcgtccaagaggatggaa cacctgtacagcatgaagtgaagaacgtcgtcctctgtccgat ctgctcctggaaatgctggacgcgcacagactctaccctatgatg ttcctgattatgcttcccgtggatgtactaaaagagaatgtga tgaccagtcaccgccactctagccttccaccgggtgagcgcg caacctgtcttgagagcctccaagacatctcaaaataacctta attggtatcaacagaagcccgacaggctcctgccttctgatcta ccacaccagccggctccattctggaatcccgtccagggtcagcgg tagcggatctgggaccgactacaccctcactatcagctcactgca gccagaggactcgtgtctattctgtcagcaagggaacaccctg ccctacaccttggacagggcaccaagctcgagattaaagggtg agggtgcagcggaggagggtgggtccggcggtggaggaagcca ggtccaactccaagaaagcggaccgggtcttgaagccatcag aaactcttactgactgtactgtgagcggaggtctctccccgatt acggggtgtcttgatcagacagccaccggggaagggtctgga atggattggagtgattggggtctgagactactactactctc cctcaagtcacgcgtcaccatctcaaggacaactctaagaatc agggtgactgaaactgtcatctgtgaccgcagccgacaccgc gtgtactattgcgtaagcattactatttgccgggagctacgcaat ggattactggggacagggtactctggtcaccgtgtccagcaccac taccacagcaccgaggccaccaccccggtcctaccatcgccct cccagcctctgtccctgcgtccggaggcatgtagaccgcagctg gtggggccgtgcatacccggttctgacttgcctgcgatatcta catttggggccctctggtggtacttgcggggtcctgctgttact cgtgatcactcttactgtaagcgcggtcggaagaagctgctgtac atcttaagcaaccctcatgaggcctgtgcagactactcaagagg aggacggctgttcatgccggtcccagaggaggaggaaggcgg ctcgaactgcgctgaaattcagccgcagcgcagatgtccag cctacaagcaggggcagaaccagctctacaacgaactcaatctt

		ggtcggagagaggagtacgacgtgctggacaagcggagagg acgggacccagaaatgggcggaagccgcgcagaaagaatc ccaagaggcctgtacaacgagctccaaaaggataagatgg cagaagcctatagcgagattggtatgaaaggggaacgcagaa gaggcaaggccacgacggactgtaccagggactcagcaccg ccaccaaggacacctatgacgctcttcacatgcaggccctgccg cctcgg (SEQ ID NO: 70)
CG#c71 FKBP _{mut} _HA_ noFurin_CAR 19	MALPVTALLPLALLHAARPG VQVETISPGDGRTPKRGQTCV VHYTGMLEDGKKVDSSRDRNK PFKFMLGKQEVIRGWEEGVAQ MSVGQRAKLITSPDYAYGATGH PGIIPPHATLVFDVELLKPEYPYD VPDYAFPVDEIVMTQSPATLSLS PGERATLSCRASQDISKYLNWY QQKPGQAPRLLIYHTSRLHSGIP ARFSGSGSGTDYTLTISLQPED FAVYFCQQGNTLPYTFGQGTKL EIKGGGSGGGGSGGGGSGQV QLQESGPGLVKPSETLSLTCTV SGVSLPDYGVSWIRQPPGKGLE WIGVIWGSETTYSSSLKSRVTI SKDNSKNQVSLKLSSVTAADTA VYYCAKHYYYGGSYAMDYWGQ GTLVTVSSTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHT RGLDFACDIYWAPLAGTCGVLL LSLVITLYCKRGRKLLYIFKQPF MRPVQTTQEEDGCSCRFPTEE EGGCELRVKFSRSADAPAYKQ GQNQLYNELNLGRREEYDVLDK RRGRDPEMGGKPRRKNPQEGL YNELQKDKMAEAYSEIGMKGER RRGKGHDGLYQGLSTATKDTY DALHMQALPPR (SEQ ID NO: 71)	atggccctccctgtcaccgcctgtgcttccgtggctcttctgctc cacgcgctcggcccgagtgaggtggaaccatctccccag gagacggcgccaccttcccaagcgcggccagacctgtgtgtg gcactacaccggatgcttgaagatggaagaaagtcgattcct ccgggacagaaacaagcccttaagtattgctaggcaagcag gaggtgatccgaggctgggaagaaggggtgccagatgagtg tgggtcagagagccaaactgactatactccagattatgcctatgg tgccactgggcacccaggcatcatccaccacatgccactctcgt cttcgatgtggagcttctaaaacgggaatacccttatgatgttcctg attatgcttcccggtggatgaaattgtgatgaccagtcacccgcc actcttagccttccacccggtagcgcgcaaccctgtcttcgagag cctcccaagacatctcaaaaacctaattggtatcaacagaagc ccggacaggctcctcgcctctgactaccacaccagccggctcc attctggaatccctgccaggtcagcggtagcggatctgggaccg actacaccctactatcagctcactgcagcagaggactcgtctgt ctattctgtcagcaagggaacaccctgccctacaccttggacag ggcaccgaagctcgagattaaaggtggaggtggcagcggaggga gggtgggtccggcggtggaggaagccaggtccaactccaagaa agcggaccgggtctgtgaagccatcagaaactcttctactgactt gtactgtgagcggagtgctctccccgattacgggggtgtcttgatc agacagccaccggggaagggctggaatggattggagtgatttg gggctctgagactactactactcttcatccctcaagtcacgcgtca ccatctcaaaggacaactctaagaatcaggtgtcactgaaactgt catctgtgaccgcagccgacaccgcggtgactattgcgctaagc attactattatggcgggagctacgcaatggattactggggacagg gtactctgtcaccgtgtccagcaccactacccagcaccgagg ccaccaccccggtcctaccatcgctcccagcctctgtccctgc gtccggaggcatgtagaccgcagctggtggggccgtgcataacc cgggggtctgactcgcctgcgatactacatttggggccctctggct gggtacttgcgggggtcctgtgcttctactcgtgatcactcttactgta agcgcggtcggaagaagctgctgtacatctttaagcaaccctcat gaggcctgtgcagactactcaagaggaggagcggctgttcagtc gggtcccagaggaggaggaagggcgtgcgaactgcgcgtga aattcagccgcagcgcagatgtccagcctacaagcaggggca gaaccagctctacaacgaactcaatcttggtcggagagaggagt acgacgtgctggacaagcggagaggacgggaccagaaaatg ggcgggaagccgcgcagaaagaatcccaagaggcctgtac aacgagctccaaaaggataagatggcagaagcctatagcgag attggtatgaaaggggaacgcagaaagggcaagggccacgac ggactgtaccaggggactcagcaccgccaccaaggacacctatg acgctcttcacatgcaggccctgccgcctcgg (SEQ ID NO: 72)
CG#c72 ER _{mut} _HA_no FurinCAR19	MALPVTALLPLALLHAARPR SSLALSLTADQMVSALLDAEPPI LYSEYDPTRPFSEASMMGLLTN LADRELVHMINWAKRVPGFVDL ALHDQVHLLCAWMEILMIGLV WRSMEHPGKLLFAPNLLLDNRN GKCVVEGGVEIFDMLLATSSRFR	atggccctccctgtcaccgcctgtgcttccgtggctcttctgctc cacgcgctcggcccggtgctggtggcacttccctgactgcg accagatggtgtccgccccttctggacgcgagcctccaattctgta ctcggagtacgatccgactcggcgttctcgaagccagcatgat gggctgttgactaacctggcgaccgcgaggttggtgcacatgat taactgggctaagcgggtgcggggtcgtggacctggccctgca cgaccaagtgcacctcctggaatgcgctggtggaatcctcat

	MMNLQGEEFVCLKSIILLNSGVY TFLSSTLKSLEEKDHIHRVLDKIT DTLIHLMAGLTLQQQHQRRLA QLLLILSHIRHMSSKRMHELYSM KCKNVVPLSDLLLEMLDAHRLY PYDVPDYAFPVDEIVMTQSPATL SLSPGERATLSCRASQDISKYL WYQQKPGQAPRLIYHTSRLHS GIPARFSGSGSGTDYTLTISSLQ PEDFAVYFCQQGNTLPYTFGQG TKLEIKGGGGSGGGSGGGGS QVQLQESGPGLVKPSSETLSLTC TVSGVSLPDYGVSWIRQPPGKG LEWIGVIWGSETTYSSSLKSRV TISKDNSKNQVSLKLSSVTAADT AVYYCAKHYYYGGSYAMDYWG QGTLVTVSSTTPAPRPPTPAPT IASQPLSLRPEACRPAAGGAVH TRGLDFACDIYWAPLAGTCGVL LLSLVITLYCKRGRKKLLYIFKQP FMRPVQTTQEEDGCSCRFPEE EEGGCELRVKFSRSADAPAYKQ GQNQLYNELNLGRREEYDVLDK RRGRDPEMGGKPRRKNPQEGL YNELQKDKMAEAYSEIGMKGER RRGKGHDGLYQGLSTATKDTY DALHMQALPPR (SEQ ID NO: 73)	gatcggcctcgtgtggagatccatggagcatcccgaaagctcct gtttgacccaacctcctgcttgatcgcaaccagggaataatgcgt ggaaggggggtgagagatttcgacatgctgctgccacctctcc cggttcggatgatgaatctgcagggagaagagttcgtgtgtctga agtcaatcatcctgctgaactccgggtctataccttctgagctcg acctcaagtcactggaggaaaaagaccacatccatcgctgct cgataagatcaccgacaccttatccatctcatggcgaaggctgg actgacctgcaacagcagcaccagaggctggcccagttgctg ctgattctgagccacatccggcacatgctgccaagaggatggaa cacctgtacagcatgaagtgaagaacgctgctgctgctccgat ctgctcctggaaatgctggacgcgcacagactctacccttatgat ttcctgattatgctttccccgtggatgaaatgtgatgaccagtcac ccgccactcttagcctttacccgggtgagcgcgaacctgtcttg cagagcctcccaagacatctcaaaataccttaattggtatcaaca gaagcccgagcaggctcctgccttctgatctaccacaccagcc ggctccattctggaatccctgccagggtcagcggtagcggatctgg gaccgactacacctcactatcagctcactgcagccagaggactt cgctgtctatttctgtagcaagggaacacctgcctacaccttg gacagggcaccaagctcgagattaagggtggaggtggcagcg gaggaggtgggtccggcggtggagggaagccaggtccaactcc aagaagcgggacccgggtctgtgaagccatcagaactcttca ctgactgtactgtgagcggaggtgtctctccccgattacggggtgt tggatcagacagccaccggggaagggtctggaatggattggagt gatttggggctctgagactacttactactcttcatccctcaagtcacg cgtcaccatctcaaaggacaactctaagaatcagggtgactgaa actgtcatctgtgaccgcagccgacaccgctgtactattgcgt aagcattactattatggcgggagctacgcaatggattactgggga cagggtactctggtcaccgtgtccagcaccactacccagcacc gaggccaccaccccggtcctaccatgcctccagcctctgtc cctgcgtccggaggcatgtagaccgcagctggtggggcgtgc atacccggggtctgactcgcctgcgatatctacatttggcccct ctggtctgtacttgcgggtcctgctgcttctactcgtgatcactt actgtaagcgcggctcgaagaagctgctgtacatctttaagcaac ccttcatgaggcctgtgcagactactcaagaggaggacggctgtt catgccggttcccagaggaggagggaaggcggctgcgaactgc gctgaaattcagccgcagcgcagatgtccagcctacaagca ggggcagaaccagctctacaacgaactcaatcttggtcggaga gaggagtacgacgtgtggacaagcggagaggacgggaccc agaaatgggcgggaagccgcgcagaagaatcccaagagg gctgtacaacgagctccaaaaggataagatggcagaagccta tagcgagattggtatgaagggaacgcagaagaggcaaagg ccacgacggactgtaccagggactcagcaccgccaccaagga cacctatgacgctctcacatgcaggccctgcgcctcgg (SEQ ID NO: 74)
CG#73 ER_{mut}_noHa_ FurinCAR19	MALPVTALLPLALLHAARPR SSLALSLTADQMVSALLDAEPPI LYSEYDPTRPFSEASMMGLLTN LADRELVHMINWAKRVPGFVDL ALHDQVHLLCAWMEILMIGLV WRSMEHPGKLLFAPNLLDRNQ GKCEGGVEIFDMLLATSSRFR MMNLQGEEFVCLKSIILLNSGVY TFLSSTLKSLEEKDHIHRVLDKIT DTLIHLMAGLTLQQQHQRRLA QLLLILSHIRHMSSKRMHELYSM KCKNVVPLSDLLLEMLDAHRLR	atggccctccctgtcaccgcctcgtgcttccgctggctcttctgctc cacgccgctcggcccggtcgtgtggcacttccctgactgccc accagatgggtgctccgcttctggacgcggagcctccaattctgta ctcggagtacgatccgactcggcgttctccgaagccagcatgat gggctcgttgactaacctggcgaccgcgagttgtgacatgat taactgggctaagcgggtgcggggtcgtggacctggccctgca cgaccaagtgcacctcctggaatgcgcctggatggaaatcctcat gatcggcctcgtgtggagatccatggagcatcccgaaagctcct gtttgacccaacctcctgcttgatcgcaaccagggaataatgcgt ggaaggggggtgagagatttcgacatgctgctgccacctctcc cggttcggatgatgaatctgcagggagaagagttcgtgtgtctga agtcaatcatcctgctgaactccgggtctataccttctgagctcg

	TKREIVMTQSPATLSLSPGERAT LSCRASQDISKYLNWYQQKPGQ APRLLIYHTSRLHSGIPARFSGS GSGTDYTLTISSLQPEDFAVYFC QQGNTLPYTFGQGTKLEIKGGG GSGGGGSGGGGSQVQLQESG PGLVKPSETLSLTCTVSGVSLPD YGVSWIRQPPGKGLEWIGVIWG SETTYSSSLKSRVTISKDNSKN QVSLKLSSVTAADTAVYYCAKH YYYGGSYAMDYWGQGLTVTVS STTTPAPRPPTPAPTIASQPLSL RPEACRPAAGGAVHTRGLDFA CDIYIWAPLAGTCGVLLLSLVL YCKRGRKKLLYIFKQPFMRPVQ TTQEEDGCSRFPEEEEGGCEL RVKFSRSADAPAYKQGQNQLY NELNLGRREEYDVLDRRRGRDP EMGGKPRRKNPQEGLYNELQK DKMAEAYSEIGMKGERRRGKG HDGLYQGLSTATKDTYDALHMQ ALPPR (SEQ ID NO: 75)	accctcaagtcactggaggaaaaagaccacatccatcgctgct cgataagatcaccgacacccttatccatctcatggcgaaggctgg actgaccctgcaacagcagcaccagaggctggcccagttgctg ctgattctgagccacatccggcacatgctgccaagaggatggaa cacctgtacagcatgaagtgaagaacgctgctcctgtgccgat ctgctcctggaaatgctggacgcgcacagactccgtactaaaag agaaattgtgatgaccagtcaccgccactcttagcctttcacc ggtgagcgcgcaaccctgtcttgacagcctcccaagacatctc aaaatacctaattggtatcaacagaagcccgacaggctcctcg ccttctgatctaccacaccagccggctcattctggaatccctgcc aggttcagcggtagcggatctgggaccgactacaccctcactatc agctcactgcagccagaggacttcgctgtctatttctgcagcaag ggaacaccctgccctacaccttggacagggcaccaagctcga gattaaagggtggagggtggcagcggaggaggtgggtccggcggt ggaggaagccagggtccaactccaagaaagcggaccgggtctt gtgaagccatcagaaactcttctactgactgtactgtgagcggag tgtctctccccgattacggggtgtcttggatcagacagccacggg gaagggtctggaatggattggagtgattggggctctgagactact tactactcttcatccctcaagtcacgcgtcaccatctcaaggaca actctaagaatcagggtgtcactgaaactgtcatctgtgaccgcagc cgacaccgcctgtactattgctgtaagcattactattatggcggg agctacgcgaatggattactggggacagggtactctggtcaccgtg tcacgacactacccagcaccgaggccaccaccccggtctc ctaccatcgctcccagcctctgtccctgctcggaggcatgtag accgcagctggtggggccgtgcatacccggggtctgacttcgc ctgcgatatctacattgggccccctgtggtgacttgcgggtcct gctgcttctactcgtgatcactcttactgtaagcgcggtcggaaga agctgctgtacatctttaagcaacccttcagtgagcctgtgcagact actcaagaggaggacggctgttcagtcgggtcccgaggagg aggaaggcggtgcgaactgcgcgtgaaattcagccgcagcgc agatgctccagcctacaagcaggggcagaaccagctctacaac gaactcaatcttggtcggagagaggagtacgacgtgctggacaa gcgagaggacgggacccagaaatggcggggaagccgcgc agaaagaatccccaagaggggcctgtacaacgagctccaaaag gataagatggcagaagcctatagcgagattggtatgaaagggg aacgcagaagaggcaaaggccacgacggactgtaccagggga ctcagcaccgccaccaaggacacctatgacgctcttcacatgca ggcctgcccgcctcgg (SEQ ID NO: 76)
CG#c74 ER _{mut} _noHa_ noFurin- CAR19	MALPVTALLPLALLHAARPR SSLALSLTADQMVSALLDAEPPI LYSEYDPTRPFSEASMMGLLTN LADRELVHMINWAKRVPGFVDL ALHDQVHLLLECAWMEILMIGLV WRSMEHPGKLLFAPNLLDRNQ GKCVEGGVEIFDMLLATSSRFR MMNLQGEEFVCLKSIILLNSGVY TFLSSTLKSLEEKDHIHRVLDKIT DTLIHLMAKAGLTLQQQHQRILA QLLLILSHIRHMSSKRMEHLYSM KCKNVVPLSDLLLEMLDAHRLEI VMTQSPATLSLSPGERATLSCR ASQDISKYLNWYQQKPGQAPRL LIYHTSRLHSGIPARFSGSGSGT DYTLTISSLQPEDFAVYFCQQG NTLPYTFGQGTKLEIKGGGGSG GGSGGGGSQVQLQESGPGLV	atggccctccctgtcaccgcctgtgcttccgctggctcttctgctc cacgcgctcggccccggtcgtcgttggcacttccctgactgcgc accagatggtgtccgcccttctggacgcgcgagcctccaattctgta ctcggagtacgatccgactcgccttctcgaagccagcatgat gggcctgttgactaacctggcgacgcgcgagttggtgcacatgat taactgggctaagcgggtgcccgggtcgtggaactggcctgca cgaccaagtgcacctcctggaatgcgcctggtggaatcctcat gatcggcctcgtgtggagatccatggagcatcccgaaagctcct gttgcacccaacctcctgcttgatcgcaaccaggggaaaatgcgt gggaaggggtgtcgagatttgcacatgctgctcgcacacctcttc cggttccggatgatgaatctgcaggggagaagagttcgtgtgtctga agtcaatcatcctgctgaactccgggtctatacctctgagctcg accctcaagtcactggaggaaaaagaccacatccatcgctgct cgataagatcaccgacacccttatccatctcatggcgaaggctgg actgaccctgcaacagcagcaccagaggctggcccagttgctg ctgattctgagccacatccggcacatgctgccaagaggatggaa cacctgtacagcatgaagtgaagaacgctgctcctgtgccgat ctgctcctggaaatgctggacgcgcacagactcgaaattgtgatg

[illegible]

	NLTESHNSRKKREIVMTQSPATL SLSPGERATLSCRASQDISKYL WYQQKPGQAPRLLIYHSTRLHS GIPARFSGSGGTDTYTLTISSQ PEDFAVYFCQQGNTLPYTFGQG TKLEIKGGGSGGGSGGGSGGGG QVQLQESGPGLVKPSSETLSLTC TVSGVSLPDYGVSWIRQPPGKG LEWIGVIWGSETTYSSSLKSRV TISKDNSKNQVSLKLSSVTAADT AVYYCAKHYYGGSYAMDYWG QGTLTVSSTTTTPAPRPPTPAPT IASQPLSLRPEACRPAAGGAVH TRGLDFACDIYWAPLAGTCGLV LLSLVITLYCKRGRKKLLYIFKQP FMRPVQTTQEEDGCSCRFPEE EEGGCELRVKFSRSADAPAYKQ GQNQLYNELNLRREEYDVLDK RRGRDPEMGGKPRRKNPQEG LYNELQKDKMAEAYSEIGMKGER RRGKGHDGLYQGLSTATKDTY DALHMQALPPR (SEQ ID NO: 103)	accctcaagtcactggaggaaaaagaccacatccatcgctgct cgataagatcaccgacacccttatccatctcatggcgaaggctgg actgaccctgcaacagcagcaccagaggctggcccagttgctg ctgattctgagccacatccggcacatgtcgtccaagaggatggaa cacctgtacagcatgaagtgaagaacgtcgtgctctgtccgat ctgctcctggaaatgtggacgcgcacagactcagtcgaattga <u>ctgagtcacacaattccaggaagaaaagggaattgtgatgacc</u> <u>cagtcaccccgccactcttagccttcacccggtagcgcgcaacc</u> <u>ctgtcttcagagcctccaagacatctcaaaataccctaattggt</u> <u>tcaacagaagcccgacaggctcctgccttctgatctaccacac</u> <u>cagccggctccattctggaatccctgccagggtcagcggtagcgg</u> <u>atctgggaccgactacaccctcactatcagctcactgcagccaga</u> <u>ggacttcgctgtctatttctgtcagcaagggaacaccctgccctac</u> <u>accttggacagggcaccaagctcgagattaaagggtggagggtg</u> <u>cagcggaggagggtgggtccggcggtggagggaagccagggtcca</u> <u>actccaagaaagcggaccgggtcttgaagccatcagaaactc</u> <u>ttcactgactgtactgtgagcggagtgctctccccgattacgggg</u> <u>tgcttgatcagacagccaccggggaagggtctggaatggattg</u> <u>gagtgattgggctctgagactactactcttcatccctcaagt</u> <u>cacgcgtcacatctcaaaggacaactcaagaatcagggtgtca</u> <u>ctgaaactgtcatctgtgaccgcagccgacccgctgtactatt</u> <u>gcgctaagcattactattatggcggagctacgcaatggattactg</u> <u>gggacagggtactctggtcaccgtgtccagcaccactacccag</u> <u>caccgaggccacccaccccggtcctaccatgcctcccagcct</u> <u>ctgtccctgcgtccggaggcatgtagaccgcagctgggtggggc</u> <u>cgtgcatacccggggtctgacttcgctgcgatactacattggg</u> <u>ccctctggctggtacttgcgggtcctgtgctttcactcgtgatca</u> <u>ctcttactgtaagcgcggtcgggaagaagctgctgtacatcttaag</u> <u>caaccctcatgaggcctgtgcagactactcaagaggaggacgg</u> <u>ctgttcatgccgttcccagaggaggaggaaggcggtcgcgaa</u> <u>ctgcgcgtgaaattcagccgcagcgcagatgtccagcctacaa</u> <u>gcaggggcagaaccagctctacaacgaactcaatcttggtcgga</u> <u>gagaggagtacgacgtgctggacaagcggagaggacgggac</u> <u>ccagaaatgggcgggaagccgcgcagaaagaatccccaaga</u> <u>gggctctgtacaacgagctccaaaaggataagatggcagaagc</u> <u>ctatagcgagattggtatgaaaggggaacgcagaagaggcaa</u> <u>aggccacgacggactgtaccagggtactcagcaccgccaccaa</u> <u>ggacacctatgacgtcttcacatgcaggccctgccgcctcgg</u> (SEQ ID NO: 104)
ER _{mut.} Furin- CAR19=Alt2	MALPVTALLLPLALLLHAARPR SSLALSLTADQMVSALLDAEPPI LYSEYDPTRPFSEASMMGLLTN LADRELVHMINWAKRVPGFVDL ALHDQVHLLCAWMEILMIGLV WRSMEHPGKLLFAPNLLDRNQ GKCVEGGVEIFDMLLATSSRFR MMNLQGEEFVCLKSIILLNSGVY TFLSSTLKSLEEKDHIHRVLDKIT DTLIHLMKAGLTLLQQHQRLA QLLLILSHIRHMSSKRMEHLYSM KCKNVVPLSDLLLEMLDAHRLG <u>TGAEDPRPSRKRREIVMTQSPA</u> <u>TLSPGERATLSCRASQDISKY</u> <u>LNWYQQKPGQAPRLLIYHSTR</u> <u>LHSGIPARFSGSGGTDTYTLTISS</u> <u>LQPEDFAVYFCQQGNTLPYTFG</u>	atggccctccctgtcaccgcctgtgcttccgctggctcttctgctc cacgcgctcggcccggtcgtcgttggcactttccctgactgccg accagatggtgtccgccccttctggacgcgcagcctccaattctgta ctcggagtacgatccgactcgcgcgttctccgaagccagcatgat gggcctgttgactaacctggcgaccgcgagtggtgacatgat taactgggctaagcgggtgcgggcttctggtgacctggccctgca cgaccaagtgcacctcctggaatgcgcctggatggaatcctcat gatcggcctcgtgtggagatccatggagcatcccggaagactcct gtttgcacccaacctcctgcttgatcgcaaccagggaataatgcgt ggaagggggtgtcgagatttgcagatgtgctcgcacacctcttc cggttccggatgatgaatctgcaggaggagaagagttcgtgtgtga agtcaatcatcctgtgaactccgggtctataccttctgagctcg accctcaagtcactggaggaaaaagaccacatccatcgctgct cgataagatcaccgacacccttatccatctcatggcgaaggctgg actgaccctgcaacagcagcaccagaggctggcccagttgctg ctgattctgagccacatccggcacatgtcgtccaagaggatggaa cacctgtacagcatgaagtgaagaacgtcgtgctctgtccgat

	QGTKLEIKGGGSGGGSGGG GSQVQLQESGPGLVKPSSETLSL TCTVSGVSLPDYGVSWIRQPPG KGLEWIGVIWGSETTYSSSLKS RVTISKDNSKNQVSLKLSSVTAA DTAIVYCAKHYYYGGSYAMDY WGQGTLLTVSSTTTPAPRPPTP APTIASQPLSLRPEACRPAAGG AVHTRGLDFACDIYIWAPLAGTC GVLLLSLVITLYCKRGRKLLYIF KQPFMRPVQTTQEEDGCSCRF PEEEEGGCELRVKFSRSADAPA YKQGQNQLYNELNLGRREEYD VLDKRRGRDPEMGGKPRRKNP QEGLYNELQKDKMAEAYSEIGM KGERRRGKGDHGLYQGLSTAT KDTYDALHMQALPPR (SEQ ID NO: 105)	ctgctcctggaaatgctggacgcgcacagactcgggacgggag <u>ctgaggaatccacgacccagcagaaagcgacgggaaattgtgat</u> gaccagtcacccgccactcttagccttcacccggtagcgcg aacctgtcttcagagcctcccaagacatctcaaaatacctta tggatcaacagaagcccgacaggctcctgcctctgatctac cacaccagccggctccattctggaatccctgccaggtcagcggt agcggtatctgggaccgactacacctcactatcagctcactgca gccagaggacttcgctgtctatttctgtagcaagggaacacctg ccctacaccttggacagggcaccaagctcgagattaaagggtg aggtggcagcgaggagggtgggtccggcggtggaggaagcca ggtccaactccaagaaagcgacggggtctgtgaagccatcag aaactcttactgactgtactgtgagcggaagtgtctctcccga acggggtgtcttggatcagacagccacggggaagggtctgga atggattggagtgatttgggctctgagactactactactctc cctcaagtcacgcgtcaccatctcaaaggacaactctaagaatc aggtgtcactgaaactgtcatctgtgaccgcagccgacacccg gtgtactattgcgtaagcattactattatggcgggagctacgca atggattactgggacaggggtactctgtgacccgtgtccagacc caccagcaccgagggccaccaccccggtcctaccatcgct ccagcctctgtccctgcgtccggaggcatgtagaccgcagctg gtggggccgtgcatacccggggtctgactcgcctgcgatact catcttggccctctggctgtactgtcggggtcctgctgttact cgtgatcactcttactgtaagcgcggtcggaagaagctgctgac atcttaagcaaccttcatgaggcctgtgcagactactcaagg aggcagcggtgtcatgcccgttccagaggaggaggaaggcg ctgcgaactgcgcgtgaaattcagccgcagcgcagatgtccag cctacaagcaggggcagaaccagctctacaacgaactcaatct ggtcggagagaggagtacgacgtgtggaagaagcgagagg acgggaccagaaatggcggggaagccgcgcagaaagaatc ccaagagggtctgtacaacgagctccaaaaggataagatgg cagaagcctatagcgagattggtatgaaaggggaacgcagaa gaggcaaaggccacgacgactgtaccagggactcagcaccg ccaccaaggacacctatgacgctcttcacatgcaggccctgcg cctcgg (SEQ ID NO: 106)
ER _{mut} .Furin- CAR19=Alt3	MALPVTALLPLALLHAARPR SSLALSLTADQMVSALLDAEPPI LYSEYDPTRPFSEASMMGLLTN LADRELVHMINWAKRVPGFVDL ALHDQVHLLCAWMEILMIGLV WRSMEHPGKLLFAPNLLDRNQ GKCVEGGVEIFDMLLATSSRFR MMNLQGEFVCLKSIILLNSGVY TFLSSTLKSLEEKDHIHRVLDKIT DTLIHLMAKAGLTLQQHQRLA QLLILSHIRHMSSKRMEHLYSM KCKNVVPLSDLLEMLDAHRLC <u>KINGYPKRGRKRREIVMTQSPA</u> <u>TLSLSPGERATLSCRASQDISKY</u> LNWYQQKPGQAPRLIYHTSRL HSGIPARFSGSGSGTDYTLTISS LQPEDFAVYFCQQGNLTPYTFG QGTKLEIKGGGSGGGSGGG GSQVQLQESGPGLVKPSSETLSL TCTVSGVSLPDYGVSWIRQPPG KGLEWIGVIWGSETTYSSSLKS RVTISKDNSKNQVSLKLSSVTAA	Atggccctccctgtcaccgccctgtgcttccgctggctcttctgct caccgcgctcggcccggtcgtcgtggcacttccctgactgccg accagatggtgtccgccctcttgacgcgcagcctccaattctgta ctgcgagtagcatccgactcgcgcgttctccgaagccagcatgat gggcctgtgactaacctggcgacccgaggtgtgacatgat taactgggctaagcggtgcgggtcgtgacgtggcctgca cgaccaagtgcacctcctggaatgcgcctggaatgaaatcctcat gatcgccctcgtgtggagatccatggagcatcccggaagactcct gttgcacccaacctcctgcttgatcgcaaccagggaagaaatgcgt ggaagggggtgtcgagatttgcacatgctgctgcaccctctcc cgggtccggatgatgaatctgcaggggagaagagttcgtgtgtga agtcaatcatcctgctgaactccgggtctatacctcctgagctcg accctcaagtactggaggaaaaagaccacatccatcgcggtct cgataagatcaccgacaccttatccatctcatggcgaaggctgg actgacctgcaacagcagcaccagaggctggcccagttgtg ctgattctgagccacatccggcacatgtcgtccaaggagatggaa cacctgtacagcatgaagtgaagaacgtcgtgctctgtccgat ctgctcctggaaatgctggacgcgcacagactcgaagatcaa <u>cggtaccctaagagggggcagaaagcgggcggaattgtgatg</u> acccagtcacccgccactcttagccttcacccggtagcgcgca acctgtctgcagagcctccaagacatctcaaaataccttaatt ggtatcaacagaagcccgacaggctcctgcctctgatctacc

	DTAVYYCAKHYYYGGSYAMDY WGQGLTVTSSTTTPAPRPPTP APTIASQPLSLRPEACRPAAGG AVHTRGLDFACDIYWAPLAGTC GVLLLSLVITLYCKRGRKKLLYIF KQPFMRPVQTTQEEDGCSCRF PEEEEGGCELRVKFSRSADAPA YKQGQNQLYNELNLGRREEYD VLDKRRGRDPEMGGKPRRKNP QEGLYNELQDKMAEAYSEIGM KGERRRGKGGHDGLYQGLSTAT KDTYDALHMQALPPR (SEQ ID NO: 107)	acaccagccggctccattctggaatccctgccaggttcagcggta gcggtatctgggaccgactacacccctactatcagctcactgcagc cagaggacttcgctgtctatttctgtcagcaagggaacacccctgcc ctacaccttggacagggcaccagctcgagattaaagggtggag gtggcagcggaggagggtgggtccggcgggtggaggaagccagg tccactccaagaaagcggaccgggtctgtgaagccatcagaa actcttctactgactgtactgtgagcggagtgctctccccgattac ggggtgtcttggatcagacagccaccggggaagggtctggaatg gattggagtgattggggctctgagactactactactcttcatccctc aagtcacgcgtcaccatctcaaaggacaactctaagaatcagggt gtcactgaaactgtcatctgtgaccgcagccgacaccgcgctgta ctattgcgctaagcattactattatggcgggagctacgcaatggatt actggggacagggtactctgtgtcaccgtgtccagcaccactacc ccagcaccgaggccacccaccccggtcctaccatcgctccc agcctctgtccctgcgtccggaggcatgtagaccgcagctgggtg gggcccgtgcatacccggtgtgtactgcctgcgatatctacatt tggccctctgtgtgtactgtcgggtcctgtgtcttctactcgtg atcactcttactgtaagcgcgggtcggagaagagctgtgtacatctt taagcaacccctcatgaggcctgtgcagactactcaagaggagg acggctgttcatgcgggtccagaggaggaggaaggcggctg cgaactgcgcgtgaaattcagccgcagcgcagatgctccagcct acaagcaggggcagaaaccagctctacaacgaactcaatcttggt cggagagaggagtagcagctgtgtggacaagcggagaggagc ggaccagaaatggcggggaagccgcgcagaaagaatcccc aagaggggcctgtacaacgagctccaaaaggataagatggcag aagcctatagcagattggtatgaaaggggaacgcagaagag gcaaaggccacgacggactgtaccagggactcagcaccgcca ccaaggacacctatgacgtcttcatatgcaggccctgccgcctc gg (SEQ ID NO: 108)
ER _{mut} .Furin- CAR19=Alt4	MALPVTALLLPLALLLHAARPR SSLALSLTADQMVSALLDAEPPI LYSEYDPTPRFSEASMMGLLTN LADRELVHMINWAKRVPGFVDL ALHDQVHLLCAWMEILMIGLV WRSMEHPGKLLFAPNLLDRNQ GKCVEGGVEIFDMLLATSSRFR MMNLQGEFVCLKSIILLNSGVY TFLSSTLKSLEEKDHIHRVLDKIT DTLIHLMAGLTLQQHQRLA QLLLILSHIRHMSSKRMEHLYSM KCKNVVPLSDLLLEMLDAHRL <u>QWLEQQVAKRRTKREIVMTQSP</u> ATLSLSPGERATLSRASQDISK YLNWYQQKPGQAPRLLIYHTSR LHSGIPARFSGSGSGTDYTLTIS SLQPEDFAVYFCQQGNTLPYTF GQGTKLEIKGGGSGGGGSGG GGSQVQLQESGPGLVKPSSETLS LTCTVSGVSLPDYGVSWIRQPP GKGLEWIGVIWGSETTYSSSL KSRVTISKDNSKNQVSLKLSSVT AADTAVYYCAKHYYYGGSYAM DYWGQGLTVTSSTTTPAPRPP TPAPTIASQPLSLRPEACRPAAG GAVHTRGLDFACDIYWAPLAGT CGVLLLSLVITLYCKRGRKKLLYI	Atggccctccctgtcaccgcctgtgtctccgctggctcttctgtc cacgcgcgtcggccccggctgtgttggcactttccctgactgcg accagatggtgtccgccctctgtgacgcgcgagcctccaattctgta ctcggagtagcatccgactcgcgcgttctccgaagccagcatgat gggctgtgtgactaacctggcggaccgcgagtggtgacatgat taactgggctaagcgggtgccgggctcgtggacctggccctgca cgaccaagtgcacctctggaatgcgcctggatggaaatcctcat gatcggcctcgtgtggagatccatggagcatcccggaagactcct gtttgcacccaacctcctgtgtatgcgaaccagggaataatgcgt ggaaggggggtgtcgagattttcgacatgtgtctgccacctctcc cgggtccggatgatgaatctgcaggggagaagagtggtgtgtga agtcaatcatcctgtgaactccgggtctataccttctgagctcg acctcaagtactggaggaaaaagaccacatccatcgctgtgt cgataagatcaccgacaccttatccatctcatggcgaaggctgg actgacctgcaacagcagcaccagaggctggcccagttgtgt ctgattctgagccacatccggcacatgtctccaagaggatggaa cacctgtacagcatgaagtgaagaacgtgtgtcctctgtccgat ctgctcctggaaatgctggacgcgcacagactcctgcaatggctg gagcagcaggtggcgaagcggagaactaagcgggaaattgtg atgaccagtcacccgccactcttagcctttacccgggtgagcgc gcaacctgtcttgagagcctcccaagacatctcaaaatacctt aattggtatcaacagaagcccgagaggctcctgccttctgatct accacaccagccggctccattctggaatccctgccaggttcagcg gtagcggatctgggaccgactacacccctactatcagctcactgc agccagaggacttcgtgtctatttctgtcagcaagggaacacct gccctacaccttggacagggcaccagctcgagattaaagggtg gaggtggcagcggaggagggtgggtccggcgggtggaggaagcc

	FKQPFMRPVQTTQEEDGCSCR FPEEEEGGCEL RVKFSRSADAP AYKQGQNQLYNELNLGRREEY DVLDKRRGRDPEMGGKPRRKN PQEGLYNELQKDKMAEAYSEIG MKGERRRRGK GHDGLYQGLSTA TKD TYDALHMQALPPR (SEQ ID NO: 109)	aggccaactccaagaaagcggaccgggtctgtgaagccatca gaaacttttactgactgtactgtgagcggagtgctctccccgat tacggggtgtcttgatcagacacccacggggaagggctgga atggattggagtgattggggctctgagactactactacttcatc cctcaagtcacgcgcaccatctcaaggacaactctaagaatc agggtgactgaaactgtcatctgtgaccgcagccgacaccgcc gtgtactattgcgctaagcattactattatggcgggagctacgcaat ggattactggggacagggtactctgggtaccgtgtccagaccac taccacagcaccgaggccaccaccccggtcctaccatcgct cccagcctctgtccctgcgtcggaggcatgtagaccgcagctg gtggggccgtgcatacccggggtctgacttcgctcgcatatcta catttggggccctctggtggtacttgcggggctctgctgttctact cgtgatcactcttactgtaagcgcgggtcggagaagctgtgtac atcttaagcaacccttcagaggcctgtgcagactactcaagagg aggacggctgttcagccggtcccagaggaggaggaaggcgg ctgcgaactgcgcgtgaaattcagccgcagcgcagatgtccag cctacaagcaggggcagaaccagctctacaacgaactcaatctt ggctggagagaggagtacgacgtgtggacaagcggagagg acgggaccagaaaatgggcgggaagccgcgcagaaaagaatc cccaagagggcctgtacaacgagctccaaaaggataagatgg cagaagcctatagcgagattggtatgaaaggggaacgcagaa gaggcaaaagccacgacgcgactgtaccagggtactcagcaccg ccaccaaggacacctatgacgctcttcacatgcaggccctgcg cctcgg (SEQ ID NO: 110)
ER _{mut} .Furin- CAR19=Alt5	MALPVTALLPLALLHAA RPR SSLALSLTADQMVSALLDAEPPI LYSEYDPTRPFSEASMMGLLTN LADREL VHMINWAKRVP GFVDL ALHDQVHLL ECAWMEILMIGLV WRSMEHPGKLLFAPNLLDRNQ GKCV EGGVEIFDMLLATSSRFR MMNLQGE EFVCLKSIILLNSGVY TFLSSTLKSLEEKDHIHRVLDKIT DTLIHLMAGLTLQQQHQR LA QLLLILSHIRHMSSSRMEHLYSM KCKNVVPLSDLLLEMLDAHRLG <u>TGAEDPRPSRKRRLG DVG EIV</u> MTQSPATLSLSPGERATLS CRA SQDISKYL N WYQQKPGQAPRLL IYH TSRLHSGIPARFSGSGSGTD YTLTISSLQPEDFAVYFCQQGNT LPYTFGQGTKLEIKGGGGSGGG GSGGGGSQVQLQESGPGLVKP SETLSLTCTVSGVSLPDYGVSWI RQPPGKGLEWIGVIWGSETTY SSSLKSRVTISKDNSKNQVSLKL SSVTAADTAVYYCAKHYYYGGS YAMDYWGQGT LVTVSSTTTPAP RPPTPAPT IASQPLSLRPEACRP AAGGAVHTRGLDFACDIYIWAPL AGTCGVLLLSLVITLYCKRGRKK LLYIFKQPFMRPVQTTQEEDGC SCR FPEEEEGGCEL RVKFSRSA DAPAYKQGQNQLYNELNLGRR EEYDVLDKRRGRDPEMGGKPR RKNPQEGLYNELQKDKMAEAY	Atggccctccctgtcaccgccctgctgtctccgtgggtcttctgctc cacgcgcgtcggccccgggtcgtgtggcactttccctgactgcg accagatgggtgtcggcccttctggacgcgagcctccaattctgta ctcggagtagatccgactcggcgttctccgaagccagcatgat gggctgttgactaacctggcggaccgcgagtggtgcacatgat taactgggctaagcgggtgcgggctctgtggacctggccctgca cgaccaagtgcacctcctggaatgcgcctggatggaaatcctcat gatcggcctcgtgtggagatccatggagcatcccgaaagctcct gttgacccaacctcctgcttgatcgcaaccagggaataatgcgt ggaagggggtgtcgagatttcgacatgctgctgccacctcttc cgggtccggatgatgaatctgcagggaagagtgctgtgtctga agtcaatcatcctgtgaactccggggtctatacccttctgagctg accctcaagtactggaggaaaaagaccacatccatcgcggtgt cgataagatcaccgacacccttatccatctcatggcgaaggctgg actgacctgcaacagcagcaccagaggctggcccagtgctg ctgattctgagccacatccggcagatgtctccaagaggatggaa cacctgtacagcatgaagtgaagaacgtcgtgcctctgtccgat ctgctcctggaatgtcggacgcgcacagactcggaaaccggcg <u>cggaagacccccggccctccaggaagcgaaggctccctcgga</u> <u>acgtgggtgaaattgtatgaccagtcaccgcactcttagcct</u> <u>ttcaccgggtgagcgcgaaccctgtcttcagagcctccaaga</u> <u>catctcaaaataccttaattggtatcaacagaagccggacaggc</u> <u>tctcgccttctgatctaccacaccagccggctccattctggaatcc</u> <u>ctgccagggtcagcggtagcggatctgggaccgactacaccctc</u> <u>actatcagctcactgcagccagaggactcgtgtctatttctgca</u> <u>gcaagggaacaccctgccctacaccttggacagggcaccag</u> <u>ctcgagattaaagggtggagggtggcagcggaggagggtgggtccg</u> <u>gcggtggaggaagccagggtccaactccaagaaagcggaccg</u> <u>ggtctgtgaagccatcagaaacttttactgactgtactgtgag</u> <u>cggagtgctctccccgattacggggtgtcttgatcagacagcca</u> <u>ccggggaagggtctggaatggattggagtgattggggtctgag</u> <u>actactactactctcatccctcaagtcacgcgtcaccatctcaaa</u>

	SEIGMKGERRRGKGHDGLYQG LSTATKDTYDALHMQALPPR (SEQ ID NO: 111)	ggacaactctaagaatcagggtgactgaaactgtcatctgtgac cgcagccgacacccgctgtactattgctgtaagcattactattat ggcgggagctacgcaatggattactggggacagggtactctggt caccgtgtccagcaccactacccagcaccgagggccaccacc ccggctcctaccatcgctcccagcctctgctccgtccggagg catgtagaccgcagctggtggggcgtgcatacccggggtcttg actcgctgctgatactacattgggcccctctggtggtacttgctg gggtcctgctgcttactcgtgatactcttactgtaagcgcggtc ggaagaagctgctgtacatctttaagcaaccctcatgaggcctgt gcagactactcaagaggaggagcggtgttcatgcccgttccag aggaggagggaaggcggtgcgaactgcgctgaaattcagcc gcagcgcagatgtccagcctacaagcaggggcagaaccagc tctacaacgaactcaatcttggtcggagagaggagtagcagctg ctggacaagcggagaggacgggaccagaaatggcggggaa gccgcgcagaaagaatccccaagaggcgctgtacaacgagct ccaaaaggataagatggcagaagcctatagcgagattggtatg aaaggggaacgcagaagaggcaaggccacgacggactgta ccagggactcagcaccgccaccaaggacacctatgacgctcttc acatgcaggccctgcccgtcgg (SEQ ID NO: 112)
ER _{mut.} Furin- CAR19=Alt6	MALPVTALLPLALLHAARPR SSLALSLTADQMVSAALLDAEPPI LYSEYDPTRFSEASMMGLLTN LADRELVHMINWAKRVPGFVDL ALHDQVHLLCAWMEILMIGLV WRSMEHPGKLLFAPNLLDRNQ GKCVEGGVEIFDMLLATSSRFR MMNLQGEFVCLKSIILLNSGVY TFLSSTLKSLEEKDHIHRVLDKIT DTLIHLMAKAGLTQQQHQLRA QLLLILSHIRHMSSKRMHELYSM KCKNVVPLSDLLLEMLDAHRLG <u>TGAEDPRPSRKRRSLGGEIVMT</u> QSPATLSLSPGERATLSCRASQ DISKYLNWYQQKPGQAPRLIY HTSRLHSGIPARFSGSGSGTDY TLTISSLQPEDFAVYFCQQGNTL PYTFGQGTKEIKGGGSGGG GSGGGGSQVQLQESGPGLVKP SETLSLTCTVSGVSLPDYGVSWI RQPPGKGLEWIGVIWGSETYY SSSLKSRVTISKDNSKNQVSLKL SSVTAADTAVYYCAKHYYYGGS YAMDYWGQGLTVSSTTTPAP RPPTPAPTIASQPLSLRPEACRP AAGGAVHTRGLDFACDIYWAPL AGTCGVLLSLVITLYCKRGRKK LLYIFKQPFMRPVQTTQEEDGC SCRFEEEEEGGCELRVKFSRSA DAPAYKQGQNQLYNELNLGRR EEYDVLDRRRGRDPEMGKPR RKNPQEGLYNELQKDKMAEAY SEIGMKGERRRGKGHDGLYQG LSTATKDTYDALHMQALPPR (SEQ ID NO: 113)	Atggccctccctgtcaccgcccgtgcttccgctggctctctgctc cacgcccgtcggccccggctgctgtggcacttccctgactgccc accagatggtgtccgcccctctgagcgcgagcctccaattctgta ctcggagtagcagatccgactcggcgttctccgaagccagcatgat gggctgttgactaacctggcggaccgcgagtggtgacatgat taactgggctaagcgggtgcccgggctcgtggacctggccctgca cgaccaagtgcacctctggaatgcgcctggaatggaatcctcat gatcgccctcgtgtggagatccatggagcatcccggaaagctcct gtttgcacccaacctcctgcttgatgcgaaccagggaataatgct ggaagggggtgtcgagattttcgacatgctgctcgcacacctctcc cggttccggatgatgaatctgcaggggagaagagtgctgtgtctga agtcaatcatcctgctgaactccggggtctataccttctgagctcg accctcaagtcactggaggaaaaagaccacatccatcgctgct cgataagatcaccgacacccttatccatctcatggcgaaggctgg actgacctgcaacagcagcaccagaggctggcccagttgctg ctgattctgagccacatccggcacatgtcgtccaagaggatggaa cacctgtacagcatgaagtgcagaacgctgctgctctgcccgt ctgctcctggaaatgctggacgcgcacagactcggcacagggtc <u>cgaggaccctcgccaagccgcaaaaggagggtcacttggcgg</u> <u>cgaaattgtatgacccagtcacccgccactcttagccttccacc</u> ggtgagcgcgcaaccctgtcttcagagcctcccaagacatctc aaaataccttaattggtatcaacagaagcccggacaggctcctcg ccttctgatctaccacaccagccggctccattctggaatccctgcc aggttcagcggtagcggatctgggaccgactacacctcactatc agctcactgcagccagaggactcgtgtctattctgtcagcaag ggaacacccctgcctacaccttggacagggcaccaagctcga gattaaagggtggagggtggcagcggaggaggtgggtcggcggt ggaggaagccagggtccaactccaagaaagcggaccgggtctt gtgaagccatcagaaactcttactgactgtactgtgagcggag tgtctctccccgattacggggtgtcttggatcagacagccaccggg gaagggtctggaatggattggagtgtattggggctctgagactact tactactcttcatccctcaagtcacgcgtcacctatctaaaggaca actctaagaatcagggtgactgaaactgtcatctgtgaccgcagc cgacaccgcccgtgtactattgctgtaagcattactattatggcggg agctacgcaatggattactggggacagggtactctgtgaccgctg tccagcaccactacccagcaccgaggccaccaccgccggctc ctaccatcgccctccagcctctgtcctgctgctcggaggcatgtg

		acccgagctggtggggccgtgcataccgggggtcttgacttcgc ctgcgatactacatttggccctctggtggtacttgcgggtcct gctgcttctactcgtgatcactcttactgtaagcgcggtcggaaga agctgctgtacatcttaagcaaccctcatgaggcctgtgcagact actcaagaggaggacggctgtcatgccggtcccagaggagg aggaaggcggtgcgaactgcgctgaaattcagccgcagcgc agatgctccagcctacaagcaggggcagaaccagctctacaac gaactcaatcttggtcggagagaggagtacgacgtgctggacaa gcgagaggacgggacccagaaatggcggggaagccgcgc agaaagaatccccaagagggcctgtacaacgagctccaaaag gataagatggcagaagcctatagcgagattggtatgaaagggg aacgcagaagaggcaaaggccacgacggactgtaccagggga ctacgacccgccaaggaacacctatgacgctcttcacatgca ggccctgcgcgcctcgg (SEQ ID NO: 114)
ER_{mut}.Furin- CAR19=Alt7	MALPVTALLPLALLHAARPR SSLALSLTADQMVSALLDAEPPI LYSEYDPTTRPFSEASMMGLLTN LADRELVHMINWAKRVPGFVDL ALHDQVHLLLECAWMEILMIGLV WRSMEHPGKLLFAPNLLLDNRNQ GKCVEGGVEIFDMLLATSSRFR MMNLQGEFVCLKSIILLNSGVY TFLSSTLKSLEEKDHIHRVLDKIT DTLIHLMAKAGLTLQQQHQRRLA QLLLILSHIRHMSSKRMEHLYSM KCKNVVPLSDLLEMLDAHRLG <u>TGAEDPRPSRKRRSLGEIVMTQ</u> SPATLSLSPGERATLSCRASQDI SKYLNWYQQKPGQAPRLLIYHT SRLHSGIPARFSGSGSGTDYTL TISSLPEDFAVYFCQQGNTLPY TFGQGTKLEIKGGGSGGGGS GGGGSQVQLQESGPGLVKPSE TSLTCTVSGVSLPDYGVSWIR QPPGKGLEWIGVIWGSETTYYS SSLKSRVTISKDNSKNQVSLKLS SVTAADTAVYYCAKHYHYGGSY AMDYWQGGLTVTVSSTTTPAP RPPTPAPTIASQPLSLRPEACRP AAGGAVHTRGLDFACDIYWAPL AGTCGVLLLSLVITLYCKRGRKK LLYIFKQPFMRPVQTTQEEDGC SCRFPEEEEGGCELRVKFSRSA DAPAYKQGQNQLYNELNLGRR EEYDVLDKRRGRDPEMGKPR RKNPQEGLYNELQKDKMAEAY SEIGMKGERRRGKGHDGLYQG LSTATKDTYDALHMQALPPR (SEQ ID NO: 115)	Atggccctccctgtcaccgccctgctgcttccgtggtcttctgctc cagccgctcggcccggtcgtgcttggcacttccctgactgcgc accagatggtgtcgccttctggacgcgcgagcctccaattctgta ctgcgagtagatccgactcgccttctccgaagccagcatgat gggcctgttgactaacctggcggaccgcgaggttggtgcacatgat taactgggctaagcgggtgcgggcttcgtggacctggccctgca cgaccaagtgcacctcctggaatgcgcctggtggaatcctcat gatcgccctcgtgtggagatccatggagcatcccgaaagctcct gttgcacccaacctcctgcttgatgcgaaccagggaatgctg ggaagggggtgctgagatttcgacatgctgctcgcacctcttc cgggtccggatgatgaatctgcaggagagaagagttcgtgtgtcga agtcaatcatcctgctgaactccgggtctatacctctcgtgactgc accctcaagtactggaggaaaaagaccacatccatcgcgtgct cgataagatcacgcacaccttatccatctcatggcgaaggctgg actgacctgcaacagcagcaccagaggctggcccagttgctg ctgattctgagccacatccggcacatgctgccaagaggatggaa cacctgtacagcatgaagtgaagaacgtcgtgctctgtccgat ctgctcctggaaatgctggacgcgcacagactcggaaccggag <u>cagaagatcccaagccaagccggaagggcggtccctgggtg</u> aaattgtagatgcccagtcacccgccaactcttagccttccaccgg gagcgcgcaacctgtcttcagagcctcccaagacatctcaaa ataccttaattggtatcaacagaagcccgacagggtcctgcctt ctgacttaccacaccagccggtccattctggaatccctgccaggt tcagcggtagcggatctgggaccgactacacctcactatcagct cactgcagccagaggacttgcgtgctatttctgtcagaagggaa caccctgcctacaccttggacagggcaccaagctcgagatta aaggtaggaggtggcagcggaggaggtgggtccggcggtggag gaagccaggtccaactccaagaaagcggaccgggtctgtgaa gccatcagaaaactcttactgactgtgtagcggaggtgtctct ccccgattacggggtgtcttgatcagacagccaccgggaagg gtctggaatggattggagtgatttgggctctgagactactactct ctcatccctcaagtcacgcgtcacatctcaaaaggacaactctaa gaatcagggtgactgaaactgtcatctgtgaccgcagccgacac cgccgtgactattgcgctaagcattactattatggcgggagctac gcaatggattactggggacagggtactctggtcaccgtgtccagc accactacccagcaccgaggccacccacccggctcctacca tcgctccagcctctgtccctgcgtccggaggcatgtagaccg cagctggtggggccgtgcataccgggggtcttgacttcgctgcg atatctacatttggccctctggtggtacttgcgggtcctgctgc ttactcgtgatcactcttactgtaagcgcggtcggaagaagctg ctgtacatcttaagcaaccctcatgaggcctgtgcagactactca agaggaggacggctgtcatgccggtcccagaggaggaggaa

		ggcggctgcgaactgcgcgtgaaattcagccgcagcgcagatg ctccagcctacaagcaggggcagaaccagctctacaacgaact caatcttggtcggagagaggagtacgacgtgctggacaagcgg agaggacgggacccagaaatgggcgggaagccgcgcagaa agaatccccaagagggcctgtacaacgagctccaaaaggata agatggcagaagcctatagcgagattggtatgaaaggggaacg cagaagaggcaaaggccacgacggactgtaccagggactca gcaccgccaccaaggacacctatgacgctcttcacatgcaggcc ctgccgcctcgg (SEQ ID NO: 116)
--	--	--

General Methods

The following general materials and methods were used for the assays described in Examples 1-13.

Generation of CAR constructs

- 5 The scFvs used in the CAR constructs that were assessed in Examples 3 were independently synthesized based on an anti-CD19 scFv sequence described above. The scFv was cloned in a heavy-to-light chain direction, with a flexible linker connecting the VH and VL domains (e.g., GGGGSGGGGSGGGGSGGGGS (SEQ ID NO: 29)), into a vector backbone containing the CD8 hinge region along with the 4-1BB molecule and the CD3zeta molecule. To this, an N-terminal furin cleavage site fused to a destabilization domain was added upstream of the scFv. The proteins used in the furin-degion constructs that were assessed in Examples 4-5 were independently synthesized based on publicly available sequence data. To this, an N-terminal furin cleavage site fused to a destabilization domain was added upstream of the protein.

Cell lines and cell transduction

- 15 Jurkat cells were obtained from the ATCC and maintained in media according to supplier's recommendations. Jurkat cell lines were transduced by spinoculation with lentiviral supernatant from 293T cells transfected with pELPS using the protein-furin domain regulated plasmid DNA.

Cancer Cells

- 20 NALM6 and K562 cell lines were obtained from the ATCC and maintained in media according to supplier's recommendations. To produce a bioluminescent model for T cell killing assays, all cells were transduced with a luciferase lentiviral construct and kept under antibiotic selection.

Flow cytometry

- 25 Cells were isolated from *in vitro* culture, washed once in PBS supplemented with 0.5% bovine serum albumin, and stained on ice using either biotinylated Protein L followed by incubated with a fluorochrome-conjugated streptavidin reagent or an antibody recognizing the given target antigen. In all analyses, the population of interest was gated based on forward vs side scatter characteristics, followed by singlet

gating, and live cells were gated. Flow cytometry was performed on a four laser Fortessa (Becton-Dickinson).

Compound treatments

5 In all instances, either 4-OHT or Shield1 was resuspended in ethanol. Trimethoprim (TMP) was resuspended in DMSO. In all instances where concentrations not indicated, compounds were added for 24 hours in total prior to analysis by flow cytometry. 3 μ M 4-OHT (ER α), 1 μ M Shield1 (FKBP), or 100 μ M TMP (ecDHFR) was used.

Killing assay

10 In brief, luciferase transduced target cell lines were incubated at the indicated ratios with effector CD19CAR or CD19CAR-FurON T cells for 18 hours. Remaining luciferase activity was measured by adding Bright-Glo (Promega) on a luminescence reader (Envision). Percentage killing was calculated using negative controls.

Cytokine secretion

15 Effector and target cells were incubated at a 3:1 ratio in RPMI containing 10% FBS for 18 hours. Supernatant was analysed by 3-plex array according the manufacturer's instructions (Invitrogen).

EXAMPLE 2: FURIN IS THE MOST HIGHLY EXPRESSED PROPROTEIN CONVERTASE IN PRIMARY HUMAN T CELLS

20 Literature sources indicated that FURIN (FUR; PACE; PCSK3; SPC1) has a broad expression profile (Seidah, et al Nature Reviews Drug Discovery 11, 367-383 (May 2012)). The expression of the proprotein convertase family members was analysed by qRT-PCR. RNA was harvested from normal donor T cells on days 0, 4, and 11 following stimulation with anti-CD3/anti-CD28 activation beads. An additional group was supplemented with 100U/mL IL-2 during culture and RNA was harvested on day 11. These data demonstrate that following activation with anti-CD3/anti-CD28 beads, FURIN mRNA is expressed more
25 highly than other members of the proprotein convertase family (FIG. 1).

EXAMPLE 3: EXPRESSION OF CD19 CAR CONTROLLED BY COMPOUND ADDITION

30 Jurkat T cells were transduced with a furin degron domain (FKBP_{FD}, ER α _{FD}, or DHFR_{FD}) fused to an anti-CD19 scFv CAR construct followed by treatment with the corresponding compound. FKBP_{FD} transduced cells treated with 1 μ M Shield1. ER α _{FD} transduced cells treated with 1 μ M Bazedoxifene. DHFR_{FD} transduced cells treated with 1mM TMP. Expression of the anti-CD19 scFv is inducible in the presence of

compound (FIG. 2). Black=UTD; Gray=construct, no compound; White=construct, compound. These data demonstrate that multiple degron domains, when combined with a furin cleavage domain, result in strict compound-dependent regulation of CAR 19 expression.

5 EXAMPLE 4: KINETICS OF CAR EXPRESSION IN JURKAT CELLS FOLLOWING COMPOUND
ADDITION

Jurkat T cells were transduced with the indicated furin degron domain (FKBP_{FD} or ER α _{FD}) fused to an anti-CD19 scFv CAR construct. These cells were treated with either 1 μ M Shield1 or 1 μ M 4-OHT for the time indicated and CAR expression was determined by FACS. These data demonstrate that induction of
10 expression using a furin degron CAR 19 occurs rapidly following compound addition and is stable throughout the period of compound treatment (FIG. 3).

EXAMPLE 5: COMPOUND INDUCIBLE CAR EXPRESSION IN PRIMARY HUMAN T CELLS

Primary human T cells were transduced with ER α furin degron domain (ER α _{FD} domain) fused to an anti-
15 CD19 scFv CAR construct. 100 U/mL IL-2 was added on day 9 following activation with anti-CD3/CD28 stimulation beads. Bazedoxifene was added on day 10, and CAR expression was determined by FACS on day 11. These data demonstrate that a furin degron domain (e.g., ER α _{FD} domain) can regulate CAR 19 expression in a compound-dependent manner in primary human T cells (FIG. 4), and that stabilization is enhanced in the presence of IL-2 in vitro (FIG. 4).

20

EXAMPLE 6: KINETICS OF CAR EXPRESSION FOLLOWING COMPOUND WASHOUT IN PRIMARY T CELLS

Primary human T cells were transduced with the indicated furin degron domain (FKBP_{FD} or ER α _{FD}) fused to an anti-CD19 scFv CAR construct. 100 U/mL IL-2 was added on day 9 following activation with anti-
25 CD3/CD28 stimulation beads. Bazedoxifene was added on day 10, and T cells were frozen on day 11. T cells were thawed, extensively washed, and placed in culture for the times indicated followed by determination of CAR expression by FACS. These data demonstrate that removal of compound results in a reduction of CAR 19 expression using a furin degron domain (FIG. 5).

EXAMPLE 7: MULTIPLE ER-ALPHA TARGETING DRUGS STABILIZE ER-ALPHA FURON CARTS

Jurkat T cells were transduced with the ER α _{FD} degradation domain fused to an anti-CD19 scFv CAR construct followed by treatment with the indicated compounds for 24 hours. Compounds were used at 10 μ M for 4-OHT, 1 μ M for Bazedoxifene, or 1 μ M for Lasofoxifene. These data demonstrate that multiple ER-alpha targeting compounds can induce CAR 19 expression using an estrogen receptor-based furin
5 degron (FurON) system (FIG. 6).

EXAMPLE 8: DOSE RESPONSE WITH BAZEDOXIFENE IN HUMAN T CELLS

Primary human T cells were transduced with ER α _{FD} furin degron domain fused to an anti-CD19 scFv CAR
10 construct or the parental CD19 CAR construct. 100 U/mL IL-2 was added on day 9 following activation with anti-CD3/CD28 stimulation beads, and T cells were frozen on day 11. T cells were thawed and placed in culture for 48 hrs with Bazedoxifene at the concentrations indicated. CAR expression was determined by FACS. These data demonstrate that physiologically relevant concentrations of Bazedoxifene can stabilize furin degron CAR 19 expression in a level that is similar to parental CAR 19
15 (FIG. 7).

EXAMPLE 9: COMPOUND-DEPENDENT TARGET SPECIFIC CELL KILLING BY ER-ALPHA FURON CART

Primary human T cells were transduced with ER α _{FD} furin degron domain fused to an anti-CD19 scFv CAR
20 construct or the parental CD19 CAR construct. 100 U/mL IL-2 and Bazedoxifene were added on day 9 following activation with anti-CD3/CD28 stimulation beads, and T cells were frozen on day 11. T cells were thawed and incubated for 20 hours with the indicated luciferized cell line targets, K562 (CD19-) or NALM6 (CD19+). Percent killing was determined by analysis of remaining luciferase activity. These data demonstrate that CAR19 with an estrogen receptor-based furin degron domain specifically kills CD19+
25 tumor cells in a manner that is compound-dependent and is noninferior to the parental CAR19 (FIG. 8).

EXAMPLE 10: COMPOUND-DEPENDENT TARGET SPECIFIC CELL KILLING BY FKBP FURON CART

Primary human T cells were transduced with FKBP_{FD} furin degron domain fused to an anti-CD19 scFv CAR construct or the parental CD19 CAR construct. 100U/mL IL-2 and Shield1 were added on day 9
30 following activation with anti-CD3/CD28 stimulation beads, and T cells were frozen on day 11. T cells were thawed and incubated for 20 hours with the indicated luciferized cell line targets, K562 (CD19-) or NALM6 (CD19+). Percent killing was determined by analysis of remaining luciferase activity. These data

demonstrate that CAR19 with an FKBP-based furin degron domain specifically kills CD19⁺ tumor cells in a manner that is compound-dependent and is noninferior to the parental CAR19 (FIG. 9).

EXAMPLE 11: COMPOUND-DEPENDENT CYTOKINE PRODUCTION OF ER-ALPHA FURON CART

5 Primary human T cells were transduced with ER α _{FD} furin degron domain fused to an anti-CD19 scFv CAR construct or the parental CD19 CAR construct. 100 U/mL IL-2 and Bazedoxifene were added on day 9 following activation with anti-CD3/CD28 stimulation beads, and T cells were frozen on day 11. T cells were thawed and incubated with the indicated cell line targets for 20 hours. Supernatants were harvested and analyzed by cytokine bead array. These data demonstrate that CAR19 with an estrogen receptor-
10 based furin degron domain specifically produces cytokines in the presence of CD19⁺ tumor cells in a manner that is compound-dependent and is noninferior to the parental CAR19 (FIG. 10).

EXAMPLE 12: COMPOUND-DEPENDENT PROLIFERATION OF ER-ALPHA FURON CART

Primary human T cells were transduced with ER α _{FD} furin degron domain fused to an anti-CD19 scFv CAR
15 construct or the parental CD19 CAR construct. 100 U/mL IL-2 and Bazedoxifene were added on day 9 following activation with anti-CD3/CD28 stimulation beads, and T cells were frozen on day 11. T cells were thawed and incubated with the indicated cell line targets for 4 days. T cell FurON-CAR numbers were analyzed by FACS. These data demonstrate that CAR19 with an estrogen receptor-based furin
20 degron domain specifically proliferates in the presence of CD19⁺ tumor cells in a manner that is compound-dependent and is noninferior to the parental CAR19 (FIG. 11).

EXAMPLE 13: MATERIALS AND METHODS FOR EXAMPLES 14-26.

The following general materials and methods were used for the assays described in Examples 14-26.

FurON constructs

25 In some embodiments, the fusion protein described herein includes a furin degron (FurON) domain, which comprises two components: a degron or degradation domain, which is a mutated protein domain unable to acquire a proper conformation in the absence of a small molecule ligand, and a furin cleavage site. The furin degron domain can be fused to a protein of interest that is expressed in the endoplasmic reticulum. The N- and/ or C-termini of the protein of interest can be used as site of fusion, provided that
30 the furin degron domain faces the lumen of the endoplasmic reticulum. The protein of interest can be either a membrane protein (regardless of the number of transmembrane domains) or a soluble protein .

The orientation of the furin cleavage site relative to the degron domain should be such that the cleavage results in the separation of the furin degron domain and protein of interest. In the absence of the small molecule ligand or stabilization compound, the furin degron domain leads to the destabilization or degradation of the entire fusion protein. In the presence of the small molecule ligand or stabilization compound, the fusion protein is spared from degradation. The furin degron domain is mutated such that the affinity to its natural endogenous ligand is abolished; the affinity to the small molecule ligand or stabilization compound is preserved; and protein instability is conferred when the small molecule is absent.

Several constructs comprising different mutations and different furin cleavage sites within the furin degron domain were created and fused to the N-terminus of the anti-CD19 scFV CAR or anti-CD123 scFV CAR. Regardless the orientation of the scFV heavy and light chains, the fusion of the furin degron domain occurs between the signal peptide leader and the scFV. The mutated protein selected within the furin degron domain was a truncated version of the estrogen receptor alpha. The small molecule ligands chosen to stabilize the furin degron domain belong to the family of selective estrogen receptor modulators or downregulators.

The efficacy of the furin degron domain at destabilizing or stabilizing the CAR structure was assessed, in the absence or presence of a small molecule ligand. The potency of the CART cell effector function, when the furin degron domain was fused, was also evaluated in the absence or presence of a small molecule ligand, and compared to the parental CAR19 construct. Cells were normalized to the same percentage of CAR expressing cells, with the addition of untransduced T cells (UTDs) from the same donor T cell expansion. The normalized populations were then used in co-cultured assays to measure CAR-mediated cytolytic function, cytokine production, and proliferation.

Generation of FurON CAR constructs

The scFVs used in the CAR constructs assessed in the examples were independently synthesized based on anti-CD19 or anti-CD123 scFV sequences described above. The scFVs were cloned in a light-to-heavy chain direction (anti-CD19) or heavy-to-light chain direction (anti-CD123), with a flexible linker connecting the VH and VL domains (e.g., GGGSGGGSGGGSGGGGS, SEQ ID NO: 29), into a vector backbone containing the CD8 hinge region along with the 4-1BB molecule and the CD3zeta molecule. To this, an N-terminal furin cleavage site fused to a destabilization domain was added upstream of the scFV. All constructs are generated in a lentiviral vector. Sequences of various FurON CAR constructs and components thereof are provided in Table 23.

Table 23. Sequences of FurON CAR constructs and components thereof

	Amino acid sequence	DNA sequence
ER1 WT (305aa-549aa)	SLALSLTADQMVSALLDAEPPI LYSEYDPTRPFSEASMMGLLT NLADRELVHMINWAKRVPGF VDLTLHDQVHLLCAWLEILMI GLVWRSMEHPGKLLFAPNLLL DRNQGKCVEGMVEIFDMLLA TSSRFRMMNLQGEEFVCLKSI ILLNSGVYTFLSSTLKSLEEKD HIHRVLDKITDTLIHLMAGALT LQQQHQRQAQLLLILSHIRHM SNKGMEHLYSMKCKNVVPLY DLLLEMLDAHRL (SEQ ID NO: 970)	tcgttggcactttccctgactgccgaccagatggtgtccgcc cttctggacgccgagcctccaattctgtactcggagtagcat ccgactcgcccggttctccgaagccagcatgatgggcctgtt gactaacctggcgaccgcgagttggtgcacatgattaac tgggctaagcgggtgccgggcttcgtggacctgactctgc acgaccaagtgcacctcctggaatgcgcctggatggaaa tctcatgatcgccctcgtgtggagatccatggagcatccc ggaaagctcctgtttgcacccaacctcctgcttgatcgcaa ccagggaataatgcgtggaagggtggtcagattttcga catgctgctgccacctcttccgggtccggatgatgaatct gcagggagaagagttcgtgtctgaagtaaatcatcctgc tgaactccgggtctataccttctgagctcgacctcaagt cactggaggaaaaagaccacatccatcgctgctcgata agatcaccgacaccttatccatctcatggcgaaggctgg actgacctgcaacagcagcaccagaggctggcccagtt gctgctgattctgagccacatccggcacatgtcgaacaag gggatggaacacctgtacagcatgaagtgaagaacgtc gtgcctctgtacgatctgctcctggaaatgtcggacgcgca cagactc (SEQ ID NO: 971)
ERmut1 (6 mutations)	SLALSLTADQMVSALLDAEPPI LYSEYDPTRPFSEASMMGLLT NLADRELVHMINWAKRVPGF VDLALHDQVHLLCAWMEILM IGLVWRSMEHPGKLLFAPNLL LDRNQGKCVEGGVEIFDMLLA TSSRFRMMNLQGEEFVCLKSI ILLNSGVYTFLSSTLKSLEEKD HIHRVLDKITDTLIHLMAGALT LQQQHQRQAQLLLILSHIRHM SSKRMEHLYSMKCKNVVPLS DLLLEMLDAHRL (SEQ ID NO: 58)	tcgttggcactttccctgactgccgaccagatggtgtccgcc cttctggacgccgagcctccaattctgtactcggagtagcat ccgactcgcccggttctccgaagccagcatgatgggcctgtt gactaacctggcgaccgcgagttggtgcacatgattaac tgggctaagcgggtgccgggcttcgtggacctggccctgc acgaccaagtgcacctcctggaatgcgcctggatggaaa tctcatgatcgccctcgtgtggagatccatggagcatccc ggaaagctcctgtttgcacccaacctcctgcttgatcgcaa ccagggaataatgcgtggaagggtggtcagattttcga catgctgctgccacctcttccgggtccggatgatgaatct gcagggagaagagttcgtgtctgaagtaaatcatcctgc tgaactccgggtctataccttctgagctcgacctcaagt cactggaggaaaaagaccacatccatcgctgctcgata agatcaccgacaccttatccatctcatggcgaaggctgg actgacctgcaacagcagcaccagaggctggcccagtt gctgctgattctgagccacatccggcacatgtcgtccaaga ggatggaacacctgtacagcatgaagtgaagaacgtc tgctctgtccgatctgctcctggaaatgtcggacgcgcac agactc (SEQ ID NO: 1110)
ERmut2 (4 mutations)	SLALSLTADQMVSALLDAEPPI LYSEYDPTRPFSEASMMGLLT NLADRELVHMINWAKRVPGF VDLTLHDQVHLLCAWMEILM IGLVWRSMEHPGKLLFAPNLL LDRNQGKCVEGGVEIFDMLLA TSSRFRMMNLQGEEFVCLKSI ILLNSGVYTFLSSTLKSLEEKD HIHRVLDKITDTLIHLMAGALT LQQQHQRQAQLLLILSHIRHM SNKRMEHLYSMKCKNVVPLS DLLLEMLDAHRL (SEQ ID NO: 121)	tcgttggcactttccctgactgccgaccagatggtgtccgcc cttctggacgccgagcctccaattctgtactcggagtagcat ccgactcgcccggttctccgaagccagcatgatgggcctgtt gactaacctggcgaccgcgagttggtgcacatgattaac tgggctaagcgggtgccgggcttcgtggacctgacctgc acgaccaagtgcacctcctggaatgcgcctggatggaaa tctcatgatcgccctcgtgtggagatccatggagcatccc ggaaagctcctgtttgcacccaacctcctgcttgatcgcaa ccagggaataatgcgtggaagggtggtcagattttcga catgctgctgccacctcttccgggtccggatgatgaatct gcagggagaagagttcgtgtctgaagtaaatcatcctgc tgaactccgggtctataccttctgagctcgacctcaagt cactggaggaaaaagaccacatccatcgctgctcgata agatcaccgacaccttatccatctcatggcgaaggctgg

		actgaccctgcaacagcagcaccagaggctggcccagtt gctgctgattctgagccacatccggcacatgtcgaacaag aggatggaacacctgtacagcatgaagtgaagaacgtc gtgcctctgtccgatctgtcctggaaatgtggacgcgca cagactc (SEQ ID NO: 122)
Furin cleavage site1	RTKR (SEQ ID NO: 123)	cgtactaaaaga (SEQ ID NO: 1112)
Furin cleavage site2	GTGAEDPRPSRKRRSLGDVG (SEQ ID NO: 125)	ggaaccggcgcggaagacccccggccctccaggaagc gaaggccctcgagacgtgggt (SEQ ID NO: 126)
Furin cleavage site3	GTGAEDPRPSRKRR (SEQ ID NO: 127)	ggaaccggcgcggaagacccccggccctccaggaagc gaagg (SEQ ID NO: 128)
Furin cleavage site4	LQWLEQQVAKRRRTKR (SEQ ID NO: 129)	ctgcaatggctggagcagcagggtggcgaagcggagaac taagcgg (SEQ ID NO: 130)
Furin cleavage site5	GTGAEDPRPSRKRRSLGG (SEQ ID NO: 131)	ggcacagggtgccgaggacctcgcccaagccgcaaaa ggaggtcacttggcggc (SEQ ID NO: 132)
Furin cleavage site6	GTGAEDPRPSRKRRSLG (SEQ ID NO: 133)	ggaaccggagcagaagatcccagaccaagccgga aggcggccctgggt (SEQ ID NO: 134)
Furin cleavage site7	SLNLTESHNSRKRR (SEQ ID NO: 135)	agtctcaatttgactgagtcacacaattccaggaagaaaa gg (SEQ ID NO: 136)
Furin cleavage site8	CKINGYPKRGRKRR (SEQ ID NO: 137)	tgcaagatcaacggctaccctaagaggggcagaaagcg ggg (SEQ ID NO: 138)
Leader sequence/ Signal peptide (SP)	MALPVTALLPLALLHAARP (SEQ ID NO: 139)	atggccctccctgtcaccgcccgtgcttccgctggctcttc tgctccacgcgcgtcggccc (SEQ ID NO: 140)
SP-Linker 1- ERmut1-Furin cleavage site 1- CD19 CAR1	MALPVTALLPLALLHAARPR SSLALSLTADQMVSALLDAEP PILYSEYDPTRPFSEASMMGL LTNLADRELVHMINWAKRVPG FVDLALHDQVHLLECAWMEIL MIGLVWRSMEHPGKLLFAPNL LLDRNQGKCEGGVEIFDMLL ATSSRFRMMNLQGEFVCLK SIILLNSGVYTFLSSTLKSLEEK DHIHRVLDKITDTLIHLMAKAG LTLQQQHQRQAQLLLILSHIRH MSSKRMEHLYSMKCKNVVPL SDLLEMLDAHRLRTKREIVM TQSPATLSLSPGERATLSCRA SQDISKYLNWYQQKPGQAPR LLIYHTSRLHSGIPARFSGSGS GTDYTLTISSLQPEDFAVYFC QQGNTLPYTFGGTKLEIKGG GGSGGGGGSGGGGSQVQLQE SGPGLVKPSETLSLTCTVSGV SLPDYGVSWIRQPPGKGLEWI GVIWGSETTYSSSLKSRVTIS KDNSKNQVSLKLSSVTAADTA VYYCAKHYHYGGSYAMDYW GQGTLVTVSSTTTPAPRPPTP APTIASQPLSLRPEACRPAAG GAVHTRGLDFACDIYWAPLA GTCGVLLLSLVITLYCKRGRKK LLYIFKQPFMRPVQTTQEEDG CSCRFPEEEEGGCELRVKFS RSADAPAYKQGQNQLYNELN LGRREEYDVLDKRRGRDPEM	atggccctccctgtcaccgcccgtgcttccgctggctcttc tgctccacgcgcgtcggccccgggtcgtgtggcacttccc tgactgccgaccagatggtgtccgccccttctggacgcga gcctccaattctgtactcggagtagatccgactcggcgtt ctccgaagccagcatgatggcctgttgactaacctggcg gaccgcgagttggtgcacatgattaactgggctaagcggg tgccgggctcgtggacctggccctgcacgaccaagtga cctcctggaatgcgcctggatggaatcctcatgatcgcc tcgtgtggagatccatggagcatcccggaagctcctgtt gcaccaacctcctcgtgatcgcaaccagggaaaatgc gtggaagggggtgtcgagatttctgacatgctgctgccac ctctcccggttccggatgatgaatctgcaggagagaagagt tcgtgtgtctgaagtcaatcatcctgctgaactccgggtct ataccttctgagctcgacctcaagtactggaggaaaa agaccacatccatcgctgctgataagatcaccgacac ccttatccatctcatggcgaaggctggactgacctgaac agcagcaccagagggtggcccagttgctgctgattctgag ccacatccgacacatgtcgtccaagaggatggaacacct gtacagcatgaagtgaagaacgtcgtgcctctgtccgat ctgctcctggaaatgtggacgcgcacagactccgtacta aaagagaaattgtgatgaccagtcacccgccactcttag ccttcacccgggtgagcgcgcaacctgtctgcagagcct cccaagacatctcaaaataccttaattggtatcaacagaa gcccggacaggctcctcgtccttctgatctaccacaccagc cggtccattctggaatccctgccaggttcagcggtagcgg atctgggaccgactacacctcactatcagctcactgcag ccagaggacttcgtgtctattctgtcagcaagggaacac cctgccctacaccttggacagggcaccagactcgagatt aaaggtggaggtggcagcggaggaggtgggtccggcg gtggaggaagccaggtccaactccaagaaagcggacc gggtctgtgaagccatcagaaacttctcactgactgtact gtgagcggagtgctctccccgattacgggggtgtcttgatc

	GGKPRRKNPQEGLYNELQKD KMAEAYSEIGMKGERRRGKG HDGLYQGLSTATKDTYDALH MQALPPR (SEQ ID NO: 141)	agacagccaccggggaagggctggaatggattggagt gattggggctctgagactacttactcttcatccctcaag tcacgcgtcaccatctcaaaggacaactctaagaatcag gtgtcactgaaactgtcatctgtgaccgcagccgacaccg ccgtgtactattgcgctaagcattactattatggcgggagct acgcaatggattactggggacaggggtactctggtcaccgt gtccagcaccactacccagcaccgaggccaccaccacc cggctcctaccatcgctcccagcctctgtccctgcgtccg gaggcatgtagaccgcagctgggtggggccgtgcatacc cggggtcttgacttcgctgcgatactacatttgggcccctc tggctgttacttgcggggtcctgtctgttctactcgtgatcac tctttactgtaagcgcgggtcggaagaagctgtgtacatcttt aagcaacccttcatgaggcctgtgcagactactcaagag gaggacggctgttcatgccggtcccagaggaggaggaa ggcggctgcgaactgcgcgtgaaattcagccgcagcgc agatgtccagcctacaagcaggggcagaaccagctct acaacgaactcaatcttggtcggagagaggagtacgacg tgctggacaagcggagaggacgggacccagaaatggg cgggaagccgcgcagaaagaatcccaagagggcctg tacaacgagctccaaaaggataagatggcagaagcctat agcgagattggtatgaaaggggaacgcagaagaggca aaggccacgacggactgtaccagggactcagcaccgccc accaaggacacctatgacgctcttcacatgcaggccctgc cgctcgg (SEQ ID NO: 142)
SP-Linker 1- ERmut1-Furin cleavage site 2- CD19 CAR1 (construct 106)	MALPVTALLLPLALLLHAARPR SSLALSLTADQMVSALLDAEP PILYSEYDPTTRPFSEASMMGL LTNLADRELVHMINWAKRVP FVDLALHDQVHLLLECAWMEIL MIGLVWRSMEHPGKLLFAPNL LLDRNQGKCEVGGVEIFDMLL ATSSRFRMMNLQGEFVCLK SIILLNSGVYTFLSSTLKSLEEK DHIHRVLDKITDTLIHLMAKAG LTLQQQHQRQAQLLLILSHIRH MSSKRMEHLYSMKCKNVVPL SDLLEMLDAHRLGTGAEDPR PSRKRRSLGDVGEIVMTQSPA TSLSPGERATLSCRASQDIS KYLNWYQQKPGQAPRLLIYHT SRLHSGIPARFSGSGSGTDYT LTISSLQPEDFAVYFCQQGNT LPYTFGQGTKLEIKGGGGSG GGGSGGGGSQVQLQESGPG LVKPSETLSLTCTVSGVSLPD YGVSWIRQPPGKGLEWIGVIW GSETTYYSSSLKSRVTISKDN SKNQVSLKLSSVTAADTAVYY CAKHYYYGGSYAMDYWGQG TLVTVSSTTTTPAPRPPTPPTI ASQPLSLRPEACRPAAGGAV HTRGLDFACDIYIWAPLAGTC GVLLLSLVITLYCKRGRKLLYI FKQPFMRPVQTTQEEDGCSC RFPEEEEEGGCELRVKFSRSA DAPAYKQGQNQLYNELNLGR	atggccctccctgtcaccgccctgtcttccgtggctcttc tgctccacgcgcgtcggccccgggtcgtgtggcacttccc tgactgccgaccagatgggtgcccccttctggacgccga gctccaattctgtactcggagtagatccgactcgcctgtt ctccgaagccagcatgatgggcctgttgactaacctggcg gaccgcgagttgggtcacatgattaactgggctaagcggg tgccgggctcgtggacctggccctgcacgaccaagtga cctcctggaatgcgcctggatggaaatcctcatgatcgcc tcgtgtggagatccatggagcatcccgaaagctcctgttt gcaccaacctcctcgttgatcgcaaccagggaatgc gtggaagggggtgtcgagatttctgacatgctgctgccac ctctcccggttccggatgatgaatctgcaggagagaagagt tcgtgtgtctgaagtaacatcctcgtgaactccggggtct ataccttctgagctcgaccctcaagtcactggaggaaaa agaccacatccatcgctgtcgataagatcacggacac ccttatccatctcatggcgaaggctggactgacctgcaac agcagcaccagaggctggcccagttgctgtgattctgag ccacatccggcacatgtcgtccaagaggatggaacacct gtacagcatgaagtgaagaacgtcgtgcctctgtccgat ctgctcctggaaatgtggacgcgcacagactcggaaacc ggcgcggaagacccccggccctccaggaaagcgaaggt ccctcggagacgtgggtgaaattgtgatgaccagtcacc cgccactcttagcctttcaccgggtgagcgcgaaccctgt cttgacagagcctccaagacatctcaaaataccttaattgg tatcaacagaagccccggacaggctcctcgccttctgatcta ccacaccagccggctccattctggaatccctgccagggttc agcggtagcggatctgggaccgactacacctcactatca gctcactgcagccagaggacttcgtgtctatttctgtcagc aagggaacacctgcccctacaccttggacagggcacca agctcgagattaaaggtggaggtggcagcggaggaggt gggtccggcggtggaggaaagcagggtccaactccaaga aagcggaccgggtctgtgaagccatcagaactcttca

	REEYDVLDKRRGRDPEMGGK PRRKNPQEGLYNELQDKMA EAYSEIGMKGERRRGKGHDG LYQGLSTATKDTYDALHMQAL PPR (SEQ ID NO: 143)	ctgacttgactgtgagcggagtgctctccccgattacggg gtgtcttgatcagacagccaccggggaagggctggaat ggattggagtgattggggctctgagactactactcttc atccctcaagtcacgcgtaccatctcaaaggacaactct aagaatcagggtgactgaaactgcatctgtgaccgcag ccgacaccgctgtactattgcgtaagcattactattatg gctggagctacgcaatggattactgggacaggggtactct ggcaccgtgtccagcaccactacccagcaccgaggcc accaccccggtcctaccatcgctctccagcctctgtccc tgctccggaggcatgtagaccgcagctggtggggcgg tgcataccggggcttgacttcgctcgatactacatttg ggccctctggctggtacttgcggggtcctgctgcttactc gtgatcactcttactgtaagcgggtcggaagaagctgct gtacatctttaagcaaccctcatgaggcctgtgcagacta ctcaagaggaggacggctgtcatgccggtcccagagg aggaggaaggcggctgcgaactgcgctgaaattcagc cgacgcgagatgtccagcctacaagcaggggcaga accagctctacaacgaactcaatcttgctggagagagg agtacgacgtgctggacaagcggagaggacgggaccc agaaatggcggggaagccgcgcagaaagaatcccaa gagggcctgtacaacgagctcaaaaggataagatggc agaagcctatagcgagattggtatgaaaggggaacgca gaagaggcaaaggccagcagcgtgtaccagggact cagcaccgccaccaaggacacctatgacgctcttcatat gcaggccctgccgctcgg (SEQ ID NO: 144)
SP-Linker 1- ERmut1-Furin cleavage site 2- CD19 CAR2	MALPVTALLPLALLHAARPR SSLALSLTADQMVSALLDAEP PILYSEYDPTRPFSEASMMGL LTNLADRELVHMINWAKRVP FVDLALHDQVHLLCAWMEIL MIGLVWRSMEHPGKLLFAPNL LLDRNQGKCEGGVEIFDMLL ATSSRFRMMNLQGEFVCLK SIILLNSGVYTFLSSTLKSLEEK DHIHRVLDKITDTLIHLMKAG LTLQQQHQLAQLLLILSHIRH MSSKRMEHLYSMKCKNVVPL SDLLEMLDAHRLGTGAEDPR PSRKRRSLGDVGEIVMTQSPA TSLSPGERATLSCRASQDIS KYLNWYQQKPGQAPRLIYHT SRLHSGIPARFSGSGSGTDYT LTISSLQPEDFAVYFCQQGNT LPYTFGQGTKLEIKGGGSG GGGSGGGGSQVQLQESGPG LVKPSETLSLTCTVSGVSLPD YGVSWIRQPPGKLEWIGVIW GSETTYSSSLKSRVTISKDN SKNQVSLKLSSVTAADTAVYY CAKHYYYGGSYAMDYWGQG TLVTVSSTTTPAPRPPTPPTI ASQPLSLRPEACRPAAGGAV HTRGLDFACDIYWAPLAGTC GVLLLSLVITLYCKRGRKLLYI FKQPFMRPVQTTQEEDGCSC RFPEEEEGGCELRVKFSRSA	atggccctccctgtcaccgcccgtgcttccgctggctcttc tgctccacgcgcgtcggccccggctgctgtggcacttccc tgactgccgaccagatgggtgcgccttctggacgccga gcctccaattctgtactcggagtagcatccgactcggcgtt ctccgaagccagcatgatgggcctgttgactaacctggcg gaccgcgagttggtgcacatgattaactgggctaagcggg tgccgggctcgtggacctggcctgcacgaccaagtga cctcctggaatgcgcctggatggaaatcctcatgatcgcc tcgtgtggagatccatggagcatcccgaaagctcctgtt gcaccaacctcctgcttgatcgcaaccagggaagatgc gtggaagggggtgctgagatttgcacatgctgctgccac ctctcccggttccggatgatgaatctgcaggagagaagagt tcgtgtgtcgaagtcaatcatcctgctgaactccggggtct ataccttctgagctcgacctcaagtactggaggaaaa agaccacatccatcgctgctgataagatcacggacac ccttatccatctcatggcgaaggctggactgacctgcaac agcagcaccagaggctggcccagttgctgctgattctgag ccacatccggcacatgtcgtccaagaggatggaacacct gtacagcatgaagtgaagaacgtcgtgcctctgtccgat ctgctcctggaaatgctggacgcgcacagactcggaacc ggcgcggaagacccccggccctccaggaagcgaaggt ccctcggagacgtgggtgaaattgtgatgaccagtcacc cgccactcttagccttccacccggtgagcgcgcaacctgt cttgacagagcctccaagacatctcaaaataccttaattgg tatcaacagaagcccgacaggctcctgccttctgatcta ccacaccagccggctccattctggaatccctgccagggtc agcggtagcggatctgggaccgactacacctcactatca gtcactgcagccagaggactcgtgctctattctgtcagc aagggaacacctgcccacaccttggacagggcacca agctcgagattaaaggtggaggtggcagcggaggaggt gggtccggcggtggaggaagccagggtccaactccaaga

	DAPAYQQGQNQLYNELNLGR REEYDVLDRRRGRDPEMGGK PRRKNPQEGLYNELQDKMA EAYSEIGMKGERRRRGKHDG LYQGLSTATKDTYDALHMQAL PPR (SEQ ID NO: 145)	aagcggaccgggtctgtgaagccatcagaaactcttca ctgactgtactgtgagcggagtgtctctcccattacggg gtgtcttgatcagacagccaccgggaagggtctggaat ggattggagtatttggggctctgagactactactcttc atccctcaagtcacgcgtcaccatctcaaaggacaactct aagaatcagggtgactgaaactgtcatctgtgaccgcag ccgacaccgctgtactattcgctaagcattactattatg gctggagctacgcaatggattactgggacagggtactct ggcaccgtgtccagcaccactacccagcaccgaggcc accaccccggtctctaccatcgctcccagcctctgtccc tgcgtccggaggcatgtagaccgcagctggtggggcgg tgcatacccggtctgtacttcgctgcgatactacattg ggccctctggctggtacttgcgggtctgctgcttctactc gtgatcactcttactgtaagcgggtcggaagaagctgt gtacatcttaagcaaccctcatgaggcctgtgcagacta ctcaagaggaggacggctgtcatgccggttcccaggagg aggaggaaggcggctgcgaactgcgctgaaattcagc cgagcgcagatgtccagcctaccagcaggggcagaa ccagctctacaacgaactcaatcttggtcggagagagga gtacgacgtgtggaagaagcggagaggacgggaccca gaaatggggcgggaagcgcgcagaaagaatccccaag agggcctgtacaacgagctccaaaaggataagatggca gaagcctatagcagattggtatgaaagggaacgcag aagaggcaaaggccacgacggactgtaccagggactc agcaccgccaccaaggacacctatgacgtcttcacatg caggccctgccgctcgg (SEQ ID NO: 146)
SP-Linker 1- ERmut1-Furin cleavage site 3- CD19 CAR1 (construct 103)	MALPVTALLPLALLHAARPR SSLALSLTADQMVSALLDAEP PILYSEYDPTPRFSEASMMGL LTNLADRELVHMINWAKRVP FVDLALHDQVHLLCAWMEIL MIGLVWRSMEHPGKLLFAPNL LLDRNQGKCEVGGVEIFDMLL ATSSRFRMMNLQGEFVCLK SIILLNSGVYTFLSSTLKSLEEK DHIHRVLDKITDTLIHLMKAG LTLQQQHQLAQLLLILSHIRH MSSKRMEHLYSMKCKNVVPL SDLLEMLDAHRLGTGAEDPR PSRKRREIVMTQSPATLSLSP GERATLSCRASQDISKYNWY QQKPGQAPRLIYHTSRLHSG IPARFSGSGSGTDYTLTISSLQ PEDFAVYFCQQGNTLPYTFG QGKLEIKGGGSGGGSGGSGG GGSQVQLQESGPGLVKPSE TSLTCTVSGVSLPDYGV WIRQPPGKGLEWIGVIWGS ETYYSSSLKSRVTISKDNS KNQVSLKLSSVTAADTAVY YCAKHYYYGGSYAMDY GQGTLVTVSSTTTPAPRPP TPAPTIASQPLSLRPEACRP AAGGAVHTRGLDFACDIYI WAPLAGTCGVLLLSLVITLY	atggccctccctgtcaccgcccgtgtcttccgtggtcttc tgctccacgcgcgtcggccccgggtcgtgtggcacttccc tgactgccgaccagatggtgtccgccccttctggacgcga gcctccaattctgtactcggagtacgatccgactcggcgtt ctccgaagccagcatgatgggcctgttgactaacctggcg gaccgcgagttggtgcacatgattaactgggctaagcggg tgccgggctcgtggacctggccctgcacgaccaagtga cctcctggaatgcgcctggatggaatcctcatgatcggcc tcgtgtggagatccatggagcatcccgaaagctcctgttt gcaccaacctcctgcttgatcgcaaccagggaagatgc gtggaaggggtgtcgagatttctgacatgctgtcgcacac ctcttccgggttccggatgatgaatctgcaggagagaagagt tcgtgtgtctgaagtcaatcatcctgctgaactccgggtct ataccttctgagctcgacctcaagtactggaggaaaa agaccacatccatcgctgtcgtataagatcaccgacac ccttatccatctcatggcgaaggctggactgacctgcaac agcagcaccagaggctggccagttgctgtgattctgag ccacatccggcacatgtcgtccaaggaggatggaacacct gtacagcatgaagtgaagaacgtcgtgcctctgtccgat ctgctcctggaaatgctggacgcgcacagactcgggacg ggagctgaagatccacgaccagcagaaagcgcaggg aaattgtgatgaccagtcacccgccactcttagcctttcac ccggtagcgcgcgaacctgtcttgagagcctcccaag acatctcaaaaataccttaattggtatcaacagaagcccg acaggctcctgccttctgatctaccacaccagccggtcc attctggaatccctgccagggtcagcggtagcggatctggg accgactacacctcactatcagctcactgcagccagag gactcgtgtctatttctgtcagcaagggaacacctgcc tacaccttggacagggcaccaagctcgagattaaagggtg gaggtggcagcggaggagggtgggtcggcggtggagg

	CKRGRKKLLYIFKQPFMRP VQTTQEEDGCSCRFPEEE EGGCELRVKFSRSADAPA YKQGQNQLYNELNLGRRE EYDVLDKRRGRDPEMGGK PRRKNPQEGLYNELQKDK MAEAYSEIGMKGERRRGK GHDGLYQGLSTATKDTYD ALHMQALPPR (SEQ ID NO: 147)	aagccagggtccaactccaagaaagcggaccgggtctgt gaagccatcagaaactcttactgactgtactgtgagcg gagtgtctctccccgattacggggtgtcttgatcagacag ccaccggggaaggggtctggaatggattggagtattggg gctctgagactactactactcttcatccctcaagtcacgct caccatctcaaaggacaactctaagaatcagggtgactg aaactgtcatctgtgaccgcagccgacaccgctgtact attgcgctaagcattactattatggcgggagctacgcaatg gattactggggacagggtactctggtcaccgtgtccagca ccactacccagcaccgaggccacccaccccgctccta ccatcgctcccagcctctgtccctgcgtccggaggcatgt agaccgcagctggtggggcgtgcataccgggggtctt gacttcgctcgatctacatttgggcccctctggtggtta cttgcggggtcctgtcttctactcgtgatcactttactgta agcgcggtcgggaagaagctgctgtacatcttaagcaacc cttcatgaggcctgtgcagactactcaagaggaggacgg ctgttcatgccggttccagaggaggaggaaggcggctg cgaactgcgctgaaattcagccgcagcgcagatgtcc agcctacaagcaggggcagaaccagctctacaacgaa ctcaatcttggtcggagagaggagtacgacgtgctggaca agcggagaggacgggaccagaaatggcggggaagc cgcgagaaagaatccccaagaggcctgtacaacga gctccaaaaggataagatggcagaagcctatagcgaga ttggtatgaaaggggaacgcagaagaggcaaaggcca cgacggactgtaccagggactcagcaccgccaaccaagg acacctatgacgctcttcacatgcaggccctgccgctcg g (SEQ ID NO: 148)
SP-Linker 1- ERmut1-Furin cleavage site 3- CD19 CAR2	MALPVTALLPLALLHAARPR SSLALSLTADQMVSALLDAEP PILYSEYDPTPRPFSEASMMGL LTNLADRELVHMINWAKRVPG FVDLALHDQVHLLCAWMEIL MIGLVWRSMEHPGKLLFAPNL LLDRNQGKCEVGGVEIFDMLL ATSSRFRMMNLQGEFVCLK SIILLNSGVYTFLSSTLKSLEEK DHIHRVLDKITDTLIHLMKAG LTQQQHQRQAQLLLILSHIRH MSSKRMEHLYSMKCKNVVPL SDLLEMLDAHRLGTGAEDPR PSRKRREIVMTQSPATLSLSP GERATLSCRASQDISKYNWY QQKPGQAPRLLIYHLSRLHSG IPARFSGSGSGTDYTLTISSLQ PEDFAVYFCQQGNTLPYTFG QGKLEIKGGGSGGGGSGG GGSQVQLQESGPGLVKPSSET LSLTCTVSGVSLPDYGVSWIR QPPGKGLEWIGVIWGSETYY SSSLKSRVTISKDNSKNQVSL KLSSVTAADTAVYYCAKHYYY GGSYAMDYWGQGLTVVSST TTPAPRPPTPAPTIASQPLSLR PEACRPAAGGAVHTRGLDFA CDIYIWAPLAGTCGVLLLSLVIT LYCKRGRKKLLYIFKQPFMRP	atggccctccctgtcaccgcccgtgcttccgctggctcttc tgctccacgcccgtcggccccggctgctgtggcacttccc tgactgccgaccagatgggtgccccccttctggacgccga gcctccaattctgtactcggagtagcatccgactcggcgtt ctccgaagccagcatgatgggcctgttgactaacctggcg gaccgcgagttggtgcacatgattaactgggctaagcggg tgccgggcttctgtggacctggccctgcacgaccaagtga cctcctggaatgcgcctggatggaaatcctcatgatcgcc tcgtgtggagatccatggagcatcccggaaagctcctgtt gcaccaaacctcctgctgtatcgcaaccagggaatgc gtggaagggggtgtcgagatttctgacatgctgctgccac ctctcccgggtccggatgatgaatctgcaggagagaagagt tcgtgtgtctgaagtaatcctcctgtgaactccggggtct ataccttctgagctcgaccctcaagtcactggaggaaaa agaccacatccatcgctgctgataagatcaccgacac ccttatccatctcatggcgaaggctggactgacctgcaac agcagcaccagaggctggcccagttgctgtgattctgag ccacatccggcacatgtcgtccaagaggatggaacacct gtacagcatgaagtgaagaacgtcgtgcctctgtccgat ctgctcctggaaatgtcggacgcgcacagactcgggacg ggagctgaagatccacgaccagcagaaagcgacggg aaattgtgatgaccagtcacccgccactcttagcctttcac ccggtgagcgcgcaacctgtcttgagagcctccaag acatctcaaaaataccttaattggtatcaacagaagccgg acaggctcctgccttctgtatctaccacaccagccggtcc attctggaatccctgccaggtcagcggtagcggatctggg accgactacacctcactatcagctcactgcagccagag gacttcgctgtctattctgtcagaagggaacacctgccc tacacctttggacagggcaccaagctcagattaaagggtg

	VQTTQEEDGCSCRFPEEEEE GCELRVKFSRSADAPAYQQG QNQLYNELNLGRREEYDVL KRRGRDPEMGGKPRRKNPQ EGLYNELQKDKMAEAYSEIGM KGERRRGKGDGLYQGLSTA TKDTYDALHMQALPPR (SEQ ID NO: 149)	gagggtggcagcggaggaggtgggtccggcgggtggagg aagccaggccaactccaagaaagcggaccgggtctgt gaagccatcagaaactcttctactgactgtactgtgagcg gagtgctctccccgattacggggtgtcttgatcagacag ccaccgggaaggggtctggaatggattggagtattggg gctctgagactactactactctcatccctcaagtcacgct caccatctcaaaggacaactctaagaatcaggtgtcactg aaactgtcatctgtgaccgcagccgacaccgccgtgtact attgctgaagcattactattatggcgggagctacgcaatg gattactggggacaggggtactctggtcaccgtgccagca ccactacccagcaccgaggccacccaccccggtccta ccatcgctcccagcctctgtccctcggtccggaggcatgt agaccgcagctggtggggcgggtgcatacccggggtctt gactcgccctgcgatactacattgggcccctctggtggt cttgccgggtcctgtgcttctactcgtgatcactcttactgta agcgcgggtcggagaagctgctgtacatcttaagcaacc ctcatgaggcctgtgcagactactcaagaggaggacgg ctgtcatgccggttccagaggaggaggaaaggcggctg cgaactgcgctgaaattcagccgcagcgcagatgtctc agcctaccagcaggggcagaaccagctctacaacgaac tcaatcttggtcggagagaggagtacgacgtgctggaca agcggagaggacgggaccagaaatggcggggaagc cgcgagaaagaatccccaagaggcctgtacaacga gctccaaaaggataagatggcagaagcctatagcgaga ttggtatgaaaggggaacgcagaagaggcaaaggcca cgacggactgtaccagggactcagcaccgccaccaagg acacctatgacgctcttcacatgcaggccctgcgcctcg g (SEQ ID NO: 150)
SP-Linker 1- ERmut2-Furin cleavage site 1- CD19 CAR1	MALPVTALLLPLALLLHAARPR SSLALSLTADQMVSALLDAEP PILYSEYDPTPRPFSEASMMGL LTNLADRELHVHMINWAKRVP FVDLTLDHQQVHLLLECAWMEIL MIGLVWRSMEHPGKLLFAPNL LLDRNQGKCEVEGGVEIFDMLL ATSSRFRMMNLQGEFVCLK SIILLNSGVYTFLSSTLKSLEEK DHIHRVLDKITDTLIHLMAKAG LTQQQHQRQAQLLLILSHIRH MSNKRMEHLYSMCKKNVPL SDLLEMLDAHRLRTKREIVM TQSPATLSLSPGERATLSCLA SQDISKYNWYQQKPGQAPR LLIYHTSRLHSGIPARFSGSGS GTDYTLTISSLQPEDFAVYFC QQGNTLPYTFGQGTKLEIKGG GGSGGGGSGGGGSQVQLQE SGPGLVKPSETLSLTCTVSGV SLPDYGVSWIRQPPGKLEWI GVIWGSETTYSSSLKSRVTIS KDNSKNQVSLKLSSVTAADTA VYYCAKHYYYGGSYAMDYW GQGTLVTVSSTTTTPAPRPPTP APTASQPLSLRPEACRPAAG GAVHTRGLDFACDIYWAPLA GTCGVLLLSLVITLYCKRGRKK	atggccctccctgtcaccgcccgtgctgtccgctggctcttc tgctccacgcgcgtcgccccgggtcgTcggtggcactttcc ctgactgccgaccagatggtgtccgcccctctggacgcgcg agcctccaattctgtactcggagtacgatccgactgcgccg ttctccgaagccagcatgatggcctgttgactaacctggc ggaccgcgagttggtgcacatgattaactgggctaagcgg gtgccgggcttcgtggacctgacctgcacgaccaagtgc acctcctggaatgcgcctggatggaaatcctatgatcgg cctcgtgtggagatccatggagcatcccgaaagctcctg ttgcacccaacctcctgctgatcgcaaccagggaagaaatg cgtggaagggggtgtcgagatttcgacatgctgctcgcca cctcttccgggttcggatgatgaatcgcaggggagaaga gttcgtgtgtctgaagtcaatcatcctgctgaactccgggt ctataccttctgagctcgacctcaagtcactggaggaaa aagaccacatccatcgctgctcgataagatcaccgaca cccttatccatctcatggcgaaggctggactgacctgcaa cagcagcaccagaggctggcccagttgctgctgattctga gccacatccggcacatgtcgaacaagaggatggaacac ctgtacagcatgaagtgcagaacgctcgtgcctctgtccg atctgctcctggaaatgctggacgcgcacagactccgtact aaaagagaaattgtgatgaccagtcacccgccactctta gcctttcaccgggtgagcgcgcaacctgtcttgacagc ctcccaagacatctcaaaataccttaattggtatcaacaga agcccgacaggctcctgccttctgatctaccacaccag ccggctccattctggaatccctgccagggtcagcggtagcg gatctgggaccgactacacctcactatcagctcactgca gccagaggacttcgctgtctattctgtcagaagggaaca ccctgccctacaccttggacagggcaccgaagctcgagat

	LLYIFKQPFMRPVQTTQEEDG CSCRFPEEEEGGCELRVKFS RSADAPAYKQGQNQLYNELN LGRREEYDVLDRRRGRDPEM GGKPRRKNPQEGLYNELQKD KMAEAYSEIGMKGERRRGKG HDGLYQGLSTATKDTYDALH MQALPPR (SEQ ID NO: 151)	taaaggtggaggtggcagcggaggaggtgggtccggcg gtggaggaagccaggtccaactccaagaaagcggacc ggggtctgtgaagccatcagaaactcttctactgactgtact gtgagcggaggtctctccccgattacgggggtgtcttgatc agacagccaccggggaagggctggaatggattggagt gatttggggctctgagactacttactcttcatccctcaag tcacgcgtcaccatctcaaaggacaactctaagaatcag gtgtcactgaaactgtcatctgtgaccgcagccgacaccg ccgtgtactattgcgtaagcattactattatggcgggagct acgcaatggattactggggacaggggtactctggtcaccgt gtccagcaccactaccccagcaccgaggccacccaccc cggctcctaccatcgctcccagcctctgctcctgctgctcg gaggcatgtagaccgcagctggtggggccgtgcatacc cgggggtctgacttcgctgcgatatctacatttggggccctc tggctggtacttgcggggtcctgctgcttctactcgtgatcac tcttactgtaagcgcgggtcggaagaagctgctgtacatctt aagcaacccttcatgaggcctgtgcagactactcaagag gaggacggctgttcatgcccgttcccagaggaggaggaa ggcggctgcgaactgcgctgaaattcagccgcagcgc agatgtccagcctacaagcaggggcagaaccagctct acaacgaactcaatcttggtcggagagaggagtacgacg tgcctggacaagcggagagaggacgggacccagaaatggg cgggaagccgcgcagaaagaatcccaagagggcctg tacaacgagctccaaaaggataagatggcagaagcctat agcagattggatgaaaggggaacgcagaagaggca aaggccacgacggactgtaccagggaactcagaccgcc accaaggacacctatgacgtcttcatatgcaggccctgc cgctcgg (SEQ ID NO: 152)
SP-Linker 1- ERmut2-Furin cleavage site 2- CD19 CAR1 (construct 130)	MALPVTALLPLALLLHAARPR SSLALSLTADQMVSALLDAEP PILYSEYDPTPRPFSEASMMGL LTNLADRELHVHMINWAKRVPG FVDLTLDHQQVHLLLECAWMEIL MIGLVWRSMEHPGKLLFAPNL LLDRNQGKCEVGGVEIFDMLL ATSSRFRMMNLQGEFVCLK SIILLNSGVYTFLSSTLKSLEEK DHIHRVLDKITDTLIHLMAKAG LTLQQQHQLAQLLLILSHIRH MSNKRMEHLYSMKCKNVVPL SDLLEMLDAHRLGTGAEDPR <u>PSRKRRSLGDVGEIVMTQSPA</u> TLSLSPGERATLSCRASQDIS KYLNWYQQKPGQAPRLLIYHT SRLHSGIPARFSGSGSGTDYT LTISSLQPEDFAVYFCQQGNT LPYTFGQGKLEIKGGGGSG GGGSGGGGSQVQLQESGPG LVKPSETLSLTCTVSGVSLPD YGVSWIRQPPGKLEWIGVIW GSETTYSSSLKSRVTISKDN SKNQVSLKLSSVTAADTAVYY CAKHYYYGGSYAMDYWGQG TLVTVSSTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAV HTRGLDFACDIYIWAPLAGTC	atggccctccctgtcaccgcctgctgcttccgctggctcttc tgctccacgcgcgtcggccccggctgctgtggcacttccc tgactgccgaccagatgggtgctccgcttctggacgcga gcctccaattctgtactcggagtagcatccgactcggcgtt ctccgaagccagcatgatgggcctgttgactaacctggcg gaccgcgagttggtgcacatgattaactgggctaagcggg tgccgggcttctgtagcctgacccgtgcacgaccaagtga cctcctggaatgcgcctggatggaaatcctcatgatcggcc tcgtgtggagatccatggagcatcccggaagctcctgttt gcaccaacctcctgctgtagcgaaccagggaatgc gtggaagggggtgtcgagatttgcagatgctgctgccac ctcttccgggtccggatgatgaatctgcagggaagaaggt tcgtgtgtctgaagtcaatcactcctgctgaactccgggtct ataccttctgagctcgaccctcaagtactggaggaaaa agaccacatccatgcggtgctgataagatcaccgacac ccttatccatctcatggcgaaggctggactgacctgcaac agcagcaccagaggctggccaggtgctgctgattctgag ccacatccggcacatgtcgaacaagaggatggaacacc tgtacagcatgaagtgaagaacgctgctgctctgtccgat ctgctcctggaaatgctggacgcgcacagactcggaacc ggcgcggaagacccccggccctccagggaagcgaagggt ccctcggagacgtgggtgaaattgtgatgaccagtcacc cgccactcttagccttccaccgggtgagcgcgcaacctgt ctgacagagcctccaagacatctcaaaataccttaattgg tatcaacagaagcccgacaggctcctgccttctgatcta ccacaccagccggctccattctggaatccctgccagggtc agcggtagcggatctgggaccgactacacctcactatca gctcactgcagccagaggacttcgtgtctattctgtcagc

	GVLLLSLVITLYCKRGRKLLYI FKQPFMRPVQTTQEEDGCSC RFPEEEEEGGCELRVKFSRSA DAPAYKQGQNQLYNELNLGR REEYDVLDRRRGRDPEMGGK PRRKNPQEGLYNELQDKMA EAYSEIGMKGERRRGKHDG LYQGLSTATKDTYDALHMQAL PPR (SEQ ID NO: 153)	aagggaacaccctgccctacaccttggacagggcacca agctcgagattaaaggtggaggtggcagcggaggaggt gggtccggcgggtggaggaagccaggtccaactccaaga aagcggaccgggtctgtgaagccatcagaaactcttca ctgactgtactgtgagcggagtgctctccccgattacggg gtgtcttgatcagacagccaccggggaagggcttgaat ggattggagtgattggggctctgagactactactactctt atccctcaagtcacgcgtcaccatctcaaaggacaactct aagaatcagggtgactgaaactgtcatctgtgaccgcag ccgacaccgcccgtgtactattgcgctaagcattactattatg gctggagctacgcaatggattactgggacaggggtactct ggtcaccgtgtccagcaccactaccccagcaccgaggcc acccaccccggtcctaccatcgctcccagcctctgtccc tgcgtccggaggtatgtagaccgcagctggtggggcgg tgcatacccggtgtgacttcgctgcgatatctacatttg ggccccctcggctggtacttgcggggctctgtcttctactc gtgatcactcttactgtaagcgcggctcgaagaagctgct gtacatcttaagcaaccctcatgaggcctgtgcagacta ctcaagaggaggacggctgttcacgctcgggtccagagg aggaggaaggcggctgcgaactgcgctgaaatcagc cgacgcgagatgctccagcctacaagcaggggcaga accagctctacaacgaactcaatcttggcgagagagg agtacgacgtgctggacaagcggagaggacgggaccc agaaatgggcggaagccgcgcagaaagaatcccaa gagggcctgtacaacgagctccaaaaggataagatggc agaagcctatagcgagattggtatgaaaggggaacgca gaagaggcaaaggccacgacggactgtaccagggact cagcaccgccaccaaggacacctatgacgctcttcatat gcaggccctgccgcctcgg (SEQ ID NO: 154)
SP-Linker 1- ERmut2-Furin cleavage site 2- CD19 CAR2	MALPVTALLLPLALLLHAARPR SSLALSLTADQMVSALLDAEP PILYSEYDPTPRPFSEASMMGL LTNLADRELVHMINWAKRVPG FVDLTLHDQVHLLCAWMEIL MIGLVWRSMEHPGKLLFAPNL LLDRNQGKCVEGGVEIFDMLL ATSSRFRMMNLQGEFVCLK SIILLNSGVYTFLSSTLKSLEEK DHIHRVLDKITDTLIHLMAKAG LTLQQQHQRQAQLLLILSHIRH MSNKRMEHLYSMKCKNVVPL SDLLLEMLDAHRLGTGAEDPR PSRKRRSLGDVGEIVMTQSPA TSLSPGERATLSCRASQDIS KYLNWYQQKPGQAPRLLIYHT SRLHSGIPARFSGSGSGTDYT LTISSLQPEDFAVYFCQQGNT LPYTFGQGTKLEIKGGGGSG GGGSGGGGSQVQLQESGPG LVKPSSETLSLTCTVSGVSLPD YGVSWIRQPPGKLEWIGVIW GETTYYSSSLKSRVTISKDN SKNQVSLKLSSVTAADTAVYY CAKHYYYGGSYAMDYWGQG TLVTVSSTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAV	atggccctccctgtcaccgcctgtgcttccgtggtcttcc tgctccacgcgcgtcggccccgggtgctgtggcacttccc tgactgcgaccagatggtgtccgcctcttgacgcgcga gcctccaattctgtactcggagtagcatcgactcgccgtt ctccgaagccagcatgatgggcctgttgactaacctggcg gaccgcgagttggtgcacatgattaactgggctaagcggg tgccgggctcgtggacctgacctgcacgaccaagtgc cctcctggaatgcgcctggatggaaatcctcatgatcgcc tcgtgtggagatccatggagcatcccggaagctcctgtt gcaccaacctcctcgtgatcgcaaccagggaaaatgc gtggaagggggtgtcgagatttgcacatgctgctgccac ctctcccggtccggatgatgaatctgcaggagagaagagt tcgtgtgtctgaagtcaatcatcctgctgaactccggggtct ataccttctgagctcgacctcaagtactggaggaaaa agaccacatccatcgctgctcgataagatcaccgacac ccttatccatctcatggcgaaggctggactgacctgcaac agcagcaccagaggctggccagttgctgctgattctgag ccacatccggcacatgtcgacaagaggatggaaacacc tgtacagcatgaagtgaagaacgctgctgctctgtccgat ctgctcctggaatgtgagcgcgcacagactcggaacc ggcgcggaagacccccggccctccaggaagcgaaggt ccctcggagacgtgggtgaaattgtgatgaccagtcacc cgccactcttagccttccaccgggtgagcgcgcaaccctgt ctgacagacccccaagacatctcaaaataccttaattgg tatcaacagaagcccgacaggctcctgccttctgatcta ccacaccagccggctccattctggaatccctgccagggtc agcggtagcggatctgggaccgactacacctcactatca

	HTRGLDFACDIYIWAPLAGTC GVLLLSLVITLYCKRGRKKLLYI FKQPFMRPVQTTQEEDGCSC RFPEEEEEGGCELRVKFSRSA DAPAYQQGQNQLYNELNLGR REEYDVLDKRRGRDPEMGGK PRRKNPQEGLYNELQKDKMA EAYSEIGMKGERRRGKGDG LYQGLSTATKDTYDALHMQAL PPR (SEQ ID NO: 155)	gtcactgcagccagaggacttcgtgtctatttctgtcagc aagggaacaccctgccctacaccttggacagggcacca agctcgagattaaaggtggaggtggcagcggaggagggt gggtcggcggtggaggaagccaggtccaactccaaga aagcggaccgggtctgtgaagccatcagaaactcttca ctgactgtactgtgagcggagtgtctctcccgttaccggg gtgtcttggatcagacagccaccggggaaggggtctggaat ggattggagtgaattggggctctgagactactactactctc atccctcaagtcacgcgtcaccatctcaaaggacaactct aagaatcagggtgtcactgaactgtcatctgtgaccgcag ccgacaccgcccgtgtactattgcgctaagcattactattatg gcgggagctacgcaatggattactggggacaggggtactct ggtcaccgtgtccagcaccactaccccagcaccgaggcc acccaccgggtctctaccatcgctcccagcctctgtccc tgcgtccggaggcatgtagaccgcagctggtggggcgg tgcatacccggggtctgtacttcgctgcgatatctacatttg ggcccctctggctgtgtacttcggggctctgtcttctactc gtgatcactcttactgtaagcgggtcggaagaagctgtct gtacatctttaagcaaccctcatgaggcctgtgcagacta ctcaagaggaggacggctgttcattgcgggtcccagagg aggaggaaggcggctgcgaactgcgcgtgaaattcagc cgacgcgcagatgtccagcctaccagcaggggcagaa ccagctctacaacgaactcaatcttggtcggagagagga gtacgacgtgtggacaagcggagaggacggggaccca gaaatggggcggaagccgcgcagaaagaatccccaag agggcctgtacaacgagctccaaaaggataaagatggca gaagcctatagcgagattggtatgaaaggggaacgcag aagaggcaaaggccacgacggactgtaccagggactc agcaccgccaccaaggacacctatgacgctcttcacatg caggccctgccgcctcgg (SEQ ID NO: 156)
SP-Linker 1- ERmut2-Furin cleavage site 3- CD19 CAR1	MALPVTALLPLALLLHAARPR SSLALSLTADQMVSALLDAEP PILYSEYDPTPRFSEASMMGL LTNLADRELHVHMINWAKRVP FVDLTLDHDLVHLECAWMEIL MIGLVWRSMEHPGKLLFAPNL LLDRNQKGCVEGGVEIFDMLL ATSSRFRMMNLQGEFVCLK SIILLNSGVYTFLSSTLKSLEEK DHIHRVLDKITDTLIHLMAKAG LTQQQHQLAQLLLILSHIRH MSNKRMEHLYSMKCKNVVPL SDLLEMLDAHRLGTGAEDPR PSRKRREIVMTQSPATLSLSP GERATLSCRASQDISKYNWY QKPGQAPRLIYHTSRLHSG IPARFSGSGSGTDYTLTISSLQ PEDFAVYFCQQGNTLPYTFG QGKLEIKGGGSGGGGSGG GGSQVQLQESGPGLVKPSSET LSLTCTVSGVSLPDYGVSWIR QPPGKLEWIGVIWGSETYY SSSLKSRVTISKDNSKNQVSL KLSSVTAADTAVYYCAKHYY GGSYAMDYWGQGLTVTVSST TTPAPRPPTPAPTIASQPLSLR	atggccctccctgtcaccgcctgtgtcttcgtgtgctcttc tgcaccacgcgcgtcgccccgggtcgTcggtggcactttcc ctgactgccgaccagatggtgtccgccccttctggacgcgcg agcctccaattctgtactcggagtacgatccgactgcgccg ttctccgaagccagcatgatgggctgttgactaacctggc ggaccgcgagttggtgcacatgattaactgggctaagcgg gtgcggggcttcgtggacctgacctgcacgaccaagtg acctcctggaatgcgcctggatggaaatcctcatgatcgg cctcgtgtggagatccatggagcatcccggaagctcctg ttgcacccaacctcctgcttgatcgcaaccagggaaaatg cgtggaaggggggtgcgagatttcgacatgctgctcgcca cctcttcccggttcggatgatgaatcgcagggagaaga gttcgtgtgtctgaagtcaatcatcctgtgaactccgggt ctatacctcctgagctcgacctcaagtcactggaggaaa aagaccacatccatcgcggtcgtcgataagatcaccgaca cccttatccatctcatggcgaaggctggactgacctgcaa cagcagcaccagaggctggcccagttgctgattctga gccacatccggcacatgtcgacaagaggatggaacac ctgtacagcatgaagtgcgaagcgtcgtgcctctgtcgg atctgctcctggaaatgctggacgcgcacagactcGgga cgggagctgaagatccacgaccagcagaaagcgacg ggaaattgtgatgacctgacccgcactcttagccttcc acccggtgagcgcgcaaccctgtcttgagagcctccca agacatctcaaaataaccttaattggtatcaacagaagccc ggacaggctcctgcctctgatctaccacaccagccggc tccattctggaatccctgccaggttcagcggtagcggatct

	PEACRPAAGGAVHTRGLDFA CDIYIWAPLAGTCGVLLLSLVIT LYCKRGRKKLLYIFKQPFMRP VQTTQEEDGCSCRFPEEEEG GCELRVKFSRSADAPAYKQG QNQLYNELNLGRREEYDVLD KRRGRDPEMGGKPRRKNPQ EGLYNELQKDKMAEAYSEIGM KGERRRGKGHDGLYQGLSTA TKDTYDALHMQALPPR (SEQ ID NO: 157)	gggaccgactacaccctcactatcagctcactgcagcca gaggacttcgctgtctatttctgcagcaagggaaacacct gccctacaccttggacagggcaccagctcgagattaa agggtggaggtggcagcggaggaggtgggtccggcggtg gaggaagccagggtccaactccaagaaagcggaccggg tctgtgaagccatcagaaactttcactgactgtactgtg agcggagtgtctctccccgattacgggggtgtcttgatcag acagccaccggggaaggggtctggaatggattggagtgt tgggggtctgagactacttacttctcatccctcaagtca cgctcaccatctcaaaggacaactctaagaatcagggtg cactgaaactgtcatctgtgaccgcagccgacaccgcgt gtactattgcgtaagcattactattatggcgggagctacgc aatggattactggggacagggtactctggcaccgtgtcca gcaccactaccccagcaccgagggcaccaccccggct cctaccatcgctcccagcctctgtccctgcgtccggaggc atgtagaccgcagctgggtggggcgtgcataccgggg tcttgacttcgctgcgatactacattggccctctggctg gtacttgcggggctctgtctgttctactcgtgatcactcttact gtaagcgcgggtcggaagaagctgtgtacatcttaagca accctcatgaggcctgtgcagactactcaagaggagga cggtgttctgcgggttcccagaggagggaagggcg ctgcgaactgcgctgaaattcagcgcagcgagatgc tccagcctacaagcaggggcagaaccagctctacaacg aactcaatctgtgctggagagaggagtacgacgtgtg acaagcggagaggacgggaccagaaatggggcgga agccgcgcagaaagaatcccaagagggtctgtacaa cgagctccaaaaggataagatggcagaagcctatagcg agattggtatgaaaggggaacgcagaagaggcaaagg ccacgacggactgtaccagggtcagcaccgccacca aggacacctatgacgtcttcacatgcaggccctgcgcgc tcgg (SEQ ID NO: 158)
SP-Linker 1- ERmut2-Furin cleavage site 3- CD19 CAR2	MALPVTALLPLALLLHAARPR SSLALSLTADQMVSALLDAEP PILYSEYDPTPRPFSEASMMGL LTNLADRELHVHMINWAKRVP FVDLTLHDQVHLLCAWMEIL MIGLVWRSMEHPGKLLFAPNL LLDRNQKGCVEGGVEIFDMLL ATSSRFRMMNLQGEFVCLK SIILLNSGVYTFLSSTLKSLEEK DHIHRVLDKITDTLIHLMAKAG LTLQQQHQLAQLLLILSHIRH MSNKRMEHLYSMKCKNVVPL SDLLLEMLDAHRLGTGAEDPR PSRKRREIVMTQSPATLSLSP GERATLSCRASQDISKYNWY QKPGQAPRLIYHTSRLHSG IPARFSGSGSGTDYTLTISSLQ PEDFAVYFCQQGNTLPYTFG QGKLEIKGGGSGGGSGG GGSQVQLQESGPGLVKPSSET LSLTCTVSGVSLPDYGVSWIR QPPGKGLEWIGVIWGSETYY SSSLKSRVTISKDNSKNQVSL KLSSVTAADTAVYYCAKHYYY GGSYAMDYWGQGLTVTSST	atggccctccctgtcaccgcctgtgtcttcgctggctcttc tgctccacgcgctcgccccgggtgcTcggtggcacttcc ctgactgccgaccagatggtgtccgcccctctggacgcg agcctccaattctgtactcggagtacgatccgactcggccg ttctccgaagccagcatgatggcctgtgactaacctggc ggaccgcgagttggtgcacatgattaactgggctaagcgg gtgccgggctctgtggacctgacctgcacgaccaagtgc acctcctggaatgcgcctggatggaaatcctatgatcgg cctcgtgtggagatccatggagcatcccgaaagctcctg tttgaccccaacctcctgttgatcgcaaccagggaatg cgtggaagggggtgtcgagatttgcacatgctgtcgcca cctcttccgggtccggatgatgaatcgcagggaaga gtcgtgtgtctgaagtcaatcctgtcgaactccgggt ctataccttctgagctcgacctcaagtcactggaggaaa aagaccacatccatcgctgtcgtgataagatcaccgaca cccttatccatctcatggcgaaggctggactgacctgcaa cagcagcaccagaggctggccaggtgtgctgattctga gccacatccggcacatgtcgacaagaaggatggaacac ctgtacagcatgaagtgaagaacgctgctgtctgtccg atctgtctctggaatgtgtggacgcgcacagactGgga cgggagctgaagatccacgaccagcagaaagcgacg ggaaattgtatgacctcagcaccgaccttagccttcc accgggtgagcgcgaacctgtcttgagagcctccca agacatctcaaaataccttaattgtatcaacagaagccc ggacaggctcctgcctctgtatctaccacaccagccggc

	TTPAPRPPTPAPTIASQPLSLR PEACRPAAGGAVHTRGLDFA CDIYWAPLAGTCGVLLLSLVIT LYCKRGRKKLLYIFKQPFMRP VQTTQEEDGCSCRFPEEEEG GCELRVKFSRSADAPAYQQG QNQLYNELNLGRREEYDVL KRRGRDPEMGKPRRKNPQ EGLYNELQKDKMAEAYSEIGM KGERRRGKGHDLGLYQGLSTA TKDTYDALHMQALPPR (SEQ ID NO: 159)	tccattctggaatccctgccaggttcagcggtagcggatct gggaccgactacaccctcactatcagctcactgcagcca gaggactcgctgtctatttctgcagcaaggaacaccct gccctacaccttggacagggcaccagctcgagattaa agggtggaggtggcagcggaggaggtgggtccggcgggtg gaggaagccaggccaactccaagaaagcggaccggg tctgtgaagccatcagaaactcttactgactgtactgtg agcggagtgtctctccccgattacgggggtgtcttgatcag acagccaccggggaagggtctggaatggattggagtgat ttggggctctgagactacttactcttcatccctcaagtca cgcgctaccatctcaaaggacaactctaagaatcagggtg cactgaaactgtcatctgtgaccgcagccgacaccgccgt gtactattgcgctaagcattactattatggcgggagctacgc aatggattactggggacagggtactctggtcaccgtgtcca gcaccactaccccagcaccgaggccacccaccccggt cctaccatcgctcccagcctctgtccctgcgtccggaggc atgtagaccgcagctgggtggggccgtgcatacccggg tcttgactcgctgcgatactacattgggccccctgtgctg gtacttgccgggtcctgtctgttctactcgtgatcactcttact gtaagcgcgggtcggaagaagctgtgtgtacatcttaagca acccttcatgaggcctgtgcagactactcaagaggagga cggctgttcatgcccgttcccagaggagggaaggcgg ctgcgaactgcgcgtgaaattcagccgcagcgcagatgc tccagcctaccagcaggggcagaaccagctctacaacg aactcaatcttggtcggagagaggagtacgacgtgtg acaagcggagaggacgggaccagaaatgggcggga agccgcgcagaaagaatcccaagagggtctgtacaa cgagctccaaaaggataagatggcagaagcctatagcg agattggtatgaaaggggaacgcagaagaggcaaagg ccacgacggactgtaccagggtactcagcaccgccacca aggacacctatgacgtcttcacatgcaggccctgccgccc tcgg (SEQ ID NO: 160)
SP-Linker 1- ERmut1-Furin cleavage site 1- CD123 CAR	MALPVTALLPLALLLHAARPR SSLALSLTADQMVSALLDAEP PILYSEYDPTPRFSEASMMGL LTNLADRELVHMINWAKRVP FVDLALHDQVHLLLECAWMEIL MIGLVWRSMEHPGKLLFAPNL LLDRNQKGCVEGGVEIFDMLL ATSSRFRMMNLQGEFVCLK SIILLNSGVYTFLSSTLKSLEEK DHIHRVLDKITDTLIHLMAKAG LTLQQQHQLAQLLLILSHIRH MSSKRMEHLYSMKCKNVVPL SDLLLEMLDAHRLRTRKQVQL VQSGAEVKKPGASVKVSKA SGYTFTGYMHWVRQAPGQ GLEWMGWINPNSGGTNYAQ KFQGRVTLTRDTSISTVYME SRLRSDDTAVYYCARDMNILA TVPFDIWGQGTMTVTSSGGG GSGGGGSGGGGSDIQMTQS PSSLSASVGDRVTITCRASQSI SSYLNWYQQKPGKAPKLLIYA ASSLQSGVPSRFSGSGSGTD FTLTVNSLQPEDFATYYCQQG	atggccctccctgtcaccgcctgtgtcttccgtggctcttc tgctccacgcgcgtcgccccgggtcgTcggtggcacttcc ctgactgccgaccagatggtgtccgccccttctggacgcg agcctccaattctgtactcggagtacgatccgactcgcgg ttctccgaagccagcatgatgggcctgtgactaacttggc ggaccgcgagtggtgcacatgattaactgggctaagcgg gtgccggggtctgtggacctggccctgcacgaccaagtgc acctcctggaatgcgcctggatggaaatcctcatgatcgg cctcgtgtggagatccatggagcatcccgaaagctcctg tttgaccccaacctcctgttgatcgcaaccagggaatg cgtggaagggggtgtcgagatttgcacatgctgtctgcca cctcttcccggttccgatgatgaatcgcagggaaga gttcgtgtgtctgaagtcaatcctgtgaactccgggt ctatacctcctgagctcgaccctcaagtcactggaggaaa aagaccacatccatcgctgtcgtcgataagatcaccgaca cccttatccatctcatggcgaaggctggactgaccctgcaa cagcagcaccagaggctggccagtgctgtgattctga gccacatccggcacatgtctgccaaggatggaacacc tgtacagcatgaagtgaagaacgtgtgctctgtccgat ctgctcctggaaatgtggacgcgcacagactccgtacta aaagacaagtgaactcgtccaaagcggagcgggaagt aagaaaccggagcgcagcgtgaaagtgtcctgcaaagc ctccggctacacctttacgggtactacatgcactgggtgc gccaggcaccaggacagggtcttgaatggatgggatgg

	DSVPLTFGGGTRLEIKTTTPAP RPPTPAPTIASQPLSLRPEAC RPAAGGAVHTRGLDFACDIYI WAPLAGTCGVLLLSLVITLYCK RGRKKLLYIFKQPFMRPVQTT QEEDGCSCRFPEEEEGGCEL RVKFSRSADAPAYQQGQNQL YNELNLGRREEYDVLDKRRG RDPEMGGKPRRKNPQEGLYN ELQKDKMAEAYSEIGMKGER RRGKGHDGLYQGLSTATKDT YDALHMQALPPR (SEQ ID NO: 161)	atcaaccctaattcgggcggaactaactacgcacagaag ttccaggggagagtactctgactcgggatacctccatctc aactgtctacatggaactctccgcttgcggtcagatgata cggcagtgactactgcgcccgcacatgaatatcctggct accgtgccgttcgacatctggggacaggggactatggta ctgtctcatcgggcggtggaggtcaggaggaggcggctc gggaggcggagggtcggacattcagatgacccagtcctc atcctctctgtcggccagcgtcggagatagggtgaccatta cctgtcgggcctcgcaaagcatctcctcgtacctcaactgg tatcagcaaaagccgggaagggcgccctaagctgctgatc tacgccgcttcgagcttgcaaagcggggtgccatccagat tctcgggatcaggctcaggaaccgacttaccctgaccgt gaacagcctccagccggaggactttgccacttactactgc cagcagggagactccgtgccgcttactttcgggggggta cccgcctggagatcaagaccactacccagcaccgagg ccaccaccccggtcctaccatcgctccagcctctgtc cctgctcggaggcatgtagaccgcagctgggtggggc cgtgcatacccggttctgacttcgctgcgatatctacatt tgggcccctctggctggtacttgcgggctcctgctgtttcac tcgtgatcactcttactgtaagcgcggctcgaagaagctg ctgtacatctttaagcaaccctcatgaggcctgtgcagact actcaagaggaggacggctgtcatgccggttccagag gaggaggaaggcggctgcgaactgcgctgaaattcag ccgcagcgcagatgtccagcctaccagcaggggcaga accagctctacaacgaactcaatcttggtcggagagagg agtacgacgtgctggacaagcggagaggacgggaccc agaaatgggcgggaagccgcgcagaaagaatcccaa gagggcctgtacaacgagctccaaaggataagatggc agaagcctatagcgagattggtatgaaaggggaacgca gaagaggcaaaggccacgacggactgtaccagggact cagcaccgccaccaaggacacctatgacgctcttcacat gcaggccctgccgcctcgg (SEQ ID NO: 162)
SP-Linker 1- ERmut1-Furin cleavage site 2- CD123 CAR (construct 119)	MALPVTALLPLALLHAARPR SSLALSLTADQMVSALLDAEP PILYSEYDPTTRPFSEASMMGL LTNLADRELVHMINWAKRVP FVDLALHDQVHLLCAWMEIL MIGLVWRSMEHPGKLLFAPNL LLDRNQGKCEGGVEIFDMLL ATSSRFRMMNLQGEFVCLK SIILLNSGVYTFLLSSTLKSLEEK DHIHRVLDKITDTLIHLMKAG LTLQQQHQLAQLLLLSHIRH MSSKRMEHLYSMKCKNVVPL SDLLEMLDAHRLGTGAEDPR PSRKRRSLGDVGQVLVQSG AEVKKPGASVKVSKASGYTF TGYMHVVRQAPGQGLEWM GWINPNSGGTNYAQKFQGRV TLTRDTSISTVYMELSRRLSD DTAVYYCARDMNILATVPFDI WGQGTMTVTVSSGGGSGGG SGGGGSDIQMTQSPSSLSA SVGDRVTITCRASQSISSYLN WYQQKPGKAPKLLIYAASSLQ SGVPSRFSGSGSGTDFTLTV	atggccctccctgtcaccgcctgtgcttccgtggtctctc tgctccacgccgctcggccccggtcgtgctggcacttccc tgactgccgaccagatgggtgccccctcttgacgccga gctccaattctgtactcggagtagcatccgactcggccgtt ctccgaagccagcatgatgggcctgttgactaactggcg gaccgcgagttggtgcacatgattaactgggctaagcggg tgccgggctcgtggacctggccctgcacgaccaagtga cctcctggaatgcgcctggatggaaatcctcatgatcgcc tcgtgtggagatccatggagcatcccgaaagctcctgtt gcaccaacctcctgctgatcgcaaccagggaatgc gtggaagggggtgtcgagatttgcacatgctgctgccac ctctcccggtccggatgatgaatctgcagggagaagagt tcgtgtgtctgaagtcaatcatcctgctgaactcggggtct atacctcctgagctcgacctcaagtcaactggaggaaaa agaccacatccatcgctgctcgataagatcaccgacac ccttatccatctcatggcgaaggctggactgacctgcaac agcagcaccagaggctggcccagttgctgctgattctgag ccacatccggcacatgtctccaagaggatggaacacct gtacagcatgaagtgaagaacgtcgtgcctctgtccgat ctgctcctggaaatgtggacgcgcacagactcggaaacc ggcgcggaagacccccggccctccaggaagcgaagggt ccctcggagacgtgggtcaagtgaactcgtccaaagcg gagcgggaagtcaagaaacccggagcgagcgtgaaagt gtcctgcaaagcctccggctacaccttacgggctactaca

	NSLQPEDFATYYCQQGDSVP LTFGGGTRLEIKTTTPAPRPPT PAPTASQPLSLRPEACRPAA GGAVHTRGLDFACDIYWAPL AGTCGVLLLLSLVITLYCKRGRK KLLYIFKQPFMRPVQTTQEED GCSCRFPEEEEGGCELRVKF SRSADAPAYQQGQNQLYNEL NLGRREEYDVLDKRRGRDPE MGGKPRRKNPQEGLYNELQK DKMAEAYSEIGMKGERRRGK GHDGLYQGLSTATKDTYDAL HMQALPPR (SEQ ID NO: 163)	tgcactgggtgcgccaggcaccaggacagggcttgaat ggatgggatggatcaaccctaattcgggaggaaactaacta cgcacagaagttccaggggagagtactctgactcggga tacctccatctcaactgtctacatggaactctcccgcttgcg gtcagatgatacggcagtgactactgcgcccgacatg aatatcctggctaccgtgccttgcacatctggggacagg ggactatggtactgtctcatcgggagggtggaggttcagga ggaggcggctcgggaggcggaggttcggacattcagat gaccagtcctccatcctctctgtcggccagcgtcggagat agggtgaccattacctgtcgggacctcgcaaagcatctcct gtacctcaactggtatcagcaaaagccgggaaaggcgc ctaagctgctgatctacgccgcttcgagcttgcaaaaggcg ggtgccatccagattctcgggatcaggctcaggaaccga cttcaccctgaccgtgaacagcctccagccggaggacttt gccacttactactgccagcagggagactccgtgcgcgtta ctttcgggggggtaccgcctggagatcaagaccacta ccccagcaccgaggccaccaccccggtctctaccatcg cctcccagcctctgtccctgcgtcgggaggtcatgtagacc gcagctggtggggcggtgcatacccggttctgactcgcg cctgcgatatctacatttgggcccctctggctggtacttgcg ggtcctgctgtcttactcgtgtatcacttctactgtaagcg gtcgggaagaagctgctgtatctttaagcaacccttcag aggcctgtgcagactactcaagaggaggacggctgttcat gccggttcccagaggaggaggaaggcggtgcgaactg cgcgtgaaattcagccgcagcgcagatgctccagcctac cagcaggggcagaaccagctctacaacgaactcaatctt ggtcggagagaggagtacgacgtgctggacaagcgga gaggacgggaccagaaatggcggaagccgcgca gaaagaatcccaagagggcctgtacaacgagctcaa aaggataagatggcagaagcctatagcgagattggtatg aaaggggaacgcagaagaggcaaaggccacgacgg actgtaccagggactcagcaccgccaccaaggacacct atgacgctcttcacatgcaggccctgcgcgctcgg (SEQ ID NO: 164)
SP-Linker 1- ERmut1-Furin cleavage site 3- CD123 CAR (construct 122)	MALPVTALLLPLALLLHAARPR SSLALSLTADQMVSALLDAEP PILYSEYDPTTRPFSEASMMGL LTNLADRELVHMINWAKRVP FVDLALHDQVHLLLECAWMEIL MIGLVWRSMEHPGKLLFAPNL LLDRNQGKCVGGVEIFDMLL ATSSRFRMMNLQGEFVCLK SIILLNSGVYTFLLSSTLKSLEEK DHIHRVLDKITDTLIHLMAKAG LTLOQQHQRLAQLLLILSHIRH MSSKRMEHLYSMKCKNVVPL SDLLEMLDAHRLGTGAEDPR PSRKRQVQLVQSGAEVKKP GASVKVSCKASGYTFTGYM HWVRQAPGQGLEWMGWINP NSGGTNYAQKFQGRVTLTRD TSISTVYMELSLRSDDTAVY YCARDMNILATVPFDIWGQGT MVTVSSGGGGSGGGGSGGG GSDIQMTQSPSSLSASVGDR VTITCRASQSISSYLNWYQQK	atggccctccctgtcaccgcctgctgcttccgctggctctt tgctccacgccgctcggccccggtcgtctgtggcacttccc tgactccgaccagatggtgtccgccttctggacgccgag cctccaattctgtactcggagtagatccgactcggcgttc tccgaagccagcatgatgggcctgttgactaacctggcgga ccgcgagttggtgcacatgattaactgggctaagcggtgc cgggcttcgtggacctggcctgcacgaccaagtgcacctc ctggaatgcgcctggatggaaatcctcatgatcggcctcgt gtggagatccatggagcatcccggaaagctcctgtttgcac ccaacctcctgcttgatcgcaaccagggaataatgcgtgga agggggtgtcgagattttcgacatgctgctgccacctctt ccggttccgagatgatgaatctgcagggaagaagagttcgtg gtctgaagtcaatcatcctgtgaactccggggtctatacct tctgagctcgacctcaagtcactggaggaaaaagacca catccatcgctgctcgataagatcaccgacaccttatcc atctcatggcgaaggctggactgacctgcaacagcagca ccagaggctggccagttgctgctgattctgagccacatcc ggcacatgtcgtccaagaggatggaacacctgtacagcat gaagtgaagaacgtcgtgcctctgtccgatctgctcctgg

	PGKAPKLLIYAASSLQSGVPS RFSGSGSGTDFTLTVNSLQPE DFATYYCQQGDSVPLTFGGG TRLEIKTTTPAPRPPTPPTI ASQPLSLRPEACRPAAGG AVHTRGLDFACDIYWAPLA GTCGVLLLSLVITLYCKRGR KKLLYIFKQPFMRPVQTTQ EEDGCSCRFPEEEEGGCE LRVKFSRSADAPAYQQGQ NQLYNELNLGRREEYDVL KRRGRDPEMGGKPRRKNP QEGLYNELQKDKMAEAYS EIGMKGERRRGKGHDGLY QGLSTATKDTYDALHMQAL PPR (SEQ ID NO: 165)	aaatgctggacgcgcacagactcggaaccggcgcggaag acccccggccctccaggaagcgaaggcaagtgaactcgt ccaaagcggagcggaagtcaagaacccggagcgagcgt gaaagtgtcctgcaaagcctccggctacacctttacgggct actacatgcactgggtgcgcagggcaccaggacaggggtct tgaatggatgggatggatcaaccctaattcgggcggaact aactacgcacagaagttccaggggagagtactctgactc gggatacctccatctcaactgtctacatggaactctccgct tgcggtcagatgatacggcagtgactactgcgcccgcgac atgaatatcctggctaccgtgccgttcgacatctggggaca ggggactatggttactgtctcatcggcggtggaggttcag gaggaggcggctcgggaggcggaggttcggacattcagat gaccagtcctccatctctgtcggccagcgtcggagata gggtgaccattacctgtcgggctcgaagcatctcctcgt acctcaactggatcagcaaaagcgggaaaggcgcttaa gctgctgatctacgccgttcgagcttgcaaagcggggtgc catccagattctcgggatcaggctcaggaaccgacttcacc ctgacctgaacagcctccagccggaggactttgccactta ctactgccagcaggagactccgtgccgttactttcgggg ggggtaccgcctggagatcaagaccactacccagcacc gaggccaccacccggctcctaccatgcctcccagcctc tgtcctgcgtccggaggcatgtagaccgcagctgggtggg gccgtgcataccggggtcttgacttcgctgcgatatctac atttgggccccttggtggtacttgcggggtcctgtgcttt cactcgtgatcactctttactgaagcgcggtcggaagaag ctgctgtacatctttaagcaaccttcatgaggcctgtgcag actactcaagaggaggacgggtgttcagccggttccaga ggaggaggaaggcggctgcgaactgcgctgaaattcag ccgcagcgcagatgctccagcctaccagcaggggcagaac cagctctacaacgaactcaatcttggtcggagagaggagt acgacgtgctggacaagcggagaggacgggaccagaaa tgggcggaagccgcgcagaaagaatcccaagagggcc tgtacaacgagctcaaaaggataagatggcagaagccta tagcgagattggtatgaaagggaacgcagaagaggcaa aggccacgacggactgtaccagggactcagcaccgccacc aaggacacctatgacgtcttcacatgcaggccctgccgcc tcgg (SEQ ID NO: 166)
SP-Linker 1- ERmut2-Furin cleavage site 1- CD123 CAR	MALPVTALLPLALLHAARPR SSLALSLTADQMVSALLDAEP PILYSEYDPTRPFSEASMMGL LTNLADRELHVHMINWAKRVP FVDLTLDQVHLLECAWMEIL MIGLVWRSMEHPGKLLFAPNL LLDRNQGKCEGGVEIFDMLL ATSSRFRMMNLQGEFVCLK SIILLNSGVYTFLSSTLKSLEEK DHIHRVLDKITDTLIHLMAKAG LTQQQHQRQAQLLLILSHIRH MSNKRMEHLYSMKCKNVVPL	atggccctccctgtcaccgcctgtgcttccgctggctcttc tgctccacgcgcgtcggccccggtcgTcgttggcactttcc ctgactgccgaccagatggtgtccgccccttcggacgcgcg agcctccaattctgtactcggagtagcatccgactcgcgcg ttcctccaagccagcatgatgggctgttgactaacctggc ggaccgcgagttggtgcacatgattaactgggctaagcgg gtgccggggtcgtggacctgacctgcacgaccaagtgc acctcctggaatgcgcctggtatgaaatcctcatgatcgg cctcgtgtggagatccatggagcatcccgaaagctcctg tttgacccaacctcctgcttgatcgcaaccagggaagaaatg cgtggaaggggggtgcgagatttcgacatgctgctcgcca cctcttcccggttccggatgatgaatgcaggggagaaga

	SDLLEMLDAHRLRTRKQVQL VQSGAEVKKPGASVKVSCKA SGYTFTGYMHVVRQAPGQ GLEWMGWNPNSGGTNYAQ KFQGRVTLTRDTSISTVYME SRLRSDDTAVYYCARDMNILA TVPDFIWGGQTMVTVSSGGG GSGGGGSGGGGSDIQMTQS PSSLASVGDRTITCRASQSI SSYLNWYQQKPGKAPKLLIYA ASSLQSGVPSRFSGSGSGTD FTLTVNSLQPEDFATYYCQQG DSVPLTFGGGTRLEIKTTTPAP RPPTPAPTIASQPLSLRPEAC RPAAGGAVHTRGLDFACDIYI WAPLAGTCGVLLLSLVITLYCK RGRKKLLYIFKQPFMRPVQTT QEEDGCSCRFPEEEEGGCEL RVKFSRSADAPAYQQGNQL YNELNLGRREEYDVLDRRG RDPEMGGKPRRKNPQEGLYN ELQKDKMAEAYSEIGMKGER RRGKGHDGLYQGLSTATKDT YDALHMQALPPR (SEQ ID NO: 167)	gttcgtgtgtctgaagtcaatcatcctgtgaactccggggt ctataccttctgagctcgaccctcaagtcactggaggaaa aagaccacatccatcgctgctgataagatcacgcaca cccttatccatctcatggcgaaggctggactgacctgcaa cagcagcaccagaggctggccagttgctgtgattctga gccacatccggcacatgtcgaacaagaggatggaacac ctgtacagcatgaagtgcagaacgtcgtgctctgtccg atctgtctctggaaatgctggacgcgcacagactccgtact aaaagacaagtgcactcgtccaaagcggagcggaagt caagaaacccggagcgagcgtgaaagtgtcctgcaaag cctccggctacacctttacgggctactacatgcactgggtg cgccaggcaccaggacagggtcttgaatggatgggatgg atcaaccctaattcgggcggaactaactacgcacagaag ttccaggggagagtactctgactcgggatacctccatctc aactgtctacatggaactctccgcttgcggtcagatgata cggcagtgtactactgcgcccgcacatgaatatcctggct accgtgccgttcgacatctggggacaggggactatggta ctgtctcatcgggctggagggttcaggaggaggcggctc gggaggcggagggttcggacattcagatgacccagtcctc atcctctgtcggccagcgtcggagatagggtgaccatta cctgtcgggctcgcgaagcattcctcgtacctaactgg tatcagcaaaagccgggaaaggcgccctaagctgctgatc tacgccgcttcgagctgcaaagcggggtgccatccagat tctcgggatcaggctcaggaaccgacttaccctgaccgt gaacagcctccagccggaggactttgccacttactactgc cagcagggagactccgtgccgttactttcggggggggta cccgcttgagatcaagaccactacccagcaccgagg ccaccaccccggtcctaccatcgctccagcctctgtc cctgcgtccggaggcatgtagaccgcagctgggtggggc cgtgcatacccggttctgacttcgctgcgatatctacatt tgggcccctctggttacttgcggggtcctgtgtttcac tcgtgatcactttactgtaagcgcggctcgaagaagctg ctgtacatctttaagcaacccttcagaggcctgtgcagact actcaagaggaggacggctgttcagccggttccagag gaggaggaaggcggctgcgaactgcgcgtgaaattcag ccgcagcgcagatgctccagcctaccagcaggggcaga accagctctacaacgaactcaatcttggtcggagagagg agtacgacgtgtcggacaagcggagaggacgggaccc agaaatgggcggaagccgcgcagaagaatcccaa gagggcctgtacaacgagctccaaaggataagatggc agaagcctatagcgagattggtatgaaaggggaacgca gaagaggcaaggccacgacggactgtaccagggact cagcaccgccaccaaggacatgatgacgctcttcacat gcaggccctgccgcctcg (SEQ ID NO: 168)
SP-Linker 1- ERmut2-Furin cleavage site 2- CD123 CAR	MALPVTALLPLALLHAARPR SSLALSLTADQMVSALLDAEP PILYSEYDPTPRPFSEASMMGL LTNLADRELVHMINWAKRVP FVDLTLDQVHLLCAWMEIL MIGLVWRSMEHPGKLLFAPNL LLDRNQGKCEGGVEIFDMLL ATSSRFRMMNLQGEFVCLK SIILLNSGVYTFLLSSTLKSLEEK DHIHRVLDKITDTLIHLMAKAG LTQQQHQRQAQLLLILSHIRH	atggccctccctgtcaccgccgtgcttccgctggctcttc tgctccacgcgcgtcggccccgggtcgTcggtggcactttcc ctgactgccgaccagatggtgtccgcccttctggacgcgg agcctccaattctgtactcggagtagcatccgactcggccg ttctccgaagccagcatgatgggctgtgactaacctggc ggaccgcgagttggtgcacatgattaactgggctaagcgg gtgccgggctcgtggacctgacctgcacgaccaagtgc acctcctggaatgcgcctggatgaaatcctcatgatcgg cctcgtgtggagatccatggagcatcccgaaagctcctg ttgcaccaacctcctgcttgatcgcaaccagggaatg cgtggaagggggtgctgagatttcgacatgctgctcgcca

	MSNKRMEHLYSMKCKNVVPL SDLLLEMLDAHRLGTGAEDPR PSRKRRSLGDVGQVQLVQSG AEVKKPGASVKVSCASGYTF TGYMHWWVRQAPGQGLEWM GWINPNSGGTNYAQKFQGRV TLTRDTSISTVYMELSRLRSD DTAVYYCARDMNILATVPFDI WGQGTMTVTVSSGGGGSGGG SGGGGGSDIQMTQSPSSLSA SVGDRVITICRASQSISSYLN WYQQKPGKAPKLLIYAASSLQ SGVPSRFSGSGSGTDFTLV NSLQPEDFATYYCQQGDSVP LTFGGGTREIKTTTPAPRPPT PAPTIASQPLSLRPEACRPAA GGAVHTRGLDFACDIYWAPL AGTCGVLLLSLVITLYCKRGRK KLLYIFKQPFMRPVQTTQEED GCSCRFPEEEEGGCELRVKF SRSDAPAYQQGQNQLYNEL NLGRREEYDVLDKRRGRDPE MGGKPRRKNPQEGLYNELQK DKMAEAYSEIGMKGERRRGK GHDGLYQGLSTATKDTYDAL HMQALPPR (SEQ ID NO: 169)	cctcttcccggttcggatgatgaatctgcaggagagaaga gttcgtgtgtctgaagtcaatcatcctgctgaactccgggt ctataccttctgagctcgacctcaagtcactggaggaaa aagaccacatccatcgctgctcgataagatcccgaca cccttatccatctcatggcgaaggctggactgacctgcaa cagcagcaccagaggctggccagttgctgctgattctga gccacatccggcacatgtcgacaagaggatggaacac ctgtacagcatgaagtgcagaacgtcgtgctctgtccg atctgctcctggaaatgctggacgcgcacagactcggaa ccggcgcggaagacccccggccctccagggaagcgaag gtccctcgagacgtgggtcaagtgcactcgtccaaag cggagcgggaagtcaagaaacccggagcgcgagcgtgaaa gtgtcctgcaaagcctccgggtacaccttaccgggtacta catgcactgggtgcgccaggcaccaggacagggtcttga atggatgggatggatcaaccctaattcgggcgggaactaac tacgcacagaagtccaggggagagtgactctgactcgg gatacctccatctcaactgtctacatggaactctcccgctg cggtcagatgatacggcagtgactactgcgcccgcgac atgaatatcctggctaccgtgcggttcgacatctggggaca ggggactatgggtactgtctcactcgggcgggtggaggtcag gaggaggcggctcgggagcggaggttcggacattcag atgaccagtcctccatcctctctcgtcgccagcgtcggag atagggtgaccattacctgtcgggcctcgcaaagcatctcc tcgtacctcaactggatcagcaaaagccgggaaaggcg cctaagctgctgatctacgcccttcgagcttgcaaagcgg ggtgccatccagattctcgggatcaggctcaggaaaccga cttcacctgaccgtgaacagcctccagccggaggacttt gccacttactactgccagcaggagactccgtgccgctta cttcgggggggggtaccgcctggagatcaagaccacta ccccagcaccgaggccacccaccccggtcctaccatcg cctccagcctctgtccctgcgtcggaggcatgtagacc gcagctggtggggccgtgcatacccggttcttgactcgg cctgcgatatctacattggggccctctggctggtacttgcgg ggtcctgctgctttactcgtgatcactttactgtaagcgg gtcgggaagaagctgctgtacatcttaagcaaccctcatg aggcctgtgcagactactcaagaggaggacggctgttcat gccggttcccagaggaggaggaaggcggctgcgaactg cgctgaaattcagccgcagcgcagatgctccagcctac cagcaggggcagaaccagctctacaacgaactcaatctt ggtcggagagaggagtacgacgtgctggacaagcggga gaggacgggaccagaaatgggcgggaagccgcgca gaaagaatcccaagagggcctgtacaacgagctcaa aaggataagatggcagaagcctatagcagattggtatg aaaggggaacgcagaagaggcaaaggccacgacgg actgtaccagggaactcagcaccgccaccaaggacacct atgacgctcttcacatgcaggccctgcgcctcgg (SEQ ID NO: 170)
SP-Linker 1- ERmut2-Furin cleavage site 3- CD123 CAR	MALPVTALLLPLALLLHAARPR SSLALSLTADQMVSALLDAEP PILYSEYDPTRPFSEASMMGL LTNLADRELVHMINWAKRVP FVDLTLDQVHLLLECAWMEIL MIGLVWRSMEHPGKLLFAPNL LLDRNQGKCEVGGVEIFDMLL ATSSRFRMMNLQGEFVCLK SIILLNSGVYTFLSSTLKSLEEK	atggccctccctgtcaccgccctgctgctccgctggctcttc tgctccacgcgcgtcggccccggctgTcggtggcactttcc ctgactgccgaccagatggtgtccgcccttctggacgcgg agcctccaattctgtactcggagtacgatccgactgcccg ttctccgaagccagcatgatgggcctgttgactaacctggc ggaccgcgagttggtgcacatgattaactgggctaagcgg gtgccgggctcgtggacctgacctgcacgaccaagtgc acctcctggaatgcgcctggtggaatcctcatgatcgg cctcgtgtggagatccatggagcatcccggaagctcctg

	DHIHRVLDKITDTLIHLMKAG LTQQQHQRQAQLLLILSHIRH MSNKRMEHLYSMKCKNVVPL SDLLEMLDAHRLGTGAEDPR PSRKRRQVQLVQSGAEVKKP GASVKVSCKASGYTFTGYM HWVRQAPGQGLEWMGWNP NSGGTNYAQKFQGRVTLTRD TSISTVYMELSRLSDDTAVY YCARDMNILATVPFDIWGQGT MVTVSSGGGGSGGGSGGGG GSDIQMTQSPSSLSASVGDR VTITCRASQSISSYLNWYQK PGKAPKLLIYAASSLQSGVPS RFSGSGSGTDFTLTVNSLQPE DFATYYCQQGDSVPLTFGGG TRLEIKTTTTAPRPPTPAPTIA SQPLSLRPEACRPAAGGAVH TRGLDFACDIYWAPLAGTCG VLLLSLVITLYCKRGRKLLYIF KQPFMRPVQTTQEEDGCSCR FPEEEEGGCELRVKFSRSAD APAYQQGQNQLYNELNLGRR EEYDVLDKRRGRDPEMGGKP RRKNPQEGLYNELQKDKMAE AYSEIGMKGERRRGKGDGL YQGLSTATKDTYDALHMQALP PR* (SEQ ID NO: 171)	tttgacccaacctcctgctgatcgcaaccagggaaaatg cgtggaaggggtgctgagatttcgacatgctgctgcc cctctcccggttcggatgatgaatgacagggagaaga gttcgtgtgtctgaagtcaatcatcctgctgaactccgggt ctatacctcctgagctcgaccctcaagtcactggaggaaa aagaccacatccatcgctgctcgataagatcaccgaca cccttatccatctcatggcgaaggctggactgacctgcaa cagcagcaccagaggctggcccagttgctgctgattctga gccacatccggcacatgtcgacaagaggatggaacac ctgtacagcatgaagtgcagaacgtgctgctgtgctcg atctgctcctggaaatgctggacgcgcacagactcggga cgggagctgaagatccacgacccagcagaaagcgacg gcaagtgcactcgtccaaagcggagcggaagtcaaga aacccggagcgagcgtgaaagtgtcctgcaaagcctcc ggctacaccttacgggctactacatgcactgggtgcgcca ggcaccaggacagggtcttgaatggatggatggatcaa ccctaattcgggcgaactaactacgcacagaagtcca ggggagagtactctgactcgggatacctccatctcaact gtctacatggaactctcccgcttgcggtcagatgatacggc agtgactactgcgcccgcacatgaatatcctggctaccg tgccgttcgacatctggggacaggggactatggttactgtct catcggggcggtggagggtcaggaggaggcggtcggga ggccggagggtcggacattcagatgacccagtcctccatcct ctctgtcggccagcgtcggagatagggtgaccattacctgt cgggcctcgcgaagcatctcctctgtacctaactggatca gcaaaagccgggaaaggcgccctaagctgctgatctacg ccgcttcgagcttgcaaaaggggtgccatccagattctcg ggatcaggctcaggaaccgacttcacctgacctgaac agcctccagccggaggactttgccacttactactgccagc agggagactccgtgcgcttactttcgggggggtaccgg cctggagatcaagaccactacccagcaccgaggccac ccaccccggtcctaccatgcctccagcctgtgtccctg cgtccggaggcatgtagaccgcagctggtggggcggtg catacccggtgttacttcgctgcgatatctacattgg gccctctgggtgttacttgcggggctcctgctgtttactcg tgatcactcttactgtaagcgcggtcggagaagctgctgt acatctttaagcaaccctcatgaggcctgtgcagactactc aagaggaggacggctgttcatgccggttccagaggagg aggaaggcggtcgcgaactgcgctgaaattcagccgc agcgagatgctccagcctaccagcaggggcagaaacca gctctacaacgaactcaatcttggtcggagagaggagtag gacgtgctggacaagcggagaggacgggaccagaaaa tgggcgggaagccgcgcagaaagaatcccaagagggg cctgtacaacgagctccaaaaggataagatggcagaag cctatagcagattggtatgaaaggggaacgcagaaga ggcaaaaggccacgacgactgtaccagggactcagca ccgccaccaaggacacatgatgcgtcttcacatgcagg cctgcccgcctcgg (SEQ ID NO: 172)
SP-Linker 1- ERmut1-Furin cleavage site 1- BCMA CAR	MALPVTALLPLALLLHAARPR SSLALSLTADQMVSALLDAEP PILYSEYDPTPRPFSEASMMGL LTNLADRELVHMINWAKRVPG FVDLALHDQVHLLLECAWMEIL MIGLVWRSMEHPGKLLFAPNL LLDRNQGKCEGGVEIFDMLL	atggccctccctgtcaccgcccgtgctgttcogctggctcttc tgcctcacgcgctcggccccggctgTcggtggcactttcc ctgactgccgaccagatggtgtccgcccttctggacgcgg agcctccaattctgtactcggagtagatccgactgcgccg ttctccgaagccagcatgatggcctgttgactaacctggc ggaccgcgagttggtgcacatgattaactgggctaagcgg gtgcccgggtcgtggacctggccctgcacgaccaagtgc

	ATSSRFRMMNLQGEFVCLK SIILLNSGVYTFLSSTLKSLEEK DHIHRVLDKITDTLIHLMKAG LTQQQHQRQAQLLLILSHIRH MSSKRMEHLYSMKCKNVVPL SDLLEMLDAHRLRTKREVQL VESGGGLVQPGSLRLSCAV SGFALSNHGMSWVRRAPGK GLEWVSGIVYSGSTYYAASVK GRFTISRDNSRNTLYLQMNSL RPEDTAIYYCSAHGGESDVW GQGTTVTVSSASGGGGSGG RASGGGSDIQLTQSPSSLSA SVGDRVITICRASQSISSYLN WYQQKPGKAPKLLIYAASSLQ SGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQSYSTPYT FGQGTKVEIKTTTPAPRPPTP APTIASQPLSLRPEACRPAAG GAVHTRGLDFACDIYWAPLA GTCGVLLLSLVITLYCKRGRKK LLYIFKQPFMRPVQTTQEEDG CSCRFPEEEEGGCELRVKFS RSADAPAYQQGQNQLYNELN LGRREEYDVLDKRRGRDPEM GKGPRRKNPQEGLYNELQKD KMAEAYSEIGMKGERRRGKG HDGLYQGLSTATKDTYDALH MQALPPR (SEQ ID NO: 173)	acctcctggaatgcgcctggatggaatcctcatgatcgg cctcgtgtggagatccatggagcatcccgaaagctcctg ttgcacccaacctcctgctgatcgcaaccagggaatg cgtggaaggggtgtcgagatttcgacatgctgctcgcca cctcttcccggtccggatgatgaatcgcagggaaga gttcgtgtgtcgaagtcaatcatcctgctgaactccgggt ctatacctcctgagctcgaccctcaagtcactggaggaaa aagaccacatccatcgctgctcgataagatcaccgaca cccttatccatctcatggcgaaggctggactgaccctgcaa cagcagcaccagaggctggcccagtgctgctgattctga gccacatccggcacatgtcgtccaagaggatggaacacc tgtacagcatgaagtgaagaacgtcgtgctctgtccgat ctgctcctggaatgtcggacgcgcacagactccgtacta aaagagaagtgaattgggtgaatcagggggaggacttg tgcagcctggaggatcgtgagactgtcatgtccgtgtcc ggctttgccctgtccaaccacgggatgtcctgggtccgcg cgcgctggaagggtcgaatgggtgtcgggtattgtgt acagcgttagcacctactatgccgatccgtgaagggga gattcaccatcagccgggacaactccaggaacactctgta cctccaaatgaattcgtgaggccagaggacactgcatc tactactgctccgcgcatggcggagagtcgacgtctggg gacaggggaccaccgtgaccgtgtctagcgcgtccggcg gaggcggcagcgggggtcgggcatcaggggcccggcg atcggacatccagctcaccagtcctccgagctcgtgtcc gccctcgtgggagatcgggtcaccatcacgtgcgcgcc agccagtcgatttccctctacctaagctgtaccaacagaa gcccgaaaagccccgaagcttctcatctacgcgcctc gagcctgcagtcaggagtgcctcctcaggttctccggctc ggttccggtactgattcaccctgaccatttccctcctgaac cggaggactcgtacttactactgcccagcagtcgtactcc acccctacacttccgacaaggcaccaggtcgaaatc aagaccactacccagcaccgaggccaccaccccg ctctaccatcgctccagcctctgtccctgcgtccggag gcatgtagaccgcagctgggtggggccgtgcatacccg ggtcttgacttcgctgcgatactacattgggcccctctg ctgggtacttgcgggtcctgctgttctactcgtgatcactt actgtaagcgcgggtcgaagaagctgtgtacatcttaag caaccctcatgaggcctgtgcagactactcaagaggag gacggctgtcatgccgttcccagaggaggaggaaggc ggctgcgaactgcgctgaaattcagccgcagcgcagat gctccagcctaccagcaggggcagaaccagctctacaa cgaactcaatcttggtcggagagaggagtacgacgtgctg gacaagcggagaggacgggacccagaaatgggcccgg aagccgcgcagaaagaatcccaagagggctgtaca acgagctccaaaaggataagatggcagaagcctatagc gagattggtatgaaaggggaacgcagaagaggcaaag gccacgacggactgtaccagggtactcagaccgccacc aaggacacctatgacgtcttcatatgcaggccctgcgc ctg (SEQ ID NO: 174)
SP-Linker 1- ERmut1-Furin cleavage site 2- BCMA CAR (construct 164)	MALPVTALLLPLALLLHAARPR SSLALSLTADQMVSALLDAEP PILYSEYDPTPRPFSEASMMGL LTNLADRELVHMINWAKRVPG FVDLALHDQVHLLLECAWMEIL MIGLVWRSMEHPGKLLFAPNL LLDRNQGKCEGGVEIFDMLL	atggccctccctgtcaccgcccgtgcttccgctggctcttc tgcctcacgcgcgtcggccccggtgcTcggtggcactttcc ctgactgccgaccagatgggtgcggccttctggacgcgcg agcctccaattctgtactcggagtacgatccgactcggccg ttctccgaagccagcatgatgggctgtgactaacctggc ggaccgcgagttggtgcacatgattaactgggctaagcgg gtgcggggtcgtggacctggcctgcacgaccaagtgc

	ATSSRFRMMNLQGEFVCLK SIILLNSGVYTFLSSTLKSLEEK DHIHRVLDKITDTLIHLMKAG LTQQQHQRQAQLLLILSHIRH MSSKRMEHLYSMKCKNVVPL SDLLEMLDAHRLGTGAEDPR PSRKRRSLGDVGEVQLVESG GGLVQPGGSLRLSCAVSGFA LSNHGMSWVRRAPGKGLEW VSGIVYSGSTYYAASVKGRFTI SRDNSRNTLYLQMNSLRPED TAIYYCSAHGGESDVWGQGT TVTVSSASGGGGSGGRASGG GGSDIQLTQSPSSLASVGDR VTITCRASQSISSYLNWYQK PGKAPKLLIYAASSLQSGVPS RFGSGSGTDFTLTISSLQPE DFATYYCQSYSTPYTFGQG TKVEIKTTTTAPRPPTPAPTIA SQPLSLRPEACRPAAGGAVH TRGLDFACDIYIWAPLAGTCG VLLLSLVITLYCKRGRKLLYIF KQPFMRPVQTTQEEDGCSCR FPEEEEGGCELRVKFSRSAD APAYQQGQNQLYNELNLGRR EEYDVLDKRRGRDPEMGKP RRKNPQEGLYNELQKDKMAE AYSEIGMKGERRRGKGHDGL YQGLSTATKDTYDALHMQALP PR (SEQ ID NO: 175)	acctcctggaatgcgcctggatggaatcctcatgatcgg cctcgtgtggagatccatggagcatcccgaaagctcctg ttgcacccaacctcctgctgatcgcaaccagggaaaatg cgtggaaggggggtgcgagatttcgacatgctgctcgcca cctcttcccggtccggatgatgaatcgcagggagaaga gttcgtgtgtcgaagtcaatcatcctgctgaactccgggt ctatacctcctgagctcgaccctcaagtcactggaggaaa aagaccacatccatcgctgctcgataagatcaccgaca cccttatccatctcatggcgaaggctggactgaccctgcaa cagcagcaccagaggctggcccagttgctgctgattctga gccacatccggcacatgctgccaagaggatggaacacc tgtacagcatgaagtgaagaacgctgctgctctgctccgat ctgctcctggaatgctggacgcgcacagactcggaacc ggcgcggaagacccccggccctccaggaagcgaaggt ccctcggagacgtgggtgaagtgaattggtggaatcag ggggaggactgtgcagcctggaggatcgctgagactgtc atgtgccgtgtccggctttgccctgtccaaccacgggatgtc ctgggtccgcgcgcgcctggaaagggcctcgaatgggt gtcgggtattgtgtacagcggtagcacctactatgccgat ccgtgaaggggagattcaccatcagccgggacaactcc aggaacactctgtacctccaaatgaattcgtgaggccag aggacactgccatctactactgctccgcgcagtgccgaga gtccgacgtctggggacaggggaccaccgtgaccgtgtc tagcgcgctccggcggaggcgccagcgggggtcgggcat cagggggcggcggatcgacatccagctcaccagctcc ccgagctcgtgtccgcctccgtgggagatcggggtacca tcacgtgccgcgcagccagctgatttccctctacctaac tggtagcaacagaagcccgaaaagccccgaagctctc atctacgcgcctcgagcctgcagtcaggagtgcctcac ggttctccggctccggttccggtactgttaccctgacct ttctccctgcaaccggaggactcgtacttactactgcc gcagtcgtactccacccctacactttcggacaaggcacc aaggctgaaatcaagaccactacccagcaccgaggcc acccaccggctcctaccatcgctcccagcctctgtccc tgcgtccggaggcatgtagaccgcagctggtggggcgg tgcatacccggggtcttgacttgcctgcgatactacattg ggccctctggctggtacttgcggggtcctgctgttctactc gtgatcactcttactgtaagcgggtcggaagaagctgct gtacatctttaagcaaccttcatgaggcctgtgcagacta ctcaagaggaggacggctgtcatgcccgttccagagg aggaggaaggcggctgcgaactgcgcgtgaaattcagc cgacgcgcagatgtccagcctaccagcaggggcagaa ccagctctacaacgaactcaatcttggtcggagagagga gtacgacgtgctggacaagcggagaggacgggaccca gaaatggggcgggaagccgcgcagaaagaatcccaag agggcctgtacaacgagctccaaaaggataagatggca gaagcctatagcgagattggtatgaaaggggaacgcag aagaggcaaaggccacgacggactgtaccagggactc agcaccgccaccaaggacacctatgacgtcttccatg caggccctgccgcctcgg (SEQ ID NO: 176)
SP-Linker 1- ERmut1-Furin cleavage site 3- BCMA CAR	MALPVTALLLPLALLLHAARPR SSLALSLTADQMVSALLDAEP PILYSEYDPTPRPFSEASMMGL LTNLADRELVHMINWAKRVPG FVDLALHDQVHLLLECAWMEIL MIGLVWRSMEHPGKLLFAPNL	atggccctccctgtcacgcctgctgcttccgtggctcttc tgcctcacgcgcgtcggccccgggtcgTcgttggcactttcc ctgactgccgaccagatggtgtccgcccttctggacgcgcg agcctccaattctgtactcggagtacgatccgactcgcgcg ttctccgaagccagcatgatggcctgttgactaacctggc ggaccgcgagttggtgcacatgattaactgggctaagcgg

	LLDRNQGKCEGGVEIFDMLL ATSSRFRMMNLQGEFVCLK SIILLNSGVYTFLSSTLKSLEEK DHIHRVLDKITDTLIHLMAKAG LTLQQQHQRLLAQLLLILSHIRH MSSKRMEHLYSMKCKNVVPL SDLLLEMLDAHRLGTGAEDPR PSRKRREVQLVESGGGLVQP GGSLRLSCAVSGFALS NHGM SWVRRAPGKGLEWVSGIVYS GSTYYAASVKGRFTISRDNRS NTLYLQMNSLRPEDTAIYYCS AHGGESDVWGQGTTVTVSSA SGGGGSGGRASGGGSDIQL TQSPSSLSASVGDRTITCRA SQSISSYLNWYQKPKGAPKL LIYAASSLQSGVPSRFSGSGS GTDFTLTISLQPEDFATYYC QQSYSTPYTFGQGTKEIKTT TPAPRPPTPAPTIASQPLSLRP EACRPAAGGAVHTRGLDFAC DIYIWAPLAGTCGVLLLSLVL YCKRGRKKLLYIFKQPFMRPV QTTQEEDGCSCRFEEEEEGG CELRVKFSRSADAPAYQQGQ NQLYNELNLGRREEYDVLDK RRGRDPEMGGKPRRKNPQE GLYNELQKDKMAEAYSEIGMK GERRRGKGDGLYQGLSTAT KDTYDALHMQALPPR (SEQ ID NO: 177)	gtgccgggcttcgtggacctggccctgcacgaccaagtgc acctcctggaatgcgcctggatggaatcctcatgatcgg cctcgtgtggagatccatggagcatcccgaaagctcctg ttgcacccaacctcctgctgatcgcaaccagggaaaatg cgtggaaggggggtgcgagatttcgacatgctgctcgcca cctcttcccggtccggatgatgaatcgcagggagaaga gtcgtgtgtctgaagtcaatcatcctgctgaactccgggt ctatacctcctgagctcgaccctcaagtcactggaggaaa aagaccacatccatcgctgctcgataagatcaccgaca cccttatccatctcatggcgaaggctggactgacctgcaa cagcagcaccagaggctggcccgagtgtgctgattctga gccacatccggcacatgtcgtccaagaggatggaacacc tgtacagcatgaagtgaagaacgtcgtgctcgtcctgat ctgctcctggaaatgtggacgcgcacagactcGggacg ggagctgaagatccacgacccagcagaaagcgacggg aagtgaattggtggaatcagggggaggactgtgcagc ctggaggatcgtgagactgtcatgtccgtgtccggcttg ccctgtccaaccacgggatgtcctgggtccgcccgcgcgc tggaaagggcctcgaatgggtgtcgggtattgtgtacagc ggtagcacctactatgccgatccgtgaaggggagattca catcagccgggacaactccaggaacactctgtacctcc aatgaattcgtgaggccagaggacactgccatctacta ctgctccgcgcgatggcggagagtccgacgtctggggaca ggggaccaccgtgaccgtgtctagcgcgtccggcggag gcgccagcgggggtcgggcatcagggggcgccggatc ggacatccagctcaccagtcctccgagctcgtgtccgcc tcgtgggagatcgggtcaccatcacgtccgcgcgcagc cagtcgatttctcctacctgaactgttaccacagaagcc cggaaaagccccgaagcttctcatctacgcgcctcgag cctgcagtcaggagtgcctcaggttctccggctccgggt ccggtactgatttaccctgaccatttctccctgcaaccgg aggacttcgctacttactactgccagcagtcgtactccacc ccctacatttccgacaaggcaccgaaggtcgaatcaag accactacccagcaccgaggccaccaccccggtcct accatcgctcccagcctctgtccctgctcggaggcatg tagaccgcgagctgtgtggggccgtgcatacccggggtct gacttcgctcgcgatactacatttgggccccctgtggtgta cttgccgggtcctgctgtcttactcgtgatcactcttactgta agcgcgggtcgaagaagctgctgtacatcttaagcaacc ctcatgaggcctgtgcagactactcaagaggaggacgg ctgttcatgccggttccagaggaggaggaaggcggctg cgaactgcgcgtgaaattcagccgcagcgcagatgctcc agcctaccagcaggggcagaaccagctctacaacgaac tcaatcttggtcggagagaggagtacgacgtgctggaca agcggagaggacgggaccagaaatgggcgggaagc cgcgcagaaagaatccccaaggggcctgtacaacga gctccaaaaggataagatggcagaagcctatagcgaga ttggtatgaaaggggaacgcagaagaggcaaaggcca cgacggactgtaccagggactcagcacgccaccaagg acacctatgacgctcttcacatgcaggccctgcccgtcg g (SEQ ID NO: 178)
SP-Linker 1- ERmut2-Furin cleavage site 1- BCMA CAR	MALPVTALLLPLALLLHAARPR SSLALSLTADQMVSALLDAEP PILYSEYDPTPRPFSEASMMGL LTNLADRELHMINWAKRVPG	atggccctccctgtcaccgcccctgctgcttccgctggctcttc tgctccacgcccgtcggccccgggtcgTcgttggcacttcc ctgactgccgaccagatggtgtccgcccttctggacgccc agcctccaattctgtactcggagtacgatccgactcggccc

	FVDLTLDQVHLLLECAWMEIL MIGLVWRSMEHPGKLLFAPNL LLDRNQGKCEGGVEIFDMLL ATSSRFRMMNLQGEFVCLK SIILLNSGVYTFLLSSTLKSLEEK DHIHRVLDKITDTLIHLMAKAG LTLQQQHQRRLAQLLLILSHIRH MSNKRMEHLYSMKCKNVVPL SDLLEMLDAHRLRTKREVQL VESGGGLVQPGSLRLSCAV SGFALSNHGMSWVRRAPGK GLEWVSGIVYSGSTYYAASVK GRFTISRDNSRNTLYLQMNSL RPEDTAIYYCSAHGGESDVW GQGTTVTVSSASGGGGSGG RASGGGSDIQLTQSPSSLSA SVGDRVTITCRASQSISSYLN WYQQKPGKAPKLLIYAASSLQ SGVPSRFSGSGSGTDFLTIS SLQPEDFATYYCQSYSTPYT FGQGTKVEIKTTTPAPRPPTP APTIASQPLSLRPEACRPAAG GAVHTRGLDFACDIYWAPLA GTCGVLLLSLVITLYCKRGRKK LLYIFKQPFMRPVQTTQEEDG CSCRFPEEEEGGCELRVKFS RSADAPAYQQGQNQLYNELN LGRREEYDVLDRRGRDPEM GGKPRRKNPQEGLYNELQKD KMAEAYSEIGMKGERRRGKG HDGLYQGLSTATKDTYDALH MQALPPR (SEQ ID NO: 179)	tttcggaagccagcatgatgggctgtgactaacctggc ggaccgagagtggtgcacatgattaactgggctaagcgg gtgccgggctcgtggacctgacctgcacgaccaagtg acctcctggaatgcgcctggatggaatcctcatgatcgg cctcgtgtggagatccatggagcatcccgaaagctcctg ttgcacccaacctcctgctgatcgcaaccagggaatg cgtggaaggggtgtcgagatttgcacatgctgctcgcca cctctcccgggtccggatgatgaatcgcagggaaga gttcgtgtgtgaagcaatcatcctgctgaactccgggt ctatacctcctgagctcgacctcaagtcactggaggaaa aagaccacatccatcgctgctgataagatcacggaca cccttatccatctcatggcgaaggctggactgacctgcaa cagcagcaccagaggtggccagtgctgctgattctga gccacatccggcacatgtcgacaagaggatggaacac ctgtacagcatgaagtgaagaacgctgctcctgtccg atctgctcctggaatgctggacgcgacagactccgtact aaaagagaagtgcaattggtggaatcagggggaggactt gtgcagcctggaggatcgctgagactgtcatgtccgtgtc cggtttgccctgtccaaccacgggatgtcctgggtccgcc gcgcgctggaaggccctgaatgggtgctgggtattgt gtacagcggtagcacctactatgcgcacatccgtgaagg gagattcaccatcagccgggacaactccaggaaactct gtacctccaaatgaattcgtgaggccagaggacactgc catctactactgtcctcgcatggcgagagtcggactcc ggggacaggggaccaccgtgacctgtctagcgcgtcc ggcgaggcgccagcgggggtcgggcatcagggggcg gcggtatcgacatccagctcaccagtcctccgagctcgc tgtccgctcctgggagatcggtcaccatcacgtccg cgccagccagtcgatttctcctactgaactgtaccaac agaagcccgaaaagccccgaagcttctcatctacgccg cctcgagcctgcagtcaggagtgcctcagcgttctccg ctccggtccggtactgattcaccctgaccatttctccctgc aaccggaggactcgtactactactgccagcagtcgtac tccacccctacacttccgacaaggcaccaggtcgaa atcaagaccactacccagcaccgaggccacccaccc ggctcctaccatcgctcctccagcctctgtccctcgctccg aggcatgtagaccgagctggtggggcggtgcataccc ggggtcttgactcgcctcgatatactattgggcccctct ggctggtacttgcgggtcctgctgttctactcgtgatcact cttactgtaagcggtcggaagaagctgctgtacatctt aagcaaccctcatgaggcctgtgcagactactcaagag gaggacggctgtcatgcgggtcccagaggaggaggaa ggcggtgcgaactgcggtgaaattcagccgagcgc agatgctccagcctaccagcggggcagaaccagctcta caacgaactcaatcttggtcgagagaggagtacgacgt gctggacaagcggagaggacgggacccagaaatgggc gggaagccgagcagaaagaatcccaagaggcctgt acaacgagctccaaaggataagatggcagaagcctat agcgagattggtatgaaaggggaacgcagaagaggca aaggccacgagcgtgtaccagggactcagcaccgcc accaaggacacctatgacgctctcacatgcaggccctgc cgctcgg (SEQ ID NO: 180)
SP-Linker 1- ERmut2-Furin cleavage site 2- BCMA CAR	MALPVTALLLPLALLLHAARPR SSLALSLTADQMVSALLDAEP PILYSEYDPTPRPFSEASMMGL LTNLADRELHMINWAKRVPG	atggccctccctgtcaccgcccgtgcttccgctggctctt tgctccacgcccgtcggccccgggtgcgtggcacttcc ctgactccgaccagatggtgtccgcccctctggacgcgg agcctccaattctgtactcggagtacgatccgactcggccg

	FVDLTLDQVHLLLECAWMEIL MIGLVWRSMEHPGKLLFAPNL LLDRNQGKCEGGVEIFDMLL ATSSRFRMMNLQGEFVCLK SIILLNSGVYTFLLSSTLKSLEEK DHIHRVLDKITDTLIHLMAKAG LTLQQQHQRLLAQLLLILSHIRH MSNKRMEHLYSMKCKNVVPL SDLLLEMLDAHRLGTGAEDPR PSRKRRSLGDVGEVQLVESG GGLVQPGGSLRLSCAVSGFA LSNHGMSWVRRAPGKGLEW VSGIVYSGSTYYAASVKGRFTI SRDNSRNTLYLQMNSLRPED TAIYYCSAHGGESDVWGQGT TVTSSASGGGGSGGRASGG GGSDIQLTQSPSSLASVGD VTITCRASQSISSYLNWYQK PGKAPKLLIYAASSLQSGVPS RFSGSGSGTDFTLTISLQPE DFATYYCQQSYSTPYTFGQG TKVEIKTTTPAPRPPTPAPTIA SQPLSLRPEACRPAAGGAVH TRGLDFACDIYIWAFLAGTCG VLLLSLVITLYCKRGR KKLLYIFKQPFMRPVQTTQEE DGCSCRFPEEEEGGCELRVK FSRSADAPAYQQGQNQLYNE LNLGRREEYDVLDKRRGRDP EMGGKPRRKNPQEGLYNELQ KDKMAEAYSEIGMKGERRRG KGHDGLYQGLSTATKDTYDAL HMQALPPR (SEQ ID NO: 181)	tttcggaagccagcatgatgggctgtgactaacctggc ggaccgaggttggtgcacatgattaactgggctaagcgg gtgccgggcttcgtggacctgacctgcacgaccaagtgc acctcctggaatgcgcctggatggaatcctcatgatcgg cctcgtgtggagatccatggagcatcccgaaagctcctg ttgcacccaacctcctgctgatcgcaaccagggaatg cgtggaaggggtgtcgagatttcgacatgctgctcgcca cctctcccggtccggatgatgaatctgcagggaaga gttcgtgtgtgaagcaatcatcctgctgaactccgggt ctatacctcctgagctcgacctcaagtcactggaggaaa aagaccacatccatcgctgctgataagatcacggaca cccttatccatctcatggcgaaggctggactgacctgcaa cagcagcaccagaggtggccaggtgctgctgattctga gccacatccggcacatgtcgacaagaggatggaacac ctgtacagcatgaagtgaagaacgctgctcctgtccg atctgctcctggaatgttgagcgccacagactcggaa cggcgcggaagaccccgccctccagggaagcgaag gtccctcggagacgtgggtgaagtgaattggtggaatca gggggaggactgtgcagcctggaggatcgtgagactg tcatgtccgtgtccggcttgcctgtccaaccacgggatg tctgggtccgcccgcgcctggaaaggcctcgaatgg gtgtcgggtattgtgtacagcggtacactactatgccgc atccgtgaaggggagattaccatcagccgggacaactc caggaaactctgtacctcaaatgaattcgtgaggcca gaggacactgccatctactgctccgcgcatggcggag agtccgacgtctgggacaggggaccacgtgacctgt ctagcgcgtccggcggaggcggcagcgggggtcgggc atcagggggcggcgatcgacatccagtcacccagtc cccgagctcgtgtccgctcgtgggagatcgggtcacc atcagtgccgcgcagccagtcgatttctctacctgaa ctggtaccaacagaagcccgaaaagccccgaagcttct catctacgcccgtcgtgagcctgcagtcaggagtgcctca cgggtctccggtccggttccggtactgatttaccctgacc atttctccctgcaaccggaggacttcgctacttactactgc cagcagtcgtactccacccctacacttccggacaaggca ccaaggtcgaatcaagaccactacccagcaccgagg ccacccaccccggtcctaccatcgctccagcctctgtc cctgctccggaggcatgtagaccgcagctggtggggc cgtgcatacccggtgttacttcgctgcgatactacatt tgggcccctctggtggtacttgcgggtcctgctgtttcac tcgtgatcacttcttactgtaagcgcggtcgaagaagctg ctgtacatctttaagcaaccttcatgaggcctgtgcagact actcaagaggaggacggctgttcagcgggttccagag gaggaggaaggcggctgcgaactgcgcgtgaaattcag ccgacgcgcagatgctccagcctaccagcaggggcaga accagctctacaacgaactcaatcttggtcggagagagg agtacgacgtgctggacaagcggagaggacgggaccc agaaatgggcggaagccgcgcagaaagaatcccaa gagggcctgtacaacgagctccaaaaggataagatggc agaagcctatagcgagattggtatgaaaggggaacgca gaagaggcaaggccacgacggactgtaccagggact cagcaccgccaccaaggacacctatgacgcttctcatat gcaggccctgccgcctcg (SEQ ID NO: 182)
SP-Linker 1- ERmut2-Furin cleavage site 3-	MALPVTALLPLALLHAARPR SSLALSLTADQMVSALLDAEP PILYSEYDPTPRPFSEASMMGL	atggccctccctgtcaccgcccgtgcttccgctggctcttc tgctccacgcccgtcggccccggctgTcggtggcacttcc ctgactgccgaccagatggtgtccgccccttctggacgcgcg

BCMA CAR	LTNLADRELVHMINWAKRVPG FVDLTLDQVHLLLECAWMEIL MIGLVWRSMEHPGKLLFAPNL LLDRNQGKCEGGVEIFDMLL ATSSRFRMMNLQGEFVCLK SIILLNSGVYTFLSSTLKSLEEK DHIHRVLDKITDTLIHLMAKAG LTLOQQHQRLAQLLLILSHIRH MSNKRMEHLYSMKCKNVVPL SDLLEMLDAHRLGTGAEDPR PSRKRREVQLVESGGGLVQP GGSLRLSCAVSGFALS NHGM SWVRRAPGKGLEWVSGIVYS GSTYYAASVKGRFTISRDNRS NTLYLQMNSLRPEDTAIYYCS AHGGESDVWGQGTTVTVSSA SGGGSGGGRASGGGSDIQL TQSPSSLSASVGDRVTITCRA SQSISSYLNWYQKPKAPKL LIYAASSLQSGVPSRFSGSGS GTDFTLTISLQPEDFATYYC QQSYSTPYTFGQGTKVEIKTT TPAPRPPTPAPTIASQPLSLRP EACRPAAGGAVHTRGLDFAC DIYIWAPLAGTCGVLLLSLVITL YCKRGRKKLLYIFKQPFMRPV QTTQEEDGCSCRFEEEEEGG CELRVKFSRSADAPAYQQGQ NQLYNELNLGRREEYDVLDK RRGRDPEMGGKPRRKNPQE GLYNELOKDKMAEAYSEIGMK GERRRGKGDGLYQGLSTAT KDTYDALHMQALPPR (SEQ ID NO: 183)	agcctccaattctgtactcggagtagcatccgactcgcccg ttctccgaagccagcatgatggcctgttgactaacctggc ggaccgcgagttggtgcacatgattaactgggctaagcgg gtgccgggcttcgtggacctgacctgcacgaccaagtgc acctcctggaatgcgcctggatggaaatcctcatgatcgg cctcgtgtggagatccatggagcatcccgaaagctcctg ttgcacccaacctcctgcttgatcgcaaccagggaatg cgtggaaggggtgtcgagatttgcacatgctgctcgcca cctcttcccggtccggatgatgaatctgcagggagaaga gttcgtgtgtctgaagcaatcatcctgctgaactccgggt ctataccttccgtgactcgacctcaagtcactggaggaaa aagaccacatccatcgctgctcgataagatcacccgaca cccttatccatctcatggcgaaggctggactgacctgcaa cagcagcaccagaggctggccaggtgctgctgattctga gccacatccggcacatgtcgaaacagaggatggaacac ctgtacagcatgaagtgaagaacgctgctcctgtccg atctgctcctggaatgtctggacgcgcacagactcggga cgggagctgaagatccacgacctcagagaaagcgacg ggaagtgaattggtggaatcagggggaggactgtgtga gcctggaggatcgctgagactgtcatgtccgtgtccggct tgccctgtccaaccacgggatgtcctgggtccgcgcgc gcctggaaaggcctcgaaatgggtgtcgggtattgtgtac agcggtagcacctactatgccgcatccgtgaaggggaga ttaccatcagccgggacaactccaggaacactctgtacc tccaaatgaattcgtgaggccagaggacactgccatcta ctactgctccgcgcagtgccggagagtcgcagctctggg acaggggaccacctgacctgtctagcgcgtccggcgg aggcggcagcgggggtcgggcacagggggcggcgga tcggacatccagctcaccagctcccgagctcgtgtccg cctccgtgggagatcgggtcaccatcacgtgccgcgcca gccagtcgatttctcctactgaactgttaccacagaag ccggaaaagccccgaagcttctcatctacgccgcctcg agcctgcagtcaggagtgccctcacggttctccggctccg gttccggctactgatttaccctgaccttctccctgcaacc ggaggacttcgctacttactactgccagcagtcgtactcca ccccctacactttcggacaaggcaccaaggctgaaatca agaccactacccagcaccgaggccacccaccccggt cctaccatcgctcccagcctctgtccctgctcggaggc atgtagaccgcagctggtggggcgtgcataccgggg tcttgacttcgctcgatatactattggccctctggctg gtacttgcggggctcctgctgcttctactcgtgatcactcttact gtaagcgcggtcggaagaagctgtgtacatcttaagca accctcatgaggcctgtgcagactactcaagaggagga cggctgtcatgcccgttcccagaggagggaaggcgg ctgcgaactgcgcgtgaaattcagccgcagcgagatgc tccagcctaccagcaggggcagaaccagctctacaacg aactcaatctgtgtcgagagaggagtacgacgtgctgg acaagcggagaggacgggaccagaaatgggcggga agccgcgcagaaagaatccccagagggtctgtacaa cgagctccaaaaggataagatggcagaagcctatagcg agattggtatgaaaggggaacgcagaagaggcaaagg ccacgacggactgtaccagggactcagcaccgccacca aggacacctatgacgcttctacatgcaggccctgcggcc tcgg (SEQ ID NO: 184)
-----------------	---	---

Cell lines and cell transduction

Jurkat cells were obtained from the ATCC and maintained in media according to supplier's recommendations. Jurkat cell lines were transduced by spinoculation with lentiviral supernatant from 293T cells transfected with the various plasmid DNAs.

5 *Cancer Cells*

NALM6, K562, Molm13 cell lines were obtained from the ATCC and maintained in media according to supplier's recommendations. To produce a bioluminescent model for T cell killing assays, all cells were transduced with a luciferase lentiviral construct and kept under antibiotic selection.

Compound treatments

- 10 4-hydroxytamoxifen (4-OHT) was resuspended in ethanol. Bazedoxifene and raloxifene were resuspended in DMSO. In all instances, where concentrations not indicated, compounds were added at 1 μ M for 24 hours prior to analysis by flow cytometry.

Flow cytometry

- 15 Cells were isolated from *in vitro* culture, washed once in PBS supplemented with 0.5% bovine serum albumin, and stained on ice using either biotinylated Protein L followed by incubated with a fluorochrome-conjugated streptavidin reagent or an antibody recognizing the given target antigen. In all analyses, the population of interest was gated based on forward vs side scatter characteristics, followed by singlet gating, and live cells were gated. Flow cytometry was performed on a four laser Fortessa (Becton-Dickinson).

20 *Tumor killing assay*

In brief, luciferase transduced target cell lines were co-cultured at the indicated ratios with effector CD19CAR, FurON-CD19CAR, CD123CAR, FurON-CD123 CAR T cells for 20 hours, in the presence or absence of bazedoxifene. Remaining luciferase activity was measured by adding Bright-Glo (Promega) on a luminescence reader (Envision). Percentage killing was calculated using negative controls.

25 *Cytokine secretion*

Effector and luciferase transduced target cell lines were co-cultured at a 3:1 ratio in RPMI containing 10% FBS for 20 hours, in the presence or absence of bazedoxifene. Supernatant was analysed by 3-plex array according the manufacturer's instructions (Invitrogen).

Proliferation assay

Effector and irradiated target cells were co-cultured for 4 days, in the presence or absence of bazedoxifene. Cells were then harvested, washed, and stained with an anti-CD3 antibody and/or protein L reagent to detect CAR surface expression. Cells were then washed, resuspended in FACS buffer and a fixed volume of Absolute Counting Beads are added to each sample. Samples were run on a Fortessa FACS analyzer and the same number of events in the Counting Beads gate was collected for all samples.

EXAMPLE 14: EVALUATION OF DIFFERENT FURIN CLEAVAGE SITES WITHIN THE FURIN DEGRON DOMAIN IN THE CONTEXT OF CAR19 (ANTI-CD19 SCFV CAR)

Gene fragments, comprising a furin degron domain fused to an anti-CD19 scFV CAR and preceded by a T7 promoter, were subjected to in vitro transcription/ translation. The differences between gene fragments lay in the furin cleavage sites created, as annotated. The *in vitro* synthesized proteins were incubated with furin as indicated, at 37°C for 1hr. The samples were loaded onto a reducing SDS-PAGE gel and analyzed by immunoblotting using an anti-CD3ζ antibody.

FIGs. 12A-12B showed the degree of furin cleavage across the various tested furin cleavage sites, in the CAR19 context. The tested furin cleavage sites are: #105 – LQWLEQQVAKRRTKR (SEQ ID NO: 129); #106 – GTGAEDPRPSRKRRSLGDVG (SEQ ID NO: 125); #107 – GTGAEDPRPSRKRRSLGG (SEQ ID NO: 131); #108 – GTGAEDPRPSRKRRSLG (SEQ ID NO: 133); #102 – SLNLTESHNSRKRR (SEQ ID NO: 135); #103 – GTGAEDPRPSRKRR (SEQ ID NO: 127); #104 – CKINGYPKRGRKRR (SEQ ID NO: 137); #73 – RTKR (SEQ ID NO: 123). A gene fragment derived from the parental CAR19 was used as a control (Ctrl) and no cleavage was observed (FIGs. 12A-12B).

EXAMPLE 15: COMPOUND INDUCIBLE CAR EXPRESSION IN PRIMARY HUMAN T CELLS

Primary human T cells were transduced with a furin degron domain fused to an anti-CD19 scFV CAR construct (construct #106). Untransduced T cells (UTD) and the parental CAR19 were used as controls. Cells were expanded for 10 days in the presence of anti-CD3/CD28 stimulation beads. 100U/mL IL-2 was added on day 7, bazedoxifene (BZA) was added on day 8. Prior to freezing down the cells, CAR expression was determined on day 10 by FACS using protein L staining. Cell number, size, and viability were also assessed.

The data demonstrated that the furin degron domain regulates CAR19 expression in a stabilizing compound-dependent manner in human primary T cells, with the MFI (mean fluorescence intensity) of the CAR being lower compared to the parental CAR construct (FIG. 13). Also, the furin degron domain had no impact on cell viability and cell proliferation (FIG. 13).

EXAMPLE 16: COMPOUND-DEPENDENT FURON CAR-MEDIATED TUMOR KILLING

Primary human T cells were transduced with a furin degron domain fused to an anti-CD19 scFV CAR (construct #106). Untransduced T cells (UTD) were used as control. The parental CAR19 construct was included as a benchmark for full CAR functional activity. Cells are expanded for 10 days in the presence of anti-CD3/CD28 stimulation beads. 100U/mL IL-2 was added on day 7, bazedoxifene was added on day 8 (samples CD19CAR+ and FurON 106+) or omitted (samples CD19CAR and FurON 106). Cells were frozen on day 10. T cells were thawed and co-cultured with the luciferized target cell lines (CD19+ NALM6 cells or CD19- K562 cells) and bazedoxifene, for 20 hours. CART cells were normalized to the same percentage of CAR expressing cells. Percent tumor lysis was determined by analysis of remaining luciferase activity.

These data demonstrated that CAR19 with the furin degron domain kills CD19+ tumor cells in a stabilizing compound dose-dependent manner and is noninferior to the parental CAR construct (FIG. 14).

EXAMPLE 17: COMPOUND- AND TUMOR-DEPENDENT CYTOKINE SECRETION BY THE FURON CAR

Primary human T cells were transduced with a furin degron domain fused to an anti-CD19 scFV CAR (construct 106). Untransduced T cells (UTD) were used as control. The parental CAR19 construct was included as a benchmark for full CAR functional activity. Cells were expanded for 10 days in the presence of anti-CD3/CD28 stimulation beads. 100U/mL IL-2 was added on day 7, bazedoxifene (BAZ) was added on day 8 (samples CD19CAR+BAZ and FurON 106+BAZ) or omitted (samples CD19CAR and FurON 106). Cells were frozen on day 10. T cells were thawed and co-cultured with luciferized NALM6, a CD19+ target cell line, for 20 hours, and bazedoxifene as indicated. CART cells were normalized to the same percentage of CAR expressing cells. Supernatants were harvested and evaluated for levels of IFN γ .

These data demonstrated that primary human T cells expressing ER α FurON CAR19 secrete IFN γ in the presence of CD19+ tumor cells, in a manner that is stabilizing compound dose-dependent and is noninferior to the parental CAR19 construct (FIG. 15).

EXAMPLE 18: COMPOUND- AND TUMOR-DEPENDENT PROLIFERATION OF THE FURON CAR

Primary human T cells were transduced with a furin degron domain fused to an anti-CD19 scFV CAR (construct 106). Untransduced T cells (UTD) were used as control. The parental CAR19 construct was included as a benchmark for full CAR functional activity. Cells were expanded for 10 days in the presence of anti-CD3/CD28 stimulation beads. 100U/mL IL-2 was added on day 7, bazedoxifene (Baz) was added on day 8 (samples CD19CAR+BAZ and FurON 106+BAZ) or omitted (samples CD19CAR and FurON 106). Cells were frozen on day 10. T cells were thawed and co-cultured with the luciferized target

cell lines (CD19+ NALM6 cells or CD19- K562 cells) and bazedoxifene. CART cells were normalized to the same percentage of CAR expressing cells. After 4 days, the samples were analyzed by FACS and 3000 events in the counting beads gate were collected for all samples.

5 These data demonstrated that primary human T cells expressing ER α FurON CAR19 proliferate in the presence of CD19+ tumor cells, in a manner that is stabilizing compound-dependent and is noninferior to the parental CAR19 construct (FIG. 16).

EXAMPLE 19: COMPOUND INDUCIBLE CAR EXPRESSION IN JURKAT T CELLS

10 Jurkat T cells were transduced with one of two furin degron domains fused to an anti-CD19 scFV CAR constructs. The two constructs share the same furin cleavage sequence but differ in the number of mutations in the degradation domain (ERmut1 or ERmut 2 shown in Table 23). The construct with more mutations was FurONCART19 #106 (with ERmut1); and the construct with fewer was FurONCART19 #130 (with ERmut2). The transduced cells were incubated with 4-OH tamoxifen, bazedoxifene, or raloxifene, at the indicated concentrations, for 42 hours. Expression of the anti-CD19 scFV was determined by FACS, using protein L.

15 These data demonstrated that the tested furin degron domains can regulate CAR19 expression in a stabilizing compound-dependent manner, regardless of the number of mutations; and no CAR surface expression is detected in the absence of compound (FIG. 17).

EXAMPLE 20: COMPOUND INDUCIBLE CAR EXPRESSION IN HUMAN PRIMARY T CELLS

20 Primary human T cells were transduced with a furin degron domain fused to an anti-CD19 scFV CAR construct (construct #130). Untransduced T cells (UTDs) and the parental CAR19 were used as controls. Cells were expanded for 10 days in the presence of anti-CD3/CD28 stimulation beads. 100U/mL IL-2 was added on day 7 or omitted, bazedoxifene (BZA) was added on day 8. Prior to freezing down the cells, CAR expression was determined on day 10 by FACS, using protein L staining.

25 These data demonstrated that the FurON domain – comprising a limited number of mutations in the degron domain - regulates CAR19 expression in a stabilizing compound- and IL-2-dependent manner in human primary T cells (FIG. 18). Also, no surface CAR expression is detected in the absence of the stabilizing compound bazedoxifene, when the FurON moiety is fused to CAR19 (FIG. 18).

EXAMPLE 21: COMPOUND-DEPENDENT FURON CAR-MEDIATED TUMOR KILLING

30 Primary human T cells were transduced with a furin degron domain fused to an anti-CD19 scFV CAR construct (construct #130). Untransduced T cells (UTDs) were used as control. The parental CAR19 construct was included as a benchmark for full CAR functional activity. Cells were expanded for 10 days in the presence of anti-CD3/CD28 stimulation beads. 100U/mL IL-2 was added on day 7. Bazedoxifene

(BZA) was added on day 8 to a fraction of the FurON 130 BZA sample, so CAR expression can be determined on day 10 by FACS, using protein L staining, prior to freezing down the cells. T cells were thawed and co-cultured with the luciferized target cell lines (CD19+ NALM6 cells or CD19- K562 cells) for 20 hours, in the presence or absence of bazedoxifene. Different ratios of CART ("effector") and target cells are used as indicated in the x-axis of FIGs. 19A-19B. CART cells were normalized to the same percentage of CAR expressing cells. Percent tumor lysis was determined by analysis of remaining luciferase activity.

These data demonstrated that CART cells expressing FurON CAR19 kill CD19+ tumor cells, comprising a limited number of mutations in the degron domain, in a stabilizing compound- and target-dependent manner and is noninferior to the parental CAR construct (FIGs. 19A-19B).

EXAMPLE 22: COMPOUND- AND TUMOR-DEPENDENT CYTOKINE SECRETION BY THE FURON CAR

Primary human T cells were transduced with a furin degron domain fused to an anti-CD19 scFV CAR construct (construct #130). Untransduced T cells (UTDs) were used as control. The parental CAR19 construct was included as a benchmark for full CAR functional activity. Cells were expanded for 10 days in the presence of anti-CD3/CD28 stimulation beads. 100U/mL IL-2 was added on day 7. Bazedoxifene (BZA) was added on day 8 to a fraction of the FurON 130 BZA sample, so CAR expression can be determined on day 10 by FACS, using protein L staining, prior to freezing down the cells. Cells were frozen on day 10. T cells were thawed and co-cultured with the luciferized target cell lines (CD19+ NALM6 cells) for 20 hours, at a 5:1 effector:target ratio, in the presence or absence of bazedoxifene. CART cells were normalized to the same percentage of CAR expressing cells. Supernatants were harvested and evaluated for levels of IFN γ .

These data demonstrated that CART cells expressing FurON CAR19, comprising a limited number of mutations in the degron domain, secrete cytokines in the presence of CD19+ tumor cells, in a manner that is stabilizing compound-dependent and is noninferior to the parental CAR construct (FIG. 20).

EXAMPLE 23: COMPOUND- AND TUMOR-DEPENDENT T CELL PROLIFERATION

Primary human T cells were transduced with a furin degron domain fused to an anti-CD19 scFV CAR (construct #130). Untransduced T cells (UTD) were used as control. The parental CAR19 construct was included as a benchmark for full CAR functional activity. Cells were expanded for 10 days in the presence of anti-CD3/CD28 stimulation beads. 100U/mL IL-2 was added on day 7. Bazedoxifene was added on day 8 to a fraction of the FurON 130 BZA sample, so CAR expression can be determined on day 10 by FACS, using protein L staining, prior to freezing down the cells. Cells were frozen on day 10. T cells were thawed and co-cultured with the indicated luciferized target cell lines for 4 days, in the presence or absence of bazedoxifene. CART cells were normalized to the same percentage of CAR

expressing cells. After 4 days, the samples were analyzed by FACS and 3000 events in the counting beads gate are collected for all samples.

These data demonstrated that CD3⁺ T cells comprising FurON CAR19 proliferate in the presence of CD19⁺ tumor cells, in a manner that is stabilizing compound-dependent and is noninferior to the parental CAR construct (FIG. 21).

EXAMPLE 24: COMPOUND INDUCIBLE CAR123 EXPRESSION IN PRIMARY HUMAN T CELLS

Primary human T cells were transduced with a furin degron domain fused to an anti-CD123 scFV CAR construct. Untransduced T cells (UTD) and the parental CAR123 were used as controls. Cells were expanded for 10 days in the presence of anti-CD3/CD28 stimulation beads. 100U/mL IL-2 was added on day 7, bazedoxifene (BZA) was added on day 8 (Furon123+BZA) or omitted (Furon123). Prior to freezing down the cells, CAR expression was determined on day 10 by FACS using protein L staining.

These data demonstrated that the FurON domain regulates CAR123 expression in primary human T cells, in a stabilizing compound-dependent manner (FIG. 22).

EXAMPLE 25: COMPOUND-DEPENDENT CAR123-MEDIATED TUMOR KILLING

Primary human T cells were transduced with a furin degron domain fused to an anti-CD123 scFV CAR construct. Untransduced T cells (UTD) were used as control. The parental CAR123 construct was included as a benchmark for full CAR functional activity. Cells were expanded for 10 days in the presence of anti-CD3/CD28 stimulation beads. 100U/mL IL-2 was added on day 7, bazedoxifene (BZA) was added on day 8 (FurON123+ BZA) or omitted (FurON123). Prior to freezing down the cells, CAR expression was determined on day 10 by FACS, using protein L staining. T cells were thawed and co-cultured with the luciferized target cell lines for 20 hours, in the presence or absence of bazedoxifene. Molm13 is a CD123⁺ cell line; very low expression of CD123⁺ observed in K562 cells. Different ratios of CART and target cells were used as indicated in the x-axis (E:T ratios) of FIG. 25. CART cells were normalized to the same percentage of CAR expressing cells. Percent tumor lysis was determined by analysis of remaining luciferase activity.

These data demonstrated that CART cells expressing FurON CAR123 kill CD123⁺ tumor cells, in a stabilizing compound- and target-dependent manner and is noninferior to the parental CAR construct (FIG. 23).

EXAMPLE 26: COMPOUND- AND TUMOR-DEPENDENT IFN- γ CYTOKINE SECRETION BY THE FURON CAR123

Primary human T cells were transduced with a furin degron domain fused to an anti-CD123 scFV CAR. Untransduced T cells (UTD) were used as control. The parental CAR123 construct was included as a

benchmark for full CAR functional activity. Cells were expanded for 10 days in the presence of anti-CD3/CD28 stimulation beads. 100U/mL IL-2 was added on day 7, bazedoxifene (BZA) was added on day 8 (FurON123+ BZA) or omitted (FurON123). Cells were frozen on day 10. T cells were thawed and co-cultured with the luciferized target cell lines for 20hrs at a 5:1 effector to target ratio, in the presence or absence of bazedoxifene. Molm13 is a CD123+ cell line; very low expression of CD123+ observed in K562 cells. Supernatants were harvested and evaluated for levels of IFN γ .

These data demonstrated that CART cells expressing FurON CAR123 secrete cytokines in the presence of CD123+ tumor cells, in a manner that is stabilizing compound-dependent and is noninferior to the parental CAR construct (FIG. 24).

EXAMPLE 27: FURON CART19 IS EFFECTIVE AGAINST CD19+ TUMOR CELLS IN AN ANIMAL MODEL ONLY WHEN BAZEDOXIFENE IS DOSED

Cell line

NALM6 (RRID: CVCL_0092) is a human leukemia cell line that was derived from the peripheral blood of a 19-year-old man with acute lymphoblastic leukemia (ALL) in relapse in 1976. Cells were grown in RMPI medium containing 10% fetal bovine serum. This cell line grows in suspension in tissue culture flasks. This cell line persists and expands in mice when implanted intravenously. The NALM6 cells have been modified to express luciferase, so that that tumor cell growth can also be monitored by imaging the mice.

Mice

6 week old NSG (NOD.Cg-*Prkdc*^{scid}*Il2rg*^{tm1Wjl}/SzJ) mice were received from the Jackson Laboratory. Animals were allowed to acclimate in the NIBR animal facility for at least 3 days prior to experimentation. Animals were handled in accordance with Novartis ACUC regulations and guidelines. Electronic transponders for animal identification were implanted on the left flank one day prior to tumor implantation.

Tumor implantation

NALM6 cells in logarithmic growth phase were harvested and washed in 50ml falcon tubes at 1200rpm for 5 minutes, once in growth media and then two times in cold sterile PBS. The cells were resuspended in PBS at a concentration of 5×10^6 per ml, placed on ice, and immediately injected in mice. Tumor cells were injected intravenously in 200ul through the caudal vein. The NALM6 model endogenously expresses CD19 and thus, can be used to test the in vivo efficacy of CD19-directed CAR T cells. This model grows well when implanted intravenously in mice and can be imaged for tumor burden measurements.

Preparation of CART19 and FurON CART19 cells for the in vivo study

CART cells were generated by starting with blood from healthy apheresed donors whose naïve T cells were obtained by negative selection for T cells, CD4+ and CD8+ lymphocytes. These cells were activated by the addition of CD3/CD28 beads (Dynabeads® Human T-Expander CD3/CD28, Thermo Fisher Scientific) at a ratio of 1:3 (T cell to bead) in T cell medium (RPMI1640, 10% heat-inactivated fetal calf serum (FCS), 2 mM L-glutamine, 1x Penicillin/Streptomycin, 100 µM non-essential amino acids, 1 mM Sodium Pyruvate, 10 mM Hepes, and 55 µM 2-mercaptoethanol) at 37°C, 5% CO₂. T cells were cultured at 4x10⁶ T cells (UTDs) or 5x10⁶ (CART19 and FurON CART19) in 1 mL medium per well of a 24-well plate. After 24 hours, when T cells were blasting, 0.5 mL of non-concentrated, or smaller volumes of concentrated viral supernatant were added; T cells were transduced at a multiplicity of infection (MOI) of 5. T cells began to divide in a logarithmic growth pattern, which is monitored by measuring the cell counts per mL, and T cells are diluted in fresh medium every two days. On day 7, 100U/ml of IL2 (PeproTech, Rocky Hill, NJ) and 1µM bazedoxifene is added to the cultures. On day 9, 1µM bazedoxifene is added. On day 10 the cells are collected and the percentage of cells transduced (expressing the CD19-specific CAR on the cell surface) was determined by flow cytometry analysis on a FACS Fortessa (BD). The viral transduction shows similar transduction efficiency; the surface expression of the FurON CART19 (mean fluorescence intensity, MFI) is lower than the observed for CART19. All CAR T cells were produced in research grade (i.e., not clinical grade) manufacturing conditions.

Treatment with CART19 or FurON CART19 cells

CD19+ NALM6 tumor cells expressing luciferase, were infused into NSG mice. Seven days later, the tumor burden was measured by whole body bioluminescence, the animals were randomized into treatment groups (5 mice per group), and infused with PBS (vehicle), CART19 (1x10⁶ or 5x10⁶ CAR+ T cells), FurON CART19 cells (5x10⁶ cells CAR+ T cells), or untransduced T cells (UTD), intravenously via the lateral tail vein. All animals received the same dose of total T cells (16.4x10⁶/mouse). Some treatment groups were dosed with bazedoxifene (BZA), bazedoxifene plus interleukin 2 (BZA/IL2), or vehicle, as indicated by the line. BZA was dosed for 10 days (single dose 200mg/kg; p.o). IL2 was dosed for 5 days, rested for two, and dosed again for 3 days (single dose 18x10⁶ IU/kg; i.p.). Tumor growth and animal health were monitored over time. The mean bioluminescence for all treatment groups is plotted in FIG. 27; the arrow indicates when administration of BZA and IL2 was discontinued.

Results

As shown in FIG. 47, while the tumor progressed in the negative control mice and mice treated with FurON CART19 only, tumor growth was inhibited in mice infused with CART19, or infused with FurON CART19 and treated with BZA alone or both BZA and IL2. Once dosing of bazedoxifene and IL2 is discontinued, only the constitutively active CART19 at the highest dose was able to control tumor growth. BZA was previously shown to have no effect on the growth of NALM6 tumor cells at the same dose and

dose regimen (data unshown). Thus, FurON CART19 in the presence of bazedoxifene shows comparable tumor inhibitory activity as the positive control CART19.

EXAMPLE 28: ADDITIONAL FURON CAR SEQUENCES

5 **Table 24. Sequences of additional FurON CAR constructs and components thereof**

	Amino acid sequence	DNA sequence
Leader sequence/ Signal peptide (SP)	MALPVTALLPLALLLHAARP (SEQ ID NO: 139)	atggccctccctgtcaccgcccgtgcttccgctggctcttc tgctccacgcccgtcggccc (SEQ ID NO: 140)
SP-Linker 2- ERmut1-Furin cleavage site 2 - CD19 CAR2	MALPVTALLPLALLLHAARPS LALSLTADQMVSALLDAEPPIL YSEYDPTRPFSEASMMGLLT NLADRELVHMINWAKRVPGF VDLALHDQVHLLCAWMEILM IGLVWRSMEHPGKLLFAPNLL LDRNQGKCEVEGVEIFDMLLA TSSRFRMMNLQGEFVCLKSI ILLNSGVYTFLSSTLKSLEEKD HIHRVLDKITDTLIHLMAKAGLT LQQQHQRLLAQLLLILSHIRHM SSKRMEHLYSMKCKNVVPLS DLLLEMLDAHRLGTGAEDPRP SRKRRSLGDVGEIVMTQSPAT LSLSPGERATLSCRASQDISK YLNWYQQKPGQAPRLLIYHTS RLHSGIPARFSGSGSGTDYTL TISSLQPEDFAVYFCQQGNL PYTFGQGTLEIKGGGGSGG GGSGGGGSQVQLQESGPG VKPSETLSLTCTVSGVSLPDY GVSWIRQPPGKLEWIGVIW GSETYYSSSLKSRVTISKDN SKNQVSLKLSSVTAADTAVYY CAKHYYYGGSYAMDYWGQG TLVTVSSTTPAPRPPTPPTI ASQPLSLRPEACRPAAGGAV HTRGLDFACDIYIWAPLAGTC GVLLLSLVITLYCKRGRKKLLYI FKQPFMRPVQTTQEEDGCSC RFPEEEEGGCELRVKFSRSA DAPAYQQGQNQLYNELNLGR REEYDVLDRRGRDPEMGGK PRRKNPQEGLYNELQKDKMA EAYSEIGMKGERRRGKGHDG LYQGLSTATKDTYDALHMQAL PPR (SEQ ID NO: 990)	atggccctccctgtcaccgcccgtgcttccgctggctcttc tgctccacgcccgtcggccc (SEQ ID NO: 140) atggccctccctgtcaccgcccgtgcttccgctggctcttc tgctccacgcccgtcggcccgtggtgacttccctgactg ccgaccagatggtgtccgccccttctggacgcccagcctcc aattctgtactcggagtacgatccgactcggcgttctccga agccagcatgatgggctgtgactaacctggcggaccg cgagttgtgcacatgattactgggtaagcgggtgccc ggctcgtggacctggccctgcacgaccaagtgcacctcc tggaatgcgcctggatggaatcctcatgatcggcctggtg tggagatccatggagcatcccgaaagctcctgtttgcac ccaacctcctgctgatcgcaaccagggaatgctgtg aagggggtgtcgagatttcgacatgctgctcgccacctt cccgggtccgcatgatgaatcgcaggaggagaagagttcgt gtgtcgaagtcaatcatcctgctgaactccgggtctatac cttctgagctcgacctcaagtcactggaggaaaaaga ccacatccatcgctgctcgataagatcaccgacacctt atccatctcatggcgaaggctggactgacctgcaacagc agcaccagaggctggcccagttgctgtgattctgagcca catccggcacatgctgccaagaggatggaacacctgta cagcatgaagtgaagaacgctgctgctctgtccgatctg ctcctggaaatgctggacgcgcacagactcggaaccggc gcggaagacccccggccctccaggaagcgaaggtccct cggagacgtgggtgaaattgtgatgacctcagtcacccgc cactcttagccttcacccgggtgagcgcgcgaacctgtctg cagagcctccaagacatctcaaaataaccttaattgtatc aacagaagcccggacaggtcctcgccttctgatctacca caccagccggctccattctggaatccctgccaggtcagc ggtagcggatctgggaccgactacacctcactatcagct cactgcagccagaggactcgtgcttattctgtcagcaa gggaacacctgcccacacctttggacagggcaccaag ctcagagattaagggtggaggtggcagcggaggaggtgg gtccggcgggtggaggaagcagggtccaactccaagaaa gcggacgggtctgtgagccatcagaaactcttactg actgtactgtgagcggagtgtctctcccgtattacgggtg tcttgatcagacagccacggggaagggtctggaatgg attggagtgtttggggtctgagactactactacttctatc cctcaagtcacgcgtcaccatctcaaggacaactctaag aatcaggtgtcactgaaactgtcatctgtgaccgacggc acaccgcccgtgtactattgcgctaagcattactattatggcg ggagctacgcaatggattactggggacagggtactctggt caccgtgtccagcaccactacccagcaccgaggccac ccacccggctcctaccatgcctcccagcctgttcctg cgtccggaggcatgtagaccgcagctggtggggccgtg

		cataccgggggtcttgacttcgctgcgatactacattgg gccccctctggctggacttgccgggtcctgctgttctactcg tgatcactctttactgtaagcgcggtcggaagaagctgctgt acatctttaagcaaccctcatgaggcctgtgcagactactc aagaggaggacggctgtcatgccgttcccagaggagg aggaaggcggtcggaactgcgctgaaattcagccgc agcgagatgtccagcctaccagcaggggcagaacca gctctacaacgaactcaatcttggtcggagagaggagtag gacgtgctggacaagcggagaggacgggaccagaaa tgggcggaagccgcgcagaaagaaatcccaagaggg cctgtacaacgagctccaaaaggataagatggcagaag cctatagcgagattggtatgaagggggaacgcagaaga ggcaaaggccacgacggactgtaccagggactcagca ccgccaccaaggacacctatgacgctctcacatgcagg ccctgcgcctcgg (SEQ ID NO: 1050)
SP-Linker 2- ERmut2-Furin cleavage site 2 - CD19 CAR2	MALPVTALLPLALLHAARPS LALSLTADQMVSALLDAEPPI YSEYDPTTRPFSEASMMGLLT NLADRELVHMINWAKRVPGF VDLTLHDQVHLLECAWMEILM IGLVWRSMHEHPGKLLFAPNLL LDRNQGKCVEGGVEIFDMLLA TSSRFRMMNLQGEFVCLKSI ILLNSGVYTFLSSTLKSLEEKD HIHRVLDKITDTLIHLMAKAGLT LQQQHQRLLAQLLLILSHIRHM SNKRMEHLYSMKCKNVVPLS DLLLEMLDAHRLGTGAEDPRP SRKRRLGVDGEIVMTQSPAT LSLSPGERATLSCRASQDISK YLNWYQQKPGQAPRLIYHTS RLHSGIPARFSGSGSGTDYTL TISSLQPEDFAVYFCQQGNTL PYTFGQGTKLEIKGGGSGG GGSGGGGSQVQLQESGPG VKPSETLSLTCTVSGVSLPDY GVSWIRQPPGKLEWIGVIW GSETYYSSSLKSRVTISKDN SKNQVSLKLSSVTAADTAVYY CAKHYYYGGSYAMDYWGQG TLVTVSSTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAV HTRGLDFACDIYWAPLAGTC GVLLLSLVITLYCKRGRKLLYI FKQPFMRPVQTTQEEDGCSC RFPEEEEGGCELRVKFSRSA DAPAYQQGQNQLYNELNLGR REEYDVLDRRGRDPEMGGK PRRKNPQEGLYNELQKDKMA EAYSEIGMKGERRRGKGDG LYQGLSTATKDTYDALHMQAL PPR (SEQ ID NO: 991)	atggccctccctgtcaccgcctgctgttcgcgtggctcttc tgctccacgcgcgtcggccctgtggcactttccctgactg ccgaccagatggtgtccgcctctgtgacgcgcgagcctcc aattctgtactcggagtacgatccgactgcgcgttctccga agccagcatgatgggctgtgactaacctggcggaccg cgagttgtgacatgattactgggtaagcgggtgcgcg ggctctgtggacctgacctgcacgaccaagtgccactcc tggaatgcgcctggatggaaatccctcatgatcgccctgtg tggagatccatggagcatcccgaaagctcctgtttgcac ccaacctcctgctgatcgcaaccagggaataatgcgtgg aagggggtgtcgagattttcgacatgctgtcgcgccactctt cccgggtccggatgatgaatcgcaggggagaagagttcgt gtgtctgaagtcaatcatcctgtgaactccgggtctatac cttctgagctcgacctcaagtcactggaggaaaaaga ccacatccatcgctgtctcgataagatcaccgacacctt atccatctcatggcgaaggctggactgacctgcaacagc agcaccagaggctggccagttgtctgtgattctgagcca catccggcacatgtcgaaagaggatggaacacctgtga cagcatgaagtgaagaacgtcgtgcctctgtccgatctg ctcctggaaatgctggacgcgcacagactcggaaccggc gcggaagacccccggccctccaggaagcgaaggctccct cggagacgtgggtgaaattgtgatgaccagtcacccgc cactcttagcctttaccgggtgagcgcgcgaacctgtcttg cagagcctccaagacatctcaaaataccttaattggtatc aacagaagcccgacaggtcctcgcctctgtatcacc caccagccggctccattctggaatccctgccaggttcagc ggtagcggatctgggaccgactacacctcactatcagct cactgcagccagaggactcgtgtctatttctgtcagcaa gggaacacctgcccacacctttggacagggcaccaag ctcagagattaaggtggagggtggcagcggaggaggtgg gtccggcggtggagggaagccaggtccaactccaagaaa gcggaccgggtctgtgaagccatcagaaactcttactg actgtactgtgagcggagtgctctccccgattacggggtg tcttgatcagacagccacgggggaagggtctggaatgg attggagtatttgggctctgagactacttactacttctatc cctcaagtcacgcgtcaccatctcaaggacaactctaag aatcaggtgtcactgaaactgtcatctgtgaccgcagccg acaccgcctgtactattgcgctaagcattactattatggcg ggagctacgcaatggattactggggacagggtactctggt caccgtgtccagcaccactacccagcaccgaggccac ccaccccggtcctaccatcgccctccagcctctgtccctg

		cgtcggaggcatgtagaccgcagctggtggggccgtg catacccggggtcttgactcgctcgatattacattgg gcccctctggctggtacttgcggggtctgctgttctactcg tgatcactctttactgtaagcgcggtcggaagaagctgctgt acatctttaagcaaccctcatgaggcctgtgcagactactc aagaggaggacggctgtcatgccggtcccagaggagg aggaaggcggtcggaactgcgctgaaattcagccgc agcgcatgtctccagcctaccagcaggggcagaacca gctctacaacgaactcaatttggctggagagaggagtac gacgtgctggacaagcggagaggacgggaccagaaa tgggcggaagccgcgagaaagaatcccaagaggg cctgtacaacgagctccaaaaggataagatggcagaag cctatagcgagattggtatgaagggggaacgcagaaga ggcaaaggccacgacggactgtaccagggactcagca ccgccaccaaggacacctatgacgctctcacatgcagg ccctgcgcctcgg (SEQ ID NO: 1051)
SP-Linker 2 – ERmut1 – Furin cleavage site 3 – CD19 CAR2	MALPVTALLPLALLHAARPS LALSLTADQMVSALLDAEPPIL YSEYDPTRPFSEASMMGLLT NLADRELVHMINWAKRVPGF VDLALHDQVHLLCAWMEILM IGLVWRSMEHPGKLLFAPNLL LDRNQGKCVVEGGVEIFDMLLA TSSRFRMMNLQGEFVCLKSI ILLNSGVYTFLSSTLKSLEEKD HIHRVLDKITDTLIHLMAGALT LQQQHQRLAQLLLILSHIRHM SSKRMEHLYSMKCKNVVPLS DLLLEMLDAHRLGTGAEDPRP SRKRREIVMTQSPATLSLSPG ERATLSCRASQDISKYNWYQ QKPGQAPRLLIYHTSRLHSGIP ARFSGSGSGTDYTLTISSLQP EDFAVYFCQQGNTLPYTFGQ GTKLEIKGGGSGGGSGGG GSQVQLQESGPGLVKPSSETL SLTCTVSGVSLPDYGVSWIRQ PPGKGLEWIGVIWGSETTYYS SSLKSRVTISKDNSKNQVSLK LSSVTAADTAVYYCAKHYYYG GSYAMDYWGQGTLVTVSSTT TPAPRPPTPAPTIASQPLSLRP EACRPAAGGAVHTRGLDFAC DIYIWAPLAGTCGVLLLSLVITL YCKRGRKLLYIFKQPFMRPV QTTQEEDGCSCRFPEEEEGG CELRVKFSRSADAPAYQQGQ NQLYNELNLGRREEYDVLDK RRGRDPEMGGKPRRKNPQE GLYNELQKDKMAEAYSEIGMK GERRRGKGDGLYQGLSTAT KDTYDALHMQALPPR (SEQ ID NO: 992)	atggccctccctgtaccgcctgtgcttccgtggtcttct tgctccacgcgcgtcgccctctgtggcactttccctgactg ccgaccagatggtgtccgcctcttgagcgcgagcctcc aattctgtactcggagtacgatccgactgcgggttctccga agccagcatgatgggcctgttgactaacctggcgagccg cgagtgtgtgcacatgattaactgggtaagcgggtgccg ggcttctgtggacctggccctgcacgaccaagtgcacctcc tggatgcgcctggatggaatcctcatgatcgccctcgtg tggagatccatggagcatcccgaaagctcctgtttgcac ccaacctcctgcttgatcgcaaccagggaagaaatgcgtgg aagggggtgtcgagatttgcacatgctgctcgccacctctt cccggttccggatgatgaatcgcagggagaagagttcgt gtgtctgaagtcaatcatcctgctgaactccggggtctatac cttctgagctcgaccctcaagtactggaggaaaaaga ccacatccatcgctgtctcgataagatcccgacaccctt atccatctcatggcgaaggctggactgacctgcaacagc agcaccagaggctggccagttgctgctgattctgagcca catccggcacatgtcgtccaagaggatggaacacctgta cagcatgaagtgaagaacgtcgtgacctgtccgatctg ctcctggaaatgctggacgcgcacagactcgggacggg agctgaagatccacgacccagcagaaagcgacgggaa attgtgatgacctcagcaccgcacctcttagcctttcacc ggtgagcgcgcaacctgtcttcagagcctcccaagac atctcaaaataaccttaattggtatcaacagaagcccgac aggctcctcgcttctgatctaccacaccagccggtccatt ctggaatccctgccaggttcagcggtagcggatctgggac cgactacacctcactatcagctactgcagccagaggga cttgcgtgtctatttctgtcagcaagggaacacctgcccta caccttggacagggcaccaagctcgagattaaagggtg agggtggcagcggaggagggtgggtccggcggtggagga agccaggtccaactccaagaaagcggaccgggtctgtg aagccatcagaaactcttctactgactgtactgtgagcgg agtgtctctccccgattacggggtgtcttgatcagacagc caccggggaagggtctggaatggattggagtatttggg ctctgagactacttactactcttcatccctcaagtacgcgtc accatctcaaaggacaacttaagaatcaggtgtactga aactgtcatctgtgaccgcagccgacaccgcggtgtactat tgcgctaagcattactattatggcgggagctacgcaatgga ttactggggacagggtactctggtcaccgtgtccagcacc

		actaccccagcaccgaggccacccaccccggtcctacc atcgctcccagcctctgtccctcggtccgaggcatgtag accgcagctggtggggccgtgcataccggggtcttgac ttcgctgcgatatctacattggccctctggctggtacttg cggggtcctgtgctttcactcgatcactcttactgtaagc gcggtcgggaagaagctgctgtacatcttaagcaaccctc atgaggcctgtgcagactactcaagaggaggacggctgtt catgccggtcccagaggaggaggaggcggtgcgaa ctgcgcgtgaaattcagccgcagcgcagatgtccagcct accagcaggggcagaaaccagctctacaacgaactcaat cttggtcggagagaggagtagcagctgtggacaagcg gagaggacgggacccagaaatggcggggaagccgcg cagaaagaatcccaagaggcgctgtacaacgagctcc aaaaggataagatggcagaagcctatagcgagattgga tgaaaggggaacgcagaagaggcaaagggcacgacg gactgtaccagggactcagcaccgccaccaaggacacc tatgacgtcttcacatgcagccctgcccgcctcgg (SEQ ID NO: 1052)
SP-Linker 2 – ERmut2 – Furin cleavage site 3 – CD19 CAR2	MALPVTALLPLALLHAARPS LALSLTADQMVSALLDAEPPIL YSEYDPTRPFSEASMMGLLT NLADRELVHMINWAKRVPGF VDLTLHDQVHLLCAWMEILM IGLVWRSMEHPGKLLFAPNLL LDRNQGKCVEGGVEIFDMLLA TSSRFRMMNLQGEFVCLKSI ILLNSGVYTFLSSTLKSLEEKD HIHRVLDKITDTLIHLMAGLT LQQQHQRQAQLLLILSHIRHM SNKRMEHLYSMKCKNVVPLS DLLLEMLDAHRLGTGAEDPRP SRKRREIVMTQSPATLSLSPG ERATLSCRASQDISKYLNWYQ QKPGQAPRLLIYHTSRLHSGIP ARFSGSGSGTDYTLTISSLQP EDFAVYFCQQGNTLPYTFGQ GTKLEIKGGGSGGGSGGG GSQVQLQESGPGLVKPSSETL SLTCTVSGVSLPDYGVSWIRQ PPGKGLEWIGVIWGSETTYYS SSLKSRVTISKDNSKNQVSLK LSSVTAADTAVYYCAKHYYYG GSYAMDYWGQGTLVTVSSTT TPAPRPPTPAPTIASQPLSLRP EACRPAAGGAVHTRGLDFAC DIYIWAPLAGTCGVLLLSLVITL YCKRGRKKLLYIFKQPFMRPV QTTQEEDGCSCRFEEEEEGG CELRVKFSRSADAPAYQQGQ NQLYNELNLGRREEYDVLDK RRGRDPEMGGKPRRKNPQE GLYNELQKDKMAEAYSEIGMK GERRRGKGDGLYQGLSTAT KDTYDALHMQALPPR (SEQ ID NO: 993)	atggccctccctgtcaccgcctgtgcttccgtggtcttc tgctccacgcgctcgcccTcggtggcacttccctgactg ccgaccagatggtgtccgcctcttgacgcgagcctcc aattctgtactcggagtacgacatccgctgcctctccga agccagcatgatgggcctgttgactaacctggcgagccg cgagttggtgcacatgattaactgggctaagcggtgcg ggcttcgtggacctgacctgcacgaccaagtgcacctcc tggaatgcgcctggatggaatcctcatgatcgccctcgtg tgagatccatggagcatcccgaaagctcctgtttgcac ccaacctcctgctgatcgcaaccagggaataatgcgtgg aaggggtgtcgagatttcgacatgctgctcgccacctctt cccggttccggatgatgaatcgcaggagagaaggttcgt gtgtcgaagtcaatcctcgtgaactccgggtctatac cttctgagctcgacctcaagtactggaggaaaaaga ccacatccatcgctgctcgataagatcaccgacacctt atccatctcatggcgaaggctggactgacctgcaacagc agcaccagaggctggcccagttgctgctgattctgagcca catccggcacatgtcgaacaagaggatggaacacctgta cagcatgaagtgaagaacgtcgtgctctgtccgatctg ctcctggaaatgctggacgcgcacagactcGggacggg agctgaagatccacgacccagcagaaagcgacgggaa attgtgatgacccagtcacccgccactcttagcctttcacc ggtgagcgcgcaacctgtcttcagagcctcccaagac atctcaaaataaccttaattggtatcaacagaagcccgac aggctcctcgcttctgatctaccacaccagccggtccatt ctggaatccctgccaggtcagcggtagcggatctgggac cgactacacctcactatcagctcactgcagccagagga cttcgctgtctattctgtcagcaagggaacacctgccta caccttggacagggcaccaagctcgagattaaagggtg agggtggcagcggaggagggtgggtccggcggtggagga agccaggtccaactccaagaaagcggacccgggtctgtg aagccatcagaaactcttactgactgtactgtgagcgg agtgtctctccccgattacgggtgtcttgatcagacagc caccggggaagggtctggaatggattggagtattgggg ctctgagactactactactctcatccctcaagtacgcgtc accatctcaaaggacaacttaagaatcaggtgtcactga aactgtcatctgtgaccgcagccgacaccgctgtactat tgcgctaagcattactattatggcgggagctacgcaatgga

		ttactggggacaggggtactctggtcaccgtgtccagcacc actaccccagcaccgagggcaccaccccggtcctacc atgcctcccagcctctgtccctcgtccggaggcatgtag accgcagctggtggggcgtgcataccggggtcttgac ttgcctgcgatatctacattgggccctctggtggtacttg cggggtcctgctgtttcactcgtgatcactttactgtaagc gcggtcggaagaagctgctgtacatcttaagcaacccttc atgaggcctgtgcagactactcaagaggaggacggctgtt catgccggtcccagaggaggaggaaggcggtgcgaa ctgcgcgtgaaattcagccgcagcgcagatgtccagcct accagcaggggcagaaccagctctacaacgaactcaat cttggtcggagagaggagtacgacgtgctggacaagcg gagaggacgggacccagaaatggcggggaagccgcg cagaaagaatcccaagaggcgctgtacaacgagctcc aaaaggataagatggcagaagcctatagcgagattggtg tgaaaggggaacgcagaagaggcaaagccacgacg gactgtaccagggactcagcaccgccaccaaggacacc tatgacgctctcacatgcaggccctgcgcctcgg (SEQ ID NO: 1053)
SP-Linker 2 – ERmut1 – Furin cleavage site 2 – CD123 CAR	MALPVTALLPLALLHAARPS LALSLTADQMVSALLDAEPPI L YSEYDPTTRPFSEASMMGLLT NLADRELVHMINWAKRVPGF VDLALHDQVHLLCAWMEILM IGLVWRSMEHPGKLLFAPNLL LDRNQGKCVEGGVEIFDMLLA TSSRFRMMNLQGEEFVCLKSI ILLNSGVYTFLSSTLKSLEEKD HIHRVLDKITDTLIHLMAGALT LQQQHQRQAQLLLLSHIRHM SSKRMEHLYSMKCKNVVPLS DLLLEMLDAHRLGTGAEDPRP SRKRRSLGDVGQVQLVQSGA EVKKPGASVKVSCKASGYTFT GYMHWVRQAPGQGLEWM GWINPNSGGTNYAQKFQGRV TLTRDTSISTVYMELSRLRSD DTAVYYCARDMNILATVPFDI WGQGTMTVTSSGGGSGGG GSGGGGSDIQMTQSPSSLSA SVGDRVTITCRASQSISSYL N WYQQKPGKAPKLLIYAASSLQ SGVPSRFSGSGSGTDFTLTV NSLQPEDFATYYCQQGDSVP LTFGGGTRLEIKTTTPAPRPPT PAPTIASQPLSLRPEACRPAA GGAVHTRGLDFACDIYWAPL AGTCGVLLLSLVITLYCKRGRK KLLYIFKQPFMRPVQTTQEED GCSCRFPEEEEGGCELRVKF SRSADAPAYQQGQNQLYNEL NLGRREEYDVLDKRRGRDPE MGGKPRRKNPQEGLYNELQK DKMAEAYSEIGMKGERRRGK GHDGLYQGLSTATKDTYDAL HMQALPPR (SEQ ID NO: 994)	atggccctccctgtcaccgcctcgtgcttccgtggtcttc tgctccacgcgcgtcggccctcgttggtcacttccctgactg ccgaccagatggtgtccgcctctgtgacgcgagcctcc aattctgtactcggagtagcatccgactcgccttctccga agccagcatgatgggcctgttgactaacctggcgaccg cgagttggtgcacatgattaactgggctaagcgggtgccg ggcttcgtggacctggccctgcacgaccaagtgcacctcc tggaatgcgcctggatggaaatcctcatgatcgccctcgtg tgagatccatggagcatcccgaaagctcctgtttgcac ccaacctcctgctgatcgcaaccagggaagaaatgcgtgg aaggggtgtcgagatttcgacatgctgctcgccacctctt cccgttccggatgatgaatcgcaggagagaagagttcgt gtgtctgaagtcaatcatcctgctgaactccgggtctatac cttctgagctcgacctcaagtcactggaggaaaaaga ccacatccatcgctgctcgataagatcaccgacaccctt atccatctcatggcgaaggctggactgacctgcaacagc agcaccagaggctggcccagttgctgctgattctgagcca catccggcacatgtcgtccaagaggatggaacacctgta cagcatgaagtgaagaacgtcgtgacctgtccgatctg ctcctggaaatgctggacgcgcacagactcggaaaccggc gcggaagacccccggccctccaggaagcgaaggtccct cggagacgtgggtcaagtgaactcgtccaaagcggag cggaagtcaagaacccggagcgcggtgaaagtgtcc tgcaaagcctccggctacacctttacgggctactacatgca ctgggtgcgcaggcaccaggacagggtcttgaatggat gggatggatcaaccctaattcgggcggaactaactacgc acagaagttccaggggagagtactctgactcgggatac ctccatctcaactgtctacatggaactctcccgttgcggtc agatgatacggcagtgtagtactcgcgcgcgcgacatgaat atcctggctaccgtgcggttcgacatctggggacagggga ctatggttactgtctcatcgggcgggtggaggtcaggagga ggcggctcgggaggcggaggttcggacattcagatgacc cagtcctccatcctctgtcggccagcgtcggagataggg gaccattacctgtcgggcctcgaaagcatctcctgtacc tcaactggtatcagcaaaagccgggaaggcgcttaag ctgctgatctacgcgccttcgagcttgcaaaagcgggtgcc atccagattctcgggatcaggctcaggaaaccgacttacc

		ctgaccgtgaacagcctccagccggaggactttgccactt actactgccagcaggagactccgtgccgttactttcggg gggggtaccgcctggagatcaagaccactacccagc accgaggccacccacccggctcctaccatcgctccca gcctctgtccctgcgtccggaggcatgtagaccgcagct ggtggggccgtgcataccggggtcttgacttcgctgcg atatctacattggggccctctggctgggtacttgcggggtcct gctgcttactcgtgatcactcttactgtaagcgcggtcgg aagaagctgctgtacatcttaagcaaccctcatgaggcc tgtgcagactactcaagaggaggacggctgtcatgccc tcccagaggaggagggaaggcggtgcgaactgcgcgt gaaattcagccgcagcgcagatgtccagcctaccagca ggggcagaaccagctctacaacgaactcaatcttggtcg gagagaggagtacgacgtgctggacaagcggagaggga cgggacccagaaatgggggggaagccgcgcagaaag aatccccaagaggcctgtacaacgagctccaaaagga taagatggcagaagcctatagcgagattggtatgaagg ggaacgcagaagaggcaagggccacgacggactgtac cagggactcagcaccgccaccaaggacacatgacgc tctcacatgcaggccctgccgctcgg (SEQ ID NO: 1054)
SP-Linker 2 – ERmut2 – Furin cleavage site 2 – CD123 CAR	MALPVTALLPLALLLHAARPS LALSLTADQMVSALLDAEPPIL YSEYDPTTRPFSEASMMGLLT NLADRELVHMINWAKRVPGF VDLTLHDQVHLLCAWMEILM IGLVWRSMEHPGKLLFAPNLL LDRNQGKCVEGGVEIFDMLLA TSSRFRMMNLQGEFVCLKSI ILLNSGVYTFLSSTLKSLEEKD HIHRVLDKITDTLIHLMAGALT LQQQHQRQAQLLLILSHIRHM SNKRMEHLYSMKCKNVVPLS DLLLEMLDAHRLGTGAEDPRP SRKRRSLGDVGQVQLVQSGA EVKKPGASVKVSCASGYTFT GYMHWRVQAPGQGLEWM GWINPNSGGTNYAQKFQGRV TLTRDTSISTVYMELSLRSD DTAVYYCARDMNILATVPDI WGQGTMTVTSSGGGSGGG SGGGGSDIQMTQSPSSLSA SVGDRVTITCRASQSISSYN WYQQKPGKAPKLLIYAASSLQ SGVPSRFSGSGSGTDFLTIV NSLQPEDFATYYCQQGDSVP LTFGGGTRLEIKTTTPAPRPPT PAPTIASQPLSLRPEACRPAA GGAVHTRGLDFACDIYWAPL AGTCGVLLLSLVITLYCKRGRK KLLYIFKQPFMRPVQTTQEED GCSCRFPETEEGGCELRVKF SRSDAPAYQQGQNQLYNEL NLGRREEYDVLDKRRGRDPE MGGKPRRKNPQEGLYNELQK DKMAEAYSEIGMKGERRRGK	atggccctccctgtcaccgccctgctgctccgctggctcttc tgctccacgccgctcggcccTcgtggcacttccctgactg ccgaccagatggtgtccgcccttctggacgccgagcctcc aattctgtactcggagtacgatccgactcgccttctccga agccagcatgatgggctgttgactaacctggcggaccg cgagtgtgtgcacatgattaactgggctaagcgggtgccg ggcttcgtggacctgacctgcacgaccaagtgcacctcc tggaatgcgctggatggaatcctcatgatcgccctcgtg tgagatccatggagcatcccgaaagctcctgtttgcac ccaacctcctgcttgatcgcaaccagggaataatgcgtgg aaggggtgtcgagatttcgacatgctgctcgccacctctt cccgggtccggatgatgaatcgcaggaggagaagagttcgt gtgtctgaagtcaatcatcctgctgaactccgggtctatac cttctgagctcgacctcaagtcactggaggaaaaaga ccacatccatcgctgctcgataagataccgacaccctt atccatctcatggcgaaggctggactgacctgcaacagc agcaccagaggctggcccagttgctgctgattctgagcca catccggcacatgtcgaacaagaggatggaacacctgta cagcatgaagtgaagaacgtcgtgacctgtccgatctg ctcctggaaatgctggacgcgcacagactcggaaccggc gcggaagacccccggccctccagggaagcgaaggctccct cggagacgtgggtcaagtgaactcgtccaaagcggag cggaagtcaagaaccccgagcgcgagcgtgaaagtgtcc tgcaaaagcctccggctacacctttacgggctactacatgca ctgggtgcgccaggcaccaggacagggtcttgaatggat gggatggatcaaccctaattcgggcggaactaactacgc acagaagttccaggggagagtgcactgactcgggatac ctccatctcaactgtctacatggaactctcccgttgcggtc agatgatacggcagtgactactgcgccgcgacatgaat atcctggctaccgtgccgttcgacatctgggacagggga ctatggttactgtctcatcgggcgggtggagggtcaggagga ggcggctcgggaggcggagggttcggacattcagatgacc cagtcctccatcctctctgctcgccagcgtcgagataggg gaccattacctgctgggcctcgaaagcatctcctgtacc tcaactggtatcagcaaaagccggggaaggcgcctaag

	GHDGLYQGLSTATKDTYDAL HMQALPPR (SEQ ID NO: 995)	ctgctgatctacgccgcttcgagcttgcaaagcgggggtgcc atccagattctcgggatcaggctcaggaaccgacttacc ctgaccgtgaacagcctccagccggaggactttgccactt actactgccagcaggagactccgtgccgttactttcggg gggggtaccgcctggagatcaagaccactaccccagc accgaggccacccaccccggtcctaccatcgccctcca gcctctgtccctgcgtccggaggcatgtagaccgcagct ggtggggccgtgcatacccggggtcttgacttcgcctgcg atatctacatttgggcccctctggctggtacttgcggggtcct gctgctttcactcgtgatcactctttactgtaagcgcggtcgg aagaagctgctgtacatctttaagcaacccttcatgaggcc tgtgcagactactcaagaggaggacgggtgttcattgcggg ttcccagaggaggagggaaggcgggtgcgaactgcgcgt gaaattcagccgcagcgcagatgctccagcctaccagca ggggcagaaccagctctacaacgaactcaatcttggtcg gagagaggagtacgacgtgctggacaagcggagagga cgggaccagaaaatggcggggaagccgcgcagaaaag aatccccaagaggcctgtacaacgagctccaaaagga taagatggcagaagcctatagcgagattggtatgaaagg ggaacgcagaagaggcaaaggccacgacgactgtac cagggactcagcaccgccaccaaggacacctatgacgc tcttcacatgcaggccctgccgcctcgg (SEQ ID NO: 1055)
SP-Linker 2 – ERmut1 – Furin cleavage site 3 – CD123 CAR	MALPVTALLLPLALLLHAARPS LALSLTADQMVSALLDAEPPIL YSEYDPTRPFSEASMMGLLT NLADRELVHMINWAKRVPGF VDLALHDQVHLLCAWMEILM IGLVWRSMEHPGKLLFAPNLL LDRNQGKCVEGGVEIFDMLLA TSSRFRMMNLQGEFVCLKSI ILLNSGVYTFLSSTLKSLEEKD HIHRVLDKITDTLIHLMKAGLT LQQQHQRQAQLLLILSHIRHM SSKRMEHLYSMKCKNVVPLS DLLLEMLDAHRLGTGAEDPRP SRKRRQVQLVQSGAEVKKPG ASVKVSCASGYTFTGYMH WVRQAPGQGLEWMGWINPN SGGTNYAQKFQGRVTLTRDT SISTVYMELSRLSDDTAVYY CARDMNILATVPFDIWQGQTM VTVSSGGGGSGGGGSGGGG SDIQMTQSPSSLSASVGDRVT ITCRASQSISSYLNWYQKPG KAPKLLIYAASSLQSGVPSRFS GSGSGTDFTLTVNSLPEDFA TYQCQGDSDVPLTFGGGTRL EIKTTTPAPRPPTPAPTASQP LSLRPEACRPAAGGAVHTR GLDFACDIYWAPLAGTCG VLLLSLVITLYCKRGRKLL YIFKQPFMRPVQTTQEEDG CSCRFPEEEEEGGCEL RVK FSRSADAPAYQQGQNQLY	atggccctccctgtcaccgcctgctgcttccgctggctcttc tgctccacgcgcgtcggccctcgttggcactttccctgactg ccgaccagatggtgtccgcccttctggacgcgagcctcca attctgtactcggagtacgatccgactcgccggttctccgaa gccagcatgatgggcctgttgactaacctggcgagaccgcg agtgtgtgcacatgattaactgggctaagcgggtgcggggc ttcgtggacctggccctgcacgaccaagtgcacctcctgga atgcgcctggatggaaatcctcatgatcgccctcgtgtgga gatccatggagcatcccggaaagctcctgtttgcacccaac ctcctgcttgatcgcaaccagggaaaatgctgggaagggg gtgtcgagattttgacatgctgctcgccaccttctccggtt ccggatgatgaatctgcaggagagaagagttcgtgtgtctga agtcaatcatcctgctgaactccggggtctataccttctctga gctcgaccctcaagtactggaggaaaaagaccacatcca tcgcgtgctcgataagatcaccgacacccttatccatctcat ggcgaaggctggactgacctgcaacagcagcaccagag gctggcccagttgctgctgattctgagccacatccggcacat gtcgtccaagaggatggaacacctgtacagcatgaagtgc aagaacgtcgtgcctctgtccgatctgctcctggaaatgctg gacgcgcacagactcggaaccggcgcggaagacccccgg ccctccaggaagcgaaggcaagtgcactcgtccaaagcg gagcggaagtcaagaaacccggagcgagcgtgaaagtgt cctgcaaagcctccggctacacctttacgggctactacatg cactgggtgcgccaggcaccaggacagggtcttgatgga tgggatggatcaaccctaattcgggcggaactaactacgca cagaagttccaggggagagtactctgactcgggatacctc catctcaactgtctacatggaactctcccgttgcggtcaga tgatacggcagtgactactgcgccgcgacatgaatatcc

	NELNLGRREEYDVLDKRR GRDPEMGGKPRRKNPQE GLYNELQKDKMAEAYSEIG MKGERRRGKGHDGLYQGL STATKDTYDALHMQALPPR (SEQ ID NO: 996)	tggctaccgtgccgttcgacatctggggacaggggactatg gttactgtctcatcgggagggtggaggttcaggaggaggcgg ctcgggaggcggagggttcggacattcagatgaccagtc ccatctctctgtcggccagcgtcggagatagggtgacat tacctgtcgggcctcgaaagcatctcctgtacctcaactg gtatcagcaaaagccgggaaaggcgcctaagctgtgatc tacgccgttcgagcttgaaagcgggtgccatccagatt ctcgggatcaggctcaggaaccgacttcacctgaccgtga acagcctccagccggaggactttgccacttactactgccag cagggagactccgtgccgttactttcgggggggtacccg cctggagatcaagaccactacccagcaccgaggccaccc accccggtcctaccatcgctcccagcctctgtccctgct ccggaggcatgtagaccgcagctggtggggccgtgcata cccggggtcttgacttcgctgcgatctacatttgggcc ctctggctggtacttgccgggtcctgctgttctactcgtgat cactctttactgtaagcgcggtcggaagaagctgctgtaca tctttaagcaacccttcagaggcctgtgcagactactcaag aggaggacggctgttcagccggtccagaggaggaggga aggcggctgcgaactgcgctgaaattcagccgcagcgca gatgtccagcctaccagcaggggcagaaccagctctaca acgaactcaatcttggtcggagagaggagtacgacgtgct ggacaagcggagaggacgggacccagaaatgggcggga agccgcgcagaaagaatcccaagagggtctgtacaacg agctcaaaaggataagatggcagaagcctatagcgagat tggtatgaaaggggaacgcagaagaggcaaaggccacga cggactgtaccagggactcagcaccgccaccaaggacacc tatgacgtcttcacatgcaggccctgccgctcgg (SEQ ID NO: 1056)
SP-Linker 2 – ERmut2 – Furin cleavage site 3 – CD123 CAR	MALPVTALLLPLALLLHAARPS LALSLTADQMVSALLDAEPPIL YSEYDPTTRPFSEASMMGLLT NLADRELVHMINWAKRVPGF VDLTLHDQVHLLECAWMEILM IGLVWRSMEHPGKLLFAPNLL LDRNQGKCVEGGVEIFDMLLA TSSRFRMMNLQGEFVCLKSI ILLNSGVYTFLSSTLKSLEEKD HIHRVLDKITDTLIHLMAKAGLT LQQQHQLRAQLLLILSHIRHM SNKRMEHLYSMKCKNVVPLS DLLLEMLDAHRLGTGAEDPRP SRKRRQVQLVQSGAEVKKPG ASVKVSKKASGYTFTGYMH WVRQAPGQGLEWMGWINPN SGGTNYAQKFQGRVTLTRDT SISTVYMELSRLSDDTAVYY CARDMNILATVPFDIWGQGT VTVSSGGGGSGGGGSGGGG SDIQMTQSPSSLSASVGDRT ITCRASQSISSYLNWYQQKPG	atggccctccctgtcaccgccctgctgctccgctggctcttc tgctccacgccgctcggcccTcgtggcacttccctgactg ccgaccagatggtgtcggcctctcgtgacgccgagcctcc aattctgtactcggagtacgatccgactcgcctgtctccga agccagcatgatgggcctgttgactaacctggcggaccg cgagttggtgcacatgattaactgggctaagcgggtgccg ggctcgtggacctgacctgcacgaccaagtgcacctcc tggaatgcgctggatggaatcctcatgatcggcctcgtg tggagatccatggagcatcccgaaagctcctgtttgcac ccaacctcctgcttgatcgcaaccagggaataatgcgtgg aagggggtgtcgagatttcgacatgctgctcgccacctctt cccgggtccggatgatgaatcgcaggagagaagagttcgt gtgtctgaagtcaatcatcctgctgaactccgggtctatac cttctgagctcgacctcaagtcactggaggaaaaaga ccacatccatcgctgctcgataagatcaccgacacctt atccatctcatggcgaaggctggactgacctgcaacagc agcaccagaggctggcccagttgctgctgattctgagcca catccggcacatgtcgaacaagaggatggaacacctgta cagcatgaagtgaagaacgtcgtgacctgtcggatctg ctcctggaaatgctggacgcgcacagactcgggacggg agctgaagatccacgaccagcagaaagcgacggcaa gtgcaactcgtccaaagcggagcgggaagtcaagaaacc

	KAPKLLIYAASSLQSGVPSRFS GSGSGTDFTLTVNSLQPEDFA TYYCQQGDSVPLTFGGGTRL EIKTTTPAPRPPTPAPTIASQP LSLRPEACRPAAGGAVHTRG LDFACDIYWAPLAGTCGVLLL SLVITLYCKRGRKLLYIFKQP FMRPVQTTQEEDGCSCRFPE EEEGGCELRVKFSRSADAPA YQQGQNQLYNELNLGRREEY DVLDKRRGRDPEMGGKPRRK NPQEGLYNELQKDKMAEAYS EIGMKGERRRGKGHDGLYQG LSTATKDTYDALHMQALPPR (SEQ ID NO: 997)	cggagcgcgagcgtgaaagtgtcctgcaaagcctccggcta cacctttacgggctactacatgcactgggtgcgccaggca ccaggacagggtcttgaatggatgggatggaacacctta attcgggcggaactaactacgcacagaagttccaggga gaggactctgactcgggatacctccatctcaactgtctaca tggaaactctcccgcttgcggtcagatgatacggcagtgat tactgcgcccgcgacatgaatacttggtaccgtgccgtt cgacatctggggacaggggactatggttactgtctcatcgg gcggtggagggtcaggaggaggcggctcgggaggcgg aggttcggacattcagatgacccagtcctccatctctgtc ggccagcgtcggagatagggtgaccattacctgtcgggc ctgcgaaagcatctcctcgtacctcaactggtatcagcaaa agccgggaaaggcgcctaagctgctgatcagccgcttc gagcttgcaaagcgggtgccaatccagattctcgggatca ggctcaggaaccgacttcacctgaccgtgaacagcctc cagccggaggacttggcacttactactgccagcaggga gactccgtgcgcttacttccggggggggtaccgcctgga gatcaagaccactacccagcaccgaggccaccacccc cggctcctaccatcgctccagcctctgtccctgcgtccg gaggcatgtagaccgcagctgggtggggccgtgcatacc cgggtcttgactcgcctgcgatactacattggggccctc tggctggtacttgcgggtcctgtcgtcttactcgtgatcac tcttactgtaagcgcggtcggaagaagctgctgtacatctt aagcaacccttcatgaggcctgtgcagactactcaagag gaggacggctgttcatgcccgttccagaggaggaggaa ggccgctgcgaactgcgctgaaattcagccgcagcgc agatgtccagcctaccagcaggggcagaaccagctcta caacgaactcaatcttggtcggagagaggagtacgacgt gctggacaagcggagaggacgggaccagaaaatgggc gggaagccgcgcagaaagaatcccaagagggcctgt acaacgagctccaaaaggataagatggcagaagcctat agcgagattggtatgaaagggaacgcagaagaggca aaggccacgacggactgtaccagggactcagaccgcgc accaaggacacctatgacgctctcactgcaggccctgc cgctcgg (SEQ ID NO: 1057)
SP-Linker 2 – ERmut1 – Furin cleavage site 2 – BCMA CAR	MALPVTALLLPLALLLHAARPS LALSLTADQMVSALLDAEPPIL YSEYDPTRPFSEASMMGLLT NLADRELVHMINWAKRVPGF VDLALHDQVHLLCAWMEILM IGLVWRSMEHPGKLLFAPNLL LDRNQGKCVEGGVEIFDMLLA TSSRFRMMNLQGEFVCLKSI ILLNSGVYFLSSTLKSLEEKD HIHRVLDKITDTLIHLMKAGLT LQQQHQRQAQLLLILSHIRHM SSKRMEHLYSMKCKNVVPLS DLLLEMLDAHRLGTGAEDPRP SRKRRSLGADVGEVQLVESGG GLVQPGGSLRLSCAVSGFALS NHGMSWVRRAPGKGLEWVS GIVYSGSTYYAASVKGRFTISR DNSRNTLYLQMNSLRPEDTAI YYCSAHGGESDVWGQGTTVT VSSASGGGGSGGRASGGGG SDIQLTQSPSSLSASVGDRVTI	atggccctccctgtcaccgccctgctgctccgctggctcttc tgctccacgcgcgtcggcccTcggtggcacttccctgactg ccgaccagatggtgtcggccttctggacgcgcagcctcc aattctgtactcggagtacgatccgactcggcgttctccga agccagcatgatgggcctgtgactaacctggcggaccg cgagttggtgcacatgattaactgggctaagcgggtgcg ggctcgtggacctggccctgcacgaccaagtgcacctcc tggaatgcgcctggatggaatcctcatgatcggcctcgtg tggagatccatggagcatcccgaaagctcctgtttgcac ccaacctcctgctgatcgcaaccagggaataatgcgtgg aagggggtgtcgagatttgcacatgctgctcgccacctctt cccgggtccggatgatgaatctgcaggaggagaagagttcgt gtgtctgaagtcaatcatcctgctgaactccgggtctatac ctctctgagctcgacctcaagtactggaggaaaaaga ccacatccatcgctgctcgataagataccgacacctt atccatctcatggcgaaggctggactgacctgcaacagc agcaccagaggctggcccagttgctgctgattctgagcca catccggcacatgctgccaagaggatggaacacctgta cagcatgaagtgaagaacgctgctgctcctctgctccgatctg ctctggaaatgctggacgcgcacagactcggaaccggc gcggaagacccccggccctccagggaagcgaaggctccct

	TCRASQSISSYLNWYQQKPG KAPKLLIYAASSLQSGVPSRFS GSGSGTDFTLTISSLQPEDFA TYYCQQSYSTPYTFGQGTKV EIKTTTPAPRPPTPPTIASQP LSLRPEACRPAAGGAVHTRG LDFACDIYWAPLAGTCGVLLL SLVITLYCKRGRKLLYIFKQP FMRPVQTTQEEDGCSCRFE EEEGGCELRVKFSRSADAPA YQQGQNQLYNELNLGRREEY DVLDKRRGRDPEMGGKPRRK NPQEGLYNELQDKMAEAYS EIGMKGERRRGKGHDGLYQG LSTATKDTYDALHMQALPPR (SEQ ID NO: 998)	cggagacgtgggtgaagtgaattgggtggaatcaggggg aggactgtgcagcctggaggatcgctgagactgtcatgtg ccgtgtccggcttggcctgtccaaccacgggatgtcctgg gtccgcccgcgcctggaaagggcctcgaatgggtgtcg ggtattgtgtacagcggtagcacctactatgccgatccgt gaaggggagattcaccatcagccgggacaactccagga acactctgtacctcaaatgaattcgctgaggccagagga cactgccatctactactgtccgcgcgatggcggagagtcc gacgtctggggacaggggaccaccgtgaccgtgtctagc gcgtccggcggaggcggcagcgggggtcgggcacatcag ggggcggcggatcgacatccagctcaccagtcgcccg agctcgctgtccgcctccgtgggagatcgggtcaccatca cgtgccgcgcagccagtcgatttctcctacctgaactgg taccacagaagcccggaaaagccccgaagcttctcatc tacgccgcctcgagcctgcagtcaggagtgccctcacggt tctccggctccggttccggtactgatttaccctgaccatttc tccctgcaaccggaggacttcgtacttactactgccagca gtcgtactccacccccctacatttcggacaaggcacc gtcgaaatcaagaccactacccagcaccgaggccacc caccggcgtcctaccatgcctccagcctctgtcctgc gtccggaggcatgtagaccgcagctgggtggggccgtgc ataccgggggtcttgacttcgcctgcgatactacatttggg cccctctggctgggtacttgcggggctcgtctgttactcgt gatcactcttactgtaagcgcggtcgggaagaagctgctgt acatctttaagcaaccctcatgaggcctgtgcagactactc aagaggaggacggctgttcatgccggttccagaggagg aggaaggcggctgcgaactgcgcgtgaaattcagccgc agcgcagatgtccagcctaccagcaggggcagaacca gctctacaacgaactcaatcttggtcggagagaggagtac gacgtgtggacaagcggagaggacgggaccagaaa tgggcgggaagccgcgcagaaagaatcccaagaggg cctgtacaacgagctccaaaaggataagatggcagaag cctatagcagattggatgaaaggggaacgcagaaga ggcaaggccacgacggactgtaccagggactcagca ccgccaccaaggacacctatgacgctcttcatatgcagg ccctgccgcctcgg (SEQ ID NO: 1058)
SP-Linker 2 – ERmut2 – Furin cleavage site 2 – BCMA CAR	MALPVTALLPLALLLHAARPS LALSLTADQMVSALLDAEPPIL YSEYDPTRPFSEASMMGLLT NLADRELVHMINWAKRVPGF VDLTLDQVHLLECAWMEILM IGLVWRSMEHPGKLLFAPNLL LDRNQGKCVEGGVEIFDMLLA TSSRFRMMNLQGEEFVCLKSI ILLNSGVYTFLSSTLKSLEEKD HIHRVLDKITDTLIHLMAKAGLT LQQQHQRLLAQLLLILSHIRHM SNKRMEHLYSMKCKNVVPLS DLLLEMLDAHRLGTGAEDPRP <u>SRKRRSLGDVGEVQLVESGG</u> GLVQPGGSLRLSCAVSGFALS NHGMSWVRRAPGKGLEWVS GIVYSGSTYYAASVKGRFTISR DNSRNTLYLQMNSLRPEDTAI YYCSAHGGESDVWGQGTTVT VSSASGGGGSGGRASGGGG	atggccctccctgtcaccgcccgtgcttccgtggtcttc tgctccacgcgcgtcggcccTcgttggcacttccctgactg ccgaccagatggtgtccgccttctggacgcgagcctcc aattctgtactcggagtacgatccgactcggcgttctccga agccagcatgatgggcctgttgactaacctggcggaccg cgagttggtgcacatgattaactgggctaagcgggtgcg ggcttctgtgacctgacctgcacgaccaagtgcacctcc tggaatgcgcctggatggaatcctcatgatcgccctgtg tggagatccatggagcatcccggaagctcctgtttgcac ccaacctcctgttgatcgcaaccagggaataatgcgtgg aagggggtgtcgagatttgcacatgctgctcgccaccttt cccgggtccggatgatgaatctgcagggaagaggtcgt gtgtctgaagtcaatcatcctgtgaactccgggtctatac cttctgagctcgacctcaagtcactggaggaaaaaga ccacatccatcgctgtcgtgataagatcccgacacctt atccatctcatggcgaaggctggactgacctgcaacagc agcaccagaggctggcccagttgtctgtgattctgagcca catccggcacatgtcgaacaagaggatggaacacctgta cagcatgaagtgaagaacgtcgtgcctctgtccgatctg ctcctggaaatgtggacgcgcacagactcggaaaccggc

	SDIQLTQSPSSLSASVGDRTV TCRASQSISSYLNWYQQKPG KAPKLLIYAASSLQSGVPSRFS GSGSGTDFTLTISSLQPEDFA TYYCQQSYSTPYTFGQGTKV EIKTTTTAPRPPTPAPTIASQP LSLRPEACRPAAGGAVHTRG LDFACDIYWAPLAGTCGVLLL SLVITLYCKRGRKKLLYIFKQP FMRPVQTTQEEDGCSCRPE EEEGGCELRVKFSRSADAPA YQQGQNQLYNELNLGRREEY DVLDKRRGRDPEMGGKPRRK NPQEGLYNELQKD KMAEAYS EIGMKGERRRGKGHDGLYQG LSTATKDTYDALHMQALPPR (SEQ ID NO: 999)	gcggaagacccccggccctcaggaaagcgaaggtccct cggagacgtgggtgaagtgcattggtggaatcaggggg aggactgtgcagcctggaggatcgctgagactgtcatgtg ccgtgtccggctttgccctgtccaaccacgggatgtctctgg gtccgcgcgcgcctggaaagggcctcgaatgggtgtcgtg ggatattgtgtacagcggtagcacctactatgccgcatccgt gaaggggagattcacctacagccgggacaactccagga acactctgtacctccaaatgaattcgctgaggccagagga cactgccatctactactgtcgcgcgcgtggcggagagtc gacgtctggggacaggggaccaccgtgaccgtgtctagc gcgtccggcggaggcggcagcgggggtcgggcatcag ggggcggcggatcgacatccagctcaccagtcctccg agctcgctgtccgcctcgtgggagatcgggtcaccatca cgtgccgcgccagccagtcgatttctctactgaactgg taccaacagaagcccggaaaagccccgaagcttctcatc tacgccgcctcgagcctgcagtcaggagtgccctcacgg tctccggctccgggtccgggtactgatttcaccctgaccatttc tccctgcaaccggaggacttcgctacttactactgccagca gtcgtactccacccccctacatttcggacaaggcaccaag gtcgaatatcaagaccactaccccagcaccgaggccacc caccocggctcctaccatcgctctccagcctctgtccctgc gtccggaggcatgtagaccgcagctgggtggggcgtgc ataccgggggtcttgacttcgctgcgatatctacatttggg ccctctgtgctggtactgtcgggggtcctgtgtcttactcgt gatcactctttactgtaagcgcggctcggaagaagctgtgt acatctttaagcaacccctcatgaggcctgtgcagactactc aagaggaggacggctgttctatgcgggttcccagaggagg aggaaggcggctcggaactgcgcgtgaaattcagccgc agcgcatgtctccagcctaccagcaggggcagaacca gctctacaacgaactcaatcttggtcggagagaggagtac gacgtgtgtgacaagcggagaggacgggacccagaaa tgggcgggaagccgcgcagaaagaatccccagaggg cctgtacaacgagctccaaaaggataagatggcagaag cctatagcgagattggtatgaaaggggaacgcagaaga ggcaaaggccacgacggactgtaccagggactcagca ccgccaccaaggacacctatgacgtcttcatatgcagg ccctgccgcctcgg (SEQ ID NO: 1059)
SP-Linker 2 – ERmut1 – Furin cleavage site 3 – BCMA CAR	MALPVTALLLPLALLLHAARPS LALSLTADQMVSALLDAEPPIL YSEYDPTRPFSEASMMGLLT NLADRELVHMINWAKRVPGF VDLALHDQVHILLECAWMEILM IGLVWRSMEHGPKLLFAPNLL LDRNQGKCVVEGGVEIFDMLLA TSSRFRMMNLQGEFVCLKSI ILLNSGVYTFLLSSTLKSLEEKD HIHRVLDKITDTLIHLMKAGLT LQQQHQRQAQLLLILSHIRHM SSKRMEHLYSMKCKNVVPLS DLLLEMLDAHRLGTGAEDPRP SRKRREVQLVESGGGLVQPG GSLRLSCAVSGFALSNHGMS WVRRAPGKGLEWVSGIVYSG STYYAASVKGRFTISRDNARN TLYLQMNSLRPEDTAIYYCSA HGGESDVWGQGTTVTVSSAS	atggccctccctgtcaccgcctgtgcttccgctggctcttc tctccacgcgcgtcggcccTcggtggcactttccctgactg ccgaccagatggtgtcgcgcctcttgagcgcgcgagcctcc aattctgtactcggagtagcatccgactgcgccgttctccga agccagcatgatgggctgtgtgactaacctggcggaccg cgagttggtgcacatgattaaactgggctaagcgggtgccg ggcttcgtggacctggccctgcacgaccaagtgcacctcc tggaatgcgcctggatggaatcctcatgatcggcctcgtg tggagatccatggagcatcccggaagctcctgttgcac ccaacctcctgctgatgcgaaccagggaataatgcgtgg aagggggtgtcgagatttgcacatgctgtcgcacacctctt ccgggttccgatgatgaatcgcagggaagaagagttcgt gtgtctgaagtcaatcatcctgtgaactccggggtctatac cttctgagctgcaccctcaagtactggaggaaaaaga ccacatccatgcgtgtcgtgataagatcaccgacacctt atcatctcatggcgaaggctggactgacctgcaacacag agcaccagaggctggcccggtgctgtgattctgagcca catccggcacatgtcgtccaagaggatggaacacctgta cagcatgaagtqcaagaacgtcgtgcctctgtccgatctg

	GGGSGGGRASGGGSDIQLT QSPSSLSASVGDRVTITCRAS QSISSYLNWYQQKPGKAPKLL IYAASSLQSGVPSRFSGSGSG TDFTLTISLQPEDFATYYCQ QSYSTPYTFGQGTKVEIKTTT PAPRPPTPAPTIASQPLSLRPE ACRPAAGGAVHTRGLDFACDI YIWAPLAGTCGVLLLSLVITLY CKRGRKLLYIFKQPFMRPVQ TTQEEDGCSCRFPEEEEGGC ELRVKFSRSADAPAYQQGQN QLYNELNLGRREEYDVLDKR RGRDPEMGGKPRRKNPQEG LYNELQKDKMAEAYSEIGMKG ERRRGKGHDLGLYQGLSTATK DTYDALHMQALPPR (SEQ ID NO: 1000)	ctcctggaaatgctggacgcgcacagactcGggacggg agctgaagatccacgaccagcagaaagcgacgggaa gtgcaattggtggaatcagggggaggactgtgcagcctg gaggatcgctgagactgtcatgtgccgtgtccggtttgcc ctgtccaaccacgggatgtcctgggtccgcgcgcgcctg gaaagggcctcgaatgggtgtcgggtattgttacagcgg tagcacctactatgccgcacgtgaaggggagattcacc atcagccgggacaactccaggaacactctgtacctcaa atgaattcgctgaggccagaggacactgccatctactact gctccgcgcgatggcggagagtgccgacgtctggggacag gggaccaccgtgaccgtgtctagcgcgtccggcggaggc ggcagcgggggtcgggcatcagggggcggcgggatcgg acatccagctcaccagtcctccgagctcgtgtccgcctc cgtgggagatcgggtcaccatcacgtgccgcgcgcagcca gtcgatttctcctacctgaactggtaccaacagaagcccg gaaaagccccgaagcttctatctacgcgcctcagacct gcagtcaggagtgcctcacggttctccggtcgggtccg gtactgatttaccctgaccatttctcctgcaaccggagg acttcgctacttactactgccagcagtcgtactccacccct acactttcggacaaggcaccagggtcgaaatcaagacc actaccccagcaccgaggccaccaccccgggtcctacc atcgctccagcctctgtcctcgcgtccggaggcgtctag acccgcagctggtggggcgcgtgcataccgggggtctgac ttcgctgcgatatctacatttggggccctctggctggtactg cggggctcgtcgtcttactcgtgatcactcttactgtaagc gcggtcgggaagaagctgctgtacatcttaagcaacccttc atgaggcctgtgcagactactcaagaggaggacggctgtt catgccggttcccagaggaggaggaaaggcggctgcgaa ctgcgcgtgaaattcagccgcagcgcagatgtccagcct accagcaggggcagaaccagctctacaacgaactcaat cttggtcggagagaggagtacgacgtgctggacaagcg gagaggacgggaccagaaatgggcgggaagccgcg cagaaagaatcccaagagggctgtacaacgagctcc aaaaggataagatggcagaagcctatagcgagattggt tgaaaggggaacgcagaagaggcaaaggccacgacg gactgtaccagggactcagcaccgccaccaaggacacc tatgacgctcttccatgcaggccctgccgcctcgg (SEQ ID NO: 1060)
SP-Linker 2 – ERmut2 – Furin cleavage site 3 – BCMA CAR	MALPVTALLPLALLHAARPS LALSLTADQMVSALLDAEPPIL YSEYDPTRPFSEASMMGLLT NLADRELVHMINWAKRVPGF VDLTLHDQVHLLCAWMEILM IGLVWRSMHPGKLLFAPNLL LDRNQGKCVEGGVEIFDMLLA TSSRFRMMNLQGEEFVCLKSI ILLNSGVYTFLSSTLKSLEEKD HIHRVLDKITDTLIHLMAGLT LQQQHQRQAQLLLILSHIRHM SNKRMEHLYSMKCKNVVPLS DLLLEMLDAHRLGTGAEDPRP SRKRREVQLVESGGGLVQPG GSLRLSCAVSGFALSNGHMS WVRRAPGKGLEWVSGIVYSG STYYAASVKGRFTISRDNARN TLYLQMNSLRPEDTAIYYCSA	atggccctccctgtcaccgcctgtgcttccgctggctcttc tgctccacgcgcgtcggcccTcgttggcacttccctgactg ccgaccagatggtgtccgccttctggacgccgagcctcc aattctgtactcggagtacgatccgactcggcgttctccga agccagcatgatgggcctgttactaaccctggcgaccg cgagttggtgcacatgattaactgggctaagcgggtgcgg ggcttcgtggacctgacctgcacgaccaagtgcacctcc tggaaatgcgcctggatggaatcctcatgatcggcctcgtg tggagatccatggagcatccggaaagctcctgttgcac ccaacctcctgcttgatcgcaaccagggaataatgcgtgg aagggggtgtcgagatttgcacatgctgctcgccaccttt cccgggtccggatgatgaatctgcaggaggagaagagttcgt gtgtctgaagtcaatcatcctgctgaactccgggtctatac cttctgagctcgacctcaagtcactggaggaaaaaga ccacatccatcgctgctcgataagatcccgacacctt atccatctcatggcgaaggctggactgacctgcaacagc agcaccagaggctggcccagttgtgtgtgattctgagcca catccggcacatgtcgaacaagaggatggaacacctgta

	HGGESDVWGQGTTVTVSSAS GGGGSGGRASGGGGSDIQLT QSPSSLSASVGDRVITICRAS QSISSYLNWYQQKPGKAPKLL IYAASSLQSGVPSRFSGSGSG TDFTLTISLQPEDFATYYCQ QSYSTPYTFGQGTKVEIKTTT PAPRPPTPAPTIASQPLSLRPE ACRPAAGGAVHTRGLDFACDI YIWAPLAGTCGVLLLSLVITLY CKRGRKKLLYIFKQPFMRPVQ TTQEEDGCSCRFPEEEEGGC ELRVKFSRSADAPAYQQGQN QLYNELNLGRREEYDVLDR RGRDPEMGGKPRRKNPQEG LYNELQKDKMAEAYSEIGMKG ERRRGKGDGLYQGLSTATK DTYDALHMQALPPR (SEQ ID NO: 1001)	cagcatgaagtgaagaacgtcgtgcctctgtccgatctg ctcctggaatgctggacgcgcacagactcgggacggg agctgaagatccacgaccagcagaaagcgacgggaa gtgcaattggtgaatcagggggaggactgtgcagcctg gaggatcgctgagactgtcatgtccgtgtccggctttgcc ctgtccaaccacgggatgtcctgggtccgccgcgcgctg gaaagggcctcgaatgggtgtcgggtattgtgtacagcg tagcacctactatgccgcacccgtgaaggggagattcacc atcagccgggacaactccaggaacactctgtacctcaa atgaattcgctgaggccagaggacactgccatctactact gctccgcgcgatggcggagagtcggacgtctggggacag gggaccaccgtgaccgtgtctagcgcgtccggcggaggc ggcagcgggggtcgggcatcagggggcggcggatcgg acatccagctcaccagtcacccagctcgcgtgtccgcctc cgtgggagatcgggtcaccatcacgtgcgcgcgcagcca gtcgatttctcctacctgaactgggtaccaacagaagcccg gaaaagccccgaagcttctcatctacgcgcgcctcgcgct gcagtcaggagtgccctcacggttctccggctccggttccg gtactgtattcaccttgaccatttctcctgcaaccggagg acttgcctacttacttgcagcagctcgtactccacccct acacttccggacaaggcaccagggtcgaatcaagacc actacccacgaccgaggccacccaccccggtcctacc atcgctcccagcctctgtccctcgtccggaggcatgtag acccgcagctggtggggccgtgcataccgggggtcttgac ttcgctgcgatatctacatttggccctctggctgtgacttg cggggctcgtcgttctactcgtgatcacttctactgtgaagc gcggtcgggaagaagctgctgtacatcttgaagcaaccctc atgaggcctgtgcagactactcaagaggaggacggctgtt catgccggtcccagaggaggaggaaaggcggctgcgaa ctgcgcgtgaaattcagccgcagcgcagatgtccagcct accagcaggggcagaaccagctctacaacgaactaat cttggtcggagagaggagtacgacgtgctggacaagcg gagaggacgggaccagaaatgggcgggaagccgcg cagaaagaatcccaagaggcctgtacaacgagctcc aaaaggataagatggcagaagcctatagcgagattgga tgaaaggggaacgcagaagaggcaaaggccacgacg gactgtaccagggactcagcaccgccaccaaggacacc tatgacgtcttcacatgcaggccctgcgcgcctcgg (SEQ ID NO: 1061)
SP-Linker 3 – ERmut1 – Furin cleavage site 2 – CD19 CAR2	MALPVTALLPLALLHAARPD SLALSLTADQMVSALLDAEPPI LYSEYDPTTRPFSEASMMGLLT NLADRELVHMINWAKRVPGF VDLALHDQVHLLCAWMEILM IGLVWRSMEHPGKLLFAPNLL LDRNQGKCVVEGGVEIFDMLLA TSSRFRMMNLQGEFVCLKSI ILLNSGVYTFLSSTLKSLEEKD HIHRVLDKITDTLIHLMAGALT LQQQHQRQAQLLLILSHIRHM SSKRMEHLYSMKCKNVVPLS DLLLEMLDAHRLGTGAEDPRP SRKRRSLGDVGEIVMTQSPAT LSLSPGERATLSCRASQDISK YLNWYQQKPGQAPRLIYHTS RLHSGIPARFSGSGSGTDYTL	atggccctccctgtcaccgcctgtgcttccgtggtcttct tgctccacgcgcgtcggcccgttctggtgacgttccctga ctgccgaccagatggtgtccgccttctgacgcgcgagcc tccaattctgtactcggagtacgatccgactcgcgcgttctc cgaagccagcatgatggcctgttgactaacctggcgga ccgcgagttggtgcacatgattaactgggctaagcgggtg ccgggcttctgtggacctggccctgcacgaccaagtgac ctcctggaatgcgcctggatggaaatcctcatgatcggcct cgtgtggagatccatggagcatcccgaaagctcctgtttg cacccaacctcctgtgatcgcaaccagggaatgcgt ggaagggggtgtcgagatttctgacatgctgtcgcacact cttcccggttccggatgatgaatcgcaggggagaagagttc gtgtgtctgaagtcaatcctcgtgtgaactccgggtctat accttctgagctcgacctcaagtcactggaggaaaaa gaccacatccatcgcgtgtcgtgataagatcaccgacacc cttatccatctcatggcgaaggctggactgacctgcaaca gcagcaccagaggctggcccagttgctgtgattctgagc

	TISSLQPEDFAVYFCQQGNTL PYTFGQGTKLEIKGGGSGG GGSGGGGSQVQLQESGPG VKPSETLSLTCTVSGVSLPDY GVSWIRQPPGKGLEWIGVIW GSETYYSSSLKSRVTISKDN SKNQVSLKLSSVTAADTAVYY CAKHYYYGGSYAMDYWGQG TLVTVSSTTTPAPRPPTPPTI ASQPLSLRPEACRPAAGGAV HTRGLDFACDIYWAPLAGTC GVLLLSLVITLYCKRGRKLLYI FKQPFMRPVQTTQEEDGCSC RFPEEEEGGCELRVKFSRSA DAPAYQQGQNQLYNELNLGR REEYDVLDKRRGRDPEMGGK PRRKNPQEGLYNELQDKMA EAYSEIGMKGERRRRGKHDG LYQGLSTATKDTYDALHMQAL PPR (SEQ ID NO: 1002)	cacatccggcacatgtcgtccaagaggatggaacacctg tacagcatgaagtgaagaacgtcgtcctctgctcatct gctcctggaaatgctggacgcgcacagactcggaaccg gcgcggaagacccccggccctccaggaagcgaaggctc cctcggagacgtgggtgaaattgtatgacctcagctaccc gccactcttagccttcacccgggtgagcgcgaaccctgtc ttgcagagcctccaagacatctcaaaataccttaattggt atcaacagaagcccgacaggctcctcgccttctgatcta ccacaccagccggctccattctggaatccctgccagggtc agcggtagcggatctgggaccgactacaccctcactatca gctcactgcagccagaggactcgtctgtctatttctgtcagc aagggaacaccctgccctacacctttggacagggcacca agctcgagattaaagggtggagggtggcagcggaggagggt gggtccggcgggtggagggaagccagggtccaactccaaga aagcggaccgggtctgtgaagccatcagaaactcttca ctgactgtactgtgagcggaggtgtctctcccgattacggg gtgtcttgatcagacagccaccggggaaggggtctggaat ggattggagtgattggggctctgagactactactactcttc atccctcaagtcacgcgtcaccatctcaaaaggacaactct aagaatcagggtgtcactgaaactgtcatctgtgaccgcag ccgacaccgcgtgtactattgcgttaagcattactattatg gcgggagctacgcaatggattactgggacaggggtactct ggtcaccgtgtccagcaccactacccagcaccgaggcc acccaccccggtcctaccatcgctcccagcctctgtccc tgcgtccggaggcatgtagaccgcagctggtggggcgcg tgcatacccggggtctgacttcgctgcgatactacattg ggccctctggctggtacttgcggggctctgtcttctactc gtgatcactcttactgtaagcgcggctcgaagaagctgtc gtacatcttaagcaaccctcatgaggcctgtgcagacta ctcaagaggaggacggctgttcacgctccagagg aggagggaagggcggctgcgaactgcgcgtgaaatcagc cgcagcgcagatgtccagcctaccagcaggggcagaa ccagctctacaacgaactcaatcttggtcggagagagga gtacgacgtgtggacaagcggagaggacgggaccca gaaatgggcggaagccgcgcagaaagaatcccaag agggcctgtacaacgagctccaaaaggataagatggca gaagcctatagcagattggtatgaaaggggaacgcag aagaggcaaaggccacgacggactgtaccagggactc agcaccgcccacaaggacacctatgacgtcttcacatg caggccctgccgctcgg (SEQ ID NO: 1062)
SP-Linker 3 – ERmut2 – Furin cleavage site 2 – CD19 CAR2	MALPVTALLPLALLHAARPD SLALSLTADQMVSALLDAEPPI LYSEYDPTRPFSEASMMGLLT NLADRELVHMINWAKRVPGF VDLTLHDQVHLLCAWMEILM IGLVWRSMEHPGKLLFAPNLL LDRNQGKCVGGVEIFDMLLA TSSRFRMMNLQGEFVCLKSI ILLNSGVYTFLSSTLKSLEEKD HIHRVLDKITDTLIHLMAKAGLT LQQQHQRALQALLILSHIRHM SNKRMEHLYSMKCKNVVPLS DLLLEMLDAHRLGTGAEDPRP SRKRRSLGDVGEIVMTQSPAT LSLSPGERATLSCRASQDISK YLNWYQQKPGQAPRLIYHTS	atggccctccctgtcaccgcctgtcgtctcgtctggtcttct tgctccacgcgcgtcggcccgattcgttgacacttccctga ctgccgaccagatggtgtccgcccttctggacgcgcagcc tccaattctgtactcggagtacgatccgactcgcctgtctc cgaagccagcatgatgggcctgtgactaaactggcgga ccgcgagttggtgcacatgattaactgggctaagcgggtg ccgggctcgtggacctgacctgcacgaccaagtgcac ctcctggaatgcgcctggatggaaatcctcatgatcggcct cgtgtggagatccatggagcatcccgaaagctcctgtttg cacccaacctcctgtgatcgcaaccagggaatgcgt ggaagggggtgtcgagatttgcacatgctgtcgcacact ctcccggttcggatgatgaatcgcaggaggagaagagttc gtgtgtcgaagtcaatcatcctgtgaactccggggtctat acctcctgagctcgacctcaagtcactggaggaaaaa gaccacatccatgcgtgtcgtgataagatcaccgacacc cttatccatctcatggcgaagggtggactgacctgcaaca

	RLHSGIPARFSGSGSGTDYTL TISSLQPEDFAVYFCQQGNTL PYTFGQGTKLEIKGGGSGG GGSGGGGSQVQLQESGPG VKPSETLSLTCTVSGVSLPDY GVSWIRQPPGKGLEWIGVIW GSETYYSSSLKSRVTISKDN SKNQVSLKLSSVTAADTAVYY CAKHYYYGGSYAMDYWGQG TLVTVSSTTTPAPRPPTPPTI ASQPLSLRPEACRPAAGGAV HTRGLDFACDIYWAPLAGTC GVLLLSLVITLYCKRGRKLLYI FKQPFMRPVQTTQEEDGCSC RFPEEEEGGCELRVKFSRSA DAPAYQQGQNQLYNELNLGR REEYDVLDKRRGRDPEMGK PRRKNPQEGLYNELQDKMA EAYSEIGMKGERRRGKHDG LYQGLSTATKDTYDALHMQAL PPR (SEQ ID NO: 1003)	gcagcaccagaggctggcccagttgctgctgattctgagc cacatccggcacatgtcgaacaagaggatggaacacct gtacagcatgaagtgaagaacgtcgtcctctgtccgat ctgctcctggaaatgtcggacgcgcacagactcggaacc ggcgcggaagacccccggccctccaggaagcgaaggt ccctcggagacgtgggtgaaattgtgatgaccagtcacc cgccactcttagcctttcaccgggtgagcgcgaaccctgt ctgagagcctcccaagacatctcaaaatacctaatgg tatcaacagaagcccgacaggctcctgcctctgatcta ccacaccagccggctccattctggaatccctgccagggtc agcggtagcggatctgggaccgactacaccctcactatca gctcactgcagccagaggactcgtcgtctattctgtcagc aagggaacaccctgccctacaccttgacagggcacca agctcgagattaaagggtggagggtggcagcggaggaggt gggtccggcgggtggaggaaagccagggtccaactcaaga aagcggaccgggtctgtgaagccatcagaaactcttca ctgactgtactgtgagcggagtgctctccccgattacggg gtgtcttgatcagacagccaccggggaaggggtctggaat ggattggagtgattggggctctgagactactactactctt atccctcaagtcacgcgtcaccatctcaaggacaactct aagaatcagggtgctactgaaactgtcatctgtgaccgag ccgacaccggcgtgtactattgcgctaagcattactattatg gcgggagctacgcaatggattactggggacaggggtactct ggtcaccgtgtccagcaccactacccagcaccgaggcc accaccccggtcctaccatcgctcccagcctctgtccc tgcgtccggaggcatgtagaccgcagctggtggggcgg tgcataccgggggtctgactcgcctgcgatatctacattg ggcccctctggctggtactgcggggctcgtcgtcttactc gtgatcactcttactgtaagcgggtcggaagaagctgct gtacatcttaagcaaccctcatgaggcctgtgcagacta ctcaagaggaggacggctgttcacgctccggtcccagagg aggaggaaggcggctgcgaactgcgctgaaattcagc cgagcgcagatgctccagcctaccagcaggggcagaa ccagctctacaacgaactcaatcttggtcggagagagga gtacgacgtgctggacaagcggagaggacgggaccca gaaatgggcggaagccgcgcagaaagaatcccaag agggcctgtacaacgagctccaaaaggataagatggca gaagcctatagcgagattggtatgaaaggggaacgcag aagaggcaaaggccacgacggactgtaccagggactc agcaccgccaccaaggacacctatgacgtcttcacatg caggccctgccgctcgg (SEQ ID NO: 1063)
SP-Linker 3 – ERmut1 – Furin cleavage site 3 – CD19 CAR2	MALPVTALLLPLALLLHAARPD SLALSLTADQMVSALLDAEPI LYSEYDPTRPFSEASMMGLLT NLADRELVHMINWAKRVPGF VDLALHDQVHLLCAWMEILM IGLVWRSMEHPGKLLFAPNLL LDRNQGKCVEGGVEIFDMLLA TSSRFRMMNLQGEFVCLKSI ILLNSGVYTFLSSTLKSLEEKD HIHRVLDKITDTLIHLMAKAGLT LQQQHQRQAQLLLILSHIRHM SSKRMEHLYSMKCKNVVPLS DLLLEMLDAHRLGTGAEDPRP SRKRREIVMTQSPATLSLSPG ERATLSCRASQDISKYLNWYQ	atggccctccctgtcaccgcctgctgcttccgtggtcttc tgctccacgcgctcggcccgattcgttgacatttccctga ctgcccagcagatggtgtccgcccttctggacgcgagcc tccaattctgtactcggagtacgatccgactcgcctgtctc cgaagccagcatgatgggctgttgactaaacctggcggga ccgcgagttggtgcacatgattaactgggctaagcgggtg ccgggcttcgtggacctggccctgcacgaccaagtgcac ctcctggaatgcgcctggatggaatcctcatgatcgccct cgtgtggagatccatggagcatcccgaaagctcctgtttg cacccaacctcctgctgatcgcaaccagggaatgcgt ggaagggggtgtcgagattttcgacatgctgctcgccacct ctcccggttcggatgatgaatcgcaggagagaagagttc gtgtgtcgaagtcaatcatcctgtgaactcgggggtctat acctcctgagctcgaccctcaagtcactggaggaaaaa gaccacatccatcgctgctcgataagatcaccgacacc

	QKPGQAPRLLIYHTSRLHSGIP ARFSGSGSGTDYTLTISSLQP EDFAVYFCQQGNTLPYTFGQ GTKLEIKGGGSGGGGSGGG GSQVQLQESGPGLVKPSSETL SLTCTVSGVSLPDYGVSWIRQ PPGKGLEWIGVIWGSETTYYS SSLKSRVTISKDNSKNQVSLK LSSVTAADTAVYYCAKHYYYG GSYAMDYWGQGTLVTVSSTT TPAPRPPTPAPTIASQPLSLRP EACRPAAGGAVHTRGLDFAC DIYIWAPLAGTCGVLLLSLVITL YCKRGRKKLLYIFKQPFMRPV QTTQEEDGCSCRFPFFFFFFG CELRVKFSRSADAPAYQQGQ NQLYNELNLGRREEYDVLDK RRGRDPEMGGKPRRKNPQE GLYNELQKDKMAEAYSEIGMK GERRRGKGDGLYQGLSTAT KDTYDALHMQALPPR (SEQ ID NO: 1004)	cttatccatctcatggcgaaggctggactgaccctgcaaca gcagcaccagaggctggcccagttgctgctgattctgagc cacatccggcacatgtctccaagaggatggaacacctg tacagcatgaagtgaagaacgtcgtcctctgctcgatct gctcctggaaatgctggacgcgcacagactcgggacgg gagctgaagatccacgaccagcagaaagcgacggga aattgtgatgaccagtcaccgccactcttagcctttcacc cggtagcgcgcaaccctgtcttcagagcctcccaaga catctcaaaataccttaattggatcaacagaagcccga caggctcctcgcttctgactaccacaccagccggctcca ttctggaatccctgccagggtcagcggtagcggatctggga ccgactacaccctcactatcagctcactgcagccagagg acttgcgtgtctatttctgcagcaagggaacaccctgccct acaccttggacagggcaccaagctcgagattaaagggtg gagggtggcagcggaggagggtgggtccggcggtggagg aagccagggtccaactccaagaaagcggaccgggtctgt gaagccatcagaaactcttctactgactgtactgtgagcg gagtgctctccccgattacgggggtgtcttgatcagacag ccaccggggaagggtctggaatggattggagtgattggg gctctgagactactactactctcatccctcaagtcacgcgt caccatctcaaaggacaacttaagaatcagggtgactcgt aaactgtcatctgtgaccgcagccgacaccgcgtgtact attgcgctaagcattactattatggcgggagctacgcaatg gattactggggacagggtactctgggtaccgttccagca ccactacccagcaccgaggccacccaccccgctccta ccatcgctcccagcctctgtcctcgctccggaggcatgt agaccgcagctggtggggcgtgcataccgggggtctt gactcgcctcgcgatactacattggccctctggctggta cttgcggggtcctgctgttctactcgtgatcactttactgta agcgcggtcggaagaagctgctgtacatcttaagcaacc ctcatgaggcctgtgcagactactcaagaggaggacgg ctgtcatgccggttccagaggaggaggaaaggcggtg cgaactgcgcgtgaaattcagccgcagcgagatgctcc agcctaccagcaggggcagaaccagctctacaacgaac tcaatcttggtcggagagaggagtagcagctgctggaca agcggagaggacgggaccagaaatgggcggaagc cgcgagaaagaatcccaagagggcctgtacaacga gctccaaaaggataagatggcagaagcctatagcgaga ttggtatgaaagggaacgcagaagaggcaaaggcca cgacggactgtaccaggactcagcaccgccaccaagg acacctatgacgctcttcacatgcaggccctgccgctcg g (SEQ ID NO: 1064)
SP-Linker 3 – ERmut2 – Furin cleavage site 3 – CD19 CAR2	MALPVTALLPLALLHAARPD SLALSLTADQMVSALLDAEPPI LYSEYDPTRPFSEASMMGLLT NLADRELVHMINWAKRVPGF VDLTLHDQVHLLCAWMEILM IGLVWRSMEHPGKLLFAPNLL LDRNQGKCVEGGVEIFDMLLA TSSRFRMMNLQGEFVCLKSI ILLNSGVYTFLSSTLKSLEEKD HIHRVLDKITDTLIHLMAGALT LQQQHQRQAQLLLLSHIRHM SNKRMEHLYSMKCKNVVPLS DLLLEMLDAHRLGTGAEDPRP SRKRREIVMTQSPATLSLSPG	atggccctccctgtcaccgcctgtgcttccgctggctcttc tgctccacgcgcgtcggcccgatTcgttggcactttccctg actgccgaccagatgggtgccgccctctggacgcgcgagc ctccaattctgtactcggagtagcatccgactcgcctgtct ccgaagccagcatgatgggcctgttgactaacctggcgg accgcgagttggtgcacatgattaactgggctaagcgggt gccgggcttctgtggacctgacctgcacgaccaagtgca cctcctggaatgcgcctggatggaaatcctcatgatcgcc tcgtgtggagatccatggagcatcccgaaagctcctgttt gcaccaacctcctgcttgatcgcaaccagggaatgc gtggaagggggtgcgagatttgcacatgctgctcgccac ctctcccggtccggatgatgaatctgcaggagagaagagt tcgtgtgtctgaagtcaatcatcctgctgaactccggggtct atacctcctgagctcgaccctcaagtcactggaggaaaa

	ERATLSCRASQDISKYLNWYQ QKPGQAPRLLIYHTSRLHSGIP ARFSGSGSGTDYTLTISSLQP EDFAVYFCQQGNTLPYTFGQ GTKLEIKGGGSGGGGSGGG GSQVQLQESGPGLVKPSL SLTCTVSGVSLPDYGVSWIRQ PPGKGLEWIGVIWGSETTYYS SSLKSRVTISKDNSKNQVSLK LSSVTAADTAVYYCAKHYYYG GSYAMDYWGQGLVTVSSTT TPAPRPPTPAPTIASQPLSLRP EACRPAAGGAVHTRGLDFAC DIYIWAPLAGTCGVLLLSLVITL YCKRGRKKLLYIFKQPFMRPV QTTQEEDGCSCRFPEEEEGG CELRVKFSRSADAPAYQQGQ NQLYNELNLGRREEYDVLDK RRGRDPEMGGKPRRKNPQE GLYNELQKDKMAEAYSEIGMK GERRRGKGDGLYQGLSTAT KDTYDALHMQALPPR (SEQ ID NO: 1005)	agaccacatccatcgctgctcgataagatcaccgacac ccttatccatctcatggcgaaggctggactgacctgcaac agcagcaccagaggctggcccagttgctgctgattctgag ccacatccggcacatgtcgaaacagaggatggaacacc tgtacagcatgaagtgaagaacgtcgctcctgtccgat ctgctcctggaatgtggacgcgcacagactcGggacg ggagctgaagatccacgaccagcagaaagcgacggg aaattgtgatgaccagtcacccgccactcttagcctttcac ccggtgagcgcgcaaccctgtcttcgagagcctccaag acatctcaaaataccctaatgtgtatcaacagaagcccg acaggctcctcgcttctgacttaccacaccagccggtcc attctggaatccctgccagggtcagcggtagcggatctggg accgactacaccctcactatcagctcactgcagccagag gacttcgctgtctatttctgcagcaagggaacaccctgcc tacaccttggacagggcaccaagctcgagattaaagggtg gagggtggcagcggaggagggtgggtccggcgggtggagg aagccaggccaactccaagaaagcgaccgggtctgt gaagccatcagaactcttctactgactgtactgtgagcg gagtgtctctcccgattacggggtgtcttgatcagacag ccaccggggaagggtctggaatggattggagtgattggg gctctgagactacttactctctcatccctcaagtcacgct caccatctcaaggacaactctaagaatcagggtgtcactg aaactgtcatctgtgaccgcagccgacaccgcggtgtact attgcgctaagcattactattatggcgggagctacgcaatg gattactggggacaggggtactctggtaaccgtgtccagca ccactacccagcaccgaggccacccacccggctccta ccatcgctcccagcctctgtccctgcgtccggaggcatgt agaccgcagctggtggggcgtgcataccgggggtctt gacttcgctcgatatactacattggccctctggctggta cttgccgggtcctgtgcttctactcgtgatcactttactgta agcgcgggtcggagaagctgctgtacatcttaagcaacc cttcatgaggcctgtgcagactactcaagaggaggacgg ctgttcatgccggttccagaggaggaggaaggcggctg cgaactgcgcgtgaaattcagccgcagcgcagatgctcc agcctaccagcaggggcagaaccagctctacaacgaac tcaatcttggtcggagagaggagtagcagctgtctggaca agcggagaggacgggaccagaaatgggagggaagc cgcgagaaagaatcccaagagggcctgtacaacga gctccaaaaggataagatggcagaagcctatagcgaga ttggtatgaaagggaacgcagaagaggcaaaggcca cgacggactgtaccaggactcagcaccgccaccaagg acacctatgacgctcttcacatgcaggccctgccgctcg g (SEQ ID NO: 1065)
SP-Linker 3 – ERmut1 – Furin cleavage site 2 – CD123 CAR	MALPVTALLPLALLHAARPD SLALSLTADQMVSALLDAEPPI LYSEYDPTPRPFSEASMMGLLT NLADRELVHMINWAKRVPGF VDLALHDQVHLLCAWMEILM IGLVWRSMEHPGKLLFAPNLL LDRNQGKCVEGGVEIFDMLLA TSSRFRMMNLQGEFVCLKSI ILLNSGVYTFLSSTLKSLEEKD HIHRVLDKITDTLIHLMAKAGLT LQQQHQRQAQLLLILSHIRHM SSKRMEHLYSMKCKNVVPLS DLLLEMLDAHRLGTGAEDPRP	atggccctccctgtcaccgccctgtgcttccgctggctcttc tgctccacgcgcgtcggcccgattcgttggcactttccctga ctgccgaccagatgggtgtccgccccttggacgccgagcc tccaattctgtactcggagtagcatccgactcgccggttctc cgaagccagcatgatggcctgttgactaacctggcggga ccgcgagttggtgcacatgattaactgggctaagcgggtg ccgggcttctggacctggccctgcacgaccaagtgcac ctcctggaatgcgcctggatggaatcctcatgatcgccct cgtgtggagatccatggagcatcccgaaagctcctgtttg cacccaacctcctgtgatgcgaaccagggaatgcgt ggaaggggtgtcgagattttcgacatgctgctcgccacct ctcccggttccggatgatgaatctgcaggagagaagagttc gtgtgtctgaagtcaatcatcctgtgaactccgggtctat

	SRKRRSLGADVGVQLVQSGA EVKKPGASVKVSCASGYTFT GYMHWWVRQAPGGGLEWM GWINPNSGGTNYAQKFQGRV TLTRDTSISTVYMELSLRSD DTAVYYCARDMNILATVPFDI WGQGTMTVTVSSGGGSGGG GSGGGGSDIQMTQSPSSLSA SVGDRVITICRASQSISSYLN WYQQKPGKAPKLLIYAASSLQ SGVPSRFSGSGSGTDFLTIV NSLQPEDFATYYCQQGDSVP LTFGGGTREIKTTTPAPRPPT PAPTIASQPLSLRPEACRPAA GGAVHTRGLDFACDIYWAPL AGTCGVLLLSLVITLYCKRGRK KLLYIFKQPFMRPVQTTQEED GCSCRFPEEEEGGCELRVKF SRADAPAYQQGQNQLYNEL NLGRREEYDVLDKRRGRDPE MGGKPRRKNPQEGLYNELQK DKMAEAYSEIGMKGERRRGK GHDGLYQGLSTATKDTYDAL HMQALPPR (SEQ ID NO: 1006)	accttctgagctcgaccctcaagtcaactggaggaaaaa gaccacatccatcgctgctgataagatcacgacacc cttatccatctcatggcgaaggctggactgaccctgaaca gcagcaccagaggctggcccagttgctgctgattctgagc cacatccggcacatgtcgtccaagaggatggaacacctg tacagcatgaagtgaagaacgtcgtgcctctgtccgatct gctcctggaaatgctggacgcgcacagactcggaaccg gcgcggaagacccccggccctccaggaagcgaaggctc cctcggagacgtgggtcaagtgaactcgtccaaagcgg agcgggaagtcaagaaacccggagcgagcgtgaaagt tctgcaaagcctccggctacacctttacgggctactacat gcactgggtgcgccaggcaccaggacagggtcttgaatg gatgggatggatcaaccctaattcgggaggaaactaactac gcacagaagttccaggggagagtgactctgactcgggat acctccatctcaactgtctacatggaactctcccgttgcgg tcagatgatacgcgcagtgactactgcgccgcgacatga atatcctggctaccgtgcggttcgacatctggggacaggg gactatggttactgtctcatcgggctggagggtcaggag gaggcggctcgggaggcggaggttcggacattcagatg accagtcctccatctctgtcggccagcgtcggagata gggtgaccattacctgtcgggctcgcaagcatctcctcg tacctcaactggtatcagcaaaagccgggaagcgccct aagctgctgatctacgccgtctcgagctgcaaagcgggg tgccatccagattctcgggatcaggctcaggaaaccgactc acctgaccgtgaacagcctccagccggaggactttgcc acttactactgccagcaggagactccgtgccgttactttc ggggggggtaccgcctggagatcaagaccactacccc agcaccgaggccaccaccccggtcctaccatgcctc ccagcctctgtccctgcgtccggaggcatgtagaccgca gctggtggggccgtgcatacccggggtcttgactcgcctg cgatatctacatttggggccctctggctggtacttgcgggt cctgctgcttactcgtgatcactcttactgtaagcgcggtc ggaagaagctgctgtacatcttaagcaacccttcatgagg cctgtgcagactactcaagaggaggacggctgttcatgcc ggttcccagaggaggagggaagggcggtgcgaactgcgc gtgaaattcagccgcagcgcagatgtccagcctaccag caggggcagaaccagctctacaacgaactcaatcttgtt cggagagaggagtagcagctgctggacaagcgggagag gacgggacccagaaatgggagggaagccgcgcagaa agaatccccaagagggcctgtacaacgagctccaaaag gataagatggcagaagcctatagcgagattggtatgaaa ggggaacgcagaagaggcaaaggccacgacggactgt accagggactcagcaccgccaccaaggacacctatgac gctcttcacatgcaggccctgcgcctcgg (SEQ ID NO: 1066)
SP-Linker 3 – ERmut2 – Furin cleavage site 2 – CD123 CAR	MALPVTALLLPLALLLHAARPD SLALSLTADQMVSALLDAEPPI LYSEYDPTRPFSEASMMGLLT NLADRELVHMINWAKRVPGF VDLTLHDQVHLLCAWMEILM IGLVWRSMEHPGKLLFAPNLL LDRNQGKCVEGGVEIFDMLLA TSSRFRMMNLQGEFVCLKSI ILLNSGVYTFLSSTLKSLEEKD HIHRVLDKITDTLIHLMAGALT LQQQHQLRAQLLLILSHIRHM	atggccctccctgtcaccgccctgctgcttccgtggctcttc tgctccacgcgcgtcggcccgatTcggtggcactttccctg actgccgaccagatggtgtccgcccttctggacgccgagc ctccaattctgtactcggagtagatccgactcgcctgtct ccgaagccagcatgatgggctgttgactaacctggcgg accgcgagttggtgcacatgattaactgggctaagcgggt gccgggctcgtggacctgacctgcacgaccaagtga cctcctggaatgcgcctggatggaaatcctcatgatcgcc tcgtgtggagatccatggagcatcccgaaagctcctgtt gcaccaacctcctgcttgatcgcaaccagggaatgc gtggaagggggtgtcgagatttgcacatgctgctcggccac

	SNKRMEHLYSMKCKNVVPLS DLLLEMLDAHRLGTGAEDPRP SRKRRSLGDIVGQVQLVQSGA EVKKPGASVKVSKASGYTFT GYMHWWVRQAPGQGLEWM GWINPNSGGTNYAQKFQGRV TLTRDTSISTVYMELSRLRSD DTAVYYCARDMNILATVPFDI WGQGTMTVTVSSGGGGSGGG GSGGGGSDIQMTQSPSSLSA SVGDRVITICRASQSISSYLN WYQQKPGKAPKLLIYAASSLQ SGVPSRFSGSGSGTDFTLV NSLQPEDFATYYCQQGDSVP LTFGGGTREIKTTTPAPRPPT PAPTIASQPLSLRPEACRPAA GGAVHTRGLDFACDIYWAPL AGTCGVLLLSLVITLYCKRGRK KLLYIFKQPFMRPVQTTQEED GCSCRFPEEEEEGGCELRVKF SRSDAPAYQQGQNQLYNEL NLGRREEYDVLDRRGRDPE MGGKPRRKNPQEGLYNELQK DKMAEAYSEIGMKGERRRGK GHDGLYQGLSTATKDYDAL HMQALPPR (SEQ ID NO: 1007)	ctctcccggtccggatgatgaatctgcagggagaagagt tcgtgtgtctgaagtcaatcatcctgctgaactccgggtct ataccttcctgagctcgaccctcaagtcactggaggaaaa agaccacatccatcgctgctgataagatcacggacac ccttatccatctcatggcgaaggctggactgacctgcaac agcagcaccagaggctggcccagtgctgctgattctgag ccacatccggcacatgtcgacaagaggatggaacacc tgtacagcatgaagtgaagaacgtcgctgctgtccgat ctgctcctggaaatgtcggacgcgcacagactcggaaacc ggcgcggaagacccccggccctccaggaagcgaaggt ccctcggagacgtgggtcaagtgaactcgtccaaagcg gagcggaaagtcaagaaacccggagcgcgagcgtgaaagt gtcctgcaaagcctccggctacaccttacgggtactaca tgactgggtgcgccaggcaccaggacagggcttgaat ggatgggatggatcaaccctaattcggggcggaactaacta cgcacagaagttccaggggagagtgactctgactcggga tacctccatctcaactgtctacatggaactctcccgttgcg gtcagatgatacggcagtgactactgcgcccgcgacatg aatatcctggctaccgtgcggttcgacatctgggacagg ggactatggttactgtctcatcgggcggtggagggtcagga ggaggcggctcgggagggcgaggttcggacattcagat gaccagtcctccatcctctgtcggcagcgtcggagat agggtgaccattacgtcgggctcgcgcaaagcatctcctc gtacctcaactggtatcagcaaaagccgggaaaggcgc ctaagctgctgatctacgcgcttcgagcttgcaaagcgg ggtgccatccagattctcgggatcaggctcaggaaccga cttcacctgaccgtgaacagcctccagccggaggacttt gccacttactactgccagcaggagactccgtgcgctta cttcgggggggggtaccgcctggagatcaagaccacta ccccagcaccgaggccacccacccggctcctaccatcg cctccagcctctgtccctgcgtccggaggcatgtagacc gcagctggtggggccgtgcatacccggttcttgacttcg cctgcgatatctacattggggccctctggctggtacttcgg ggtcctgctgctttactcgtgatcactttactgtaagcgcg gtcggagaagctgctgtacatcttaagcaaccctcatg aggcctgtgcagactactcaagaggaggacggctgttcat gccggttcccagaggaggaggaaggcggctgcgaactg cgcgtgaaattcagccgcagcgcagatgctccagcctac cagcaggggcagaaccagctctacaacgaactcaatctt ggtcggagagaggagtacgacgtgctggacaagcggga gaggacgggaccagaaatgggcgggaagccgcgca gaaagaatcccaagagggcctgtacaacgagctccaa aaggataagatggcagaagcctatagcgagattggtatg aaaggggaacgcagaagaggcaaaggccacgacgg actgtaccagggactcagcaccgccaccaaggacacct atgacgctcttcacatgcaggccctgcgcctcgg (SEQ ID NO: 1067)
SP-Linker 3 – ERmut1 – Furin cleavage site 3 – CD123 CAR	MALPVTALLLPLALLHAARPD SLALSLTADQMVSALLDAEPPI LYSEYDPTRPFSEASMMGLLT NLADRELVHMINWAKRVPGF VDLALHDQVHLLCAWMEILM IGLVWRSMEHPGKLLFAPNLL LDRNQGKCVVEGGVEIFDMLLA TSSRFRMMNLQGEFVCLKSI ILLNSGVYTFLSSTLKSLEEKD	atggccctccctgtcaccgcctgctgcttccgtggctcttc tgctccacgcgcctcggcccgattcgttggcactttccctga ctgccgaccagatgggtgtccgccttctggacgccgagcct ccaattctgtactcggagtacgatccgactcggcgttctcc gaagccagcatgatgggcctgttgactaacctggcggacc gcgagttggtgcacatgattaactgggctaagcgggtgccg ggcttcgtggacctggcctgcacgaccaagtgcacctcct

	HIHRVLDKITDTLIHLMAKAGLT LQQQHQRRLAQLLLILSHIRHM SSKRMEHLYSMKCKNVVPLS DLLLEMLDAHRLGTGAEDPRP SRKRRQVQLVQSGAEVKKPG ASVKVSKASGYTFTGYMH WVRQAPGQGLEWMGWINPN SGGTNYAQKFQGRVTLTRDT SISTVYMELSRRLRSDDTAVYY CARDMNILATVPFDIWGQGT MTVSSGGGGSGGGGSGGGG SDIQMTQSPSSLSASVGDRT ITCRASQSISSYLNWYQKPG KAPKLLIYAASSLQSGVPSRFS GSGSGTDFTLTVNSLPEDFA TYYCQQGDSVPLTFGGGTRL EIKTTTTAPRPPTPAPTIASQP LSLRPEACRPAAGGAVHTR GLDFACDIYIWAPLAGTCG VLLLVLITLYCKRGRKLL YIFKQPFMRPVQTTQEEDG CSCRFPEEEEGGCELRVK FRSADAPAYQQGQNQLY NELNLGRREEYDVLDKRR GRDPEMGGKPRRKNPQE GLYNELQDKMAEAYSEIG MKGERRRRGKGGHDGLYQGL STATKDTYDALHMQALPPR (SEQ ID NO: 1008)	ggaatgcgcctggatggaaatcctcatgatcgccctcgtgt ggagatccatggagcatcccggaaagctcgtgttgcaccc aacctcctgctgatcgcaaccagggaagctcgtggaag ggggtgtcgagattttcgacatgctgctgccacctctccc ggttccggatgatgaatctgcaggagagaagagttcgtgtgt ctgaagtcaatcatcctgctgaactccgggtctataccttc ctgagctcgaccctcaagtcactggaggaaaaagaccaca tccatcgctgctcgataagatcacccgacaccccttatccatc tcatggcgaaggctggactgacctgcaacagcagcacca gaggtggcccagttgctgctgattctgagccatccggc acatgtcgtccaagaggatggaacacctgtacagcatgaa gtgcaagaacgtcgtgctcctgtccgatctgctcctggaat gctggacgcgcagactcggaaccggcgcggaagaccc ccggccctccaggaagcgaaggcaagtgaactcgtccaa agcggagcgggaagtcaagaaacccggagcgagcgtgaaa gtgtcctgcaaagcctccggctacacctttacgggtactac atgcactgggtgcgcaggcaccaggacagggtcttgaat ggatgggatggatcaaccctaattcgggcggaactaacta cgacagaagttccaggggagagtactctgactcgggat acctcatctcaactgtctacatggaactctcccgttgcg tcgatgatacggcagtgactactgcgccgcgacatgaa tatcctggctaccgtgccgttcgacatctggggacaggga ctatggttactgtctcatcgggcgggtggagggtcaggagga ggcggctcgggaggcggaggttcggacattcagatgacc agtccccatcctctgtcggccagcgtcggagatagggtg accattacctgtcgggcctcgaaagcatctcctctacctc aactggtatcagcaaaagcgggaaaggcgcctaagctgc tgatctacgcccttcgagcttgcaaagcggggtgcatcc agattctcgggatcaggctcaggaaccgacttcacctgac cgtgaacagcctccagccggaggactttgccacttactact gccagcaggagactccgtgccgttactttcggggggggt acccgctggagatcaagaccactacccagcaccgaggc caccaccccgctcctaccatgcctccagcctctgtccc tgcgtcggaggcatgtagaccgcagctgggtgggcccgt gcataccggggtcttgaactcgctgcgatctacatttg ggcccctctggctggtacttgcggggtcgtgcttctactc gtgatcactcttactgtaagcgggtcggaagaagctgct gtacatctttaagcaaccttcagaggcctgtgcagactac tcaagaggaggacggctgttcagccggttccagaggag gaggaaggcggctgcgaactgcgctgaaattcagccgca gcgcagatgctccagcctaccagcaggggcagaaccagct ctacaacgaactcaatcttggtcggagagaggagtacgac gtgctggacaagcggagaggacgggaccagaaatgggc gggaagccgcgagaaagaatcccaagagggcctgtac aacgagctccaaaaggataagatggcagaagcctatagc gagattggtatgaaagggaacgcagaagaggcaaggc cacgacggactgtaccagggactcagcaccgccaccaagg acacctatgacgctcttcacatgcaggccctgccgctcgg
--	--	---

		(SEQ ID NO: 1068)
SP-Linker 3 – ERmut2 – Furin cleavage site 3 – CD123 CAR	MALPVTALLLPLALLLHAARPD SLALSLTADQMVSALLDAEPPI LYSEYDPTRPFSEASMMGLLT NLADRELVHMINWAKRVPGF VDLTLHDQVHLLECAWMEILM IGLVWRSMEHPGKLLFAPNLL LDRNQGKCVEGGVEIFDMLLA TSSRFRMMNLQGEFVCLKSI ILLNSGVYTFLSSTLKSLEEKD HIHRVLDKITDTLIHLMAKAGLT LQQQHQRQAQLLLILSHIRHM SNKRMEHLYSMKCKNVVPLS DLLLEMLDAHRLGTGAEDPRP SRKRRQVQLVQSGAEVKKPG ASVKVSCASGYTFTGYMH WVRQAPGQGLEWMGWINPN SGGTNYAQKFQGRVTLTRDT SISTVYMELSRLSDDTAVYY CARDMNILATVPFDIWGGTM VTVSSGGGGSGGGSGGGG SDIQMTQSPSSLSASVGDRT ITCRASQSISSYLNWYQKPG KAPKLLIYAASSLQSGVPSRFS GSGSGTDFTLTVNSLQPEDFA TYCQGGDSVPLTFGGGTRL EIKTTTPAPRPPTPAPTASQP LSLRPEACRPAAGGAVHTRG LDFACDIYWAPLAGTCGVLLL SLVITLYCKRGRKLLYIFKQP FMRPVQTTQEEDGCSCRFPE EEEGGCELRVKFSRSADAPA YQQGQNQLYNELNLGRREEY DVLDKRRGRDPEMGGKPRRK NPQEGLYNELQKDKMAEAYS EIGMKGERRRGKGHDGLYQG LSTATKDTYDALHMQALPPR (SEQ ID NO: 1009)	atggccctccctgtcaccgcccgtgcttccgctggctcttc tgctccacgcccgtcggcccgatTcggtggcactttccctg actgccgaccagatggtgtccgccccttctggacgccgagc ctccaattctgtactcggagtagcatccgactcggcgttct ccgaagccagcatgatgggcctgtgactaacctggcgg accgcgagttggtgcacatgattaactgggctaagcgggt gccgggctcgtggacctgacctgcacgaccaagtga cctcctggaatgcgcctggatggaaatcctcatgatcggcc tcgtgtggagatccatggagcatcccgaaagctcctgttt gcaccaacctcctgcttgatcgcaaccagggaatgc gtggaaggggtgtcgagatttcgacatgctgctgccac ctctcccggtccggatgatgaatctgcaggagagaagagt tcgtgtgtctgaagtcaatcatcctgctgaactccgggtct ataccttctgagctcgacctcaagtactggaggaaaa agaccacatccatcgcgtgctcgataagatcacggacac ccttatccatctcatggcgaaggctggactgacctgcaac agcagcaccagaggctggcccagttgctgctgattctgag ccacatccggcacatgtcgaaagaggatggaacacc tgtacagcatgaagtgcgaagcgtcgtgctctgtccgat ctgctcctggaaatgtcggacgcgcacagactcgggacg ggagctgaagatccacgaccagcagaaagcagcggc aagtgcactcgtccaaagcggagcggagtaagtaagaaa cccggagcgcgagcgtgaaagtgtcctgcaaacgctccggc tacacctttacgggctactacatgcactgggtgcgccaggc accaggacagggcttgaatggatgggatggaacacct aattcgggcggaactaactacgcacagaagtccagggg agagtgcactgcactcgggatacctccatctcaactgtctac atggaactctcccgttgcggtcagatgatacggcagtgta ctactgcggccgcacatgaatacctggtaccgtgccgt tcgacatctggggacaggggactatggtactgtctcatcg ggcgggtggaggttcaggaggaggcggctcgggaggcg gaggttcggacattcagatgacctcagctcccatcctctgt cggccagcgtcggagatagggtgaccattacgttcggg cctcgcaagcatctcctgctacctaactggtatcagcaa aagccgggaaaggcgctaagctgctgatctacggcgt tcgagcttgcaagcgggggtgccatccagattctcgggat caggctcaggaaccgacttcacctgacctgaacagcc tcagccggaggactttgccacttacttgcagcaggc agactccgtgcgcttacttccgggggggtaccgcctgg agatcaagaccactacccagcaccgaggccaccacc cggctcctaccatcgctcccgacctctgtccctgcgtccg gaggcatgtagaccgcagctggtggggcggatgcatacc cggggtcttgacttcgctgcgatactacatttgggcccctc tggctggtacttcggggtcctgctgcttctactcgtgatcac tcttactgtaagcgcggtcggagaagctgctgtacatctt aagcaaccttcatgaggcctgtgcagactactcaagag gaggacggctgttcatgccggtccagaggaggaggaa ggcggctgcgaactgcgcgtgaaattcagccgcagcgc agatgctccagcctaccagcaggggcagaaccagctcta caacgaactcaatcttggtcggagagaggagtacgacgt gctggacaagcggagaggacgggaccagaaaatgggc gggaagccgcgcagaaagaatcccaagaggggcctgt acaacgagctccaaaaggataagatggcagaagcctat agcgagattggtatgaaaggggaacgcagaagaggca aaggccacgacggactgtaccagggactcagcaccgcc

		accaaggacacctatgacgctcttcacatgcaggccctgc cgctcgg (SEQ ID NO: 1069)
SP-Linker 3 – ERmut1 – Furin cleavage site 2 – BCMA CAR	MALPVTALLLPLALLLHAARPD SLALSLTADQMVSALLDAEPI LYSEYDPTRPFSEASMMGLLT NLADRELVHMINWAKRVPGF VDLALHDQVHLLECAWMEILM IGLVWRSMEHPGKLLFAPNLL LDRNQGKCVEGGVEIFDMLLA TSSRFRMMNLQGEFVCLKSI ILLNSGVYTFLSSTLKSLEEKD HIHRVLDKITDTLIHLMAGALT LQQQHQLRAQLLLILSHIRHM SSKRMEHLYSMKCKNVVPLS DLLLEMLDAHRLGTGAEDPRP <u>SRKRRLG</u> DVGEVQLVESGG GLVQPGGSLRLSCAVSGFALS NHGMSWVRRAPGKGLEWVS GIVYSGSTYYAASVKGRFTISR DNSRNTLYQMNSLRPEDTAI YYCSAHGGESDVWGQTTVT VSSASGGGGSGGRASGGGG SDIQLTQSPSSLSASVGDRVTI TCRASQSISSYLNWYQQKPG KAPKLLIYAASSLQSGVPSRFS GSGSGTDFTLTISLQPEDFA TYYCQQSYSTPYTFGQGTKV EIKTTTPAPRPPTPAPTASQP LSLRPEACRPAAGGAVHTRG LDFACDIYWAPLAGTCGVLLL SLVITLYCKRGRKKLLYIFKQP FMRPVQTTQEEDGCSCRPE EEEGGCELRVKFSRSADAPA YQQGQNQLYNELNLGRREEY DVLDKRRGRDPEMGGKPRRK NPQEGLYNELQKDKMAEAYS EIGMKGERRRGKGHDGLYQG LSTATKDTYDALHMQALPPR (SEQ ID NO: 1010)	atggccctccctgtcaccgccctgctgcttccgctggctcttc tgctccacgccgctcggcccgatTcgtggcactttccctg actgccgaccagatggtgtccgcccttctggacgccgagc ctccaattctgtactcggagtacgatccgactcgcctgtct ccgaagccagcatgatgggcctgttgactaacctggcgg accgcgagttggtgcacatgattaactgggctaagcgggt gccgggctcgtggacctggccctgcacgaccaagtga cctcctggaatgcgcctggatggaaatcctcatgatcggcc tcgtgtggagatccatggagcatcccgaaagctcctgttt gcaccaacctcctgcttgatcgcaaccagggaaaatgc gtggaaggggtgtcgagatttcgacatgctgctgccac ctctcccggttccggatgatgaatctgcaggagagaagagt tcgtgtgtctgaagtcaatcatcctgctgaactccgggtct ataccttctgagctcgacctcaagtactggaggaaaa agaccacatccatcgcgtgtcgataagatcacggacac ccttatccatctcatggcgaaggctggactgacctgcaac agcagcaccagaggctggcccggtgtgtgtgattctgag ccacatccggcacatgtcgtccaagaggatggaacacct gtacagcatgaagtgaagaacgtcgtgcctctgtccgat ctgctcctggaaatgtcggacgcgcacagactcggaacc ggcgcggaagacccccggccctccaggaaagcgaaggt ccctcggagacgtgggtgaagtgaattggtggaatcag ggggaggactgtgcagcctggaggatcgctgagactgtc atgtgccgtgtccggcttgcctgtccaaccacgggatgtc ctgggtccgcgcgcgcctggaaagggcctcgaatgggt gtcgggtattgtgtacagcggtagcacctactatgccgat ccgtgaaggggagattcaccatcagccgggacaactcc aggaacactctgtacctcaaatgaattcgtgaggccag aggacactgccatctactactgtccgcgatggcggaga gtccgacgtctggggacaggggaccaccgtgaccgtgtc tagcgcgtccggcggaggcggcagcggggctgggcat cagggggcggcggatcggacatccagctcaccagctcc ccgagctcgtctgcgcctccgtgggagatcgggtcacca tcacgtgccgcgcagccagtcgatttctcctacctaac tggtaccaacagaagcccgaaaagccccgaagcttctc atctacgccgcctcgagcctgcagtcaggagtgcctcac ggttctccggctccggttccggtactgattcacctgacct ttcctccctgaaccggaggacttcgctacttactactgcca gcagctgtactccacccctacactttcgacaaggcacc aaggtcgaaatcaagaccactacccagcaccgaggcc accacccccggctcctaccatcgccctccagcctctgtcc tgcgtccggaggcatgtagaccgcagctggtggggcgg tgcatacccggggtcttgacttcgcctgcgatatctacattg ggccctctggctggtacttgcggggtcctgctgttctactc gtgatcactcttactgtaagcgggtcggaagaagctgct gtacatcttaagcaaccctcataggcctgtgcagacta ctcaagaggaggacggctgtcatgccgttcccaggagg aggaggaagggcgtcgaactgcgcgtgaaattcagc cgcagcgcagatgtccagcctaccagcaggggcagaa ccagctctacaacgaactcaatcttggtcggagagagga gtacgacgtgtggacaagcggagaggacgggaccca gaaatgggcgggaagccgcgcagaaagaatcccaag agggcctgtacaacgagctccaaaaggataagatggca gaagcctatagcagattggtatgaaaggggaacgcag

		aagaggcaaaagggccacgacggactgtaccagggactc agcaccgccaccaaggacacctatgacgctcttcacatg caggccctgccgcctcgg (SEQ ID NO: 1070)
SP-Linker 3 – ERmut2 – Furin cleavage site 2 – BCMA CAR	MALPVTALLPLALLLHAARPD SLALSLTADQMVSALLDAEPPI LYSEYDPTRPFSEASMMGLLT NLADRELVHMINWAKRVPGF VDLTLDHQQVHLLECAWMEILM IGLVWRSMEHPGKLLFAPNLL LDRNQGKCVVEGGVEIFDMLLA TSSRFRMMNLQGEFVCLKSI ILLNSGVYTFLSSTLKSLEEKD HIHRVLDKITDTLIHLMAGALT LQQQHQRQAQLLLILSHIRHM SNKRMEHLYSMKCKNVVPLS DLLLEMLDAHRLGTGAEDPRP <u>SRKRRLGDUVEVQLVESGG</u> GLVQPGGSLRLSCAVSGFALS NHGMSWVRRAPGKLEWVS GIVYSGSTYYAASVKGRFTISR DNSRNTLYLQMNSLRPEDTAI YYCSAHGGESDVWGQGTTVT VSSASGGGGSGGRASGGGG SDIQLTQSPSSLSASVGDRVIT TCRASQSISSYLNWYQQKPG KAPKLLIYAASSLQSGVPSRFS GSGSGTDFTLTISSLQPEDFA TYYCQQSYSTPYTFGQGTKV EIKTTTTAPRPPTPAPTIASQP LSLRPEACRPAAGGAVHTRG LDFACDIYWAPLAGTCGVLLL SLVITLYCKRGRKKLLYIFKQP FMRPVQTTQEEDGCSCRFE EEEGGCELRVKFSRSADAPA YQQGQNQLYNELNLGRREEY DVLDKRRGRDPEMGGKPRRK NPQEGLYNELQDKMAEAYS EIGMKGERRRGKGHDGLYQG LSTATKDTYDALHMQALPPR (SEQ ID NO: 1011)	atggccctccctgtcaccgccctgtgcttccgctggctcttc tgctccacgcccgtcggcccgatTcggtggcactttccctg actgccgaccagatgggtccgccccttctggacgccgagc ctccaattctgtactcggagtagcatccgactcggcgttct ccgaagccagcatgatgggcctgttgactaacctggcgg accgcgagttggtgcacatgattaactgggctaagcgggt gccgggcttctgtggacctgacctgcacgaccaagtca cctcctggaatgcgcctggatggaaatcctcatgatcggcc tcgtgtggagatccatggagcatcccgaaagctcctgttt gcaccaacctcctgtgtgatcgcaaccagggaaaatgc gtggaagggggtgtcgagatttctgacatgctgctgccac ctctcccggttccggatgatgaatctgcaggagagaagagt tcgtgtgtctgaagtcaatcatcctgtgaactccggggtct ataccttctgagctcgacctcaagtcactggaggaaaa agaccacatccatcgctgtcgtataagatcaccgacac ccttatccatctcatggcgaaggctggactgacctgcaac agcagcaccagaggctggcccagttgtctgtgattctgag ccacatccggcacatgtcgaaacagaggatggaacacc tgtacagcatgaagtgcgaagaacgtcgtgctctgtccgat ctgctcctggaaatgtcggacgcgcacagactcggaacc ggcgcggaagacccccggccctccaggaaagcgaaggt ccctcggagacgtgggtgaagtgaattggtggaatcag ggggaggactgtgcagcctggaggatcgctgagactgtc atgtgccgtgtccggcttggcctgtccaaccacgggatgtc ctgggtccgcgcgcgcctggaaagggcctcgaatgggt gtcgggtattgtgtacagcggtagcacctactatgccgat ccgtgaaggggagattcaccatcagccgggacaactcc aggaacactctgtacctcaaatgaattcgtgaggccag aggacactgccatctactactgtccgcgcagcgggagaga gtccgacgtctggggacaggggaccaccgtgacctgtc tagcgcgtccggcggaggcggcagcgggggtcgggcat cagggggcggcggatcggacatccagctcaccagctcc ccgagctcgtgtccgcctccgtgggagatcgggtcacca tcacgtgccgcgcagccagtcgatttctcctacctaagc tggtaccaacagaagcccggaaaagccccgaagcttctc atctacgccgcctcgagcctgcagtcaggagtgcctcac ggttctccggctccgggtccggtagtattcacctgacctat ttcctccctgcaaccggaggacttcgctacttactactgcca gcagtcgtactccacccctacactttcgacaaggcacc aaggtcgaaatcaagaccactacccagcaccgaggcc accaccccggtcctaccatcgctccagcctctgtccc tgctcggaggcatgtagaccgcagctggtggggccg tgcataccgggggtcttgacttcgctgcgatactacattg ggccctctggctgggtacttgcggggtcctgctgcttactc gtgatcactcttactgtaagcgcgggtcggaagaagctgct gtacatcttaagcaaccctcataggcctgtgcagacta ctcaagaggaggacggctgtcatgccgttcccagagg aggaggaagggcgtgcgaactgcgctgaaattcagc cgcagcgcagatgtccagcctaccagcaggggcagaa ccagctctacaacgaactcaatcttggtcggagagagga gtacgacgtgtgcgaagcggagaggacggggaccca gaaatgggcgggaagccgcgcagaaagaatccccaag agggcctgtacaacgagctccaaaaggataagatggca

		gaagcctatagcgagattggtatgaaaggggaacgcag aagaggcaaaggccacgacggactgtaccagggactc agcaccgccaccaaggacacctatgacgctctcacatg caggccctgccgcctcgg (SEQ ID NO: 1071)
SP-Linker 3 – ERmut1 – Furin cleavage site 3 – BCMA CAR	MALPVTALLPLALLLHAARPD SLALSLTADQMVSALLDAEPI LYSEYDPTRPFSEASMMGLLT NLADRELVHMINWAKRVPGF VDLALHDQVHLLCAWMEILM IGLVWRSMEHPGKLLFAPNLL LDRNQGKCVVEGGVEIFDMLLA TSSRFRMMNLQGEFVCLKSI ILLNSGVYTFLSSTLKSLEEKD HIHRVLDKITDTLIHLMAKAGLT LQQQHQRQAQLLLILSHIRHM SSKRMEHLYSMKCKNVVPLS DLLLEMLDAHRLGTGAEDPRP SRKRREVQLVESGGGLVQPG GSLRLSCAVSGFALSNGHMS WVRRAPGKGLEWVSGIVYSG STYYAASVKGRFTISRDNARN TLYLQMNSLRPEDTAIYYCSA HGGESDVWGQGTTVTVSSAS GGGGSGGRASGGGGSDIQLT QSPSSLSASVGDRVITCRAS QSISSYLNWYQQKPKAPKLL IYAASSLQSGVPSRFSGSGSG TDFTLTISLQPEDFATYYCQ QSYSTPYTFGGGTKVEIKTTT PAPRPPTPAPTIASQPLSLRPE ACRPAAGGAVHTRGLDFACDI YIWAPLAGTCGVLLLSLVITLY CKRGRKLLYIFKQPFMRPVQ TTQEEDGCSCRFPEEEEGGC ELRVKFSRSADAPAYQQGQN QLYNELNLGRREEYDVLDR RGRDPEMGGKPRRKNPQEG LYNELQDKMAEAYSEIGMKG ERRRGKGDGLYQGLSTATK DTYDALHMQALPPR (SEQ ID NO: 1012)	atggccctccctgtcaccgcctgtgcttccgtggtcttc tgctccacgccgtcggcccgatTcgttggcactttccctg actgccgaccagatggtgtccgcccttctggacgccgagc ctccaattctgtactcggagtagcatccgactcgcctgtct ccgaagccagcatgatgggcctgttgactaacctggcgg accgcgagttggtgcacatgattaactgggctaagcgggt gccgggcttctgtggacctggccctgcacgaccaagtga cctcctggaatgcgcctggatggaaatcctcatgatcggcc tcgtgtggagatccatggagcatcccggaagctcctgttt gcaccaacccctcgtgtgatcgcaaccagggaataatgc gtggaagggggtgtcgagatttctgacatgctgctgccac ctctcccggttccggatgatgaatctgcaggagagaagagt tcgtgtgtctgaagtcaatcctcgtgaactccggggtct ataccttctgagctcgaccctcaagtcactggaggaaaa agaccacatccatcgctgtcgtgataagatcaccgacac ccttatccatctcatggcgaaggctggactgacctgcaac agcagcaccagaggctggccagtgctgtgattctgag ccacatccggcacatgtcgtccaagaggatggaacacct gtacagcatgaagtgaagaacgtcgtgcctcgtcctgat ctgctcctggaaatgtggacgcgcacagactcGggacg ggagctgaagatccacgacccagcagaaagcgacggg aagtgaattggtggaatcagggggaggactgtgcagc ctggaggatcgctgagactgtcatgtccgtgtccgctttg ccctgtccaaccacgggatgtcctgggtccgcgcgcgcgc tggaagggcctcgaatgggtgtcgggtattgtgtacagc ggtagcacctactatgccgatccgtgaaggggagattca ccatcagccgggacaactccaggaaactctgtacctcc aaatgaattcgtgaggccagaggacactgccatctacta ctgctccgcgcgatggcggagagtccgacgtctggggaca ggggaccaccgtgaccgtgtctagcgcgtccggcggag gcggcagcgggggtcgggcatcagggggcggcggatc ggacatccagctcaccagtcctcccgagctcgtgtccgcc tccgtgggagatcgggtcaccatcacgtgccgcgccagc cagtcgatttctcctacctgaactggtaccaacagaagcc cggaaaagccccgaagcttctcatctacgcgcctcgag cctgcagtcaggagtgcctcaccggttctccggtccggtt ccggtactgatttaccctgaccatttctccttgcaaccgg aggacttcgtacttactactgccagcagtcgtactccacc ccctacacttccggacaaggcaccaggtcgaaatcaag accactacccagcaccgaggccaccaccccggtcct accatcgctcctccagcctctgtccctgcgtccggaggcatg tagaccgcagctggtggggcgtgcatacccggggtctt gacttcgcctcgcgatactacattggggccctctggctgga cttgccgggtcctgtgcttctactcgtgatcacttctactgta agcgcgggtcggaagaagctgctgtacatctttaagcaacc cttcatgaggcctgtgcagactactcaagaggaggacgg ctgttcatgccggttccagaggaggaggaagggcgtg cgaactgcgcgtgaaatcagccgcagcgcagatgtcc agcctaccagcaggggcagaaccagctctacaacgaac tcaatcttggtcggagagaggagtacgacgtgtggaca agcggagaggacgggaccagaaatgggcgggaagc cgcgcagaaagaatccccaaggggcctgtacaacga

		gctccaaaaggataagatggcagaagcctatagcgaga ttggatgaaaggggaacgcagaagaggcaaaggcca cgacggactgtaccaggactcagcaccgccaccaagg acacctatgacgctcttcacatgcaggccctgccgctcg g (SEQ ID NO: 1072)
SP-Linker 3 – ERmut2 – Furin cleavage site 3 – BCMA CAR	MALPVTALLPLALLLHAARPD SLALSLTADQMVSALLDAEPPI LYSEYDPTRPFSEASMMGLLT NLADRELVHMINWAKRVPGF VDLTLHDQVHLLCAWMEILM IGLVWRSMEHPGKLLFAPNLL LDRNQKGCVEGGVEIFDMLLA TSSRFRMMNLQGEFVCLKSI ILLNSGVYTFLSSTLKSLEEKD HIHRVLDKITDTLIHLMAGALT LQQQHQRQAQLLLILSHIRHM SNKRMEHLYSMKCKNVVPLS DLLLEMLDAHRLGTGAEDPRP SRKRREVQLVESGGGLVQPG GSLRLSCAVSGFALSNHGMS WVRRAPGKGLEWVSGIVYSG STYYAASVKGRFTISRDNARN TLYLQMNSLRPEDTAIYYCSA HGGESDVWGQGTTVTVSSAS GGGGSGGRASGGGGSDIQLT QSPSSLSASVGDRVITCRAS QSISSYLNWYQQKPKAPKLL IYAASSLQSGVPSRFSGSGSG TDFTLTISLQPEDFATYYCQ QSYSTPYTFGGGTKVEIKTTT PAPRPPTPAPTIASQPLSLRPE ACRPAAGGAVHTRGLDFACDI YIWAPLAGTCGVLLLSLVITLY CKRGRKLLYIFKQPFMRPVQ TTQEEDGCSCRFPEEEEGGC ELRVKFSRSADAPAYQQGQN QLYNELNLGRREEYDVLDR RGRDPEMGGKPRRKNPQEG LYNELQKDKMAEAYSEIGMKG ERRRGKGHDGLYQGLSTATK DTYDALHMQALPPR (SEQ ID NO: 1013)	atggccctccctgtcaccgccctgtgcttccgctggctcttc tgctccacgccgctcgcccgatTcggtggcactttccctg actgccgaccagatgggtccgccccttctggacgccgagc ctccaattctgtactcggagtagatccgactcgcctgtct ccgaagccagcatgatgggcctgttgactaacctggcgg accgcgagttgggtcacatgattaactgggctaagcgggt gccgggcttcgtggacctgacctgcacgaccaagtgca cctcctggaatgcgcctggatggaaatcctcatgatcgcc tcgtgtggagatccatggagcatcccgaaagctcctgtt gcaccaacctcctgctgtgatcgcaaccagggaatgc gtggaaggggggtgtcgagatttcgacatgctgtcgccac ctctcccggttccgagatgaatctgcaggagagaagagt tcgtgtgtgaagtcaatcactcctgctgaactccgggtct ataccttctgagctcgacctcaagtcactggaggaaaa agaccacatccatcgcggtgtcgataagatcaccgacac ccttatccatctcatggcgaaggctggactgacctgcaac agcagcaccagaggctggccaggtgtgctgtgattctgag ccacatccggcacatgtcgacaagaggatggaaacacc tgtacagcatgaagtgcagaacgctgtgctctgtccgat ctgctcctggaaatgtggacgcgcacagactcgggacg ggagctgaagatccacgacctcagcagaagcgacggg aagtgaattgggtgaatcagggggaggactgtgcagc ctggaggatcgctgagactgtcatgtccgtgtccgcttg ccctgtccaaccacgggatgtctgggtccgcccgcgcgc tggaagggcctcgaatgggtgtcgggtattgtgtacagc ggtagcacctactatgccgatccgtgaaggggagattca ccatcagccgggacaactccaggaaactctgtacctcc aatgaattcgctgaggccagaggacactgccatctacta ctgctccgcgatggcggagagtcgacgtctggggaca ggggaccaccgtgaccgtgtctagcgcgtccggcggag gcggcagcgggggtcgggcatcagggggcggcggatc ggacatccagctcaccagtcctccgagctcgtgtccgcc tccgtgggagatcgggtcaccatcacgtgccgcgccagc cagtcgatttctcctacctgaactgttaccacagaagcc cggaaaagccccgaagcttctcatctacgcgcctcgag cctgcagtcaggagtgcctcaccggttctccggtccggt ccggtactgatttaccctgaccttctccctgcaaccgg aggacttcgtactactactgccaagcagtcgtactccacc cctacacttccggacaaggcaccaggctgaaatcaag accactacccagcaccgaggccaccaccccggtcct accatcgctccagcctctgtccctgcgtccggaggcatg tagaccgcgagctgggtggggccgtgcataccggggtctt gacttcgctcgcgatactacatttgggccccttggtggtgta cttgccgggtcctgtgcttctactcgtgatcactttactgta agcgcgggtcggaagaagctgctgtacatcttaagcaacc cttcatgaggcctgtgcagactactcaagaggaggacgg ctgttcatgccggttcccagaggaggaggaaggcggctg cgaactgcgcgtgaaattcagccgcagcgcagatgtcc agcctaccagcaggggcagaaccagctctacaacgaac tcaatcttggtcggagagaggagtacgacgtgctggaca agcggagaggacgggaccagaaatgggcgggaagc

		cgcgagaaagaatccccaagagggcctgtacaacga gctccaaaaggataagatggcagaagcctatagcgaga ttggatgaaaggggaacgcagaagaggcaaaggcca cgacggactgtaccagggactcagcaccgccaccaagg acacatgacgctcttcacatgcaggccctgccgctcg g (SEQ ID NO: 1073)
SP-Linker 4 – ERmut1 – Furin cleavage site 2 – CD19 CAR2	MALPVTALLPLALLLHAARPN SLALSLTADQMVSALLDAEPPI LYSEYDPTRPFSEASMMGLLT NLADRELVHMINWAKRVPGF VDLALHDQVHLLCAWMEILM IGLVWRSMEHPGKLLFAPNLL LDRNQGKCVVEGGVEIFDMLLA TSSRFRMMNLQGEFVCLKSI ILLNSGVYTFLSSTLKSLEEKD HIHRVLDKITDTLIHLMKAGLT LQQQHQLAQLLLILSHIRHM SSKRMEHLYSMKCKNVVPLS DLLLEMLDAHRLGTGAEDPRP SRKRRSLGDVGEIVMTQSPAT LSLSPGERATLSCRASQDISK YLNWYQQKPGQAPRLIYHTS RLHSGIPARFSGSGSGTDYTL TISSLQPEDFAVYFCQQGNTL PYTFGQGTKLEIKGGGGSGG GGSGGGGSQVQLQESGPG VKPSETLSLTCTVSGVSLPDY GVSWIRQPPGKGLEWIGVIW GSETYYSSSLKSRVTISKDN SKNQVSLKLSSVTAADTAVYY CAKHYYYGGSYAMDYWGQG TLVTVSSTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAV HTRGLDFACDIYIWAPLAGTC GVLLLSLVITLYCKRGRKLLYI FKQPFMRPVQTTQEEDGCSC RFPEEEEGGCELRVKFSRSA DAPAYQQGQNQLYNELNLGR REEYDVLDRRGRDPEMGGK PRRKNPQEGLYNELQKDKMA EAYSEIGMKGERRRRGKHDG LYQGLSTATKDTYDALHMQAL PPR (SEQ ID NO: 1014)	atggccctccctgtcaccgcccgtgcttccgctggctcttc tgctccacgcccgtcgcccaactcgttggcactttccctga ctgccgaccagatgggtgctcgccctcttgacgccgagcc tccaattctgtactcggagtacgatccgactcgccggttctc cgaagccagcatgatggcctgttgactaactggcgga ccgaggttgggtgcacatgattaactgggctaagcgggtg ccgggcttcgtggacctggccctgcacgaccaagtgcac ctcctggaatgcgcctggatggaatcctcatgatcgccct cgtgtggagatccatggagcatcccgaaagctcgtgttg caccacacccctcgttgatgcgaaccagggaatgcgt ggaaggggtgtcgagatttgcacatgctgctcgccacct ctcccggttccgatgatgaatcgcaggagagaagagttc gtgtgtgaagtcaatcatcctgtgaactccggggtctat accttctgagctcgaccctcaagtcactggaggaaaaa gaccacatccatcgctgctcgataagatcaccgacacc cttatccatctcatggcgaaggctggactgacctgcaaca gcagcaccagaggctggccagttgctgctgattctgagc cacatccggcacatgctcgaagaggatggaacacctg tacagcatgaagtgaagaacgctgctgctctgctcgatct gctcctggaaatgctggacgcgcacagactcggaaccg gcgcggaagacccccggccctccaggaagcgaaggctc cctcgagacgtgggtgaaattgtatgacctgacacc gccactctagccttcacccggtgagcgcgaacctgtc ttgagagcctccaagacatctcaaaataccttaattgt atcaacagaagccggacaggctcctgccttctgatcta ccacaccagccgctcattctggaatccctgccagggtc agcggtagcggatctgggaccgactacacctactatca gctcactgcagccagaggactcgtgctatttctgtcagc aagggaacacctgcccctacaccttgacaggggcacca agctcgagattaaagggtggagggtggcagcggaggagg gggtccggcggtggagggaagccagggtccaactccaaga aagcggaccgggtcttgaagccatcagaaactcttca ctgactgtactgtgagcggagtgtctctcccgattacggg gtgtcttgatcagacagccaccgggaaggggtctggaat ggattggagtattggggctctgagactactactactctc atccctcaagtcacgcgtcaccatctcaaaggacaactct aagaatcagggtgctactgaaactgtcatctgtgaccgcag ccgacaccgctgtactattgcgctaagcattactattatg gcgggagctacgcaatggattactggggacagggtactct ggtcaccgtgtccagcaccactacccagcaccgaggcc acccacccggctcctaccatcgctctccagcctctgtccc tgctccggaggcatgtagaccgcagctggtggggccg tgcataccgggggtctgacttcgctgcgatactacattg ggccctctgggtggtacttgccgggtcctgctgcttctactc gtgatcactcttactgtaagcgggtcggaagaagctgct gtacatcttaagcaaccttcagaggcctgtgcagacta ctcaagaggaggacggctgtcatgcccgttcccagagg aggaggaagggcggtgcgaactgcgcgtgaaattcagc cgagcgcagatgctccagcctaccagcaggggcagaa ccagctctacaacgaactcaatcttggtcggagagagga

		gtacgacgtgctggacaagcggagaggacgggaccca gaaatgggcggaagccgcgcagaaagaatccccaag agggcctgtacaacgagctccaaaaggataaatggca gaagcctatagcgagattggtatgaaaggggaacgcag aagaggcaaaggccacgacggactgtaccagggactc agcaccgccaccaaggacacctatgacgctctcacatg caggccctgccgcctcgg (SEQ ID NO: 1074)
SP-Linker 4 – ERmut2 – Furin cleavage site 2 – CD19 CAR2	MALPVTALLPLALLHAARPN SLALSLTADQMVSALLDAEPPI LYSEYDPTRPFSEASMMGLLT NLADRELVHMINWAKRVPGF VDLTLHDQVHLLCAWMEILM IGLVWRSMEHPGKLLFAPNLL LDRNQGKCEGGVEIFDMLLA TSSRFRMMNLQGEFVCLKSI ILLNSGVYTFLSSTLKSLEEKD HIHRVLDKITDTLIHLMAKAGLT LQQQHQRRLAQLLLILSHIRHM SNKRMEHLYSMKCKNVVPLS DLLLEMLDAHRLGTGAEDPRP SRKRRSLGDVGEIVMTQSPAT LSLSPGERATLSCRASQDISK YLNWYQQKPGQAPRLIYHTS RLHSGIPARFSGSGSGTDYTL TISSLQPEDFAVYFCQQGNTL PYTFGQGTKLEIKGGGGSGG GGSGGGGSQVQLQESGPG VKPSETSLTCTVSGVSLPDY GVSWIRQPPGKGLEWIGVIW GSETYYSSSLKSRVTISKDN SKNQVSLKLSSVTAADTAVYY CAKHYYYGGSYAMDYWGQG TLVTVSSTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAV HTRGLDFACDIYWAPLAGTC GVLLLSLVITLYCKRGRKLLYI FKQPFMRPVQTTQEEDGCSC RFPEEEEGGCELRVKFSRSA DAPAYQQGQNQLYNELNLGR REEYDVLDRRRGRDPEMGGK PRRKNPQEGLYNELQKDKMA EAYSEIGMKGERRRRGKHDG LYQGLSTATKDTYDALHMQAL PPR (SEQ ID NO: 1015)	atggccctccctgtcaccgcccctgtgcttccgtggtcttc tgctccacgcccgtcggcccaactcgttggcactttccctga ctgccgaccagatggtgtcggccctcttgacgccgagcc tccaattctgtactcggagtagatccgactcggccgttctc cgaagccagcatgatggcctgttgactaactggcgga ccgcgagttggtgcacatgattaactgggctaagcgggtg ccgggctcgtggacctgaccctgcacgaccaagtgcac ctcctggaatgcgcctggatggaatcctcatgatcgccct cgtgtggagatccatggagcatcccgaaagctcctgtttg caccacacctcctgtgtatgcgaaccagggaatgcgt ggaaggggtgtcgagatttgcacatgctgctcgccacct cttcccggttccgatgatgaatctgcaggagagaagagttc gtgtgtgaagtcaatcatcctgtgaactccggggtctat accttctgagctcgaccctcaagtcactggaggaaaaa gaccacatccatcgctgtcgtatagatcaccgacacc cttatccatctcatggcgaaggctggactgaccctgcaaca gcagcaccagaggctggcccagttgctgtgattctgagc cacatccggcacatgtcgaacaagaggatggaacacct gtacagcatgaagtgaagaacgtcgtgcctctgtccgat ctgctcctggaaatgtggacgcgcacagactcggaaacc ggcgcggaagacccccggccctccaggaagcgaagggt ccctcggagacgtgggtgaaattgtatgaccagtcacc cgccactcttagcctttaccgggtgagcgcgaaccctgt cttgagagcctccaagacatctcaaaataccttaattgg tatcaacagaagcccgacagggtcctgccttctgatcta ccacaccagccggtccattctggaatccctgccagggtc agcggtagcggatctgggaccgactacaccctcactatca gctcactgcagccagaggactcgtgtctatttctgtcagc aagggaacaccctgccctacaccttggacagggcacca agctcgagattaaggtggaggtggcagcggaggagggt gggtccggcggtggagggaagccagggtccaactccaaga aagcggaccgggtctgtgaagccatcagaaactcttca ctgactgtactgtgagcggaggtgtctctcccgattacggg gtgtcttgatcagacagccaccgggaaggggtctggaat ggattggagtattggggctctgagactacttactacttctc atccctcaagtcacgcgtcaccatctcaaaggacaactct aagaatcagggtgtcactgaactgtcatctgtgaccgcag ccgacaccgctgtactattgcgctaagcattactattatg gctcaccgtgtccagcaccactacccagcaccgaggcc acccaccccggtcctaccatcgctctccagcctctgtccc tgctccggaggcatgtagaccgcagctggtggggcgg tgcataccgggggtctgacttcgctgcgatactacattg ggccctctgggtggtacttgccgggtcctgctgcttctactc gtgatcactcttactgtaagcgggtcggaagaagctgt gtacatcttaagcaaccctcatgaggcctgtgcagacta ctcaagaggaggacgggtgtcatgcccgttccagagg aggaggaagggcggtgcgaactgcgctgaaattcagc cgacgcgagatgtccagcctaccagcaggggcagaa

		ccagctctacaacgaactcaatcttggtcggagagagga gtacgacgtgctggacaagcggagaggacgggaccca gaaatgggcggaagccgcgcagaaagaatcccaag agggcctgtacaacgagctccaaaaggataagatggca gaagcctatagcgagattggtatgaaaggggaacgcag aagaggcaaaggccacgacggactgtaccagggactc agcaccgccaccaaggacacctatgacgctctcacatg caggccctgccgcctcgg (SEQ ID NO: 1075)
SP-Linker 4 – ERmut1 – Furin cleavage site 3 – CD19 CAR2	MALPVTALLPLALLHAARPN SLALSLTADQMVSALLDAEPP LYSEYDPTPRFSEASMMGLLT NLADRELVHMINWAKRVPGF VDLALHDQVHLLCAWMEILM IGLVWRSMHEHPGKLLFAPNLL LDRNQGKCVGGVEIFDMLLA TSSRFRMMNLQGEFVCLKSI ILLNSGVYTFLSSTLKSLEEKD HIHRVLDKITDTLIHLMKAGLT LQQQHQRQAQLLLSHIRHM SSKRMEHLYSMCKKNVPLS DLLLEMLDAHRLGTGAEDPRP SRKRREIVMTQSPATLSLSPG ERATLSCRASQDISKYNWYQ QKPGQAPRLLIYHLSRLHSGIP ARFSGSGSGTDYTLTISLQ EDFAVYFCQQGNTLPYTFGQ GTKLEIKGGGSGGGSGGG GSQVQLQESGPGLVKPS SLTCTVSGVSLPDYGVSWIRQ PPGKGLEWIGVIWGSETTYYS SSLKSRVTISKDNSKNQVSLK LSSVTAADTAVYYCAKHYYYG GSYAMDYWGQGTLLTVSSTT TPAPRPPTPAPTIASQPLSLRP EACRPAAGGAVHTRGLDFAC DIYIWAPLAGTCGVLLLSLVITL YCKRGRKKLLYIFKQPFMRPV QTTQEEDGCSCRFPEEEEGG CELRVKFSRSADAPAYQQGQ NQLYNELNLGRREEYDVLK RRGRDPEMGGKPRRKNPQE GLYNELQKDKMAEAYSEIGMK GERRRGKGDHGLYQGLSTAT KDYDALHMQALPPR (SEQ ID NO: 1016)	atggccctccctgtcaccgcctgtgcttccgtggctctc tgctccacgccgctcggcccaactcgttggcacttccctga ctgccgaccagatggtgtccgcctcttgacgccgagcc tccaattctgtactcggagtagatccgactcgcctgtctc cgaagccagcatgatggcctgttgactaacctggcggga ccgcgagttggtgcacatgattaactgggctaagcgggtg ccgggctcgtggacctggccctgcacgaccaagtgcac ctcctggaatgcgcctggatggaatcctcatgatcggcct cgtgtggagatccatggagcatcccgaaagctcctgtttg caccacacctcctgctgtatgcgaaccagggaatgcgt ggaaggggtgtcgagatttgcacatgctgctcgccacct ctcccggttccgatgatgaatctgcaggagagaagagttc gtgtgtgaagtcaatcatcctgctgaactccggggtctat acctcctgagctcgaccctcaagtcactggaggaaaaa gaccacatccatcgctgtcgtcgataagatcaccgacacc cttatccatctcatggcgaaggctggactgacctgcaaca gcagcaccagaggctggccagttgctgtgattctgagc cacatccggcacatgtcgtccaagaggatggaacacctg tacagcatgaagtgaagaacgctgctcctctgtccgatct gctcctggaaatgctggacgcgcacagactcgggacgg gagctgaagatccacgaccagcagaaagcgacggga aattgtgatgaccagtcaccgccactctagccttcacc cggtagcgcgcgaaccctgtctgcagagcctccaaga catctcaaaataccttaattggtatcaacagaagcccgga caggctcctgccttctgatctaccacaccagccggctcca ttctggaatccctgccagggtcagcggtagcggatctggga ccgactacaccctcactatcagctcactgcagccagagg acttgcgtgtctatttctgtcagcaagggaacaccctgccct acaccttggacagggcaccaagctcgagattaaagggtg gagggtggcagcggaggagggtgggtccggcggtggagg aagccaggccaactccaagaaagcggaccgggtctgt gaagccatcagaaactcttactgactgtactgtgagcg gagtgctctccccgattacggggtgtcttgatcagacag ccaccggggaagggtctggaatggattggagtgtattggg gctctgagactacttactcttcatccctcaagtcacgcgt caccatctcaaaggacaactctaagaatcaggtgtcactg aaactgtcatctgtgaccgcagccgacaccgcgtgtact attgcgctaagcattactattatggcgggagctacgcaatg gattactggggacaggggtactctggtcaccgtgtccagca ccactacccagcaccgaggccacccacccggctccta ccatcgccctccagcctctgtccctgcgtccggaggcatgt agaccgcagctggtggggccgtgcataccgggggtctt gactcgcctcgcgatactacatttggccctctggctggtg cttgccgggtcctgtgcttctactcgtgatcacttctactgta agcgggtcggaagaagctgctgtacatcttaagcaacc cttcatgaggcctgtgcagactactcaagaggaggacgg ctgttcatgccggttccagaggaggaggaaaggcggctg cgaactgcgcgtgaaattcagccgcagcgcagatgctcc

		agcctaccagcaggggcagaaccagctctacaacgaac tcaatcttggtcggagagaggagtagcagctgctggaca agcggagaggacgggaccagaaatggcggggaagc cgcgagaaagaatccccaagaggcctgtacaacga gctccaaaaggataagatggcagaagcctatagcgaga ttggtatgaaaggggaacgcagaagaggcaaggcca cgacggactgtaccagggactcagcaccgccaccaagg acacatgacgctcttcacatgcaggccctgccgctcg g (SEQ ID NO: 1076)
SP-Linker 4 – ERmut2 – Furin cleavage site 3 – CD19 CAR2	MALPVTALLPLALLHAARPN SLALSLTADQMVSALLDAEPP LYSEYDPTPRFSEASMMGLLT NLADRELVHMINWAKRVPGF VDLTLHDQVHLLCAWMEILM IGLVWRSMHEHPGKLLFAPNLL LDRNQGKCVGGVEIFDMLLA TSSRFRMMNLQGEFVCLKSI ILLNSGVYTFLSSTLKSLEEKD HIHRVLDKITDTLIHLMAKAGLT LQQQHQLAQLLILSHIRHM SNKRMEHLYSMKCKNVVPLS DLLLEMLDAHRLGTGAEDPRP SRKRREIVMTQSPATLSLSPG ERATLSCRASQDISKYNWYQ QKPGQAPRLLIYHLSRLHSGIP ARFSGSGSGTDYTLTISSLQP EDFAVYFCQQGNTLPYTFGQ GTKLEIKGGGSGGGSGGG GSQVQLQESGPGLVKPSSETL SLTCTVSGVSLPDYGVSWIRQ PPGKGLEWIGVIWGSETTYYS SSLKSRVTISKDNSKNQVSLK LSSVTAADTAVYYCAKHYYYG GSYAMDYWGQGTLVTVSSTT TPAPRPPTPAPTIASQPLSLRP EACRPAAGGAVHTRGLDFAC DIYIWAPLAGTCGVLLLSLVITL YCKRGRKKLLYIFKQPFMRPV QTTQEEDGCSCRFPETEEGG CELRVKFSRSADAPAYQQGQ NQLYNELNLGRREEYDVLDK RRGRDPEMGGKPRRKNPQE GLYNELQDKMAEAYSEIGMK GERRRGKGDGLYQGLSTAT KDYDALHMQALPPR (SEQ ID NO: 1017)	atggccctccctgtcaccgccctgtgcttccgtggtcttc tgctccacgccgctcggcccaacTcgttggtcacttccctg actgccgaccagatggtgtccgccctcttgacgccgagc ctccaattctgtactcggagtagatccgactcgcctgtct ccgaagccagcatgatgggcctgttgactaacctggcgg accgcgagttggtgcacatgattaactgggctaagcgggt gccgggcttcgtggacctgacctgcacgaccaagtga cctcctggaatgcgcctggatggaaatcctcatgatcgcc tcgtgtggagatccatggagcatcccgaaagctcctgttt gcaccaacctcctgttgatcgcaaccagggaataatgc gtggaagggggtgtcgagatttgcacatgtgtcgcac ctctcccggttcggatgatgaatctgcagggaagaggt tcgtgtgtctgaagtcaatcctgtgtaactccgggtct ataccttcctgagctcgacctcaagtactggaggaaaa agaccacatccatcgctgtcgataagatcaccgacac ccttatccatctcatggcgaaggctggactgacctgcaac agcagcaccagaggctggccagttgtgtgattctgag ccacatccggcacatgtcgaaagaggatggaacacc tgtacagcatgaagtgaagaacgtgtgctctgtccgat ctgtcctggaaatgtgtgacgcgcacagactGggacg ggagctgaagatccacgaccagcagaaagcgacggg aaattgtatgacctcagcaccgacctttagcctttcac ccggtgagcgcgaacctgtctgtcagagcctcccaag acatctcaaaataccttaattggtatcaacagaagcccg acaggctcctgcctctgtatctaccacaccagccggtcc attctggaatccctgccaggttagcggtagcggatctggg accgactacacctcactatcagctcactgcagccagag gacttcgtgtctattctgtcagcaagggaacacctgcc tacaccttgacagggcaccaagctcgagattaaagggtg gaggtggcagcggaggaggtgggtccggcggtggagg aagccaggccaactccaagaaagcggaccgggtctgt gaagccatcagaaactcttactgactgtactgtgagcg gagtgctctccccgattacggggtgtcttgatcagacag ccaccgggaagggtctggaatggattggagtgattggg gctctgagactactactcttcatccctcaagtcacgcgt caccatctcaaaggacaactctaagaatcagggtgtcactg aaactgtcatctgtgaccgcagccgacaccgctgtact attgcgctaagcattactattatggcgggagctacgcaatg gattactggggacaggggtactctggtaccgtgtccagca ccactacccagcaccgaggccacccacccggctccta ccatcgctcccagcctctgtccctgcgtccggaggcatgt agaccgcagctggtggggcgtgcatacccggggtctt gactcgctcgcgatactacatttggccctctggctggtgta cttggggtcctgtgcttctactcgtgatcactttactgta agcgggtcggaagaagctgtgtacatcttaagcaacc cttcatgaggcctgtgcagactactcaagaggaggacgg ctgtcatgccggtcccagaggaggaggaaggcggctg

		cgaactgcgcgtgaaattcagccgcagcgcagatgctcc agcctaccagcaggggcagaaccagctctacaacgaac tcaatcttggtcggagagaggtagcagctgctggaca agcggagaggacgggaccagaaatggcggggaagc cgcgagaaagaatcccaagaggcctgtacaacga gctccaaaaggataagatggcagaagcctatagcgaga ttggtatgaaaggggaacgcagaagaggcaaggcca cgacggactgtaccaggactcagcaccgccaccaagg acacctatgacgctcttcacatgcaggccctgccgcctcg (SEQ ID NO: 1077)
SP-Linker 4 – ERmut1 – Furin cleavage site 2 – CD123 CAR	MALPVTALLPLALLHAARPN SLALSLTADQMVSALLDAEPPI LYSEYDPTPRFSEASMMGLLT NLADRELVHMINWAKRVPGF VDLALHDQVHLLCAWMEILM IGLVWRSMHEHPGKLLFAPNLL LDRNQGKCVEGGVEIFDMLLA TSSRFRMMNLQGEFVCLKSI ILLNSGVYTFLSSTLKSLEEKD HIHRVLDKITDTLIHLMKAGLT LQQQHQRRLAQLLLILSHIRHM SSKRMEHLYSMKCKNVVPLS DLLLEMLDAHRLGTGAEDPRP SRKRRSLGDVGQVQLVQSGA EVKKPGASVKVSCASGYTFT GYMHWWVRQAPGQGLEWM GWINPNSGGTNYAQKFQGRV TLTRDTSISTVYMELSRLRSD DTAVYYCARDMNILATVPFDI WGQGTMTVTVSSGGGSGGG GSGGGGSDIQMTQSPSSLSA SVGDRVTITCRASQSISSYLN WYQQKPGKAPKLLIYAASSLQ SGVPSRFSGSGSGTDFLT NSLQPEDFATYYCQQGDSVP LTFGGGTRLEIKTTTPAPRPPT PAPTIASQPLSLRPEACRPAA GGAVHTRGLDFACDIYWAPL AGTCGVLLLSLVITLYCKRGRK KLLYIFKQPFMRPVQTTQEED GCSCRFPETEEEGGCELRVKF SRADAPAYQQGQNQLYNEL NLGRREEYDVLDRRGRDPE MGGKPRRKNPQEGLYNELQK DKMAEAYSEIGMKGERRRGK GHDGLYQGLSTATKDTYDAL HMQALPPR (SEQ ID NO: 1018)	atggccctccctgtcaccgccctgctgctccgctggctctc tgctccacgcgcgtcggcccaactcgtggcacttccctga ctgccgaccagatggtgtccgccctctggacgccgagcc tccaattctgtactcggagtagatccgactcgcctgtctc cgaagccagcatgatggcctgttgactaacctggcgga ccgcgagttggtgcacatgattaactgggctaagcgggtg ccgggctcgtggacctggccctgcacgaccaagtgcac ctcctggaatgcgcctggatggaatcctcatgatcggcct cgtgtggagatccatggagcatcccgaaagctcctgtttg caccacacctcctgctgtatcgcaaccagggaagatgcgt ggaaggggtgtcgagatttgcacatgctgctcgccacct cttcccggttccggtgatgaatctgcaggagagaagagttc gtgtgtctgaagtcaatcatcctgctgaactccggggtctat acctcctgagctcgaccctcaagtcactggaggaaaaa gaccacatccatcgctgctcgataagatcaccgacacc cttatccatctcatggcgaaggctggactgacctgcaaca gcagcaccagaggctggccagttgctgctgattctgagc cacatccggcacatgtctccaagaggatggaacacctg tacagcatgaagtgaagaacgctgctcctctgctcgatct gctcctggaaatgctggacgcgcacagactcggaaccg gcgcggaagacccccggccctccaggaaagcgaaggctc cctcgagacgtgggtcaagtgaactcgtccaaagcgg agcgggaagtcaagaaacccggagcgagcgtgaagtg tctgcaaagcctccggctacacctttacgggctactacat gactgggtgcgccaggcaccaggacagggtcttgaatg gatgggatggatcaaccctaattcgggcggaactaactac gcacagaagtccaggggagagtgactctgactcgggat acctccatctcaactgtctacatggaactctcccgttgagg tcagatgatacgcgagtgactactgcgccgcgacatga atatcctggctaccgtgcccgttcgacatctggggacaggg gactatggttactgtctcatcgggcgggtggaggttcaggag gaggcggctcgggaggcggaggttcggacattcagatg accagtcctccatcctctgtcggccagcgtcggagata gggtgaccattacctgtcgggctcgcgaagcatctcctcg tacctcaactggatcagcaaaagccgggaaggcgct aagctgctgatctacgcgcgttcgagctgcaaaagcggg tgccatccagattctcgggatcaggctcaggaaaccgactc acctgaccgtgaacagcctccagccggaggactttgcc acttactactgccagcaggagactcgcgtgccgttacttcc gggggggggtaccgcctggagatcaagaccactacccc agcaccgaggccacccaccccgctcctaccatgcctc ccagcctctgtccctgcgtccggaggcatgtagaccgcga gctggtggggccgtgcatacccggggtcttgactcgcctg cgatatctacatttgggccctctggctggtacttgcgggt cctgctgcttactcgtgatcactcttactgtaagcgcggtc ggaagaagctgctgtacatcttaagcaaccctcatgagg

		cctgtgcagactactcaagaggaggacggctgttcatgcc gggtcccagaggaggaggaaaggcggctgcaactgcgc gtgaaattcagccgcagcgagatgtccagcctaccag caggggcagaaccagctctacaacgaactcaatcttgt cggagagaggagtacgacgtgctggacaagcggagag gacgggacccagaaatgggcgggaagccgcgcagaa agaatccccaagaggggcctgtacaacgagctccaaaag gataagatggcagaagcctatagcgagattggtatgaaa ggggaacgcagaagaggcaaaggccacgacggactgt accagggactcagcaccgccaccaaggacacctatgac gctcttcacatgcaggccctgccgcctcgg (SEQ ID NO: 1078)
SP-Linker 4 – ERmut2 – Furin cleavage site 2 – CD123 CAR	MALPVTALLPLALLLHAARPN SLALSLTADQMVSALLDAEPP LYSEYDPTTRPFSEASMMGLLT NLADRELVHMINWAKRVPGF VDLTLHDQVHLLCAWMEILM IGLVWRSMHPGKLLFAPNLL LDRNQGKCVGGVEIFDMLLA TSSRFRMMNLQGEFVCLKSI ILLNSGVYTFLSSTLKSLEEKD HIHRVLDKITDTLIHLMAGALT LQQQHQRALQALLILSHIRHM SNKRMEHLYSMKCKNVVPLS DLLLEMLDAHRLGTGAEDPRP SRKRRSLGDIVGQVQLVQSGA EVKKPGASVKVSCASGYTFT GYMHWWVRQAPGGGLEWM GWINPNSGGTNYAQKFQGRV TLTRDTSISTVYMELSRRLSD DTAVYYCARDMNILATVPFDI WGQGTMTVTVSSGGGSGGG GSGGGGSDIQMTQSPSSLSA SVGDRVTITCRASQSISSYLN WYQQKPKGKAPKLLIYAASSLQ SGVPSRFSGSGSGTDFTLTV NSLQPEDFATYYCQQGDSVP LTFGGGTRLEIKTTTPAPRPPT PAPTIASQPLSLRPEACRPAA GGAVHTRGLDFACDIYWAPL AGTCGVLLLSLVITLYCKRGRK KLLYIFKQPFMRPVQTTQEED GCSCRFEEEEEGGCELRVKF GRSADAPAYQQGQNQLYNEL NLGRREEYDVLDKRRGRDPE MGGKPRRKNPQEGLYNELQK DKMAEAYSEIGMKGERRRGK GHDGLYQGLSTATKDTYDAL HMQALPPR (SEQ ID NO: 1019)	atggccctccctgtcaccgccctgtgcttccgtggctcttc tgctccacgccgctcggcccaacTcgttggcactttccctg actgccgaccagatggtgtccgcccttctggacgccgagc ctccaattctgtactcggagtagatccgactcggcgttct ccgaagccagcatgatgggcctgttgactaacctggcgg accgcgagttggtgcacatgattaactgggctaagcgggt gccgggctcgtggacctgacctgcacgaccaagtga cctcctggaatgcgcctggatggaaatcctcatgatcggcc tcgtgtggagatccatggagcatcccggaagctcctgtt gcaccaacctcctgtgtgatcgcaaccagggaatgc gtggaaggggtgtcgagatttgcacatgtgctcgccac ctctcccggttccggatgatgaatctgcaggagagaagagt tcgtgtgtctgaagtcaatcatcctgctgaactccgggtct ataccttctgagctcgacctcaagtactggaggaaaa agaccacatccatcgcgtgtcgataagatcacggacac ccttatccatctcatggcgaaggctggactgacctgcaac agcagcaccagaggctggcccggtgtgctgattctgag ccacatccggcacatgtcgaaagaggatggaacacc tgtacagcatgaagtgaagaacgtcgtgctctgtccgat ctgctcctggaaatgtcggacgcgcacagactcggaacc ggcgcggaagacccccggccctccaggaagcgaaggt ccctcggagacgtgggtcaagtgaactcgtcacaagcg gagcgggaagtcaagaaacccggagcgagcgtgaaagt gtcctgcaaagcctccggctacacctttacgggtactaca tgactgggtgcgccaggcaccaggacagggcttgaat ggatgggatggatcaaccctaattcggggcggaactaacta cgacagaagttccaggggagagtgactctgactcggga tacctccatctcaactgtctacatggaactctcccgcttgcg gtcagatgatacggcagtgactactgcgcccgacatg aatatcctggctaccgtgcgttcgacatctgggacagg ggactatgggtactgtctatcgggcgggtggaggttcagga ggaggcggctcgggaggcggaggttcggacattcagat gaccagtcctccatcctctctgtcggccagcgtcggagat agggtgaccattacctgtcgggcctcgcaagcatctcctc gtacctcaactggtatcagcaaaagccgggaaggcgc ctaagctgtgatctacgcgcgttcgagcttgaagcgg ggtgccatccagattctcgggatcaggctcaggaaccga cttcacctgaccgtgaacagcctccagccggaggacttt gccacttactactgccagcaggagactccgtgccgctta ctttcgggggggtaccgcctggagatcaagaccacta ccccagcaccgaggccacccaccccggtcctaccatcg cctccagcctctgtcctgtcgtcggaggcatgtagacc gcagctggtggggccgtgcatacccggttctgacttcg cctgcgatctacatttgggccctctggctggtacttcgg

		ggctcgtgctttcactcgtgatcactcttactgtaagcgcg gtcgaagaagctgctgtacatcttaagcaaccctcatg aggcctgtgcagactactcaagaggaggacggctgtcat gccggtcccagaggaggaggaaggcggctgcgaactg cgcgtgaaattcagccgcagcgcagatgctccagcctac cagcaggggcagaaccagctctacaacgaactcaatctt ggtcggagagaggagtacgacgtgctggacaagcggga gaggacgggaccagaaatgggcgggaagccgcgca gaaagaatcccaagagggcctgtacaacgagctcaa aaggataagatggcagaagcctatagcgagattggtatg aaaggggaacgcagaagaggcaaaggccacgacgg actgtaccagggactcagcaccgccaccaaggacacct atgacgctcttcacatgcaggccctgccgcctcgg (SEQ ID NO: 1079)
SP-Linker 4 – ERmut1 – Furin cleavage site 3 – CD123 CAR	MALPVTALLPLALLLHAARPN SLALSLTADQMVSALLDAEPPI LYSEYDPTTRPFSEASMMGLLT NLADRELVHMINWAKRVPGF VDLALHDQVHLLCAWMEILM IGLVWRSMEHPGKLLFAPNLL LDRNQGKCVEGGVEIFDMLLA TSSRFRMMNLQGEFVCLKSI ILLNSGVYTFLSSTLKSLEEKD HIHRVLDKITDTLIHLMAKAGLT LQQQHQRQAQLLLILSHIRHM SSKRMEHLYSMKCKNVVPLS DLLLEMLDAHRLGTGAEDPRP SRKRRQVQLVQSGAEVKKPG ASVKVSKASGYTFTGYMH WVRQAPGQGLEWMGWINPN SGGTNYAQKFQGRVTLTRDT SISTVYMELSRRLRSDDTAVYY CARDMNILATVPFDIWQGQTM VTVSSGGGGSGGGGSGGGG SDIQMTQSPSSLSASVGDRT ITCRASQSISSYLNWYQQKPG KAPKLLIYAASSLQSGVPSRFS GSGSGTDFTLTVNSLQPEDFA TYYCQQGDSVPLTFGGGTRL EIKTTTPAPRPPTPAPTIASQP LSLRPEACRPAAGGAVHTR GLDFACDIYIWAPLAGTCG VLLLSLVITLYCKRGRKLL YIFKQPFMRPVQTTQEEDG CSCRFPEEEEEGGCELRVK FSRSADAPAYQQGQNQLY NELNLGRREEYDVLDKRR GRDPEMGGKPRRKNPQE GLYNELQKDKMAEAYSEIG MKGERRRGKGHDGLYQGL STATKDTYDALHMQALPPR (SEQ ID NO: 1020)	atggccctccctgtcaccgccctgctgcttccgctggctctt tgctccacgccgctcggcccaactcgttggcactttccctga ctgccgaccagatgggtgtccgccttctggacgccgagcct ccaattctgtactcggagtacgatccgactcggcgttctcc gaagccagcatgatgggcctgttgactaacctggcggacc gcgagttgggtgcacatgattaactgggctaagcgggtgccg ggcttcgtggacctggcctgcacgaccaagtgcacctcct ggaatgcgcctggatggaaatcctcatgatcgccctcgtgt ggagatccatggagcatcccgaaagctcctgtttgaccc aacctcctgcttgatcgcaaccagggaaatgcgtggaag ggggtgtcgagattttcgacatgctgctgccacctcttccc ggttccgatgatgaatctgcaggagagaagagttcgtgtgt ctgaagtcaatcatcctgctgaactccggggtctataccttc ctgagctcgacctcaagtcactggaggaaaaagaccaca tccatcgctgctcgataagatcaccgacaccttatccatc tcattggcgaaggctggactgacctgcaacagcagcacca gaggctggcccagttgctgctgattctgagccacatccggc acatgtcgtccaagaggatggaacacctgtacagcatgaa gtgcaagaacgtcgtgcctctgtccgatctgctcctggaat gctggacgcgcacagactcggaaccggcgcggaagaccc ccggccctccaggaagcgaaggcaagtgaactcgtccaa agcggagcgggaagtcaagaaaccggagcgagcgtgaaa gtgtcctgcaaagcctccggctacacctttacgggctactac atgcactgggtgcgccaggcaccaggacagggtcttgaat ggatgggatggatcaaccctaattcgggcggaactaacta cgacagaagttccaggggagagtactctgactcgggat acctccatctcaactgtctacatggaactctcccgttgccg tcagatgatacggcagtgactactgcgcccgacatgaa tatcctggctaccgtgccgttcgacatctggggacagggga ctatgggtactgtctcatcgggcgggtggaggttcaggagga ggcggctcgggaggcggaggttcggacattcagatgaccc agtccccatcctctctgtcggccagcgtcggagatagggtg accattacctgtcgggcctcgaaagcatctcctgtacctc aactggtatcagaaaagccgggaaaggcgctaagctgc tgatctacgccgttcgagcttcaaagcggggtgcatcc agattctcgggatcaggctcaggaaccgacttcacctgac

		cgtaacagcctccagccggaggactttgccacttactact gccagcagggagactccgtgccgttactttcgggggggt acccgctggagatcaagaccactacccagcaccgaggc caccaccccggtcctaccatcgctcccagcctctgtccc tgctccggaggcatgtagaccgcagctgggtggggcgt gcatacccggggtcttgacttcgctgcgatctacatttg ggccctctggctggtacttgcggggtctgtgctttcactc gtgatcactctttactgtaagcgcggtcgaagaagctgct gtacatctttaagcaaccctcatgaggcctgtgcagactac tcaagaggaggacggctgttcatgccggttccagaggag gaggaaggcggtgcgaactgcgctgaaattcagccga gcgcagatgctccagcctaccagcaggggcagaaccagct ctacaacgaactcaatcttggtcggagagaggagtacgac gtgctggacaagcggagaggacgggaccagaaatgggc gggaagccgcgcagaaagaatcccaagaggcgctgtac aacgagctccaaaaggataagatggcagaagcctatagc gagattggtatgaaaggggaacgcagaagaggcaaggc cacgacggactgtaccagggactcagcaccgccaccaagg acacctatgacgctcttcacatgcaggccctgccgctcgg (SEQ ID NO: 1080)
SP-Linker 4 – ERmut2 – Furin cleavage site 3 – CD123 CAR	MALPVTALLPLALLHAARPN SLALSLTADQMVSALLDAEPPI LYSEYDPTRPFSEASMMGLLT NLADRELVHMINWAKRVPGF VDLTLHDQVHLLCAWMEILM IGLVWRSMEHPGKLLFAPNLL LDRNQGKCVEGGVEIFDMLLA TSSRFRMMNLQGEFVCLKSI ILLNSGVYTFLSSTLKSLEEKD HIHRVLDKITDTLIHLMAGALT LQQQHQRQAQLLLILSHIRHM SNKRMEHLYSMKCKNVVPLS DLLLEMLDAHRLGTGAEDPRP SRKRRQVQLVQSGAEVKKPG ASVKVSCASGYTFTGYMH WVRQAPGQGLEWMGWINPN SGGTNYAQKFQGRVTLTRDT SISTVYMELSRLRSDDTAVYY CARDMNILATVPFDIWGGTM VTVSSGGGSGGGGSGGGG SDIQMTQSPSSLSASVGDRV ITCRASQSISSYLNWYQKPG KAPKLLIYAASSLQSGVPSRFS GSGSGTDFTLTVNSLPEDFA TYQCQGDVPLTFGGGTRL EIKTTTPAPRPPTPAPTASQP LSLRPEACRPAAGGAVHTRG LDFACDIYWAPLAGTCGVLL SLVITLYCKRGRKKLLYIFKQP FMRPVQTTQEEDGCSCRFPE EEEGGCELRVKFSRSADAPA YQQGQNQLYNELNLGRREEY DVLDKRRGRDPEMGGKPRRK	atggccctccctgtaccgcccgtgcttccgctggctcttc tgctccacgcgctcggcccaacTcggtggcactttccctg actgccgaccagatggtgtccgcccctctggacgcccagc ctccaattctgtactcggagtagcgaatccgactcggcgttct ccgaagccagcatgatgggcctgttgactaacctggcgg accgcgagttggtgcacatgattaactgggctaagcgggt gccgggcttcgtggacctgacctgcacgaccaagtga cctcctggaatgcgctggatggaaatcctcatgatcgcc tcgtgtggagatccatggagcatcccgaaagctcctgttt gcaccaaacctcctgcttgatcgcaaccagggaatgc gtggaagggggtgcgagatttgcacatgctgctgccac ctctcccggtccggatgatgaatctgcaggagagaagagt tcgtgtgtctgaagtaactcatcctgctgaactccggggtct atacctcctgagctcgacctcaagtcactggaggaaaa agaccacatccatcgctgctgataagatcaccgacac ccttatccatctcatggcgaaggctggactgacctgcaac agcagcaccagaggctggcccagttgctgctgattctgag ccacatccggcacatgtcgaacaagaggatggaacacc tgtacagcatgaagtgaagaacgtgctgctctgtccgat ctgctcctggaaatgtggaacgcgcacagactcgggacg ggagctgaagatccacgaccagcagaaagcgacggc aagtgaactcgtccaaagcggagcggaaagtcaagaaa cccgagcgcgagcgtgaaagtgcctgcaaagcctccggc tacaccttacgggctactacatgcactgggtgcgcaggc accaggacagggctctgaatggatggatggaatcaacct aattcgggcggaactaactacgcacagaagtccagggg agagtactctgactcgggatacctccatctcaactgtctac atggaactctccgctgctgagatgatacggcagtgta ctactgcgcccgcgacatgaatacctggctacgtgctg tcgacatctggggacaggggactatggtactgtctcatcg ggcgggtggaggtcaggaggaggcggctcgggaggcg gaggttcggacattcagatgacctcagctcccatcctctgt cggccagcgtcggagatagggtgaccattacgtcggg

	NPQEGLYNELQKDKMAEAYS EIGMKGERRRRGKHDGLYQG LSTATKDTYDALHMQALPPR (SEQ ID NO: 1021)	cctcgcaaagcatctcctcgtaacctcaactggtatcagcaa aagccgggaaaggcgccctaagctgctgatctacgccgt tcgagcttgcaaagcggggtgccatccagattctcggtat caggctcaggaaccgacttcacctgaccgtgaacagcc tccagccggaggactttgccacttactactgccagcaggg agactccgtgccgttactttcggggggggtacccgcctgg agatcaagaccactacccagcaccgaggccaccacc ccggctcctaccatcgctcccagcctctgtccctgcgtccg gaggcatgtagaccgcagctggtggggccgtgcatacc cggggtcttgacttcgctgcgatactacatttggggccctc tggctggtacttgccgggtcctgctgctttcactcgtgatcac tctttactgtaagcgcgggtcggaagaagctgctgtacatctt aagcaacccttcatgaggcctgtgcagactactcaagag gaggacggctgttcatgccggtcccagaggaggaggaa ggcggctgcgaactgcgcgtgaaattcagccgcagcgc agatgtccagcctaccagcaggggcagaaccagctcta caacgaactcaatcttggtcggagagaggagtacgacgt gctggacaagcggagaggacgggaccagaaaatgggc gggaagccgcgcagaaagaatcccaagagggcctgt acaacgagctccaaaaggataagatggcagaagcctat agcgagattggtatgaagggggaacgcagaagaggca aaggccacgacggactgtaccagggactcagcaccgcc accaaggacacctatgacgctcttcacatgcaggccctgc cgctcgg (SEQ ID NO: 1081)
SP-Linker 4 – ERmut1 – Furin cleavage site 2 – BCMA CAR	MALPVTALLLPLALLLHAARPN SLALSLTADQMVSALLDAEPPI LYSEYDPTPRPFSEASMMGLLT NLADRELVHMINWAKRVPGF VDLALHDQVHLLECAWMEILM IGLVWRSMEHPGKLLFAPNLL LDRNQGKCVEGGVEIFDMLLA TSSRFRMMNLQGEFVCLKSI ILLNSGVYTFLSSTLKSLEEKD HIHRVLDKITDTLIHLMAKAGLT LQQQHQLRAQLLLILSHIRHM SSKRMEHLYSMKCKNVVPLS DLLLEMLDAHRLGTGAEDPRP <u>SRKRRSLGDVGEVQLVESGG</u> GLVQPGGSLRLSCAVSGFALS NHGMSWVRRAPGKGLEWVS GIVYSGSTYYAASVKGRFTISR DNSRNTLYLQMNSLRPEDTAI YYCSAHGGESDVWGQGTVT VSSASGGGGSGGRASGGGG SDIQLTQSPSSLSASVGDRVTI TCRASQSISSYLNWYQQKPG KAPKLLIYAASSLQSGVPSRFS GSGSGTDFTLTISSLQPEDFA TYYCQQSYSTPYTFGQGTKV EIKTTTPAPRPPTPAPTIASQP LSLRPEACRPAAGGAVHTRG LDFACDIYWAPLAGTCGVLLL SLVITLYCKRGRKKLLYIFKQP FMRPVQTTQEEDGCSCRFPE EEEGGCELRVKFSRSADAPA YQQGQNQLYNELNLGRREEY	atggccctccctgtcaccgccctgctgctccgctggctcttc tgctccacgcgcgtcggcccaacTcgttggcactttccctg actgccgaccagatggtgtccgccccttctggacgccgagc ctccaattctgtactcggagtagatccgactcgcctgtct ccgaagccagcatgatgggcctgtgactaacctggcgg accgcgagttggtgcacatgattaactgggctaagcgggt gccgggctcgtggacctggccctgcacgaccaagtga cctcctggaatgcgcctggatggaaatcctcatgatcgcc tcgtgtggagatccatggagcatcccgaaagctcctgttt gcaccaacctcctgcttgatcgcaaccagggaatgc gtggaagggggtgtcagagatttcgacatgctgctgccac ctctcccggttccggatgatgaatctgcaggagagaagagt tcgtgtgtctgaagtcaatcatcctgctgaactccggggtct ataccttctgagctcgacctcaagtactggaggaaaa agaccacatccatcgctgctgataagatcacggacac ccttatccatctcatggcgaaggctggactgacctgcaac agcagcaccagaggctggcccagttgctgctgattctgag ccacatccggcacatgtcgtccaagaggatggaacacct gtacagcatgaagtgaagaacgtcgtgcctctgtccgat ctgctcctggaaatgtggacgcgcacagactcggaacc ggcgcggaagaccccgccctccaggaaagcgaaggt ccctcggagacgtgggtgaagtgaattggtggaatcag ggggaggacttgtgcagcctggaggatcgctgagactgtc atgtgccgtgtccggcttgcctgtccaaccacgggatgtc ctgggtccgcgcgcgcctggaaagggcctcgaatgggt gtcgggtattgtgtacagcggtagcacctactatgccgcat ccgtgaaggggagattcaccatcagccgggacaactcc aggaacactctgtacctccaaatgaattcgtgaggccag aggacactgccatctactactgtccgcgcagtgccggaga gtccgacgtctggggacaggggaccaccgtgaccgtgtc tagcgcgtccggcggaggcggcagcgggggtcgggcat cagggggcggcggatcggacatccagctcaccagctcc

	DVLDKRRGRDPEMGGKPRRK NPQEGLYNELQDKMAEAYS EIGMKGERRRRGKHDGLYQG LSTATKDTYDALHMQALPPR (SEQ ID NO: 1022)	ccgagctcgctgtccgcctccgtgggagatcgggtcacca tcacgtgccgcgccagccagtcgatttctctacctaac tggtaccaacagaagcccggaagccccaagcttctc atctacgccgcctcgagcctgcagtcaggagtcacctac ggttctccggctccggttccggtactgatttaccctgaccat ttctccctgcaaccggaggacttcgctacttactactgcca gcagtcgtactccacccctacactttcggaacaaggcacc aaggtcgaaatcaagaccactacccagcaccgaggcc accaccccggtctctaccatcgctctccagcctctgtccc tgcttccggaggcatgtagaccgcagctggtggggccg tgcataccgggggtctgacttcgctgcgatactacattg ggccctctggctggtacttgcggggctctgctgcttactc gtgatcactcttactgtaagcgggctcggaagaagctgt gtacatctttaagcaaccctcatgaggcctgtgcagacta ctcaagaggaggacggctgtcatgccggttcccaggagg aggaggaaggcggctgcgaactgcgctgaaattcagc cgagcgcagatgtccagcctaccagcaggggcagaa ccagctctacaacgaactcaatcttggtcggagagagga gtacgacgtgtcggacaagcggagaggacgggaccca gaaatgggcggaagccgcgcagaagaatccccaag agggcctgtacaacgagctccaaaaggataagatggca gaagcctatagcgagattggtatgaaaggggaacgcag aagaggcaaaggccacgacggactgtaccagggactc agcaccgccaccaaggacacatgacgctcttcacatg caggccctgccgcctcgg (SEQ ID NO: 1082)
SP-Linker 4 – ERmut2 – Furin cleavage site 2 – BCMA CAR	MALPVTALLLPLALLLHAARPN SLALSLTADQMVSALLDAEPP LYSEYDPTTRPFSEASMMGLLT NLADRELVHMINWAKRVPGF VDLTLHDQVHLLCAWMEILM IGLVWRSMEHPGKLLFAPNLL LDRNQGKCVEGGVEIFDMLLA TSSRFRMMNLQGEFVCLKSI ILLNSGVYTFLSSTLKSLEEKD HIHRVLDKITDTLIHLMAKAGLT LQQQHQLRAQLLLILSHIRHM SNKRMEHLYSMKCKNVVPLS DLLLEMLDAHRLGTGAEDPRP SRKRRLGDDVGEVQLVESGG GLVQPGGSLRLSCAVSGFALS NHGMSWVRRAPGKGLEWVS GIVYSGSTYYAASVKGRFTISR DNSRNTLYLQMNSLRPEDTAI YYCSAHGGESDVWGQTTVT VSSASGGGSGGRASGGGG SDIQLTQSPSSLSASVGDRVIT TCRASQSISSYLNWYQQKPG KAPKLLIYAASSLQSGVPSRFS GSGSGTDFTLTISSLQPEDFA TYYCQQSYSTPYTFGQGTKV EIKTTTPAPRPPTPAPTIASQP LSLRPEACRPAAGGAVHTRG LDFACDIYWAPLAGTCGVLLL SLVITLYCKRGRKKLLYIFKQP FMRPVQTTQEEDGCSCRFPE EEEGGCELRVKFSRSADAPA	atggccctccctgtcaccgcctgtgcttccgtggctcttc tgctccacgcgcgtcggcccaacTcgttggcactttccctg actgcgcaccagatggtgtccgcctcttgacgcgcgagc ctccaattctgtactcggagtacgatccgactcgcctgtct ccgaagccagcatgatgggcctgtgactaacctggcgg accgcgagttggtgcacatgattaactgggctaagcgggt gccgggctctgtggacctgacctgcacgaccaagtga cctcctggaatgcgcctggatggaatcctcatgatcggcc tcgtgtggagatccatggagcatcccgaaagctcctgttt gcaccaacctcctgcttgatcgcaaccagggaagatgc gtggaagggggtgtcgagatttgcacatgctgctgccac ctcttccgggtccggatgatgaatctgcaggagagaagagt tcgtgtgtctgaagtcaatcatcctgctgaactccggggtct ataccttctgagctcgacctcaagtactggaggaaaa agaccacatccatcgctgctcgataagatcacggacac ccttatccatctcatggcgaaggctggactgacctgcaac agcagcaccagaggctggcccagttgtctgtgattctgag ccacatccggcacatgtcgaacaagaggatggaacacc tgtacagcatgaagtgaagaacgtcgtgctctgtccgat ctgctcctggaaatgtggacgcgcacagactcggaacc ggcgcggaagaccccgccctccaggaaagcgaagggt ccctcggagacgtgggtgaagtgaattggtggaatcag ggggaggacttgtgcagcctggaggatcgctgagactgtc atgtgccgtgtccggcttgcctgtccaaccacgggatgtc ctgggtccgcgcgcgcctggaaagggcctcgaatgggt gtcgggtattgtgtacagcggtagcacctactatgccgat ccgtgaaggggagattcaccatcagccgggacaactcc aggaacactctgtacctccaaatgaattcgtgaggccag aggacactgccatctactactgtccgcgcagtgccggaga gtccgacgtctggggacaggggaccaccgtgaccgtgtc tagcgcgtccggcgaggcgccagcgggggtcgggcat

	YQQGQNQLYNELNLGRREEY DVLDKRRGRDPEMGGKPRRK NPQEGLYNELQKDKMAEAYS EIGMKGERRRRGKHDGLYQG LSTATKDTYDALHMQALPPR (SEQ ID NO: 1023)	cagggggcgggcgatcgacatccagctcaccagtc ccgagctcgtgtccgctcgtgggagatcggtcacca tcagtgccgcccagccagctgatttctctacctaac tggtaccaacagaagcccgaaaagcccgaaagcttct atctacgcccctcgagcctgcagtcaggagtgccctcac ggttctccggtccggttcgggtactgatttcaccctgaccat ttctccctgcaaccggaggacttcgctacttactactgcc gcagtcgtactccacccctacactttcggaacaaggcacc aaggtcgaaatcaagaccactacccagcaccgaggcc accaccccggtcctaccatcgctcccagcctctgtccc tgctccgaggcatgtagaccgcagctggtggggcgg tgcataccggggtctgacttcgctcgatatactacattg ggccctctgggtgacttgccgggtcctgctgcttctactc gtgatcactcttactgtaagcgggtcggaagaagctgct gtacatcttaagcaaccctcatgaggcctgtgcagacta ctcaagaggaggacggtgttcacgcccgttcccagagg aggaggaaggcggctgcgaactgcgctgaaattcagc cgagcgcagatgtccagcctaccagcaggggcagaa ccagctctacaacgaactcaatcttggtcgagagagga gtacgacgtgtggaacaagcggagaggacgggaccca gaaatggggcggaagccgcgcagaagaatccccaag agggcctgtacaacgagctccaaaaggataagatggca gaagcctatagcagattggtatgaaaggggaacgcag aagaggcaaaggccacgacggactgtaccagggactc agcaccgccaccaaggacacatgacgctcttcacatg caggccctgccgctcgg (SEQ ID NO: 1083)
SP-Linker 4 – ERmut1 – Furin cleavage site 3 – BCMA CAR	MALPVTALLPLALLLHAARPN SLALSLTADQMVSALLDAEPI LYSEYDPTTRPFSEASMMGLLT NLADRELVHMINWAKRVPGF VDLALHDQVHLLECAWMEILM IGLVWRSMEHGPKLLFAPNLL LDRNQGKCVEGGVEIFDMLLA TSSRFRMMNLQGEFVCLKSI ILLNSGVYTFLSSTLKSLEEKD HIHRVLDKITDTLIHLMAKAGLT LQQQHQLAQLLLILSHIRHM SSKRMEHLYSMKCKNVVPLS DLLLEMLDAHRLGTGAEDPRP SRKRREVQLVESGGGLVQPG GSLRLSCAVSGFALSNGHMS WVRRAPGKGLEWVSGIVYSG STYYAASVKGRFTISRDNRSR TLYLQMNSLRPEDTAIYYCSA HGGESDVWGQGTTVTVSSAS GGGSGGRASGGGSDIQLT QSPSSLSASVGDRVTITCRAS QSISSYLNWYQQKPKAPKLL IYAASSLQSGVPSRFSGSGSG TDFTLTISLQPEDFATYYCQ QSYSTPYTFGGQTKVEIKTTT PAPRPPTPAPTIASQPLSLRPE ACRPAAGGAVHTRGLDFACDI YIWAPLAGTCGVLLLSLVITLY CKRGRKKLLYIFKQPFMRPVQ TTQEEDGCSCRFPEEEEGGC	atggccctccctgtcaccgcccgtgcttccgctggctcttc tgctccacgcccgtcggcccaacTcgttggaactttccctg actgccgaccagatggtgtccgccccttctggacgccgagc ctccaattctgtactcggagtacgatccgactcggcgttct ccgaagccagcatgatgggcctgtgactaacctggcgg accgcgagttggtgcacatgattaactgggctaagcgggt gccgggcttctgtgacactggccctgcacgaccaagtga cctcctggaatgcgcctggatggaatcctcatgatcggcc tcgtgtggagatccatggagcatcccgaaagctcctgttt gcaccaaacctcctgctgatcgcaaccagggaagatgc gtggaagggggtgtcgagattttcgacatgctgctgccac ctcttccgggttccggatgatgaatctgcaggagagaagagt tcgtgtgtctgaagtcaatcatcctgctgaactccggggtct ataccttctgagctcgacctcaagtactggaggaaaa agaccacatccatcgctgctgataagatcaccgacac ccttatccatctcatggcgaaggctggactgacctgcaac agcagcaccagaggctggcccagttgctgctgattctgag ccacatccggcacatgtcgtccaagaggatggaacacct gtacagcatgaagtgaagaacgtcgtgcctctgtccgat ctgctcctggaaatgctggacgcgcacagactcGggacg ggagctgaagatccacgaccagcagaaagcgacggg aagtgaattggtggaatcagggggaggactgtgcagc ctggaggatcgctgagactgtcatgtccgtgtccgcttctg ccctgtccaaccacgggatgtctgggtccgcccgcgcgc tggaagggcctcgaatgggtgtcgggtattgtgtacagc ggtagcacctactatgccgatccgtgaaggggagattca ccatcagccgggacaactccaggaaactctgtacctcc aatgaattcgtgaggccagaggacactgccatctacta ctgctccgcgatggcggagagtcgcagctctggggaca ggggaccaccgtgaccgtgtctagcgcgtccggcggag

	ELRVKFSRSADAPAYQQGN QLYNELNLGRREEYDVLDKR RGRDPEMGGKPRRKNPQEG LYNELQKDKMAEAYSEIGMKG ERRRGKGHDGLYQGLSTATK DTYDALHMQALPPR (SEQ ID NO: 1024)	gcggcagcgggggtcgggcatcagggggcgggcgatc ggacatccagctcaccagtcacccgagctcgctgtccgcc tccgtgggagatcgggtcaccatcacgtgccgcccagc cagtcgatttctctacctgaactggtaccaacagaagcc cggaaaagccccgaagcttctcatctacgccgctcgag cctgcagtcaggagtgccctcacggttctccggtccggtt ccggtactgatttaccctgaccatttctccctgaaccgg aggacttcgctacttactactgccagcagtcgtactccacc ccctacatttcggacaaggcaccagggtcgaaatcaag accactacccagcaccgaggccaccaccccggtcct accatcgctcccagcctctgtccctgctcggaggcatg tagacccgcagctggtggggccgtgcatacccggggtctt gacttcgctcgatattctacatttgggcccctctggctggt cttgcggggtcctgctgttctactcgtgatcactttactgta agcgcggtcggaagaagctgctgtacatcttaagcaacc cttcagtaggacctgagactactcaagaggaggacgg ctgttcagtcgggttccagaggaggaggaaaggcggtg cgaactgcgctgaaattcagccgcagcgcagatgctcc agcctaccagcaggggcagaaccagctctacaacgaac tcaatcttggtcgagagaggagtacgacgtgctggaca agcgagaggacgggaccagaaatggcggggaagc cgcgagaaagaatccccaagaggcgctgtacaacga gctccaaaaggataagatggcagaagcctatagcgaga ttggtatgaaagggaacgcagaagaggcaaaggcca cgacggactgtaccagggactcagcaccgcccaccaagg acacctatgacgctcttcacatgcaggccctgccgctcg g (SEQ ID NO: 1084)
SP-Linker 4 – ERmut2 – Furin cleavage site 3 – BCMA CAR	MALPVTALLLPLALLLHAARP SLALSLTADQMVSALLDAEPI LYSEYDPTTRPFSEASMMGLLT NLADRELVHMINWAKRVPGF VDLTLDHQQVHLLCAWMEILM IGLVWRSMEHGPKLLFAPNLL LDRNQGKCVGGVEIFDMLLA TSSRFRMMNLQGEFVCLKSI ILLNSGVYTFLSSTLKSLEEKD HIHRVLDKITDTLIHLMAKAGLT LQQQHQRQAQLLLILSHIRHM SNKRMEHLYSMKCKNVVPLS DLLLEMLDAHRLGTGAEDPRP SRKRREVQLVESGGGLVQPG GSLRLSCAVSGFALSNGHMS WVRRAPGKGLEWVSGIVYSG STYYAASVKGRFTISRDNRN TLYLQMNSLRPEDTAIYYCSA HGGESDVWGQGTTVTVSSAS GGGGSGGRASGGGGSDIQLT QSPSSLSASVGDRVITCRAS QSISSYLNWYQQKPKGKAPKLL IYAASSLQSGVPSRFSGSGSG TDFTLTISLQPEDFATYYCQ QSYSTPYTFGGQTKVEIKTTT PAPRPPTPAPTIASQPLSLRPE ACRPAAGGAVHTRGLDFACDI YIWAPLAGTCGVLLLSLVITLY CKRGRKKLLYIFKQPFMRPVQ	atggccctccctgtcaccgcccgtgcttccgctggctcttc tgctccacgcccgtcggcccaacTcgttggaactttccctg actgccgaccagatggtgtccgccccttctggacgccgagc ctccaattctgtactcggagtacgatccgactcgcctgtct ccgaagccagcatgatgggctgtgactaacctggcgg accgaggtggtgcacatgattaactgggctaagcggtg gccgggcttctgtggacctgacctgcacgaccaagtga cctcctggaatgcgcctggatggaaatcctcatgatcgcc tcgtgtggagatccatggagcatcccgaaagctcctgtt gcaccaacctcctgctgtatcgcaaccagggaatgc gtggaagggggtgtcgagatttctgacatgctgctgccac ctcttccgggtccggatgatgaatctgcaggagagaagagt tcgtgtgtctgaagtcaatcctcctgctgaactccgggtct ataccttctgagctcgacctcaagtactggaggaaaa agaccacatccatcgctgctgataagatcaccgacac ccttatccatctcatggcgaaggctggactgacctgcaac agcagcaccagaggctggcccagttgctgtgattctgag ccacatccggcacatgtcgaacaagaggatggaacacc tgtacagcatgaagtgcagaacgtgctgtcctctgtccgat ctgctcctggaaatgtggacgcgcacagactcgggacg ggagctgaagatccacgaccagcagaaagcgacggg aagtgcattggtggaatcagggggaggactgtgcagc ctggaggatcgctgagactgtcatgtccgtgtccgcttctg cctgtccaaccacgggatgtcctgggtccgcccgcgcgc tggaagggcctcgaatgggtgtcgggtattgtgtacagc ggtagcacctactatgccgatccgtgaaggggagattca ccatcagccgggacaactccaggaaactctgtacctcc aatgaattcgtgaggccagaggacactgccatctacta ctgctccgcatggcgagagtccgacgtctggggaca

	TTQEEDGCSCRFPEEEEEGGC ELRVKFSRSADAPAYQQGQN QLYNELNLGRREEYDVLDKR RGRDPEMGGKPRRKNPQEG LYNELQKDKMAEAYSEIGMKG ERRRGKGDGLYQGLSTATK DTYDALHMQALPPR (SEQ ID NO: 1025)	ggggaccaccgtgaccgtgtctagcgcgtccggcggag gcgccagcgggggtcgggcatcagggggcgccggatc ggacatccagctcaccagtcacccagctcgtgtccgcc tccgtgggagatcggtcaccatcacgtccgcgccagc cagtcgatttctctacctgaactgtaccaacagaagcc cggaaaagccccgaagcttctcatctacgcgcctcgag cctgcagtcaggagtgccctcacggttctccggtccggt ccggtactgatttaccctgaccatttctccctgcaaccgg aggacttcgctacttactactgccagcagtcgtactccacc ccctacacttctcgacaaggcaccaggctgaaatcaag accactaccccagcaccgaggccacccaccccggtcct accatcgctcccagcctctgtccctgcgtccggaggcatg tagaccgcagctggtggggcggtgcatacccggggtctt gacttcgctcgatatactatttgggcccctctggtggtta cttgcgggtcctgctgttctactcgtgatcactttactgta agcgcggtcggaagaagctgctgtacatcttaagcaacc cttcatgaggcctgtgcagactactcaagaggaggacgg ctgttcatgccggttccagaggaggaggaaaggcggtg cgaactgcgctgaaattcagccgcagcgcagatgctcc agcctaccagcaggggcagaaccagctctacaacgaac tcaatcttggtcgagagaggagtacgacgtgctggaca agcggagaggacgggaccagaaatgggcgggaagc cgccagaaagaatccccaaggggcctgtacaacga gctccaaaaggataagatggcagaagcctatagcgaga ttggtatgaaaggggaacgcagaagaggcaaaggcca cgacggactgtaccagggactcagcacccgccaacgaag acacctatgacgctcttcacatgcaggccctgcgcctcg g (SEQ ID NO: 1085)
SP-Linker 5 – ERmut1 – Furin cleavage site 2 – CD19 CAR2	MALPVTALLLPLALLLHAARPE SLALSLTADQMVSALLDAEPPI LYSEYDPTRPFSEASMMGLLT NLADRELVHMINWAKRVPGF VDLALHDQVHLLCAWMEILM IGLVWRSMEHPGKLLFAPNLL LDRNQGKCVVEGGVEIFDMLLA TSSRFRMMNLQGEFVCLKSI ILLNSGVYTFLSSTLKSLEEKD HIHRVLDKITDTLIHLMAGALT LQQQHQLRAQLLLILSHIRHM SSKRMEHLYSMKCKNVVPLS DLLLEMLDAHRLGTGAEDPRP SRKRRSLGDVGEIVMTQSPAT LSLSPGERATLSCRASQDISK YLNWYQQKPGQAPRLIYHTS RLHSGIPARFSGSGSGTDYTL TISSLQPEDFAVYFCQQGNL PYTFGQGTKLEIKGGGSGG GGSGGGGSQVQLQESGPG VKPSETLSLTCTVSGVSLPDY GVSWIRQPPGKLEWIGVIW GSETTYSSSLKSRVTISKDN SKNQVSLKLSSVTAADTAVYY CAKHYYYGGSYAMDYWGQG TLVTVSSTTTPAPRPPTPPTI ASQPLSLRPEACRPAAGGAV HTRGLDFACDIYWAPLAGTC	atggccctccctgtcaccgcctgctgttccgctggctcttc tgctccacgcgcgtcgcccgagtcgttggcactttccctg actgccgaccagatggtgtccgccccttctggacgcgcgagc ctccaattctgtactcggagtacgatccgactcgcgcgttct ccgaagccagcatgatgggcctgttgactaacctggcgg accgcgagttggtgcacatgattaactgggctaagcgggt gccgggcttctgtggacctggccctgcacgaccaagtgca cctcctggaatgcgcctggatggaaatcctcatgatcgcc tcgtgtggagatccatggagcatcccgaaagctcctgttt gcaccaacctcctgctgtgatcgcaaccagggaatgc gtggaagggggtgtcgagatttctgacatgctgctgccac cttctccggttccggtatgataatctgcaggagagaagagt tcgtgtgtctgaagtcaatcactcctgctgaactccgggtct ataccttctgagctcgaccctcaagtactggaggaaaa agaccacatccatcgctgtcgtgataagatcaccgacac ccttatcatctcatggcgaaggctggactgacctgcaac agcagcaccagaggctggcccagttgctgtgattctgag ccacatccggcacatgtcgtccaagaggatggaacacct gtacagcatgaagtgaagaacgtcgtgcctctgtccgat ctgctcctggaaatgctggacgcgcacagactcggaacc ggcgcggaagacccccggccctccaggaaagcgaagggt ccctcggagacgtgggtgaaattgtgatgaccagtcacc cgccactcttagccttccaccggtgagcgcgcaacctgt cttgacagcctcccaagacatctcaaaataccttaattgg tatcaacagaagcccgacaggctcctgccttctgatcta ccacaccagccggtccattctggaatccctgccagggtc agcggtagcggatctgggaccgactacacctcactatca gctcactgcagccagaggacttcgtgtctatttctgtcagc

	GVLLLSLVITLYCKRGRKKLLYI FKQPFMRPVQTTQEEDGCSC RFPEEEEEGGCELRVKFSRSA DAPAYQQGQNQLYNELNLGR REEYDVLDKRRGRDPEMGGK PRRKNPQEGLYNELQDKMA EAYSEIGMKGERRRGKHDG LYQGLSTATKDTYDALHMQAL PPR (SEQ ID NO: 1026)	aagggaacaccctgccctacaccttggacagggcacca agctcgagattaaaggtggaggtggcagcggaggaggt gggtccggcgggtggaggaagccaggtccaactccaaga aagcggaccgggtctgtgaagccatcagaaactcttca ctgactgtactgtgagcggagtgtctctcccgttacggg gtgtcttgatcagacagccaccggggaaggggtcggaa ggattggagtatttggggctctgagactactactactctc atccctcaagtcacgcgtcaccatctcaaaggacaactct aagaatcagggtgactgaaactgtcatctgtgaccgcag ccgacaccgcccgtgtactattgcgctaagcattactattatg gctgggagctacgcaatggattactgggacaggggtactct ggtcaccgtgtccagcaccactaccccagcaccgaggcc acccaccccggtcctaccatcgctcccagcctctgtccc tgcgtccggaggcatgtagaccgcagctggtggggcgg tgcatacccggggtctgacttcgctgcgatatctacattt ggccccctcggctggtacttgcggggctctgtcttctactc gtgatcactcttactgtaagcgggtcggaagaagctgt gtacatcttaagcaaccctcatgaggcctgtgcagacta ctcaagaggaggacggctgttcacgctccgggtccagagg aggaggaaggcggctgcgaactgcgctgaaatcagc cgacgcgagatgtccagcctaccagcaggggcagaa ccagctctacaacgaactcaatcttggtcggagagagga gtacgacgtgctggacaagcggagaggacgggaccca gaaatgggcccgaagccgcgcagaaagaatcccaag agggcctgtacaacgagctccaaaaggataagatggca gaagcctatagcagattggtatgaaaggggaacgcag aagaggcaaaggccacgacggactgtaccagggaactc agcaccgccaccaaggacacctatgacgctcttcacatg caggccctgccgcctcgg (SEQ ID NO: 1086)
SP-Linker 5 – ERmut2 – Furin cleavage site 2 – CD19 CAR2	MALPVTALLPLALLLHAARPE SLALSLTADQMVSALLDAEPI LYSEYDPTRPFSEASMMGLLT NLADRELVHMINWAKRVPGF VDLTLHDQVHLLCAWMEILM IGLVWRSMEHPGKLLFAPNLL LDRNQGKCVVEGGVEIFDMLLA TSSRFRMMNLQGEFVCLKSI ILLNSGVYTFLSSTLKSLEEKD HIHRVLDKITDTLIHLMAKAGLT LQQQHQRQAQLLLILSHIRHM SNKRMEHLYSMKCKNVVPLS DLLLEMLDAHRLGTGAEDPRP SRKRRSLGDVGEIVMTQSPAT LSLSPGERATLSCRASQDISK YLNWYQQKPGQAPRLIYHTS RLHSGIPARFSGSGSGTDYTL TISSLQPEDFAVYFCQQGNTL PYTFGQGTKLEIKGGGSGG GGSGGGGSQVQLQESGPG VKPSETLSLTCTVSGVSLPDY GVSWIRQPPGKGLEWIGVIW GSETYYSSSLKSRVTISKDN SKNQVSLKLSSVTAADTAVYY CAKHYYYGGSYAMDYWGQG TLVTVSSTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAV	atggccctccctgtcaccgcccgtgcttccgtggtcttct tgctccacgcccgtcggcccagatcgttggcacttccctg actgccgaccagatggtgtccgccccttctggacgccgagc ctccaattctgtactcggagtacgatccgactcgcctgtct ccgaagccagcatgatgggcctgtgactaacctggcgg accgcgagttggtgcacatgattaactgggctaagcgggt gccgggcttctgtggacctgacctgcacgaccaagtgca cctcctggaatgcgcctggatggaaatcctcatgatcgcc tcgtgtggagatccatggagcatcccggaagctcctgtt gcaccaacctcctgctgtatcgcaaccagggaatgc gtggaaggggtgtcgagatttgcagatgtctgcgccac ctctcccggtccggatgatgaatctgcagggaagaagagt tcgtgtgtctgaagtcaatcctcgtgtaactccggggtct ataccttctgagctcgacctcaagtcactggaggaaaa agaccacatccatcgctgtcgtgataagatcaccgacac ccttatccatctcatggcgaaggctggactgacctgcaac agcagcaccagaggctggcccagttgctgctgattctgag ccacatccggcacatgtcgacaagaggatggaaacacc tgtacagcatgaagtgcagaacgctgctgctctgtccgat ctgctcctggaatgtgagcgcgcacagactcggaaacc ggcgcggaagacccccggccctccagggaagcgaagggt ccctcggagacgtgggtgaaattgtgatgaccagtcacc cgccactcttagccttccaccgggtgagcgcgcaaccctgt ctgacagacctcccaagacatctcaaaatccttaattgg tatcaacagaagcccgacaggctcctgccttctgatcta ccacaccagccggctccattctggaatccctgccagggtc agcggtagcggatctgggaccgactacacctcactatca

	HTRGLDFACDIYIWAPLAGTC GVLLLSLVITLYCKRGRKLLYI FKQPFMRPVQTTQEEDGCSC RFPEEEEEGGCELRVKFSRSA DAPAYQQGQNQLYNELNLGR REEYDVLDKRRGRDPEMGGK PRRKNPQEGLYNELQKDKMA EAYSEIGMKGERRRRGKHDG LYQGLSTATKDTYDALHMQAL PPR (SEQ ID NO: 1027)	gtcactgcagccagaggacttcgctgtctatttctgtcagc aagggaacaccctgccctacaccttggacagggcacca agctcgagattaaaggtggaggtggcagcggaggagggt gggtcggcggtggaggaagccaggtccaactccaaga aagcggaccgggtctgtgaagccatcagaaactcttca ctgactgtactgtgagcggagtgtctctcccgttactcggg gtgtcttggatcagacagccaccggggaaggggtctggaat ggattggagtgaattggggctctgagactactactactctc atccctcaagtcacgcgtcaccatctcaaaggacaactct aagaatcagggtgtcactgaactgtcatctgtgaccgcag ccgacaccgcccgtgtactattgcgctaagcattactattatg gcgggagctacgcaatggattactggggacaggggtactct ggtcaccgtgtccagcaccactaccccagcaccgaggcc acccaccggctcctaccatcgctcccagcctctgtccc tgcgtccggaggcatgtagaccgcagctggtggggccg tgcatacccggggtctgtacttcgctgcgatactacatttg ggcccctctggctgtgtacttcggggtcctgtcttctactc gtgatcactcttactgtaagcgggtcggaagaagctgtct gtacatctttaagcaaccctcatgaggcctgtgcagacta ctcaagaggaggacggctgttcatgcgggtcccagagg aggagggaaggcggctgcgaactgcgcgtgaaattcagc cgcagcgcagatgctccagcctaccagcaggggcagaa ccagctctacaacgaactcaatcttggtcggagagagga gtacgacgtgtggacaagcggagaggacggggaccca gaaatgggcggaagccgcgcagaaagaatccccaag agggcctgtacaacgagctccaaaaggataaagatggca gaagcctatagcgagattggtatgaaaggggaacgcag aagaggcaaaggccacgacggactgtaccagggactc agcaccgccaccaaggacacctatgacgctcttcacatg caggccctgccgcctcgg (SEQ ID NO: 1087)
SP-Linker 5 – ERmut1 – Furin cleavage site 3 – CD19 CAR2	MALPVTALLLPLALLLHAARPE SLALSLTADQMVSALLDAEPPI LYSEYDPTRPFSEASMMGLLT NLADRELVHMINWAKRVPGF VDLALHDQVHILLECAWMEILM IGLVWRSMEHPGKLLFAPNLL LDRNQGKCVVEGGVEIFDMLLA TSSRFRMMNLQGEFVCLKSI ILLNSGVYTFLSSTLKSLEEKD HIHRVLDKITDTLIHLMAGALT LQQQHQLRAQLLLILSHIRHM SSKRMEHLYSMKCKNVVPLS DLLLEMLDAHRLGTGAEDPRP SRKRREIVMTQSPATLSLSPG ERATLSCRASQDISKYLNWYQ QKPGQAPRLLIYHTSRLHSGIP ARFSGSGSGTDYTLTISSLQP EDFAVYFCQQGNTLPYTFGQ GTKLEIKGGGSGGGSGGG GSQVQLQESGPGLVKPSSETL SLTCTVSGVSLPDYGVSWIRQ PPGKGLEWIGVIWGSETTYYS SSLKSRVTISKDNSKNQVSLK LSSVTAADTAVYYCAKHYYYG GSYAMDYWGQGTLLTVSSTT TPAPRPPTPAPTIASQPLSLRP	atggccctccctgtcaccgcccgtgtcttccgtggtcttct tgcctcacgcgcgtcggcccagtcgttggcactttccctg actgccgaccagatggtgtccgccccttctggacgccgagc ctccaattctgtactcggagtacgatccgactcgcgcgttct ccgaagccagcatgatgggcctgttgactaacctggcgg accgcgagttggtgcacatgattaactgggctaagcgggt gccgggcttctgtggacctggccctgcacgaccaagtga cctcctggaatgcgcctggatggaaatcctcatgatcgccc tcgtgtggagatccatggagcatcccggaagctcctgttt gcaccaacctcctgttgatcgcaaccagggaaaatgc gtggaagggggtgtcgagatttctgacatgtctgtcgccac ctcttccgggtccggatgatgaatctgcaggagagaagagt tcgtgtgtctgaagtcaatcctcctgctgaactccggggtct atacctcctgagctcgaccctcaagtcactggaggaaaa agaccacatccatcgcgtgtcgataagatcaccgacac ccttatccatctcatggcgaaggctggactgacctgcaac agcagcaccagaggctggcccagttgctgctgattctgag ccacatccggcacatgtctgccaaggagatggaacacct gtacagcatgaagtgaagaacgtcgtgcctctgtccgat ctgctcctggaatgtggacgcgcacagactcgggacg ggagctgaagatccacgaccagcagaaagcgacggg aaattgtatgacctcagtcacccgacctttagcctttcac ccggtgagcgcgaacctgtctgtcagagcctcccaag acatctcaaaaataccttaattggtatcaacagaagcccg acaggctcctgccttctgtatctaccacaccagccggtcc attctggaatccctgccaggttcagcggtagcggatctggg

	EACRPAAGGAVHTRGLDFAC DIYIWAPLAGTCGVLLLSLVITL YCKRGRKKLLYIFKQPFMRPV QTTQEEDGCSCRFPEEEEGG CELRVKFSRSADAPAYQQGQ NQLYNELNLGRREEYDVLDK RRGRDPEMGGKPRRKNPQE GLYNELQKDKMAEAYSEIGMK GERRRGKGHDLGLYQGLSTAT KDTYDALHMQALPPR (SEQ ID NO: 1028)	accgactacaccctcactatcagctcactgcagccagag gacttcgctgtctatttctgtcagcaaggggaacaccctgcc tacaccttggacagggcaccaagctcgagattaaaggtg gaggtggcagcggaggaggtgggtccggcggtggagg aagccaggccaactccaagaaagcggaccgggtctgt gaagccatcagaaactcttctactgactgtactgtgagcg gagtgctctccccgattacgggggtgcttggatcagacag ccaccggggaaggggtctggaatggattggagtgattggg gctctgagactacttactactcttcatccctcaagtcacgct caccatctcaaaggacaactctaagaatcagggtgactg aaactgtcatctgtgaccgcagccgacaccgcggtgact attgcgctaagcattactattatggcgggagctacgcaatg gattactggggacaggggtactctggtaaccgtgccagca ccactacccagcaccgagggccacccaccccggtccta ccatcgctcccagcctctgtccctgcgtccggaggcatgt agaccgcagctggtggggcgtgcataccgggggtctt gacttcgctcgatatactacatttggccctctggctgga cttgcgggtcctgtgcttctactcgtgatcacttctactgta agcgcgggtcggagaagctgctgtacatcttaagcaacc cttcatgaggcctgtgcagactactcaagaggaggacgg ctgttcagccgggtccagaggaggaggaagcggtg cgaactgcgcgtgaaattcagccgcagcgagatgctcc agcctaccagcaggggcagaaccagctctacaacgaac tcaatcttggtcggagagaggagtagcagctgctggaca agcggagaggacgggaccagaaatggcggggaagc cgcgagaaagaatcccaagaggcctgtacaacga gctccaaaaggataagatggcagaagcctatagcgaga ttggtatgaaaggggaacgcagaagaggcaaaggcca cgacggactgtaccaggactcagcaccgccaccaagg acacctatgacgctcttcacatgcaggccctgcgcctcg g (SEQ ID NO: 1088)
SP-Linker 5 – ERmut2 – Furin cleavage site 3 – CD19 CAR2	MALPVTALLPLALLLHAAPE SLALSLTADQMVSALLDAEPI LYSEYDPTPRFSEASMMGLLT NLADRELVHMINWAKRVPGF VDLTLDQVHLLCAWMEILM IGLVWRSMHEHPGKLLFAPNLL LDRNQGKCVGGVEIFDMLLA TSSRFRMMNLQGEEFVCLKSI ILLNSGVYTFLSSTLKSLEEKD HIHRVLDKITDTLIHLMAKAGLT LQQHQRLAQLLLILSHIRHM SNKRMEHLYSMCKKNVPLS DLLLEMLDAHRLGTGAEDPRP SRKRREIVMTQSPATLSLSPG ERATLSCRASQDISKYNWYQ QKPGQAPRLLIYHTRSRLHSGIP ARFSGSGSGTDYTLTISSLQP EDFAVYFCQQGNTLPYTFGQ GTKLEIKGGGSGGGGSGGG GSQVQLQESGPGLVKPSSETL SLTCTVSGVSLPDYGVSWIRQ PPGKGLEWIGVIWGSETTYYS SSLKSRVTISKDNSKNQVSLK LSSVTAADTAVYYCAKHYYYG	atggccctccctgtcaccgcctgctgcttccgctggctcttc tgctccacgcccgtcggcccagTcggtggcacttccctg actgccgaccagatggtgtccgcccctctggacgccgagc ctccaattctgtactcggagtagatccgactcgcctgtct ccgaagccagcatgatgggcctgttgactaacctggcgg accgcgagttggtgcacatgattaactgggctaagcgggt gccgggcttcgtggacctgacctgcacgaccaagtga cctcctggaatgcgcctggatggaaatcctcatgatcgcc tcgtgtggagatccatggagcatcccgaaagctcctgttt gcaccaacctcctgcttgatcgcaaccagggaatgc gtggaaggggggtgagagatttcgacatgctgctgccac ctctcccggtccggatgatgaatctgcaggagagaagagt tcgtgtgtctgaagtcaatcatcctgctgaactccgggtct ataccttctgagctcgacctcaagtcactggaggaaa agaccacatccatcgctgtcgtgataagatcaccgacac ccttatccatctcatggcgaaggctggactgacctgcaac agcagcaccagaggctggcccagttgctgctgattctgag ccacatccggcacatgtcgaaagaggatggaacacc tgtacagcatgaagtgaagaacgtcgtgctctgtccgat ctgctcctggaaatgctggacgcgcacagactGggacg ggagctgaagatccacgaccagcagaaagcgacggg aaattgtatgaccagtcaccgcctacttagcctttcac ccggtgagcgcgcaacctgtctgtcagagcctccaag acatctcaaaataccttaattggtatcaacagaagcccg

	GSYAMDYWGQGTTLTVSSTT TPAPRPPTPAPTIASQPLSLRP EACRPAAGGAVHTRGLDFAC DIYIWAPLAGTCGVLLLSLVITL YCKRGRKKLLYIFKQPFMRPV QTTQEEDGCSCRFPEEEEEGG CELRVKFSRSADAPAYQQGQ NQLYNELNLGRREEYDVLDK RRGRDPEMGGKPRRKNPQE GLYNELQKDKMAEAYSEIGMK GERRRGKGDGLYQGLSTAT KDTYDALHMQALPPR (SEQ ID NO: 1029)	acaggctcctcgcttctgatctaccacaccagccggctcc attctggaatccctgccagggtcagcggtagcggatctggg accgactacaccctcactatcagctcactgcagccagag gacttcgctgtctattctgtcagcaagggaacaccctgcc tacaccttggacagggcaccaagctcgagattaaggtg gagggtggcagcggaggagggtgggtccggcggtggagg aagccagggtccaactccaagaaagcggaccgggtctgt gaagccatcagaaactcttctactgactgtactgtgagcg gagtgctctccccgattacgggggtgtcttgatcagacag ccaccggggaaggggtctggaatggattggagtgattggg gctctgagactacttactactcttcatccctcaagtcacgcg caccatctcaaaggacaactctaagaatcagggtgtactg aaactgtcatctgtgaccgcagccgacaccgcccgtgtact attgcgctaagcattactattatggcgggagctacgcaatg gattactggggacaggggtactctggtcaccgtgtccagca ccactaccccagcaccgaggccacccaccccggtccta ccatcgccctccagcctctgtccctgcgtccggaggcatgt agaccgcagctggtggggcggtgcataccgggggtctt gacttcgctgcgatatctacattgggccccctctggctgga cttgcgggtctgtgcttctactcgtgatcactcttactgta agcgcgggtcggaagaagctgctgtacatctttaagcaacc cttcatgaggcctgtgcagactactcaagaggagagcgg ctgttcatgccggttcccagaggaggaggaagcggtg cgaactgcgctgaaattcagccgcagcgcagatgctcc agcctaccagcaggggcagaaccagctctacaacgaac tcaatcttggtcggagagaggagtagcagctgtctggaca agcggagaggacgggaccagaaatggcggggaagc cgcgagaaagaatccccaagaggcctgtacaacga gctccaaaaggataagatggcagaagcctatagcgaga ttggtatgaaaggggaacgcagaagaggcaaggcca cgacggactgtaccagggtactcagcaccgccaccaagg acacatgacgctcttcacatgcaggccctgccgcctcg g (SEQ ID NO: 1089)
SP-Linker 5 – ERmut1 – Furin cleavage site 2 – CD123 CAR	MALPVTALLPLALLHAARPE SLALSLTADQMVSALLDAEPP LYSEYDPTPRPFSEASMMGLLT NLADRELVHMINWAKRVPGF VDLALHDQVHLLCAWMEILM IGLVWRSMHEHPGKLLFAPNLL LDRNQGKCVGGVEIFDMLLA TSSRFRMMNLQGEFVCLKSI ILLNSGVYTFLSSTLKSLEKD HIHRVLDKITDTLIHLMKAGLT LQQHQRLAQLLLILSHIRHM SSKRMEHLYSMKCKNVVPLS DLLLEMLDAHRLGTGAEDPRP SRKRRSLGDVGQVQLVQSGA EVKKPGASVKVSCASGYTFT GYMHWWVRQAPGQGLEWM GWINPNSGGTNYAQKFQGRV TLTRDTSISTVYMELSRRLSD DTAVYYCARDMNILATVPFDI WGQGTMTVTSSGGGSGGG SGGGGSDIQMTQSPSSLSA SVGDRVTITCRASQSISSYLN WYQQKPGKAPKLLIYAASSLQ	atggccctccctgtcaccgccctgctgctccgctggctctt tgctccacgccgctcggcccgagtgctggcacttccctg actgccgaccagatggtgtccgccccttctggacgccgagc ctccaattctgtactcggagtacgatccgactcggcgttct ccgaagccagcatgatgggcctgtgactaacctggcgg accgcgagtggtgcacatgattaactgggctaagcgggt gccgggcttcgtggacctggccctgcacgaccaagtga cctcctggaatgcgcctggatggaaatcctcatgatcgcc tcgtgtggagatccatggagcatcccgaaagctcctgtt gcaccaacctcctgctgtatcgcaaccagggaataatgc gtggaagggggtgtcgagatttgcacatgctgctgccac ctctcccggttccggatgatgaatctgcagggaagaaggt tcgtgtgtctgaagtcaatcatcctgctgaactccgggtct ataccttctgagctcgaccctcaagtcactggaggaaaa agaccacatccatcgctgtcgataagatcaccgacac ccttatccatctcatggcgaaggctggactgacctgcaac agcagcaccagaggctggccagtgctgctgattctgag ccacatccggcacatgtctccaagaggatggaacacct gtacagcatgaagtgaagaacgtcgtgcctctgtccgat ctgctcctggaaatgctggacgcgcacagactcggaaacc ggcgcggaagacccccggccctccagggaagcgaaggt ccctcgagacgtgggtcaagtgaactcgtccaaagcg gagcgggaagtcaagaaacccggagcgcgagcgtgaaagt

	SGVPSRFSGSGSGTDFTLTV NSLQPEDFATYYCQQGDSVP LTFGGGTRLEIKTTTPAPRPPT PAPTIASQPLSLRPEACRPAA GGAVHTRGLDFACDIYWAPL AGTCGVLLLLSLVITLYCKRGRK KLLYIFKQPFMRPVQTTQEED GCSCRFPEEEEEGGCELRVKF SRSADAPAYQQGQNQLYNEL NLGRREEYDVLDRRRGRDPE MGGKPRRKNPQEGLYNELQK DKMAEAYSEIGMKGERRRGK GHDGLYQGLSTATKDTYDAL HMQALPPR (SEQ ID NO: 1030)	gtcctgcaaagcctccggtacacctttacgggctactaca tgcactgggtgcgccaggcaccaggacagggcttgaat ggatgggatggatcaaccctaattcgggcggaactaacta cgcacagaagttccaggggagagtgactctgactcggga tacctccatctcaactgtctacatggaactctcccgcttgcg gtcagatgatacggcagtgactactgcgcccgcgacatg aatatcctggctaccgtgcggtcgacatctggggacagg ggactatggttactgtctcatcgggcggtggaggtcagga ggaggcggtcgggaggcgaggttcggacattcagat gaccagtcctccatcctctgtcggccagcgtcggagat agggtgaccattacgtcgggctcgcgcaaagcatctcctc gtacctcaactggtatcagcaaaagccgggaaaggcgc ctaagctgctgatctacgcgcgttcgagcttgcaaaaggc ggtgccatccagattcgggacaggctcaggaaaccga cttcaccctgaccgtgaacagcctccagccggaggacttt gccacttactactgccagcaggagactccgtgcgctta cttcgggggggtaccgcctggagatcaagaccacta cccagcaccgaggccaccaccccggtcctaccatcg cctccagcctctgtcctgcgtcgggaggcatgtagacc gcagctggtggggcggtgcatacccggttctgacttcg cctgcgatatctacattgggcccctctggctggtacttcg ggctcgtcgtcttactcgtgatcactcttactgtaagcg gtcgggaagaagctgctgtacatcttaagcaaccctcatg aggcctgtgcagactactcaagaggaggacggctgttcat gccggttcccagaggaggaggaaggcggtgcgaactg cgctgaaattcagccgcagcgcagatgctccagcctac cagcaggggcagaaccagctctacaacgaactcaatctt ggtcggagagaggagtacgacgtgctggacaagcgga gaggacgggaccagaaatggcggaagccgcgca gaaagaatcccaagagggtgtacaacgagctcaa aaggataagatggcagaagcctatagcgagattggtatg aaaggggaacgcagaagaggcaaaggccacgacgg actgtaccagggactcagcaccgccaccaaggacacct atgacgctcttcatgacggcctgcccgcctcgg (SEQ ID NO: 1090)
SP-Linker 5 – ERmut2 – Furin cleavage site 2 – CD123 CAR	MALPVTALLPLALLLHAARPE SLALSLTADQMVSALLDAEPPI LYSEYDPTTRPFSEASMMGLLT NLADRELVHMINWAKRVPGF VDLTLHDQVHLLCAWMEILM IGLVWRSMEHPGKLLFAPNLL LDRNQGKCVEGGVEIFDMLLA TSSRFRMMNLQGEFVCLKSI ILLNSGVYTFLSSTLKSLEEKD HIHRVLDKITDTLIHLMAGALT LQQQHQRQAQLLLILSHIRHM SNKRMEHLYSMKCKNVVPLS DLLLEMLDAHRLGTGAEDPRP SRKRRSLGDIVGQVQLVQSGA EVKKPGASVKVSCASGYTFT GYMHWWVRQAPGQGLEWM GWINPNSGGTNYAQKFQGRV TLTRDTSISTVYMELSRRLSD DTAVYYCARDMNILATVPFDI WGQGTMTVTSSGGGSGGG SGGGGSDIQMTQSPSSLSA	atggccctccctgtcaccgccctgctgctccgctggctctt tgctccacgccgctcggcccgagTcgttggcactttccctg actgccgaccagatggtgtccgccccttctggacgccgagc ctccaattctgtactcggagtacgatccgactcggcgttct ccgaagccagcatgatgggcctgtgactaacctggcgg accgcgagttggtgcacatgattaactgggctaagcgggt gccgggctcgtggacctgacctgcacgaccaagtga cctcctggaatgcgcctggatggaaatcctcatgatcggcc tcgtgtggagatccatggagcatcccggaaagctcctggtt gcacccaacctcctgcttgatcgcaaccagggaatgc gtggaagggggtgtcgagatttcgacatgctgctgcacac ctctcccggtccggatgatgaatctgcaggagagaagagt tcgtgtgtctgaagtcaatcatcctgctgaactccggggtct ataccttctgagctgcacctcaagtactggaggaaaa agaccacatccatcgcgtgctcgataagatcacgacac ccttatccatctcatggcgaaggctggactgacctgcaac agcagcaccagaggctggcccagttgctgctgattctgag ccacatccggcacatgtcgaaagaggatggaacacc tgtacagcatgaagtgaagaacgtcgtgctcctgtccgat ctgctcctggaaatgctggacgcgcacagactcggaaacc ggcgcggaagacccccggccctccagggaagcgaaggt

	SVGDRVITICRASQSISSYLN WYQQKPGKAPKLLIYAASSLQ SGVPSRFSGSGSGTDFLT NSLQPEDFATYYCQQGDSVP LTFGGGTRLEIKTTTPAPRPPT PAPTIASQPLSLRPEACRPAA GGAVHTRGLDFACDIYWAPL AGTCGVLLLSLVITLYCKRGRK KLLYIFKQPFMRPVQTTQEED GCSCRFPEEEEGGCELRVKF SRSADAPAYQQGQNQLYNEL NLGRREEYDVLDKRRGRDPE MGGKPRRKNPQEGLYNELQK DKMAEAYSEIGMKGERRRGK GHDGLYQGLSTATKDTYDAL HMQALPPR (SEQ ID NO: 1031)	ccctcggagacgtgggtcaagtgaactcgtccaaagcg gagcgggaagtcaagaaacccggagcgagcgtgaaagt gtcctgcaaagcctccggctacacctttacgggtactaca tgcactgggtgcgccaggcaccaggacagggtcttgaat ggatgggatggatcaaccctaattcgggagggaactaacta cgacagaagttccaggggagagtgtactgtactcggga tacctccatctcaactgtctacatggaactctcccgcttgcg gtcagatgatacggcagtgactgtactgcgcccgcgacatg aatatcctggctaccgtgccgttcgacatctggggacagg ggactatggttactgtctcatcgggagggtggaggttcagga ggaggcggctcgggaggcggagggttcggacattcagat gaccagtcctccatcctctctgtcggccagcgtcggagat agggtgaccattacgtcgggcccctcgcaaagcatctcctc gtacctcaactggtatcagcaaaagccgggaaaggcgc ctaagctgtgtatcagccgcttcgagcttgcaaaggcg ggtgccatccagattctcgggacaggtcaggaaaccga ctcacctgaccgtgaacagcctccagccggaggacttt gccacttactgtccagcaggagactccgtgcgctta cttcgggggggttaccgcctggagatcaagaccacta cccagcaccgaggccaccacccggctcctaccatcg cctccagcctctgtccctgcgtcggaggcatgtagacc gcagctggtggggccgtgcataccggggtcttgacttcg cctgcgatatctacattggggccctctggctggacttcg ggctcgtgtcttactcgtgtatcactcttactgtaagcgcg gtcgggaagaagctgtgtacatctttaagcaacccttcag aggcctgtgcagactactcaagaggaggacggctgttcag gccggtcccagaggaggagggaaggcggctgcgaactg cgcgtgaaattcagccgcagcgcagatgtccagcctac cagcaggggcagaaccagctctacaacgaactcaatctt ggtcggagagaggagtacgacgtgtggacaagcggga gaggacgggaccagaaatgggcgggaagccgcgca gaaagaatcccaagaggggcctgtacaacgagctcaa aaggataagatggcagaagcctatagcgagattggtatg aaaggggaacgcagaagaggcaaggccacgacgg actgtaccagggaactcagcaccgccaccaaggacacct atgacgctcttcacatgcaggccctgcgcctcgg (SEQ ID NO: 1091)
SP-Linker 5 – ERmut1 – Furin cleavage site 3 – CD123 CAR	MALPVTALLPLALLHAARPE SLALSLTADQMVSALLDAEPPI LYSEYDPTTRPFSEASMMGLLT NLADRELVHMINWAKRVPGF VDLALHDQVHLLECAWMEILM IGLVWRSMEHPGKLLFAPNLL LDRNQGKCVEGGVEIFDMLLA TSSRFRMMNLQGEFVCLKSI ILLNSGVYTFLSSTLKSLEEKD HIHRVLDKITDTLIHLMAGALT LQQHQRLAQLLLILSHIRHM SSKRMEHLYSMKCKNVVPLS DLLLEMLDAHRLGTGAEDPRP SRKRRQVQLVQSGAEVKKPG ASVKVSCASGYTFTGYMH WVRQAPGQGLEWMGWINPN SGGTNYAQKFQGRVTLTRDT SISTVYMELSRLSDDTAVYY CARDMNILATVPFDIWGQGT	atggccctccctgtcaccgcctgtcgttccgctggctcttc tgctccacgccgctcggcccgagtcgttggcacttccctga ctgccgaccagatgggtgtccgccttctggacgccgagcct ccaattctgtactcggagtacgatccgactgcgccgttctcc gaagccagcatgatgggcctgttgactaacctggcggacc gcgagttggtgcacatgattaactgggctaagcgggtgccg ggcttcgtggacctggccctgcacgaccaagtgcacctcct ggaatgcgcctggatggaatcctcatgatcgccctcgtgt ggagatccatggagcatcccgaaagctcctgtttgaccc aacctcctgcttgatcgcaaccagggaagaatgcgtggaag ggggtgtcgagatttgcacatgtgtcgtccacctcttccc ggttccggatgatgaatctgcagggagaagagttcgtgtgt ctgaagtcaatcatcctgtgtaactccggggtctataccttc ctgagctcgacctcaagtcactggaggaaaaagaccaca tccatcgcgtgtcgtgataagatcaccgacaccttatccatc tcatggcgaaggctggactgacctgcaacagcagcacca

	VTVSSGGGGSGGGGSGGGG SDIQMTQSPSSLSASVGDRT ITCRASQSISSYLNWYQKPG KAPKLLIYAASSLQSGVPSRFS GSGSGTDFTLTVNSLQPEDFA TYCQQGDVPLTFGGGTRL EIKTTTPAPRPPTPAPTIASQP LSLRPEACRPAAGGAVHTR GLDFACDIYIWAPLAGTCG VLLLVLITLYCKRGRKLL YIFKQPFMRPVQTTQEEDG CSCRFPEEEEGGCELRVK FRSADAPAYQQGQNQLY NELNLGRREEYDVLDRR GRDPEMGGKPRRKNPQE GLYNELQKDKMAEAYSEIG MKGERRRGKGHGGLYQGL STATKDTYDALHMQALPPR (SEQ ID NO: 1032)	gaggctggcccagttgctgctgattctgagccacatccggc acatgtcgtccaagaggatggaacacctgtacagcatgaa gtgcaagaacgtcgtgcctctgtccgatctgctcctggaat gctggacgcgcacagactcggaaccggcgcggaagaccc ccggccctccaggaagcgaaggcaagtgaactcgtccaa agcggagcggagtgcaagaaaccggagcgagcgtgaaa gtgtcctgcaaagcctccggctacacctttacgggtactac atgcactgggtgcgcaggcaccaggacagggtcttgaat ggatgggatggatcaaccctaattcgggcggaactaacta cgacagaagttccaggggagagtactctgactcgggat acctcatctcaactgtctacatggaactctccgcttgcg tcagatgatacggcagtgactactgcgccgcgacatgaa tatcctggctaccgtgccgttcgacatctggggacaggga ctatggttactgtctcatcgggcggtggagggtcaggagga ggcggtcgggagggcgagggttcggacattcagatgacc agtccccatcctctctgtcggccagcgtcgagatagggtg accattacctgtcgggcctcgaaagcatctcctgtacctc aactggtatcagaaaagccgggaaaggcgctaagctgc tgatctacgccgttcgagcttgcaaagcgggtgccatcc agattctcgggatcaggctcaggaaccgacttcacctgac cgtgaacagcctccagccggaggactttgccattactact gccagcaggagactccgtgccgttactttcggggggggt accgcctggagatcaagaccactacccagcaccgaggc caccaccccgctcctaccatcgctcctccagcctctgtcc tgcgtccggagggcatgtagaccgcagctgggtggggcgt gcataccggggtcttgacttcgctgcgatattctacattg ggcccctctggctggtacttcggggtcctgtgctttcactc gtgatcactctttactgtaagcggtcggaagaagctgct gtacatctttaagcaacccttcagaggcctgtgcagactac tcaagaggaggacggctgttcagccggtccagaggag gaggaaggcggctgcgaactgcgctgaaattcagccgca gcgcagatgctccagcctaccagcaggggcagaaccagct ctacaacgaactcaatcttggtcggagagaggagtacgac gtgctggacaagcggagaggacgggaccagaaatgggc gggaagccgcgcagaaagaatcccaagagggcctgtac aacgagctccaaaaggataagatggcagaagcctatagc gagattggtatgaaaggggaacgcagaagaggcaaaggc cagcagcgtgtaccagggactcagcaccgccaccaagg acacctatgacgtcttcacatgcaggccctgccgctcgg (SEQ ID NO: 1092)
SP-Linker 5 – ERmut2 – Furin cleavage site 3 – CD123 CAR	MALPVTALLPLALLHAAPE SLALSLTADQMVSALLDAEPI LYSEYDPTPRPFSEASMMGLLT NLADRELVHMINWAKRVPGF VDLTLHDQVHLLCAWMEILM IGLVWRSMEHPGKLLFAPNLL LDRNQGKCVGGVEIFDMLLA TSSRFRMMNLQGEFVCLKSI	atggccctccctgtaccgccctgctgctccgctggctcttc tgcctccagccgctcggcccgagTcgttggcactttccctg actgccgaccagatggtgtccgccccttcggagcccgagc ctccaattctgtactcggagtacgatccgactcggcgttct ccgaagccagcatgatgggcctgtgactaacctggcgg accgcgagttggtgcacatgattaaactgggctaagcgggt gccgggctcgtggacctgacctgcacgaccaagtga cctcctggaatgcgcctggatggaaatcctcatgatcgcc

	ILLNSGVYTFLSSTLKSLEEKD HIHRVLDKITDTLIHLMAKAGLT LQQHQRLAQLLLILSHIRHM SNKRMEHLYSMKCKNVVPLS DLLLEMLDAHRLGTGAEDPRP SRKRRQVQLVQSGAEVKKPG ASVKVSKASGYTFTGYMH WVRQAPGQGLEWMGWINPN SGGTNYAQKFQGRVTLTRDT SISTVYMELSRLSDDTAVYY CARDMNILATVPFDIWGQGT MTVSSGGGGSGGGGSGGGG SDIQMTQSPSSLSASVGDRT ITCRASQSISSYLNWYQQKPG KAPKLLIYAASSLQSGVPSRFS GSGSGTDFTLTVNSLQPEDFA TYQCQGDSDVPLTFGGGTRL EIKTTTPAPRPPTPAPTASQP LSLRPEACRPAAGGAVHTRG LDFACDIYWAPLAGTCGVLLL SLVITLYCKRGRKLLYIFKQP FMRPVQTTQEEDGCSCRFPE EEEGGCELRVKFSRSADAPA YQQGQNQLYNELNLGRREEY DVLDKRRGRDPEMGGKPRRK NPQEGLYNELQDKMAEAYS EIGMKGERRRGKGHDGLYQG LSTATKDTYDALHMQALPPR (SEQ ID NO: 1033)	tcgtgtggagatccatggagcatcccgaaagctcctgtt gcaccaacccctcgtgctgacgaaccagggaatgc gtggaaggggtgctgagatttcgacatgctgctgccac ctctcccggtccggatgatgaatcgcaggagagaagagt tcgtgtgtgaagtcaatcatcctgctgaactccgggtct ataccttcctgagctcgacctcaagtcactggaggaaaa agaccacatccatcgctgctgataagatcaccgacac ccttatccatctcatggcgaaggctggactgacctgcaac agcagcaccagaggctggcccagttgctgctgattctgag ccacatccggcacatgtcgacaagaggatggaacacc tgtacagcatgaagtgaagaacgtgctgctctgtccgat ctgctcctggaaatgctggacgcgcacagactcgggacg ggagctgaagatccacgacccagcagaaagcgacggc aagtgaactcgtccaaagcggagcggaaagtcaagaaa cccggagcgcgctgaaagtgtcctgcaaagcctccggc tacaccttacgggtactacatgcactgggtgcgcaggc accaggacagggtcttgatggatggatggaacacct aattcgggcggaactaactacgcacagaagtccagggg agagtgaactcgtactcgggatacctccatctcaactgtctac atggaactctccgctgctgctgcatgatacggcagtgta ctactgcgcccgcacatgaatactcgtgctaccgtgcgt tcgacatctggggacaggggactatggttactgtctcatcg ggcggtggagggtcaggaggaggcggtcgggaggcg gaggttcggacattcagatgacctagctcccatcctctgt cggccagcgtcggagatagggtgaccattacgtcggg cctcgcaaagcatctcctgtacctcaactggtatcagcaa aagccgggaaaggcgctaagctgctgatctacgcgct tcgagcttgcaaagcgggtgccatccagattcgggat caggctcaggaaccgacttcacctgacctgaacagcc tccagccggaggactttgccacttactgcccagcaggg agactccgtgcccgttacttccgggggggtaccgcctgg agatcaagaccactacccagcaccgaggccaccacc ccggtcctaccatcgctcccagcctctgtccctgcgtccg gaggcattgtagaccgcagctggtggggcgtgcatacc cggggtcttgacttcgctgcgatactacatttgggcccctc tggctggtacttgcggggtcctgctgtcttactcgtgatcac tcttactgtaagcgcggtcggagaagctgctgtacatctt aagcaacccttcatgaggcctgtgcagactactcaagag gaggacggctgttcatgcccgttcccagaggaggaggaa ggcggtgcgaactgcgctgaaattcagccgcagcgc agatgtccagcctaccagcggggcagaaccagctcta caacgaactcaatcttggtcggagagaggagtacgacgt gctggacaagcggagaggacgggaccagaaaatgggc gggaagcgcgcagaaaagaatccccaagagggcctgt acaacgagctccaaaaggataagatggcagaagcctat agcgagattggtatgaaaggggaacgcagaagaggca aaggccacgacggactgtaccagggactcagcaccgcc accaaggacacctatgacgtcttcacatgcaggccctgc cgctcgg (SEQ ID NO: 1093)
SP-Linker 5 – ERmut1 – Furin cleavage site 2 – BCMA CAR	MALPVTALLPLALLLHAARPE SLALSLTADQMVSALLDAEPPI LYSEYDPTRPFSEASMMGLLT NLADRELVHMINWAKRVPGF VDLALHDQVHLLCAWMEILM IGLVWRSMEHPGKLLFAPNLL LDRNQGKCVEGGVEIFDMLLA	atggccctccctgtcaccgcccgtgctgtccgctggtctt tgcctccagcgcgctcggcccagTcgttggcactttccctg actgccgaccagatggtgtccgccccttctggacgcgagc ctccaattctgtactcggagtacgatccgactcgcctgtct ccgaagccagcatgatgggcctgtgactaacctggcgg accgcgagttggtgcacatgattaactgggctaagcgggt gccgggctcgtggacctggccctgcacgaccaagtga

	TSSRFRMMNLQGEEFVCLKSI ILLNSGVYTFLSSTLKSLEEKD HIHRVLDKITDTLIHLMAKAGLT LQQQHQRRLAQLLLILSHIRHM SSKRMEHLYSMKCKNVVPLS DLLLEMLDAHRLGTGAEDPRP <u>SRKRRSLGDVGEVQLVESGG</u> GLVQPGGSLRLSCAVSGFALS NHGMSWVRRAPGKGLEWVS GIVYSGSTYYAASVKGRFTISR DNSRNTLYLQMNSLRPEDTAI YYCSAHGGESDVWGQGTTVT VSSASGGGGSGGRASGGGG SDIQLTQSPSSLSASVGDRVTI TCRASQSISSYLNWYQQKPG KAPKLLIYAASSLQSGVPSRFS GSGSGTDFTLTISSLQPEDFA TYYCQQSYSTPYTFGQGTKV EIKTTTPAPRPPTPAPTIASQP LSLRPEACRPAAGGAVHTRG LDFACDIYWAPLAGTCGVLLL SLVITLYCKRGRKLLYIFKQP FMRPVQTTQEEDGCSCRFE EEEGGCELRVKFSRSADAPA YQQGQNQLYNELNLGRREEY DVLDKRRGRDPEMGGKPRRK NPQEGLYNELQDKMAEAYS EIGMKGERRRGKGHDGLYQG LSTATKDTYDALHMQALPPR (SEQ ID NO: 1034)	cctcctggaatgcgcctggatggaatcctcatgatcgcc tcgtgtggagatccatggagcatcccgaaagctcctgtt gcaccaacccctcgtgtgatcgcaaccagggaaaatgc gtggaaggggtgtcgagatcttcgacatgctgctgccac ctctcccggtccggatgatgaatcgcagggagaagagt tcgtgtgtcgaagtcaatcatcctgctgaactccgggtct ataccttcctgagctcgacctcaagtcactggaggaaaa agaccacatccatcgctgctcgataagatcaccgacac ccttatccatctcatggcgaaggctggactgacctgcaac agcagcaccagaggctggcccagtgctgctgattctgag ccacatccggcacatgctgctccaagaggatggaacacct gtacagcatgaagtgaagaacgctgctgctcctgtccgat ctgctcctggaaatgtcggacgcgcacagactcggaacc ggcgcggaagacccccggccctccaggaagcgaaggt ccctcggagacgtgggtgaagtgaattggtggaatcag ggggaggactgtgcagcctggaggatcgctgagactgtc atgtgccgtgtccggcttggcctgccaaccacgggatgtc ctgggtccgcgcgcgcctggaaagggcctcgaatgggt gtcgggtattgtgtacagcggtagcacctactatgccgat ccgtgaaggggagattcaccatcagcgggacaactcc aggaacactctgtacctccaatgaattcgtgaggccag aggacactgccatctactactgctccgcgcagtgccgaga gtccgacgtctggggacaggggaccaccgtgaccgtgtc tagcgcgtccggcggaggcggcagcgggggtcgggcac cagggggcggcggatcggacatccagctcaccagctcc ccgagctcgtgtccgcctcgtgggagatcgggtcacca tcacgtccgcgcgcagccagtcgatttccctctacctaac tggtaccaacagaagcccgaaaagccccgaagctctc atctacgcgcctcagcctgcagtcaggagtgcctcac ggttctccggctccggttcgggtactgttaccctgacct ttctccctgcaaccggaggactcgtacttactactgcc gcagtcgtactccacccctacactttcggacaaggcacc aaggctgaaatcaagaccactacccagcaccgaggcc acccaccccggtcctaccatcgctcccagcctctgtccc tgctcggaggcatgtagaccgcagctggtggggccg tgcatacccggggtctgtacttcgctgcgatactacattg ggccctctggctggtacttgccgggtcctgctgcttctact gtgatcactcttactgtaagcgggtcggaagaagctgct gtacatctttaagcaaccttcagtaggcctgtgcagacta ctcaagaggaggacggctgtcatgcccgttccagagg aggaggaaggcggctgcgaactgcgcgtgaaattcagc cgacgcgagatgtccagcctaccagcaggggcagaa ccagctctacaacgaactcaatcttggtcggagagagga gtacgacgtgctggacaagcggagaggacgggaccca gaaatggggcgggaagccgcgcgagaagaatcccaag agggcctgtacaacgagctccaaaaggataagatggca gaagcctatagcagattggtatgaaaggggaacgcag aagaggcaaaggccacgacggactgtaccagggactc agcaccgccaccaaggacacctatgacgtcttcacatg caggccctgccgcctcgg (SEQ ID NO: 1094)
SP-Linker 5 – ERmut2 – Furin cleavage site 2 – BCMA CAR	MALPVTALLLPLALLLHAARPE SLALSLTADQMVSALLDAEPII LYSEYDPTRPFSEASMMGLLT NLADRELVHMINWAKRVPGF VDLTLDHQQVHLLCAWMEILM IGLVWRSMEHGPKLLFAPNLL	atggccctccctgtcaccgcctgctgcttccgctggctcttc tgctccacgcgcgtcggcccgagTcgttggcactttccctg actgccgaccagatggtgtccgccccttctggacgccgagc ctccaattctgtactcggagtacgatccgactcggcgttct ccgaagccagcatgatgggcctgtgactaacctggcgg accgcgagttggtgcacatgattaactgggctaagcgggt

	LDRNQGKCVVEGGVEIFDMLLA TSSRFRMMNLQGEFVCLKSI ILLNSGVYTFLSSTLKSLEEKD HIHRVLDKITDTLIHLMAKAGLT LQQQHQRRLAQLLLILSHIRHM SNKRMEHLYSMKCKNVVPLS DLLLEMLDAHRLGTGAEDPRP SRKRRSLGDVGEVQLVESGG GLVQPGGSLRLSCAVSGFALS NHGMSWVRRAPGKLEWVS GIVYSGSTYYAASVKGRFTISR DNSRNTLYLQMNSLRPEDTAI YYCSAHGGESDVWQGTTVT VSSASGGGGSGGRASGGGG SDIQLTQSPSSLSASVGDRVTI TCRASQSISSYLNWYQQKPG KAPKLLIYAASSLQSGVPSRFS GSGSGTDFTLTISSLQPEDFA TYYCQQSYSTPYTFGQGTKV EIKTTTPAPRPPTPAPTIASQP LSLRPEACRPAAGGAVHTRG LDFACDIYWAPLAGTCGVLLL SLVITLYCKRGRKKLLYIFKQP FMRPVQTTQEEDGCSCRFPE EEEGGCELRVKFSRSADAPA YQQGQNQLYNELNLGRREEY DVLDKRRGRDPEMGGKPRRK NPQEGLYNELQDKMAEAYS EIGMKGERRRRGKGHDLGYQG LSTATKDTYDALHMQALPPR (SEQ ID NO: 1035)	gccgggcttcgtggacctgacctgcacgaccaagtgc cctcctggaatcgccctggatggaaatcctcatgatcgcc tcgtgtggagatccatggagcatcccgaaagctcctgtt gcaccaacctcctgcttgatcgcaaccagggaaaatgc gtggaaggggtgtcgagatttcgacatgctgctgccac ctctcccggtccggatgatgaatctgcaggagagaagagt tcgtgtgtctgaagtcaatcatcctgctgaactccgggtct atacctcctgagctcgacctcaagtcactggaggaaaa agaccacatccatcgctgctcgataagatcaccgacac ccttatccatctcatggcgaaggctggactgacctgcaac agcagcaccagaggctggcccagttgctgctgattctgag ccacatccggcacatgtcgaaacagaggatggaacacc tgtacagcatgaagtgaagaacgtgctgctctgtccgat ctgctcctggaaatgtggacgcgcacagactcggaaacc ggcgcggaagacccccggccctccaggaagcgaaggt ccctcggagacgtgggtgaagtgaattggtggaatcag ggggaggactgtgcagcctggaggatcgctgagactgtc atgtgccgtgtccggctttgccctgtccaaccacgggatgtc ctgggtccgcgcgcgcctggaaagggcctcgaatgggt gtcgggtattgtgtacagcgttagcacctactatgccgat ccgtgaaggggagattcaccatcagccgggacaactcc aggaacactctgtacctccaaatgaattcgctgaggccag aggacactgccatctactactgctccgcgcgtggcggaga gtccgacgtctggggacaggggaccaccgtgacctgtc tagcgcgtccggcggaggcggcagcgggggtcgggcat cagggggcggcggatcggacatccagctcaccagctcc ccgagctcgtgtccgcctcgtgggagatcgggtcacca tcacgtccgcgcgcagccagctgatttccctactacgaac tggtaccaacagaagcccggaagcccggaagcttctc atctacgcgcctcagcctgcagtcaggagtgcctcac ggttctccggctccgggtccgggtactgttaccctgacct ttctccctgcaaccggaggacttcgtacttactactgcca gcagtcgtactccacccctacactttcggacaaggcacc aaggctcgaatcaagaccactacccagcaccgaggcc acccaccccggtcctaccatcgctcccagcctctgtccc tgctcctggaggcatgtagaccgcagctggtggggcgg tgcatacccggtgtgtgacttcgctgcgatactacattg ggccctctggctggtacttcgggggtcctgctgcttactc gtgatcactcttactgtaagcgggtcggaagaagctgct gtacatctttaagcaaccctcatgaggcctgtgcagacta ctcaagaggaggacggctgtcatgcccgttccagagg aggaggaaggcggctgcgaactgcgcgtgaaattcagc cgacgcgcagatgtccagcctaccagcaggggcagaa ccagctctacaacgaactcaatcttggtcggagagagga gtacgacgtgtggacaagcggagagggacgggacca gaaatgggcggggaagccgcgcagaaagaatccccag agggcctgtacaacgagctccaaaaggataagatggca gaagcctatagcagattggtatgaaaggggaacgcag aagaggcaaaggccacgacggactgtaccagggactc agcaccgccaccaaggacacatgatgcgtcttcacatg caggccctgccgcctcgg (SEQ ID NO: 1095)
SP-Linker 5 – ERmut1 – Furin cleavage site 3 – BCMA CAR	MALPVTALLLPLALLHAARPE SLALSLTADQMVSALLDAEPI LYSEYDPTRPFSEASMMGLLT NLADRELVHMINWAKRVPGF VDLALHDQVHILLECAWMEILM	atggccctccctgtcaccgcctgctgcttccgtggtcttc tgctccacgcgcgtcggcccagTcgttggaacttccctg actgccgaccagatggtgtccgccttctggacgcgcgagc ctcaattctgtactcggagtacgatccgactcgccttct ccgaagccagcatgatgggcctgttgactaacctggcgg

	IGLVWRSMEHPGKLLFAPNLL LDRNQGKCEGGVEIFDMLLA TSSRFRMMNLQGEFVCLKSI ILLNSGVYTFLSSTLKSLEEKD HHRVLDKITDTLIHLMAKAGLT LQQQHQRQAQLLLILSHIRHM SSKRMEHLYSMKCKNVVPLS DLLLEMLDAHRLGTGAEDPRP SRKRREVQLVESGGGLVQPG GSLRLSCAVSGFALSNGHMS WVRAPGKGLEWVSGIVYSG STYYAASVKGRFTISRDNARN TLYLQMNSLRPEDTAIYYCSA HGGESDVWGQGTTVTVSSAS GGGGSGGRASGGGSDIQLT QSPSSLSASVGDRVTITCRAS QSISSYLNWYQQKPKAPKLL IYAASSLQSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQ QSYSTPYTFGQGTKVEIKTTT PPRPPTPAPTIASQPLSLRPE ACRPAAGGAVHTRGLDFACDI YIWAPLAGTCGVLLLSLVITLY CKRGRKKLLYIFKQPFMRPVQ TTQEEDGCSCRFPEEEEGGC ELRVKFSRSADAPAYQQGQN QLYNELNLGRREEYDVLDR RGRDPEMGGKPRRKNPQEG LYNELQDKMAEAYSEIGMKG ERRRGKGHDGLYQGLSTATK DTYDALHMQALPPR (SEQ ID NO: 1036)	accgcgagttggtgcacatgattaactgggctaagcgggt gccgggcttcgtggacctggccctgcacgaccaagtga cctcctggaatgcgcctggatggaaatcctcatgatcgcc tcgtgtggagatccatggagcatcccgaaagctcctgtt gcaccaacctcctgctgacgaaccagggaatgc gtggaaggggtgtcgagatttcgacatgctgctgccac ctctcccggtccggatgatgaatctgcaggagagaagagt tcgtgtgtctgaagtcaatcatcctgctgaactccgggtct atacctcctgagctcgacctcaagtcactggaggaaaa agaccacatccatcgctgctcgataagatcacggacac ccttatccatctcatggcgaaggctggactgacctgcaac agcagcaccagaggctggcccagttgctgctgattctgag ccacatccggcacatgtcgtccaaggaggatggaacacct gtacagcatgaagtgaagaacgtcgtgctcctgtccgat ctgctcctggaaatgtcggacgcgcacagactcGggacg ggagctgaagatccacgacctcagcagaagcgacggg aagtgaattggtggaatcagggggaggactgtgcagc ctggaggatcgtgagactgtcatgtccgtgtccggtttg ccctgtccaaccacgggatgtcctgggtccgcgcgcgc tggaaagggcctcgaatgggtgtcgggtattgtgtacagc ggtagcacctactatgccgatccgtgaaggggagattca ccacagccgggacaactccaggaaactcgttacctcc aaatgaattcgtgaggccagaggacactgccatctacta ctgctccgcgcgtggcggagagtccgacgtctggggaca ggggaccacgtgacgtgtctagcgcgtccggcgggag ggggcagcgggggtcgggcatcagggggcggcggatc ggacatccagctcaccagctcccgagctcgtgtccgcc tccgtgggagatcgggtcaccatcacgtccgcgcgcagc cagtcgatttctcctactgaactgttaccaacagaagcc cggaaaagccccgaagcttctcatctacgcgcctcgag cctgcagtcaggagtgcctcaccgttctccggtccgggt ccggtactgatttaccctgaccttctcctgcaaccgg aggacttcgctacttactactgccagcagtcgtactccacc cctacacttctcgacaaggcaccgaaggtcgaaatcaag accactacccagcaccgaggccaccaccccggtcct accatcgctcccagcctctgtccctgctcggaggcatg tagaccgcagctggtggggcgtgcatacccggggtctt gacttcgctcgcgatactacatttgggcccccttggtgta ctgctggggctcctgctgttctactcgtgatcactttactgta agcgcgggtcggaagaagctgctgtacatcttaagcaacc ctcatgaggcctgtgcagactactcaagaggaggacgg ctgttcagtcgggtcccgaggaggagggaaggcggctg cgaactgcgcgtgaaattcagccgcagcgcagatgctcc agcctaccagcaggggcagaaccagctctacaacgaac tcaatctggtcggagagaggagtacgacgtgctggaca agcggagaggacgggaccagaaatgggctgggaagc cgcgcagaaagaatccccaaggggcctgtacaacga gctccaaaaggataagatggcagaagcctatagcgaga ttggtatgaaaggggaacgcagaagaggcaaaggcca cgacggactgtaccaggactcagcaccgcccaccaagg acacatgacgctcttcacatgcaggccctgcgcctcg g (SEQ ID NO: 1096)
SP-Linker 5 – ERmut2 – Furin cleavage site 3 – BCMA CAR	MALPVTALLLPLALLHAARPE SLALSLTADQMVSALLDAEPI LYSEYDPTRPFSEASMMGLLT NLADRELVHMINWAKRVPGF	atggccctccctgtcaccgcctgctgcttcgctggctcttc tgcctcacgcgcgtcggcccgagTcgttggcactttccctg actgcccagcagatggtgtccgccccttctggacgcgcgagc ctccaattctgtactcggagtacgatccgactcgcgccttct

	VDLTLHDQVHLLCAWMEILM IGLVWRSMEHPGKLLFAPNLL LDRNQGKCVEGGVEIFDMLLA TSSRFRMMNLQGEFVCLKSI ILLNSGVYTFLSSTLKSLEEKD HIHRVLDKITDTLIHLMAGLT LQQQHQRQAQLLLILSHIRHM SNKRMEHLYSMKCKNVVPLS DLLLEMLDAHRLGTGAEDPRP SRKRREVQLVESGGGLVQPG GSLRLSCAVSGFALSNGMS WVRRAPGKGLEWVSGIVYSG STYYAASVKGRFTISRDNRN TLYLQMNSLRPEDTAIYYCSA HGGESDVWGGQTTVTVSSAS GGGGSGGRASGGGSDIQLT QSPSSLASVGDRTITCRAS QSISSYLNWYQQKPGKAPKLL IYAASSLQSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQ QSYSTPYTFGQGTKVEIKTTT PPRPPTPAPTIASQPLSLRPE ACRPAAGGAVHTRGLDFACDI YIWAPLAGTCGVLLLSLVITLY CKRGRKKLLYIFKQPFMRPVQ TTQEEDGCSCRFPEEEEGGC ELRVKFSRSADAPAYQQGQN QLYNELNLGRREEYDVLDRK RGRDPEMGGKPRRKNPQEG LYNELQDKMAEAYSEIGMKG ERRRGKGDGLYQGLSTATK DTYDALHMQALPPR (SEQ ID NO: 1037)	ccgaagccagcatgatgggctgtgactaacctggcgg acccgaggttggtgcacatgattaactgggctaagcgggt gccgggcttcgtggacctgacctgcacgaccaagtga cctcctggaatgcgcctggatggaaatcctcatgatcgcc tcgtgtggagatccatggagcatcccgaaagctcctgtt gcaccaacctcctgctgtatcgcaaccagggaatgc gtggaaggggtgtcgagatttgcacatgctgctgccac ctctcccggtccggatgatgaatctgcaggagagaagagt tcgtgtgtctgaagtcaatcatcctgctgaactccgggtct atacctcctgagctcgacctcaagtactggaggaaaa agaccacatccatcgctgctgataagatcaccgacac ccttatccatctcatggcgaaggctggactgacctgcaac agcagcaccagaggctggcccagttgctgctgattctgag ccacatccggcacatgtcgaaagaggatggaacacc tgtacagcatgaagtgaagaacgtgctgctgtccgat ctgctcctggaatgtggacgcgcacagactcgggacg ggagctgaagatccacgacctcagaaagcgacggg aagtgaattggtggaatcagggggaggactgtgcagc ctggaggatcgtgagactgtcatgtccgtgtccggctttg ccctgtccaaccacgggatgtctgggtccgcgcgcgc tggaaaggccctcgaatgggtgtcgggtattgtgacagc ggtagcacctactatgccgcacatcgtaaggggagattca ccatcagccgggacaactccaggaaactctgtacctcc aaatgaattcgtgaggccagaggacactgccatctacta ctgctccgcgcgtggcggagagtccgacgtctggggaca ggggaccaccgtgacctgtctagcgcgtccggcggag gcggcagcgggggtcgggcatcagggggcgccggatc ggacatccagctcaccagctcccgagctcgtgtccgcc tccgtgggagatcgggtaccatcagctccgcgcgcagc cagtcgatttctcctacctgaactgttaccacagaagcc cggaaaagccccgaagcttctcatctacgcgcgcctcgag cctgcagtcaggagtgcctcagcgttctccggtcgggt ccggtactgatttaccctgaccttctccctgcaaccgg aggacttcgctacttactactgccagcagtcgtactccacc ccctacacttctcgacaaggcaccgaaggtcgaaatcaag accactacccagcaccgaggccaccaccccggtcct accatgcctcccagcctctgtccctgctcggaggcatg tagaccgcgagctggtggggccgtgcatacccggggtctt gacttcgctcgcgatactacatttgggcccccttggtgta ctgcggggtcctgctgttctactcgtgatcacttttactgta agcgcgggtcggaagaagctgctgtatctttaaagcaacc ctctcatgaggcctgtgcagactactcaagaggaggacgg ctgttcagtcgggttcccagaggagggaaggcggctg cgaactgcgcgtgaaattcagccgcagcagatgctcc agcctaccagcaggggcagaaccagctctacaacgaac tcaatcttggtcggagagaggagtacgacgtgctggaca agcggagaggacgggaccagaaatgggcggaagc cgcgagaaagaatccccaaggggcctgtacaacga gctccaaaaggataagatggcagaagcctatagcgaga ttggtatgaaaggggaacgcagaagaggcaaaggcca cgacggactgtaccaggactcagcaccgccaccaagg acacctatgacgctcttcacatgcaggccctgccgcctcg g (SEQ ID NO: 1097)
SP-Linker 6 – ERmut1 – Furin	MALPVTALLLPLALLLHAARPQ SLALSLTADQMVSALLDAEPP	atggccctccctgtcaccgcccctgctgcttccgctggctctt tgcctccacgcccgtcggccccagtcgttggcacttccctga

cleavage site 2 – CD19 CAR2	LYSEYDPTRPFSEASMMGLLT NLADRELVHMINWAKRVPGF VDLALHDQVHLLCAWMEILM IGLVWRSMEHPGKLLFAPNLL LDRNQGKCVEGGVEIFDMLLA TSSRFRMMNLQGEFVCLKSI ILLNSGVYTFLSSTLKSLEEKD HIHRVLDKITDTLIHLMAGALT LQQQHQRQAQLLLILSHIRHM SSKRMEHLYSMKCKNVVPLS DLLLEMLDAHRLGTGAEDPRP SRKRRSLGVDGEIVMTQSPAT LSLSPGERATLSCRASQDISK YLNWYQQKPGQAPRLIYHTS RLHSGIPARFSGSGSGTDYTL TISSLQPEDFAVYFCQQGNTL PYTFGGQTKLEIKGGGSGG GGSGGGGSQVQLQESGPG VKPSETLSLTCTVSGVSLPDY GVSWIRQPPGKGLEWIGVIW GSETTYYSSSLKSRVTISKDN SKNQVSLKLSSVTAADTAVYY CAKHYYYGGSYAMDYWGQG TLVTVSSTTTPAPRPPTPPTI ASQPLSLRPEACRPAAGGAV HTRGLDFACDIYWAPLAGTC GVLLLSLVITLYCKRGRKKLLYI FKQPFMRPVQTTQEEDGCSC RFPEEEEEGGCELRVKFSRSA DAPAYQQGQNQLYNELNLGR REEYDVLDKRRGRDPEMGGK PRRKNPQEGLYNELQKDKMA EAYSEIGMKGERRRGKGHDG LYQGLSTATKDTYDALHMQAL PPR (SEQ ID NO: 1038)	ctgccgaccagatgggtgccgacctctggacgccgagcc tccaattctgtactcggagtagatccgactcgccgttctc cgaagccagcatgatgggctgttgactaacctggcgga ccgaggttggtgcacatgattaactgggctaagcgggtg ccgggctcgtggacctggccctgcacgaccaagtgcac ctcctggaatgcgctggatggaatcctcatgatcgccct cgtgtggagatccatggagcatcccgaaagctcctgtttg cacccaacctcctgctgatcgcaaccagggaatgcgt ggaaggggtgtcgagatttcgacatgctgctcgccacct cttcccggttccggatgatgaatcgaggagagaagagttc gtgtgtctgaagtcaatcatcctgctgaactccggggtctat acctcctgagctcgaccctcaagtactggaggaaaaa gaccacatccatcgctgctcgataagatcaccgacacc cttatccatctcatggcgaaggctggactgacctgcaaca gcagcaccagaggctggccaggtgtgctgattctgagc cacatccggcacatgtcgccaagaggatggaacacctg tacagcatgaagtgaagaacgctgctcctctgcccagatc gctcctggaatgctggacgcgcacagactcggaaccg gcgcggaagacccccggccctccaggaaagcgaaggctc cctcggagacgtgggtgaaattgtatgaccagtcacc gccactcttagccttccaccgggtgagcgcgaaccctgtc ttgcagagcctccaagacatctcaaaataaccttaattgt atcaacagaagcccgacaggctcctgcctctgatcta ccacaccagccgctccattctggaatccctgccagggtc agcggtagcggatctgggacgactacacctcactatca gctcactgcagccagaggactcgtgtctattctgtcagc aagggaacacctgcccacaccttggacagggcacca agctcgagattaaagggtggagggtggcagcggaggaggt gggtccggcggtggaggaaagcagggtccaactccaaga aagcggaccgggtctgtgaagccatcagaaactcttca ctgactgtactgtgagcggagtgtctctcccagattacggg gtgtcttgatcagacagccaccggggaagggtctggaat ggattggagtatttggggctctgagactactactactctc atccctcaagtacgcgtcaccatctcaaaggacaactct aagaatcagggtgtactgaaactgtcatctgtgaccgcag ccgacaccgctgtactattgcgctaagcattactattatg gcgggagctacgcaatggattactgggacaggggtactct ggtcacctgtccagcaccactacccagcaccgaggcc accaccccggtcctaccatcgctcccagcctctgtccc tgcgtccggaggcatgtagaccgcagctggtggggcgg tgcatacccggttctgacttcgctgcgatactacatttg ggccctctggctggtacttgcggggtcctgtgcttctactc gtgatcactcttactgtaagcgcgggtcggagaagctgct gtacatctttaagcaacccttcaggcctgtgcagacta ctcaagaggaggacggctgtcatgcccgttccagagg aggagggaaggcggctgcgaactgcggtgaaattcagc cgcagcgcagatgctccagcctaccagcagggggcagaa ccagctctacaacgaactcaatcttggtcggagagagga gtacgacgtgctggacaagcggagaggacgggaccca gaaatgggcggggaagccgcgcagaaagaatcccaag agggcctgtacaacgagctccaaaaggataagatggca gaagcctatagcagattggtatgaaaggggaacgcag aagaggcaaaggccacgacggactgtaccagggactc agcaccgccaccaaggacacctatgacgctctcacatg caggccctgccgctcgg (SEQ ID NO: 1098)
SP-Linker 6 –	MALPVTALLLPLALLLHAARPQ	atggccctccctgtcaccgacctgctgcttccgtggtctctc

ERmut2 – Furin cleavage site 2 – CD19 CAR2	SLALSLTADQMVSALLDAEPPI LYSEYDPTRPFSEASMMGLLT NLADRELVHMINWAKRVPGF VDLTLHDQVHLLCAWMEILM IGLVWRSMEHPGKLLFAPNLL LDRNQGKCVEGGVEIFDMLLA TSSRFRMMNLQGEFVCLKSI ILLNSGVYTFLSSTLKSLEEKD HIHRVLDKITDTLIHLMAGALT LQQQHQRQAQLLLILSHIRHM SNKRMEHLYSMKCKNVVPLS DLLLEMLDAHRLGTGAEDPRP SRKRRSLGDVGEIVMTQSPAT LSLSPGERATLSCRASQDISK YLNWYQQKPGQAPRLIYHTS RLHSGIPARFSGSGSGTDYTL TISSLQPEDFAVYFCQQGNLT PYTFGQGKLEIKGGGSGG GGSGGGGSQVQLQESGPG VKPSETLSLTCTVSGVSLPDY GVSWIRQPPGKGLEWIGVIW GSETTYYSSSLKSRVTISKDN SKNQVSLKLSSVTAADTAVYY CAKHYYYGGSYAMDYWGQG TLVTVSSTTTPAPRPPTPPTI ASQPLSLRPEACRPAAGGAV HTRGLDFACDIYWAPLAGTC GVLLLSLVITLYCKRGRKKLLYI FKQPFMRPVQTTQEEDGCSC RFPEEEEEGGCELRVKFSRSA DAPAYQQGQNQLYNELNLGR REEYDVLDKRRGRDPEMGK PRRKNPQEGLYNELQKDKMA EAYSEIGMKGERRRGKGHG LYQGLSTATKDTYDALHMQAL PPR (SEQ ID NO: 1039)	tgctccacgcccgtcgccccagtcgttggcactttccctga ctgccgaccagatggtgtccgcccttctggacgccgagcc tccaattctgtactcggagtagatccgactcgccgttctc cgaagccagcatgatggcctgttgactaacctggcgga ccgcgagttggtgcacatgattaactgggctaagcgggtg ccgggctcgtggacctgacctgcacgaccaagtgcac ctcctggaatgcgcctggatggaatcctcatgatcgccct cgtgtggagatccatggagcatcccgaaagctcctgtttg cacccaacctcctgctgatcgcaaccagggaatgcgt ggaaggggtgtcgagatfttcgacatgctgctgccacct cttcccggttccggatgatgaatgcgaggagagaggttc gtgtgtctgaagtcaatcatcctgctgaactccggggtctat accttctgagctcgacctcaagtactggaggaaaaa gaccacatccatcgctgctcgataagatcacgcacacc cttatccatctcatggcgaaggctggactgacctgcaaca gcagcaccagaggctggccaggtgtgctgattctgagc cacatccggcacatgtcgacaagaggatggaacacct gtacagcatgaagtgaagaacgtcgtgacctgtccgat ctgctcctggaatgtggacgcgcacagactcggaacc ggcgcggaagacccccggccctccaggaagcgaaggt ccctcgagacgtgggtgaatgtgatgaccagtcacc cgccactcttagcctttcaccgggtgagcgcgaacctgt cttgacagagcctccaagacatctcaaatcttaattgg tatcaacagaagcccgacaggctcctgccttctgatcta ccacaccagccgctccattctggaatccctgccagggttc agcggtagcggatctgggaccgactacacctcactatca gctcactgcagccagaggactcgtgtctattctgtcagc aagggaacacctgcccacaccttggacagggcacca agctcgagattaaaggtggagggtggcagcggaggaggt gggtccggcggtggagggaagccagggtccaactccaaga aagcggaccgggtctgtgaagccatcagaaactcttca ctgactgtactgtgagcggagtgtctctcccgtattacggg gtgtcttgatcagacagccaccggggaaggggtctggaat ggattggagtatttggggctctgagactactactactctc atcccctcaagtcacgcgtcaccatctcaaggacaactct aagaatcagggtgactgaaactgtcatctgtgaccgcag ccgacaccgcccgtgtactattgcgctaagcattactattatg gccccgagctacgcaatggattactgggacaggggtactct ggtcaccgtgtccagcaccactacccagcaccgaggcc accacccccggctcctaccatcgccctccagcctctgtccc tgctccggaggcatgtagaccgcagctggtggggccg tgcataccggggctgtacttgcctgcgatactacatttg ggccctctggctggtacttgcggggtcctgctgtcttactc gtgatcactcttactgtaagcgcggtcggaagaagctgct gtacatctttaagcaaccttcatgaggcctgtgcagacta ctcaagaggaggacggctgttcacgctccagagg aggagggaagggcgtcgcaactgcgctgaaattcagc cgcagcgcagatgctccagcctaccagcaggggcagaa ccagctctacaacgaactcaatcttggtcgagagagga gtacgacgtgtggacaagcggagaggacgggaccca gaaatgggcccgaagccgcgagaaagaatcccaag agggcctgtacaacgagctccaaaaggataagatggca gaagcctatagcagattggtatgaaaggggaacgcag aagaggcaaaggccacgacggactgtaccagggactc agcaccgcccacaaaggacacctatgacgctctcacatg caggccctgccgcctcgg (SEQ ID NO: 1099)
---	--	--

SP-Linker 6 – ERmut1 – Furin cleavage site 3 – CD19 CAR2	MALPVTALLLPLALLLHAARPO SLALSLTADQMVSALLDAEPPI LYSEYDPTRPFSEASMMGLLT NLADRELVHMINWAKRVPGF VDLALHDQVHLLCAWMEILM IGLVWRSMHEHPGKLLFAPNLL LDRNQGKCEVEGGVEIFDMLLA TSSRFRMMNLQGEEFVCLKSI ILLNSGVYTFLSSTLKSLEEKD HIHRVLDKITDTLIHLMAKAGLT LQQQHQRALQALLILSHIRHM SSKRMEHLYSMKCKNVVPLS DLLLEMLDAHRLGTGAEDPRP SRKRREIVMTQSPATLSLSPG ERATLSCRASQDISKYLWYQ QKPGQAPRLLIYHTSRLHSGIP ARFSGSGSGTDYTLTISSLQP EDFAVYFCQQGNTLPYTFGQ GTKLEIKGGGSGGGSGGG GSQVQLQESGPGLVKPSETL SLTCTVSGVSLPDYGVSWIRQ PPGKGLEWIGVIWGSETTYYS SSLKSRVTISKDNSKNQVSLK LSSVTAADTAVYYCAKHYYYG GSYAMDYWGQGLTVTSSTT TPAPRPPTPAPTASQPLSLRP EACRPAAGGAVHTRGLDFAC DIYIWAPLAGTCGVLLLSLVITL YCKRGRKKLLYIFKQPFMRPV QTTQEEDGCSCRFPEEEEEGG CELRVKFSRSADAPAYQQGQ NQLYNELNLGRREEYDVLDK RRGRDPEMGGKPRRKNPQE GLYNELQKDKMAEAYSEIGMK GERRRGKGGHDGLYQGLSTAT KDTYDALHMQALPPR (SEQ ID NO: 1040)	atggccctccctgtcaccgcccctgtgcttccgctggctcttc tgctccacgcgcgtcgccccagtcgttggcacttccctga ctgccgaccagatgggtgtccgcccttctggacgcgagcc tccaattctgtactcggagtagatccgactcgccgttctc cgaagccagcatgatggcctgttgactaacctggcgga ccgcgagttgggtgcacatgattaactgggctaagcgggtg ccgggctcgtggacctggccctgcacgaccaagtgcac ctcctggaatgcgcctggatggaaatcctcatgatcgccct cgtgtggagatccatggagcatcccgaaagctcctgtttg caccacacctcctgcttgatcgcaaccagggaatgcgt ggaagggggtgtcgagatttgcacatgctgctcgccacct cttcccggttccggaatgatgaatcgcaggaggagaagagttc gtgtgtctgaagtcaatcatcctgtgaactccggggtctat acctcctgagctcgacctcaagtcactggaggaaaaa gaccacatccatcgctgctcgataagatcacgcacacc cttatccatctcatggcgaaggctggactgacctgcaaca gcagcaccagaggctggccagtgctgtgattctgagc cacatccggcacatgtcgtccaagaggatggaacacctg tacagcatgaagtgaagaacgtcgtgctctgtccgatct gctcctggaatgtctggacgcgcacagactcgggacgg gagctgaagatccacgaccagcagaagcgcagcggga aatgtgatgaccagtcacccgccactcttagcctttcacc cggtgagcgcgaacccctgtcttcagagcctcccaaga catctcaaaataccttaattggtatcaacagaagcccga caggctcctcgcttctgactaccacaccagccggctcca ttctggaatccctgccagggtcagcggtagcggatctggga ccgactacacctcactatcagctcactgcagccagagg acttcgctgtctattctgtcagcaagggaacacctgcct acaccttggacagggcaccaagctcgagattaaagggtg gagggtggcagcggaggagggtgggtccggcggtggagg aagccagggtcaactccaagaaagcggaccgggtctgt gaagccatcagaaactcttactgactgtactgtgagcg gagtgctctccccgattacgggggtgttgatcagacag ccaccggggaagggtctggaatggattggagtgattggg gctctgagactacttactcttcatccctcaagtcacgcgt caccatctcaaaggacaactctaagaatcagggtgtactg aaactgtcatctgtgaccgcagccgacaccgcccgtgact attgcgctaagcattactattatggcgggagctacgcaatg gattactggggacagggtactctggtaccggtgccagca ccactaccccagcaccgaggccacccacccggctccta ccatcgccctccagcctctgtccctgcgtccggaggcatgt agaccgcagctggtggggcgtgcataccgggggtctt gacttcgctgcgatatctacatttggccctctggctggta cttgccgggtcctgctgcttactcgtgatcactcttactgta agcgcgggtcggaagaagctgctgtacatctttaagcaacc cttcatgaggcctgtgcagactactcaagaggaggacgg ctgttcatgccggttcccagaggaggagggaaggcggctg cgaactgcgcgtgaaattcagccgcagcgcagatgctcc agcctaccagcaggggcagaaccagctctacaacgaac tcaatcttggtcggagagaggtagcagctgctggaca agcggagaggacgggaccagaaatgggcgggaagc cgcgagaaagaatcccaagagggtctgtacaacga gctccaaaaggataagatggcagaagcctatagcgaga ttggtatgaaaggggaacgcagaagaggcaaggcca cgacggactgtaccagggtactcagcaccgccaccaagg acacctatgacgctcttcacatgcaggccctgcgcctcg
---	--	---

		g (SEQ ID NO: 1100)
SP-Linker 6 – ERmut2 – Furin cleavage site 3 – CD19 CAR2	MALPVTALLLPLALLLHAARPQ SLALSLTADQMVSALLDAEPPI LYSEYDPTRPFSEASMMGLLT NLADRELVHMINWAKRVPGF VDLTLHDQVHLLECAWMEILM IGLVWRSMHEHPGKLLFAPNLL LDRNQGKCVVEGGVEIFDMLLA TSSRFRMMNLQGEEFVCLKSI ILLNSGVYTFLSSTLKSLEEKD HIHRVLDKITDTLIHLMAKAGLT LQQQHQRQAQLLLILSHIRHM SNKRMEHLYSMKCKNVVPLS DLLLEMLDAHRLGTGAEDPRP SRKRREIVMTQSPATLSLSPG ERATLSCRASQDISKYNWYQ QKPGQAPRLLIYHTSRLHSGIP ARFSGSGSGTDYTLTISSLQ EDFAVYFCQQGNTLPYTFGQ GTLKLEIKGGGSGGGSGGG GSQVQLQESGPGLVKPSETL SLTCTVSGVSLPDYGVSWIRQ PPGKGLEWIGVIWGSETTYYS SSLKSRVTISKDNSKNQVSLK LSSVTAADTAVYYCAKHYYG GSYAMDYWGQGLTVTSSTT TPAPRPPTPAPTIASQPLSLRP EACRPAAGGAVHTRGLDFAC DIYIWAPLAGTCGVLLLSLVITL YCKRGRKKLLYIFKQPFMRPV QTTQEEDGCSCRFPEEEEGG CELRVKFSRSADAPAYQQGQ NQLYNELNLGRREEYDVLDK RRGRDPEMGGKPRRKNPQE GLYNELQKDKMAEAYSEIGMK GERRRGKGGHDGLYQGLSTAT KDTYDALHMQALPPR (SEQ ID NO: 1041)	atggccctccctgtcaccgcccctgtgcttccgctggctcttc tgctccacgcccgtcggccccagTcgtggcactttccctg actgccgaccagatggtgtccgccccttctggacgccgagc ctccaattctgtactcggagtagcatccgactcggcgttct ccgaagccagcatgatgggcctgtgactaacctggcgg accgcgagttggtgcacatgattaactgggctaagcgggt gccgggctcgtggacctgacctgcacgaccaagtga cctcctggaatgcgcctggatggaaatcctcatgatcggcc tcgtgtggagatccatggagcatcccgaaagctcctgttt gcaccaacctcctgcttgatcgcaaccagggaatgc gtggaaggggtgtcgagatttcgacatgctgctgccac ctctcccggtccggatgatgaatctgcaggagagaagagt tcgtgtgtctgaagtcaatcatcctgctgaactccgggtct ataccttctgagctcgacctcaagtactggaggaaaa agaccacatccatcgcgtgtcgataagatcacggacac ccttatccatctcatggcgaaggctggactgacctgaac agcagcaccagaggctggcccagttgctgtgattctgag ccacatccggcacatgtcgaacaagaggatggaacacc tgtacagcatgaagtgcgaagcgtcgtgctctgtccgat ctgctcctggaatgtcggacgcgcacagactcGggacg ggagctgaagatccacgaccagcagaagcggacggg aaattgtgatgaccagtcaccggccactcttagccttcac ccggtgagcgcgcaacctgtcttcgagagcctccaag acatctcaaaataccttaattggtatcaacagaagcccg acaggctcctcgccttctgatctaccacaccagccggtcc attctggaatccctgccagggtcagcggtagcggatctggg accgactacacctcactatcagctcactgcagccagag gacttcgctgtctattctgtcagcaagggaacacctgccc tacaccttggacagggcaccaagctcgagattaaagggtg gagggtggcagcggaggagggtgggtccggcgggtgagg aagccagggtccaactccaagaaagcggaccgggtctgt gaagccatcagaaactcttactgactgtactgtgagcg gagtgctctccccgattacgggggtgttgatcagacag ccaccggggaagggtctggaatggattggagtgattggg gctctgagactacttactacttctatccctcaagtcacggt caccatctcaaaggacaactctaagaatcagggtgtactg aaactgtcatctgtgaccgcagccgacacgcgggtact attgcgctaagcattactattatggcgggagctacgcaatg gattactggggacagggtactctggtaccgtgtccagca ccactacccagcaccgaggccacccaccccggtccta ccatcgccctccagcctctgtccctgctcggaggcatgt agaccgcagctggtgggcccgtgcataccgggggtctt gacttcgctcgcgatactacatttggccctctggctggta cttgccgggtcctgctgttctactcgtgatcacttctactgta agcgcgggtcggaagaagctgctgtacatctttaagcaacc cttcatgaggcctgtgcagactactcaagaggaggacgg ctgttcatgccggttccagaggaggagggaaggcggctg cgaactgcgcgtgaaattcagccgcagcgcagatgctcc agcctaccagcaggggcagaaccagctctacaacgaac tcaatcttggtcggagagaggtagcagctgtctggaca agcggagaggacgggaccagaaatgggcgggaagc cgcgagaaagaatcccaagagggcctgtacaacga gctccaaaaggataagatggcagaagcctatagcgaga ttggtatgaaaggggaacgcagaagaggcaaggcca cgacggactgtaccagggtactcagcaccgccaccaagg

		acacctatgacgctcttcacatgcaggccctgccgcctcg g (SEQ ID NO: 1101)
SP-Linker 6 – ERmut1 – Furin cleavage site 2 – CD123 CAR	MALPVTALLPLALLLHAARPQ SLALSLTADQMVSALLDAEPPI LYSEYDPTRPFSEASMMGLLT NLADRELVHMINWAKRVPGF VDLALHDQVHLLECAWMEILM IGLVWRSMEHPGKLLFAPNLL LDRNQGKCVEGGVEIFDMLLA TSSRFRMMNLQGEFVCLKSI ILLNSGVYTFLSSTLKSLEEKD HIHRVLDKITDTLIHLMAKAGLT LQQQHQRQAQLLLILSHIRHM SSKRMEHLYSMKCKNVVPLS DLLLEMLDAHRLGTGAEDPRP SRKRRLGQVQVQLVQSGA EVKKPGASVKVSCKASGYTFT GYMHWVRQAPGQGLEWM GWINPNSGGTNYAQKFQGRV TLTRDTSISTVYMELSRLRSD DTAVYYCARDMNILATVPFDI WGQGTMTVTVSSGGGSGGG GSGGGGSDIQMTQSPSSLSA SVGDRVITICRASQSISSYLN WYQQKPGKAPKLLIYAASSLQ SGVPSRFSGSGSGTDFTLTV NSLQPEDFATYYCQQGDSVP LTFGGGTREIKTTTPAPRPPT PAPTIASQPLSLRPEACRPAA GGAVHTRGLDFACDIYWAPL AGTCGVLLLSLVITLYCKRGRK KLLYIFKQPFMRPVQTTQEED GCSCRFPEEEEGGCELRVKF SRSADAPAYQQGQNQLYNEL NLGRREEYDVLDKRRGRDPE MGGKPRRKNPQEGLYNELQK DKMAEAYSEIGMKGERRRGK GHDGLYQGLSTATKDTYDAL HMQALPPR (SEQ ID NO: 1042)	atggccctccctgtcaccgccctgtgcttcgctggctcttc tgctccacgccgctcggccccagtcgttgccactttccctga ctgccgaccagatggtgtccgcccttctggacgccgagcc tccaattctgtactcggagtagatccgactcggcgttctc cgaagccagcatgatggcctgttgactaacctggcggga ccgagagtggtgcacatgattaactgggctaagcgggtg ccgggctcgtggacctggccctgcacgaccaagtgcac ctcctggaatgcgcctggatggaatcctcatgatcgccct cgtgtggagatccatggagcatcccgaaagctcctgtttg caccacacccctcctgtgatcgcaaccagggaagcgtggt ggaagggggtgtcgagatttgcacatgctgctcgccacct cttcccggttcgggatgatgaatcgcaggagagaagagttc gtgtgtcgaagtcaatcatcctgtgaactccggggtctat acctcctgagctcgacctcaagtcactggaggaaaaa gaccacatccatcgctgctcgataagatcaccgacacc cttatccatcctatggcgaaggctggactgacctgcaaca gcagaccagaggctggccaggtgctgtgattctgagc cacatccggcacatgtcgtccaagaggatggaacactg tacagcatgaagtgaagaacgtcgtcctcgtcctgatct gctcctggaatgctggacgcgcacagactcgggaaccg gcgcggaagacccccggccctccagggaagcgaaggtc cctcggagacgtgggtcaagtgaactcgtccaaagcgg agcgggaagtcaagaaacccggagcgagcgtgaaagt tctgcaaagcctccggctacacctttacgggtactacat gcactgggtgcgccaggcaccaggacagggtcttgaatg gatgggatggatcaaccctaattcgggcggaactaactac gcacagaagtccaggaggaggtgactctgactcgggat acctccatcctaactgtctacatggaactctccgcttgccg tcagatgatacggcagtgactactgcgcccgcgacatga atatcctggctaccgtgccgttcgacatctggggacagg gactatggttactgtctcatcgggcgggtggaggtcaggag gaggcggctcgggaggcggaggttcggacattcagatg accagtcctccatcctcctcgtcggccagcgtcggagata gggtgaccattacctgtcggggcctcgcaagcatctcctcg tacctcaactggtatcagcaaaagccgggaaaggcgcc aagctgctgatctacgccgcttcgagcttcaaagcgggg tgccatccagattctcgggatcaggctcaggaaaccgactc accctgaccgtgaacagcctccagccggaggactttgcc acttactactgccagcaggagactcctgctccgcttacttc gggggggtaccgcctggagatcaagaccactacccc agcaccgaggccaccaccccggtcctaccatcgccctc ccagcctcgtccctgcgtcggaggcatgtagaccgcga gctgggtggggcgtgcatacccggggtcttgactcgcctg cgatatctacatttggggccctcgtgggtgacttgcgggt cctgctgcttctactcgtgatcactcttactgtaagcgcggtc ggaagaagctgctgtacatcttaagcaaccctcatgagg cctgtgcagactactcaagaggaggacggctgttcatgcc ggttcccagaggaggaggaaggcgggtgcgaactgcgc gtgaaattcagccgcagcgcagatgctccagcctaccag caggggcagaaccagctctacaacgaactcaatcttgt cggagagaggagtacgacgtgctggacaagcgggagag gacgggacccagaaatggggcgggaagccgcgcagaa agaatccccaagaggggcctgtacaacgagctccaaaag

		gataagatggcagaagcctatagcgagattggatgaaa ggggaacgcagaagaggcaaagggccacgacggactgt accagggactcagcaccgccaccaaggacacatgac gctcttcacatgcaggccctgccgcctcgg (SEQ ID NO: 1102)
SP-Linker 6 – ERmut2 – Furin cleavage site 2 – CD123 CAR	MALPVTALLLPLALLLHAARPQ SLALSLTADQMVSALLDAEPPI LYSEYDPTRPFSEASMMGLLT NLADRELVHMINWAKRVPGF VDLTLHDQVHLLCAWMEILM IGLVWRSMEHPGKLLFAPNLL LDRNQGKCVVEGGVEIFDMLLA TSSRFRMMNLQGEFVCLKSI ILLNSGVYTFLSSTLKSLEEKD HIHRVLDKITDTLIHLMKAGLT LQQQHQLRAQLLLILSHIRHM SNKRMEHLYSMKCKNVVPLS DLLLEMLDAHRLGTGAEDPRP <u>SRKRRSLGDVGVQVLVQSGA</u> EVKKPGASVKVSCASGYTFT GYMHWVRQAPGGGLEWM GWINPNSGGTNYAQKFQGRV TLTRDTSISTVYMELSRRLSD DTAVYYCARDMNILATVPFDI WGQGTMTVTVSSGGGSGGG GSGGGGSDIQMTQSPSSLSA SVGDRVTITCRASQSISSYLN WYQQKPGKAPKLLIYAASSLQ SGVPSRFSGSGSGTDFLT NSLQPEDFATYYCQQGDSVP LTFGGGTREIKTTTPAPRPPT PAPTIASQPLSLRPEACRPAA GGAVHTRGLDFACDIYWAPL AGTCGVLLLSLVITLYCKRGRK KLLYIFKQPFMRPVQTTQEED GCSCRFPEEEEGGCELRVKF SRSADAPAYQQGQNQLYNEL NLGRREEYDVLDKRRGRDPE MGGKPRRKNPQEGLYNELQK DKMAEAYSEIGMKGERRRGK GHDGLYQGLSTATKDTYDAL HMQALPPR (SEQ ID NO: 1043)	atggccctccctgtcaccgcccctgtgcttccgtggtcttc tgctccacgcccgtcgccccagTcggtggcactttccctg actgccgaccagatggtgtccgccccttctggacgccgagc ctccaattctgtactcggagtacgatccgactcgcctgtct ccgaagccagcatgatgggcctgttgactaacctggcgg accgcgagttggtgcacatgattaactgggctaagcgggt gccgggcttcgtggacctgacctgcacgaccaagtga cctcctggaatgcgcctggatggaaatcctcatgatcgcc tcgtgtggagatccatggagcatcccgaaagctcctgttt gcaccaaacctcctgcttgatcgcaaccagggaaaatgc gtggaagggggtgtcgagatttctgacatgctgctgccac ctctcccggtccggatgatgaatctgcaggagagaagagt tcgtgtgtctgaagtcaatcatcctgctgaactccggggtct ataccttctgagctcgaccctcaagtcactggaggaaaa agaccacatccatcgcggtgctcgataagatcaccgacac ccttatccatctcatggcgaaggctggactgacctgcaac agcagcaccagaggctggccagttgctgctgattctgag ccacatccggcacatgtcgacaagaggatggaacacc tgtacagcatgaagtgaagaacgtgctgctctgtccgat ctgctcctggaatgtggacgcgcacagactcggaacc ggcgcggaagacccccggccctccaggaagcgaagggt ccctcggagacgtgggtcaagtgaactcgtccaaagcg gagcgggaagtcaagaaacccggagcgagcgtgaaagt gtcctgcaaagcctccggctacacctttacgggctactaca tgactgggtgcgccaggcaccaggacagggtcttgaat ggatgggatggatcaaccctaattcgggcggaactaacta cgacagaagttccaggggagagtactctgactcgga tacctccatctcaactgtctacatggaactctcccgcttgcg gtcagatgatacggcagtgactactgcgcccgcgacatg aatatcctggctaccgtgccgttcgacatctgggacagg ggactatggttactgtctcatcgggcggttgagggtcagga ggaggcggtcgggaggcgagggttcggacattcagat gaccagtcctccatcctctgtcgccagcgctcgagat agggtgaccattacctgtcgggcctcgcaaagcatctcctc gtacctcaactggtatcagcaaaagccgggaaaggcgc ctaagctgtgatctacgcgcttcgagcttgcaaagcgg ggtgccatccagattctcggtatcaggctcaggaaccga cttcacctgacctgaacagcctccagccggaggacttt gccacttactgtccagcaggagactccgtgcccgtta ctttcggggggggtaccgcctggagatcaagaccacta ccccagcaccgaggccacccaccccggtcctaccatcg cctcccagcctctgtccctgcgtccggaggcatgtagacc gcagctggtggggccgtgcataccggggtcttgacttcg cctgcgatatctacatttggggccctctggctggtacttcgg ggtcctgctgtttactcgtgatcactcttactgtaagcgcg gtcggagaagaagctgtgtacatcttaagcaacccttcag aggcctgtgcagactactcaagaggaggacggctgttcat gccggttcccagaggaggaggaaggcggtgcgaactg cgctgaaattcagccgcagcgcagatgtccagcctac cagcagggggcagaaccagctctacaacgaactcaatctt

		ggtcggagagaggagtacgacgtgctggacaagcggga gaggacgggaccagaaatgggcgggaagccgcgca gaaagaatccccaagagggcctgtacaacgagctcaa aaggataagatggcagaagcctatagcgagattggtatg aaaggggaacgcagaagaggcaaaggccacgacgg actgtaccagggactcagcaccgccaccaaggacacct atgacgctcttcacatgcaggccctgccgcctcgg (SEQ ID NO: 1103)
SP-Linker 6 – ERmut1 – Furin cleavage site 3 – CD123 CAR	MALPVTALLLPLALLLHAARPQ SLALSLTADQMVSALLDAEPPI LYSEYDPTPRPFSEASMMGLLT NLADRELVHMINWAKRVPGF VDLALHDQVHLLCAWMEILM IGLVWRSMHEHPGKLLFAPNLL LDRNQGKCVGGVEIFDMLLA TSSRFRMMNLQGEFVCLKSI ILLNSGVYTFLSSTLKSLEEKD HIHRVLDKITDTLIHLMKAGLT LQQHQRLAQLLLILSHIRHM SSKRMEHLYSMKCKNVVPLS DLLLEMLDAHRLGTGAEDPRP SRKRRQVQLVQSGAEVKKPG ASVKVSKASGYTFTGYMH WVRQAPGQGLEWMGWINPN SGGTNYAQKFQGRVTLTRDT SISTVYMELSRLSDDTAVYY CARDMNILATVPFDIWQGGM VTVSSGGGGSGGGGSGGGG SDIQMTQSPSSLSASVGDRT ITCRASQSISSYLNWYQQKPG KAPKLLIYAASSLQSGVPSRFS GSGSGTDFTLTVNSLPEDFA TYQCQQGDSVPLTFGGGTRL EIKTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGG AVHTRGLDFACDIYIWAPLA GTCGVLLLSLVITLYCKRGR KKLLYIFKQPFMRPVQTTQ EEDGCSCRFPEEEEGGCE LRVKFSRSADAPAYQQGQ NQLYNELNLGRREEYDVL KRRGRDPPEMGGKPRRKNP QEGLYNELQKDKMAEAYS EIGMKGERRRGKGHDGLY QGLSTATKDTYDALHMQAL PPR (SEQ ID NO: 1044)	atggccctccctgtcaccgccctgtgcttccgtggctcttc tgctccacgccgctcgccccagctgttgccactttccctga ctgccgaccagatgggtgtccgccttctggacgccgagcct ccaattctgtactcggagtacgatccgactcgccgttctcc gaagccagcatgatgggcctgttgactaacctggcggacc gcgagttgggtgcacatgattaactgggctaagcgggtgccg ggcttcgtggacctggccctgcacgaccaagtgcacctct ggaatgcgcctggatggaaatcctcatgatcgccctcgtgt ggagatccatggagcatcccgaaagctcctgtttgcacc aacctcctgcttgatcgcaaccagggaagaaatgcgtggaag ggggtgtcgagattttcgacatgctgctgccacctcttccc ggttccggatgatgaatctgcaggagagaagagttcgtgtgt ctgaagtcaatcatcctgctgaactccggggtctataccttc ctgagctcgacctcaagtactggaggaaaaagaccaca tccatcgctgctcgataagatcacccgacaccttatccatc tcatggcgaaggctggactgacctgcaacagcagcacca gaggctggcccagttgctgctgattctgagccacatccggc acatgtcgtccaagaggatggaacacctgtacagcatgaa gtgcaagaacgtcgtgcctctgtccgatctgctcctggaat gctggacgcgcacagactcggaaccggcgcggaagacc ccggccctccaggaagcgaaggcaagtgaactcgtccaa agcggagcgggaagtcaagaaaccggagcgagcgtgaaa gtgtcctgcaaagcctccggctacaccttacgggctactac atgcactgggtgcgcaggcaccaggacagggtcttgaat ggatgggatggatcaaccctaattcgggcggaactaacta cgacagaagttccaggggagagtgactctgactcgggat acctccatctcaactgtctacatggaactctcccgttgccg tcagatgatacggcagtgactactcgccccgcagatgaa tatcctggctaccgtgccgttcgacatctggggacagggga ctatgggtactgtctcatcgggcgggtggaggttcaggagga ggcggctcgggagggcggaggttcggacattcagatgacc agtcccatcctctctgtcggccagcgtcggagatagggtg accattacctgtcgggcctcgaaagcatctcctgtacctc aactggatatcagcaaaagccgggaaggcgctaagctgc tgatctacgccgcttcgagcttgcaagcggggtgccatcc agattctcgggatcaggctcaggaaccgacttcacctgac cgtgaacagcctccagccggaggactttgccacttactact gccagcaggagactccgtgcgcttactttcggggggggt acccgctggagatcaagaccactacccagcaccgaggc caccacccggctcctaccatcgctcccagcctctgtccc tgctcggaggcatgtagaccgcagctgggtggggcgt

		gcataccgggggtcttgacttcgctgcgatattacatttg ggcccctctggctggacttgccgggctctgctgttctactc gtgatcactctttactgtaagcgcggctcgaagaagctgct gtacatctttaagcaacccttcatgaggcctgtgcagactac tcaagaggaggacggctgttcatgccggttccagaggag gaggaaaggcggctgcgaactgcgctgaaattcagccgca gcgcatgctccagcctaccagcaggggcagaaccagct ctacaacgaactcaatcttggtcggagagaggagtacgac gtgctggacaagcggagaggacgggaccagaaatgggc gggaagccgcgcagaaagaatcccaagaggcctgtac aacgagctccaaaaggataagatggcagaagcctatagc gagattggtatgaaagggaacgcagaagaggcaaaaggc cacgacggactgtaccagggactcagcaccgccaccaagg acacctatgacgctcttcacatgcaggccctgccgctcgg (SEQ ID NO: 1104)
SP-Linker 6 – ERmut2 – Furin cleavage site 3 – CD123 CAR	MALPVTALLPLALLHARPQ SLALSLTADQMVSALLDAEPI LYSEYDPTTRPFSEASMMGLT NLADRELVHMINWAKRVPGF VDLTLHDQVHLLCAWMEILM IGLVWRSMHEHPGKLLFAPNLL LDRNQGKCVGGVEIFDMLLA TSSRFRMMNLQGEFVCLKSI ILLNSGVYTFLSSTLKSLEEKD HIHRVLDKITDTLIHLMKAGLT LQQQHQRQAQLLLILSHIRHM SNKRMEHLYSMKCKNVVPLS DLLLEMLDAHRLGTGAEDPRP SRKRRQVQLVQSGAEVKKPG ASVKVSCASGYTFTGYMH WVRQAPGQGLEWMGWINPN SGGTNYAQKFQGRVTLTRDT SISTVYMELSRRLSDDTAVYY CARDMNILATVPFDIWQGGM VTVSSGGGGSGGGGSGGGG SDIQMTQSPSSLSASVGDRT ITCRASQSISSYLNWYQKPG KAPKLLIYAASSLQSGVPSRFS GSGSGTDFTLTVNSLPEDFA TYQCQGDSDVPLTFGGGTRL EIKTTTPAPRPPTPAPTASQP LSLRPEACRPAAGGAVHTRG LDFACDIYWAPLAGTCGVLL SLVITLYCKRGRKKLLYIFKQP FMRPVQTTQEEDGCSCRFPE EEEGGCELRVKFSRSADAPA YQQGQNQLYNELNLGRREEY DVLDKRRGRDPEMGGKPRRK NPQEGLYNELQKDKMAEAYS EIGMKGERRRGKGHDGLYQG LSTATKDTYDALHMQALPPR (SEQ ID NO: 1045)	atggccctccctgtcaccgccctgctgcttccgctggctcttc tgctccacgcgcgctcggcccccagTcggtggcacttccctg actgccgaccagatggtgtccgccccttctggacgccgagc ctccaattctgtactcggagtacgatccgactcggcgttct ccgaagccagcatgatgggctgtgtactaacctggcgg accgcgagttggtgcacatgattaactgggctaagcgggt gccgggctcgtggacctgacctgcacgaccaagtga cctcctggaatgcgcctggatggaatcctcatgatcgcc tcgtgtggagatccatggagcatcccggaagctcctgtt gcaccaacctcctgctgtatgcgaaccagggaatgc gtggaagggggtgtcgagatttcgacatgctgctcgccac ctctcccggtccggatgatgaatctgcagggagaagagt tcgtgtgtctgaagtcaatcatcctgctgaactccgggtct ataccttctgagctcgacctcaagtcactggaggaaaa agaccacatccatcgctgctcgataagatcaccgacac ccttatccatctcatggcgaaggctggactgacctgcaac agcagcaccagaggctggccagttgctgctgattctgag ccacatccggcacatgtcgaaagaggatggaacacc tgtacagcatgaagtgaagaacgtcgtgctctgtccgat ctgctcctggaatgctggacgcgcacagactcgggacg ggagctgaagatccacgaccagcagaaagcgacggc aagtgaactcgtccaaagcggagcgggaagtcaagaaa cccgagcagcgtgaaagtgtcctgcaaagcctccggc tacacctttacgggctactacatgcactgggtgcgaccaggc accaggacagggtottgatggatggatggatgaaccct aattcgggcggaactaactacgcacagaagttccagggg agagtgactctgactcgggatacctccatctcaactgtctac atggaactctcccgttgcggtcagatgatacggcagtgta ctactgcgcccgcgacatgaatacctggctaccgtgacct tcgacatctggggacaggggactatggttactgtctcatcg ggcgggtggaggtcaggaggaggcggctcgggaggcg gaggttcggacattcagatgaccagtcctccatcctctgt cggccagcgtcggagatagggtgaccattacctgtcggg cctcgcaaagcatctcctgtaacctcaactggatcagcaa aagccgggaaaggcgccgaagctgtgatctacgacct tcgagcttgcgaagcgggggtgccatccagattctcggat caggctcagggaaccgactcaccctgaccgtgaacagcc

		tcagccggaggactttgccacttactactgccagcaggg agactccgtgccgttactttcgggggggtaccgcctgg agatcaagaccactacccagcaccgaggccaccacc ccggctcctaccatgcctcccagcctctgctcctgcgtccg gaggcatgtagaccgcagctgggtggggccgtgcatacc cggggtcttgacttcgcctgcgatatctacattgggcccctc tggctggacttgccgggtcctgctgtttcactcgtgatcac tcttactgtaagcgcggtcggaagaagctgctgtacatctt aagcaaccctcatgaggcctgtgcagactactcaagag gaggacggctgtcatgccggtcccagaggaggaggaa ggcggctgcgaactgcggtgaaattcagccgcagcgc agatgctccagcctaccagcaggggcagaaccagctcta caacgaactcaatcttggtcggagagaggagtacgacgt gctggacaagcggagaggacgggacccagaaatgggc gggaagccgcgcagaaagaatcccaagaggggcctgt acaacgagctccaaaaggataagatggcagaagcctat agcgagattggtatgaaagggaacgcagaagaggca aaggccacgacggactgtaccagggactcagcaccgcc accaaggacacctatgacgctctcacatgcaggccctgc cgctcgg (SEQ ID NO: 1105)
SP-Linker 6 – ERmut1 – Furin cleavage site 2 – BCMA CAR	MALPVTALLPLALLLHAARPQ SLALSLTADQMVSALLDAEPPI LYSEYDPTRPFSEASMMGLLT NLADRELVHMINWAKRVPGF VDLALHDQVHLLCAWMEILM IGLVWRSMEHPGKLLFAPNLL LDRNQGKCVGGVEIFDMLLA TSSRFRMMNLQGEFVCLKSI ILLNSGVYTFLSSTLKSLEEKD HIHRVLDKITDTLIHLMAGALT LQQQHQRQAQLLLILSHIRHM SSKRMEHLYSMKCKNVVPLS DLLLEMLDAHRLGTGAEDPRP SRKRRSLGDVGEVQLVESGG GLVQPGGSLRLSCAVSGFALS NHGMSWVRRAPGKGLEWVS GIVYSGSTYYAASVKGRFTISR DNSRNTLYLQMNSLRPEDTAI YYCSAHGGESDVWGQGTTVT VSSASGGGSGGRASGGGG SDIQLTQSPSSLSASVGDRVTI TCRASQSISSYLNWYQQKPG KAPKLLIYAASSLQSGVPSRFS GSGSGTDFTLTISSLQPEDFA TYQCQSYSTPYTFGQGTKV EIKTTTPAPRPPTPAPTIASQP LSLRPEACRPAAGGAVHTRG LDFACDIYWAPLAGTCGVLLL SLVITLYCKRGRKKLLYIFKQP FMRPVQTTQEEDGCSCRFPE EEEGGCELRVKFSRSADAPA YQQGQNQLYNELNLGRREEY DVLDKRRGRDPEMGGKPRRK NPQEGLYNELQDKMAEAYS EIGMKGERRRGKGHDGLYQG LSTATKDTYDALHMQALPPR	atggccctccctgtcaccgcccgtgcttccgtggtcttc tgctccacgccgctcggccccagTcgtggcactttccctg actgccgaccagatgggtccgcccctctggacgccgagc ctccaattctgtactcggagtacgatccgactcggcgttct ccgaagccagcatgatgggcctgttgactaacctggcgg accgcgagttggtgcacatgattaactgggctaagcgggt gccgggcttcgtggacctggccctgcacgaccaagtga cctcctggaatgcgcctggatggaaatcctcatgatcgcc tcgtgtggagatccatggagcatcccgaaagctcctgtt gcaccaacctcctcgtgatcgcaaccagggaatgc gtggaaggggtgtcgagatttcgacatgctgctgccac ctctcccggtccggatgatgaatcgcaggagagaagagt tcgtgtgtcgaagtcaatcatcctgctgaactccgggtct atacctcctgagctcgacctcaagtcactggaggaaaa agaccacatccatcgctgctcgataagatcaccgacac ccttatccatctcatggcgaaggctggactgacctgcaac agcagcaccagaggctggcccagttgctgctgattctgag ccacatccggcacatgtcgtccaagaggatggaacacct gtacagcatgaagtgaagaacgtcgtgcctctgtccgat ctgtcctggaaatgtcggacgcgcacagactcggaaacc ggcgcggaagacccccggccctccaggaagcgaaggt ccctcggagacgtgggtgaagtgaattggtggaatcag gggaggactgtgcagcctggaggatcgtgagactgtc atgtgccgtgtccggcttgcctgtccaaccacgggatgtc ctgggtccgcccgcgcctggaaagggcctcgaatgggt gtcgggtattgtgtacagcggtagcacctactatgccgat ccgtgaaggggagattcaccatcagccgggacaactcc aggaacactctgtacctccaaatgaattcgtgaggccag aggacactgccatctactactgctccgcgcagtgccggaga gtccgacgtctggggacaggggaccaccgtgaccgtgtc tagcgcgtccggcggaggcggcagcgggggtcgggcat cagggggcggcggatcggacatccagctcaccagctcc ccgagctcgtgtccgcctcctgtggagatcgggtacca tcacgtccgcgcagccagctgattcctcctacctaac tggtaccaacagaagcccggaagccccaagcttctc atctacgccgcctcagcctgcagtcaggagtgcctcac

	(SEQ ID NO: 1046)	gggttcctccggctccgggtccgggtactgatttcacccctgaccat ttcctccctgcaaccggaggacttcgctacttactactgccca gcagtcgtactccacccctacactttcggacaaggcacc aaggctcgaataagaccactacccagcaccgaggcc accaccccggtcctaccatcgctccagcctctgtccc tgcgtccggaggcatgtagaccgcagctggtggggcgg tgcatacccggttctgacttcgctcgatattacattg ggccctctggctggtacttgcggggtcctgctgttctactc gtgatcactcttactgtaagcgcggtcggaagaagctgct gtacatctttaagcaacccttcagaggcctgtgcagacta ctcaagaggaggacggctgttcagtcgggtcccagagg aggaggaaggcgggtgcgaactgcgctgaaattcagc cgcagcgcagatgtccagcctaccagcaggggcagaa ccagctctacaacgaactcaatcttggtcggagagagga gtacgacgtgtggacaagcggagaggacggggacca gaaatgggcggaagccgcgcagaaagaatccccaag agggcctgtacaacgagctccaaaaggataagatggca gaagcctatagcgagattggtatgaaaggggaacgcag aagaggcaaaggccacgacggactgtaccagggactc agcaccgccaccaaggacacctatgacgctctcacatg caggcctgcgcctcgg (SEQ ID NO: 1106)
SP-Linker 6 – ERmut2 – Furin cleavage site 2 – BCMA CAR	MALPVTALLPLALLHAARPQ SLALSLTADQMVSALLDAEPPI LYSEYDPTRPFSEASMMGLLT NLADRELVHMINWAKRVPGF VDLTLHDQVHLLCAWMEILM IGLVWRSMEHPGKLLFAPNLL LDRNQGKCVEGGVEIFDMLLA TSSRFRMMNLQGEFVCLKSI ILLNSGVYTFLSSTLKSLEEKD HIHRVLDKITDTLIHLMAGALT LQQQHQRQAQLLLILSHIRHM SNKRMEHLYSMKCKNVVPLS DLLLEMLDAHRLGTGAEDPRP SRKRRSLGDVGEVQLVESGG GLVQPGGSLRLSCAVSGFALS NHGMSWVRRAPGKGLEWVS GIVYSGSTYYAASVKGRFTISR DNSRNTLYLQMNSLRPEDTAI YYCSAHGGESDVWQGQTTVT VSSASGGGSGGRASGGGG SDIQLTQSPSSLSASVGDRVTI TCRASQSISSYLNWYQQKPG KAPKLLIYAASSLQSGVPSRFS GSGSGTDFTLTISSLQPEDFA TYQCQSYSTPYTFGQGTKV EIKTTTPAPRPPTPAPTASQP LSLRPEACRPAAGGAVHTRG LDFACDIYWAPLAGTCGVLLL SLVITLYCKRGRKLLYIFKQP FMRPVQTTQEEDGCSCRFPE EEEGGCELRVKFSRSADAPA YQQGQNQLYNELNLGRREEY DVLDKRRGRDPEMGGKPRRK NPQEGLYNELQDKMAEAYS EIGMKGERRRGKGHDGLYQG	atggccctccctgtcaccgacctgctgctccgctggctcttc tgctccacgcccgtcggccccagTcgtggcactttccctg actgccgaccagatggtgtccgcccctctggacgccgagc ctccaattctgtactcggagtagatccgactcgcctgtct ccgaagccagcatgatgggcctgttgactaacctggcgg accgcgagttggtgcacatgattaactgggctaagcgggt gccgggcttcgtggacctgacctgcacgaccaagtga cctcctggaatgcgcctggatggaaatcctcatgatcgcc tcgtgtggagatccatggagcatcccgaaagctcctgtt gcaccaacctcctcctgtgatcgcaaccagggaatgc gtggaaggggtgtcgagatttgcacatgctgctcgccac ctctcccggtccggatgatgaatctgcaggagagaagagt tcgtgtgtctgaagtcaatcatcctgctgaactccggggtc ataccttccctgagctcgacctcaagtcaactggaggaaaa agaccacatccatcgcgtgtcgataagatcaccgacac ccttatccatctcatggcgaaggctggactgacctgcaac agcagcaccagaggctggcccagttgctgctgattctgag ccacatccggcacatgtcgaaacagaggatggaacacc tgtacagcatgaagtgaagaacgtcgtgctctgtccgat ctgctcctggaaatgtggacgcgcacagactcggaaacc ggcgcggaagacccccggcctccaggaagcgaaggt ccctcggagacgtgggtgaagtgaattggtggaatcag ggggaggactgtgcagcctggaggatcgtgagactgtc atgtgccgtgtccggctttgcctgtccaaccacgggatgtc ctgggtccgcccgcgcgctggaaagggcctcgaatgggt gtcgggtattgtgtacagcggtagcacctactatgccgcat ccgtgaaggggagattcaccatcagccgggacaactcc aggaacactctgtacctccaatgaattcgtgaggccag aggacactgccatctactactgctccgcgcatggcggaga gtccgacgtctggggacaggggaccaccgtgaccgtgtc tagcgcgtccggcggaggcggcagcgggggtcgggcat cagggggcggcggatcggacatccagctcaccagctcc ccgagctcgtgtccgctcctgtgggagatcgggtacca tcacgtgccgcgcagccagtcgatttctcctacctaag tggtaccaacagaagcccggaagccccgaagcttctc

	LSTATKDTYDALHMQALPPR (SEQ ID NO: 1047)	atctacgccgctcgagcctgcagtcaggagtgccctcac ggttctccggctccgggtccgggtactgattcacccctgaccat ttcctccctgcaaccggaggacttcgctactactactgcc gcagtcgtactccacccctacactttcggacaaggcacc aaggtcgaaatcaagaccactacccagcaccgaggcc accaccccggtcctaccatgcctcccagcctctgtccc tgcgtccggaggcatgtagaccgcagctggtggggcgg tgcatacccggtgtgtgacttcgctgcgatatctacattg ggccctctggctggtacttgcggggctcgtgctttcactc gtgatcactctttactgtaagcgcggtcggaagaagctgt gtacatctttaagcaacccttcagaggcctgtgcagacta ctcaagaggaggacggctgttcagtcgggtcccagagg aggaggaaggcgggtgcgaactgcgctgaaattcagc cgcagcgcagatgtccagcctaccagcaggggcagaa ccagctctacaacgaactcaatcttggtcggagagagga gtacgacgtgtgcgaagcggagaggacgggaccca gaaatgggcggaagccgcgcagaaagaatccccaag agggcctgtacaacgagctccaaaaggataagatggca gaagcctatagcgagattggtatgaaaggggaacgcag aagaggcaaaggccacgacggactgtaccagggactc agcaccgcaccacgaagacacctatgacgtcttcacatg caggccctgcgcctcgg (SEQ ID NO: 1107)
SP-Linker 6 – ERmut1 – Furin cleavage site 3 – BCMA CAR	MALPVTALLPLALLHAARPQ SLALSLTADQMVSALLDAEPPI LYSEYDPTTRPFSEASMMGLLT NLADRELVHMINWAKRVPGF VDLALHDQVHLLCAWMEILM IGLVWRSMHPGKLLFAPNLL LDRNQGKCVGGVEIFDMLLA TSSRFRMMNLQGEFVCLKSI ILLNSGVYTFLSSTLKSLEEKD HIHRVLDKITDTLIHLMAGALT LQQQHQLRAQLLLILSHIRHM SSKRMEHLYSMKCKNVVPLS DLLLEMLDAHRLGTGAEDPRP SRKRREVQLVESGGGLVQPG GSLRLSCAVSGFALSNGHMS WVRRAPGKGLEWVSGIVYSG STYYAASVKGRFTISRDNARN TLYLQMNSLRPEDTAIYYCSA HGGESDVWGGQTTVTVSSAS GGGSGGRASGGGSDIQLT QSPSSLSASVGDRTVITCRAS QSISSYLNWYQQKPGKAPKLL IYAASSLQSGVPSRFSGSGSG TDFTLTISLQPEDFATYYCQ QSYSTPYTFGGTKVEIKTTT PAPRPPTPAPTIASQPLSLRPE ACRPAAGGAVHTRGLDFACDI YIWAPLAGTCGVLLLSLVITLY CKRGRKKLLYIFKQPFMRPVQ TTQEEDGCSCRFPEEEEGGC ELRVKFSRSADAPAYQQGQN QLYNELNLGRREEYDVLDRK RGRDPEMGGKPRRKNPQEG LYNELQKDKMAEAYSEIGMKG	atggccctccctgtcaccgctgctgctccgctggctcttc tgctccacgcccgtcggccccagTcgtggcactttccctg actgccgaccagatggtgtccgcccctctggacgccgagc ctccaattctgtactcggagtacgatccgactcggcgttct ccgaagccagcatgatgggcctgtgactaacctggcgg accgcgagttggtgcacatgattaactgggctaagcgggt gccgggctcgtggacctggccctgcacgaccaagtga cctcctggaatgcgcctggatggaaatcctcatgatcgcc tcgtgtggagatccatggagcatcccgaaagctcctgtt gcaccaacccctcctgtgatcgcaaccagggaatgc gtggaagggggtgtcgagattttcgacatgtgctcgccac ctctcccggtccggatgatgaatcgcagggaagaggt tcgtgtgtctgaagtcaatcatcctgctgaactccggggtc ataccttctgagctcgacctcaagtcactggaggaaaa agaccacatccatcgctgtcgataagatcacccgacac ccttatccatctcatggcgaaggctggactgacctgcaac agcagcaccagaggctggccagttgctgtgattctgag ccacatccggcacatgtctccaagaggatggaacacct gtacagcatgaagtgaagaacgtcgtgacctgtccgat ctgctcctggaatgtggacgcgcacagactcGggacg ggagctgaagatccacgaccagcagaaagcgacggg aagtgaattggtgaatcagggggaggactgtgcagc ctggaggatcgctgagactgtcatgtccgtgtccggtttg ccctgtccaaccacgggatgtcctgggtccgcccgcgcgc tggaagggcctcgaatgggtgtcgggtattgtgtacagc ggtagcacctactatgccgatccgtgaaggggagattca ccatcagccgggacaactccaggaaactctgtacctcc aatgaattcgtgaggccagaggacactgccatctacta ctgctccgcgcagtcgggagagtcgcagctgtggggaca ggggaccaccgtgaccgtgtctagcgcgtccggcggag gcggcagcgggggtcgggcatcagggggcggcggatc ggacatccagctcaccagtcacccagctcgtgtccgccc tcgtgggagatcgggtaccatcagctgcgcgcgcagc cagtcgatttctcctacctgaactggtaccaacagaagcc

	ERRRGKGHDLGLYQGLSTATK DTYDALHMQALPPR (SEQ ID NO: 1048)	cggaaaagccccgaagcttctcatctacgccgcctcgag cctgcagtcaggagtgccctcacgggttccggctccgggt ccgggtactgatttcaccctgaccatttctccctgcaaccgg aggacttcgctacttactactgccagcagtcgtactccacc ccctacactttcggacaaggcaccaaggtcgaaatcaag accactacccagcaccgaggccaccaccccggtcct accatcgctcccagcctctgtccctgctcggaggcatg tagacccgcagctgggtggggccgtgcataccggggtctt gacttcgctcgatactacattgggccccctctggctggta cttgcggggtcctgctgttctactcgtgatcactttactgta agcgcggtcggaagaagctgctgtacatcttaagcaacc cttcatgaggcctgtgcagactactcaagaggaggacgg ctgttcatgccggttcccagaggaggagggaaggcggctg cgaactgcgcgtgaaatcagccgcagcgcagatgctcc agcctaccagcaggggcagaaccagctctacaacgaac tcaatcttggtcggagagaggagtagcagctgtggaca agcggagaggacgggaccagaaatggcggggaagc cgcgagaaagaatccccagagggcctgtacaacga gctccaaaaggataagatggcagaagcctatagcgaga ttggtatgaaaggggaacgcagaagaggcaaggcca cgacggactgtaccagggactcagcaccgccaccaagg acacctatgacgctctcacatgcaggccctgcgcctcg g (SEQ ID NO: 1108)
SP-Linker 6 – ERmut2 – Furin cleavage site 3 – BCMA CAR	MALPVTALLLPLALLLHAARPQ SLALSLTADQMVSALLDAEPPI LYSEYDPTRPFSEASMMGLLT NLADRELVHMINWAKRVPGF VDLTLHDQVHLLCAWMEILM IGLVWRSMEHPGKLLFAPNLL LDRNQGKCVEGGVEIFDMLLA TSSRFRMMNLQGEFVCLKSI ILLNSGVYTFLSSTLKSLEEKD HIHRVLDKITDTLIHLMAGALT LQQQHQRQAQLLLILSHIRHM SNKRMEHLYSMKCKNVVPLS DLLLEMLDAHRLGTGAEDPRP SRKRREVQLVESGGGLVQPG GSLRLSCAVSGFALSNGMS WVRRAPGKGLEWVSGIVYSG STYYAASVKGRFTISRDNARN TLYLQMNSLRPEDTAIYYCSA HGGESDVWGQGTTVTVSSAS GGGSGGGRASGGGSDIQLT QSPSSLSASVGDRVITCRAS QSISSYLNWYQKPKAPKLL IYAASSLQSGVPSRFSGSGSG TDFTLTISLQPEDFATYYCQ QSYSTPYTFGQGTKVEIKTTT PAPRPPTPAPTIASQPLSLRPE ACRPAAGGAVHTRGLDFACDI YIWAPLAGTCGVLLLSLVITLY CKRGRKKLLYIFKQPFMRPVQ TTQEEDGCSCRFPEEEEGGC ELRVKFSRSADAPAYQQGQN QLYNELNLGRREEYDVLDR RGRDPEMGGKPRRKNPQEG	atggccctccctgtcaccgccctgctgctccgctggctctt tgctccacgccgctcggccccagTcggtggcactttccctg actgccgaccagatgggtgcgccccttctggacgccgagc ctccaattctgtactcggagtagatccgactcggcgttct ccgaagccagcatgatgggcctgttgactaacctggcgg accgcgagttggtgcacatgattaactgggctaagcgggt gccgggctcgtggacctgacctgcacgaccaagtga cctcctggaatgcgcctggatggaatcctcatgatcgcc tcgtgtggagatccatggagcatcccgaaagctcctgtt gcaccaacctcctgcttgatcgcaaccagggaatgc gtggaagggggtgctgagatttgcagatgctgctgccac ctctcccggttcggatgatgaatctgcaggagagaagagt tcgtgtgtctgaagtcaatcatcctgctgaactccgggtct ataccttctgagctcgacctcaagtactggaggaaaa agaccacatccatcgctgctgataagatcacggacac ccttatccatctcatggcgaaggctggactgacctgcaac agcagcaccagaggctggccagtgctgctgattctgag ccacatccggcacatgtcgaaagaggatggaacacc tgtacagcatgaagtgaagaacgtcgtgctctgtccgat ctgctcctggaaatgctggacgcgcacagactcgggacg ggagctgaagatccacgaccagcagaaagcgacggg aagtgaattgggtgaatcagggggaggactgtgacgc ctggaggatcgtgagactgtcatgtgccgtgcccgttgg ccctgtccaaccacgggatgtcctgggtccgcccgcgcgc tggaaggggctcgaatgggtgtcgggtattgtgtacagc ggtagcacctactatgccgatccgtgaaggggagattca ccatcagccgggacaactccaggaaactctgtacctcc aatgaattcgtgaggccagaggacactgccatctacta ctgctccgcgcatggcggagagtccgacgtctggggaca ggggaccaccgtgaccgtgtctagcgcgtccggcggag gcggcagcgggggtcgggcatcagggggcggcggatc ggacatccagctcaccagtcctccgagctcgtgtccgcc tcctgtgggagatcgggtaccatcacgtgcgcgcgcagc

	LYNELQKDKMAEAYSEIGMKG ERRRGKGDGLYQGLSTATK DTYDALHMQALPPR (SEQ ID NO: 1049)	cagtcgatttctcctacctaactgggtaccaacagaagcc cggaaaagccccgaagcttctcatctacgccgctcgag cctgcagtcaggagtgccctcacgggtctccggctccggt ccggtactgatttcaccctgaccatttctccctgcaaccgg aggacttcgctacttactactgccagcagtcgtactccacc ccctacactttcggacaaggcaccagggtcgaaatcaag accactacccagcaccgaggccacccacccggctcct accatcgctcccagcctctgtccctgctcggaggcatg tagacccgcagctgggtggggccgtgcataccggggtctt gacttcgctcgatactacattgggcccctctggctggtgta cttgcggggtcctgctgcttctactcgatcactttactgta agcgcgggtcggaagaagctgctgtacatcttaagcaacc cttcatgaggcctgtgcagactactcaagaggaggacgg ctgttcatgccggttccagaggaggaggaaaggcggctg cgaactgcgctgaaattcagccgcagcgcagatgctcc agcctaccagcaggggcagaaccagctctacaacgaac tcaatcttggtcggagagaggagtacgacgtgtggaca agcggagaggacgggaccagaaatgggcggaagc cgcgcaaaagaatccccaaggggcctgtacaacga gctccaaaaggataagatggcagaagcctatagcgaga ttggtatgaaaggggaacgcagaaggaggcaaaggcca cgacggactgtaccagggactcagcaccgcccacaaagg acacctatgacgctctcacatgcaggccctgccgctcg g (SEQ ID NO: 1109)
--	---	---

EXAMPLE 29: TEMPORALLY CONTROLLED TOTAL B CELL DEPLETION.

The materials and methods employed in these experiments are now described.

Construction of CAR constructs including suicide genes. Constructs using the FMC63 (anti-CD19) single-chain variable fragment (scFv) used the previously described vector (pRRLSIN.cPPT.gene-
of interest-WPRE with a human EF1alpha promoter), which was modified for caspase-9 expression as follows:

1. For expression of the inducible caspase-9 3' of the FMC63-bbz CAR, the transmembrane domain and the cytoplasmic tail were removed by digestion with EcoRV and Sall and replaced with a geneblock (IDT), that encoded the same transmembrane domain and cytoplasmic tail followed by a 2A site and FKBP12F36V followed by a short GS-linker and the caspase-9 promolecule domain.

2. For expression of the inducible caspase-9 5' of the FMC63-bbz CAR, the signal peptide and the part of FMC63 ScFv were removed by digestion with XbaI and Tth111I and replaced with a geneblock (IDT), that encoded the same inducible caspase-9 domain as described in 1. followed by a 2A site and the sequence encoding the previously removed part of the original plasmid.

3. For expression of the reversible caspase-9 3' of the FMC63-bbz CAR, the transmembrane domain and the cytoplasmic tail were removed by digestion with EcoRV and Sall and replaced with a geneblock (geneart, Thermofisher), that encoded the same transmembrane domain and cytoplasmic tail followed by a 2A site and 2 repeats of FKBP12F36M followed by a short GS-linker (SGGGS, SEQ ID NO:3036) and the caspase-9 promolecule domain.

4. For expression of an anti-human CD20 ScFv, the FMC63 ScFv and the CD8 hinge were removed from the constructs described in 1-3 and replaced with a codon-optimized gene block (IDT) encoding the amino acid sequence ofveltuzumab.

Construction of CAR constructs including conditional aggregation domains. For expression of the conditional aggregation domains 5' of the FMC63-bbz CAR, the plasmid was cut with BamHI between signal peptide and ScFv and a gene block encoding (geneart) 4 repeats of FKBP12F36M followed by a furin recognition sequence were inserted between signal peptide and ScFv.

Lentiviral production. VSV-G pseudotyped lentiviral particles were produced using a 4th generation packaging system. 293T cells were transfected at a confluency of 90% with a mixture of the pRRLSIN.cPPT.EF1 α -gene-of-interest.WPRE, the envelope plasmid pMD2.G (Addgene #12252), the packaging plasmids pRSVRev (Addgene #12253) and pMDLgM/pRRE (Addgene #12251) in a complex with Lipofectamine 2000 (Life Technologies). Lentivirus containing supernatant was harvested after 24 and 48 hours, filtered through a 0.4 micron PES membrane, concentrated at 12,000xg for 12 hours at 4°C and stored at -80°C.

Stimulation and expansion of primary human T cells. Primary human T cells were cultured in RPMI1640, 10% FBS, 10 mM HEPES, 1% penicillin/streptomycin. Bulk T cells (CD4⁺ and CD8⁺) were stimulated with anti-CD3 and anti-CD28 beads (Dynabeads, Life Technologies) at a bead:cell ratio of 3:1. The culture medium was supplemented with 100 IU/mL interleukin 2. 24 hours after stimulation, 10⁶ T cells were transduced with lentiviral particles encoding various CAR constructs or control constructs or mock transduced. Expansion of the T cells was monitored for 8-12 days by measurement of cell volume and concentration (Coulter counter, Beckman Coulter). Cell surface expression of the CAR constructs was validated by flow cytometry (BD LSRII) with polyclonal antibodies against the human or mouse heavy and light chain. CAR staining was performed for 25 minutes at room temperature. All staining procedures were performed under saturating conditions. For some experiments, transduced T cells were previously frozen in 90% FBS and 10% DMSO. Experiments were performed when cells were rested after stimulation (i.e. volume of <450fl).

In vitro cytotoxicity and cytokine assays. *In vitro* killing of Nalm-6 cells was tested with a ⁵¹Cr-release assay. 5x10⁵ target cells were loaded with 50 μ Ci of Na₂⁵¹CrO₄ (Perkin Elmer) for 90-120 minutes, washed twice and resuspended in phenol red-free medium with 5% FBS. CAR, control CAR, or mock transduced T cells (8-10 days after initial activation) were co-incubated with loaded target cells for 4 hours at various effector:target (E:T) ratios, and chromium release into the supernatant was measured with a MicroBeta2 plate counter (Perkin Elmer). Spontaneous release by target cells (without effector cells) was analyzed in the same volume, and maximum release was assessed by lysing target cells with SDS at a final concentration of 5%. Percent specific lysis = [(Experimental Release – Spontaneous Release)/ (Maximum Release – Spontaneous Release)] *100. All experiments were performed with at least 3 replicates.

Elimination of CD19 CAR T cells. CD19 sCAR T cells were incubated in the presence of the indicated concentrations AP20187 for 16 hours at 37°C. Dead cells were detected with live/dead-violet dye and quantified by flow cytometry.

CD19 sCAR T Cells Retain Biologic Efficacy In Vivo. Mice were pretreated with IVIG (Privigen, CSL Behring) at a dose of 600 mg/kg i.v. for 2 days in order to block FcγRs on monocytes and neutrophils. NSG mice were then injected with 1×10^6 CD19+ Nalm6 cells expressing click-beetle luciferase to allow for bioluminescence detection. Five days later, mice were treated either with 5×10^6 CD19 CAR T cells that express an inducible caspase9 or with nontransduced control T cells. Peripheral blood was obtained by retro-orbital bleeding, and the presence of B cells and T-cell engraftment was determined by flow cytometry using BD TruCOUNT (BD Biosciences) tubes as described in the manufacturer's instructions. Bioluminescence was assessed on day 5, 6, 7, 10, 13 and 18 after B cell injection, which was combined with intraperitoneally administered IVIG (600 mg/kg). Mice were euthanized for organ harvest according to local IACUC guidelines, and bone marrow, spleen and blood samples were assessed by flow cytometry.

The results of the experiments are now described.

B cell depletion, if 100% complete, should be curative in pemphigus vulgaris (PV) and other antibody-mediated diseases, because the pathogenic B cells should be eliminated, and a brand new B cell repertoire must form. Given the multiple tolerance checkpoints that prevent autoimmunity, it is unlikely that B cell autoreactivity will recur.

The advantage of the CD19 CAR T cell approach is that it is a universal approach to the treatment of any B cell or antibody-mediated disease and has been validated in human clinical trials to be highly effective at CD19⁺ B cell depletion. Thus, the target antigen for the disease does not need to be known. This therapeutic approach could be applied to any disease in which B cells or the antibodies they produce cause autoimmunity or disease. In addition, the CD19 CAR could be used to eliminate alloantibodies to non-self proteins that prevent functional rescue of genetic diseases, such as HLA or beta2 microglobulin antibodies from organ transplant, blood group or Rh antibodies from transfusion or pregnancy, or Factor VIII, α-L-iduronidase, and many other protein replacement therapies in clinical use or development.

CD19 CAR T cells have shown efficacy for B cell depletion in human clinical trials without significant off-target cytotoxicity, although B cell depletion is permanent, resulting in lifelong immunosuppression. CD20 is also a clinical target for B cell depletion. Thus, the incorporation of a suicide gene into the anti-CD19 or anti-CD20 CAR design (sCAR), or selective activation of CAR-T function (via a reversible suicide cassette or conditional expression of the CAR), will allow temporal control of CAR-mediated B cell depletion as an important safety measure.

An example of a suicide gene in a sCAR includes fusion of human caspase 9 to a modified human FK-binding protein, which allows conditional dimerization upon exposure to a synthetic dimerizing

drug such as AP1903. Upon dimerization caspase 9 becomes activated, leading to death of cells expressing the suicide gene. Thus, infusion of CD19 sCAR T cells would result in complete B cell depletion, which would cure B cell- or antibody-mediated disease. Subsequent activation of the suicide gene with AP1903, AP20187, or similar agent would then eliminate the sCAR T cells, allowing B cell
5 repopulation to occur, thereby regenerating normal immune function. An example of a reverse suicide gene in a revCAR includes fusion of human caspase 9 to a modified human FK-binding protein, whose default state is to dimerize and cause death of cells expressing the suicide gene. Upon solubilization of dimerization domains, caspase 9 activity is inhibited and cell death is prevented, allowing CAR T cell function to occur. An example of a regulatory on-CAR system includes fusion of the CAR to modified
10 human FK-binding protein domains, whose default state is to dimerize and cause aggregation and degradation of proteins in the secretory system of the cell. Solubilization of the dimerization domains allows egress and processing of the CAR in the secretory system of the cell, including furin cleavage of the CAR from the FKBP domains to allow functional cell surface expression of the CAR.

To evaluate these approaches for temporal control of CAR T cell function, several constructs
15 were engineered; for one embodiment, one with a suicide gene in front of the CAR and one with the suicide gene after the CAR construct (FIG. 27). For another embodiment, a reverse suicide gene (either in front of or after the CAR construct) (FIG. 28). For yet another embodiment, a regulatory onCAR (FIG. 26). Primary human T cells were shown to efficiently express the CD19 sCARs, CD19 revCAR, and CD20 CAR (FIGS. 29A-29F) and CD19 sCAR T cells demonstrated specific cytotoxicity against their intended
20 targets (FIG. 30). Additionally, primary human T cells expressing the CD19 sCAR were specifically killed by activation of the suicide switch with AP20187 *in vitro*, whereas nontransduced T cells showed no cell death after AP20187 treatment (FIG. 31). Additionally, CD19 sCAR T cells remained effective at eliminating CD19⁺ B cells in an *in vivo* mouse model (FIG. 32) and demonstrated engraftment (FIG. 33).

As seen in the killing assay in FIG. 34, CD20sCAR, 20revCAR and CD20 onCAR show
25 equivalent and specific killing of the CD20+ target cells. On-CAR was tested in presence of 500nM Shield-1.

As seen in FIG. 35, the absence of solubilizing FKBP ligand (e.g. shield-1) inhibits CAR function. At lower E:T ratio's the On-CAR function is strongly inhibited if no FKBP ligand is present.

As seen in FIG. 36, the CAR surface expression could be modulated with FKBP ligand Shield-1.
30 Shield-1 resulted in a dose-dependent increase in CAR expression while the absence of Shield-1 resulted in ~60% reduction of CD20 on-CAR expression.

As seen in FIG. 37, Shield-1 was titrated in CD19rev CAR system and lower doses of Shield-1 resulted in higher caspase-9 activation and increased apoptosis.

As seen in FIG. 38, the *in vivo* assessment of apoptosis efficiency in anti CD19 revCAR T cells
35 indicated a sufficient *in vivo* apoptosis of revCAR T cells (FIG. 38). The *in vivo* efficacy of CD19 revCAR T cells was also evaluated (FIG. 39).

As seen in FIGS. 40, 41 and 42, the suicide gene activation resulted in peripheral depletion of the suicide CAR T cells (e.g. depletion of sCAR T cells from lymphoid organs in FIG. 42).

The timeline for T cell production of the present invention is outlined in a schematic in FIG. 43 and the timeline of the experimental design of the *in vivo* experiment of the present invention is outlined in a schematic in FIG. 44.

As shown in FIG. 45, 'Universal' sCAR T cells can deplete peripheral B cells in non-autologous BT mice and human B cells in a non-cancer humanized mouse model. Furthermore, FIG. 46 demonstrates that the universal sCAR T cells can be depleted with AP1903 treatment.

The relevant sequences of the some experimental results presented herein are as follows:

CD19 sCAR:

Suicide gene followed by CD19 CAR (nt)
 Suicide gene followed by CD19 CAR (aa)
 CD19 CAR followed by suicide gene (nt)
 CD19 CAR followed by suicide gene (aa)

CD20 CAR and sCAR:

CD20bbz CAR (nt and aa)
 CD20 CAR followed by suicide gene (nt and aa)
 suicide gene followed by CD20 CAR (nt and aa)

CD19 revCAR:

CD19 CAR followed by reversible suicide cassette (nt and aa)

CD19 onCAR:

CD19 on-CAR (nt and aa)

CD20 revCAR:

CD20 CAR followed by reversible suicide cassette (nt and aa)

CD20 onCAR:

CD20 on-CAR (nt and aa)

Suicide gene = inducible caspase9 (activates apoptosis upon dimerization with small molecule activators)

2A site = ribosome skipping site

CD19 CAR, comprising a CD8 transmembrane domain, CD137 and CD3-zeta (CD3-zeta is also known as CD247, collectively the CD137-CD3zeta is also known as bbz) cytoplasmic signaling domains

Inducible caspase9-2A-CD19bbz nucleotide sequence (SEQ ID NO: 3018)

ATGCTCGAGGGGGTTTCAGGTGGAGACTATCAGCCCGGGCGACGGACGGACATTCCCAAAGCGCGGGCAGACGT
 GTGTGGTGCATTACACCGGGATGCTTGAGGACGGAAAGAAAGTGGACTCTTCCCGAGACCGAAATAAACCATT
 CAAGTTCATGTTGGGCAAGCAGGAGGTTATCAGAGGGTGGGAGGAGGGCGTCGCTCAGATGAGTGTCTGGACA
 GAGGGCCAAGCTCACGATCTCCCTGATTACGCCTACGGGGCAACTGGTCACCCCGGAATCATCCCCCTCACGC
 AACCTCGTGTTTCGACGTCGAGCTGCTCAAACCTGGAATCAGGCGGAGGCAGTGGCGCTAGCGGGTTTGGCGAT

GTCGGTGCCCTTGAAAGCTTGAGAGGAAATGCCGATCTCGCTTACATCTTGAGCATGGAGCCCTGTGGGCACTG
 TCTGATCATCAACAATGTAACTTTGCCGGGAGTCCGGCCTGCGCACACGCACAGGCTCCAACATTGACTGCGA
 AAAACTTCGAAGGAGGTTTAGCTCTCTGCATTTATGTTAGAGGTGAAGGGGGATCTGACCGCCAAGAAAATG
 GTTCTCGCCCTTCTCGAGCTTGCGCAGCAGGACCATGGAGCGCTTGACTGTTGTGTCTGTTGTGATACTGAGCCAT
 5 GGCTGTCAGGCTTCCCATCTCCAGTTTCCAGGGGCCGTGTACGGAACCGATGGATGCCCTGTGTCAGTTGAAAA
 GATCGTAAACATCTTTAACGGAACATCTTGCCGAGCCTCGGCGGTAAACCGAAGCTTTTTTTATCCAGGCCTG
 CGGCGGTGAACAGAAAGATCATGGCTTCGAGGTTGCCAGTACCAGCCCTGAAGACGAATCCCCGGGTCAAAT
 CCTGAACCAGATGCGACCCCTTCCAGGAAGGACTCCGCACTTTTGACCAGCTTGACGCCATTTCTCCCTGCCAA
 CACCTCCGACATATTTGTAAGCTACTCCACCTTCCAGGATTCGTGAGCTGGCGCGACCCAAAATCCGGCAGTT
 10 GGTATGTTGAAACCTGGACGATATTTTCGAACAATGGGCCCACAGTGAGGACCTGCAGTCCCTTCTTCTGCGCG
 TAGCCAATGCCGTGTCAGTCAAAGGGATTACAAGCAGATGCCAGGCTGCTTAATTTCTGCGCAAGAACTG
 TTTTAAAGACCAGTGGCTCCGGCGCAACAAATTTCTCCTTGCTGAAACAGGCAGGCGACGTTGAGGAAAATCCC
 GGCCCAATGGCCTTACCAGTGACCGCCTTGCTCCTGCCGCTGGCCTTGCTGCTCCACGCCGCCAGGCCGGACATCCA
 GATGACACAGACTACATCTCCCTGTCTGCCTCTCTGGGAGACAGAGTACCATCAGTTGCAGGGCAAGTCAGGAC
 15 ATTAGTAAATATTTAAATGGTATCAGCAGAAACCAGATGGAAGTGTAACTCCTGATCTACCATACATCAAGATT
 AACTCAGGAGTCCCATCAAGGTTCAAGTGGCAGTGGGTCTGGAACAGATTATTCTCTCACCATTAGCAACCTGGAG
 CAAGAAGATATTGCCACTTACTTTTGCCAACAGGGTAATACGTTCCGTACACGTTCCGAGGGGGGACTAAGTTGG
 AAATAACAGGTGGCGGTGGCTCGGGCGGTGGTGGGTGGCGGCGGATCTGAGGTGAACTGCAGGAGTC
 AGGACCTGGCCTGGTGGCGCCCTCACAGAGCCTGTCCGTACATGCACTGTCTCAGGGGTCTCATTACCCGACTAT
 20 GGTGTAAGCTGGATTGCGCCAGCTCCACGAAAGGGTCTGGAGTGGCTGGGAGTAATATGGGGTAGTGAAACCAC
 ATACTATAATTCAGCTCTCAAATCCAGACTGACCATCATCAAGGACAACCTCAAGAGCCAAGTTTTCTTAAAAATGA
 ACAGTCTGCAAACCTGATGACACAGCCATTACTACTGTGCCAAACATTATTACTACGGTGGTAGCTATGCTATGGAC
 TACTGGGGTCAAGGAACCTCAGTCACCGTCTCTCAACCACGACGCCAGCGCCGCGACCAACACCGGCGCCCA
 CCATCGCGTCGAGCCCCCTGTCCCTGCGCCCAGAGGCGTGCCGGCCAGCGCGGGGGGCGCAGTGCACACGAGG
 25 GGGCTGGACTTCGCTGTGATATCTACATCTGGGCGCCCTTGCCGGGACTTGTTGGGGTCTTCTCCTGTCACTGGT
 TATCACCTTTACTGCAAACGGGGCAGAAAGAACTCCTGTATATATTCAAACAACCATTTATGAGACCAGTACAAA
 CTACTCAAGAGGAAGATGGCTGTAGCTGCCGATTTCCAGAAGAAGAAGGAGGATGTGAAGTGAAGTGAAG
 TTCAGCAGGAGCGCAGACGCCCCCGGTACCAGCAGGGCCAGAACAGCTCTATAACGAGCTCAATCTAGGACGA
 AGAGAGGAGTACGATGTTTTGGACAAGAGACGTGGCCGGGACCCTGAGATGGGGGGAAAGCCGAGAAGGAAGA
 30 ACCCTCAGGAAGGCCTGTACAATGAACTGCAGAAAGATAAGATGGCGGAGGCCTACAGTGAGATTGGGATGAAA
 GGCGAGCGCCGAGGGGCAAGGGGCACGATGGCCTTACCAGGGTCTCAGTACAGCCACCAAGGACACCTACGA
 CGCCCTTCACATGCAGGCCCTGCCCCCTCGCTAA

35 **Inducible caspase9-2A-CD19bbz** amino acid sequence (SEQ ID NO: 3019)

MLEGVQVETISPGDGRTPKRGQTCVVHYTGMLEDGKKVDSSRDNRNPKFKMLGKQEVIRGWEEGVAQMSVGQ
 RAKLTISPDIYAGATGHPGIIPPHATLVFDVELLKLESGGSGASGFGDVGALESRLGNADLAYILSMPCGHCLINN
 VNFRESGLRTRTGSNIDCEKLRRRFSSLHFMVEVKGDLTAKKMLVLALELAQQDHGALDCCVVVILSHGCQASHLQ
 40 FPGAVYGTGDCPVSEKIVNIFNGTSCPSLGGKPKLFFIQACGGEQKDHGFVASTSPEDESPGSNPEPDATPFQEGL
 RTFDQLDAISSLPSTDFVSYSFPGFVSWRDPKSGSWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMP
 GCFNFLRKKLFFKTSGSGATNFSLLKQAGDVEENPGPMALPVTALLPLALLHAARPDQMTQTSSLSASLGDRVTISC

RASQDISKYLNWYQQKPDGTVKLLIYHTSRLHSGVPSRFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPYTFGGGTKL
 EITGGGGSGGGSGGGGSEVKLQESGPGLVAPSQSLSVTCTVSGVSLPDYGVSWIRQPPRKGLEWLGVWVGSETTYYN
 SALKSRLTIKDNSKSQVFLKMNSLQTDDTAIYYCAKHYYYGGSYAMDYWGQGSVTVSSTTTPAPRPPTPAPTIASQPL
 SLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRF
 5 PEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDRRGRDPEMGGKPRRKNPQEGLYNELQKDK
 MAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR

CD19bbz - 2A-inducible caspase9 nucleotide sequence (SEQ ID NO: 3020)

10 ATGGCCTTACCAGTGACCGCCTTGCTCCTGCCGCTGGCCTTGCTGCTCCACGCCGCCAGGCCGGACATCCAGATGAC
 ACAGACTACATCCTCCCTGTCTGCCTCTCTGGGAGACAGAGTCACCATCAGTTGCAGGGCAAGTCAGGACATTAGT
 AAATATTTAAATTGGTATCAGCAGAAACCAGATGGAAGTGTAACTCCTGATCTACCATACATCAAGATTACACTC
 AGGAGTCCCATCAAGGTTCAAGTGGCAGTGGGTCTGGAACAGATTATTCTCTCACCATTAGCAACCTGGAGCAAGAA
 15 GATATTGCCACTTACTTTTGCCAACAGGGTAATACGCTTCCGTACACGTTCCGGAGGGGGGACTAAGTTGGAAATAA
 CAGGTGGCGGTGGCTCGGGCGGTGGTGGGTGGGTGGCGGCGGATCTGAGGTGAAACTGCAGGAGTCAGGACC
 TGGCCTGGTGGCGCCCTCACAGAGCCTGTCCGTACATGCACTGTCTCAGGGGTCTCATTACCCGACTATGGTGTA
 AGCTGGATTGCGCAGCCTCCACGAAAGGGTCTGGAGTGGCTGGGAGTAATATGGGGTAGTGAAACCACATACTAT
 AATTCAGCTCTCAAATCCAGACTGACCATCATCAAGGACAACCTCCAAGAGCCAAGTTTTCTTAAAAATGAACAGTCT
 20 GCAAACCTGATGACACAGCCATTTACTACTGTGCCAAACATTATTACTACGGTGGTAGCTATGCTATGGACTACTGG
 GGTCAAGGAACCTCAGTCACCGTCTCCTCAACCACGACGCCAGCGCCGCGACCAACACCCGGCGCCCAACCATCG
 CGTCGCAGCCCCTGTCCCTGCGCCAGAGGCGTGGCGGCCAGCGGCGGGGGGCGCAGTGCACACGAGGGGGGCTG
 GACTTCGCCTGTGATATCTACATCTGGGCGCCCTTGCCGGGACTTGTGGGGTCCTTCTCCTGTCACTGGTTATCAC
 CCTTTACTGCAAACGGGGCAGAAAGAACTCCTGTATATATTCAAACAACCATTTATGAGACCAGTACAACTACTC
 25 AAGAGGAAGATGGCTGTAGCTGCCGATTTCCAGAAGAAGAAGAAGGAGGATGTGAACTGAGAGTGAAGTTCAGC
 AGGAGCGCAGACGCCCCCGCTACCAGCAGGGCCAGAACCAGCTCTATAACGAGCTCAATCTAGGACGAAGAGA
 GGAGTACGATGTTTTGGACAAGAGACGTGGCCGGGACCCTGAGATGGGGGGAAAGCCGAGAAGGAAGAACCCT
 CAGGAAGGCCTGTACAATGAACTGCAGAAAGATAAGATGGCGGAGGCCTACAGTGAGATTGGGATGAAAGGCG
 AGCGCCGGAGGGGGCAAGGGGACGATGGCCTTTACCAGGGTCTCAGTACAGCCACCAAGGACACCTACGACGCCC
 30 TTCACATGCAGGCCCTGCCCCCTCGCTCGGAAGCGACGGGGCTCCGGCGCAACAAATTTCTCCTTGCTGAAACAGG
 CAGGCGACGTTGAGGAAAATCCCGGCCAGGGGTTGAGGTGGAGACTATCAGCCCCGGGCGACGGACGGACATTC
 CCAAAGCGCGGGCAGACGTGTGTGGTGATTACACCGGGATGCTTGAGGACGGAAAGAAAGTGGACTCTTCCC
 GAGACCGAAATAAACCATTCAAGTTCATGTTGGGCAAGCAGGAGGTTATCAGAGGGTGGGAGGAGGGCGTCG
 CTCAGATGAGTGTGCGACAGAGGGCCAAGCTCACGATCTCCCTGATTACGCCTACGGGGCAACTGGTCACCCC
 35 GGAATCATCCCCCTCACGCAACCTCGTGTTCGACGTCGAGCTGCTCAAACCTGGAATCAGGCGGAGGCAGTGG
 CGGGTTTGGCGATGTCGGTGGCCTTGAAAGCTTGAGAGGAAATGCCGATCTCGCTTACATCTTGAGCATGGAGC
 CCTGTGGGCACTGTCTGATCATCAACAATGTTAACTTTGCCGGGAGTCCGGCCTGCGCACACGCACAGGCTCCA
 ACATTGACTGCGAAAACTTCGAAGGAGGTTAGCTCTCTGCATTTTCATGGTAGAGGTGAAGGGGGATCTGACC
 GCCAAGAAAATGGTTCTCGCCCTTCTCGAGCTTGCAGCAGGACCATGGAGCGCTTGACTGTTGTGTCGTTGTG
 40 ATACTGAGCCATGGCTGTCAGGCTTCCATCTCCAGTTTCCAGGGGCCGTGTACGGAACCGATGGATGCCCTGTG
 TCAGTTGAAAAGATCGTAAACATCTTTAACGGAACATCTTCCCCGAGCCTCGGCGGTAAACCGAAGCTTTTTTT
 ATCCAGGCCTGCGGCGGTGAACAGAAAGATCATGGCTTCGAGGTTGCCAGTACCAGCCCTGAAGACGAATCCCC

CGGGTCAAATCCTGAACCAGATGCGACCCCTTTCCAGGAAGGACTCCGCACTTTTGACCAGCTTGACGCCATTTCC
 CTCCTGCCAACACCTTCCGACATATTTGTAAGCTACTCCACCTTTCCAGGATTCGTGAGCTGGCGCGACCCAAAA
 TCCGGCAGTTGGTATGTTGAAACCTGGACGATATCTTCGAACAATGGGCCCACAGTGAGGACCTGCAGTCCCTT
 CTTCTGCGCGTAGCCAATGCCGTGTAGTCAAAGGGATTACAAGCAGATGCCAGGCTGCTTTAATTTCTGCGC
 5 AAGAAACTGTTTTTAAGACCAGTTGAGTCGACGGAGGAGGAG

CD19bbz -2A-inducible caspase9 amino acid sequence (SEQ ID NO: 3021)

10 MALPVTALLPLALLHAARPDQM TQTSSLSASLGDRVTISCRASQDISKYNWYQQKPDGTVKLLIYHSTRHSGVPS
 RFGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPYTFGGGKLEITGGGGSGGGGSGGGGSEVKLQESGPGLVAPSQSL
 SVTCTVSGVSLPDYGVSWIRQPPRKGLEWLGVWGETTYNSALKSRLTIKDNSKSQVFLKMNSLQTDDTAIYYCAKH
 YYYGGSYAMDYWGQGSVTVSSTTPAPRPPTAPTASQPLSLRPEACRPAAGGAVHTRGLDFACDIYWAPLAGTCG
 VLLLSLVITLYCKRGRKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNL
 15 GRREEYDVLDRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGGHGLYQGLSTATKDTYD
 ALHMQALPPRRKRRGSGATNFSLLKQAGDVEENPGPGVQVETISPGDGRTFPRKRGQTCVVHYTGMLEDGKKVDSSR
 DRNKPFFKMLGKQEVIRGWEEGVAQMSVQGQRAKLITSPDYAYGATGHPGIIPPHATLVFDVELLKLESGGSGGFG
 DVGALSLRGNADLAYILSMEPCGHCLINNVNFCRESGLRTRTGSNIDCEKLRFRFSSLHFMVEVKGDLTAKKMVLA
 LLELAQQDHGALDCCVVVILSHGCQASHLQFPGAVYGTGDCPVSVEKIVNIFNGTSCPSLGGKPKLFFIQACGGEQKD
 20 HGFEVASTSPEDESPGSNPEPDATPFQEGRLTFDQLDAISSLPTPSDIFVSYSTFPGFVSWRDPKSGSWYVETLDDIFE
 QWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNFLRKKLFFKTS

Signal peptide-Anti-human CD20-CD8 hinge-CD8transmembrane-CD137-CD247 nucleotide sequence
 25 (SEQ ID NO:3022)

ATGGCCTTACCAGTGACCGCCTTGCTCCTGCCGCTGGCCTTGCTGCTCCACGCCGCCAGGCCGGGATCCGATATTC
 AACTTACACAGTCCCCTAGTTCCTTGCTCCGCTCCGCTCGGCGACAGAGTTACCATGACTTGTCGAGCGTCTTCTAGC
 GTTTCCTACATTCATTGGTTCACAGAAAGCCCGGAAAGGCACCAAAACCTTGGATCTACGCCACGTCCAATTTGG
 30 CTAGTGGTGTTCGGGTGCGATTTTCCGGGTCAGGTAGCGGGACGGACTATACTTTTACCATTTCAGCCCTCAGCC
 TGAAGACATCGCGACGTACTATTGTCAGCAGTGGACCTCTAACCCCTCTACCTTTGGCGGTGGAACAAAGCTGGA
 GATCAAACGAGGCGGGGGTGGCTCTGGGGGAGGAGGTTCGGGTGGGGGAGGCTCTCAAGTACAACGCAACAA
 AGTGGGGCTGAAGTGAAGAAGCCCGTTCTTCAGTCAAAGTATCATGTAAGGCAAGTGGTTATACCTTTACGTCTT
 ATAACATGCATTGGGTAAAGCAAGCCCTGGTCAGGGCCTCGAGTGGATTGGTGCGATCTACCCTGGAATGGGTG
 35 ATACGAGCTATAATCAGAAATTCAAGGGGAAAGCCACCTTGACTGCAGACGAATCTACGAACACGGCTTACATGG
 AGCTTAGCTCACTCAGATCAGAGGATACAGCCTTTTACTACTGCGCTAGATCAACTTATTACGGAGGAGACTGGTA
 TTTTGATGTATGGGGTCAGGGGACCACAGTCACTGTTAGCTCTGCTAGCACCACGACGCCAGCGCCGCGACCACC
 AACACCGGCGCCACCATCGCGTCGACGCCCTGTCCCTGCGCCAGAGGCGTGCCGGCCAGCGGCGGGGGGCG
 CAGTGACACGAGGGGGCTGGACTTCGCTGTGATTCCGGAATCTACATCTGGGCGCCCTTGGCCGGGACTTGTG
 40 GGGTCCTTCTCCTGTCACTGGTTATCACCTTTACTGCAAACGGGGCAGAAAGAACTCCTGTATATATTCAAACAA
 CCATTTATGAGACCAGTACAACTACTCAAGAGGAAGATGGCTGTAGCTGCCGATTTCAGAAGAAGAAGAAGGA
 GGATGTGAACTGAGAGTGAAGTTCAGCAGGAGCGCAGACGCCCCCGGTACCAGCAGGGCCAGAACCAGCTCTA

TAACGAGCTCAATCTAGGACGAAGAGAGGAGTACGATGTTTTGGACAAGAGACGTGGCCGGGACCCCTGAGATGG
GGGGAAAGCCGAGAAGGAAGAACCCTCAGGAAGGCCTGTACAATGAACTGCAGAAAGATAAGATGGCGGAGGC
CTACAGTGAGATTGGGATGAAAGGCGAGCGCCGGAGGGGGCAAGGGGCACGATGGCCTTTACCAGGGTCTCAGTA
CAGCCACCAAGGACACCTACGACGCCCTTCACATGCAGGCCCTGCCCCCTCGC

5

Signal peptide-Anti-human CD20-CD8 hinge-*CD8transmembrane*-CD137-CD247 amino acid sequence
(SEQ ID NO: 3023)

10 MALPVTALLPLALLHAARPGSDIQLTGSPSSLSASVGDRVTMTCRASSSVSYIHWFOQKPGKAPKPWIYATSNLASG
VPVRFSGSGSGTDYFTISSLOPEDATYYCQQWTSNPPTFGGGTKLEIKRGGGSGGGGSGGGGSGVQLQQSGAEVK
KPGSSVKVSKASGYTFTSYNMHWVKQAPGQGLEWIGAIYPMGDTSYNOKFKGKATLTADESTNTAYMELSSLRSE
DTAFYYCARSTYYGGDWYFDVWVGQGTITVSSASTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFAC
DSGIYIWAPLAGTCGVLLSLVITLYCKRGRKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAY
15 QQQQNQLYNELNLRREYDVLDRRRGRDPEMGGKPRRKNPQEGLYNELQDKMAEAYSEIGMKGERRRGKGHDG
LYQGLSTATKDTYDALHMQALPPRZ

Anti-human CD20bbz-2A-**iCasp9** nucleotide sequence (SEQ ID NO: 3024)

20

ATGGCTCTGCCTGTGACAGCTCTGCTGCTGCCTCTGGCCCTGCTGCTGCATGCTGCCAGACCTGGCTCCGATATTCA
ACTTACACAGTCCCCTAGTTTCCTTGTCGCCCTCCGTCGGCGACAGAGTTACCATGACTTGTCGAGCGTCTTCTAGCG
TTTCTACATTCAATTGGTTCCAACAGAAGCCCGGAAAGGCACCAAAACCTTGGATCTACGCCACGTCCAATTTGGCT
AGTGGTGTTCCGGTGCATTTTCCGGGTGAGGTAGCGGGACGGACTATACTTTACCATTCAAGCCTTCAGCCTG
25 AAGACATCGCGACGTACTATTGTCAGCAGTGGACCTCTAACCTCTACCTTTGGCGGTGGAACAAAGCTGGAGAT
CAAACGAGGCGGGGGTGGCTCTGGGGGAGGAGGTTCCGGTGGGGGAGGCTCTCAAGTACAACCTGCAACAAAGT
GGGGCTGAAGTGAAGAAGCCCGGTTCTTCAGTCAAAGTATCATGTAAGGCAAGTGGTTATACTTTACGTCTTATA
ACATGCATTGGGTAAAGCAAGCCCCTGGTCAGGGCCTCGAGTGGATTGGTGGCATCTACCCTGGAATGGGTGATA
CGAGCTATAATCAGAAATTCAAGGGGAAAGCCACCTTGACTGCAGACGAATCTACGAACACGGCTTACATGGAGC
30 TTAGCTCACTCAGATCAGAGGATACAGCCTTTTACTACTGCGCTAGATCAACTTATTACGGAGGAGACTGGTATTTT
GATGTATGGGGTCAGGGGACCACAGTCACTGTTAGCTCTGCTAGCACCACGACGCCAGCGCCGCGACCACCAACA
CCGGCGCCACCATCGCGTCGAGCCCTGTCCCTGCGCCAGAGGCGTGCCGGCCAGCGGCGGGGGGCGCAGT
GCACACGAGGGGGCTGGACTTCGCCTGTGATTCCGGAATCTACATCTGGGCGCCCTTGGCCGGGACTTGTGGGGT
CCTTCTCCTGTCACTGGTTATCACCTTTACTGCAAACGGGGCAGAAAGAACTCCTGTATATATTCAAACAACCAT
35 TTATGAGACCAGTACAACTACTCAAGAGGAAGATGGCTGTAGCTGCCGATTTCCAGAAGAAGAAGAAGGAGGA
TGTGAAGTGAAGTGAAGTTCAGCAGGAGCGCAGACGCCCCCGGTACCAGCAGGGCCAGAACCAGCTCTATAA
CGAGCTCAATCTAGGACGAAGAGAGGAGTACGATGTTTTGGACAAGAGACGTGGCCGGGACCCCTGAGATGGGG
GGAAAGCCGAGAAGGAAGAACCCTCAGGAAGGCCTGTACAATGAACTGCAGAAAGATAAGATGGCGGAGGCCT
ACAGTGAGATTGGGATGAAAGGCGAGCGCCGGAGGGGGCAAGGGGCACGATGGCCTTTACCAGGGTCTCAGTAC
40 AGCCACCAAGGACACCTACGACGCCCTTCACATGCAGGCCCTGCCCCCTCGCGGTCCGGGCGCAACAAATTTCTCC
TTGCTGAAACAGGCAGGCGACGTTGAGGAAAATCCCCGGCCAGGGGTTTCAGGTGGAGACTATCAGCCCGGGCG
ACGGACGGACATTCCCAAAGCGCGGGCAGACGTGTGTGGTGCATTACACCGGGATGCTTGAGGACGGAAAGA

AAGTGGACTCTTCCCGAGACCGAAATAAACCATTCAAGTTCATGTTGGGCAAGCAGGAGGTTATCAGAGGGTG
 GGAGGAGGGCGTCGCTCAGATGAGTGTGCGACAGAGGGCCAAGCTCACGATCTCCCTGATTACGCCTACGGG
 GCAACTGGTCACCCCGGAATCATCCCCCTCACGCAACCCTCGTGTTGACGTCGAGCTGCTCAAACCTGGAATCA
 GCGGAGGCAGTGGCGGGTTTGGCGATGTCGGTGCCTTGAAAGCTTGAGAGGAAATGCCGATCTCGCTTACA
 5 TCTTGAGCATGGAGCCCTGTGGGCACTGTCTGATCATCAACAATGTAACTTTGCCGGGAGTCCGGCCTGCGCA
 CACGCACAGGCTCCAACATTGACTGCGAAAACTTCGAAGGAGGTTAGCTCTCTGCATTCATGGTAGAGGTG
 AAGGGGGATCTGACCGCCAAGAAAATGGTTCTCGCCCTTCTCGAGCTTGCGCAGCAGGACCATGGAGCGCTTGA
 CTGTTGTGTCGTTGTGATACTGAGCCATGGCTGTGAGGCTTCCCATCTCCAGTTTCCAGGGGGCGTGTACGGAAC
 CGATGGATGCCCTGTGTGAGTTGAAAAGATCGTAAACATCTTTAACGGAACATCTTGCCCGAGCCTCGGCGGTA
 10 AACCGAAGCTTTTTTTTATCCAGGCCTGCGGCGGTGAACAGAAAGATCATGGCTTCGAGGTTGCCAGTACCAGC
 CCTGAAGACGAATCCCCGGGTCAAATCCTGAACCAGATGCGACCCCTTCCAGGAAGGACTCCGCACTTTTAC
 CAGCTTGACGCCATTTCTCCCTGCCAACACCTTCCGACATATTTGTAAGCTACTCCACCTTCCAGGATTCTGTGAG
 CTGGCGCGACCCAAAATCCGGCAGTTGGTATGTTGAAACCCTGGACGATATCTTCGAACAATGGGCCACAGTG
 AGGACCTGCAGTCCCTTCTTCTGCGCGTAGCCAATGCCGTGTGAGTCAAAGGGATTACAAGCAGATGCCAGGC
 15 TGCTTAATTCCTGCGCAAGAACTGTTTTTAAGACCAGTTGA

Anti-human CD20bbz-2A-iCasp9 amino acid sequence (SEQ ID NO: 3025)

20 MALPVTALLPLALLHAARPGSDIQLTQSPSSLSASVGDRVTMTCRASSSVSYIHWFQQKPGKAPKPWIYATSNLASG
 VPVRFSGSGSGTDYFTISSLPEDIATYYCQQWTSNPPTFGGGTKLEIKRGGGSGGGGSGGGGSGVQLQQSGAEVK
 KPGSSVKVSKASGYTFTSYNMHWVKQAPGQGLEWIGAIYPGMGDTSYNQKFKGKATLTADSTNTAYMELSSLRSE
 DTAFYFCARSTYYGGDWYFDVWVGQGTITVSSASTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFAC
 DSGIYWAPLAGTCGVLLSLVITLYCKRGRKLLYIFKQPFMRPVQTTQEEDGCSRFPETEEGGCELRVKFSRSADAPAY
 25 QQQQNQLYNELNLRREYDVLDRGRDPENGGKPRRKNPQEGLYNELQDKMAEAYSEIGMKGERRRGKGHG
 LYQGLSTATKDYDALHMQALPPRGSGATNFSLLKQAGDVEENPGPGVQVETISPGDGRTPFKRGQTCVVHYTGML
 EDGKKVDSSRDNRNPKFKMLGKQEVIRGWEEGVAQMSVGRRAKLITSPDYAYGATGHPGIIPPHATLVFDVELLKE
 SGGGSGGFGDVGALSLRGNADLAYILSMEPCGHCLINNVNFCRESGLRTRTGSNIDCEKLRRRFFSLHFMVEVKGD
 LTAKKMLVALLLELAQQDHGALDCCVVILSHGCQASHLQFPAVYGTGDCPVSEKIVNIFNGTSCPSLGGKPKLFFI
 30 QACGGEQKDHGFEVASTPEDESPGSNPEPDATPFQEGRLTFDQLDAISSLPTPSDIFVSYSTFPGFVSWRDPKSGS
 WYVETLDDIFEQWAHSEDLQSLLRVANAVSVKGIYKQMPGCFNFLRKKLFFKTSZ

iCasp9-2A-anti-human CD20bbz nucleotide sequence (SEQ ID NO: 3026)

35 ATGCTCGAGGGGGTTCAGGTGGAGACTATCAGCCCGGGCGACGGACGGACATTCCCAAAGCGCGGGCAGACGT
 GTGTGGTGCATTACACCGGGATGCTTGAGGACGGAAAGAAAGTGGACTCTTCCCGAGACCGAAATAAACCATT
 CAAGTTCATGTTGGGCAAGCAGGAGGTTATCAGAGGGTGGGAGGAGGGCGTCGCTCAGATGAGTGTGCGACA
 GAGGGCCAAGCTCACGATCTCCCTGATTACGCCTACGGGGCAACTGGTCACCCCGGAATCATCCCCCTCACGC
 40 AACCTCGTGTTGACGTCGAGCTGCTCAAACCTGGAATCAGGCGGAGGCAGTGGCGCTAGCGGGTTTGGCGAT
 GTCGGTGCCTTGAAAGCTTGAGAGGAAATGCCGATCTCGCTTACATCTTGAGCATGGAGCCCTGTGGGCACTG
 TCTGATCATCAACAATGTAACTTTGCCGGGAGTCCGGCCTGCGCACACGCACAGGCTCCAACATTGACTGCGA

AAAACTTCGAAGGAGGTTTAGCTCTCTGCATTTTCATGGTAGAGGTGAAGGGGGATCTGACCGCCAAGAAAATG
 GTTCTCGCCCTTCTCGAGCTTGCGCAGCAGGACCATGGAGCGCTTACTGTTGTGTCGTTGTGATACTGAGCCAT
 GGCTGTCAGGCTTCCCATCTCCAGTTTCCAGGGGCCGTGTACGGAACCGATGGATGCCCTGTGTCAGTTGAAAA
 GATCGTAAACATCTTTAACGGAACATCTTGCCGAGCCTCGGCGGTAAACCGAAGCTTTTTTTATCCAGGCTG
 5 CGGCGGTGAACAGAAAGATCATGGCTTCGAGGTTGCCAGTACCAGCCCTGAAGACGAATCCCCGGGTCAAAT
 CCTGAACCAGATGCGACCCCTTCCAGGAAGGACTCCGCACTTTTGACCAGCTTGACGCCATTTCTCCCTGCCAA
 CACCTTCCGACATATTTGTAAGCTACTCCACCTTCCAGGATTCGTGAGCTGGCGCGACCCAAAATCCGGCAGTT
 GGTATGTTGAAACCTGGACGATATTTTCGAACAATGGGCCACAGTGAGGACCTGCAGTCCCTTCTTCTGCGCG
 TAGCCAATGCCGTGTCAGTCAAAGGGATTACAAGCAGATGCCAGGCTGCTTAATTTCTGCGCAAGAACTG
 10 TTTTAAAGACCAAGTGGCTCCGGCGCAACAAATTTCTCTTGCTGAAACAGGCAGGCGACGTTGAGGAAAATCCC
 GGCCCAATGGCCTTACCAGTGACCGCCTTGCTCCTGCCGCTGGCCTTGCTGCTCCACGCCGCCAGGCCGGGATCCG
 ATATTCAACTTACACAGTCCCCTAGTTCCTTGTCGCGCTCCGTGCGCGACAGAGTTACCATGACTTGTCGAGCGTCT
 TCTAGCGTTTCTACATTCATTGGTTCCAACAGAAGCCCGGAAAGGCACCAAAACCTTGGATCTACGCCACGTCCA
 ATTTGGCTAGTGGTGTTCGGGTGCGATTTCCGGGTGAGGTAGCGGGACGGACTATACTTTTACCATTCAAGCCT
 15 TCAGCCTGAAGACATCGCGACGTACTATTGTCAGCAGTGAGCCTCTAACCTCCTACCTTTGGCGGTGGAACAAAG
 CTGGAGATCAAACGAGGCGGGGGTGGCTCTGGGGGAGGAGGTTCCGGTGGGGGAGGCTCTCAAGTACAACTGC
 AACAAAGTGGGGCTGAAGTGAAGAAGCCCGGTTCTTCAGTCAAAGTATCATGTAAGGCAAGTGGTTATACTTTA
 CGTCTTATAACATGCATTGGGTAAAGCAAGCCCTGGTCAGGGCCTCGAGTGGATTGGTGGCATCTACCCTGGAA
 TGGGTGATACGAGCTATAATCAGAAATTCAAGGGGAAAGCCACCTTGACTGCAGACGAATCTACGAACACGGCTT
 20 ACATGGAGCTTAGCTCACTCAGATCAGAGGATACAGCCTTTTACTACTGCGCTAGATCAACTTATTACGGAGGAGA
 CTGGTATTTTGTATGTATGGGGTCAAGGGGACCACAGTCACTGTTAGCTCTGCTAGCACCACGACGCCAGCGCCGCG
 ACCACCAACACCGGCGCCCAACCATCGCGTCGAGCCCTGTCCCTGCGCCAGAGGCGTGCCGGCCAGCGGCGGG
 GGGCGCAGTGACACGAGGGGGTGGACTTCGCCTGTGATTCCGGAATCTACATCTGGGCGCCCTTGGCCGGGA
 CTTGTGGGGTCTTCTCCTGTCACTGGTTATCACCTTTACTGCAAACGGGGCAGAAAGAACTCCTGTATATATTC
 25 AAACAACCATTTATGAGACCAGTACAACTACTCAAGAGGAAGATGGCTGTAGCTGCCGATTTCCAGAAGAAGAA
 GAAGGAGGATGTGAAGTGAAGTGAAGTTCAGCAGGAGCGCAGACGCCCCCGGTACCAGCAGGGCCAGAACC
 AGCTCTATAACGAGCTCAATCTAGGACGAAGAGAGGAGTACGATGTTTTGGACAAGAGACGTGGCCGGGACCCT
 GAGATGGGGGGAAAGCCGAGAAGGAAGAACCTCAGGAAGGCCTGTACAATGAAGTGCAGAAAGATAAGATGG
 CGGAGGCCTACAGTGAGATTGGGATGAAAGGCGAGCGCCGGAGGGGGCAAGGGGCACGATGGCCTTTACCAGGG
 30 TCTCAGTACAGCCACCAAGGACACCTACGACGCCCTTACATGCAGGCCCTGCCCCCTCGC

iCasp9-2A-anti-human CD20bbz amino acid sequence (SEQ ID NO: 3027)

35 MLEGVQVETISPGDGRFTPKRGQTCVVHYTGMLDGGKVDSSRDNRNPKFKFMLGKQEVIRGWEEGVAQMSVGQRA
 KLTISPDYAYGATGHPGIIPPHATLVFDVELLKLESGGGSGASGFGDVGALES LRGNADLAYILSMEPCGHCLINNVNFC
 RESGLRTRTGSNIDCEKLRRRFSSLHFMVEVKGDLTAKKMVLALLELAQQDHGALDCCVVVILSHGCQASHLQFPGAVY
 GTDGPVSVEKIVNIFNGTSCPSLGGKPKLFFIQACGGEQKDHFGEVASTPEDESPGSNPEPDATPFQEGLRFTDQLDA
 ISSLPSPDIFVSYSTFPGFVSWRDPKSGSWYVETLDDIFEQWAHSEDLQSLLRVANAVSVKGIYKQMPGCFNFLRKKL
 40 FFKTSGSGATNFSLLKQAGDVEENPGPMALPVTALLPLALLHAARPGSDIQLTQSPSSLSASVGDRVTMTCRASSV
 SYIHWFFQKPKGKAPKPIWIYATSNLASGVPRFSGSGTDTFTISSLPEDIATYYCQQWTSNPPTFGGGTKLEIKR
 GGGGSGGGGSGGGGSQVQLQSGAEVKKPGSSVKVSKASGYTFTSYNMHWVKQAPGQGLEWIGAIYPGMGD

TSYNQKFKGKATLTADSTNTAYMELSSLRSEDYAFYYCARSTYYGGDWYFDVWVGQTTTVSSASTTTPAPRPPT
 PAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDSGIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPV
 QTTQEEDGCSCRFPEEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREYDVLDKRRGRDPEMGGKPRRK
 NPQEGLYNELQKDKMAEAYSEIGMKGERRRGKHDGLYQGLSTATKDTYDALHMQALPPRZ

5

FMC63-bbz-2A- revCasp9 nucleotide sequence (SEQ ID NO: 3028)

10 ATGGCCTTACCAGTGACCGCCTTGCTCCTGCCGCTGGCCTTGCTGCTCCACGCCGCCAGGCCGGGATCCGACATCC
 AGATGACACAGACTACATCCTCCCTGTCTGCCTCTCTGGGAGACAGAGTCACCATCAGTTGCAGGGCAAGTCAGG
 ACATTAGTAAATATTTAAATTGGTATCAGCAGAAACCAGATGGAACCTGTTAACTCCTGATCTACCATACATCAAG
 ATTAACTCAGGAGTCCCATCAAGGTTCAAGTGGCAGTGGGTCTGGAACAGATTATTCTCTCACCATTAGCAACCTG
 GAGCAAGAAGATATTGCCACTTACTTTGCCAACAGGGTAATACGCTTCCGTACACGTTCCGAGGGGGGACTAAG
 TTGGAAATAACAGGTGGCGGTGGCTCGGGCGGTGGTGGGTGGGGTGGCGGCGGATCTGAGGTGAAACTGCAGG
 15 AGTCAGGACCTGGCCTGGTGGCGCCCTCACAGAGCCTGTCCGTACATGCACTGTCTCAGGGGTCTCATTACCCGA
 CTATGGTGTAAAGCTGGATTCGCCAGCCTCCACGAAAGGGTCTGGAAGTGGCTGGGAGTAATATGGGGTAGTGAAA
 CCACATACTATAATTCAAGCTCTCAAATCCAGACTGACCATCATCAAGGACAACCTCAAGAGCCAAGTTTCTTAAAA
 ATGAACAGTCTGCAAACTGATGACACAGCCATTTACTACTGTGCCAAACATTATTACTACGGTGGTAGCTATGCTAT
 GGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCAGCTAGCACCACGACGCCAGCGCCGCGACCAAC
 20 ACCGGCGCCCAACATCGCGTCGCAGCCCTGTCCCTGCGCCAGAGGCGTGCCGGCCAGCGGCGGGGGGCGCAG
 TGCACACGAGGGGGGCTGGACTTCGCCTGTGATTCCGGAATCTACATCTGGGCCCTCTGGCCGGCACCTGTGGCG
 TGCTGCTGCTGTCTCTCGTGATCACCCTGTACTGCAAGCGGGGAGAGAAAGAGCTGCTGTACATCTTCAAGCAGCC
 CTTTCATGCGGCCCGTGCAGACCACCCAGGAAGAGGACGGCTGCTCCTGCAGATTCCCCGAGGAAGAAGAAGGCG
 GCTGCGAGCTGAGAGTGAAGTTCAGCAGAAGCGCCGACGCCCTGCTATCAGCAGGGCCAGAACCAGCTGTAC
 25 AACGAGCTGAACCTGGGCAGACGGGAAGAGTACGACGTGCTGGACAAGCGGAGAGGCAGGGACCTGAGATGG
 GCGGCAAGCCAGAAAGAAAGAACCCCAAGGAAGGCCTGTATAACGAACTGCAGAAAGACAAGATGGCCGAGGC
 CTACAGCGAGATCGGAATGAAGGGCGAGCGGAGAAGAGGCAAGGGCCACGATGGCCTGTACCAGGGCCTGAGC
 ACCGCCACCAAGGACACCTATGACGCCCTGCACATGCAGGCCCTGCCTCCAAGAGGAAGCGGCGCCACCAATTC
 AGCCTGCTGAAACAGGCCGCGGACGTGGAAGAGAACCCTGGCCCTAGAGGCGTGCAAGTGGAACCATCTCTCC
 30 CGGCGACGGCAGAACCTTCCCTAAGAGGGGCCAGACCTGCGTGGTGCCTACACCGGCATGCTGGAAGATGGC
 AAGAAGATGGACAGCTCCCGGGACCGGAACAAGCCCTTCAAGTTCATGCTGGGCAAGCAGGAAGTGATCCGGG
 GCTGGGAAGAGGGCGTGGCACAGATGTCTGTGGGCCAGAGAGCCAAGCTGACCATCAGCCCCGATTACGCCTA
 CGGCGCCACAGGCCACCCTGGCATCATTCTCCACACGCCCACTGGTGTTCGATGTGGAAGTGTGAAGCTGGA
 AACCAGGGGAGTGACAGGTGGAACAATCAGCCCTGGCGACGGCCGACCTTTCCAAAACGGGGACAGACATGT
 35 GTGGTGCATTATACAGGGATGCTGGAAGATGGGAAAAAATGGATAGCAGCCGCGACCGCAACAAACCTTTTA
 AGTTTATGCTGGGGAAACAGGAAGTGATTAGAGGCTGGGAAGAGGGGGTGGCACAGATGAGCGTGGGACAG
 CGGGCCAACTGACAATCTCCCCGACTATGCCTATGGGGCCACCGGACACCCCGGAATCATCCACCTCATGCT
 ACCCTGGTGTGACGTGGAAGTGTGAACTGGAACAAGCGGCGGAGGCAGCGGCGGCTTTGGAGATGTGG
 GAGCCCTGGAAGCCTGCGGGGCAATGCCGATCTGGCCTACATCTGAGCATGGAACCCTGCGGCCACTGCCTG
 40 ATTATCAACAACGTGAACTTCTGCAGAGAGAGCGGCCTGCGGACCAGAACCAGGAGCAACATCGACTGCGAGA
 AGCTGCGGCGGAGATTCAGCAGCTGCACTTCATGGTGGAGTGAAGGGGGACCTGACCGCCAAGAAAATGGT
 GCTGGCTCTGCTGGAAGTGGCCAGCAGGATCATGGCGCCCTGGACTGTTGCGTGGTGTGATCCTGAGCCACG

GCTGCCAGGCCAGCCATCTGCAGTTTCCCGGCGCTGTGTATGGCACCGATGGCTGCCCTGTGTCCGTGGAAAAG
 ATCGTGAATATCTTCAACGGCACCAGCTGCCCCAGCCTGGGCGGAAAGCCTAAGCTGTTCTTTATTCAAGCCTGT
 GGGGGCGAGCAGAAGGACCACGGATTTGAGGTGGCCAGCACCTCCCCGAGGATGAGAGCCCTGGCAGCAAC
 CCTGAGCCTGACGCCACCCATTCCAGGAAGGACTGCGGACCTTCGACCAGCTGGACGCCATCTCTAGCCTGCCC
 5 ACCCCAGCGACATCTTCGTGTCCTACAGCACCTTCCCTGGCTTTGTGTCCTGGCGGGACCCCAAGTCCGGCTCTT
 GGTACGTGGAAACCTGGACGACATCTTTGAGCAGTGGGCCCATAGCGAGGACCTGCAGAGCCTGCTGCTGAG
 GGTGGCCAATGCCGTGTCCGTGAAGGGCATCTACAAGCAGATGCCCGGCTGCTTCAACTTCTGCGGAAGAAGC
 TGTTTTTCAAGACCAGC

10

FMC63-bbz-2A- **revCasp9** amino acid sequence (SEQ ID NO:3029)

15

MALPVTALLPLALLHAARPGSDIQMTQTSSLSASLGDRVTISCRASQDISKYLNWYQOKPDGTVKLIYHTSRLHSGV
 PSRF5SGSGSGTDYSLTISNLEQEDIATYFCQOGNTLPYTFGGGKLEITGGGSGGGGSGGGGSEVKIQESGPGLVAPS
 15 QLSVTCTVSGVSLPDYGVSWIRQPPRKGLEWLGVIWGSSETTYNSALKSRLTIKDNSKSQVFLKMNSLQDDTAIYYC
 AKHYYYGGSYAMDYWGQTSVTVSSASTTPAPRPPTPAPTASQPLSLRPEACRPAAGGAVHTRGLDFACDSGIYW
 APLAGTCGVLLSLVITLYCKRGRKLLYIFKQPFMRPVQTTQEEDGCSRFPEEEEGGCELRVKFSRSADAPAYQQGQN
 QLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELOKDKMAEAYSEIGMKGERRRGKGHDGLYQGLS
 TATKDTYDALHMOALPPRGSGATNFSLLKQAGDVEENPGPRGVQVETISPGDGRTFPKRGQTCVVHYTGMLLEDGKK
 20 MDSSRDRNKPFFKMLGKQEVIRGWEEGVAQMSVGQRAKLTISPDIYAGATGHPGIIPPHATLVFDVELLKLETRGV
 QVETISPGDGRTFPKRGQTCVVHYTGMLLEDGKKMDSSRDRNKPFFKMLGKQEVIRGWEEGVAQMSVGQRAKLT
 SPDYAGATGHPGIIPPHATLVFDVELLKLETSGGGSGGFGDVGALSLRGNADLAYILSMPCGHCLINNPNFCRES
 GLRTRTGSNIDCEKLRRRFSSLHFMVEVKGDLTAKKMVLALLELAQQDHGALDCCVVVILSHGCQASHLQFPGAVYG
 TDGCPVSVEKIVNIFNGTSCPSLGGKPKLFFIQACGGEQKDHGFVASTSPEDESPGSNPEPDATPFQEGLRTFDQLD
 25 AISSLPTPSDIFVSYSTFPGFVSWRDPKSGSWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNFLR
 KKLFFKTS

30

CD19bbz on-CAR nucleotide sequence, CD19 on-CAR (SEQ ID NO: 977, also provided previously herein)
 Signal peptide-conditional aggregation domains (4 repeats)- Furin site-FMC63bbz

35

40

ATGGCCTTACCAGTGACCGCCTTGCTCCTGCCGCTGGCCTTGCTGCTCCACGCCGCCAGGCCGGGATCCCGGGGCG
 TGCAGGTTGAGACAATTCCCCAGGAGATGGGCGAACGTTCCCCAAGCGCGGACAGACATGCGTTGTGCACTACA
 CAGGAATGTTGGAGGACGGAAAGAAAATGGACAGTTCAAGAGATCGGAACAAACCATTCAAATTCATGTTGGGA
 35 AAACAGGAAGTGATACGGGGCTGGGAAGAGGGTGTAGCGCAAATGTCCGTTGGTCAACGAGCAAACTCACGAT
 AAGTCCCGATTATGCTTACGGCGCAACCGGTCACCCGGGCATCATACCGCCTCATGCGACTTTGGTCTTTGATGTG
 GAGCTGTTGAACTTGAACTCGCGGAGTACAGGTTGAAACAATATCACCCGGGGACGGGCGGACTTTCCGAAG
 AGAGGTCAGACCTGCGTCGTCCATTATACCGGTATGCTGGAGGACGGAAAGAAAATGGACAGCTCACGGGACCG
 AAATAAACCATTCAAATTTATGTTGGGGAAACAAGAGGTTATCAGGGGCTGGGAGGAGGGTGTGGCCAGATGT
 40 CTGTGCGGTACGCGCGGAAACTCACAATCTCTCCGATTATGCGTATGGGGCGACAGGGCATCCGGGAATTATCC
 CTCCCCACGCTACCTTGGTTTTCGATGTTGAGCTTCTGAAGTTGGAGACCAGAGGAGTTCAAGTGGAGACAATATC
 TCCTGGGGATGGACGGACGTTCCCCAAGCGCGGCCAGACCTGTGTAGTCCACTACACAGGGATGCTTGAAGACG

5 GAAAAAAGATGGATAGCAGTAGAGATCGCAACAAACCATTTAAGTTCATGCTGGGGAAGCAGGAAGTAATACGC
 GGCTGGGAGGAAGGCGTGGCACAGATGAGTGTGGTCAACGGGCCAAACTTACTATTTCTCCCGATTATGCGTAT
 GGAGCCACCGGGCACCTGGCATTATCCACCCCATGCCACATTGGTTTTGACGTTGAATTGCTTAAATTGGAGA
 CCAGGGGAGTCCAAGTGGAAACAATATCACCGGGGGATGGTCGGAAGTTTCTTAAAGGGGCCAAACCTGTGTA
 10 GTCCATTATACCGGAATGCTCGAAGACGGAAAGAAAATGGACTCTTCTAGAGACCGCAATAAGCCCTTCAAGTTCA
 TGTGGGTAAGCAAGAGGTGATCCGGGGCTGGGAAGAGGGGGTGGCTCAAATGTCCGTGGTCAGCGAGCTAAA
 CTGACTATTTCCCGAGACTACGCATATGGAGCGACTGGCCACCCCGGTATTATTCCTCCCATGCGACTCTCGTGTT
 CGACGTAGAAGTCTTGAATTGGAAACGTCAGCCCGGAACAGGCGGAAGAGAGGATCCGACATCCAGATGACAC
 AGACTACATCCTCCCTGTCTGCCTCTCTGGGAGACAGAGTCACCATCAGTTGCAGGGCAAGTCAGGACATTAGTAA
 15 ATATTTAAATTGGTATCAGCAGAAACCAGATGGAAGTGTAACTCCTGATCTACCATACATCAAGATTACACTCAG
 GAGTCCCATCAAGGTTCAAGTGGCAGTGGGTCTGGAACAGATTATTCTCTCACCATTAGCAACCTGGAGCAAGAAG
 ATATTGCCACTTACTTTTGCCAACAGGGTAATACGCTTCCGTACACGTTCCGAGGGGGGACTAAGTTGGAAATAAC
 AGGTGGCGGTGGCTCGGGCGGTGGTGGGTGGGTGGCGCGGATCTGAGGTGAAACTGCAGGAGTCAGGACCT
 GGCCTGGTGGCGCCCTCACAGAGCCTGTCCGTACATGCACTGTCTCAGGGGTCTCATTACCCGACTATGGTGTA
 20 GCTGGATTGCGCAGCCTCCACGAAAGGTCTGGAGTGGCTGGGAGTAATATGGGGTAGTGAAACCACATACTATA
 ATTCAGCTCTCAAATCCAGACTGACCATCATCAAGGACAACTCCAAGAGCCAAGTTTTCTTAAAAATGAACAGTCT
 GCAAAGTATGACACAGCCATTTACTACTGTGCCAAACATTATTACTACGGTGGTAGCTATGCTATGGACTACTGG
 GGTCAAGGAACCTCAGTACCGTCTCCTCAGCTAGCACCACGACGCCAGCGCCGCGACCACCAACACCGGCGCCC
 ACCATCGCGTCGCGAGCCCTGTCCCTGCGCCCAGAGGCGTGCCGGCCAGCGGCGGGGGGCGCAGTGACACAGAG
 25 GGGGCTGGACTTCGCTGTGATTCCGGAATCTACATCTGGGCGCCCTTGCGCGGGGACTTGTGGGGTCTTCTCTG
 TCACTGGTTATCACCTTTACTGCAAACGGGGCAGAAAGAACTCCTGTATATATTCAAACAACCATTTATGAGACC
 AGTACAACTACTCAAGAGGAAGATGGCTGTAGCTGCCGATTTCCAGAAGAAGAAGAAGGAGGATGTGAAGTGA
 GAGTGAAGTTCAGCAGGAGCGCAGACGCCCCCGGTACCAGCAGGGCCAGAACCAGCTCTATAACGAGCTCAAT
 CTAGGACGAAGAGAGGAGTACGATGTTTTGGACAAGAGACGTGGCCGGGACCTGAGATGGGGGGAAAGCCGA
 30 GAAGGAAGAACCCTCAGGAAGGCCTGTACAATGAACTGCAGAAAGATAAGATGGCGGAGGCCTACAGTGAGATT
 GGGATGAAAGGCGAGCGCCGGAGGGGCAAGGGGCACGATGGCCTTACCAGGGTCTCAGTACAGCCACCAAGG
 ACACCTACGACGCCCTTCACATGCAGGCCCTGCCCCCTCGCTAA

30 CD19bbz on-CAR amino acid sequence (SEQ ID NO: 978, also provided previously herein)

Signal peptide-conditional aggregation domains (4 repeats)-Furin site-FMC63bbz

35 MALPVTALLPLALLHAARPGSRGVQVETISPGDGRTPKRGQTCVVHYTGMLEDGKKMDSSRDRNKPFFKMLGKQ
 EVIRGWEEGVAQMSVGQRAKLITSPDYAYGATGHPGIIPPHATLVFDVELLKLETRGVQVETISPGDGRTPKRGQTCV
 VHYTGMLEDGKKMDSSRDRNKPFFKMLGKQEVIRGWEEGVAQMSVGQRAKLITSPDYAYGATGHPGIIPPHATLVFD
 VELLKLETRGVQVETISPGDGRTPKRGQTCVVHYTGMLEDGKKMDSSRDRNKPFFKMLGKQEVIRGWEEGVAQMS
 VGQRAKLITSPDYAYGATGHPGIIPPHATLVFDVELLKLETRGVQVETISPGDGRTPKRGQTCVVHYTGMLEDGKKMD
 SSRDRNKPFFKMLGKQEVIRGWEEGVAQMSVGQRAKLITSPDYAYGATGHPGIIPPHATLVFDVELLKLETSARNRRKR
 40 GSDIQMTQTSSLSASLGDRVTISCRASQDISKYLNWYQKPDGTVKLLIYHTSRLHSGVPSRFSGSGSGTDYSLTISNLE
 QEDIATYFCQQGNTLPYTFGGGKLEITGGGGSGGGGSGGGGSEVKLQESGPGLVAPSQSLSVTCTVSGVSLPDYGV
 WIRQPPRKGLEWLGVWGSSETTYNSALKSRLLIKDNSKSQVFLKMNSLQTDITAIYYCAKHYYYGGSYAMDYWGQG
 TSVTVSSASTTTPAPRPPTPAPTASQPLSLRPEACRPAAGGAVHTRGLDFACDSGIYIWAPLAGTCGVLLSLVITLYCKR

GRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKR
RGRDPEMGGKPRRKNPQEGLYNELQDKDMAEAYSEIGMIKGERRRRGKHDGLYQGLSTATKDTYDALHMQALPPRZ

- 5 *Signal peptide-Anti-human CD20-CD8 hinge-CD8transmembrane-CD137-CD247-2A- revCasp9* amino acid sequence nucleotide sequence (SEQ ID NO: 3030)

ATGGCCTTACCAGTGACCGCCTTGCTCCTGCCGCTGGCCTTGCTGCTCCACGCCGCCAGGCCGGGATCCGATATTCA
ACTTACACAGTCCCCTAGTTCCCTTGTCGCGCTCCGTCGGCGACAGAGTTACCATGACTTGTCGAGCGTCTTCTAGCG
10 TTTCCTACATTTCATTGGTTCCAACAGAAGCCCGGAAAGGCACCAAAACCTTGGATCTACGCCACGTCCAATTTGGCT
AGTGGTGTTCGGTGCGATTTCCGGGTGAGGTAGCGGGACGGACTATACTTTTACCATTTCAAGCCTTCAGCCTG
AAGACATCGCGACGTACTATGTGACGAGTGGACCTCTAACCTCCTACCTTTGGCGGTGGAACAAAGCTGGAGAT
CAAACGAGGCGGGGGTGGCTCTGGGGGAGGAGGTTCCGGTGGGGGAGGCTCTCAAGTACAACCTGCAACAAAGT
GGGGCTGAAGTGAAGAAGCCCGGTTCTTCAGTCAAAGTATCATGTAAGGCAAGTGGTTATACTTTTACGTCTTATA
15 ACATGCATTGGGTAAAGCAAGCCCTGGTCAAGGCGCTCGAGTGGATTGGTGGGATCTACCTGGAATGGGTGATA
CGAGCTATAATCAGAAATTCAGGGGAAAGCCACCTTGACTGCAGACGAATCTACGAACACGGCTTACATGGAGC
TTAGCTCACTCAGATCAGAGGATACAGCCTTTTACTACTGCGCTAGATCAACTTATTACGGAGGAGACTGGTATTTT
GATGTATGGGGTCAGGGGACCACAGTCACTGTTAGCTCTGCTAGCACCACGACGCCAGCGCCGCGACCAACAAC
ACCGGCGCCCAACATCGCGTCGACAGCCCCTGTCCCTGCGCCAGAGGCGTGCCGCCAGCGGCGGGGGGCGCA
20 GTGCACACGAGGGGGCTGGACTTCGCTGTGATTCCGGAATCTACATCTGGGCGCCCTTGCCCGGACTTGTGG
GGTCTTCTCCTGTCACTGGTTATCACCTTTACTGCAAACGGGGCAGAAAGAACTCCTGTATATATTCAAACAAC
CATTTATGAGACCAGTACAACTACTCAAGAGGAAGATGGCTGTAGCTGCCGATTTCCAGAAGAAGAAGGA
GGATGTGAAGTGAAGTTCAGCAGGAGCGCAGACGCCCCCGCTACCAGCAGGGCCAGAACCAGCTCTA
TAACGAGCTCAATCTAGGACGAAGAGAGGAGTACGATGTTTTGGACAAGAGACGTGGCCGGGACCTGAGATGG
25 GGGGAAAGCCGAGAAGGAAGAACCTCAGGAAGGCCTGTACAATGAAGTGCAGAAAGATAAGATGGCGGAGGC
CTACAGTGAGATTGGGATGAAAGGCGAGCGCCGGAGGGGCAAGGGGCACGATGGCCTTTACCAGGGTCTCAGT
ACAGCCACCAAGGACACCTACGACGCCCTTACATGCAGGCCCTGCCCCCTCGCGGAAGCGGCGCCACCAATTTCA
GCCTGCTGAAACAGGCGCGGACGTGGAAGAGAACCCTGGCCCTAGAGGCGTGCAGGTGGAACCATCTCTCCC
GGCGACGGCAGAACCTTCCCTAAGAGGGGCCAGACCTGCGTGGTGCCTACACGGCATGCTGGAAGATGGCA
30 AGAAGATGGACAGCTCCCGGGACCGGAACAAGCCCTTCAAGTTCATGCTGGGCAAGCAGGAAGTGATCCGGGG
CTGGGAAGAGGGCGTGGCACAGATGTCTGTGGGCCAGAGAGCCAAGCTGACCATCAGCCCCGATTACGCCTAC
GGCGCCACAGGGCCACCCTGGCATATTCTCCACACGCCACACTGGTGTTCGATGTGGAAGTCTGAAGCTGGAA
ACCCGGGGAGTGCAGGTGGAACAATCAGCCCTGGCGACGGCCGGACCTTTCAAACGGGGACAGACATGTG
TGGTGCATTATACAGGGATGCTGGAAGATGGGAAAAAATGGATAGCAGCCGCGACCGCAACAAACCTTTTAA
35 GTTTATGCTGGGGAAACAGGAAGTGATTAGAGGCTGGGAAGAGGGGGTGGCACAGATGAGCGTGGGACAGC
GGGCCAAACTGACAATCTCCCCGACTATGCCTATGGGGCCACCGGACACCCCGGAATCATCCACCTCATGCTAC
CCTGGTGTGTTGACGTGGAAGTCTGAAACTGGAACAAGCGGCGGAGGCAGCGGCGGCTTTGGAGATGTGGGA
GCCCTGGAAGCCTGCGGGGCAATGCCGATCTGGCCTACATCTGAGCATGGAACCTGCGGCCACTGCCTGATT
ATCAACAACGTGAACTTCTGCAGAGAGAGCGGCTGCGGACCAGAACCGGCAGCAACATCGACTGCGAGAAGC
40 TGCGGCGGAGATTACGACGCTGCACTTCATGGTGGAAAGTGAAGGGGGACCTGACCGCCAAGAAAATGGTGCT
GGCTCTGCTGGAAGTGGCCAGCAGGATCATGGCGCCCTGGACTGTTGCGTGGTTCGTGATCCTGAGCCACGGCT
GCCAGGCCAGCCATCTGCAGTTTCCCGGCGCTGTGTATGGCACCGATGGCTGCCCTGTGTCCGTGGAAAAGATCG

TGAATATCTTCAACGGCACCAGCTGCCCCAGCCTGGGCGGAAAGCCTAAGCTGTTCTTTATTCAAGCCTGTGGGG
 GCGAGCAGAAGGACCACGGATTTGAGGTGGCCAGCACCTCCCCGAGGATGAGAGCCCTGGCAGCAACCCTGA
 GCCTGACGCCACCCCATTCAGGAAGGACTGCGGACCTTCGACCAGCTGGACGCCATCTCTAGCCTGCCCCACCC
 AGCGACATCTTCGTGTCTACAGCACCTTCCTGGCTTTGTGTCTGGCGGGACCCCAAGTCGGGCTCTTGGTACG
 5 TGGAAACCCTGGACGACATCTTTGAGCAGTGGGCCCATAGCGAGGACCTGCAGAGCCTGCTGCTGAGGGTGGCC
 AATGCCGTGTCCGTGAAGGGCATCTACAAGCAGATGCCCGGCTGCTTCAACTTCTGCGGAAGAAGCTGTTTTTC
 AAGACCAGC

- 10 Signal peptide-~~Anti human CD20~~-**CD8 hinge**-~~CD8transmembrane-CD137-CD247-2A~~- *revCasp9* amino acid sequence (SEQ ID NO: 3031)

MALPVTALLPLALLHAARPGSDIQLTQSPSSLASVGDRTMTCRASSSVSYIHWFOQKPGKAPKPWIYATSNLASG
 VPVRFSGSGSGTDYFTTSSLOPEDIAITYCQQWTSNPPTFGGGTKLEIKRGGGSGGGGSGGGGSGVQLQQSGAEVK
 15 KPGSSVKVSKASGYTFTSYNMHWVKQAPGQGLEWIGAIYPGMGDTSYNQKFKGKATLTADSTNTAYMELSSLRSE
 DTAFYFCARSTYYGGDWYFDVWGQGTFTVYSASTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFA
 CDSGIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSRFPEEEEGGCELRVKFSRSADAP
 AYQQGQNQLYNELNLGRREYDVLDKRRGRDPENGGKPRRKNPQEGLYNELQDKMAEAYSEIGMKGERRRGKGH
 DGLYQGLSTATKDTYDALHMQALPPRGSGATNFSLLKQAGDVEENPGPRGVQVETISPGDGRTFPKRGQTCVVHYT
 20 GMLEDGKKMDSSRDRNKPFFKMLGKQEVIRGWEEGVAQMSVGQRAKLTISPDYAYGATGHPGIIPPHATLVFDVE
 LLKLETRGVQVETISPGDGRTFPKRGQTCVVHYTGMLEDGKKMDSSRDRNKPFFKMLGKQEVIRGWEEGVAQMSV
 GQRAKLTISPDYAYGATGHPGIIPPHATLVFDVELLKLETSGGGSGGFGDVGALES LRGNADLAYILSMEPCGHCLIN
 NVNFCRESGLRTRTGSNIDCEKLRRRFSSLHFMVEVKGDLTAKKMVLALLELAQQDHGALDCCVVVILSHGCQASHL
 QFPGAVYGTGCPVSVEKIVNIFNGTSCPSLGGKPKLFFIQACGGEQKDHGFEVASTSPEDESPGSNPEPDATPFQEG
 25 LRTFDQLDAISSLPTSDIFVSYSTFPGFVSWRDPKSGSWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQM
 PGCNFRKKLFFKTS

CD20bbz on-CAR nucleotide sequence, CD20 on-CAR (SEQ ID NO: 3032)

- 30 Signal peptide-~~conditional aggregation domains (4 repeats)~~- Furin site-anti-CD20bbz

ATGGCCTTACCAGTGACCGCCTTGCTCCTGCCGCTGGCCTTGCTGCTCCACGCCGCCAGGCCGGGATCCCGGGCGC
 TGCAGGTTGAGACAATTCCCCAGGAGATGGGCGAACGTTCCCAAGCGCGGACAGACATGCGTTGTGCACTACA
 CAGGAATGTTGGAGGACGGAAAGAAAATGGACAGTTCAAGAGATCGGAACAAACCATTCAAATTCATGTTGGGA
 35 AAACAGGAAGTGATACGGGGCTGGGAAGAGGGTGTAGCGCAAATGTCCGTTGGTCAACGAGCAAACTCACGAT
 AAGTCCCGATTATGCTTACGGCGCAACCGGTCACCCGGGCATCATACCGCCTCATGCGACTTTGGTCTTTGATGTG
 GAGCTGTTGAACTTGAACTCGCGGAGTACAGGTTGAAACAATATCACCCGGGGACGGGCGGACTTTCCGAAG
 AGAGGTCAGACCTGCGTCGTCCATTATACCGGTATGCTGGAGGACGGAAAGAAAATGGACAGCTCACGGGACCG
 AAATAAACCATTCAAATTTATGTTGGGGAAACAAGAGGTTATCAGGGGCTGGGAGGAGGGTGTGGCCAGATGT
 40 CTGTCGGTCAGCGCGGAAACTCACAATCTCTCCGATTATGCGTATGGGGCGACAGGGCATCCGGGAATTATCC
 CTCCCCACGCTACCTTGGTTTTCGATGTTGAGCTTCTGAAGTTGGAGACCAGAGGAGTTCAAGTGGAGACAATATC
 TCCTGGGGATGGACGGACGTTCCCAAGCGCGGCCAGACCTGTGTAGTCCACTACACAGGGATGCTTGAAGACG

5 GAAAAAAGATGGATAGCAGTAGAGATCGCAACAAACCATTAAAGTTCATGCTGGGGAAGCAGGAAGTAATACGC
 GGCTGGGAGGAAGGCGTGGCACAGATGAGTGTGGTCAACGGGGCAAACCTTACTATTTCTCCCGATTATGCGTAT
 GGAGCCACCGGGCACCTGGCATTATCCACCCCATGCCACATTGGTTTTGACGTTGAATTGCTTAAATTGGAGA
 CCAGGGGAGTCCAAGTGGAAACAATATCACCGGGGGATGGTCGGACTTTTCTTAAAGGGGGCAAACCTGTGTA
 GTCCATTATACCGGAATGCTCGAAGACGGAAAGAAAATGGACTCTTCTAGAGACCGCAATAAGCCCTTCAAGTTCA
 TGTGGGTAAGCAAGAGGTGATCCGGGGCTGGGAAGAGGGGGTCTCAAATGTCCGTCCGTCAGCGAGCTAAA
 CTGACTATTTCCCGAGACTACGCATATGGAGCGACTGGCCACCCCGGTATTATTCCTCCCATGCGACTCTCGTGT
 CGACGTAGAAGTCTTGAAATTGGAAACGTCAGCCCGGAACAGGCGGAAGAGAGATATTCAACTTACACAGTCCCC
 TAGTTCCTTGCCGCTCCGTCGGCGACAGAGTTACCATGACTTGTGAGCGTCTTCTAGCGTTTCTACATTCATT
 10 GGTTCCAACAGAAGCCCGGAAAGGCCACCAAAACCTTGATCTACGCCACGTCCAATTTGGCTAGTGGTGTTCGG
 TGCGATTTTCCGGGTAGGTAGCGGGACGGACTATACTTTTACCATTTCAGCCTTGAAGACATCGCGAC
 GTACTATTGTCAGCAGTGGACCTCTAACCTCTACCTTTGGCGGTGGAACAAAGCTGGAGATCAAACGAGGCGG
 GGGTGGCTCTGGGGGAGGAGGTTCCGGTGGGGGAGGCTCTCAAGTACAAGTGAACAAAGTGGGGCTGAAGTG
 AAGAAGCCCCGTTCTTCAAGTATCATGTAAGGCAAGTGGTTATACTTTACGTCTTATAACATGCATTGGG
 15 TAAAGCAAGCCCTGGTCAGGCGCTCGAGTGGATTGGTGCATCTACCCTGGAATGGGTGATACGAGCTATAATC
 AGAAATTCAAGGGGAAAGCCACCTTGACTGCAGACGAATCTACGAACACGGCTTACATGGAGCTTAGCTCACTCA
 GATCAGAGGATACAGCCTTTTACTACTGCGCTAGATCAACTTATTACGGAGGAGACTGGTATTTGATGTATGGGG
 TCAGGGGACCACAGTCACTGTAGCTCTGCTAGCACCACGACGCCAGCGCCGACCAACACCGGCGCCAC
 CATCGCGTCGACGCCCCGTGCCCTGCGCCCAGAGGCGTGCCGGCCAGCGCGGGGGGGCGCAGTGCACACGAGGG
 20 GGCTGGACTTCGCTGTGATTCCGGAATCTACATCTGGGCGCCCTTGCCCGGACTTGTGGGGTCTTCTCTGTC
 ACTGGTTATCACCTTTACTGCAAACGGGGCAGAAAGAACTCTGTATATATTCAAACAACCATTTATGAGACCA
 GTACAACTACTCAAGAGGAAGATGGCTGTAGCTGCCGATTTCCAGAAGAAGAAGAGGAGGATGTGAAGTGAAG
 AGTGAAGTTCAGCAGGAGCGCAGACGCCCCCGCTACCAGCAGGGCCAGAACCAGCTCTATAACGAGCTCAATCT
 AGGACGAAGAGAGGAGTACGATGTTTTGGACAAGAGACGTGGCCGGGACCCTGAGATGGGGGGAAAGCCGAGA
 25 AGGAAGAACCCTCAGGAAGGCTGTACAATGAAGTGCAGAAAGATAAGATGGCGGAGGCCTACAGTGAAGTTGG
 GATGAAAGGCGAGCGCCGGAGGGGGCAAGGGGCACGATGGCCTTTACCAGGGTCTCAGTACAGCCACCAAGGAC
 ACCTACGACGCCCTTACATGCAGGCCCTGCCCCCTCGC

30 CD20bbz on-CAR amino acid sequence (SEQ ID NO: 3033)

Signal peptide-conditional aggregation domains (4 repeats)-Furin site-anti-CD20bbz

MALPVTALLPLALLHAARPGSRGVQVETISPGDGRTFPKRGQTCVVHYTGMLDGGKMDSSRDNRNPKFKFMLGKQ
 EVIRGWEEGVAQMSVGQRAKLISPDIYAGATGHPGIIPPHATLVFDVELLKLETRGVQVETISPGDGRTFPKRGQTCV
 VHYTGMLDGGKMDSSRDNRNPKFKFMLGKQEVIRGWEEGVAQMSVGQRAKLISPDIYAGATGHPGIIPPHATLVFD
 35 VELLKLETRGVQVETISPGDGRTFPKRGQTCVVHYTGMLDGGKMDSSRDNRNPKFKFMLGKQEVIRGWEEGVAQMS
 VGQRAKLISPDIYAGATGHPGIIPPHATLVFDVELLKLETRGVQVETISPGDGRTFPKRGQTCVVHYTGMLDGGKMD
 SSRDNRNPKFKFMLGKQEVIRGWEEGVAQMSVGQRAKLISPDIYAGATGHPGIIPPHATLVFDVELLKLETSARNRRKR
 GSDIQLTQSPSSLSASVGDRVTMTCRASSVSYSIHWFQKPKGKPKWIYATSNLASGVPVRFSGSGSGTDYFTFTISLQ
 PEDIATYYCQWTSNPPTFGGGTKLEIKRGGGSGGGGSGGGGSGVQLQQSGAEVKKPGSSVKVSKASGYTFTSYN
 40 MHWVKQAPGQGLEWIGAIYPGMGDSYNQKFKGKATLTADSTNTAYMELSSLRSEDTAFYYCARSTYYGGDWYFD
 VWGQGTTVTSSASTTTPAPRPPTPAPTASQPLSLRPEACRPAAGGAVHTRGLDFACDSGIYIWAPLAGTCGVLLSLV
 ITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSRFPFEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLRREEY

DVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQ
ALPPR

OTHER EMBODIMENTS

The disclosures of each and every patent, patent application, and publication cited herein are hereby incorporated herein by reference in their entirety. While this invention has been disclosed with reference to specific embodiments, it is apparent that other embodiments and variations of this invention may be devised by others skilled in the art without departing from the true spirit and scope of the invention. The appended claims are intended to be construed to include all such embodiments and equivalent variations.

The reference in this specification to any prior publication (or information derived from it), or to any matter which is known, is not, and should not be taken as an acknowledgment or admission or any form of suggestion that that prior publication (or information derived from it) or known matter forms part of the common general knowledge in the field of endeavour to which this specification relates.

Throughout this specification and the claims which follow, unless the context requires otherwise, the word “comprise”, and variations such as “comprises” and “comprising”, will be understood to imply the inclusion of a stated integer or step or group of integers or steps but not the exclusion of any other integer or step or group of integers or steps.

THE CLAIMS DEFINING THE INVENTION ARE AS FOLLOWS:

1. A fusion protein, comprising two protein domains separated by a heterologous protease cleavage site, wherein a first of said protein domains is a degradation domain, and a second of said protein domains is a chimeric antigen receptor (CAR), wherein the degradation domain has a first state associated with a first level of surface expression of the fusion protein and a second state associated with a second level of surface expression of the fusion protein, and wherein the second level is increased over the first level in the presence of a stabilization compound.
2. The fusion protein of claim 1, wherein the degradation domain is chosen from an estrogen receptor (ER) domain, an FKB protein (FKBP) domain or an dihydrofolate reductase (DHFR).
3. The fusion protein of claim 1 or claim 2, wherein:
 - (i) the degradation domain is from an estrogen receptor (ER) and comprises an amino acid sequence that is at least 90, 95, 97, 98, 99, or 100% identical to either of SEQ ID NOs: 58 or 121;
 - (ii) the degradation domain is a FKB protein (FKBP) domain and comprises an amino acid sequence that is at least 90, 95, 97, 98, 99, or 100% identical to SEQ ID NO: 56; or
 - (iii) the degradation domain is a dihydrofolate reductase (DHFR) domain and comprises an amino acid sequence that is at least 90, 95, 97, 98, 99, or 100% identical to SEQ ID NO: 57.
4. The fusion protein of any one of claims 1-3, wherein the second level is increased by at least 2, 3, 4, 5, 10, 20 or 30 fold over the first level in the presence of the stabilization compound.
5. The fusion protein of any one of claims 1-4, wherein said stabilization compound is:
 - (i) selected from Bazedoxifene or 4-hydroxy tamoxifen (4-OHT) when the fusion protein comprises a degradation domain that is an ER domain; or
 - (ii) Shield-1 when the fusion protein comprises a degradation domain derived from an FKBP domain.
6. The fusion protein of any one of claims 1-5, wherein:
 - (i) said heterologous protease cleavage site is cleaved by a mammalian intracellular protease;
 - (ii) said heterologous protease cleavage site comprises a polypeptide comprising a cleavage motif selected from the group consisting of RX(K/R)R consensus motif, RXXX[KR]R consensus motif, RRX consensus motif, I-E-P-D-X consensus motif (SEQ ID NO: 35), Glu/Asp-Gly-Arg, Asp-Asp-Asp-Asp-Lys (SEQ ID NO: 36), Pro-Gly-Ala-Ala-His-Tyr (SEQ ID NO: 37), LPXTG/A consensus motif, Leu-Glu-Val-Phe-Gln-Gly-Pro (SEQ ID NO: 38), Leu-Val-Pro-Arg-Gly-Ser (SEQ ID NO: 40), E-N-L-Y-F-Q-G (SEQ ID

NO: 41), and [AGSV]-x (SEQ ID NO: 42); or

(iii) said heterologous protease cleavage site is cleaved by a mammalian extracellular protease.

7. The fusion protein of claim 6, wherein:

(i) said heterologous protease cleavage site is cleaved by a protease selected from the group consisting of furin, PCSK1, PCSK5, PCSK6, PCSK7, cathepsin B, Granzyme B, Factor XA, Enterokinase, genenase, sortase, precision protease, thrombin, TEV protease, and elastase 1;

(ii) said mammalian extracellular protease is selected from the group consisting of Factor XA, Enterokinase, genenase, sortase, precision protease, thrombin, TEV protease, and elastase 1; or

(iii) said heterologous protease cleavage site comprises a polypeptide having an amino acid sequence selected from the group consisting of Glu/Asp-Gly-Arg, Asp-Asp-Asp-Asp-Lys (SEQ ID NO: 36), Pro-Gly-Ala-Ala-His-Tyr (SEQ ID NO: 37), LPXTG/A consensus motif, Leu-Glu-Val-Phe-Gln-Gly-Pro (SEQ ID NO: 38), Leu-Val-Pro-Arg-Gly-Ser (SEQ ID NO: 40), E-N-L-Y-F-Q-G (SEQ ID NO: 41), and [AGSV]-x (SEQ ID NO: 42).

8. The fusion protein of any one of claims 1-7, wherein said heterologous protease cleavage site is cleaved by furin.

9. The fusion protein of claim 8, wherein the fusion protein comprises a furin cleavage site selected from RTKR (SEQ ID NO: 123); GTGAEDPRPSRKRRSLGDVG (SEQ ID NO: 125); GTGAEDPRPSRKRR (SEQ ID NO: 127); LQWLEQQVAKRRTKR (SEQ ID NO: 129); GTGAEDPRPSRKRRSLGG (SEQ ID NO: 131); GTGAEDPRPSRKRRSLG (SEQ ID NO: 133); SLNLTESHNSRKKR (SEQ ID NO: 135); or CKINGYPKRGRKKR (SEQ ID NO: 137).

10. The fusion protein of any one of claims 1-9, wherein said CAR comprises, in a N-terminal to C-terminal direction, an antigen binding domain, a transmembrane domain, and one or more intracellular signaling domains.

11. The fusion protein of claim 10, wherein:

(i) said intracellular signaling domain comprises one or more primary signaling domains; or
(ii) said intracellular signaling domain comprises one or more costimulatory signaling domains.

12. The fusion protein of claim 11, wherein:

(i) one of said one or more primary signaling domains comprises a CD3-zeta stimulatory domain; or

(ii) one or more of said costimulatory signaling domains is an intracellular domain from a costimulatory protein selected from the group consisting of CD27, CD28, 4-1BB (CD137), OX40, GITR, CD30, CD40, ICOS, BAFFR, HVEM, ICAM-1, lymphocyte function-associated antigen-1 (LFA-1), CD2, CD7, CD287, LIGHT, NKG2C, NKG2D, SLAMF7, NKp80, NKp30, NKp44, NKp46, CD160, B7-H3, and a ligand that specifically binds with CD83.

13. The fusion protein of any one of claims 10-12, wherein:

(i) said antigen binding domain is an scFv; or

(ii) said antigen binding domain binds an antigen selected from the group consisting of CD19; CD123; CD22; CD30; CD171; CS-1; C-type lectin-like molecule-1, CD33; epidermal growth factor receptor variant III (EGFRvIII); ganglioside G2 (GD2); ganglioside GD3; TNF receptor family member B cell maturation (BCMA); Tn antigen ((Tn Ag) or (GalNAc α -Ser/Thr)); prostate-specific membrane antigen (PSMA); Receptor tyrosine kinase-like orphan receptor 1 (ROR1); Fms-Like Tyrosine Kinase 3 (FLT3); Tumor-associated glycoprotein 72 (TAG72); CD38; CD44v6; Carcinoembryonic antigen (CEA); Epithelial cell adhesion molecule (EPCAM); B7H3 (CD276); KIT (CD117); Interleukin-13 receptor subunit alpha-2; Mesothelin; Interleukin 11 receptor alpha (IL-11Ra); prostate stem cell antigen (PSCA); Protease Serine 21; vascular endothelial growth factor receptor 2 (VEGFR2); Lewis(Y) antigen; CD24; Platelet-derived growth factor receptor beta (PDGFR-beta); Stage-specific embryonic antigen-4 (SSEA-4); CD20; Folate receptor alpha; Receptor tyrosine-protein kinase ERBB2 (Her2/neu); Mucin 1, cell surface associated (MUC1); epidermal growth factor receptor (EGFR); neural cell adhesion molecule (NCAM); Prostase; prostatic acid phosphatase (PAP); elongation factor 2 mutated (ELF2M); Ephrin B2; fibroblast activation protein alpha (FAP); insulin-like growth factor 1 receptor (IGF-I receptor), carbonic anhydrase IX (CAIX); Proteasome (Prosome, Macropain) Subunit, Beta Type, 9 (LMP2); glycoprotein 100 (gp100); oncogene fusion protein consisting of breakpoint cluster region (BCR) and Abelson murine leukemia viral oncogene homolog 1 (Abl) (bcr-abl); tyrosinase; ephrin type-A receptor 2 (EphA2); Fucosyl GM1; sialyl Lewis adhesion molecule (sLe); ganglioside GM3; transglutaminase 5 (TGS5); high molecular weight-melanoma-associated antigen (HMWMAA); o-acetyl-GD2 ganglioside (OAcGD2); Folate receptor beta; tumor endothelial marker 1 (TEM1/CD248); tumor endothelial marker 7-related (TEM7R); claudin 6 (CLDN6); thyroid stimulating hormone receptor (TSHR); G protein-coupled receptor class C group 5, member D (GPRC5D); chromosome X open reading frame 61 (CXORF61); CD97; CD179a; anaplastic lymphoma kinase (ALK); Polysialic acid; placenta-specific 1 (PLAC1); hexasaccharide portion of globoH glycosphingolipid (GloboH); mammary gland differentiation antigen (NY-BR-1); uroplakin 2 (UPK2); Hepatitis A virus cellular receptor 1 (HAVCR1); adrenoceptor beta 3 (ADRB3); pannexin 3 (PANX3); G protein-coupled receptor 20 (GPR20); lymphocyte antigen 6 complex, locus K 9 (LY6K); Olfactory receptor 51E2 (OR51E2); TCR Gamma Alternate Reading Frame Protein (TARP); Wilms tumor protein (WT1); Cancer/testis antigen 1 (NY-ESO-1); Cancer/testis antigen 2 (LAGE-1a); Melanoma-associated antigen 1 (MAGE-A1); ETS translocation-variant gene 6, located on chromosome 12p (ETV6-AML); sperm protein

17 (SPA17); X Antigen Family, Member 1A (XAGE1); angiopoietin-binding cell surface receptor 2 (Tie 2); melanoma cancer testis antigen-1 (MAD-CT-1); melanoma cancer testis antigen-2 (MAD-CT-2); Fos-related antigen 1; tumor protein p53 (p53); p53 mutant; prostein; surviving; telomerase; prostate carcinoma tumor antigen-1, melanoma antigen recognized by T cells 1; Rat sarcoma (Ras) mutant; human Telomerase reverse transcriptase (hTERT); sarcoma translocation breakpoints; melanoma inhibitor of apoptosis (ML-IAP); ERG (transmembrane protease, serine 2 (TMPRSS2) ETS fusion gene); N-Acetyl glucosaminyl-transferase V (NA17); paired box protein Pax-3 (PAX3); Androgen receptor; Cyclin B1; v-myc avian myelocytomatosis viral oncogene neuroblastoma derived homolog (MYCN); Ras Homolog Family Member C (RhoC); Tyrosinase-related protein 2 (TRP-2); Cytochrome P450 1B1 (CYP1B1); CCCTC-Binding Factor (Zinc Finger Protein)-Like, Squamous Cell Carcinoma Antigen Recognized By T Cells 3 (SART3); Paired box protein Pax-5 (PAX5); proacrosin binding protein sp32 (OY-TES1); lymphocyte-specific protein tyrosine kinase (LCK); A kinase anchor protein 4 (AKAP-4); synovial sarcoma, X breakpoint 2 (SSX2); Receptor for Advanced Glycation Endproducts (RAGE-1); renal ubiquitous 1 (RU1); renal ubiquitous 2 (RU2); legumain; human papilloma virus E6 (HPV E6); human papilloma virus E7 (HPV E7); intestinal carboxyl esterase; heat shock protein 70-2 mutated (mut hsp70-2); CD79a; CD79b; CD72; Leukocyte-associated immunoglobulin-like receptor 1 (LAIR1); Fc fragment of IgA receptor (FCAR or CD89); Leukocyte immunoglobulin-like receptor subfamily A member 2 (LILRA2); CD300 molecule-like family member f (CD300LF); C-type lectin domain family 12 member A (CLEC12A); bone marrow stromal cell antigen 2 (BST2); EGF-like module-containing mucin-like hormone receptor-like 2 (EMR2); lymphocyte antigen 75 (LY75); Glypican-3 (GPC3); Fc receptor-like 5 (FCRL5); and immunoglobulin lambda-like polypeptide 1 (IGLL1).

14. The fusion protein of claim 13, wherein:

- (i) said antigen is CD19;
- (ii) the fusion protein comprises an antigen binding domain comprising an amino acid sequence selected from any one of SEQ ID NOs: 356-368 or 381;
- (iii) the fusion protein comprises a chimeric antigen receptor comprising an amino acid sequence selected from any one of SEQ ID NOs: 897, 902, 907, 912, 917, 922, 927, 932, 937, 942, 947, 952, 956;
- (iv) said antigen is CD123;
- (v) the fusion protein comprises an antigen binding domain comprising an amino acid sequence selected from any one of SEQ ID NOs: 751, 756, 761, or 766;
- (vi) the fusion protein comprises a chimeric antigen receptor comprising an amino acid sequence selected from any one of SEQ ID NOs: 750, 755, 760, or 765;
- (vii) said antigen is BCMA;
- (viii) the fusion protein comprises an antigen binding domain comprising an amino acid sequence selected from any one of SEQ ID NOs: 382, 386, 390, 394, 398, 402, 406, 410, 414, 418, 422,

426, 430, 434, 438, 442, 446, 450, 454, 458, 462, 466, 470, 474, 478, 482, 486, 490, 494, 498, 502, 506, 510, 514, 518, 522, 528, 531, 534, or 537;

(ix) the fusion protein comprises a chimeric antigen receptor comprising an amino acid sequence selected from any one of SEQ ID NOs: 789, 791, 793, 795, 797, 799, 801, 803, 805, 807, 809, 811, 813, 815, 817, 819, 821, 823, 825, 827, 829, 831, 833, 835, 837, 839, 841, 843, 845, 847, 849, 851, 853, 855, 857, or 859;

(x) said antigen is CD20;

(xi) the fusion protein comprises an antigen binding domain comprising an amino acid sequence located at positions 470-712 or 470-939 of SEQ ID NO: 3033; or

(xii) the fusion protein comprises a chimeric antigen receptor comprising an amino acid sequence of SEQ ID NO: 3033.

15. The fusion protein of any one of claims 1-14, wherein:

(i) the conditional expression domain, e.g., aggregation domain or degradation domain, is located:

(a) N-terminal to said second protein domain; or

(b) C-terminal to said second protein domain; or

(ii) said fusion protein further comprises a signal peptide, comprises a signal peptide N-terminal to said degradation domain, or comprises a linker positioned between the signal peptide and another domain of the fusion protein, or positioned between the signal peptide and said degradation domain.

16. The fusion protein of claim 15, wherein the signal peptide comprises the amino acid sequence of SEQ ID NO: 3035.

17. The fusion protein of any one of claims 1-16, comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 59, 61, 63, 65, 67, 69, 75, 103, 105, 107, 109, 111, 113, 115, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, and 990-1049.

18. A nucleic acid encoding the fusion protein of any one of claims 1-17.

19. A vector comprising the nucleic acid of claim 18.

20. The vector of claim 19, wherein said vector is a viral vector.

21. The vector of claim 19, wherein said vector is a lentiviral vector.

22. A viral particle comprising the vector of any one of claims 19-21.
23. A cell comprising the fusion protein of any one of claims 1-17, the nucleic acid of claim 18, or the vector of any one of claims 19-21.
24. A method of conditionally expressing a CAR on the surface of a cell, said method comprising: contacting the fusion protein of any one of claims 1-17, or the cell of claim 23 with the stabilization compound, wherein:
 - (a) in the presence of said stabilization compound, the level of surface expression of said CAR is increased relative to the level of surface expression of said CAR in the absence of said stabilization compound; and
 - (b) in the absence of said stabilization compound, the level of surface expression of said CAR is substantially decreased relative to the level of surface expression of said CAR in the presence of the stabilization compound;
 - (c) the presence of said stabilization compound is associated with a change in conformation of the degradation domain from a first folding state to second folding state, wherein the first folding state is more susceptible to degradation relative to the second folding state; or
 - (d) the presence of said stabilization compound exposes said protease cleavage site to a greater extent relative to the exposure of the protease cleavage site in the absence of said stabilization compound.
25. A method of conditionally expressing a CAR, said method comprising contacting the cell of claim 23 with a stabilization compound, wherein:
 - (a) in the presence of said stabilization compound, said degradation domain assumes a conformation more permissive to cleavage of the heterologous protease cleavage site relative to a conformation in the absence of said stabilization compound,
thereby resulting in cleavage of said degradation domain from the CAR and the expression of said CAR; and
 - (b) in the absence of said stabilization compound, said degradation domain assumes a conformation more resistant to cleavage of the heterologous protease cleavage site relative to a conformation in the presence of said stabilization compound, thereby resulting in degradation of said CAR.
26. A method of conditionally expressing a CAR, said method comprising contacting the cell of claim 23 with a stabilization compound, wherein:

(a) in the presence of said stabilization compound said degradation domain assumes a conformation more resistant to cellular degradation relative to a conformation in the absence of the stabilization compound; and

(b) in the absence of said stabilization compound, said degradation domain assumes a conformation more permissive to cellular degradation relative to a conformation in the presence of stabilization compound.

27. A method of treating a subject having a disease associated with expression of a tumor antigen, comprising administering to the subject an effective amount of the fusion protein of any one of claims 1-17, the nucleic acid of claim 18, the vector of any one of claims 19-21, or the cell of claim 23.

28. Use of the fusion protein of any one of claims 1-17, the nucleic acid of claim 18, the vector of any one of claims 19-21, or the cell of claim 23 in the manufacture of a medicament for treating a subject having a disease associated with expression of a tumor antigen.

29. The method of claim 27, or the use of claim 28, wherein the disease associated with expression of a tumor antigen is a cancer.

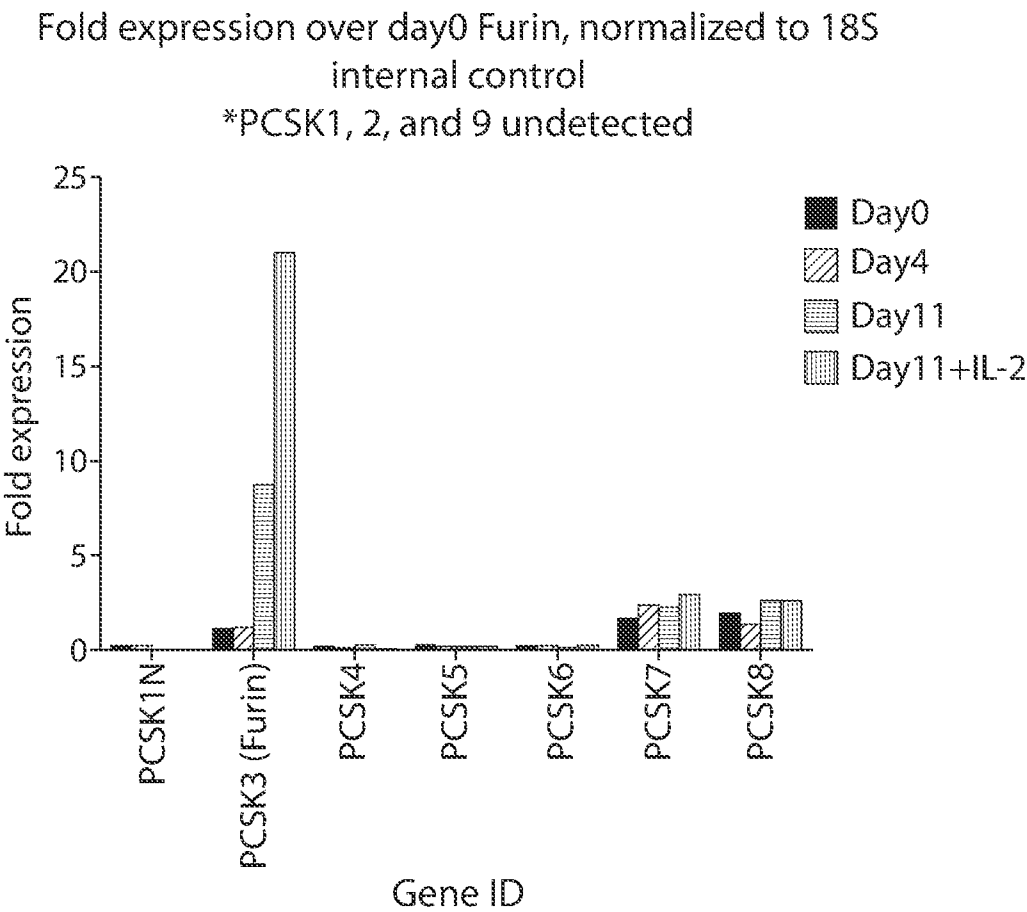


FIG. 1

2/48

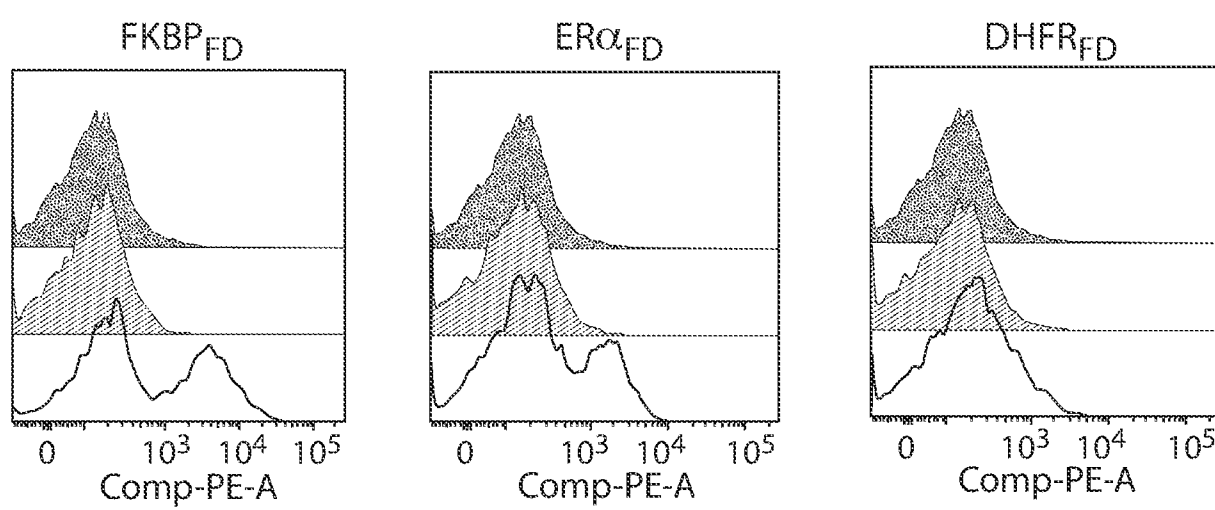


FIG. 2

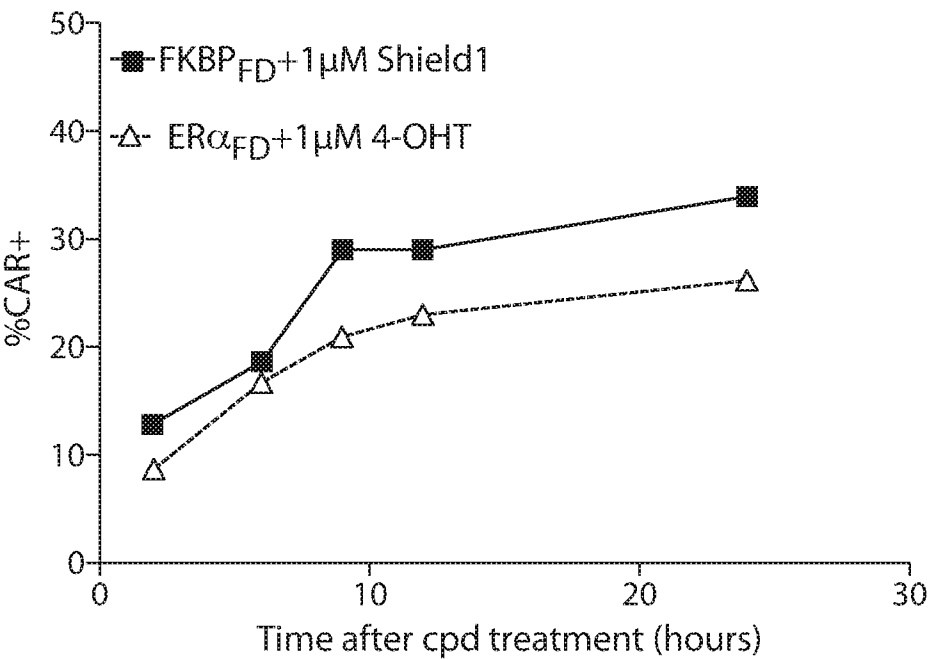


FIG. 3

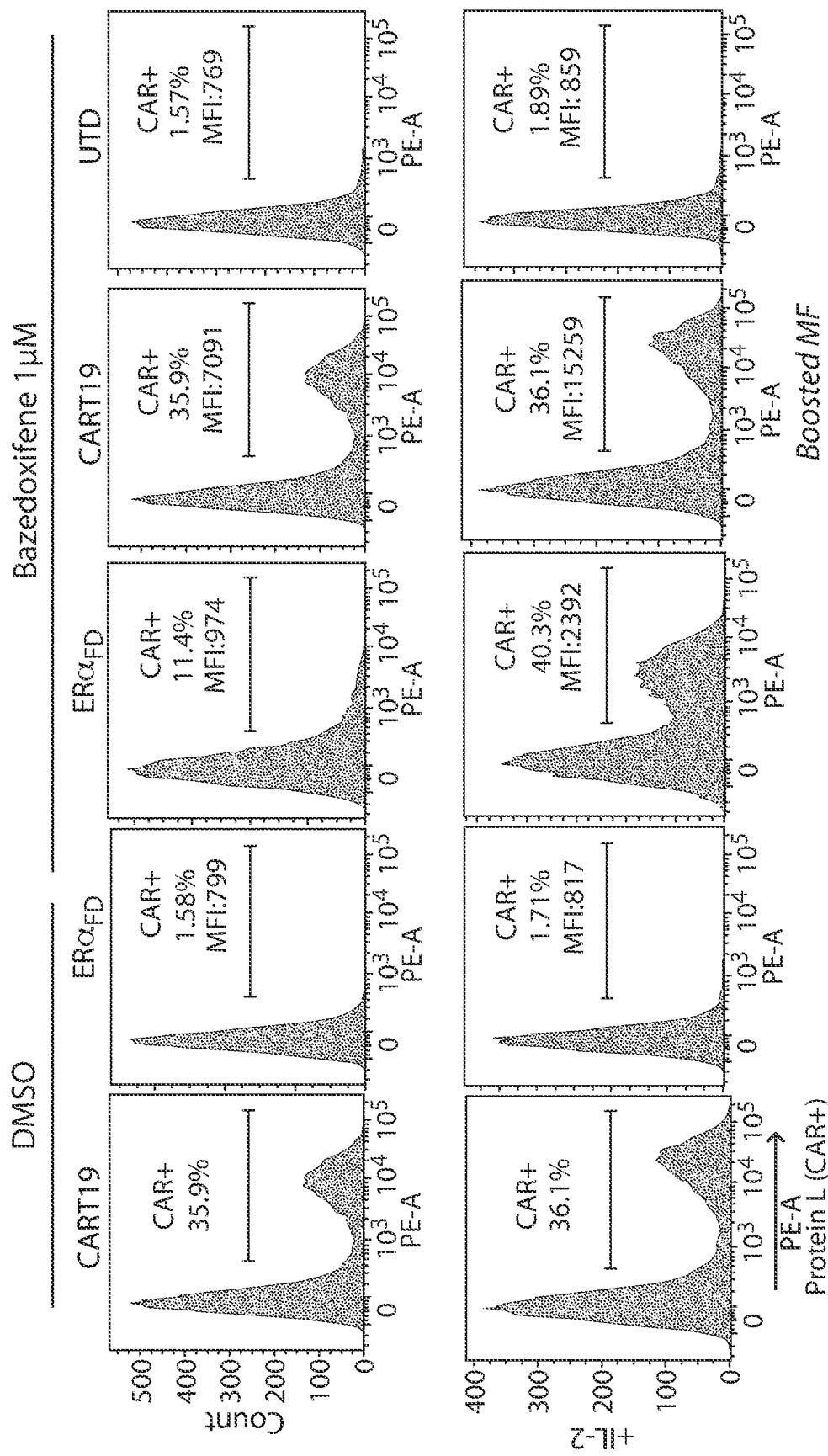


FIG. 4

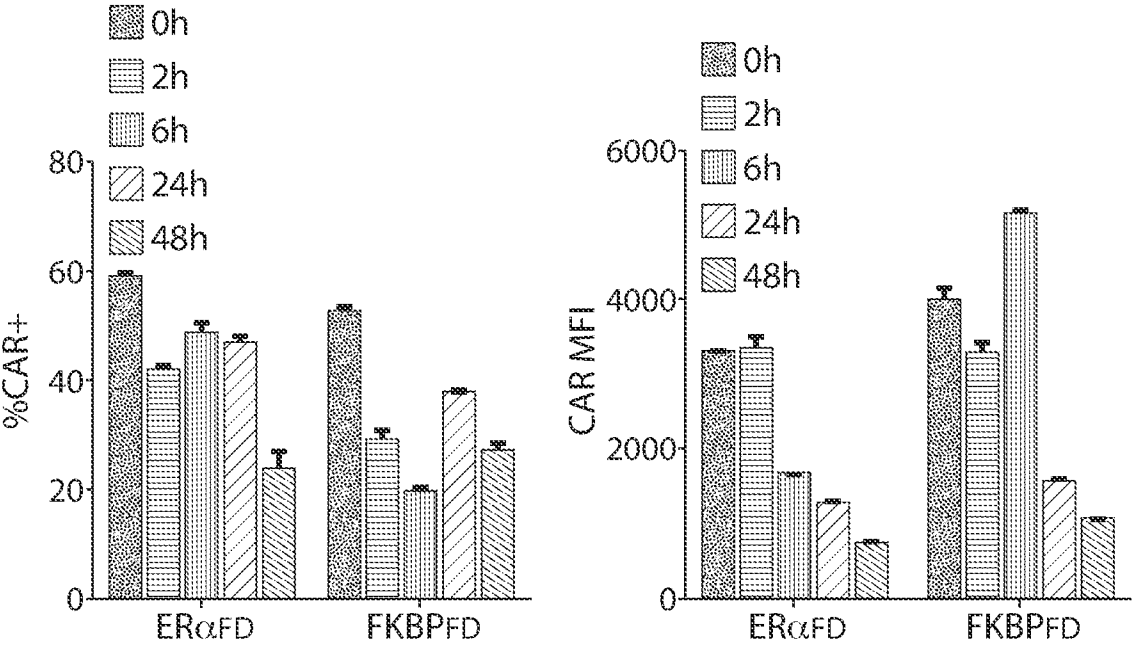


FIG. 5

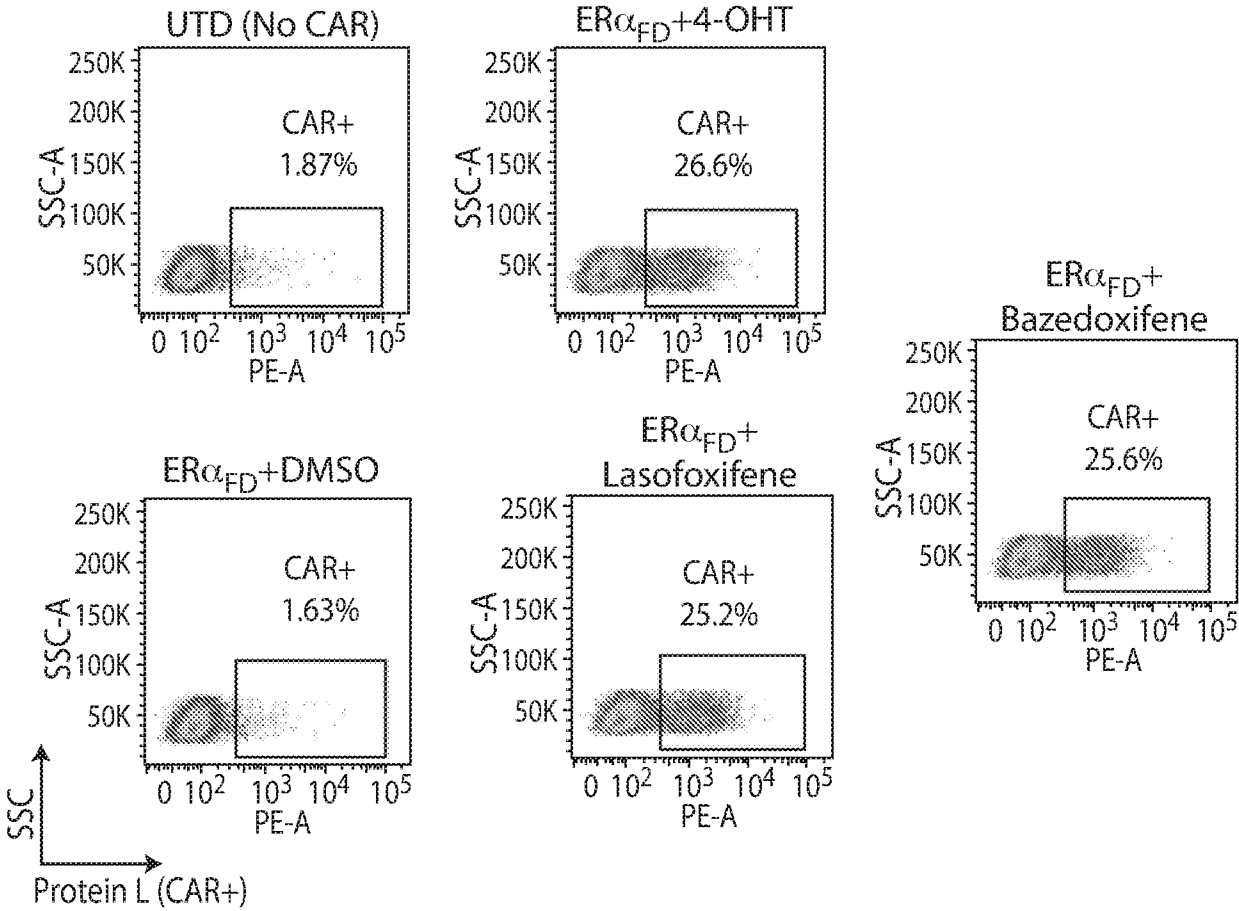


FIG. 6

7/48

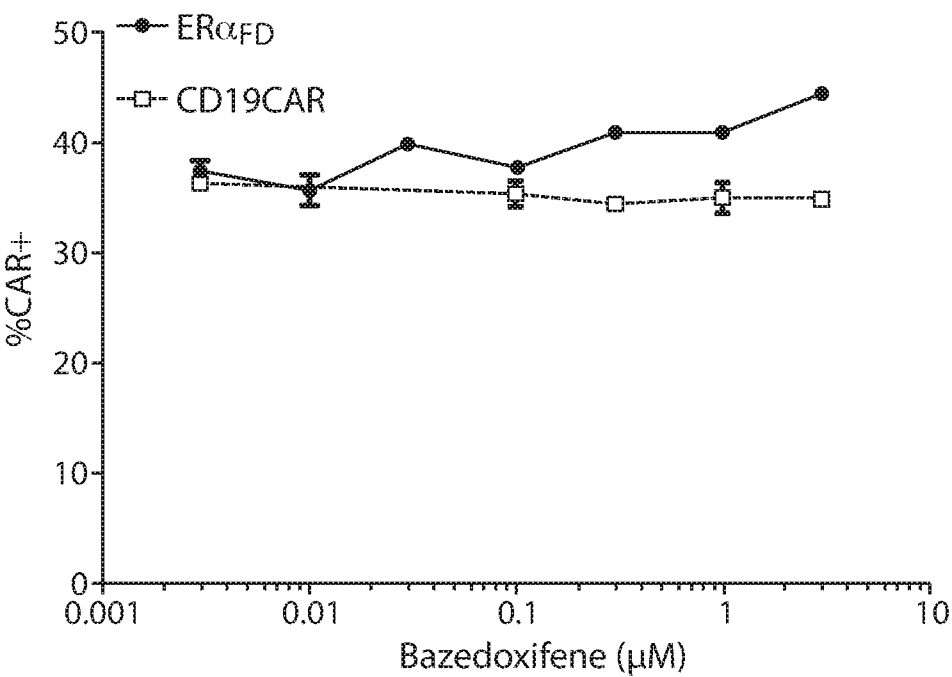


FIG. 7

8/48

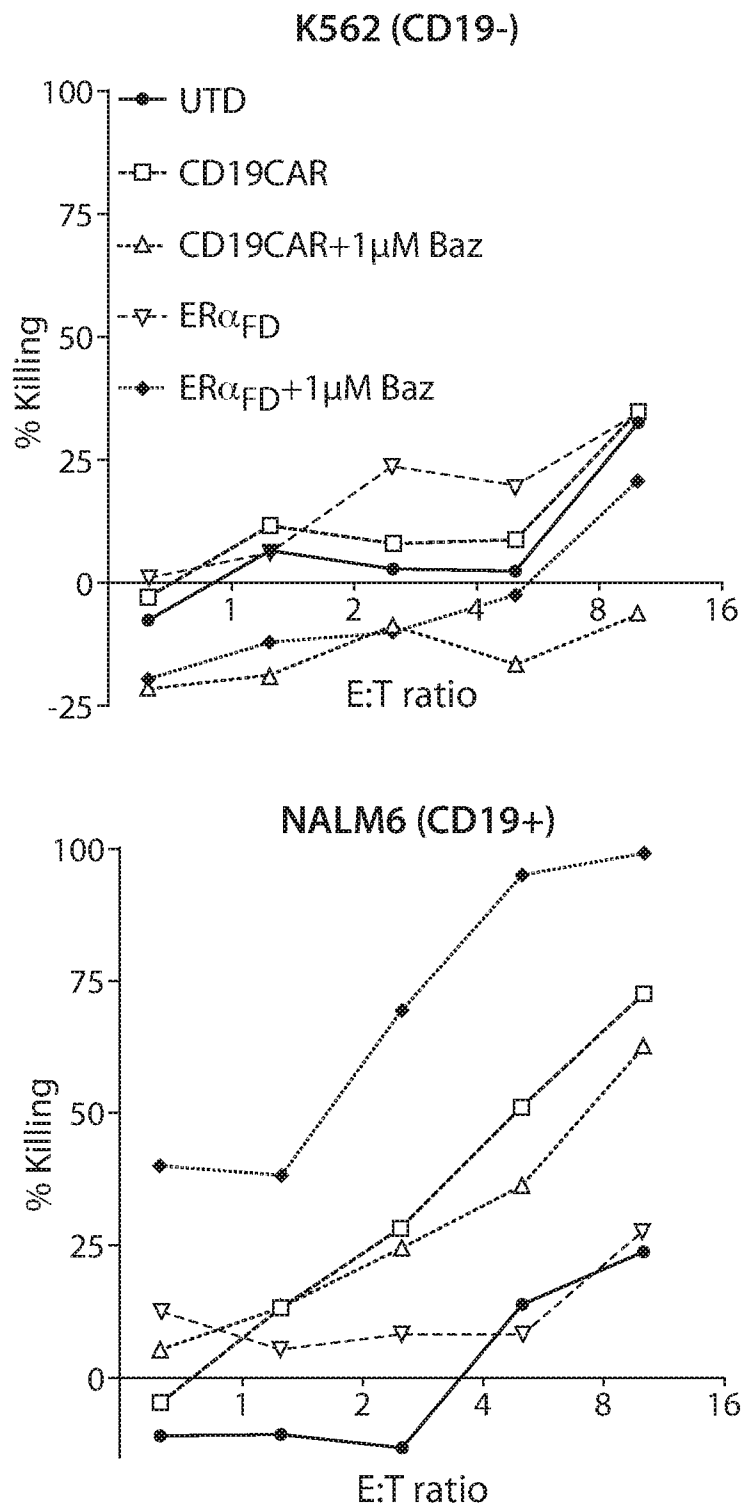


FIG. 8

9/48

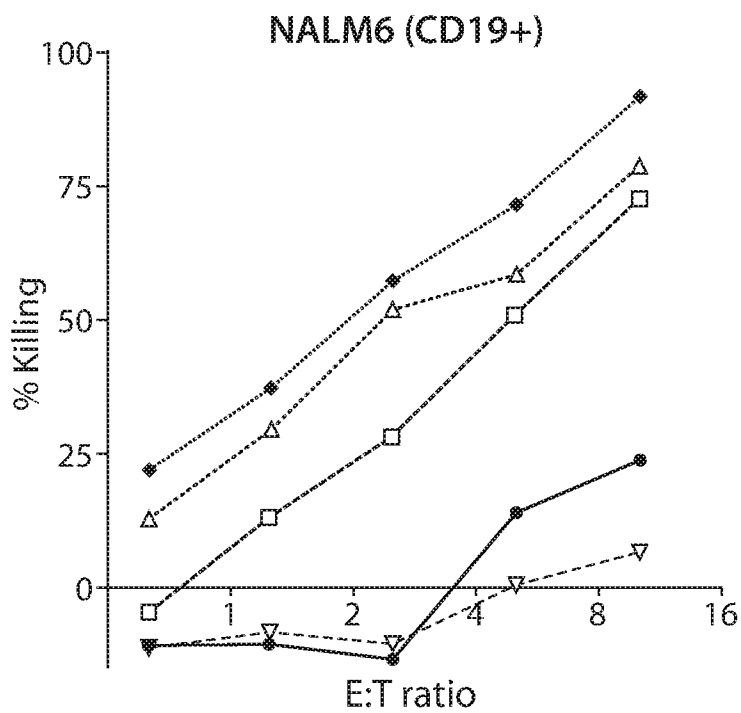
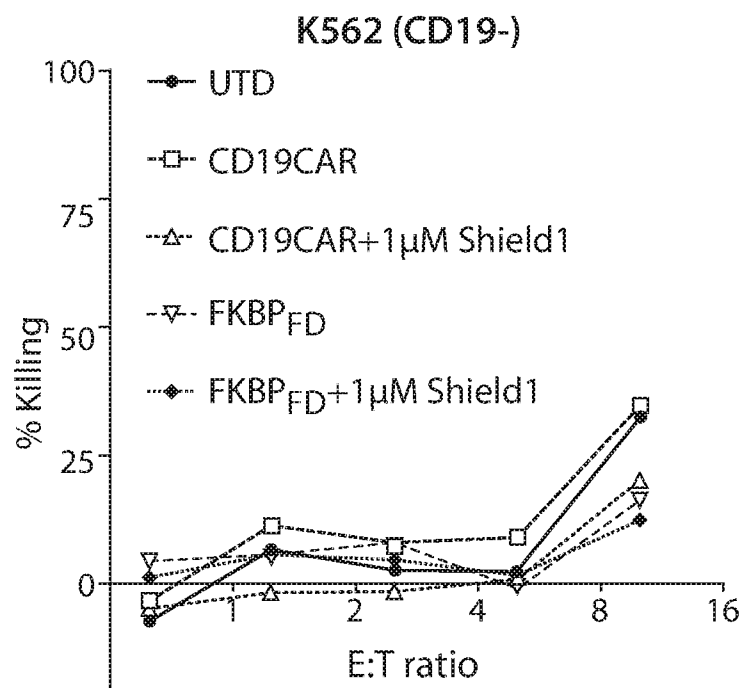


FIG. 9

10/48

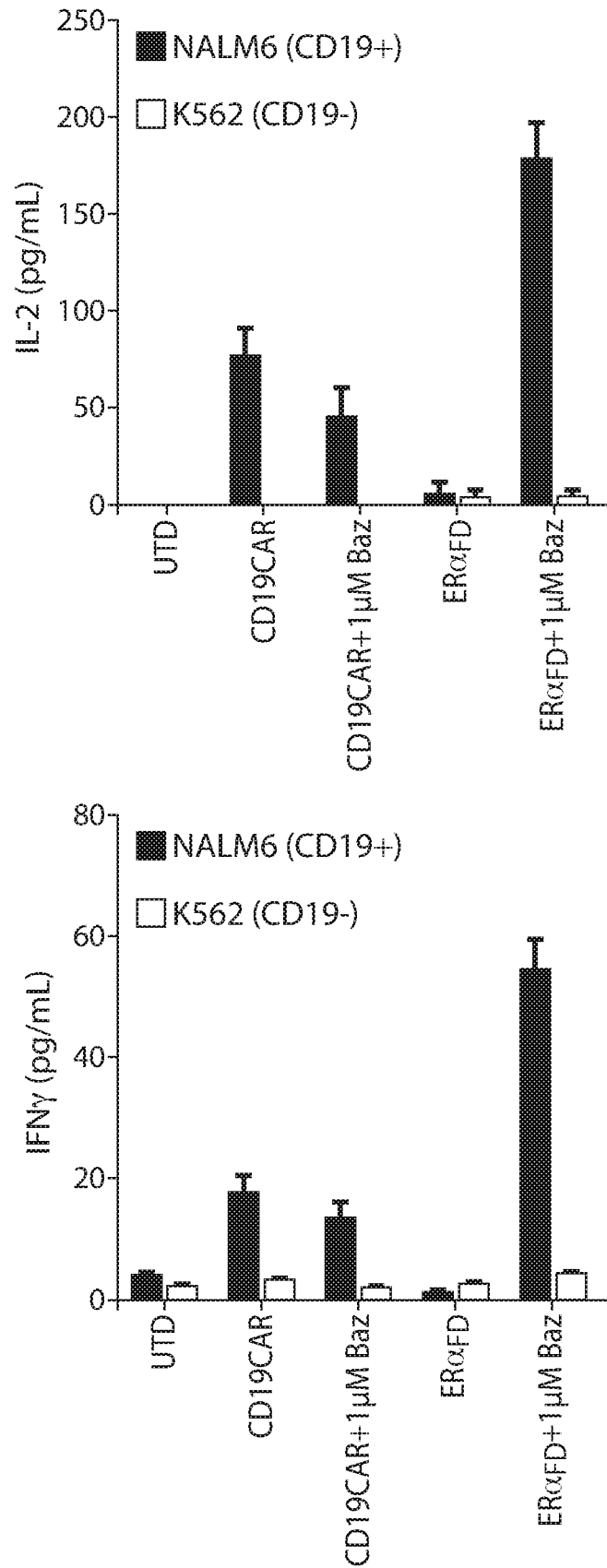


FIG. 10

11/48

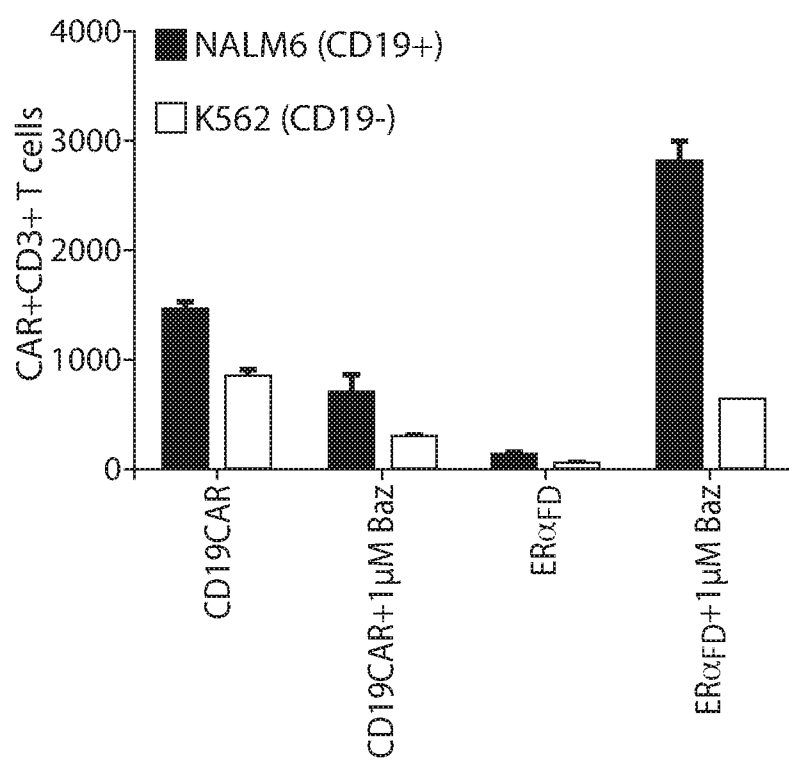


FIG. 11

12/48

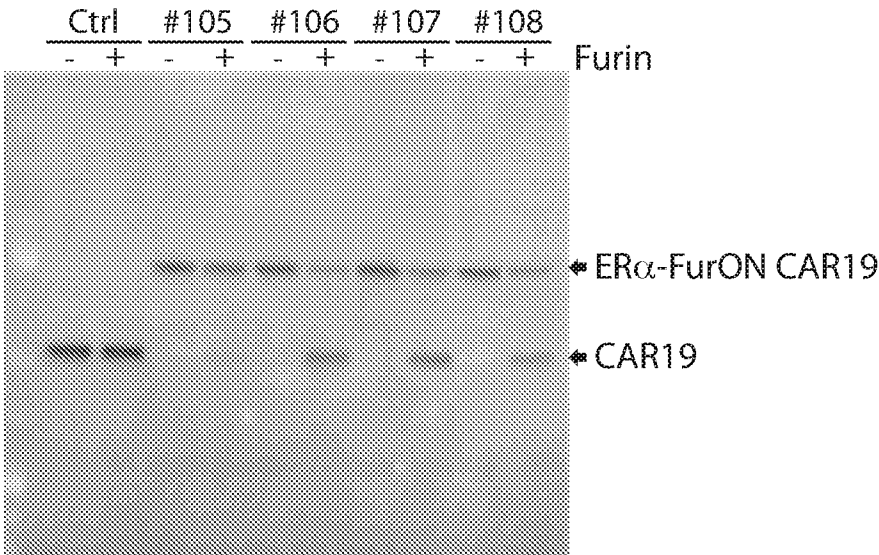


FIG. 12A

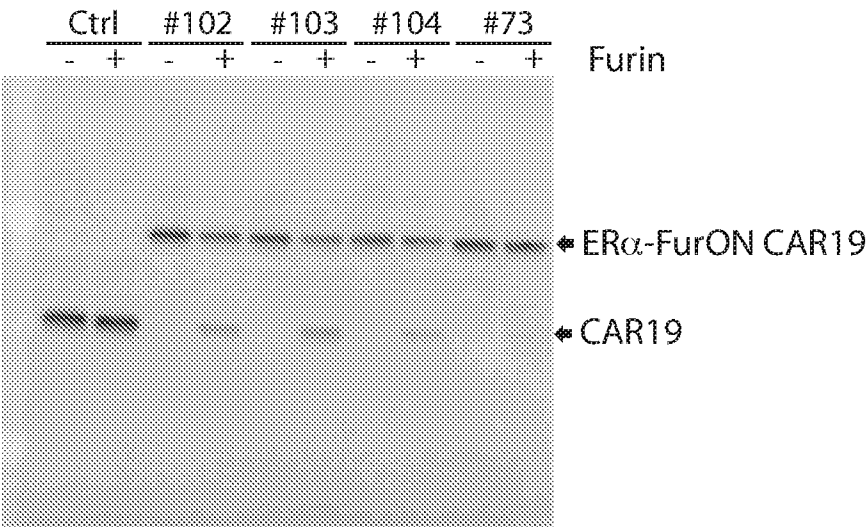


FIG. 12B

13/48

Construct	Fold expansion	Viability (%)	Size (uM)	Size (pL)	CAR+ (%)	CAR+ (Geo. Mean)
UTD	119	92.1	9.63	0.468	-	-
CART19	143	92.3	9.52	0.451	44	6708
CART19+ BZA	162	92	9.56	0.458	45	6514
Furon106	100	92.4	9.61	0.465	-	-
Furon106+ BZA	124	93.8	9.61	0.465	52	3414

FIG. 13

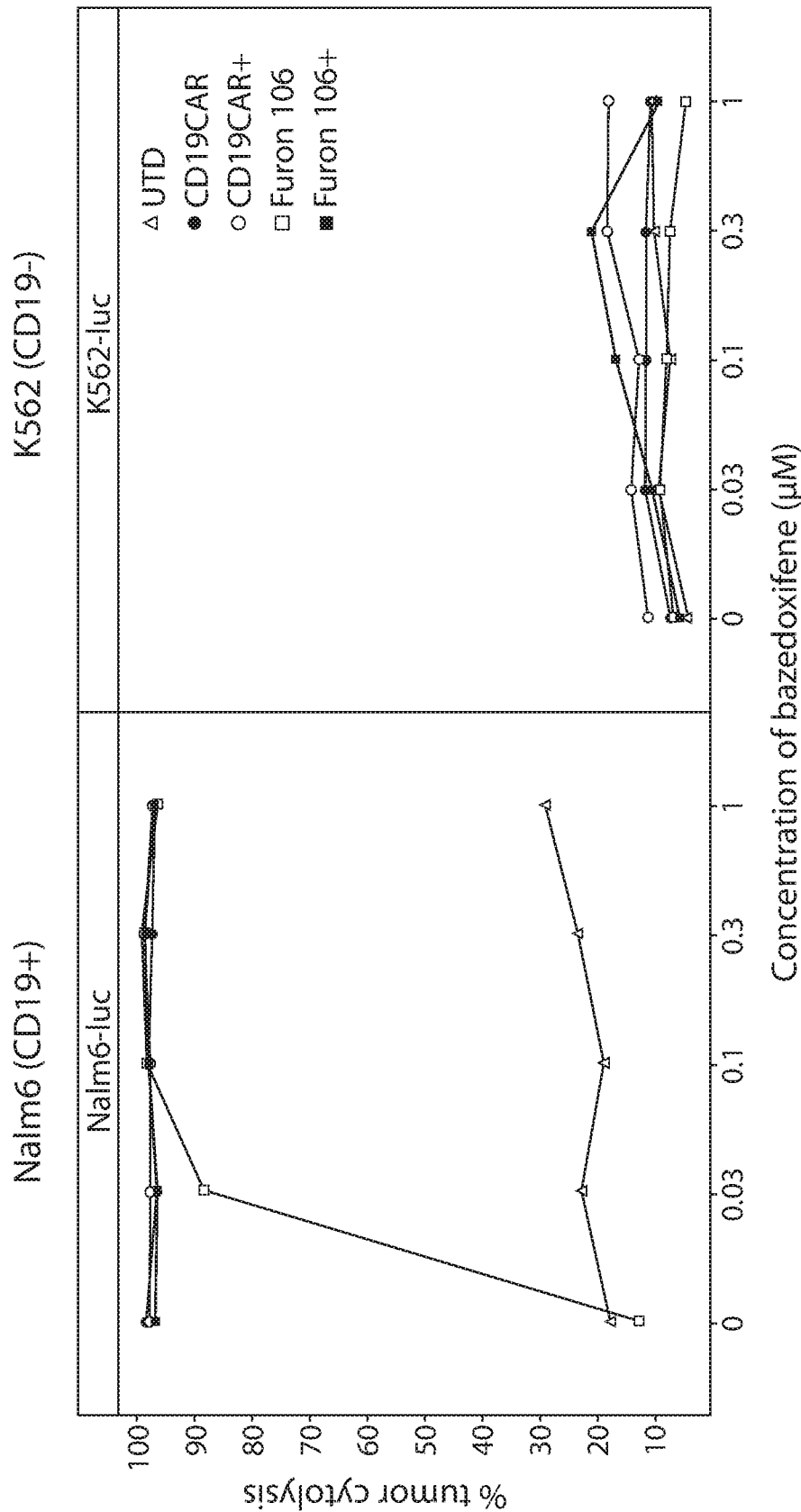


FIG. 14

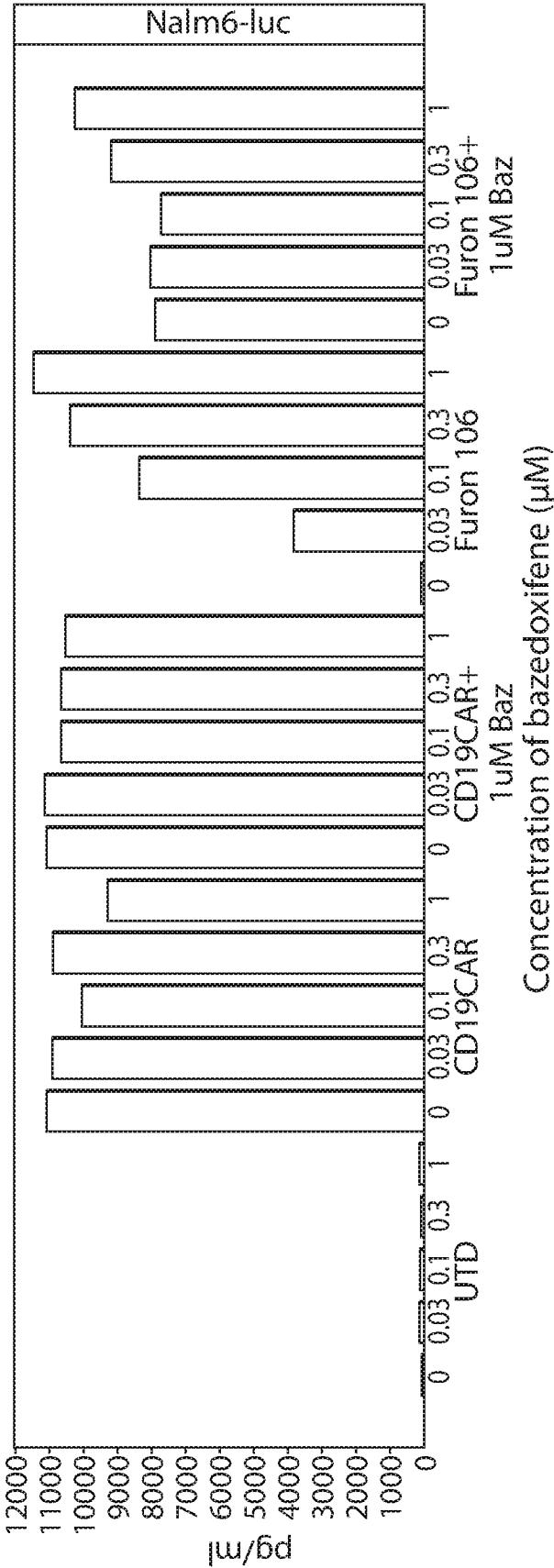


FIG. 15

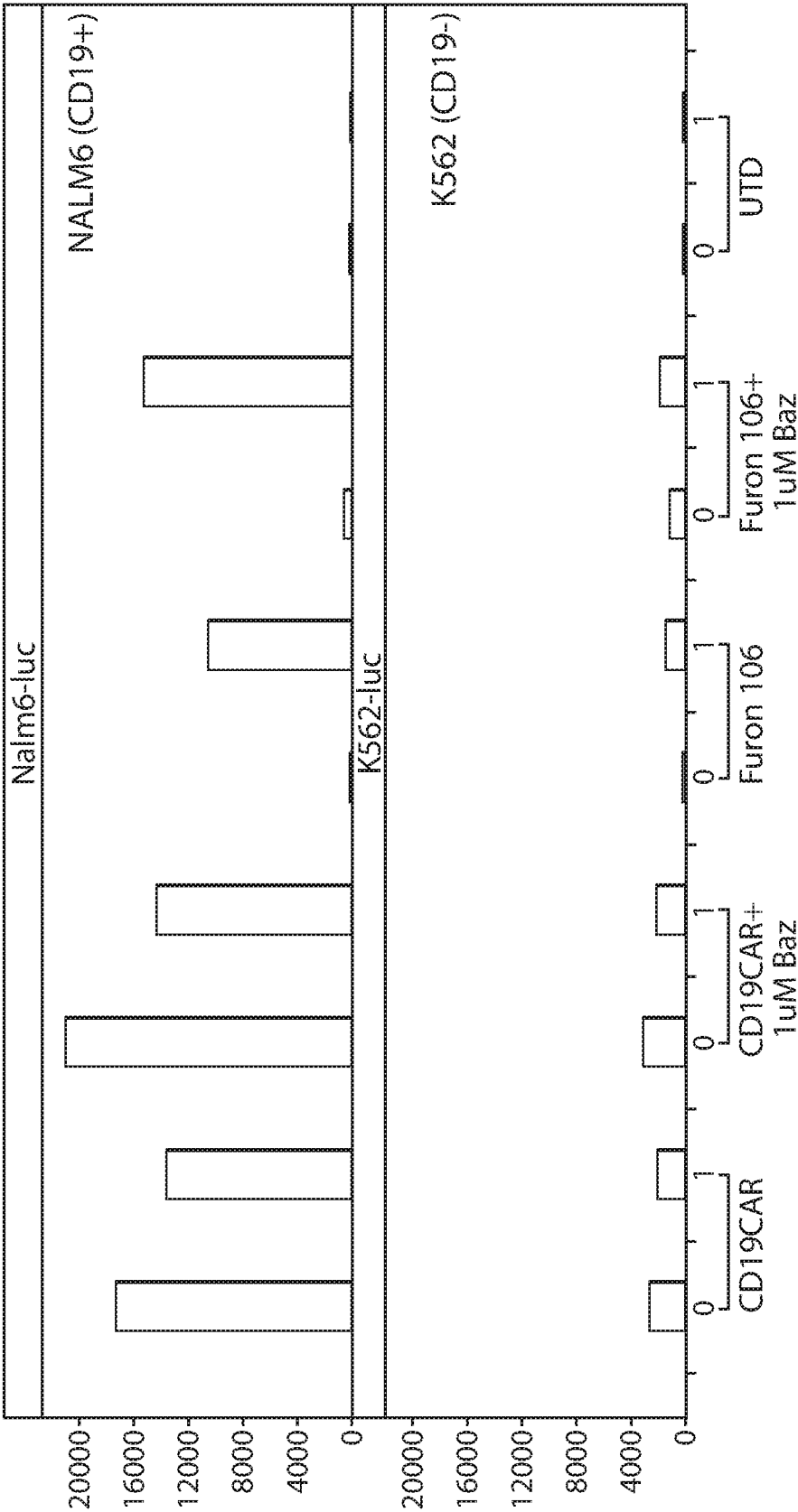


FIG. 16

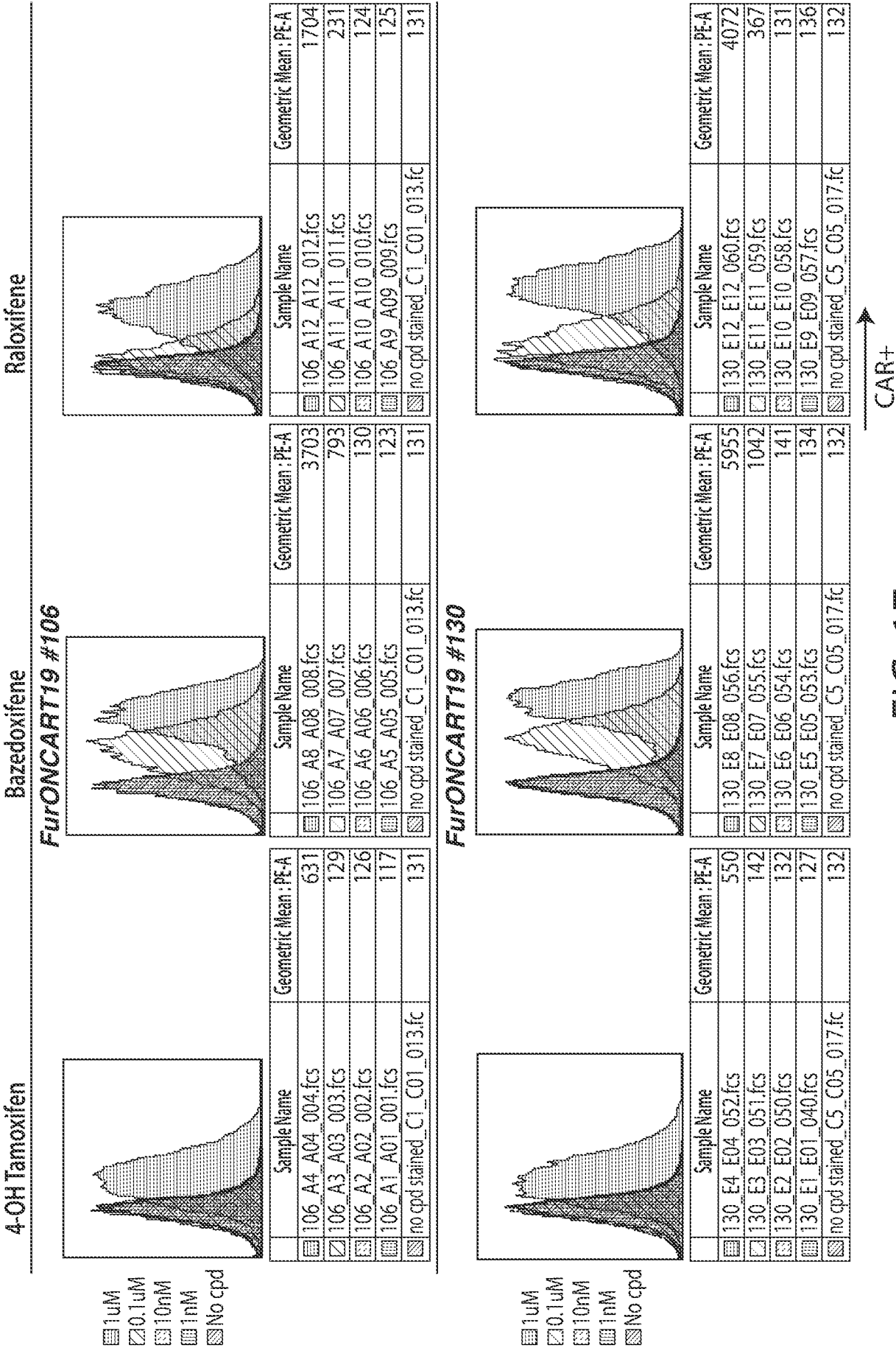


FIG. 17

18/48

	UTD		FurON 130		CART 19	
Treatment	%CAR	MFI	%CAR	MFI	%CAR	MFI
None	2.91	1952	2.85	1722	38.8	3305
BZA	6.86	2857	9.29	3482	36.5	7999
BZA + IL2	1.09	2600	38.8	6863	34.2	8142
+ IL2	0.53	962	0.72	988	37.9	2977

FIG. 18

19/48

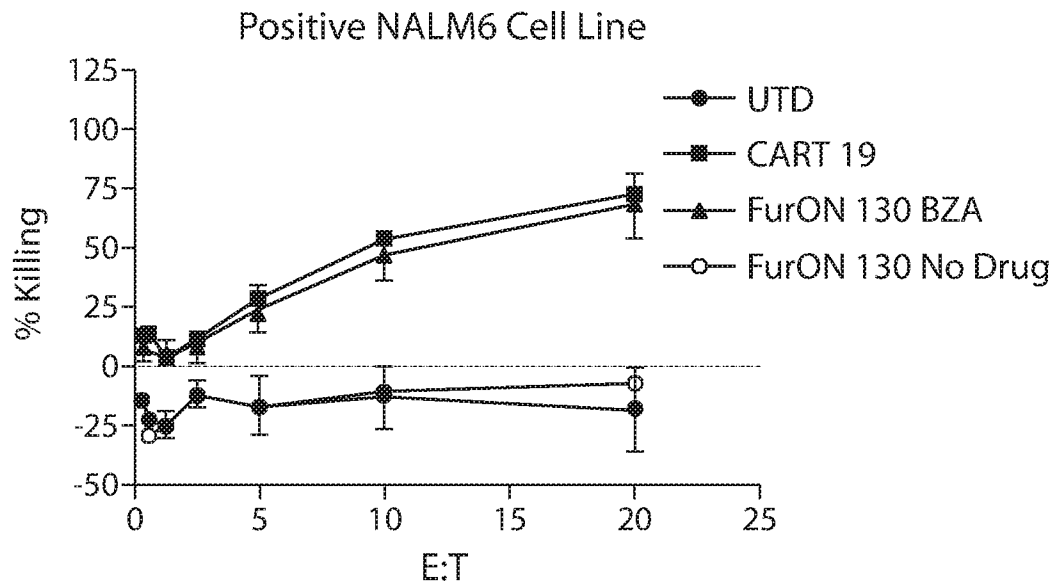


FIG. 19A

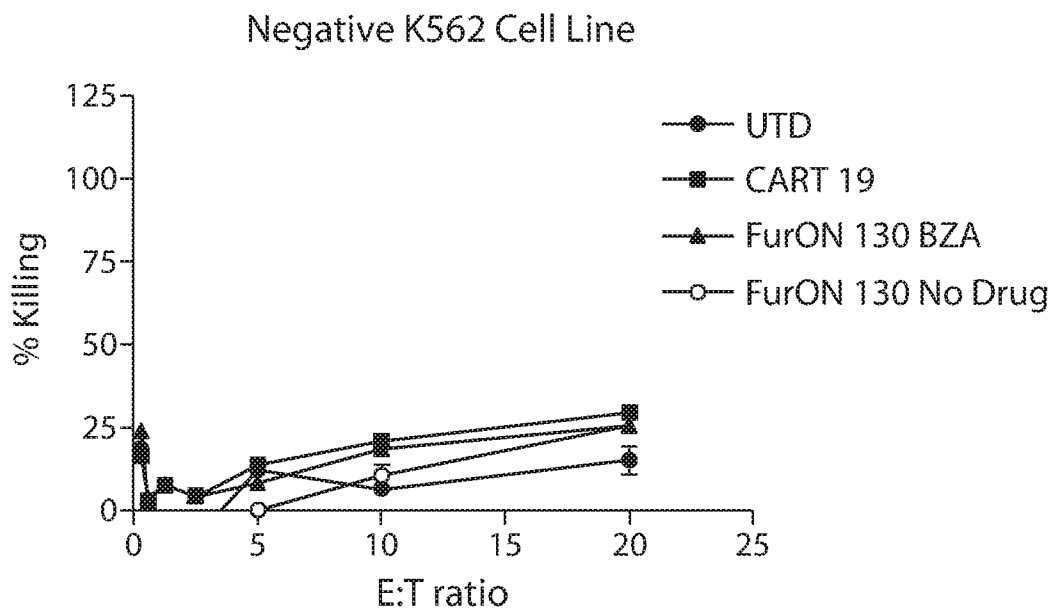
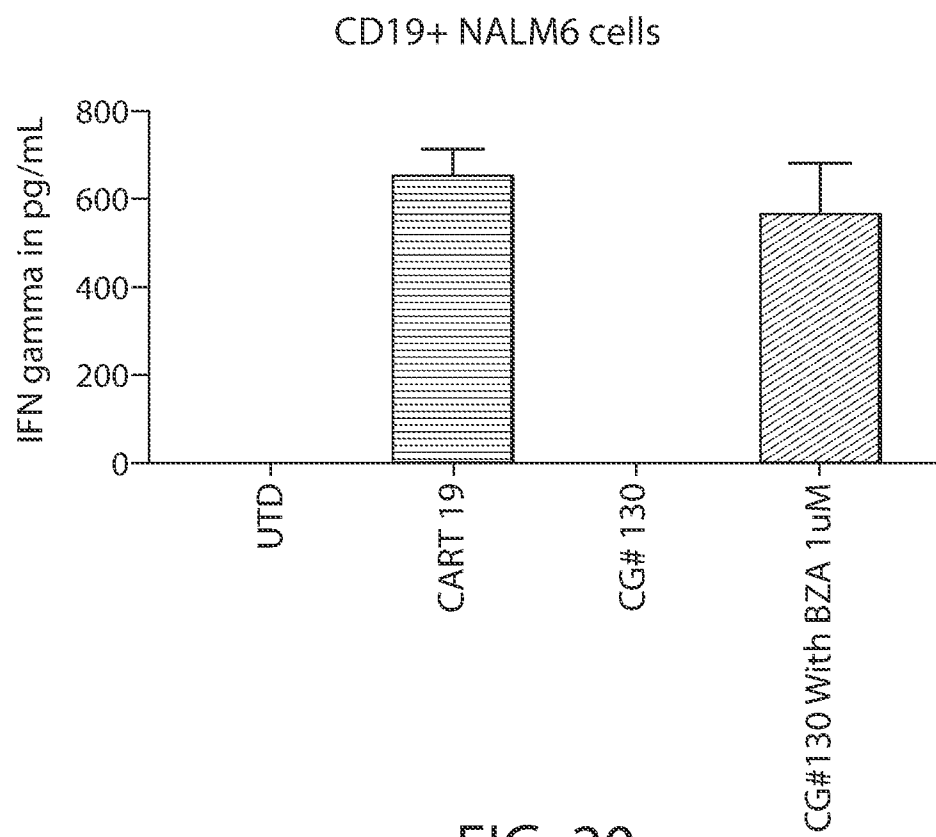


FIG. 19B

20/48



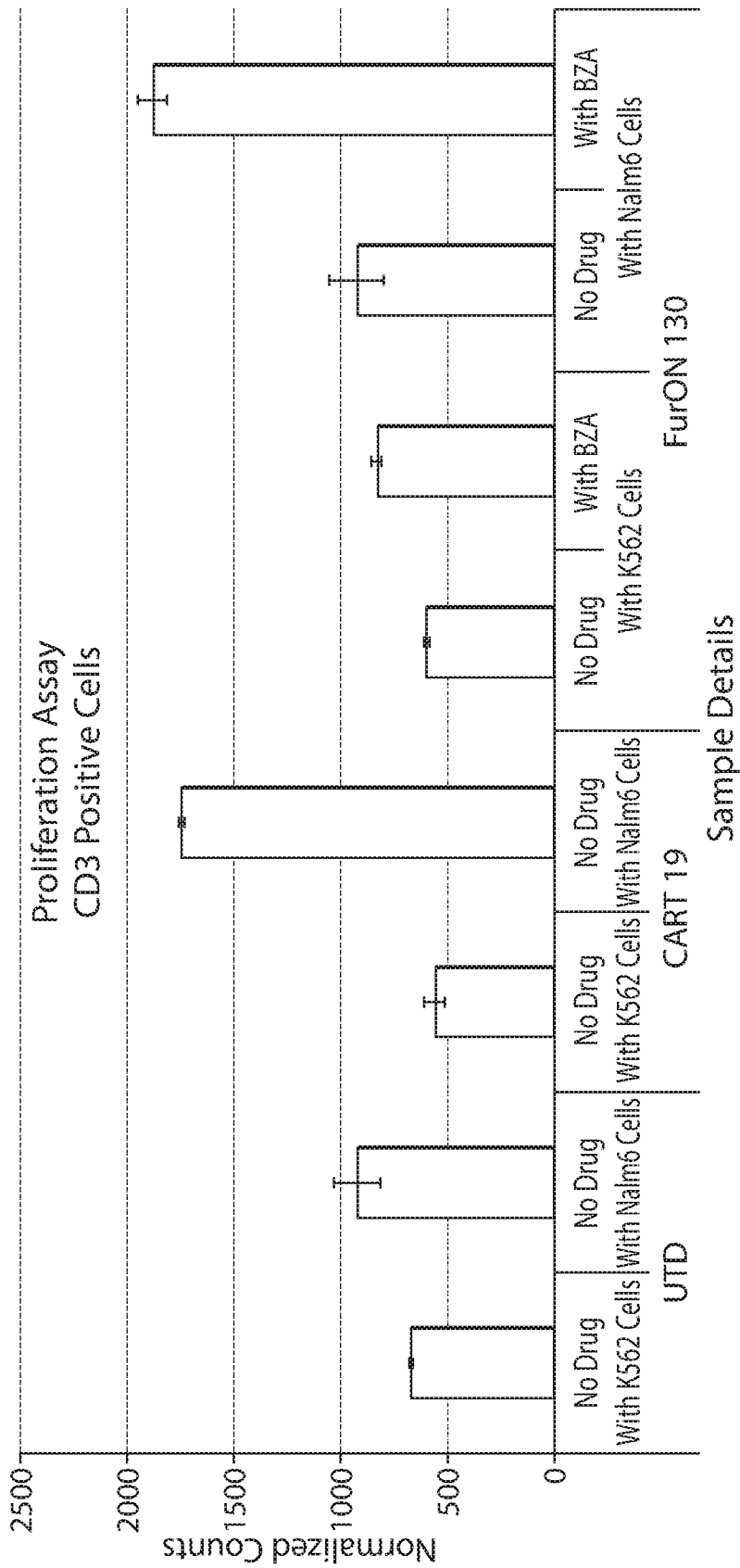


FIG. 21

22/48

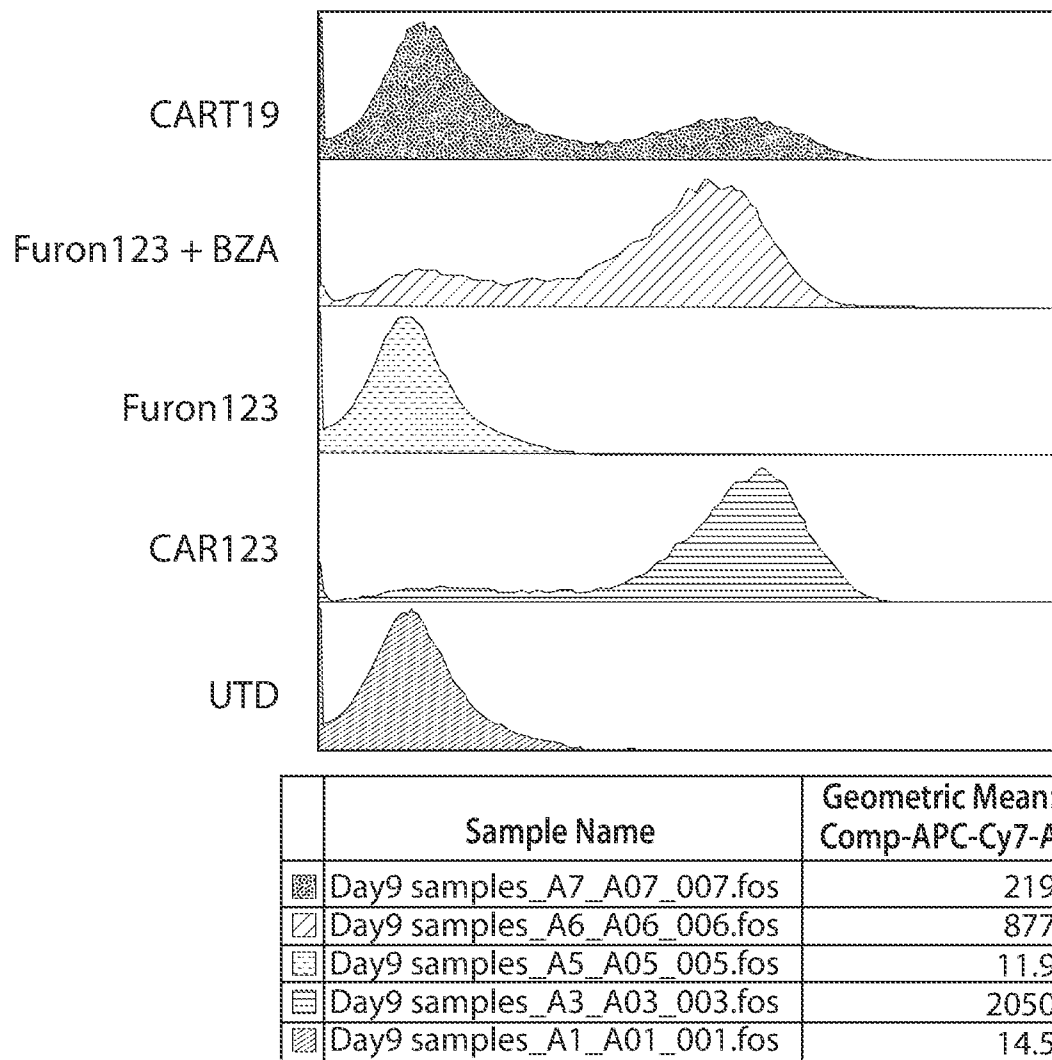


FIG. 22

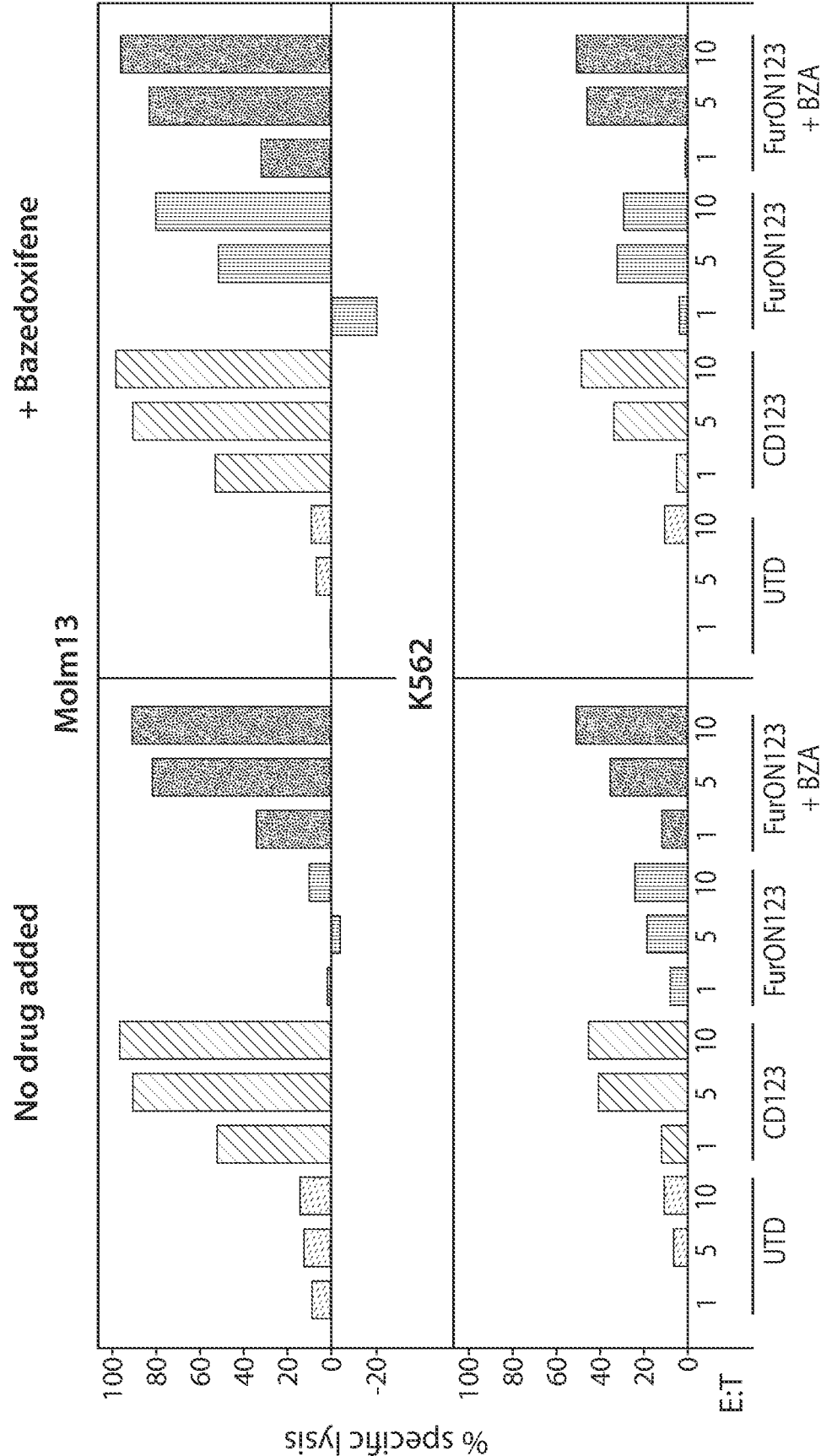


FIG. 23

24/48

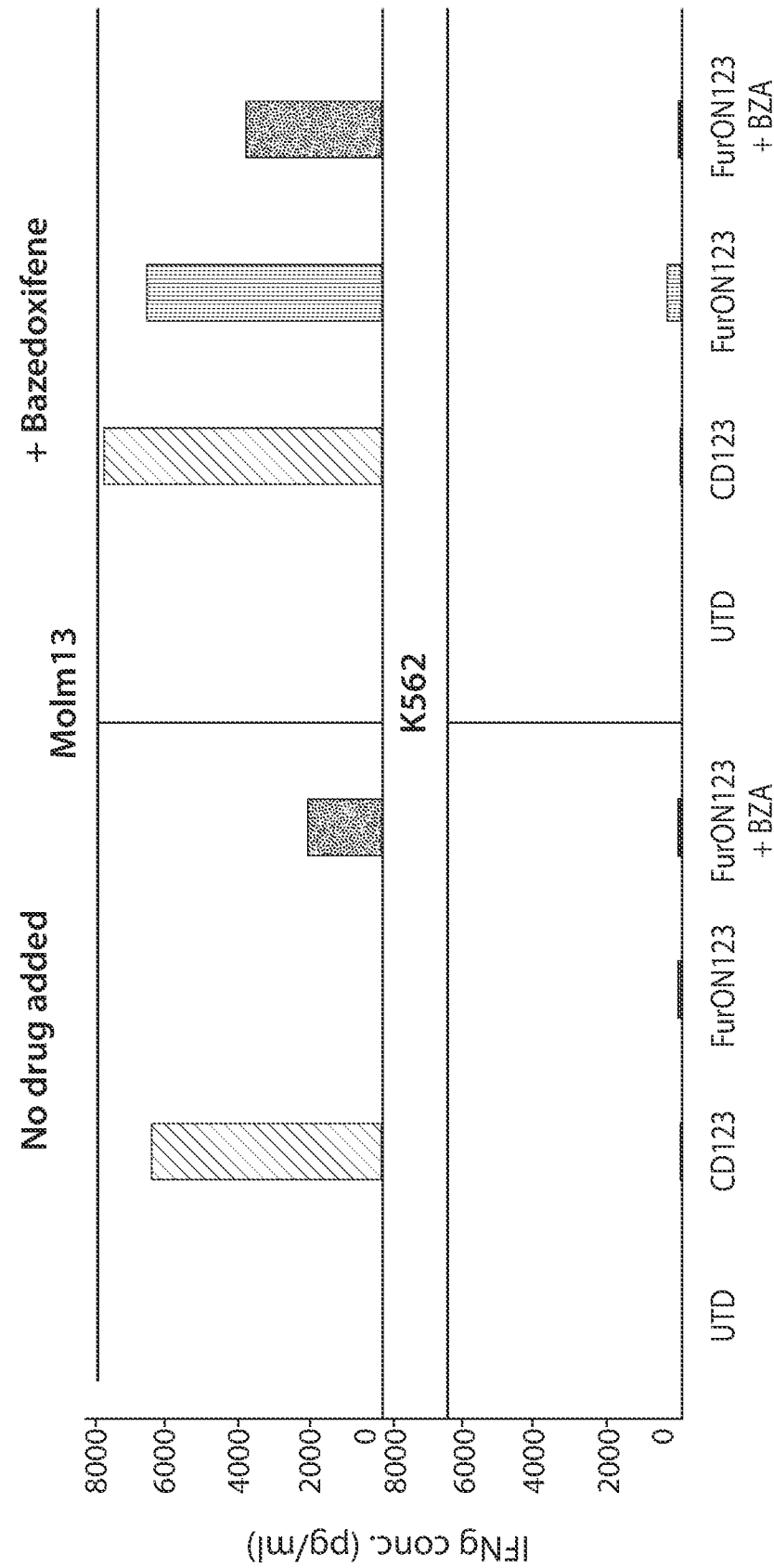


FIG. 24

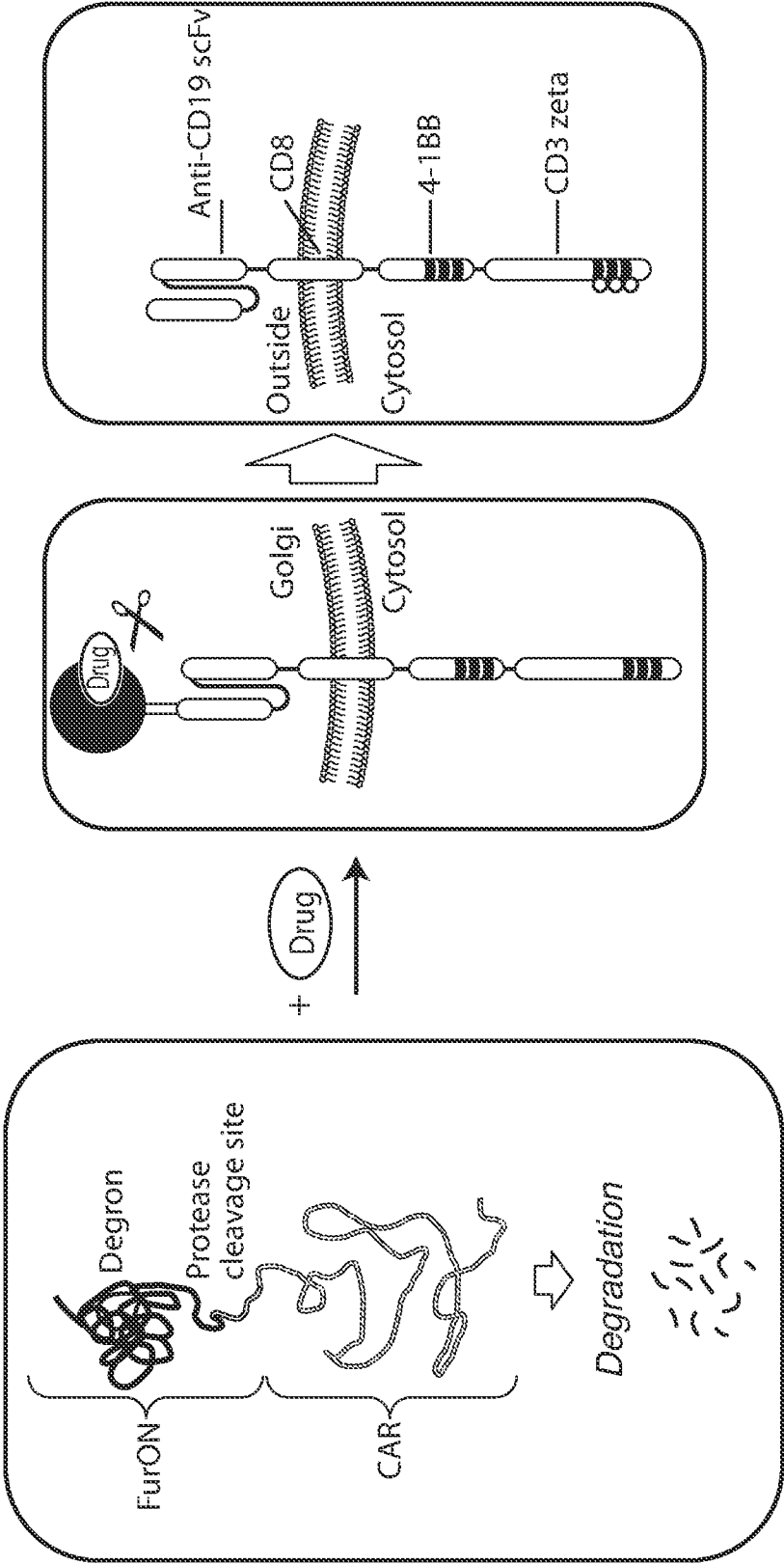


FIG. 25

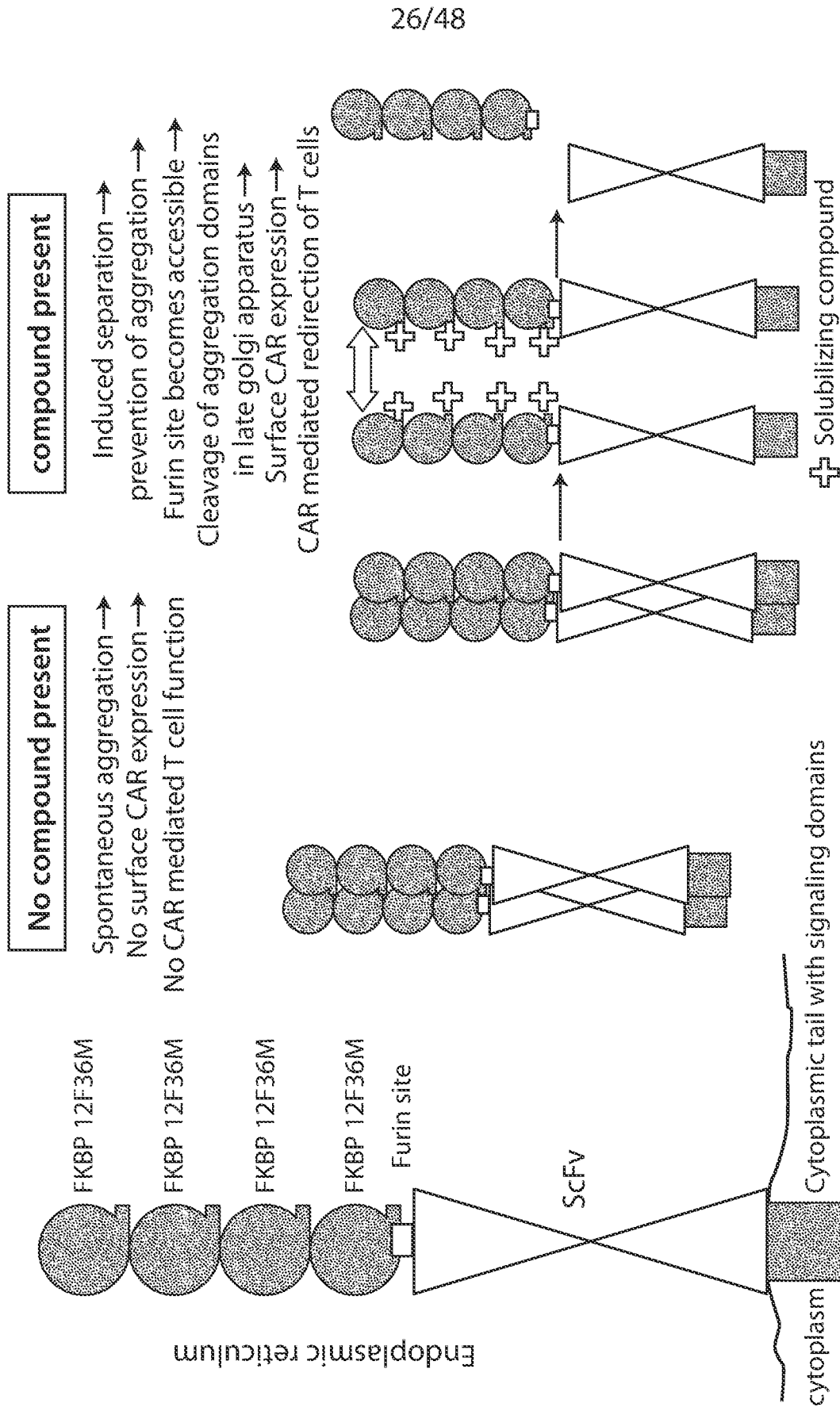


FIG. 26

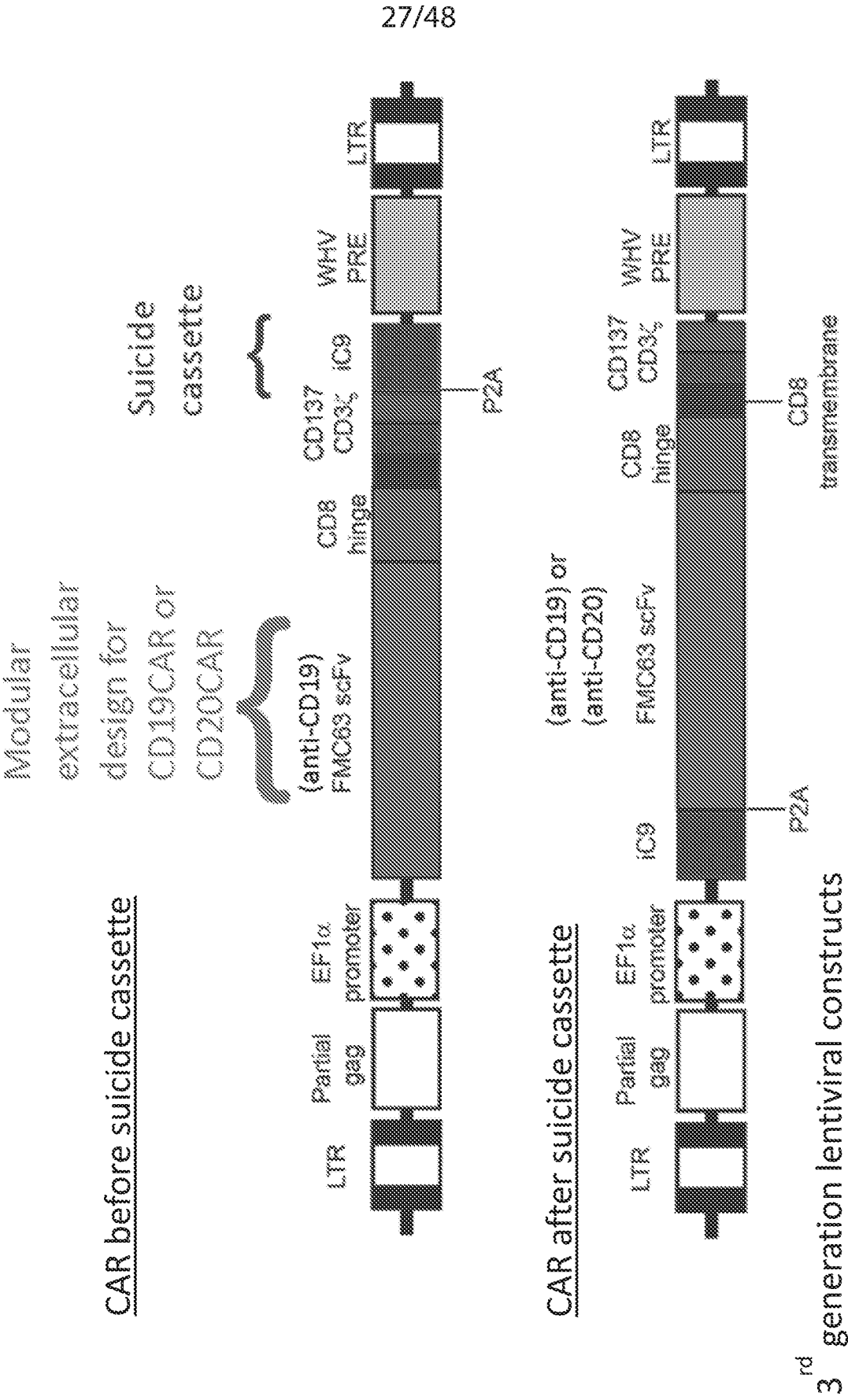


FIG. 27

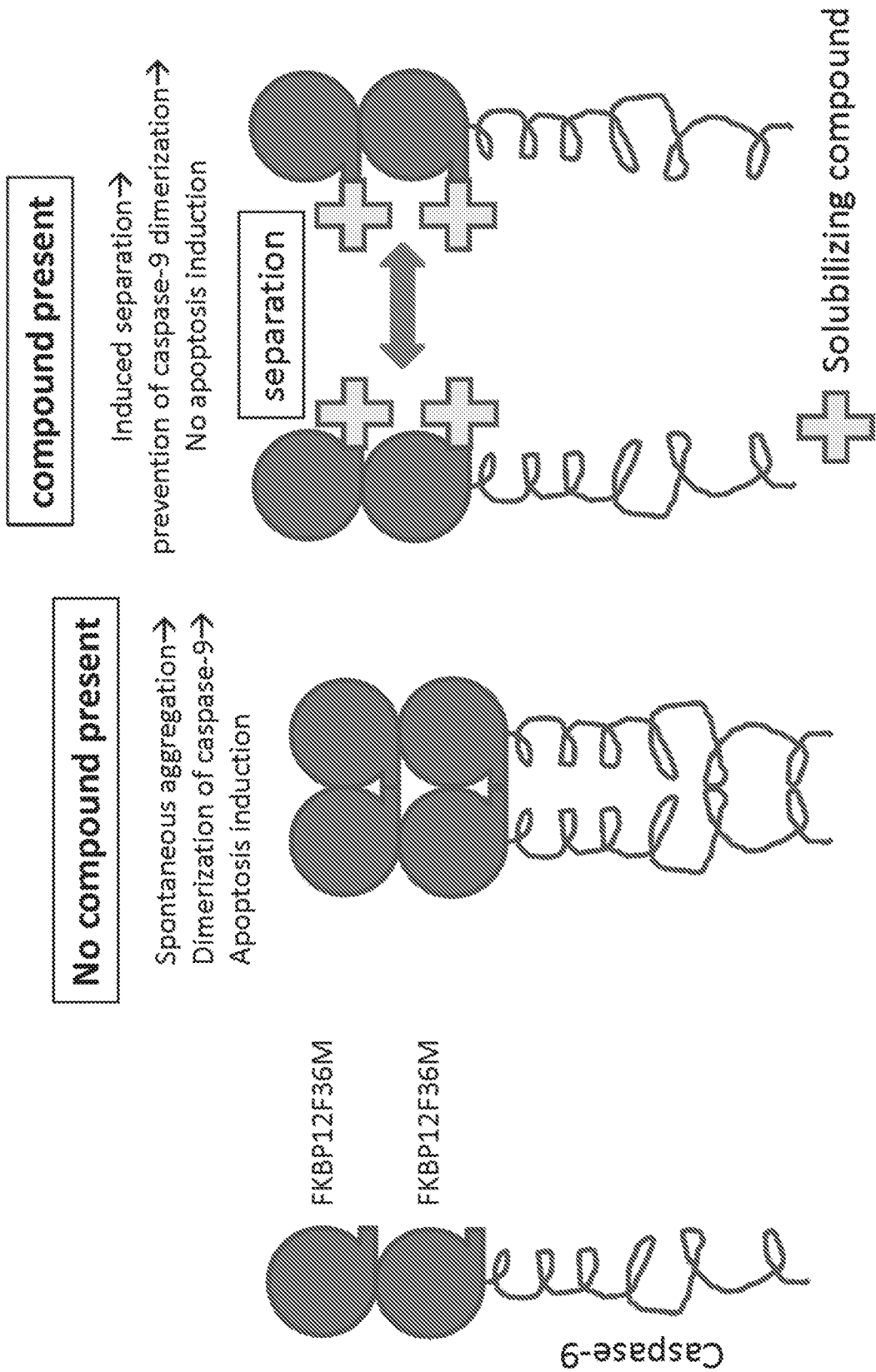


FIG. 28

Suicide cassette then anti-CD19:
5'*inducible* caspase→FMC63 3'

nontransduced

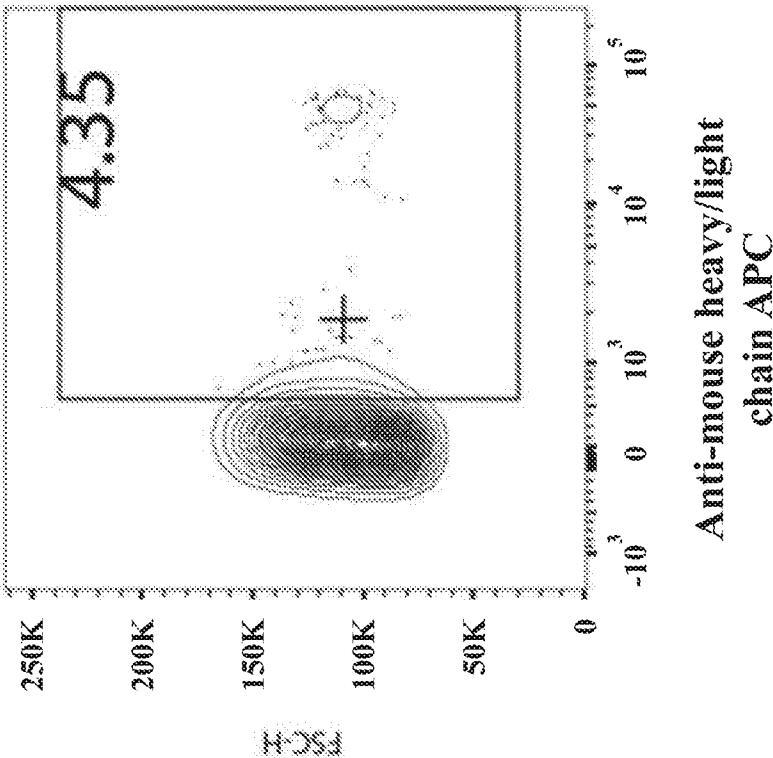


FIG. 29A

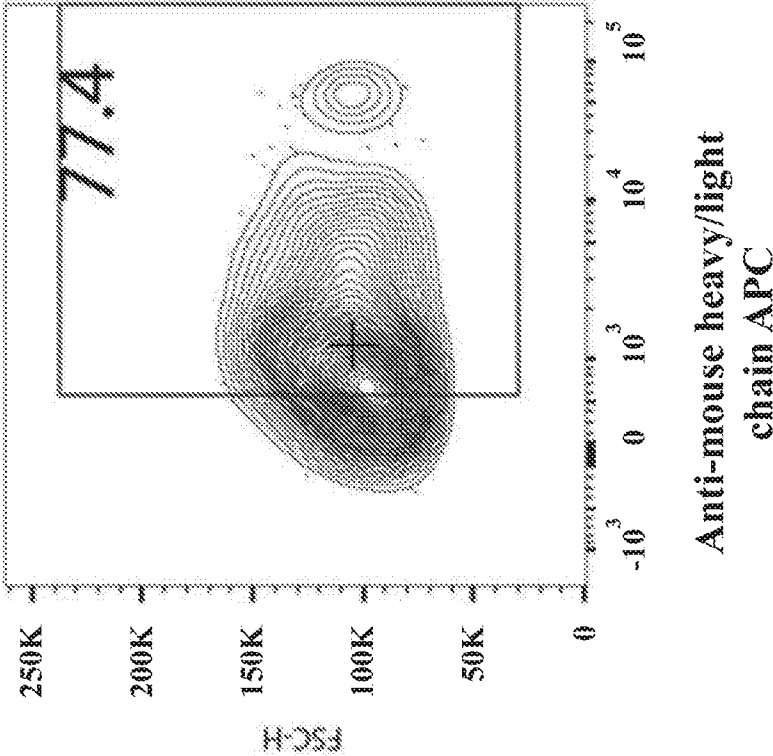


FIG. 29B

Anti-CD19 then reversible
suicide cassette:
5' FMC63→*reversible*
caspase 3'

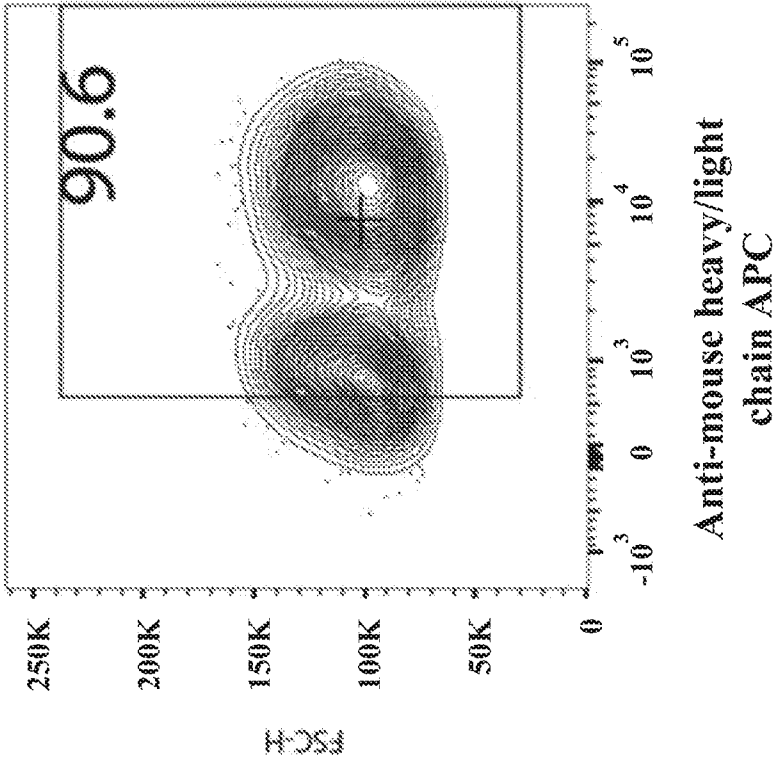


FIG. 29D

Anti-CD19 then suicide cassette:
5' FMC63→*inducible* caspase 3'

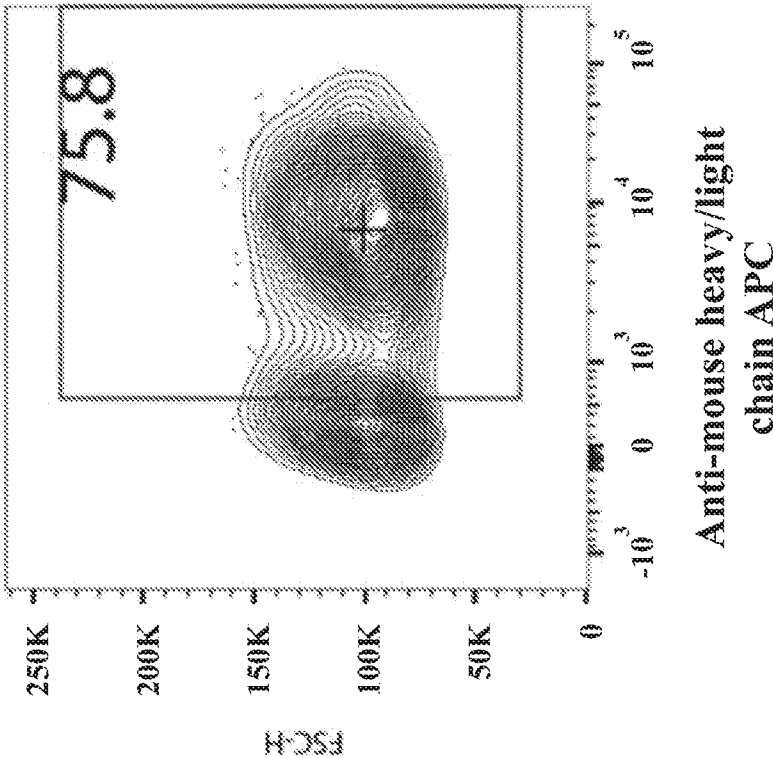
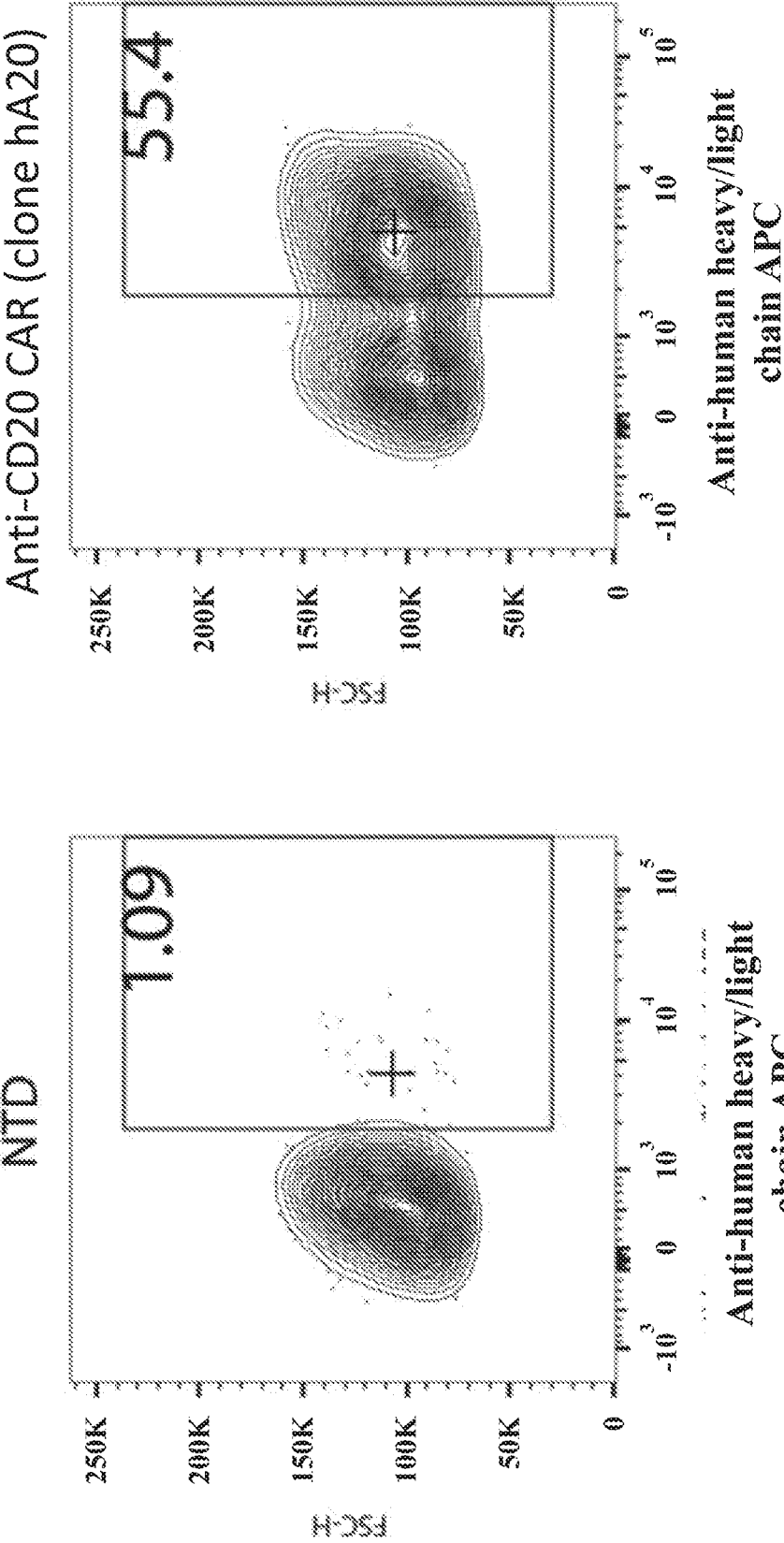


FIG. 29C



32/48

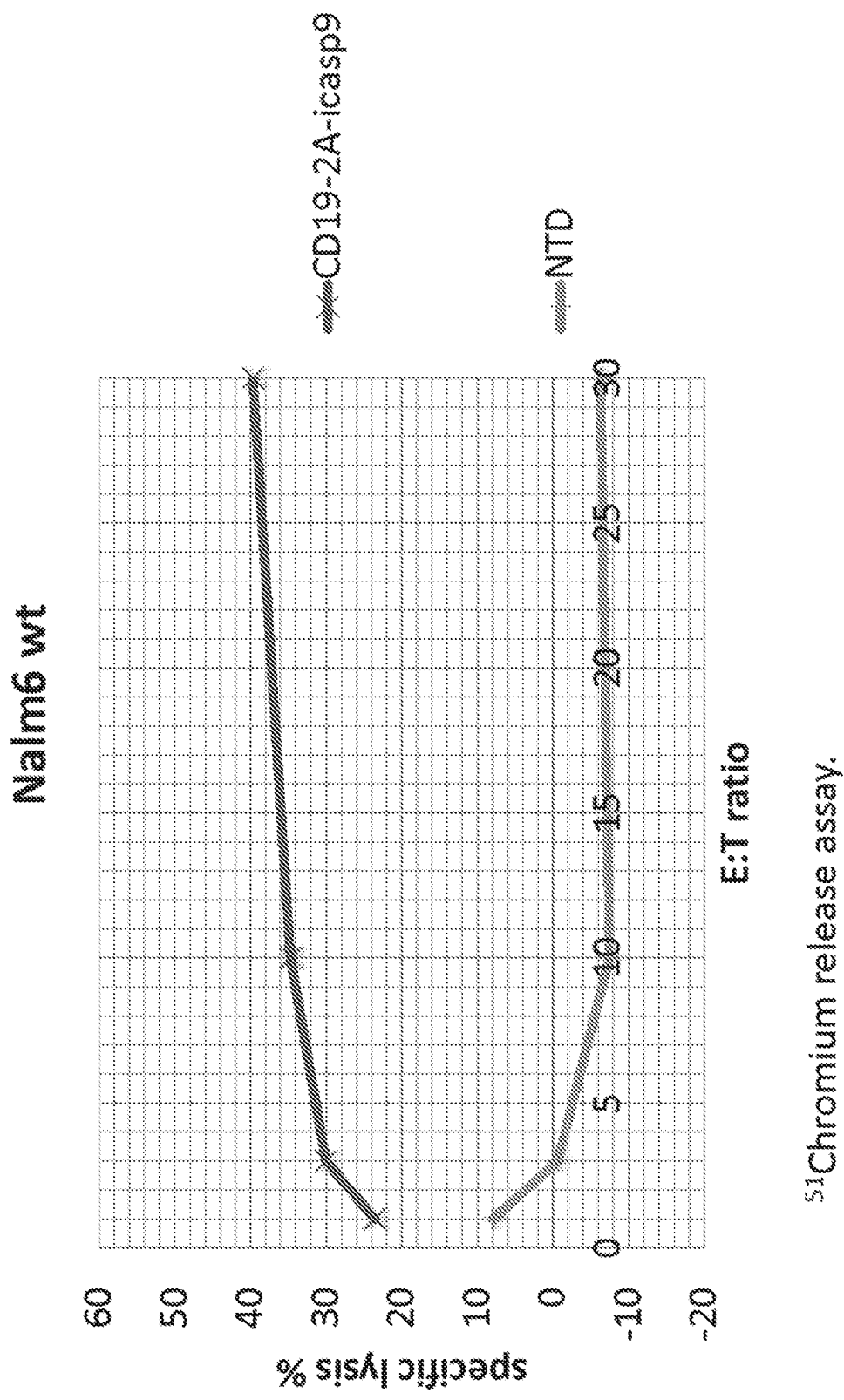


FIG. 30

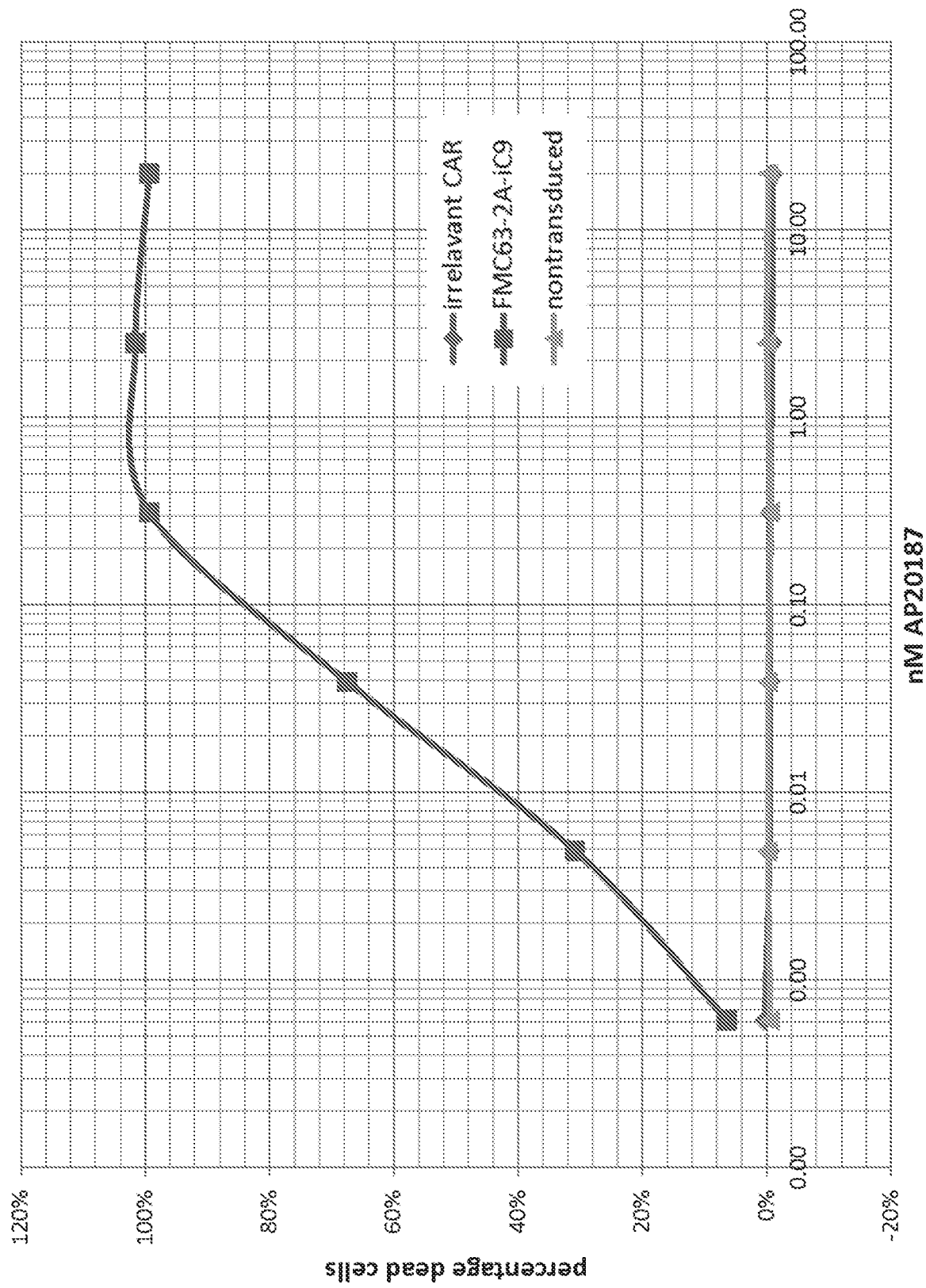


FIG. 31

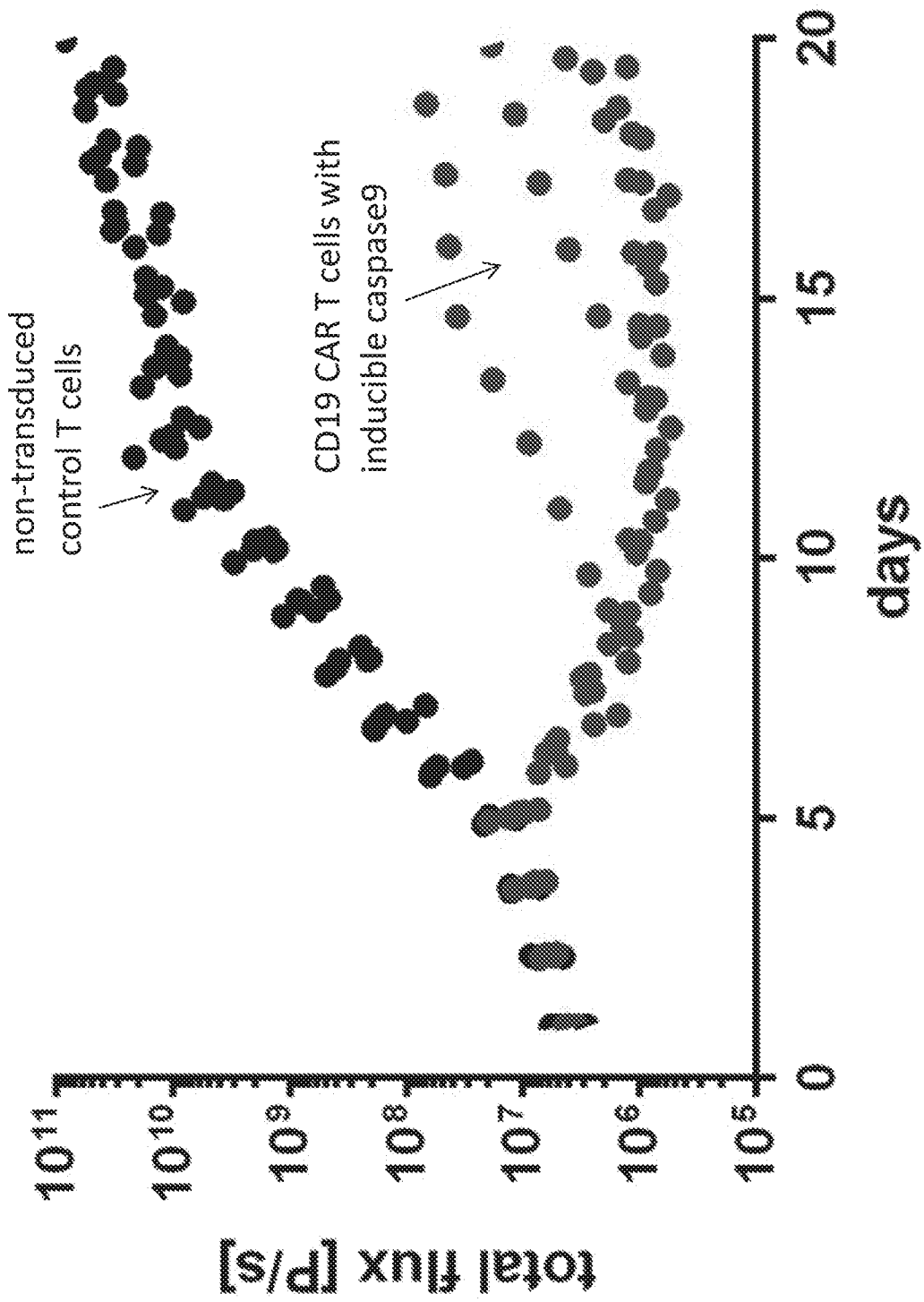


FIG. 32

35/48

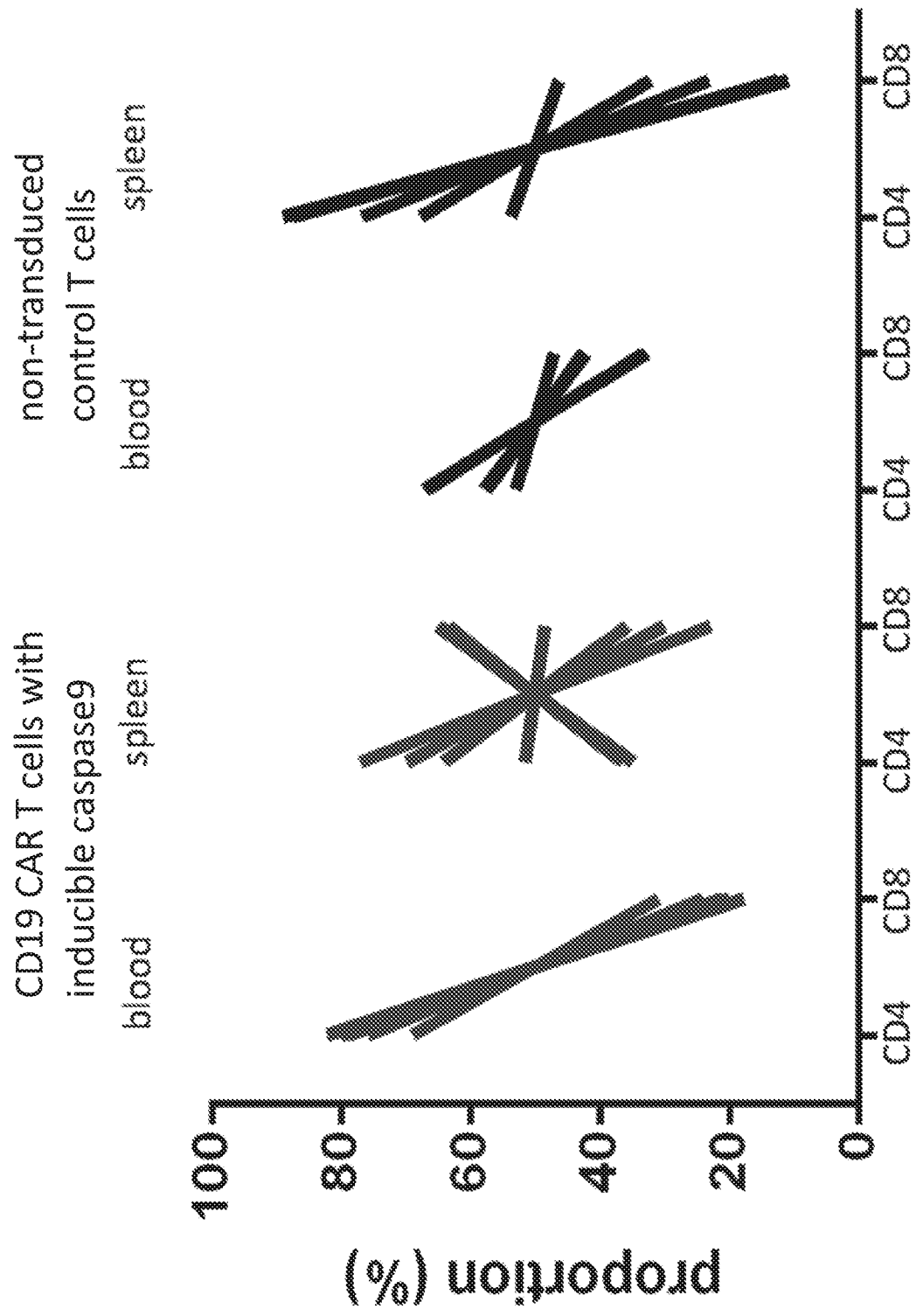


FIG. 33

36/48

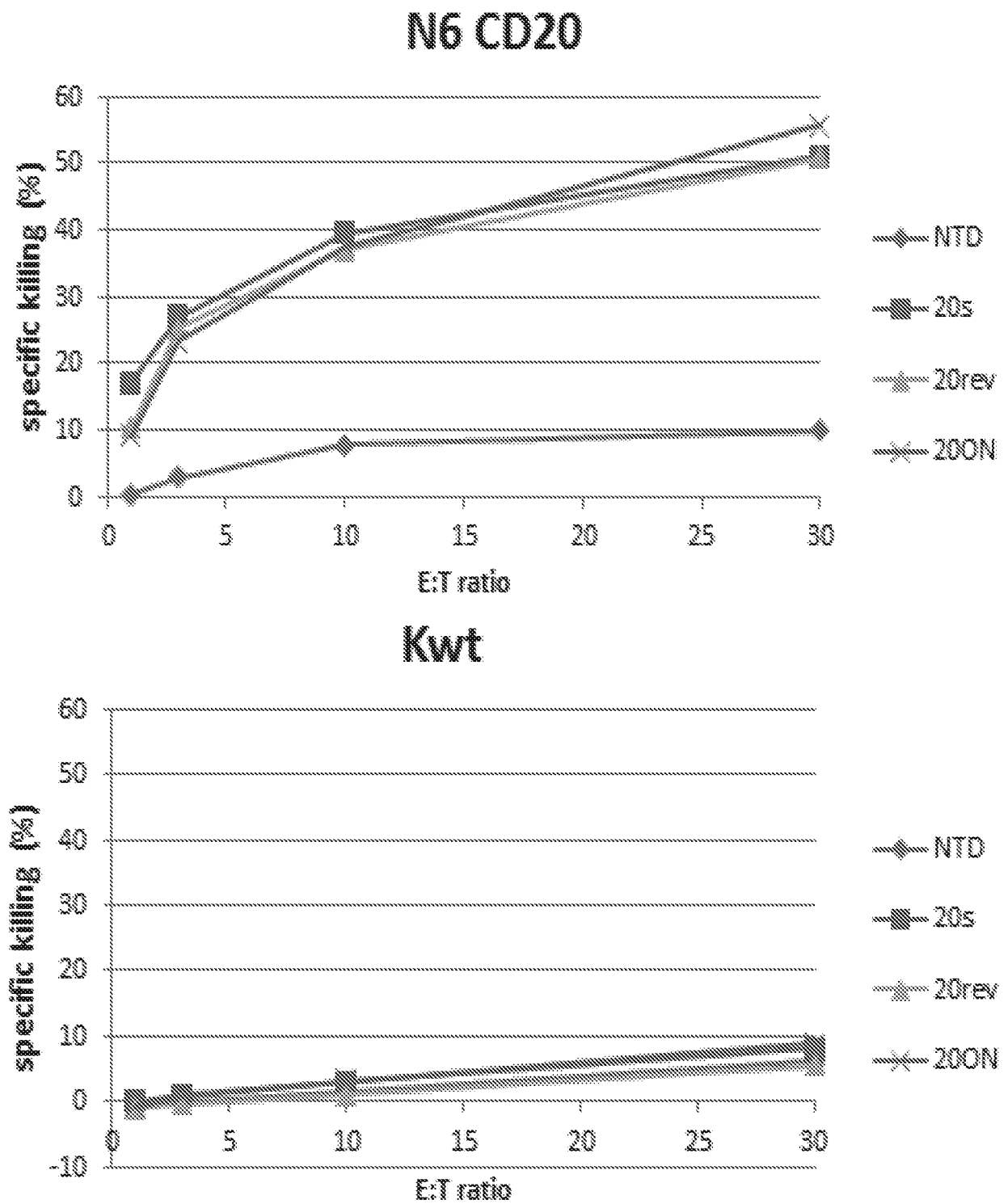


FIG. 34

37/48

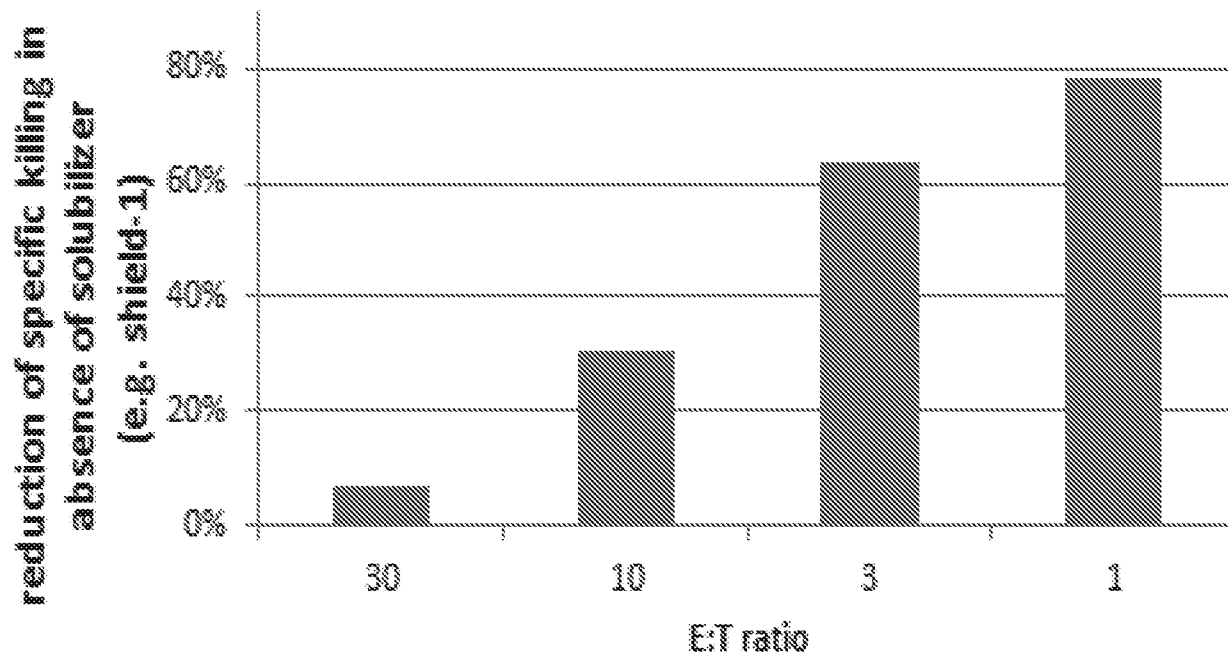
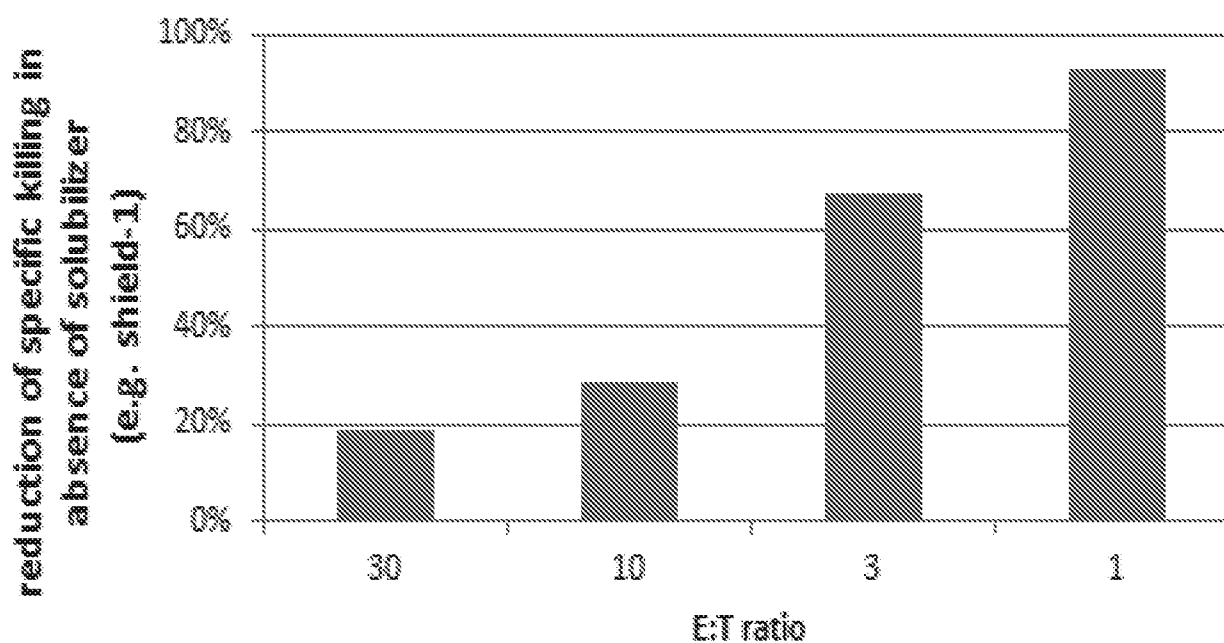
Jeko**Nalm6 CD20**

FIG. 35

38/48

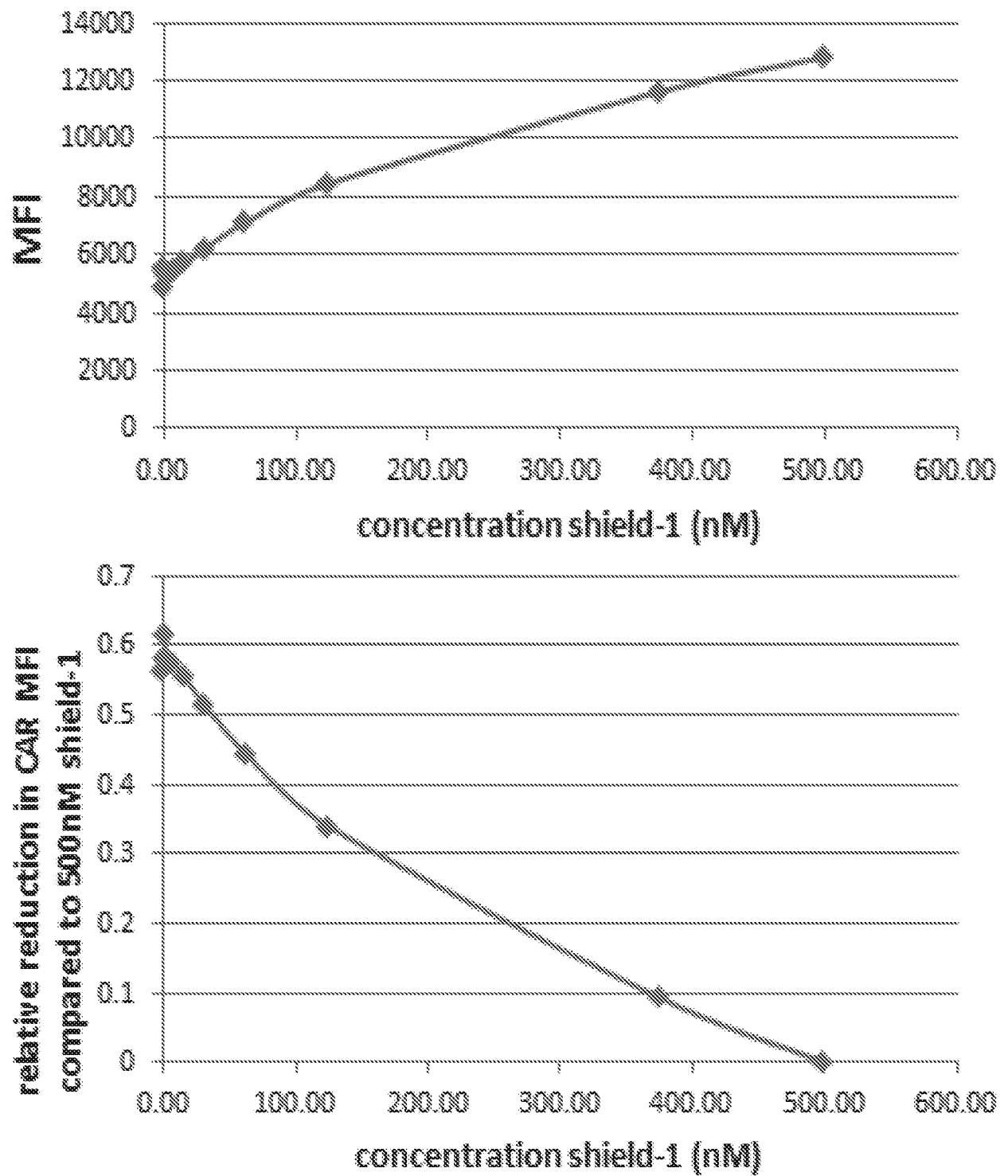
CAR+

FIG. 36

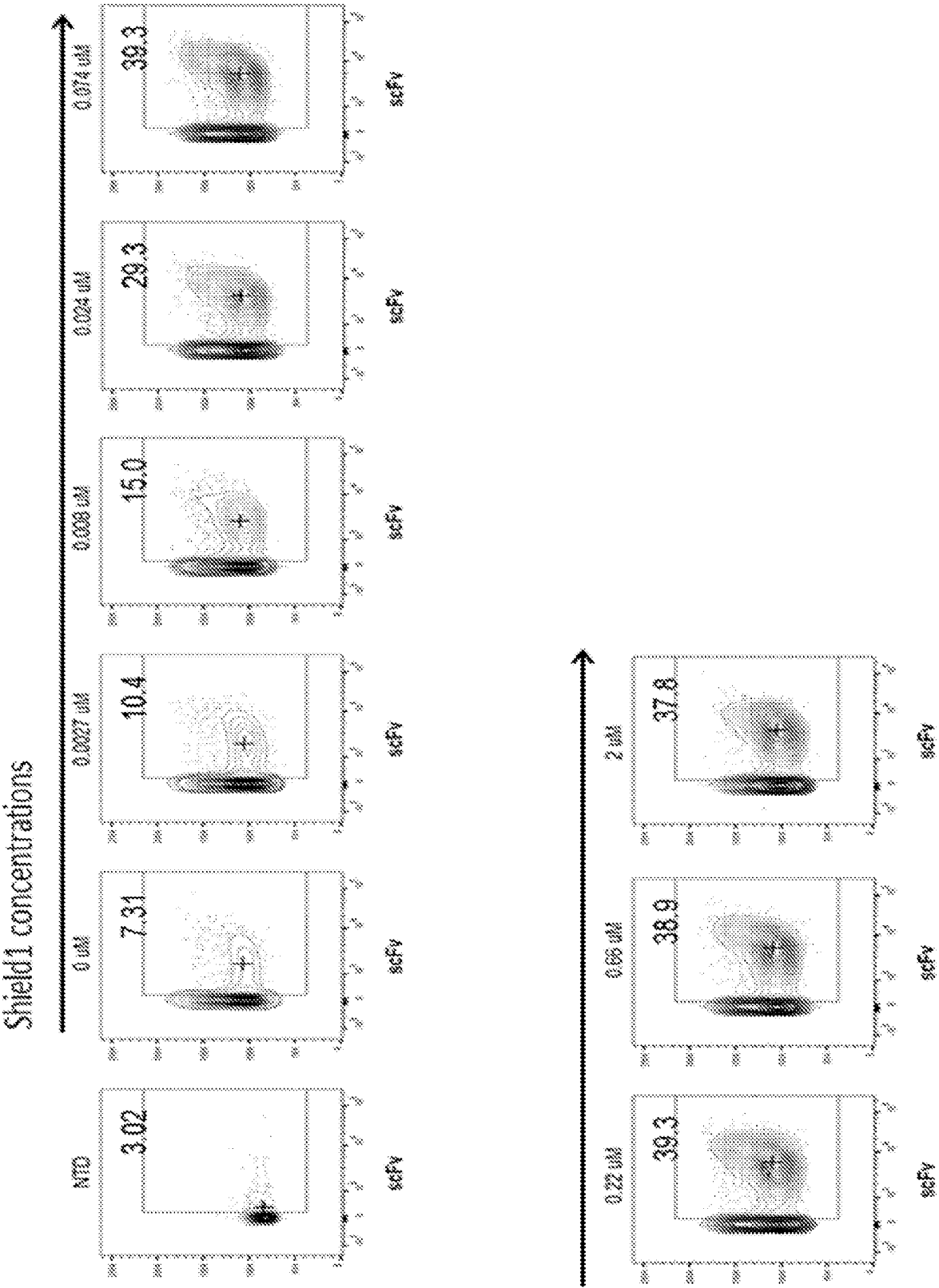


FIG. 37

40/48

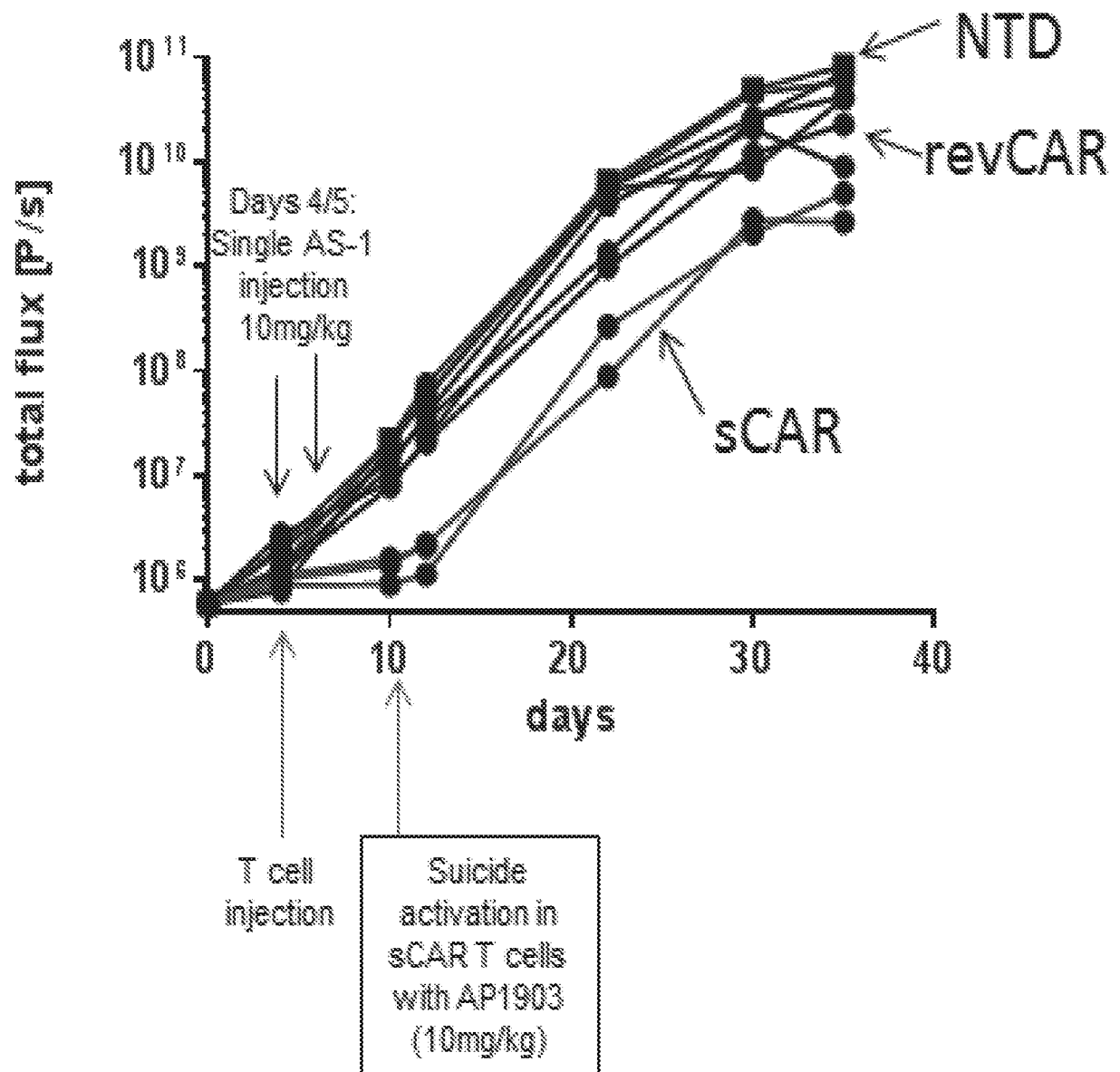


FIG. 38

41/48

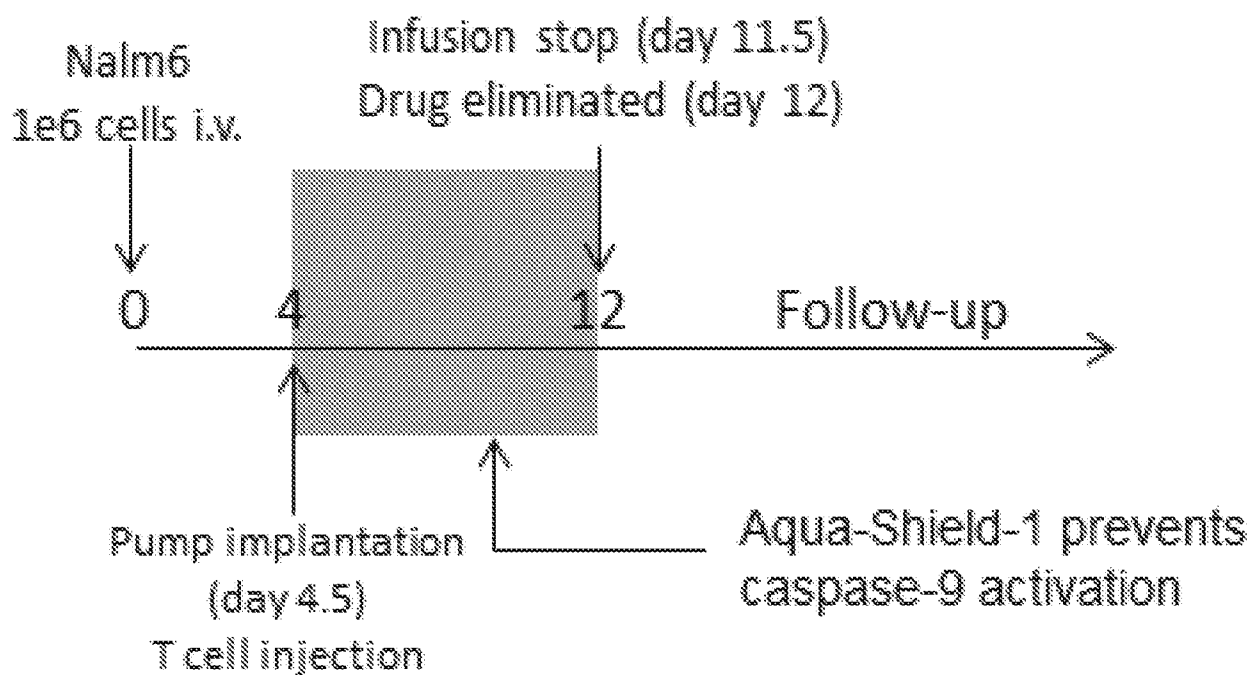
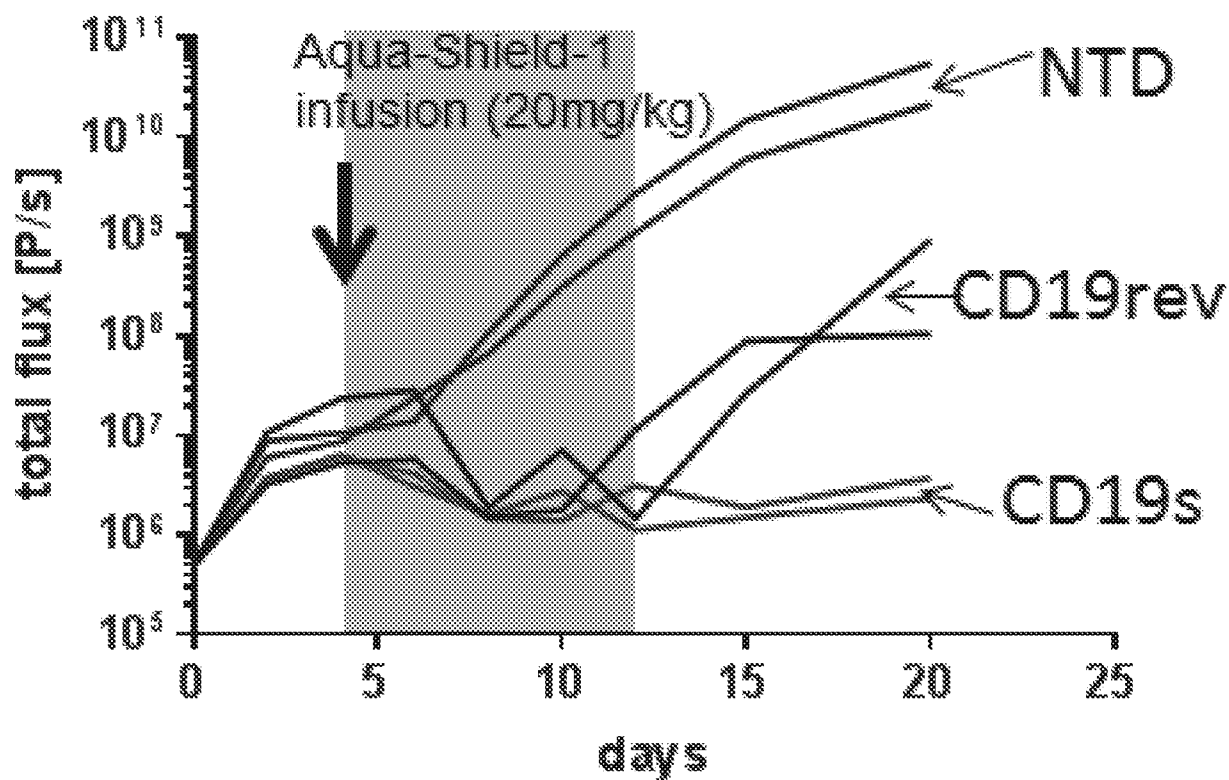
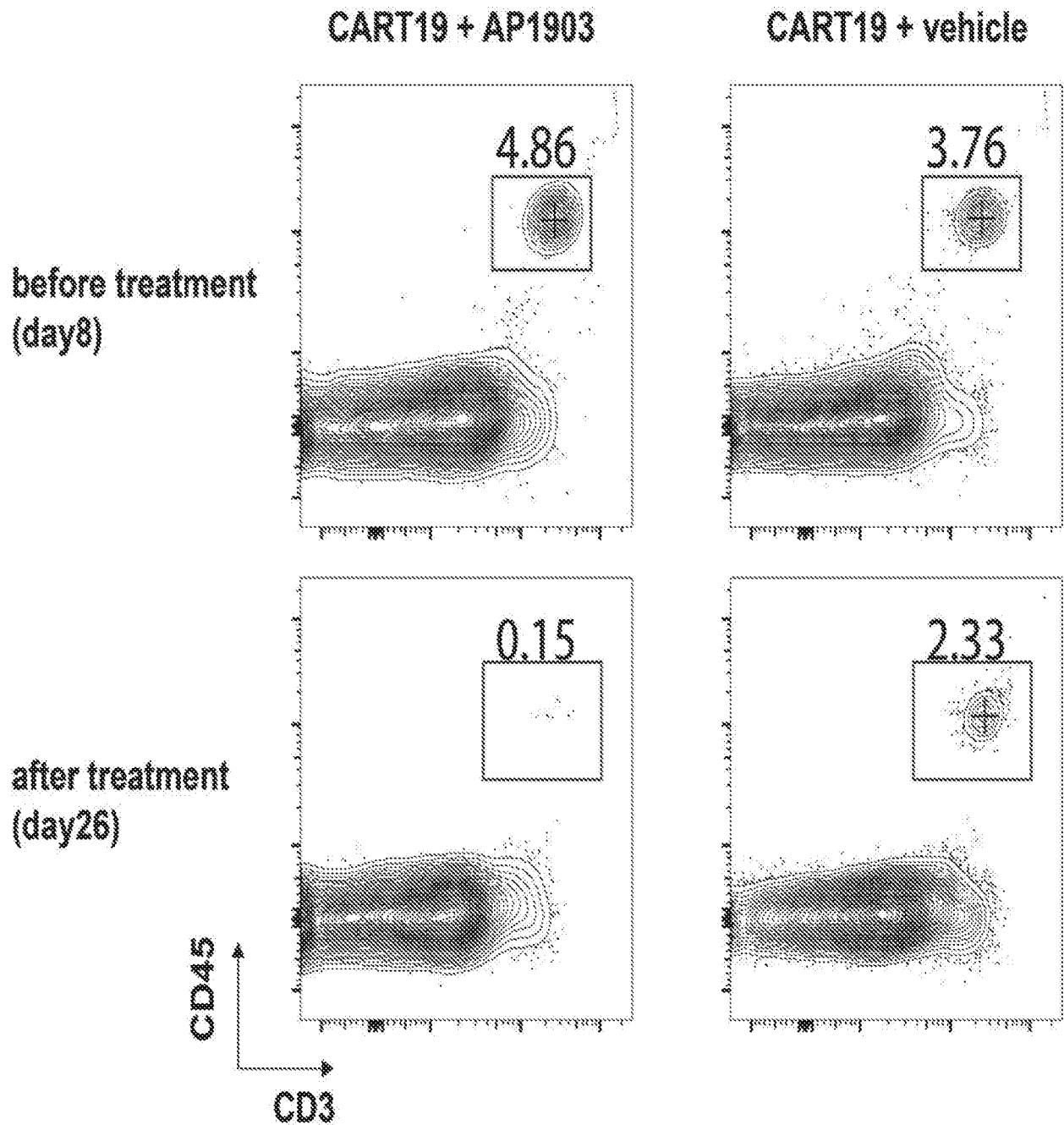
**19Rev 20mg/kg**

FIG. 39

42/48



Whole blood, gated on singlets → lymphocytes

FIG. 40

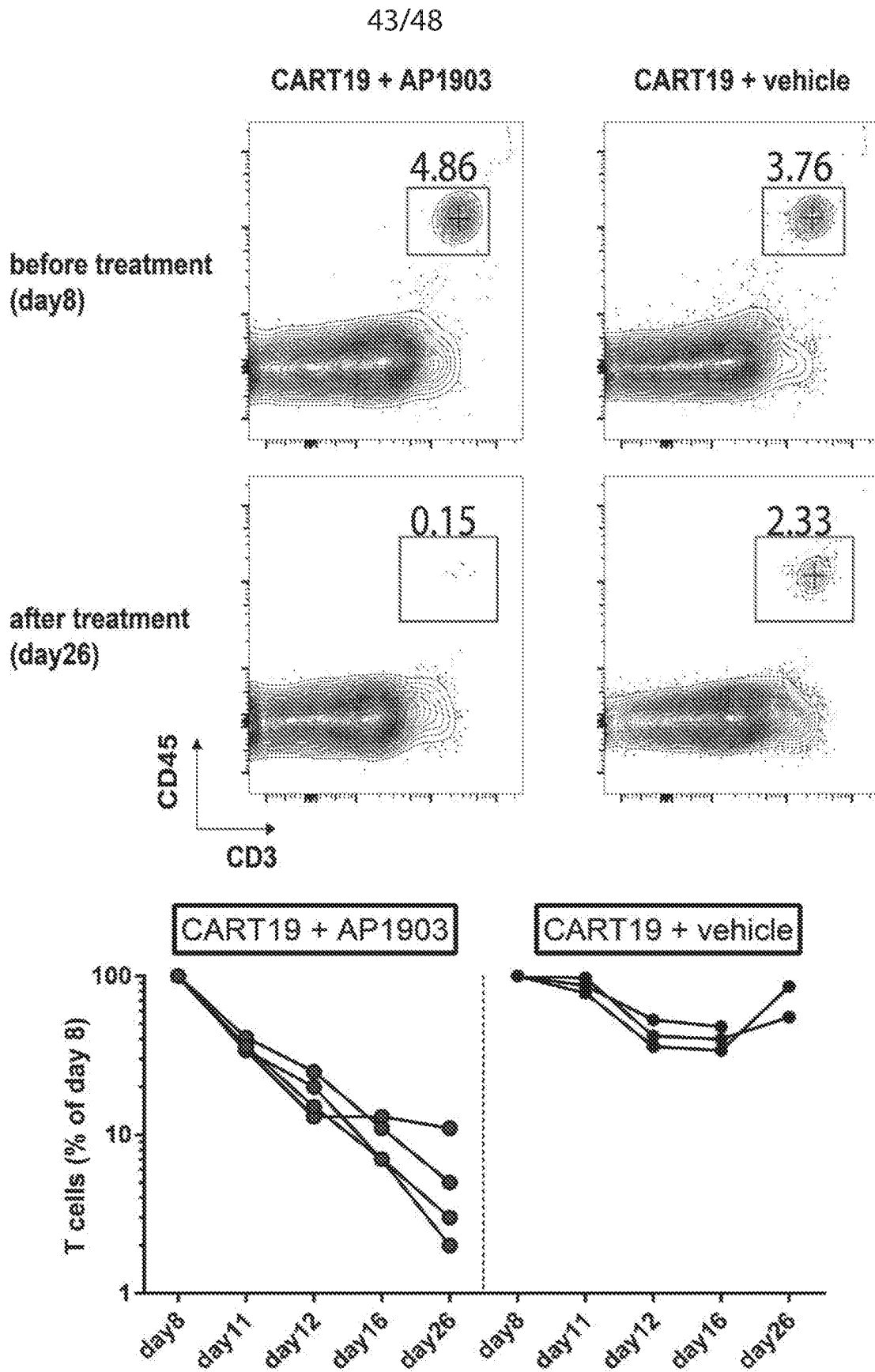


FIG. 41

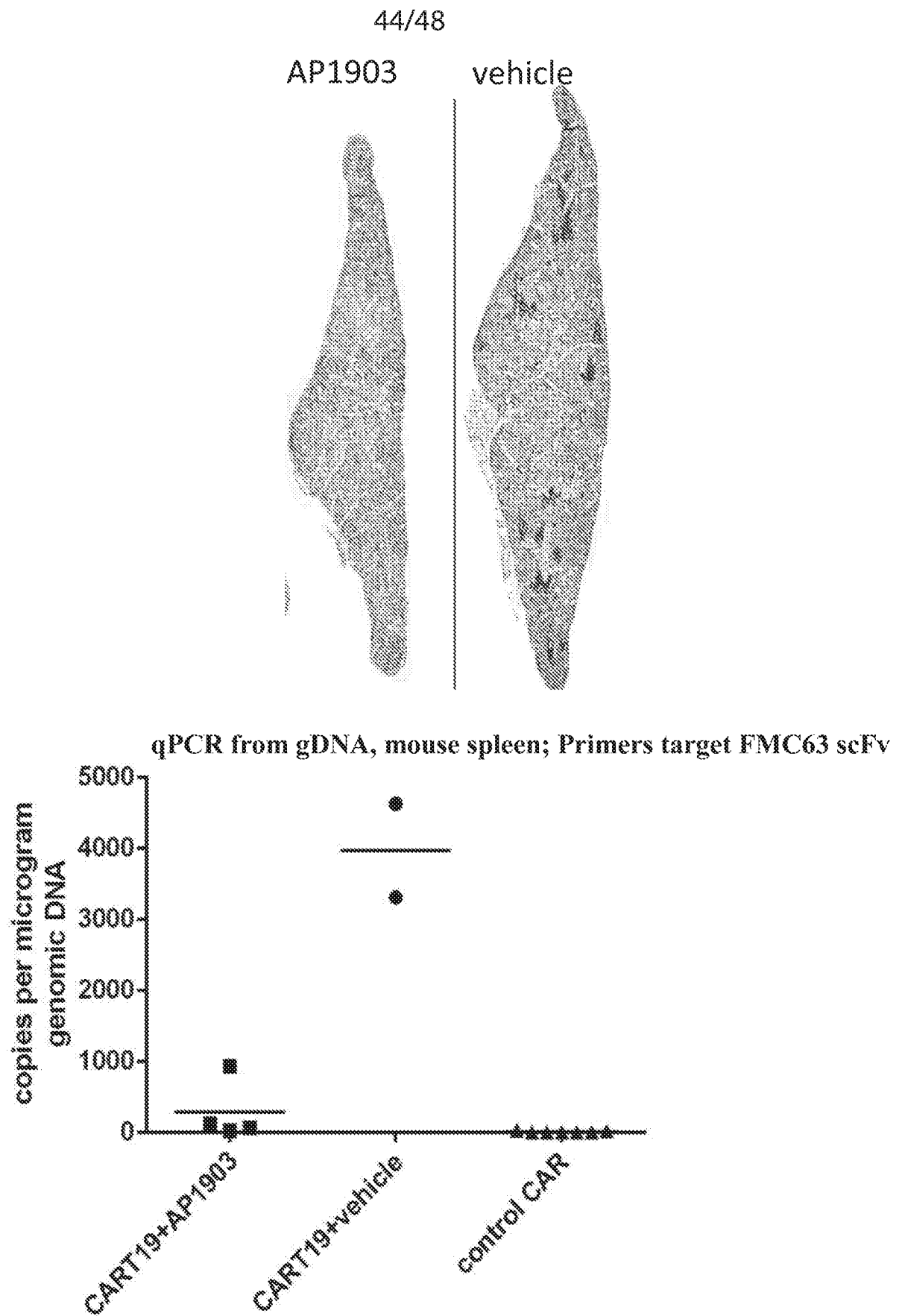


FIG. 42

45/48

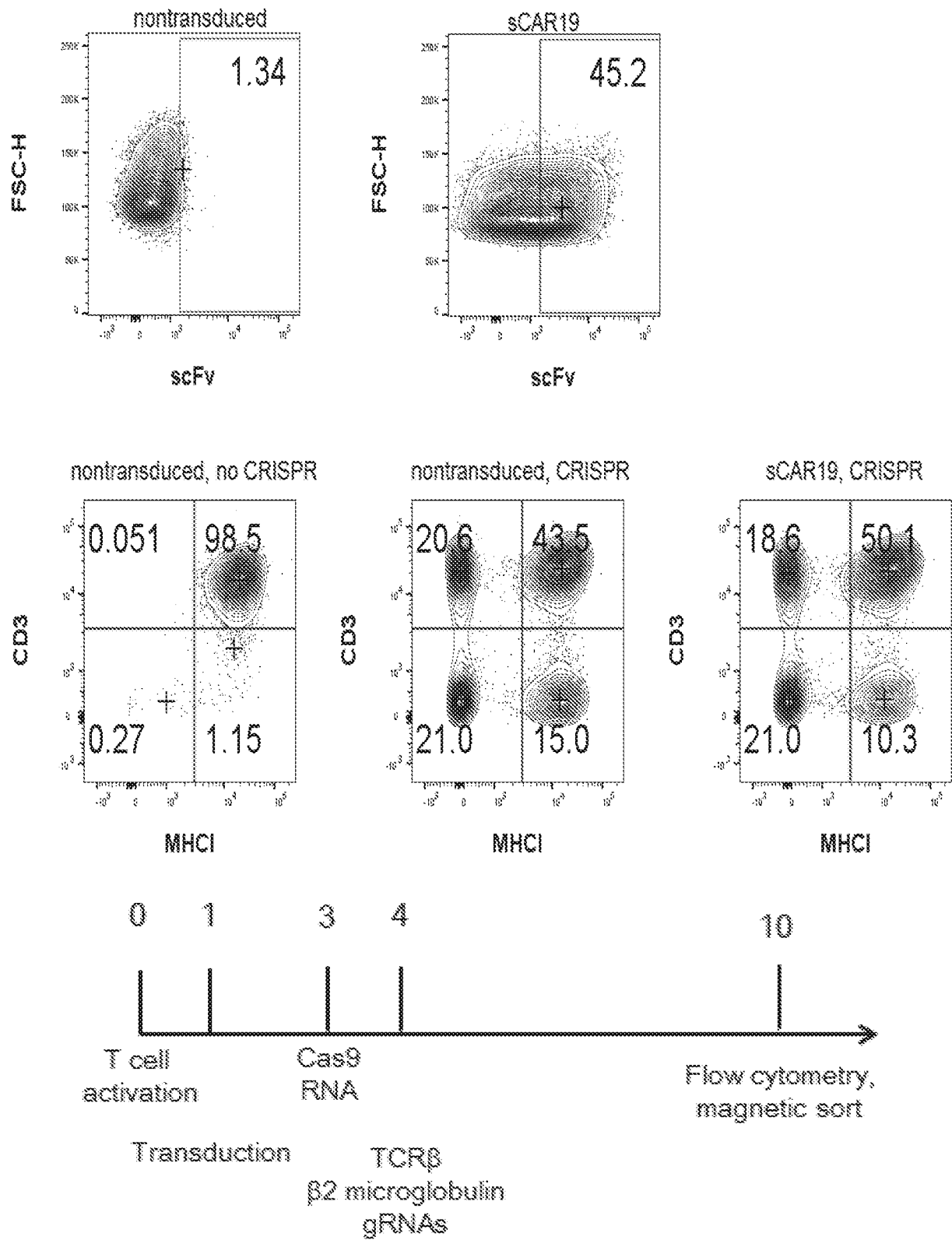


FIG. 43

46/48

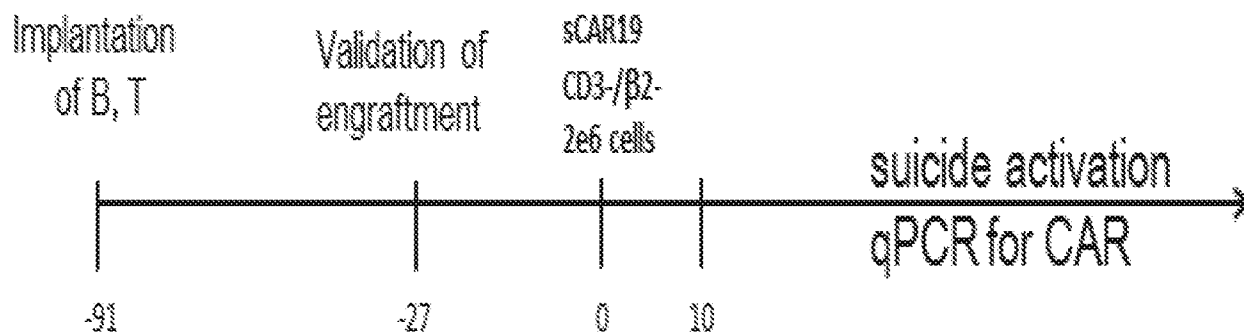


FIG. 44

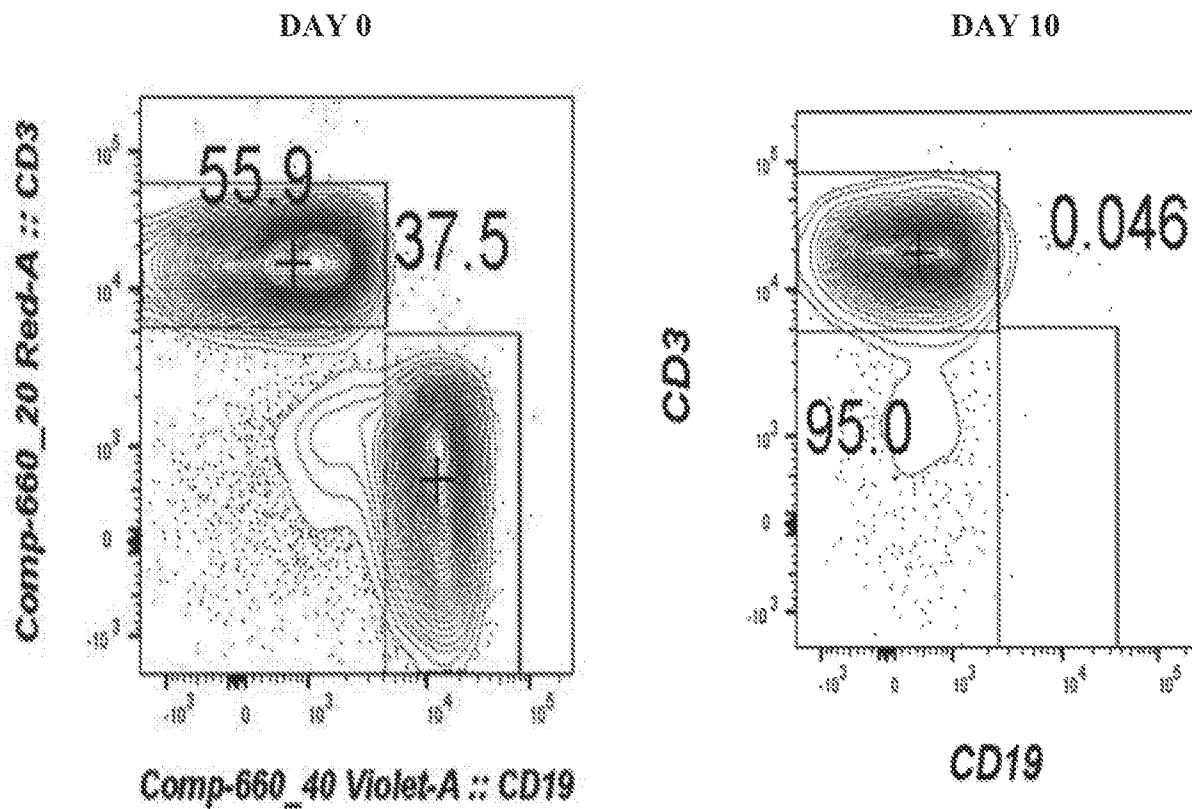


FIG. 45

47/48

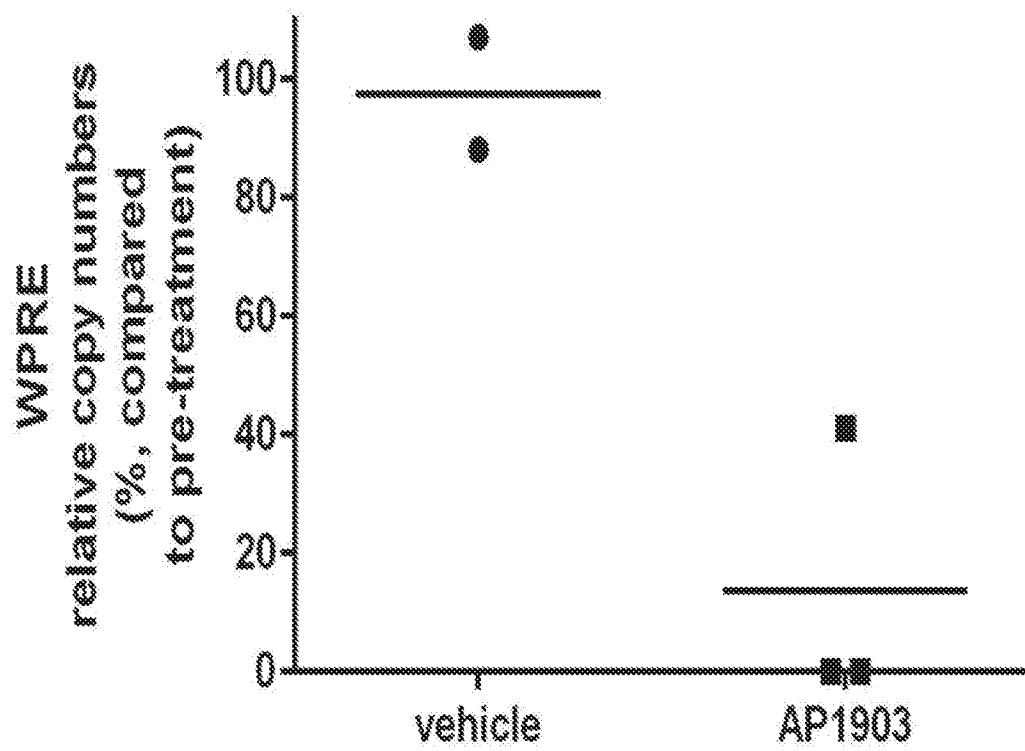


FIG. 46

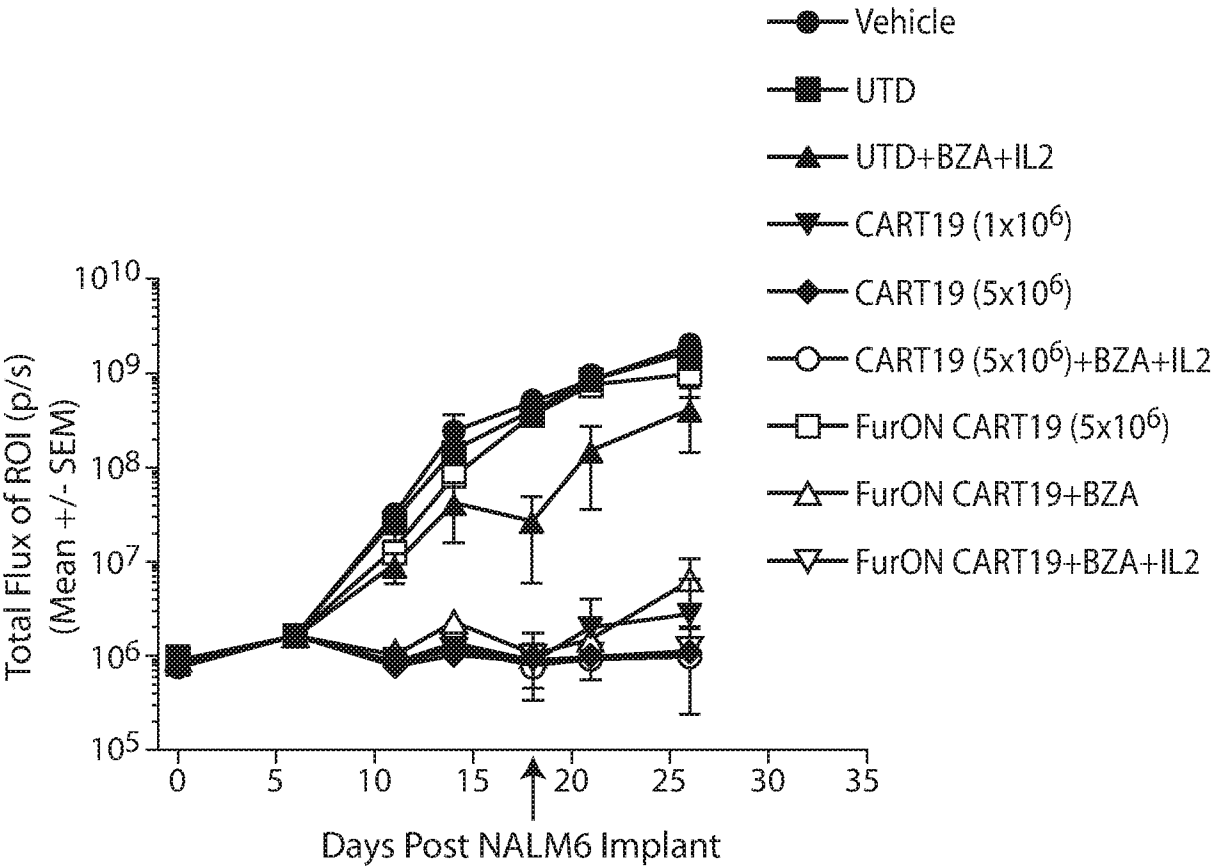


FIG. 47

_SL
SEQUENCE LISTING

<110> NOVARTIS AG
THE TRUSTEES OF THE UNIVERSITY OF PENNSYLVANIA

<120> COMPOSITIONS AND METHODS FOR SELECTIVE PROTEIN EXPRESSION

<130> N2067-7128W0

<140>

<141>

<150> 62/322,931

<151> 2016-04-15

<150> 62/481,094

<151> 2017-04-03

<160> 3036

<170> PatentIn version 3.5

<210> 1

<211> 1184

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1

cgtagaggctc	cggtgcccgt	cagtgggcag	agcgcacatc	gccacagtc	cccgagaagt	60
tggggggagg	ggtcggcaat	tgaaccggtg	cctagagaag	gtggcgcggg	gtaaactggg	120
aaagtgatgt	cgtgtactgg	ctccgccttt	ttcccagagg	tgggggagaa	ccgtatataa	180
gtgcagtagt	cgccgtgaac	gttctttttc	gcaacggggt	tgccgccaga	acacaggtaa	240
gtgccgtgtg	tggttcccg	gggcctggcc	tctttacggg	ttatggccct	tgcgtgcctt	300
gaattacttc	cacctggctg	cagtacgtga	ttcttgatcc	cgagcttcgg	gttggaagtg	360
ggtagggagag	ttcagggcct	tgcgcttaag	gagccccttc	gcctcgtgct	tgagttgagg	420
cctggcctgg	gcgctggggc	cgccgcgtgc	gaatctggtg	gcaccttcgc	gcctgtctcg	480
ctgctttcga	taagtctcta	gccatttaaa	atttttgatg	acctgctgcg	acgctttttt	540
tctggcaaga	tagtcttgta	aatgcggggc	aagatctgca	cactgggtatt	tcggtttttg	600
gggccgcggg	cggcgacggg	gcccgtgcgt	cccagcgcac	atgttcggcg	aggcggggcc	660
tgcgagcgcg	gccaccgaga	atcggacggg	ggtagtctca	agctggccgg	cctgctctgg	720
tgcctggcct	cgcgccgccg	tgtatcgccc	cgccctgggc	ggcaaggctg	gcccggctcg	780
caccagttgc	gtgagcgga	agatggccgc	ttcccggccc	tgctgcaggg	agctcaaaat	840
ggaggacgcg	gcgctcgga	gagcgggcgg	gtgagtcacc	cacacaaagg	aaaagggcct	900
ttccgtcctc	agccgtcgct	tcatgtgact	ccacggagta	ccgggcgccg	tccaggcacc	960
tcgattagtt	ctcgagcttt	tggagtacgt	cgtcttttagg	ttggggggag	gggttttatg	1020
cgatggagtt	tccccacact	gagtgggtgg	agactgaagt	taggccagct	tggcacttga	1080

_SL

tgtaattctc cttggaattt gccctttttg agtttggatc ttggttcatt ctcaagcctc 1140
agacagtggg tcaaagtttt tttcttccat ttcaggtgtc gtga 1184

<210> 2
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 2
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro
20

<210> 3
<211> 63
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic oligonucleotide"

<400> 3
atggccctgc ctgtgacagc cctgctgctg cctctggctc tgctgctgca tgccgctaga 60
ccc 63

<210> 4
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 4
Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala
1 5 10 15

Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly
20 25 30

Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp
35 40 45

<210> 5
<211> 135
<212> DNA
<213> Artificial Sequence

_SL

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 5

accacgacgc cagcgccgcg accaccaaca ccggcgccca ccatcgcgtc gcagcccctg 60

tccctgcgcc cagaggcgtg ccggccagcg gcggggggcg cagtgcacac gagggggctg 120

gacttcgcct gtgat 135

<210> 6

<211> 230

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 6

Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe
1 5 10 15

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
20 25 30

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
35 40 45

Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val
50 55 60

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser
65 70 75 80

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
85 90 95

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser
100 105 110

Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
115 120 125

Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln
130 135 140

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
145 150 155 160

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
165 170 175

_SL

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu
180 185 190

Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser
195 200 205

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
210 215 220

Leu Ser Leu Gly Lys Met
225 230

<210> 7
<211> 690
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 7
gagagcaagt acggccctcc ctgccccct tgccctgccc ccgagttcct gggcggaccc 60
agcgtgttcc tgttcccccc caagcccaag gacaccctga tgatcagccg gacccccgag 120
gtgacctgtg tgggtggtgga cgtgtcccag gaggaccccg aggtccagtt caactggtac 180
gtggacggcg tggaggtgca caacgccaag accaagcccc gggaggagca gttcaatagc 240
acctaccggg tgggtgtccgt gctgaccgtg ctgcaccagg actggctgaa cggcaaggaa 300
tacaagtgtg aggtgtccaa caagggcctg cccagcagca tcgagaaaac catcagcaag 360
gccaagggcc agcctcgga gccccagggtg tacaccctgc cccctagcca agaggagatg 420
accaagaacc aggtgtccct gacctgcctg gtgaagggt tctaccccag cgacatcgcc 480
gtggagtggg agagcaacgg ccagcccag aacaactaca agaccacccc cctgtgctg 540
gacagcgacg gcagcttctt cctgtacagc cggctgaccg tggacaagag ccggtggcag 600
gagggcaacg tctttagctg ctccgtgatg cagaggccc tgcacaacca ctacaccag 660
aagagcctga gcctgtccct gggcaagatg 690

<210> 8
<211> 282
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 8
Arg Trp Pro Glu Ser Pro Lys Ala Gln Ala Ser Ser Val Pro Thr Ala
1 5 10 15

Gln Pro Gln Ala Glu Gly Ser Leu Ala Lys^{-SL} Ala Thr Thr Ala Pro Ala
 20 25 30
 Thr Thr Arg Asn Thr Gly Arg Gly Gly Glu Glu Lys Lys Lys Glu Lys
 35 40 45
 Glu Lys Glu Glu Gln Glu Glu Arg Glu Thr Lys Thr Pro Glu Cys Pro
 50 55 60
 Ser His Thr Gln Pro Leu Gly Val Tyr Leu Leu Thr Pro Ala Val Gln
 65 70 75 80
 Asp Leu Trp Leu Arg Asp Lys Ala Thr Phe Thr Cys Phe Val Val Gly
 85 90 95
 Ser Asp Leu Lys Asp Ala His Leu Thr Trp Glu Val Ala Gly Lys Val
 100 105 110
 Pro Thr Gly Gly Val Glu Glu Gly Leu Leu Glu Arg His Ser Asn Gly
 115 120 125
 Ser Gln Ser Gln His Ser Arg Leu Thr Leu Pro Arg Ser Leu Trp Asn
 130 135 140
 Ala Gly Thr Ser Val Thr Cys Thr Leu Asn His Pro Ser Leu Pro Pro
 145 150 155 160
 Gln Arg Leu Met Ala Leu Arg Glu Pro Ala Ala Gln Ala Pro Val Lys
 165 170 175
 Leu Ser Leu Asn Leu Leu Ala Ser Ser Asp Pro Pro Glu Ala Ala Ser
 180 185 190
 Trp Leu Leu Cys Glu Val Ser Gly Phe Ser Pro Pro Asn Ile Leu Leu
 195 200 205
 Met Trp Leu Glu Asp Gln Arg Glu Val Asn Thr Ser Gly Phe Ala Pro
 210 215 220
 Ala Arg Pro Pro Pro Gln Pro Gly Ser Thr Thr Phe Trp Ala Trp Ser
 225 230 235 240
 Val Leu Arg Val Pro Ala Pro Pro Ser Pro Gln Pro Ala Thr Tyr Thr
 245 250 255
 Cys Val Val Ser His Glu Asp Ser Arg Thr Leu Leu Asn Ala Ser Arg
 260 265 270
 Ser Leu Glu Val Ser Tyr Val Thr Asp His
 275 280

_SL

<210> 9
<211> 847
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 9
aggtggcccg aaagtcccaa ggcccaggca tctagtgttc ctactgcaca gccccaggca 60
gaaggcagcc tagccaaagc tactactgca cctgccacta cgcgcaatac tggccgtggc 120
ggggaggaga agaaaaagga gaaagagaaa gaagaacagg aagagaggga gaccaagacc 180
cctgaatgtc catcccatac ccagccgctg ggcgtctatc tcttgactcc cgcagtacag 240
gacttgtggc ttagagataa ggccaccttt acatgtttcg tcgtgggctc tgacctgaag 300
gatgccatt tgacttggga ggttgccgga aaggtaccca caggggggggt tgaggaaggg 360
ttgctggagc gccattccaa tggctctcag agccagcact caagactcac ctttccgaga 420
tccctgtgga acgccgggac ctctgtcaca tgtactctaa atcatcctag cctgccccca 480
cagcgtctga tggcccttag agagccagcc gcccaggcac cagttaagct tagcctgaat 540
ctgctcgcca gtagtgatcc cccagaggcc gccagctggc tcttatgcga agtgtccggc 600
tttagcccg ccaacatctt gctcatgtgg ctggaggacc agcgagaagt gaacaccagc 660
ggcttcgctc cagcccggcc cccaccccag ccgggttcta ccacattctg ggcctggagt 720
gtcttaaggg tcccagcacc acctagcccc cagccagcca catacacctg tgttgtgtcc 780
catgaagata gcaggaccct gctaaatgct tctaggagtc tggaggtttc ctacgtgact 840
gaccatt 847

<210> 10
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 10
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10

<210> 11
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic oligonucleotide"

<400> 11

ggtggcggag gttctggagg tggaggttcc

_SL

30

<210> 12
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 12
Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu
1 5 10 15

Ser Leu Val Ile Thr Leu Tyr Cys
20

<210> 13
<211> 72
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic oligonucleotide"

<400> 13
atctacatct gggcgccctt ggccgggact tgtgggggtcc ttctcctgtc actggttatc 60
accctttact gc 72

<210> 14
<211> 42
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 14
Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met
1 5 10 15

Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe
20 25 30

Pro Glu Glu Glu Gly Gly Cys Glu Leu
35 40

<210> 15
<211> 126
<212> DNA
<213> Artificial Sequence

<220>
<221> source

_SL

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 15
aaacggggca gaaagaaact cctgtatata ttcaaacaac catttatgag accagtacaa 60
actactcaag aggaagatgg ctgtagctgc cgatttccag aagaagaaga aggaggatgt 120
gaactg 126

<210> 16
<211> 48
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 16
Gln Arg Arg Lys Tyr Arg Ser Asn Lys Gly Glu Ser Pro Val Glu Pro
1 5 10 15

Ala Glu Pro Cys Arg Tyr Ser Cys Pro Arg Glu Glu Glu Gly Ser Thr
20 25 30

Ile Pro Ile Gln Glu Asp Tyr Arg Lys Pro Glu Pro Ala Cys Ser Pro
35 40 45

<210> 17
<211> 123
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 17
aggagtaaga ggagcaggct cctgcacagt gactacatga acatgactcc ccgccgcccc 60
gggcccaccc gcaagcatta ccagccctat gccccaccac gcgacttcgc agcctatcgc 120
tcc 123

<210> 18
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 18
Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly
1 5 10 15

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
Page 8

20 25 _SL 30															
Asp	Val	Leu	Asp	Lys	Arg	Arg	Gly	Arg	Asp	Pro	Glu	Met	Gly	Gly	Lys
		35					40					45			
Pro	Arg	Arg	Lys	Asn	Pro	Gln	Glu	Gly	Leu	Tyr	Asn	Glu	Leu	Gln	Lys
	50					55					60				
Asp	Lys	Met	Ala	Glu	Ala	Tyr	Ser	Glu	Ile	Gly	Met	Lys	Gly	Glu	Arg
65					70					75					80
Arg	Arg	Gly	Lys	Gly	His	Asp	Gly	Leu	Tyr	Gln	Gly	Leu	Ser	Thr	Ala
				85					90					95	
Thr	Lys	Asp	Thr	Tyr	Asp	Ala	Leu	His	Met	Gln	Ala	Leu	Pro	Pro	Arg
			100					105					110		

```
<210> 19
<211> 336
<212> DNA
<213> Artificial Sequence
```

```
<220>  
<221> source  
<223> /note="Description of Artificial Sequence: Synthetic  
polynucleotide"
```

<400> 19							
agagtgaagt	tcagcaggag	cgcagacgcc	cccgcgtaca	agcagggcca	gaaccagctc		60
tataacgagc	tcaatctagg	acgaagagag	gagtacgatg	ttttggacaa	gagacgtggc		120
cgggaccctg	agatgggggg	aaagccgaga	aggaagaacc	ctcaggaagg	cctgtacaat		180
gaactgcaga	aagataagat	ggcggaggcc	tacagtgaga	ttgggatgaa	aggcgagcgc		240
cggaggggca	aggggcacga	tggcctttac	cagggctctca	gtacagccac	caaggacacc		300
tacgacgccc	ttcacatgca	ggccctgccc	cctcgc				336

```
<210> 20
<211> 112
<212> PRT
<213> Artificial Sequence
```

```
<220>  
<221> source  
<223> /note="Description of Artificial Sequence: Synthetic  
polypeptide"
```

<400> 20
Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly
1 5 10 15

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
20 25 30

Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
35 40 45

_SL

Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
50 55 60

Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
65 70 75 80

Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala
85 90 95

Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
100 105 110

<210> 21
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 21
agagtgaagt tcagcaggag cgcagacgcc cccgcgtacc agcagggcca gaaccagctc 60
tataacgagc tcaatctagg acgaagagag gagtacgatg ttttggacaa gagacgtggc 120
cgggaccctg agatgggggg aaagccgaga aggaagaacc ctcaggaagg cctgtacaat 180
gaactgcaga aagataagat ggcggaggcc tacagtgaga ttgggatgaa aggcgagcgc 240
cggaggggca aggggcacga tggcctttac caggggtctca gtacagccac caaggacacc 300
tacgacgccc ttcacatgca ggccctgccc cctcgc 336

<210> 22
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 22
Gly Gly Gly Gly Ser
1 5

<210> 23
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 23

ggtggcggag gttctggagg tggaggttcc

<210> 24
 <211> 150
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 24
 Pro Gly Trp Phe Leu Asp Ser Pro Asp Arg Pro Trp Asn Pro Pro Thr
 1 5 10 15

Phe Ser Pro Ala Leu Leu Val Val Thr Glu Gly Asp Asn Ala Thr Phe
 20 25 30

Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser Phe Val Leu Asn Trp Tyr
 35 40 45

Arg Met Ser Pro Ser Asn Gln Thr Asp Lys Leu Ala Ala Phe Pro Glu
 50 55 60

Asp Arg Ser Gln Pro Gly Gln Asp Cys Arg Phe Arg Val Thr Gln Leu
 65 70 75 80

Pro Asn Gly Arg Asp Phe His Met Ser Val Val Arg Ala Arg Arg Asn
 85 90 95

Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile Ser Leu Ala Pro Lys Ala
 100 105 110

Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu Arg Val Thr Glu Arg Arg
 115 120 125

Ala Glu Val Pro Thr Ala His Pro Ser Pro Ser Pro Arg Pro Ala Gly
 130 135 140

Gln Phe Gln Thr Leu Val
 145 150

<210> 25
 <211> 450
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 25
 cccggatggt ttctggactc tccggatcgc ccgtggaatc cccaacctt ctcaccggca 60

ctcttggttg tgactgaggg cgataatgcg accttcacgt gctcgttctc caacacctcc 120

_SL

gaatcattcg tgctgaactg gtaccgcatg agcccgtaa accagaccga caagctcgcc 180
gcgtttccgg aagatcggtc gcaaccggga caggattgtc ggttccgct gactcaactg 240
ccgaatggca gagacttcca catgagcgtg gtccgcgcta ggcgaaacga ctccgggacc 300
tacctgtgcg gagccatctc gctgggcct aaggccaaa tcaaagagag cttgagggcc 360
gaactgagag tgaccgagcg cagagctgag gtgccaactg cacatccatc cccatgcct 420
cggcctgctg ggcagtttca gaccctggtc 450

<210> 26

<211> 394

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 26

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Pro Gly Trp Phe Leu Asp Ser Pro Asp Arg Pro
20 25 30

Trp Asn Pro Pro Thr Phe Ser Pro Ala Leu Leu Val Val Thr Glu Gly
35 40 45

Asp Asn Ala Thr Phe Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser Phe
50 55 60

Val Leu Asn Trp Tyr Arg Met Ser Pro Ser Asn Gln Thr Asp Lys Leu
65 70 75 80

Ala Ala Phe Pro Glu Asp Arg Ser Gln Pro Gly Gln Asp Cys Arg Phe
85 90 95

Arg Val Thr Gln Leu Pro Asn Gly Arg Asp Phe His Met Ser Val Val
100 105 110

Arg Ala Arg Arg Asn Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile Ser
115 120 125

Leu Ala Pro Lys Ala Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu Arg
130 135 140

Val Thr Glu Arg Arg Ala Glu Val Pro Thr Ala His Pro Ser Pro Ser
145 150 155 160

Pro Arg Pro Ala Gly Gln Phe Gln Thr Leu Val Thr Thr Thr Pro Ala
165 170 175

_SL

Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser
180 185 190

Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr
195 200 205

Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala
210 215 220

Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys
225 230 235 240

Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met
245 250 255

Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe
260 265 270

Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg
275 280 285

Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn
290 295 300

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
305 310 315 320

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
325 330 335

Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
340 345 350

Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
355 360 365

Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
370 375 380

Ala Leu His Met Gln Ala Leu Pro Pro Arg
385 390

<210> 27
<211> 1182
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 27

_SL

atggccctcc ctgtcactgc cctgcttctc cccctcgcac tcctgctcca cgccgctaga	60
ccacccggat ggtttctgga ctctccggat cgcccgtgga atcccccaac cttctcaccg	120
gcactcttgg ttgtgactga gggcgataat gcgaccttca cgtgctcggt ctccaacacc	180
tccgaatcat tcgtgctgaa ctggtaccgc atgagcccggt caaaccagac cgacaagctc	240
gccgcgtttc cggaagatcg gtcgcaaccg ggacaggatt gtcggttccg cgtgactcaa	300
ctgccgaatg gcagagactt ccacatgagc gtggtccgcg ctaggcgaaa cgactccggg	360
acctacctgt gcggagccat ctcgctggcg cctaaggccc aaatcaaaga gagcttgagg	420
gccgaactga gagtgaccga gcgcagagct gaggtgccaa ctgcacatcc atccccatcg	480
cctcggcctg cggggcagtt tcagaccctg gtcacgacca ctccggcgcc gcgcccaccg	540
actccggccc caactatcgc gagccagccc ctgtcgtgta ggccggaagc atgccgcctt	600
gccgccggag gtgctgtgca taccggggga ttggacttcg catgcgacat ctacatttgg	660
gctcctctcg ccggaacttg tggcgtgctc cttctgtccc tggatcatcac cctgtactgc	720
aagcggggtc ggaaaaagct tctgtacatt ttcaagcagc ctttcatgag gcccgtgcaa	780
accacccagg aggaggacgg ttgctcctgc cggttccccg aagaggaaga aggaggttgc	840
gagctgcgcg tgaagtctc ccggagcgcc gacgcccccg cctataagca gggccagaac	900
cagctgtaca acgaactgaa cctgggacgg cggaagagt acgatgtgct ggacaagcgg	960
cgcgggccggg accccgaaat gggcggggaag cctagaagaa agaaccctca ggaaggcctg	1020
tataacgagc tgcagaagga caagatggcc gaggcctact ccgaaattgg gatgaaggga	1080
gagcggcgga ggggaaagg gcacgacggc ctgtaccaag gactgtccac cgccaccaag	1140
gacacatacg atgccctgca catgcaggcc cttccccctc gc	1182

<210> 28
 <211> 40
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
 <221> MISC_FEATURE
 <222> (1)..(40)
 <223> /note="This sequence may encompass 1-10 'Gly Gly Gly Ser' repeating units"

<400> 28
 Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
 1 5 10 15

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
 20 25 30

Gly Gly Gly Ser Gly Gly Gly Ser

<210> 29
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 29
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15

Gly Gly Gly Ser
20

<210> 30
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 30
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 31
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 31
Gly Gly Gly Ser
1

<210> 32
<211> 5000
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<220>
<221> misc_feature
<222> (1)..(5000)
<223> /note="This sequence may encompass 50-5000 nucleotides"

<220>

<221> source

<223> /note="See specification as filed for detailed description of substitutions and preferred embodiments"

<400> 32

aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	60
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	120
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	180
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	240
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	300
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	360
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	420
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	480
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	540
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	600
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	660
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	720
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	780
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	840
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	900
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	960
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	1020
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	1080
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	1140
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	1200
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	1260
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	1320
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	1380
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	1440
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	1500
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	1560
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	1620
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	1680
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	1740
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	1800
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	1860

						_SL	
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa		3960
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa		4020
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa		4080
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa		4140
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa		4200
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa		4260
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa		4320
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa		4380
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa		4440
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa		4500
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa		4560
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa		4620
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa		4680
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa		4740
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa		4800
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa		4860
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa		4920
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa		4980
aaaaaaaaaa	aaaaaaaaaa						5000

<210> 33
 <211> 63
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 oligonucleotide"

<400> 33	
atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg	60
ccc	63

<210> 34
 <211> 72
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 oligonucleotide"

<400> 34	
atctacattt gggcccctct ggctggtact tgcgggggtcc tgctgctttc actcgtgatc	60

actctttact gt

<210> 35
<211> 5
<212> PRT
<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown:
Granzyme B sequence"

<220>
<221> MOD_RES
<222> (5)..(5)
<223> Any amino acid

<400> 35
Ile Glu Pro Asp Xaa
1 5

<210> 36
<211> 5
<212> PRT
<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown:
Enterokinase sequence"

<400> 36
Asp Asp Asp Asp Lys
1 5

<210> 37
<211> 6
<212> PRT
<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown:
Genenase sequence"

<400> 37
Pro Gly Ala Ala His Tyr
1 5

<210> 38
<211> 7
<212> PRT
<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown:
PreScission protease sequence"

<400> 38
Leu Glu Val Phe Gln Gly Pro
1 5

_SL

<210> 39
<211> 373
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 39
Pro Gly Trp Phe Leu Asp Ser Pro Asp Arg Pro Trp Asn Pro Pro Thr
1 5 10 15

Phe Ser Pro Ala Leu Leu Val Val Thr Glu Gly Asp Asn Ala Thr Phe
20 25 30

Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser Phe Val Leu Asn Trp Tyr
35 40 45

Arg Met Ser Pro Ser Asn Gln Thr Asp Lys Leu Ala Ala Phe Pro Glu
50 55 60

Asp Arg Ser Gln Pro Gly Gln Asp Cys Arg Phe Arg Val Thr Gln Leu
65 70 75 80

Pro Asn Gly Arg Asp Phe His Met Ser Val Val Arg Ala Arg Arg Asn
85 90 95

Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile Ser Leu Ala Pro Lys Ala
100 105 110

Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu Arg Val Thr Glu Arg Arg
115 120 125

Ala Glu Val Pro Thr Ala His Pro Ser Pro Ser Pro Arg Pro Ala Gly
130 135 140

Gln Phe Gln Thr Leu Val Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr
145 150 155 160

Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala
165 170 175

Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe
180 185 190

Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val
195 200 205

Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys
210 215 220

Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe^{-SL} Met Arg Pro Val Gln Thr
 225 230 235 240
 Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu
 245 250 255
 Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro
 260 265 270
 Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly
 275 280 285
 Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro
 290 295 300
 Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr
 305 310 315 320
 Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly
 325 330 335
 Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln
 340 345 350
 Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln
 355 360 365
 Ala Leu Pro Pro Arg
 370

<210> 40
 <211> 6
 <212> PRT
 <213> Unknown

<220>
 <221> source
 <223> /note="Description of Unknown:
 Thrombin sequence"

<400> 40
 Leu Val Pro Arg Gly Ser
 1 5

<210> 41
 <211> 7
 <212> PRT
 <213> Unknown

<220>
 <221> source
 <223> /note="Description of Unknown:
 TEV protease sequence"

<400> 41
 Glu Asn Leu Tyr Phe Gln Gly
 1 5

_SL

<210> 42
<211> 2
<212> PRT
<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown:
Elastase 1 sequence"

<220>
<221> VARIANT
<222> (1)..(1)
<223> /replace="Gly" or "Ser" or "Val"

<220>
<221> MOD_RES
<222> (2)..(2)
<223> Any amino acid

<220>
<221> MISC_FEATURE
<222> (1)..(2)
<223> /note="Variant residues given in the sequence have no
preference with respect to those in the annotations
for variant positions"

<400> 42
Ala Xaa
1

<210> 43
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 43
Met Leu Leu Leu Val Thr Ser Leu Leu Leu Cys Glu Leu Pro His Pro
1 5 10 15

Ala Phe Leu Leu Ile Pro
20

<210> 44
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 44
Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu
1 5 10 15

_SL

Val Thr Asn Ser
20

<210> 45
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 45
Met Ala Gln Val Lys Leu Gln Glu Ser Gly Thr Glu Leu Ala Lys Pro
1 5 10 15

Gly Ala Ala Val Lys
20

<210> 46
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 46
Met Arg Phe Leu Ala Ala Thr Phe Leu Leu Leu Ala Leu Ser Thr Ala
1 5 10 15

Ala Gln Ala

<210> 47
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 47
Lys Asp Glu Leu
1

<210> 48
<211> 787
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

_SL

<400> 48

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Arg Ser Ser Leu Ala Leu Ser Leu Thr Ala Asp
20 25 30

Gln Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser
35 40 45

Glu Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu
50 55 60

Leu Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala
65 70 75 80

Lys Arg Val Pro Gly Phe Val Asp Leu Ala Leu His Asp Gln Val His
85 90 95

Leu Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp
100 105 110

Arg Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu
115 120 125

Leu Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe
130 135 140

Asp Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln
145 150 155 160

Gly Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly
165 170 175

Val Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp
180 185 190

His Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu
195 200 205

Met Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala
210 215 220

Gln Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Ser Lys Arg
225 230 235 240

Met Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Ser
245 250 255

Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu Arg Thr Lys Arg
260 265 270

_SL

Ile Trp Glu Leu Lys Lys Asp Val Tyr Val Val Glu Leu Asp Trp Tyr
275 280 285

Pro Asp Ala Pro Gly Glu Met Val Val Leu Thr Cys Asp Thr Pro Glu
290 295 300

Glu Asp Gly Ile Thr Trp Thr Leu Asp Gln Ser Ser Glu Val Leu Gly
305 310 315 320

Ser Gly Lys Thr Leu Thr Ile Gln Val Lys Glu Phe Gly Asp Ala Gly
325 330 335

Gln Tyr Thr Cys His Lys Gly Gly Glu Val Leu Ser His Ser Leu Leu
340 345 350

Leu Leu His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Lys
355 360 365

Asp Gln Lys Glu Pro Lys Asn Lys Thr Phe Leu Arg Cys Glu Ala Lys
370 375 380

Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Thr Ile Ser Thr
385 390 395 400

Asp Leu Thr Phe Ser Val Lys Ser Ser Arg Gly Ser Ser Asp Pro Gln
405 410 415

Gly Val Thr Cys Gly Ala Ala Thr Leu Ser Ala Glu Arg Val Arg Gly
420 425 430

Asp Asn Lys Glu Tyr Glu Tyr Ser Val Glu Cys Gln Glu Asp Ser Ala
435 440 445

Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile Glu Val Met Val Asp Ala
450 455 460

Val His Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe Ile Arg
465 470 475 480

Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn Leu Gln Leu Lys Pro Leu
485 490 495

Lys Asn Ser Arg Gln Val Glu Val Ser Trp Glu Tyr Pro Asp Thr Trp
500 505 510

Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Cys Val Gln Val Gln
515 520 525

Gly Lys Ser Lys Arg Glu Lys Lys Asp Arg Val Phe Thr Asp Lys Thr
530 535 540

_SL

Ser Ala Thr Val Ile Cys Arg Lys Asn Ala Ser Ile Ser Val Arg Ala
545 550 555 560

Gln Asp Arg Tyr Tyr Ser Ser Ser Trp Ser Glu Trp Ala Ser Val Pro
565 570 575

Cys Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Arg Asn
580 585 590

Leu Pro Val Ala Thr Pro Asp Pro Gly Met Phe Pro Cys Leu His His
595 600 605

Ser Gln Asn Leu Leu Arg Ala Val Ser Asn Met Leu Gln Lys Ala Arg
610 615 620

Gln Thr Leu Glu Phe Tyr Pro Cys Thr Ser Glu Glu Ile Asp His Glu
625 630 635 640

Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu Ala Cys Leu Pro Leu
645 650 655

Glu Leu Thr Lys Asn Glu Ser Cys Leu Asn Ser Arg Glu Thr Ser Phe
660 665 670

Ile Thr Asn Gly Ser Cys Leu Ala Ser Arg Lys Thr Ser Phe Met Met
675 680 685

Ala Leu Cys Leu Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Val
690 695 700

Glu Phe Lys Thr Met Asn Ala Lys Leu Leu Met Asp Pro Lys Arg Gln
705 710 715 720

Ile Phe Leu Asp Gln Asn Met Leu Ala Val Ile Asp Glu Leu Met Gln
725 730 735

Ala Leu Asn Phe Asn Ser Glu Thr Val Pro Gln Lys Ser Ser Leu Glu
740 745 750

Glu Pro Asp Phe Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu His
755 760 765

Ala Phe Arg Ile Arg Ala Val Thr Ile Asp Arg Val Met Ser Tyr Leu
770 775 780

Asn Ala Ser
785

<210> 49
<211> 816
<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 49

```
atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgtcca cgccgctcgg      60
ccccggtcgt cgttggcact ttccctgact gccgaccaga tgggtgtccgc ctttctggac      120
gccgagcctc caattctgta ctcggagtac gatccgactc gcccgttctc cgaagccagc      180
atgatggggc tgttgactaa cctggcggac cgcgagttgg tgcacatgat taactgggct      240
aagcgggtgc cgggcttcgt ggacctggcc ctgcacgacc aagtgcacct cctggaatgc      300
gcctggatgg aaatcctcat gatcggcctc gtgtggagat ccatggagca tcccggaaag      360
ctcctgtttg caccacacct cctgcttgat cgcaaccagg gaaaatgcgt ggaagggggg      420
gtcgagattt tcgacatgct gtcgccacc tcttcccggg tccggatgat gaatctgcag      480
ggagaagagt tcgtgtgtct gaagtcaatc atcctgctga actccggggg ctataccttc      540
ctgagctcga ccctcaagtc actggaggaa aaagaccaca tccatcgcgt gctcgataag      600
atcaccgaca cccttatcca tctcatggcg aaggctggac tgaccctgca acagcagcac      660
cagaggctgg cccagttgct gctgattctg agccacatcc ggcacatgtc gtccaagagg      720
atggaacacc tgtacagcat gaagtgaag aacgtcgtgc ctctgtccga tctgtcctg      780
gaaatgctgg acgcgcacag actccgtact aaaaga                                816
```

<210> 50

<400> 50

000

<210> 51

<400> 51

000

<210> 52

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 52

```
Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Arg Asn Leu Pro
1           5           10           15
```

Val

_SL

<210> 53
<211> 63
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 53
gtggtggcgg tggaagcggc ggtggcggaa gcggcggtgg cggcagcaga aacctccccg 60
tgg 63

<210> 54

<400> 54
000

<210> 55

<400> 55
000

<210> 56
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 56
Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe Pro
1 5 10 15

Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu Asp
20 25 30

Gly Lys Lys Val Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys Phe
35 40 45

Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val Ala
50 55 60

Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp Tyr
65 70 75 80

Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala Thr
85 90 95

Leu Val Phe Asp Val Glu Leu Leu Lys Pro Glu
100 105

<210> 57

_SL

<211> 158
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 57
Ile Ser Leu Ile Ala Ala Leu Ala Val Asp Tyr Val Ile Gly Met Glu
1 5 10 15

Asn Ala Met Pro Trp Asn Leu Pro Ala Asp Leu Ala Trp Phe Lys Arg
20 25 30

Asn Thr Leu Asn Lys Pro Val Ile Met Gly Arg His Thr Trp Glu Ser
35 40 45

Ile Gly Arg Pro Leu Pro Gly Arg Lys Asn Ile Ile Leu Ser Ser Gln
50 55 60

Pro Ser Thr Asp Asp Arg Val Thr Trp Val Lys Ser Val Asp Glu Ala
65 70 75 80

Ile Ala Ala Cys Gly Asp Val Pro Glu Ile Met Val Ile Gly Gly Gly
85 90 95

Arg Val Ile Glu Gln Phe Leu Pro Lys Ala Gln Lys Leu Tyr Leu Thr
100 105 110

His Ile Asp Ala Glu Val Glu Gly Asp Thr His Phe Pro Asp Tyr Glu
115 120 125

Pro Asp Asp Trp Glu Ser Val Phe Ser Glu Phe His Asp Ala Asp Ala
130 135 140

Gln Asn Ser His Ser Tyr Cys Phe Glu Ile Leu Glu Arg Arg
145 150 155

<210> 58
<211> 245
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 58
Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln Met Val Ser Ala Leu Leu
1 5 10 15

Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu Tyr Asp Pro Thr Arg Pro
20 25 30

_SL

Phe Ser Glu Ala Ser Met Met Gly Leu Leu Thr Asn Leu Ala Asp Arg
35 40 45

Glu Leu Val His Met Ile Asn Trp Ala Lys Arg Val Pro Gly Phe Val
50 55 60

Asp Leu Ala Leu His Asp Gln Val His Leu Leu Glu Cys Ala Trp Met
65 70 75 80

Glu Ile Leu Met Ile Gly Leu Val Trp Arg Ser Met Glu His Pro Gly
85 90 95

Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu Asp Arg Asn Gln Gly Lys
100 105 110

Cys Val Glu Gly Gly Val Glu Ile Phe Asp Met Leu Leu Ala Thr Ser
115 120 125

Ser Arg Phe Arg Met Met Asn Leu Gln Gly Glu Glu Phe Val Cys Leu
130 135 140

Lys Ser Ile Ile Leu Leu Asn Ser Gly Val Tyr Thr Phe Leu Ser Ser
145 150 155 160

Thr Leu Lys Ser Leu Glu Glu Lys Asp His Ile His Arg Val Leu Asp
165 170 175

Lys Ile Thr Asp Thr Leu Ile His Leu Met Ala Lys Ala Gly Leu Thr
180 185 190

Leu Gln Gln Gln His Gln Arg Leu Ala Gln Leu Leu Leu Ile Leu Ser
195 200 205

His Ile Arg His Met Ser Ser Lys Arg Met Glu His Leu Tyr Ser Met
210 215 220

Lys Cys Lys Asn Val Val Pro Leu Ser Asp Leu Leu Leu Glu Met Leu
225 230 235 240

Asp Ala His Arg Leu
245

<210> 59

<211> 610

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 59

Met Ala Leu Pro Val Thr Ala Leu Leu Leu^{-SL} Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp
20 25 30

Gly Arg Thr Phe Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr
35 40 45

Gly Met Leu Glu Asp Gly Lys Lys Val Asp Ser Ser Arg Asp Arg Asn
50 55 60

Lys Pro Phe Lys Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp
65 70 75 80

Glu Glu Gly Val Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr
85 90 95

Ile Ser Pro Asp Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile
100 105 110

Pro Pro His Ala Thr Leu Val Phe Asp Val Glu Leu Leu Lys Pro Glu
115 120 125

Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Phe Pro Val Asp Arg Thr Lys
130 135 140

Arg Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro
145 150 155 160

Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys
165 170 175

Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
180 185 190

Ile Tyr His Thr Ser Arg Leu His Ser Gly Ile Pro Ala Arg Phe Ser
195 200 205

Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln
210 215 220

Pro Glu Asp Phe Ala Val Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro
225 230 235 240

Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly
245 250 255

Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gln Val Gln Leu Gln
260 265 270

Glu Ser Gly₂₇₅ Pro Gly Leu Val Lys₂₈₀ Pro Ser^{-SL} Glu Thr Leu₂₈₅ Ser Leu Thr
 Cys Thr₂₉₀ Val Ser Gly Val Ser₂₉₅ Leu Pro Asp Tyr Gly₃₀₀ Val Ser Trp Ile
 Arg₃₀₅ Gln Pro Pro Gly Lys₃₁₀ Gly Leu Glu Trp Ile₃₁₅ Gly Val Ile Trp Gly₃₂₀
 Ser Glu Thr Thr Tyr₃₂₅ Tyr Ser Ser Ser Leu₃₃₀ Lys Ser Arg Val Thr₃₃₅ Ile
 Ser Lys Asp Asn₃₄₀ Ser Lys Asn Gln Val₃₄₅ Ser Leu Lys Leu Ser₃₅₀ Ser Val
 Thr Ala Ala₃₅₅ Asp Thr Ala Val Tyr₃₆₀ Tyr Cys Ala Lys His₃₆₅ Tyr Tyr Tyr
 Gly Gly₃₇₀ Ser Tyr Ala Met Asp₃₇₅ Tyr Trp Gly Gln Gly₃₈₀ Thr Leu Val Thr
 Val₃₈₅ Ser Ser Thr Thr Thr₃₉₀ Pro Ala Pro Arg Pro₃₉₅ Pro Thr Pro Ala Pro₄₀₀
 Thr Ile Ala Ser Gln₄₀₅ Pro Leu Ser Leu Arg₄₁₀ Pro Glu Ala Cys Arg₄₁₅ Pro
 Ala Ala Gly Gly₄₂₀ Ala Val His Thr Arg₄₂₅ Gly Leu Asp Phe Ala₄₃₀ Cys Asp
 Ile Tyr Ile₄₃₅ Trp Ala Pro Leu Ala₄₄₀ Gly Thr Cys Gly Val₄₄₅ Leu Leu Leu
 Ser Leu₄₅₀ Val Ile Thr Leu Tyr₄₅₅ Cys Lys Arg Gly Arg₄₆₀ Lys Lys Leu Leu
 Tyr₄₆₅ Ile Phe Lys Gln Pro Phe Met Arg Pro Val₄₇₅ Gln Thr Thr Gln Glu₄₈₀
 Glu Asp Gly Cys Ser₄₈₅ Cys Arg Phe Pro Glu₄₉₀ Glu Glu Glu Gly Gly₄₉₅ Cys
 Glu Leu Arg Val₅₀₀ Lys Phe Ser Arg Ser₅₀₅ Ala Asp Ala Pro Ala₅₁₀ Tyr Lys
 Gln Gly Gln₅₁₅ Asn Gln Leu Tyr Asn₅₂₀ Glu Leu Asn Leu Gly₅₂₅ Arg Arg Glu
 Glu Tyr₅₃₀ Asp Val Leu Asp Lys₅₃₅ Arg Arg Gly Arg Asp₅₄₀ Pro Glu Met Gly

Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu ^{-SL}Gly Leu Tyr Asn Glu Leu
 545 550 555 560

Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly
 565 570 575

Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser
 580 585 590

Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro
 595 600 605

Pro Arg
 610

<210> 60
 <211> 1830
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 60
 atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60
 cccggagtgc aggtggaaac catctcccca ggagacgggc gcaccttccc caagcgcggc 120
 cagacctgtg tgggtgacta caccgggatg cttgaagatg gaaagaaagt cgattcctcc 180
 cgggacagaa acaagccctt taagtttatg ctaggcaagc aggaggtgat ccgaggctgg 240
 gaagaagggg ttgccagat gagtgtgggt cagagagcca aactgactat atctccagat 300
 tatgcctatg gtgccactgg gcaccaggc atcatccac cacatgccac tctcgtcttc 360
 gatgtggagc ttctaaaacc ggaataccct tatgatgttc ctgattatgc tttcccctg 420
 gatcgtacta aaagagaaat tgtgatgacc cagtcaccgc ccactcttag cctttcaccc 480
 ggtgagcgcg caaccctgtc ttgcagagcc tccaagaca tctcaaaata ccttaattgg 540
 tatcaacaga agcccggaca ggctcctcgc cttctgatct accacaccag ccgggtccat 600
 tctggaatcc ctgccaggtt cagcggtagc ggatctggga ccgactacac cctcactatc 660
 agctcactgc agccagagga cttcgtgtc tatttctgtc agcaagggaa caccctgccc 720
 tacacctttg gacagggcac caagctcgag attaaagggt gaggtggcag cggaggaggt 780
 ggggccggcg gtggaggaag ccaggtccaa ctccaagaaa gcggaccggg tcttgtgaag 840
 ccatcagaaa ctctttcact gacttgtact gtgagcggag tgtctctccc cgattacggg 900
 gtgtcttggg tcagacagcc accggggaag ggtctggaat ggattggagt gatttggggc 960
 tctgagacta ctactactc ttcattccctc aagtcacgcg tcaccatctc aaaggacaac 1020
 tctaagaatc aggtgtcact gaaactgtca tctgtgaccg cagccgacac cgccgtgtac 1080
 tattgcgcta agcattacta ttatggcggg agctacgcaa tggattactg gggacaggg 1140

_SL

actctgggtca ccgtgtccag caccactacc ccagcaccga ggccaccac cccggctcct 1200
accatcgctt cccagcctct gtccctgcgt ccggaggcat gtagaccgc agctgggtggg 1260
gccgtgcata cccgggggtct tgacttcgcc tgcgatatct acatttgggc ccctctggct 1320
gggtacttgcg gggtcctgct gctttcactc gtgatcactc tttactgtaa gcgcgggtcgg 1380
aagaagctgc tgtacatctt taagcaaccc ttcattgaggc ctgtgcagac tactcaagag 1440
gaggacggct gttcatgccg gttcccagag gaggaggaag gcggctgcga actgcgcgtg 1500
aaattcagcc gcagcgcaga tgctccagcc tacaagcagg ggcagaacca gctctacaac 1560
gaactcaatc ttggtcggag agaggagtac gacgtgctgg acaagcggag aggacgggac 1620
ccagaaatgg gcgggaagcc gcgcagaaag aatccccaag agggcctgta caacgagctc 1680
caaaaggata agatggcaga agcctatagc gagattggta tgaaagggga acgcagaaga 1740
ggcaaaggcc acgacggact gtaccaggga ctacgaccg ccaccaagga cacctatgac 1800
gctcttcaca tgcaggccct gccgcctcgg 1830

<210> 61

<211> 610

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 61

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp
20 25 30

Gly Arg Thr Phe Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr
35 40 45

Gly Met Leu Glu Asp Gly Lys Lys Val Asp Ser Ser Arg Asp Arg Asn
50 55 60

Lys Pro Phe Lys Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp
65 70 75 80

Glu Glu Gly Val Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr
85 90 95

Ile Ser Pro Asp Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile
100 105 110

Pro Pro His Ala Thr Leu Val Phe Asp Val Glu Leu Leu Lys Pro Glu
115 120 125

_SL

Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Phe Pro Val Asp Ala Thr Lys
130 135 140

Arg Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro
145 150 155 160

Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys
165 170 175

Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
180 185 190

Ile Tyr His Thr Ser Arg Leu His Ser Gly Ile Pro Ala Arg Phe Ser
195 200 205

Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln
210 215 220

Pro Glu Asp Phe Ala Val Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro
225 230 235 240

Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly
245 250 255

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln
260 265 270

Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr
275 280 285

Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile
290 295 300

Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Val Ile Trp Gly
305 310 315 320

Ser Glu Thr Thr Tyr Tyr Ser Ser Ser Leu Lys Ser Arg Val Thr Ile
325 330 335

Ser Lys Asp Asn Ser Lys Asn Gln Val Ser Leu Lys Leu Ser Ser Val
340 345 350

Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr
355 360 365

Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
370 375 380

Val Ser Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro
385 390 395 400

_SL

Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro
405 410 415

Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp
420 425 430

Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu
435 440 445

Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu
450 455 460

Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu
465 470 475 480

Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys
485 490 495

Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys
500 505 510

Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu
515 520 525

Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly
530 535 540

Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu
545 550 555 560

Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly
565 570 575

Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser
580 585 590

Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro
595 600 605

Pro Arg
610

<210> 62
<211> 1830
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 62

	_SL	
atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg	60	
cccggagtgc aggtggaaac catctcccca ggagacgggc gcaccttccc caagcgcggc	120	
cagacctgtg tggcgcacta caccgggatg cttgaagatg gaaagaaagt cgattcctcc	180	
cgggacagaa acaagccctt taagtttatg ctaggcaagc aggaggtgat ccgaggctgg	240	
gaagaagggg ttgccagat gagtgtgggt cagagagcca aactgactat atctccagat	300	
tatgcctatg gtgccactgg gcaccaggc atcatccac cacatgccac tctcgtcttc	360	
gatgtggagc ttctaaaacc ggaataccct tatgatgttc ctgattatgc tttccccgtg	420	
gatgtacta aaagagaaat tgtgatgacc cagtcacccg ccactcttag cctttcaccc	480	
ggtgagcgcg caaccctgtc ttgcagagcc tccaagaca tctcaaaata ccttaattgg	540	
tatcaacaga agcccggaac ggctcctcgc cttctgatct accacaccag ccggctccat	600	
tctggaatcc ctgccagggt cagcggtagc ggatctggga ccgactacac cctcactatc	660	
agctcactgc agccagagga cttcgtgtc tatttctgtc agcaagggaa caccctgccc	720	
tacacctttg gacagggcac caagctcgag attaaaggtg gaggtggcag cggaggaggt	780	
gggtccggcg gtggaggaag ccaggtccaa ctccaagaaa gcggaccggg tcttgtgaag	840	
ccatcagaaa ctctttcact gacttgtact gtgagcggag tgtctctccc cgattacggg	900	
gtgtcttga tcagacagcc accggggaag ggtctggaat ggattggagt gatttggggc	960	
tctgagacta ctactactc ttcattccctc aagtcacgcg tcaccatctc aaaggacaac	1020	
tctaagaatc aggtgtcact gaaactgtca tctgtgaccg cagccgacac cgccgtgtac	1080	
tattgcgcta agcattacta ttatggcggg agctacgcaa tggattactg gggacaggg	1140	
actctgggtc ccgtgtccag caccactacc ccagcaccga ggccaccac cccggctcct	1200	
accatcgcct cccagcctct gtccctgcgt ccggaggcat gtagaccgc agctgggtggg	1260	
gccgtgcata cccggggtct tgacttcgcc tgcgatatct acatttgggc ccctctggct	1320	
ggtacttgcg gggctctgct gctttcactc gtgatcactc tttactgtaa gcgcggctcgg	1380	
aagaagctgc tgtacatctt taagcaaccc ttcattgaggc ctgtgcagac tactcaagag	1440	
gaggacggct gttcatgccg gttcccagag gaggaggaag gcggctgcga actgcgcgtg	1500	
aaattcagcc gcagcgcaga tgctccagcc tacaagcagg ggcagaacca gctctacaac	1560	
gaactcaatc ttggctcgag agaggagtac gacgtgctgg acaagcggag aggacgggac	1620	
ccagaaatgg gcgggaagcc gcgcagaaag aatccccaag agggcctgta caacgagctc	1680	
caaaaggata agatggcaga agcctatagc gagattggta tgaaagggga acgcagaaga	1740	
ggcaaaggcc acgacggact gtaccaggga ctcagcaccg ccaccaagga cacctatgac	1800	
gctcttcaca tgcaggccct gccgcctcgg	1830	

<210> 63

<211> 661

<212> PRT

<213> Artificial Sequence

_SL

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 63

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Ile Ser Leu Ile Ala Ala Leu Ala Val Asp Tyr
20 25 30

Val Ile Gly Met Glu Asn Ala Met Pro Trp Asn Leu Pro Ala Asp Leu
35 40 45

Ala Trp Phe Lys Arg Asn Thr Leu Asn Lys Pro Val Ile Met Gly Arg
50 55 60

His Thr Trp Glu Ser Ile Gly Arg Pro Leu Pro Gly Arg Lys Asn Ile
65 70 75 80

Ile Leu Ser Ser Gln Pro Ser Thr Asp Asp Arg Val Thr Trp Val Lys
85 90 95

Ser Val Asp Glu Ala Ile Ala Ala Cys Gly Asp Val Pro Glu Ile Met
100 105 110

Val Ile Gly Gly Gly Arg Val Ile Glu Gln Phe Leu Pro Lys Ala Gln
115 120 125

Lys Leu Tyr Leu Thr His Ile Asp Ala Glu Val Glu Gly Asp Thr His
130 135 140

Phe Pro Asp Tyr Glu Pro Asp Asp Trp Glu Ser Val Phe Ser Glu Phe
145 150 155 160

His Asp Ala Asp Ala Gln Asn Ser His Ser Tyr Cys Phe Glu Ile Leu
165 170 175

Glu Arg Arg Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Phe Pro Val Asp
180 185 190

Arg Thr Lys Arg Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser
195 200 205

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Asp
210 215 220

Ile Ser Lys Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
225 230 235 240

Arg Leu Leu Ile Tyr His Thr Ser Arg Leu His Ser Gly Ile Pro Ala
245 250 255

_SL

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser
260 265 270

Ser Leu Gln Pro Glu Asp Phe Ala Val Tyr Phe Cys Gln Gln Gly Asn
275 280 285

Thr Leu Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Gly
290 295 300

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val
305 310 315 320

Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu
325 330 335

Ser Leu Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val
340 345 350

Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Val
355 360 365

Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Ser Ser Ser Leu Lys Ser Arg
370 375 380

Val Thr Ile Ser Lys Asp Asn Ser Lys Asn Gln Val Ser Leu Lys Leu
385 390 395 400

Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Lys His
405 410 415

Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr
420 425 430

Leu Val Thr Val Ser Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr
435 440 445

Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala
450 455 460

Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe
465 470 475 480

Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val
485 490 495

Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys
500 505 510

Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr
515 520 525

_SL

Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu
530 535 540

Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro
545 550 555 560

Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly
565 570 575

Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro
580 585 590

Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr
595 600 605

Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly
610 615 620

Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln
625 630 635 640

Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln
645 650 655

Ala Leu Pro Pro Arg
660

<210> 64
<211> 1983
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 64
atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60
cccatctctc tgattgccgc tctggccgtg gactacgtga tcgggatgga aaacgctatg 120
ccatggaatc tgcccgccga tctggcttgg ttcaagagga acaccctgaa caagccagtg 180
atcatgggca gacacacttg ggagtccatt ggccggcccc tgcctggacg caagaacatc 240
attctgagct cccagccctc taccgacgac aggggtgacat ggggtgaaaag tgtggacgaa 300
gccattgccg cttgcggaga tgtgcccagag atcatggtca tcggcggagg gagagtgatc 360
gagcagttcc tgcctaaggc ccagaaactg tacctgactc acattgacgc tgagggtggaa 420
ggggacaccc attttcctga ttatgagcca gacgattggg aaagcgtgtt ctccgagttt 480
cacgacgccg atgctcagaa ctctcatagt tattgctttg agatcctgga aaggagatac 540
ccttatgatg ttcttgatta tgctttcccc gtggatcgta ctaaaagaga aattgtgatg 600

_SL

accagtcac ccgccactct tagcctttca cccggtgagc gcgcaaccct gtcttgcaga 660
gcctcccaag acatctcaaa ataccttaat tggatatcaac agaagcccgg acaggctcct 720
cgctttctga tctaccacac cagccggctc cattctggaa tccctgccag gttcagcggt 780
agcggatctg ggaccgacta caccctcact atcagctcac tgcagccaga ggacttcgct 840
gtctatttct gtcagcaagg gaacaccctg ccctacacct ttggacaggg caccaagctc 900
gagattaaag gtggaggtgg cagcggagga ggtgggtccg gcggtggagg aagccaggtc 960
caactccaag aaagcggacc gggctcttggt aagccatcag aaactctttc actgacttgt 1020
actgtgagcg gagtgtctct ccccgattac ggggtgtctt ggatcagaca gccaccgggg 1080
aagggctctg aatggattgg agtgatttgg ggctctgaga ctacttacta ctcttcatcc 1140
ctcaagtcac gcgtcacat ctcaaaggac aactctaaga atcaggtgtc actgaaactg 1200
tcctctgtga ccgcagccga caccgccgtg tactattgct ctaagcatta ctattatggc 1260
gggagctacg caatggatta ctggggacag ggtactctgg tcaccgtgtc cagcaccact 1320
acccagcac cgaggccacc caccgccgt cctaccatcg cctcccagcc tctgtccctg 1380
cgtccggagg catgtagacc cgcagctggt ggggccgtgc ataccggggg tcttgacttc 1440
gcctgcgata tctacatttg ggccctctg gctggtactt gcggggtcct gctgctttca 1500
ctcgtgatca ctctttactg taagcgcggt cggaagaagc tgctgtacat ctttaagcaa 1560
cccttcatga ggcctgtgca gactactcaa gaggaggacg gctgttcatg ccggttccca 1620
gaggaggagg aaggcggctg cgaactgctg gtgaaattca gccgcagcgc agatgctcca 1680
gcctacaagc aggggcagaa ccagctctac aacgaactca atcttggtcg gagagaggag 1740
tacgacgtgc tggacaagcg gagaggacgg gaccagaaa tgggcgggaa gccgcgcaga 1800
aagaatcccc aagagggcct gtacaacgag ctccaaaagg ataagatggc agaagcctat 1860
agcgagattg gtatgaaagg ggaacgcaga agaggcaaag gccacgacgg actgtaccag 1920
ggactcagca ccgccacaa ggacacctat gacgctcttc acatgcaggc cctgccgcct 1980
cgg 1983

<210> 65

<211> 661

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 65

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Ile Ser Leu Ile Ala Ala Leu Ala Val Asp Tyr
20 25 30

_SL

Val Ile Gly Met Glu Asn Ala Met Pro Trp Asn Leu Pro Ala Asp Leu
35 40 45

Ala Trp Phe Lys Arg Asn Thr Leu Asn Lys Pro Val Ile Met Gly Arg
50 55 60

His Thr Trp Glu Ser Ile Gly Arg Pro Leu Pro Gly Arg Lys Asn Ile
65 70 75 80

Ile Leu Ser Ser Gln Pro Ser Thr Asp Asp Arg Val Thr Trp Val Lys
85 90 95

Ser Val Asp Glu Ala Ile Ala Ala Cys Gly Asp Val Pro Glu Ile Met
100 105 110

Val Ile Gly Gly Gly Arg Val Ile Glu Gln Phe Leu Pro Lys Ala Gln
115 120 125

Lys Leu Tyr Leu Thr His Ile Asp Ala Glu Val Glu Gly Asp Thr His
130 135 140

Phe Pro Asp Tyr Glu Pro Asp Asp Trp Glu Ser Val Phe Ser Glu Phe
145 150 155 160

His Asp Ala Asp Ala Gln Asn Ser His Ser Tyr Cys Phe Glu Ile Leu
165 170 175

Glu Arg Arg Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Phe Pro Val Asp
180 185 190

Ala Thr Lys Arg Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser
195 200 205

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Asp
210 215 220

Ile Ser Lys Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
225 230 235 240

Arg Leu Leu Ile Tyr His Thr Ser Arg Leu His Ser Gly Ile Pro Ala
245 250 255

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser
260 265 270

Ser Leu Gln Pro Glu Asp Phe Ala Val Tyr Phe Cys Gln Gln Gly Asn
275 280 285

Thr Leu Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Gly
290 295 300

_SL

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val
305 310 315 320

Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu
325 330 335

Ser Leu Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val
340 345 350

Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Val
355 360 365

Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Ser Ser Ser Leu Lys Ser Arg
370 375 380

Val Thr Ile Ser Lys Asp Asn Ser Lys Asn Gln Val Ser Leu Lys Leu
385 390 395 400

Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Lys His
405 410 415

Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr
420 425 430

Leu Val Thr Val Ser Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr
435 440 445

Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala
450 455 460

Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe
465 470 475 480

Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val
485 490 495

Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys
500 505 510

Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr
515 520 525

Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu
530 535 540

Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro
545 550 555 560

Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly
565 570 575

_SL

Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro
580 585 590

Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr
595 600 605

Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly
610 615 620

Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln
625 630 635 640

Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln
645 650 655

Ala Leu Pro Pro Arg
660

<210> 66
<211> 1983
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 66
atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60
cccatctctc tgattgccgc tctggccgtg gactacgtga tcgggatgga aaacgctatg 120
ccatggaatc tgcccgccga tctggcttgg ttcaagagga acaccctgaa caagccagtg 180
atcatgggca gacacacttg ggagtccatt ggccggcccc tgccctggacg caagaacatc 240
attctgagct cccagccctc taccgacgac aggggtgacat ggggtgaaaag tgtggacgaa 300
gccattgccg cttgcggaga tgtgcccag atcatggtca tcggcgaggagg gagagtgatc 360
gagcagttcc tgcctaaggc ccagaaactg tacctgactc acattgacgc tgaggtggaa 420
ggggacaccc attttcctga ttatgagcca gacgattggg aaagcgtgtt ctccgagttt 480
cacgacgccg atgctcagaa ctctcatagt tattgctttg agatcctgga aaggagatac 540
ccttatgatg ttcctgatta tgctttcccc gtggatgcta ctaaaagaga aattgtgatg 600
accagtcac ccgccactct tagcctttca cccggtgagc gcgcaaccct gtcttgacaga 660
gcctcccaag acatctcaaa ataccttaat tggatatcaac agaagcccgg acaggctcct 720
cgccttctga tctaccacac cagccggctc cattctggaa tccctgccag gttcagcggg 780
agcggatctg ggaccgacta caccctcact atcagctcac tgcagccaga ggacttcgct 840
gtctatttct gtcagcaagg gaacaccctg ccctacacct ttggacaggg caccaagctc 900
gagattaaag gtggaggtgg cagcggagga ggtgggtccg gcggtggagg aagccaggtc 960

_SL

caactccaag aaagcggacc gggctcttgtg aagccatcag aaactctttc actgacttgt	1020
actgtgagcg gagtgtctct ccccgattac ggggtgtctt ggatcagaca gccaccgggg	1080
aagggctctgg aatggattgg agtgatttgg ggctctgaga ctacttacta ctcttcatcc	1140
ctcaagtcac gcgtcaccat ctcaaaggac aactctaaga atcaggtgtc actgaaactg	1200
tcatctgtga ccgcagccga caccgccgtg tactattgcg ctaagcatta ctattatggc	1260
gggagctacg caatggatta ctggggacag ggtactctgg tcaccgtgtc cagcaccact	1320
accccgacac cgaggccacc caccgggct cctaccatcg cctcccagcc tctgtccctg	1380
cgtccggagg catgtagacc cgcagctggg ggggccgtgc ataccggggg tcttgacttc	1440
gcctgcgata tctacatttg ggcccctctg gctggtactt gcggggtcct gctgctttca	1500
ctcgtgatca ctctttactg taagcgcggg cggaagaagc tgctgtacat ctttaagcaa	1560
cccttcatga ggctgtgca gactactcaa gaggaggacg gctgttcatg ccggttccca	1620
gaggaggagg aaggcggctg cgaactgcmc gtgaaattca gccgcagcmc agatgctcca	1680
gcctacaagc aggggcagaa ccagctctac aacgaactca atcttggtcg gagagaggag	1740
tacgacgtgc tggacaagcg gagaggacgg gaccagaaa tgggcgggaa gccgcgcaga	1800
aagaatcccc aagaggcct gtacaacgag ctccaaaagg ataagatggc agaagcctat	1860
agcgagattg gtatgaaagg ggaacgcaga agaggcaaag gccacgacgg actgtaccag	1920
ggactcagca ccgccaccaa ggacacctat gacgctcttc acatgcaggc cctgccgcct	1980
cgg	1983

<210> 67
 <211> 750
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 67
 Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
 1 5 10 15

His Ala Ala Arg Pro Arg Ser Ser Leu Ala Leu Ser Leu Thr Ala Asp
 20 25 30

Gln Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser
 35 40 45

Glu Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu
 50 55 60

Leu Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala
 65 70 75 80

Lys Arg Val Pro Gly Phe Val Asp Leu Ala^{-SL} Leu His Asp Gln Val His
 85 90 95
 Leu Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp
 100 105 110
 Arg Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu
 115 120 125
 Leu Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe
 130 135 140
 Asp Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln
 145 150 155 160
 Gly Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly
 165 170 175
 Val Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp
 180 185 190
 His Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu
 195 200 205
 Met Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala
 210 215 220
 Gln Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Ser Lys Arg
 225 230 235 240
 Met Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Ser
 245 250 255
 Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu Tyr Pro Tyr Asp
 260 265 270
 Val Pro Asp Tyr Ala Phe Pro Val Asp Arg Thr Lys Arg Glu Ile Val
 275 280 285
 Met Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala
 290 295 300
 Thr Leu Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr Leu Asn Trp
 305 310 315 320
 Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr His Thr
 325 330 335
 Ser Arg Leu His Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser
 340 345 350

Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser ^{-SL} Leu Gln Pro Glu Asp Phe
 355 360 365
 Ala Val Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr Phe Gly
 370 375 380
 Gln Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Ser Gly Gly Gly
 385 390 395 400
 Gly Ser Gly Gly Gly Ser Gln Val Gln Leu Gln Glu Ser Gly Pro
 405 410 415
 Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser
 420 425 430
 Gly Val Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln Pro Pro
 435 440 445
 Gly Lys Gly Leu Glu Trp Ile Gly Val Ile Trp Gly Ser Glu Thr Thr
 450 455 460
 Tyr Tyr Ser Ser Ser Leu Lys Ser Arg Val Thr Ile Ser Lys Asp Asn
 465 470 475 480
 Ser Lys Asn Gln Val Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp
 485 490 495
 Thr Ala Val Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly Ser Tyr
 500 505 510
 Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Thr
 515 520 525
 Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser
 530 535 540
 Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly
 545 550 555 560
 Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp
 565 570 575
 Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile
 580 585 590
 Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys
 595 600 605
 Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys
 610 615 620

Ser Cys Arg Phe Pro Glu Glu Glu Gly^{-SL} Gly Cys Glu Leu Arg Val
 625 630 635 640
 Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn
 645 650 655
 Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val
 660 665 670
 Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg
 675 680 685
 Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys
 690 695 700
 Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg
 705 710 715 720
 Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys
 725 730 735
 Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
 740 745 750

<210> 68

<211> 2250

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 68

atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg	60
ccccggtcgt cgttggcact ttccctgact gccgaccaga tgggtgtccgc ctttctggac	120
gccgagcctc caattctgta ctcggagtac gatccgactc gcccgttctc cgaagccagc	180
atgatggggc tgttgactaa cctggcggac cgcgagttgg tgcacatgat taactgggct	240
aagcgggtgc cgggcttcgt ggacctggcc ctgcacgacc aagtgcacct cctggaatgc	300
gcctggatgg aaatcctcat gatcggcctc gtgtggagat ccatggagca tcccggaaag	360
ctcctgtttg cacccaacct cctgcttgat cgcaaccagg gaaaatgcgt ggaaggggggt	420
gtcgagattt tcgacatgct gctcgccacc tcttcccgggt tccggatgat gaatctgcag	480
ggagaagagt tcgtgtgtct gaagtcaatc atcctgctga actccgggggt ctataccttc	540
ctgagctcga ccctcaagtc actggaggaa aaagaccaca tccatcgcgt gctcgataag	600
atcaccgaca cccttatcca tctcatggcg aaggctggac tgaccctgca acagcagcac	660
cagaggctgg cccagttgct gctgattctg agccacatcc ggcacatgtc gtccaagagg	720
atggaacacc tgtacagcat gaagtgaag aacgtcgtgc ctctgtccga tctgtcctg	780

_SL

gaaatgctgg acgcgcacag actctaccct tatgatgttc ctgattatgc tttccccgtg 840
gatcgtacta aaagagaaat tgtgatgacc cagtcacccg ccactcttag cttttcaccc 900
ggtgagcgcg caaccctgtc ttgcagagcc tccaagaca tctcaaaata ctttaattgg 960
tatcaacaga agcccggaag ggctcctcgc cttctgatct accacaccag cgggtccat 1020
tctggaatcc ctgccaggtt cagcggtagc ggatctggga cggactacac cctcactatc 1080
agctcactgc agccagagga cttcgctgtc tatttctgtc agcaagggaa caccctgccc 1140
tacacctttg gacagggcac caagctcgag attaaaggtg gaggtggcag cggaggaggt 1200
gggtccggcg gtggaggaag ccaggtccaa ctccaagaaa gcggaaccggg tcttgtgaag 1260
ccatcagaaa ctctttcact gacttgtact gtgagcggag tgtctctccc cgattacggg 1320
gtgtcttga tcagacagcc accggggaag ggtctggaat ggattggagt gatttggggc 1380
tctgagacta ctactactc ttcatccctc aagtcacgcy tcaccatctc aaaggacaac 1440
tctaagaatc aggtgtcact gaaactgtca tctgtgaccg cagccgacac cgccgtgtac 1500
tattgcgcta agcattacta ttatggcggg agctacgcaa tggattactg gggacaggg 1560
actctgggtc ccgtgtccag caccactacc ccagcaccga ggccaccac cccggctcct 1620
accatcgctt cccagcctct gtccctgctt ccggaggcat gtagaccgc agctgggtgg 1680
gccgtgcata cccgggggtt tgacttcgcc tgcgatatct acatttgggc ccctctggct 1740
ggtacttgcg gggtcctgct gctttcactc gtgatcactc tttactgtaa gcgcggctcg 1800
aagaagctgc tgtacatctt taagcaacc ttcatgaggc ctgtgcagac tactcaagag 1860
gaggacggct gttcatgccg gttcccagag gaggaggaag gcggctgcga actgcgcgtg 1920
aaattcagcc gcagcgcaga tgctccagcc tacaagcagg ggcagaacca gctctacaac 1980
gaactcaatc ttggtcggag agaggagtac gacgtgctgg acaagcggag aggacgggac 2040
ccagaaatgg gcgggaagcc gcgcagaaag aatccccaag agggcctgta caacgagctc 2100
caaaaggata agatggcaga agcctatagc gagattggta tgaaagggga acgcagaaga 2160
ggcaaaggcc acgacggact gtaccagga ctcagcaccg ccaccaagga cacctatgac 2220
gctcttcaca tgcaggccct gccgcctcgg 2250

<210> 69

<211> 750

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 69

Met Ala Leu Pro Val Thr Ala Leu Leu Pro Leu Ala Leu Leu
1 5 10 15

His Ala Ala Arg Pro Arg Ser Ser Leu Ala Leu Ser Leu Thr Ala Asp

_SL															
20				25				30							
Gln	Met	Val 35	Ser	Ala	Leu	Leu	Asp 40	Ala	Glu	Pro	Pro	Ile 45	Leu	Tyr	Ser
Glu	Tyr 50	Asp	Pro	Thr	Arg	Pro 55	Phe	Ser	Glu	Ala	Ser 60	Met	Met	Gly	Leu
Leu 65	Thr	Asn	Leu	Ala	Asp 70	Arg	Glu	Leu	Val	His 75	Met	Ile	Asn	Trp	Ala 80
Lys	Arg	Val	Pro	Gly 85	Phe	Val	Asp	Leu	Ala 90	Leu	His	Asp	Gln	Val 95	His
Leu	Leu	Glu	Cys 100	Ala	Trp	Met	Glu	Ile 105	Leu	Met	Ile	Gly	Leu 110	Val	Trp
Arg	Ser	Met 115	Glu	His	Pro	Gly	Lys 120	Leu	Leu	Phe	Ala	Pro 125	Asn	Leu	Leu
Leu	Asp 130	Arg	Asn	Gln	Gly	Lys 135	Cys	Val	Glu	Gly	Gly 140	Val	Glu	Ile	Phe
Asp 145	Met	Leu	Leu	Ala	Thr 150	Ser	Ser	Arg	Phe	Arg 155	Met	Met	Asn	Leu	Gln 160
Gly	Glu	Glu	Phe	Val 165	Cys	Leu	Lys	Ser	Ile 170	Ile	Leu	Leu	Asn	Ser 175	Gly
Val	Tyr	Thr	Phe 180	Leu	Ser	Ser	Thr	Leu 185	Lys	Ser	Leu	Glu	Glu 190	Lys	Asp
His	Ile	His 195	Arg	Val	Leu	Asp	Lys 200	Ile	Thr	Asp	Thr	Leu 205	Ile	His	Leu
Met	Ala 210	Lys	Ala	Gly	Leu	Thr 215	Leu	Gln	Gln	Gln	His 220	Gln	Arg	Leu	Ala
Gln 225	Leu	Leu	Leu	Ile	Leu 230	Ser	His	Ile	Arg	His 235	Met	Ser	Ser	Lys	Arg 240
Met	Glu	His	Leu	Tyr 245	Ser	Met	Lys	Cys	Lys 250	Asn	Val	Val	Pro	Leu 255	Ser
Asp	Leu	Leu	Leu 260	Glu	Met	Leu	Asp	Ala 265	His	Arg	Leu	Tyr	Pro 270	Tyr	Asp
Val	Pro	Asp 275	Tyr	Ala	Phe	Pro	Val 280	Asp	Ala	Thr	Lys	Arg 285	Glu	Ile	Val
Met	Thr	Gln	Ser	Pro	Ala	Thr	Leu	Ser	Leu	Ser	Pro	Gly	Glu	Arg	Ala

_SL

290		295		300											
Thr 305	Leu	Ser	Cys	Arg	Ala 310	Ser	Gln	Asp	Ile	Ser 315	Lys	Tyr	Leu	Asn	Trp 320
Tyr	Gln	Gln	Lys	Pro 325	Gly	Gln	Ala	Pro	Arg 330	Leu	Leu	Ile	Tyr	His 335	Thr
Ser	Arg	Leu	His 340	Ser	Gly	Ile	Pro	Ala 345	Arg	Phe	Ser	Gly	Ser 350	Gly	Ser
Gly	Thr	Asp 355	Tyr	Thr	Leu	Thr	Ile 360	Ser	Ser	Leu	Gln	Pro 365	Glu	Asp	Phe
Ala	Val 370	Tyr	Phe	Cys	Gln	Gln 375	Gly	Asn	Thr	Leu	Pro 380	Tyr	Thr	Phe	Gly
Gln 385	Gly	Thr	Lys	Leu	Glu 390	Ile	Lys	Gly	Gly	Gly 395	Gly	Ser	Gly	Gly	Gly 400
Gly	Ser	Gly	Gly	Gly 405	Gly	Ser	Gln	Val	Gln 410	Leu	Gln	Glu	Ser	Gly 415	Pro
Gly	Leu	Val	Lys 420	Pro	Ser	Glu	Thr	Leu 425	Ser	Leu	Thr	Cys	Thr 430	Val	Ser
Gly	Val	Ser 435	Leu	Pro	Asp	Tyr	Gly 440	Val	Ser	Trp	Ile	Arg 445	Gln	Pro	Pro
Gly	Lys 450	Gly	Leu	Glu	Trp	Ile 455	Gly	Val	Ile	Trp	Gly 460	Ser	Glu	Thr	Thr
Tyr 465	Tyr	Ser	Ser	Ser	Leu 470	Lys	Ser	Arg	Val	Thr 475	Ile	Ser	Lys	Asp	Asn 480
Ser	Lys	Asn	Gln	Val 485	Ser	Leu	Lys	Leu	Ser 490	Ser	Val	Thr	Ala	Ala 495	Asp
Thr	Ala	Val	Tyr 500	Tyr	Cys	Ala	Lys	His 505	Tyr	Tyr	Tyr	Gly	Gly 510	Ser	Tyr
Ala	Met	Asp 515	Tyr	Trp	Gly	Gln	Gly 520	Thr	Leu	Val	Thr	Val 525	Ser	Ser	Thr
Thr 530	Thr	Pro	Ala	Pro	Arg	Pro 535	Pro	Thr	Pro	Ala	Pro 540	Thr	Ile	Ala	Ser
Gln 545	Pro	Leu	Ser	Leu	Arg 550	Pro	Glu	Ala	Cys	Arg 555	Pro	Ala	Ala	Gly	Gly 560
Ala	Val	His	Thr	Arg	Gly	Leu	Asp	Phe	Ala	Cys	Asp	Ile	Tyr	Ile	Trp

565 570^{-SL} 575

Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile
 580 585 590

Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys
 595 600 605

Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys
 610 615 620

Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val
 625 630 635 640

Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn
 645 650 655

Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val
 660 665 670

Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg
 675 680 685

Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys
 690 695 700

Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg
 705 710 715 720

Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys
 725 730 735

Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
 740 745 750

<210> 70

<211> 2250

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 70

atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg	60
ccccggtcgt cgttggcact ttccctgact gccgaccaga tgggtgtccgc ccttctggac	120
gccgagcctc caattctgta ctcggagtac gatccgactc gcccgttctc cgaagccagc	180
atgatggggc tgttgactaa cctggcggac cgcgagttgg tgcacatgat taactgggct	240
aagcgggtgc cgggcttcgt ggacctggcc ctgcacgacc aagtgcacct cctggaatgc	300

						_SL	
gcctggatgg	aaatcctcat	gatcggcctc	gtgtggagat	ccatggagca	tcccggaaag		360
ctcctgtttg	caccaacct	cctgcttgat	cgcaaccagg	gaaaatgcgt	ggaagggggt		420
gtcgagattt	tcgacatgct	gctcgccacc	tcttcccgtt	tccggatgat	gaatctgcag		480
ggagaagagt	tcgtgtgtct	gaagtcaatc	atcctgctga	actccggggt	ctataccttc		540
ctgagctcga	ccctcaagtc	actggaggaa	aaagaccaca	tccatcgcgt	gctcgataag		600
atcaccgaca	cccttatcca	tctcatggcg	aaggctggac	tgaccctgca	acagcagcac		660
cagaggctgg	cccagttgct	gctgattctg	agccacatcc	ggcacatgtc	gtccaagagg		720
atggaacacc	tgtacagcat	gaagtgcaag	aacgtcgtgc	ctctgtccga	tctgctcctg		780
gaaatgctgg	acgcgcacag	actctaccct	tatgatgttc	ctgattatgc	tttcccctgt		840
gatgctacta	aaagagaaat	tgtgatgacc	cagtcacccg	ccactcttag	cctttcaccc		900
ggtgagcgcg	caaccctgtc	ttgcagagcc	tccaagaca	tctcaaaata	ccttaattgg		960
tatcaacaga	agcccggaca	ggctcctcgc	cttctgatct	accacaccag	ccggctccat		1020
tctggaatcc	ctgccaggtt	cagcggtagc	ggatctggga	ccgactacac	cctcactatc		1080
agctcactgc	agccagagga	cttcgctgtc	tatttctgtc	agcaagggaa	caccctgccc		1140
tacacctttg	gacagggcac	caagctcgag	attaaaggtg	gaggtggcag	cggaggaggt		1200
gggtccggcg	gtggaggaag	ccaggtccaa	ctccaagaaa	gcggaaccgg	tcttgtgaag		1260
ccatcagaaa	ctctttcact	gacttgtact	gtgagcggag	tgtctctccc	cgattacggg		1320
gtgtcttggg	tcagacagcc	accggggaag	ggtctggaat	ggattggagt	gatttggggc		1380
tctgagacta	cttactactc	ttcatccctc	aagtcacgcg	tcaccatctc	aaaggacaac		1440
tctaagaatc	aggtgtcact	gaaactgtca	tctgtgaccg	cagccgacac	cgccgtgtac		1500
tattgcgcta	agcattacta	ttatggcggg	agctacgcaa	tggattactg	gggacagggg		1560
actctgggtc	ccgtgtccag	caccactacc	ccagcaccga	ggccaccac	cccggctcct		1620
accatcgcct	cccagcctct	gtccctgcgt	ccggaggcat	gtagaccgcg	agctgggtgg		1680
gccgtgcata	cccgggggtct	tgacttcgcc	tgcgatatct	acatttgggc	ccctctgggt		1740
ggtacttgcg	gggtcctgct	gctttcactc	gtgatcactc	tttactgtaa	gcgcggctcg		1800
aagaagctgc	tgtacatctt	taagcaaccc	ttcatgaggc	ctgtgcagac	tactcaagag		1860
gaggacggct	gttcatgccg	gttcccagag	gaggaggaag	gcggtctgca	actgcgcgtg		1920
aaattcagcc	gcagcgcaga	tgctccagcc	tacaagcagg	ggcagaacca	gctctacaac		1980
gaactcaatc	ttggtcggag	agaggagtac	gacgtgctgg	acaagcggag	aggacgggac		2040
ccagaaatgg	gcgggaagcc	gcgcagaaa	aatccccaag	agggcctgta	caacgagctc		2100
caaaaggata	agatggcaga	agcctatagc	gagattggta	tgaaagggga	acgcagaaga		2160
ggcaaaggcc	acgacggact	gtaccaggga	ctcagcaccg	ccaccaagga	cacctatgac		2220
gctcttcaca	tgcaggccct	gccgcctcgg					2250

_SL

<211> 606

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 71

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp
20 25 30

Gly Arg Thr Phe Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr
35 40 45

Gly Met Leu Glu Asp Gly Lys Lys Val Asp Ser Ser Arg Asp Arg Asn
50 55 60

Lys Pro Phe Lys Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp
65 70 75 80

Glu Glu Gly Val Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr
85 90 95

Ile Ser Pro Asp Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile
100 105 110

Pro Pro His Ala Thr Leu Val Phe Asp Val Glu Leu Leu Lys Pro Glu
115 120 125

Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Phe Pro Val Asp Glu Ile Val
130 135 140

Met Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala
145 150 155 160

Thr Leu Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr Leu Asn Trp
165 170 175

Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr His Thr
180 185 190

Ser Arg Leu His Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser
195 200 205

Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe
210 215 220

Ala Val Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr Phe Gly
225 230 235 240

_SL

Gln Gly Thr Lys Leu₂₄₅ Glu Ile Lys Gly Gly₂₅₀ Gly Gly Ser Gly Gly₂₅₅ Gly
Gly Ser Gly Gly₂₆₀ Gly Gly Ser Gln Val₂₆₅ Gln Leu Gln Glu Ser₂₇₀ Gly Pro
Gly Leu Val₂₇₅ Lys Pro Ser Glu Thr₂₈₀ Leu Ser Leu Thr Cys₂₈₅ Thr Val Ser
Gly Val₂₉₀ Ser Leu Pro Asp Tyr₂₉₅ Gly Val Ser Trp Ile₃₀₀ Arg Gln Pro Pro
Gly₃₀₅ Lys Gly Leu Glu Trp₃₁₀ Ile Gly Val Ile Trp₃₁₅ Gly Ser Glu Thr Thr₃₂₀
Tyr Tyr Ser Ser Ser₃₂₅ Leu Lys Ser Arg Val₃₃₀ Thr Ile Ser Lys Asp₃₃₅ Asn
Ser Lys Asn Gln₃₄₀ Val Ser Leu Lys Leu₃₄₅ Ser Ser Val Thr Ala₃₅₀ Ala Asp
Thr Ala Val₃₅₅ Tyr Tyr Cys Ala Lys₃₆₀ His Tyr Tyr Tyr Gly₃₆₅ Gly Ser Tyr
Ala Met₃₇₀ Asp Tyr Trp Gly Gln₃₇₅ Gly Thr Leu Val Thr₃₈₀ Val Ser Ser Thr
Thr₃₈₅ Thr Pro Ala Pro Arg₃₉₀ Pro Pro Thr Pro Ala₃₉₅ Pro Thr Ile Ala Ser₄₀₀
Gln Pro Leu Ser Leu₄₀₅ Arg Pro Glu Ala Cys₄₁₀ Arg Pro Ala Ala Gly₄₁₅ Gly
Ala Val His Thr₄₂₀ Arg Gly Leu Asp Phe₄₂₅ Ala Cys Asp Ile Tyr₄₃₀ Ile Trp
Ala Pro Leu₄₃₅ Ala Gly Thr Cys Gly₄₄₀ Val Leu Leu Leu Ser₄₄₅ Leu Val Ile
Thr Leu₄₅₀ Tyr Cys Lys Arg Gly₄₅₅ Arg Lys Lys Leu Leu₄₆₀ Tyr Ile Phe Lys
Gln₄₆₅ Pro Phe Met Arg Pro₄₇₀ Val Gln Thr Thr Gln₄₇₅ Glu Glu Asp Gly Cys₄₈₀
Ser Cys Arg Phe Pro₄₈₅ Glu Glu Glu Glu Gly₄₉₀ Gly Cys Glu Leu Arg₄₉₅ Val
Lys Phe Ser Arg₅₀₀ Ser Ala Asp Ala Pro₅₀₅ Ala Tyr Lys Gln Gly₅₁₀ Gln Asn

_SL

Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val
515 520 525

Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg
530 535 540

Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys
545 550 555 560

Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg
565 570 575

Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys
580 585 590

Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
595 600 605

<210> 72

<211> 1818

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 72

atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60

cccggagtgc aggtggaaac catctcccca ggagacgggc gcaccttccc caagcgcggc 120

cagacctgtg tgggtgacta caccgggatg cttgaagatg gaaagaaagt cgattcctcc 180

cgggacagaa acaagccctt taagtttatg ctaggcaagc aggaggtgat ccgaggctgg 240

gaagaagggg ttgccagat gagtgtgggt cagagagcca aactgactat atctccagat 300

tatgcctatg gtgccactgg gcaccaggc atcatccac cacatgccac tctcgtcttc 360

gatgtggagc ttctaaaacc ggaataccct tatgatgttc ctgattatgc tttccccgtg 420

gatgaaattg tgatgacca gtcacccgcc actcttagcc tttcaccggg tgagcgcgca 480

accctgtctt gcagagcctc ccaagacatc tcaaaatacc ttaattggta tcaacagaag 540

cccggacagg ctctctgcct tctgatctac cacaccagcc ggctccattc tggaatccct 600

gccaggttca gcggtagcgg atctgggacc gactacaccc tcactatcag ctactgcag 660

ccagaggact tcgctgtcta tttctgtcag caaggaaca ccctgcccta cacctttgga 720

cagggcacca agctcgagat taaaggtgga ggtggcagcg gaggaggtgg gtccggcggt 780

ggaggaagcc aggtccaact ccaagaaagc ggaccgggtc ttgtgaagcc atcagaaact 840

ctttcactga cttgtactgt gagcggagtg tctctccccg attacggggt gtcttggatc 900

agacagccac cggggaaggg tctggaatgg attggagtga tttggggctc tgagactact 960

_SL

tactactctt catccctcaa gtcacgcgtc accatctcaa aggacaactc taagaatcag 1020
gtgtcactga aactgtcatc tgtgaccgca gccgacaccg ccgtgtacta ttgcgctaag 1080
cattactatt atggcgggag ctacgcaatg gattactggg gacagggtac tctggtcacc 1140
gtgtccagca ccactacccc agcaccgagg ccacccaccc cggctcctac catcgcctcc 1200
cagcctctgt ccctgcgtcc ggaggcatgt agaccgcgag ctgggtggggc cgtgcatacc 1260
cggggtcttg acttcgcctg cgatatctac atttggggccc ctctggctgg tacttgcggg 1320
gtcctgctgc tttcactcgt gatcactctt tactgtaagc gcggtcggaa gaagctgctg 1380
tacatcttta agcaaccctt catgaggcct gtgcagacta ctcaagagga ggacggctgt 1440
tcatgccggt tcccagagga ggaggaaggc ggctgcgaac tgcgcgtgaa attcagccgc 1500
agcgcagatg ctccagccta caagcagggg cagaaccagc tctacaacga actcaatctt 1560
ggtcggagag aggagtacga cgtgctggac aagcggagag gacgggaccc agaaatgggc 1620
gggaagccgc gcagaaagaa tccccaagag ggcctgtaca acgagctcca aaaggataag 1680
atggcagaag cctatagcga gattggtatg aaaggggaac gcagaagagg caaaggccac 1740
gacggactgt accagggact cagcaccgcc accaaggaca cctatgacgc tcttcacatg 1800
caggccctgc cgcctcgg 1818

<210> 73

<211> 746

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 73

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Arg Ser Ser Leu Ala Leu Ser Leu Thr Ala Asp
20 25 30

Gln Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser
35 40 45

Glu Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu
50 55 60

Leu Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala
65 70 75 80

Lys Arg Val Pro Gly Phe Val Asp Leu Ala Leu His Asp Gln Val His
85 90 95

Leu Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp

_SL

100	105	110
Arg Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu	115	120
Leu Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe	130	140
Asp Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln	145	155
Gly Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly	165	175
Val Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp	180	185
His Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu	195	205
Met Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala	210	215
Gln Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Ser Lys Arg	225	235
Met Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Ser	245	255
Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu Tyr Pro Tyr Asp	260	265
Val Pro Asp Tyr Ala Phe Pro Val Asp Glu Ile Val Met Thr Gln Ser	275	285
Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys	290	295
Arg Ala Ser Gln Asp Ile Ser Lys Tyr Leu Asn Trp Tyr Gln Gln Lys	305	315
Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr His Thr Ser Arg Leu His	325	335
Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr	340	345
Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Val Tyr Phe	355	365
Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gln Gly Thr Lys		

370					375					_SL		380				
Leu 385	Glu	Ile	Lys	Gly	Gly 390	Gly	Gly	Ser	Gly	Gly 395	Gly	Gly	Ser	Gly	Gly 400	
Gly	Gly	Ser	Gln	Val 405	Gln	Leu	Gln	Glu	Ser 410	Gly	Pro	Gly	Leu	Val 415	Lys	
Pro	Ser	Glu	Thr 420	Leu	Ser	Leu	Thr	Cys 425	Thr	Val	Ser	Gly	Val 430	Ser	Leu	
Pro	Asp	Tyr 435	Gly	Val	Ser	Trp	Ile 440	Arg	Gln	Pro	Pro	Gly 445	Lys	Gly	Leu	
Glu	Trp 450	Ile	Gly	Val	Ile	Trp 455	Gly	Ser	Glu	Thr	Thr 460	Tyr	Tyr	Ser	Ser	
Ser 465	Leu	Lys	Ser	Arg	Val 470	Thr	Ile	Ser	Lys	Asp 475	Asn	Ser	Lys	Asn	Gln 480	
Val	Ser	Leu	Lys	Leu 485	Ser	Ser	Val	Thr	Ala 490	Ala	Asp	Thr	Ala	Val 495	Tyr	
Tyr	Cys	Ala	Lys 500	His	Tyr	Tyr	Tyr	Gly 505	Gly	Ser	Tyr	Ala	Met 510	Asp	Tyr	
Trp	Gly	Gln 515	Gly	Thr	Leu	Val	Thr 520	Val	Ser	Ser	Thr	Thr 525	Thr	Pro	Ala	
Pro	Arg 530	Pro	Pro	Thr	Pro	Ala 535	Pro	Thr	Ile	Ala	Ser 540	Gln	Pro	Leu	Ser	
Leu 545	Arg	Pro	Glu	Ala	Cys 550	Arg	Pro	Ala	Ala	Gly 555	Gly	Ala	Val	His	Thr 560	
Arg	Gly	Leu	Asp	Phe 565	Ala	Cys	Asp	Ile	Tyr 570	Ile	Trp	Ala	Pro	Leu 575	Ala	
Gly	Thr	Cys	Gly 580	Val	Leu	Leu	Leu	Ser 585	Leu	Val	Ile	Thr	Leu 590	Tyr	Cys	
Lys	Arg	Gly 595	Arg	Lys	Lys	Leu	Leu 600	Tyr	Ile	Phe	Lys	Gln 605	Pro	Phe	Met	
Arg	Pro 610	Val	Gln	Thr	Thr	Gln 615	Glu	Glu	Asp	Gly	Cys 620	Ser	Cys	Arg	Phe	
Pro 625	Glu	Glu	Glu	Glu	Gly 630	Gly	Cys	Glu	Leu	Arg 635	Val	Lys	Phe	Ser	Arg 640	
Ser	Ala	Asp	Ala	Pro	Ala	Tyr	Lys	Gln	Gly	Gln	Asn	Gln	Leu	Tyr	Asn	

_SL

645	650	655
Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg	660	665
Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro	675	685
Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala	690	700
Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His	705	715
Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp	725	735
Ala Leu His Met Gln Ala Leu Pro Pro Arg	740	745

<210> 74

<211> 2238

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 74

atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgtcca cgccgctcgg	60
ccccggtcgt cgttggcact ttccctgact gccgaccaga tgggtgtccgc ctttctggac	120
gccgagcctc caattctgta ctcggagtac gatccgactc gcccgttctc cgaagccagc	180
atgatggggc tgttgactaa cctggcggac cgcgagttgg tgcacatgat taactgggct	240
aagcgggtgc cgggcttcgt ggacctggcc ctgcacgacc aagtgcacct cctggaatgc	300
gcctggatgg aaatcctcat gatcggcctc gtgtggagat ccatggagca tcccggaaag	360
ctcctgtttg cacccaacct cctgcttgat cgcaaccagg gaaaatgcgt ggaaggggggt	420
gtcgagattt tcgacatgct gctcgccacc tcttcccggg tccggatgat gaatctgcag	480
ggagaagagt tcgtgtgtct gaagtcaatc atcctgctga actccggggg ctataccttc	540
ctgagctcga ccctcaagtc actggaggaa aaagaccaca tccatcgcgt gctcgataag	600
atcaccgaca cccttatcca tctcatggcg aaggctggac tgaccctgca acagcagcac	660
cagaggctgg ccagttgct gctgattctg agccacatcc ggcacatgtc gtccaagagg	720
atggaacacc tgtacagcat gaagtgaag aacgtcgtgc ctctgtccga tctgtcctg	780
gaaatgctgg acgcgcacag actctaccct tatgatgttc ctgattatgc tttcccctg	840
gatgaaattg tgatgacca gtcacccgcc actcttagcc tttcacccgg tgagcgcgca	900

_SL

```

accctgtctt gcagagcctc ccaagacatc tcaaaatacc ttaattggta tcaacagaag      960
cccggacagg ctctcgcct tctgatctac cacaccagcc ggctccattc tggaatccct      1020
gccaggttca gcggtagcgg atctgggacc gactacaccc tcactatcag ctactgcag      1080
ccagaggact tcgctgtcta tttctgtcag caaggaaca ccctgcccta cacctttgga      1140
cagggcacca agctcgagat taaaggtgga ggtggcagcg gaggaggtgg gtccggcggt      1200
ggaggaagcc aggtccaact ccaagaaagc ggaccgggtc ttgtgaagcc atcagaaact      1260
ctttcactga cttgtactgt gagcggagtg tctctccccg attacggggt gtcttggatc      1320
agacagccac cggggaaggg tctggaatgg attggagtga tttggggctc tgagactact      1380
tactactctt catccctcaa gtcacgcgtc accatctcaa aggacaactc taagaatcag      1440
gtgtcactga aactgtcatc tgtgaccgca gccgacaccg ccgtgtacta ttgcgctaag      1500
cattactatt atggcgggag ctacgcaatg gattactggg gacaggggtac tctggtcacc      1560
gtgtccagca ccactacccc agcaccgagg ccaccaccc cggctcctac catcgcctcc      1620
cagcctctgt ccctgcgtcc ggaggcatgt agaccgcag ctggtggggc cgtgcatacc      1680
cggggtcttg acttcgcctg cgatatctac atttggggccc ctctggctgg tacttgcggg      1740
gtcctgctgc tttcactcgt gatcactctt tactgtaagc gcggtcggaa gaagctgctg      1800
tacatcttta agcaaccctt catgaggcct gtgcagacta ctcaagagga ggacggctgt      1860
tcatgccggt tcccagagga ggaggaaggc ggctgcgaac tgcgcgtgaa attcagccgc      1920
agcgagatg ctccagccta caagcagggg cagaaccagc tctacaacga actcaatctt      1980
ggtcggagag aggagtacga cgtgctggac aagcggagag gacgggaccc agaaatgggc      2040
gggaagccgc gcagaaagaa tccccaagag ggcctgtaca acgagctcca aaaggataag      2100
atggcagaag cctatagcga gattggtatg aaaggggaac gcagaagagg caaaggccac      2160
gacggactgt accagggact cagcaccgcc accaaggaca cctatgacgc tcttcacatg      2220
caggccctgc cgcctcgg                                2238

```

<210> 75

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 75

```

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1           5           10          15

```

```

His Ala Ala Arg Pro Arg Ser Ser Leu Ala Leu Ser Leu Thr Ala Asp
      20          25          30

```

```

Gln Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser
      35          40          45

```


_SL

Glu Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu
50 55 60

Leu Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala
65 70 75 80

Lys Arg Val Pro Gly Phe Val Asp Leu Ala Leu His Asp Gln Val His
85 90 95

Leu Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp
100 105 110

Arg Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu
115 120 125

Leu Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe
130 135 140

Asp Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln
145 150 155 160

Gly Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly
165 170 175

Val Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp
180 185 190

His Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu
195 200 205

Met Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala
210 215 220

Gln Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Ser Lys Arg
225 230 235 240

Met Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Ser
245 250 255

Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu Arg Thr Lys Arg
260 265 270

Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
275 280 285

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr
290 295 300

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
305 310 315 320

_SL

Tyr His Thr Ser Arg₃₂₅ Leu His Ser Gly₃₃₀ Ile Pro Ala Arg Phe Ser₃₃₅ Gly
Ser Gly Ser Gly₃₄₀ Thr Asp Tyr Thr₃₄₅ Thr Ile Ser Ser₃₅₀ Leu Gln Pro
Glu Asp Phe₃₅₅ Ala Val Tyr Phe₃₆₀ Cys Gln Gln Gly Asn₃₆₅ Thr Leu Pro Tyr
Thr Phe₃₇₀ Gly Gln Gly Thr₃₇₅ Lys Leu Glu Ile Lys₃₈₀ Gly Gly Gly Gly Ser
Gly₃₈₅ Gly Gly Gly Ser₃₉₀ Gly Gly Gly Ser₃₉₅ Val Gln Leu Gln₄₀₀ Glu
Ser Gly Pro Gly₄₀₅ Leu Val Lys Pro Ser₄₁₀ Glu Thr Leu Ser₄₁₅ Leu Thr Cys
Thr Val Ser₄₂₀ Gly Val Ser Leu Pro₄₂₅ Asp Tyr Gly Val Ser₄₃₀ Trp Ile Arg
Gln Pro Pro₄₃₅ Gly Lys Gly Leu₄₄₀ Glu Trp Ile Gly Val₄₄₅ Ile Trp Gly Ser
Glu Thr₄₅₀ Thr Tyr Tyr Ser₄₅₅ Ser Ser Leu Lys Ser₄₆₀ Arg Val Thr Ile Ser
Lys₄₆₅ Asp Asn Ser Lys₄₇₀ Asn Gln Val Ser Leu₄₇₅ Lys Leu Ser Ser₄₈₀ Val Thr
Ala Ala Asp Thr₄₈₅ Ala Val Tyr Tyr Cys₄₉₀ Ala Lys His Tyr Tyr₄₉₅ Tyr Gly
Gly Ser Tyr₅₀₀ Ala Met Asp Tyr Trp₅₀₅ Gly Gln Gly Thr Leu₅₁₀ Val Thr Val
Ser Ser₅₁₅ Thr Thr Thr Pro Ala₅₂₀ Pro Arg Pro Pro Thr₅₂₅ Pro Ala Pro Thr
Ile Ala₅₃₀ Ser Gln Pro Leu₅₃₅ Ser Leu Arg Pro Glu₅₄₀ Ala Cys Arg Pro Ala
Ala₅₄₅ Gly Gly Ala Val₅₅₀ His Thr Arg Gly Leu₅₅₅ Asp Phe Ala Cys Asp Ile₅₆₀
Tyr Ile Trp Ala₅₆₅ Pro Leu Ala Gly Thr₅₇₀ Cys Gly Val Leu Leu₅₇₅ Leu Ser
Leu Val Ile₅₈₀ Thr Leu Tyr Cys Lys₅₈₅ Arg Gly Arg Lys Lys₅₉₀ Leu Leu Tyr

_SL

Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu
595 600 605

Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu
610 615 620

Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln
625 630 635 640

Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu
645 650 655

Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly
660 665 670

Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln
675 680 685

Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu
690 695 700

Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr
705 710 715 720

Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro
725 730 735

Arg

<210> 76
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 76
atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60
ccccggtcgt cgttggcact ttccctgact gccgaccaga tgggtgtccgc ctttctggac 120
gccgagcctc caattctgta ctcggagtac gatccgactc gcccgttctc cgaagccagc 180
atgatgggcc tgttgactaa cctggcggac cgcgagttgg tgcacatgat taactgggct 240
aagcgggtgc cgggcttcgt ggacctggcc ctgcacgacc aagtgcacct cctggaatgc 300
gcctggatgg aaatcctcat gatcggcctc gtgtggagat ccatggagca tcccggaaag 360
ctcctgtttg cacccaacct cctgcttgat cgcaaccagg gaaaatgcgt ggaaggggggt 420
gtcgagattt tcgacatgct gctcgccacc tcttcccgggt tccggatgat gaatctgcag 480

_SL

ggagaagagt tcgtgtgtct gaagtcaatc atcctgctga actccgggggt ctataccttc 540
ctgagctcga ccctcaagtc actggaggaa aaagaccaca tccatcgcggt gctcgataag 600
atcaccgaca cccttatcca tctcatggcg aaggctggac tgaccctgca acagcagcac 660
cagaggctgg cccagttgct gctgattctg agccacatcc ggcacatgtc gtccaagagg 720
atggaacacc tgtacagcat gaagtgcaag aacgtcgtgc ctctgtccga tctgctcctg 780
gaaatgctgg acgcgcacag actccgtact aaaagagaaa ttgtgatgac ccagtcaccc 840
gccactctta gcctttcacc cggtagagcg gcaaccctgt cttgcagagc ctcccaagac 900
atctcaaaat accttaattg gtatcaacag aagcccgagc aggcctcctcg ctttctgac 960
taccacacca gccggctcca ttctggaatc cctgccaggt tcagcggtag cggatctggg 1020
accgactaca ccctcactat cagctcactg cagccagagg acttcgctgt ctatttctgt 1080
cagcaaggga acacctgccc ctacaccttt ggacagggca ccaagctcga gattaaaggt 1140
ggaggtggca gcggaggagg tgggtccggc ggtggaggaa gccaggtcca actccaagaa 1200
agcggaccgg gtcttgtgaa gccatcagaa actctttcac tgacttgtac tgtgagcgga 1260
gtgtctctcc ccgattacgg ggtgtcttgg atcagacagc caccggggaa gggctctggaa 1320
tggattggag tgatttgggg ctctgagact atttactact cttcatccct caagtcacgc 1380
gtcaccatct caaaggacaa ctctaagaat caggtgtcac tgaaactgtc atctgtgacc 1440
gcagccgaca ccgccgtgta ctattgcgct aagcattact attatggcgg gagctacgca 1500
atggattact ggggacaggg tactctggtc accgtgtcca gcaccactac cccagcaccg 1560
aggccacca ccccggtccc taccatcgcc tcccagcctc tgtccctgcg tccggaggca 1620
tgtagacccg cagctggtgg ggccgtgcat acccggggtc ttgacttcgc ctgcatatc 1680
tacatttggg cccctctggc tgggtacttg ggggtcctgc tgctttcact cgtgatcact 1740
ctttactgta agcgcggtcg gaagaagctg ctgtacatct ttaagcaacc cttcatgagg 1800
cctgtgcaga ctactcaaga ggaggacggc tgttcatgcc ggttcccaga ggaggaggaa 1860
ggcggctgcg aactgcgcgt gaaattcagc cgcagcgag atgctccagc ctacaagcag 1920
gggcagaacc agctctacaa cgaactcaat cttggtcggg gagaggagta cgacgtgctg 1980
gacaagcgga gaggacggga cccagaaatg ggcggaagc cgcgcagaaa gaatcccaa 2040
gagggcctgt acaacgagct ccaaaaggat aagatggcag aagcctatag cgagattggt 2100
atgaaagggg aacgcagaag aggcaaaggc cagcagggac tgtaccaggg actcagcacc 2160
gccaccaagg acacctatga cgctcttcac atgcaggccc tgccgcctcg g 2211

<210> 77

<211> 733

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic

_SL
polypeptide"

<400> 77

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Arg Ser Ser Leu Ala Leu Ser Leu Thr Ala Asp
20 25 30

Gln Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser
35 40 45

Glu Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu
50 55 60

Leu Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala
65 70 75 80

Lys Arg Val Pro Gly Phe Val Asp Leu Ala Leu His Asp Gln Val His
85 90 95

Leu Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp
100 105 110

Arg Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu
115 120 125

Leu Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe
130 135 140

Asp Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln
145 150 155 160

Gly Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly
165 170 175

Val Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp
180 185 190

His Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu
195 200 205

Met Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala
210 215 220

Gln Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Ser Lys Arg
225 230 235 240

Met Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Ser
245 250 255

Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu Glu Ile Val Met

_SL

260 265 270

Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr
275 280 285

Leu Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr Leu Asn Trp Tyr
290 295 300

Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr His Thr Ser
305 310 315 320

Arg Leu His Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly
325 330 335

Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
340 345 350

Val Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gln
355 360 365

Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly
370 375 380

Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly
385 390 395 400

Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly
405 410 415

Val Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln Pro Pro Gly
420 425 430

Lys Gly Leu Glu Trp Ile Gly Val Ile Trp Gly Ser Glu Thr Thr Tyr
435 440 445

Tyr Ser Ser Ser Leu Lys Ser Arg Val Thr Ile Ser Lys Asp Asn Ser
450 455 460

Lys Asn Gln Val Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr
465 470 475 480

Ala Val Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala
485 490 495

Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Thr Thr
500 505 510

Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln
515 520 525

Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala

530					535					_SL		540				
Val 545	His	Thr	Arg	Gly	Leu 550	Asp	Phe	Ala	Cys	Asp 555	Ile	Tyr	Ile	Trp	Ala 560	
Pro	Leu	Ala	Gly	Thr 565	Cys	Gly	Val	Leu	Leu 570	Leu	Ser	Leu	Val	Ile 575	Thr	
Leu	Tyr	Cys	Lys 580	Arg	Gly	Arg	Lys	Lys 585	Leu	Leu	Tyr	Ile	Phe 590	Lys	Gln	
Pro	Phe	Met 595	Arg	Pro	Val	Gln	Thr 600	Thr	Gln	Glu	Glu	Asp 605	Gly	Cys	Ser	
Cys	Arg 610	Phe	Pro	Glu	Glu	Glu 615	Glu	Gly	Gly	Cys	Glu 620	Leu	Arg	Val	Lys	
Phe 625	Ser	Arg	Ser	Ala	Asp 630	Ala	Pro	Ala	Tyr	Lys 635	Gln	Gly	Gln	Asn	Gln 640	
Leu	Tyr	Asn	Glu	Leu 645	Asn	Leu	Gly	Arg	Arg 650	Glu	Glu	Tyr	Asp	Val 655	Leu	
Asp	Lys	Arg	Arg 660	Gly	Arg	Asp	Pro	Glu 665	Met	Gly	Gly	Lys	Pro 670	Arg	Arg	
Lys	Asn	Pro 675	Gln	Glu	Gly	Leu	Tyr 680	Asn	Glu	Leu	Gln	Lys 685	Asp	Lys	Met	
Ala	Glu 690	Ala	Tyr	Ser	Glu	Ile 695	Gly	Met	Lys	Gly	Glu 700	Arg	Arg	Arg	Gly	
Lys 705	Gly	His	Asp	Gly	Leu 710	Tyr	Gln	Gly	Leu	Ser 715	Thr	Ala	Thr	Lys	Asp 720	
Thr	Tyr	Asp	Ala	Leu 725	His	Met	Gln	Ala	Leu 730	Pro	Pro	Arg				

```
<210> 78
<211> 2199
<212> DNA
<213> Artificial Sequence
```

<211> 2199

<212> DNA

<213> Artificial Sequence

$\langle 220 \rangle$

<221> source

```
<223> /note="Description of Artificial Sequence: Synthetic  
polynucleotide"
```

<400> 78

atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60

ccccggtcgt cgttggcact ttccctgact gccgaccaga tggtgtccgc ctttctggac 120

gccgagcctc caattctgta ctcggagtac gatccgactc gcccgttctc cgaagccagc 180

						_SL	
atgatgggccc	tgttgactaa	cctggcggac	cgcgagttgg	tgcacatgat	taactgggct		240
aagcgggtgc	cgggcttcgt	ggacctggcc	ctgcacgacc	aagtgcacct	cctggaatgc		300
gcctggatgg	aaatcctcat	gatcggcctc	gtgtggagat	ccatggagca	tcccggaaag		360
ctcctgtttg	cacccaacct	cctgcttgat	cgcaaccagg	gaaaatgcgt	ggaaggggggt		420
gtcgagattt	tcgacatgct	gctcgccacc	tcttcccgggt	tccggatgat	gaatctgcag		480
ggagaagagt	tcgtgtgtct	gaagtcaatc	atcctgtctga	actccgggggt	ctataaccttc		540
ctgagctcga	ccctcaagtc	actggaggaa	aaagaccaca	tccatcgcggt	gctcgataag		600
atcaccgaca	cccttatcca	tctcatggcg	aaggctggac	tgaccctgca	acagcagcac		660
cagaggctgg	cccagttgct	gctgattctg	agccacatcc	ggcacatgtc	gtccaagagg		720
atggaacacc	tgtacagcat	gaagtgcaag	aacgtcgtgc	ctctgtccga	tctgtctctg		780
gaaatgctgg	acgcgcacag	actcgaaatt	gtgatgacct	agtcacccgc	cactcttagc		840
ctttcacccg	gtgagcgcgc	aaccctgtct	tgcagagcct	ccaagacat	ctcaaaatac		900
cttaattgggt	atcaacagaa	gcccggacag	gctcctcgcc	ttctgatcta	ccacaccagc		960
cggctccatt	ctggaatccc	tgccagggttc	agcggtagcg	gatctggggac	cgactacacc		1020
ctcactatca	gctcactgca	gccagaggac	ttcgtgtgtct	atttctgtca	gcaagggaac		1080
accctgccct	acacctttgg	acagggcacc	aagctcgaga	ttaaagggtgg	aggtggcagc		1140
ggaggagggtg	ggtccggcgg	tggaggaagc	caggtccaac	tccaagaaag	cggaccgggt		1200
cttgtgaagc	catcagaaac	tctttcactg	acttgtactg	tgagcggagt	gtctctcccc		1260
gattacgggg	tgtcttggat	cagacagcca	ccggggaagg	gtctggaatg	gattggagtg		1320
atttgggggt	ctgagactac	ttactactct	tcatccctca	agtcacgcgt	caccatctca		1380
aaggacaact	ctaagaatca	ggtgtcactg	aaactgtcat	ctgtgaccgc	agccgacacc		1440
gccgtgtact	attgcgctaa	gcattactat	tatggcggga	gctacgcaat	ggattactgg		1500
ggacagggtg	ctctggtcac	cgtgtccagc	accactaccc	cagcaccgag	gccacccacc		1560
ccggctccta	ccatcgccctc	ccagcctctg	tccctgcgtc	cggaggcatg	tagacccgca		1620
gctgggtggg	ccgtgcatac	ccggggtctt	gacttcgcct	gcgatatcta	catttggggc		1680
cctctggctg	gtacttgctg	ggtcctgctg	ctttcactcg	tgatcactct	ttactgtaag		1740
cgcggtcggg	agaagctgct	gtacatcttt	aagcaaccct	tcatgaggcc	tgtgcagact		1800
actcaagagg	aggacggctg	ttcatgccgg	ttcccagagg	aggaggaagg	cggctgcgaa		1860
ctgcgcgtga	aattcagccg	cagcgcagat	gctccagcct	acaagcaggg	gcagaaccag		1920
ctctacaacg	aactcaatct	tggtcggaga	gaggagtacg	acgtgctgga	caagcggaga		1980
ggacgggacc	cagaaatggg	cgggaagccg	cgcagaaaga	atccccaaga	gggcctgtac		2040
aacgagctcc	aaaaggataa	gatggcagaa	gcctatagcg	agattgggtat	gaaaggggaa		2100
cgcagaagag	gcaaaggcca	cgacggactg	taccagggac	tcagcaccgc	caccaaggac		2160
acctatgacg	ctcttcacat	gcaggccctg	ccgcctcgg				2199

<210> 79

<400> 79
000

<210> 80

<400> 80
000

<210> 81

<400> 81
000

<210> 82

<211> 5000

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<220>

<221> misc_feature

<222> (1)..(5000)

<223> /note="This sequence may encompass 100-5000 nucleotides"

<220>

<221> source

<223> /note="See specification as filed for detailed description of
substitutions and preferred embodiments"

<400> 82

aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 60

aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 120

aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 180

aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 240

aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 300

aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 360

aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 420

aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 480

aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 540

aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 600

aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 660

aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 720

aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 780

aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 840

_SL

[illegible]

_SL

[illegible]

_SL

aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa	4980
aaaaaaaaa aaaaaaaaaa	5000

<210> 83

<400> 83
000

<210> 84

<400> 84
000

<210> 85

<400> 85
000

<210> 86

<400> 86
000

<210> 87

<400> 87
000

<210> 88

<400> 88
000

<210> 89

<400> 89
000

<210> 90

<400> 90
000

<210> 91

<400> 91
000

<210> 92

<400> 92
000

_SL

<210> 93

<400> 93
000

<210> 94

<400> 94
000

<210> 95

<400> 95
000

<210> 96

<400> 96
000

<210> 97

<400> 97
000

<210> 98

<400> 98
000

<210> 99

<400> 99
000

<210> 100

<400> 100
000

<210> 101

<400> 101
000

<210> 102

<400> 102
000

<210> 103

<211> 747

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic

_SL
polypeptide"

<400> 103

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Arg Ser Ser Leu Ala Leu Ser Leu Thr Ala Asp
20 25 30

Gln Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser
35 40 45

Glu Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu
50 55 60

Leu Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala
65 70 75 80

Lys Arg Val Pro Gly Phe Val Asp Leu Ala Leu His Asp Gln Val His
85 90 95

Leu Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp
100 105 110

Arg Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu
115 120 125

Leu Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe
130 135 140

Asp Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln
145 150 155 160

Gly Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly
165 170 175

Val Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp
180 185 190

His Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu
195 200 205

Met Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala
210 215 220

Gln Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Ser Lys Arg
225 230 235 240

Met Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Ser
245 250 255

Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu Ser Leu Asn Leu
Page 75

_SL

260	265	270
Thr Glu Ser His Asn Ser Arg Lys Lys Arg Glu Ile Val Met Thr Gln		
275	280	285
Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser		
290	295	300
Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr Leu Asn Trp Tyr Gln Gln		
305	310	315
Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr His Thr Ser Arg Leu		
325	330	335
His Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp		
340	345	350
Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Val Tyr		
355	360	365
Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gln Gly Thr		
370	375	380
Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly		
385	390	395
Gly Gly Gly Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val		
405	410	415
Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Val Ser		
420	425	430
Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly		
435	440	445
Leu Glu Trp Ile Gly Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Ser		
450	455	460
Ser Ser Leu Lys Ser Arg Val Thr Ile Ser Lys Asp Asn Ser Lys Asn		
465	470	475
Gln Val Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val		
485	490	495
Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met Asp		
500	505	510
Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Thr Thr Thr Pro		
515	520	525
Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu		

						_SL	
ccccggtcgt	cgttggcact	ttccctgact	gccgaccaga	tgggtgtccgc	ccttctggac		120
gccgagcctc	caattctgta	ctcggagtac	gatccgactc	gcccgttctc	cgaagccagc		180
atgatgggcc	tgttgactaa	cctggcggac	cgcgagttgg	tgcacatgat	taactgggct		240
aagcgggtgc	cggttctcgt	ggacctggcc	ctgcacgacc	aagtgcacct	cctggaatgc		300
gcctggatgg	aaatcctcat	gatcggcctc	gtgtggagat	ccatggagca	tcccggaaag		360
ctcctgtttg	cacccaacct	cctgcttgat	cgcaaccagg	gaaaatgcgt	ggaaggggggt		420
gtcgagattt	tcgacatgct	gctcgccacc	tcttcccggg	tccggatgat	gaatctgcag		480
ggagaagagt	tcgtgtgtct	gaagtcaatc	atcctgctga	actccgggggt	ctataccttc		540
ctgagctcga	ccctcaagtc	actggaggaa	aaagaccaca	tccatcgcg	gctcgataag		600
atcaccgaca	cccttatcca	tctcatggcg	aaggctggac	tgaccctgca	acagcagcac		660
cagaggctgg	cccagttgct	gctgattctg	agccacatcc	ggcacatgtc	gtccaagagg		720
atggaacacc	tgtacagcat	gaagtgcaag	aacgtcgtgc	ctctgtccga	tctgctcctg		780
gaaatgctgg	acgcgcacag	actcagtctc	aatttgactg	agtcacacaa	ttccaggaag		840
aaaagggaaa	ttgtgatgac	ccagtcaccc	gccactctta	gcctttcacc	cggtgagcgc		900
gcaaccctgt	cttgacagagc	ctcccaagac	atctcaaaat	accttaattg	gtatcaacag		960
aagcccggac	aggctcctcg	ccttctgata	taccacacca	gccggctcca	ttctggaatc		1020
cctgccaggt	tcagcggtag	cggatctggg	accgactaca	ccctcactat	cagctcactg		1080
cagccagagg	acttcgctgt	ctatttctgt	cagcaagggg	acaccctgcc	ctacaccttt		1140
ggacagggca	ccaagctcga	gattaaaggt	ggaggtggca	gcggaggagg	tgggtccggc		1200
ggtggaggaa	gccaggtcca	actccaagaa	agcggaccgg	gtcttgtgaa	gccatcagaa		1260
actctttcac	tgacttgtac	tgtgagcgga	gtgtctctcc	ccgattacgg	ggtgtcttgg		1320
atcagacagc	caccggggaa	gggtctggaa	tggattggag	tgatttgggg	ctctgagact		1380
acttactact	cttcatccct	caagtcacgc	gtcaccatct	caaaggacaa	ctctaagaat		1440
caggtgtcac	tgaactgtc	atctgtgacc	gcagccgaca	ccgccgtgta	ctattgcgct		1500
aagcattact	attatggcgg	gagctacgca	atggattact	ggggacaggg	tactctggtc		1560
accgtgtcca	gcaccactac	cccagcaccg	aggccacca	ccccggctcc	taccatcgcc		1620
tcccagcctc	tgtccctgcg	tccggaggca	tgtagaccgg	cagctgggtg	ggccgtgcat		1680
accgggggtc	ttgacttcgc	ctgcgatata	tacatttggg	cccctctggc	tggtacttgc		1740
ggggtcctgc	tgctttcact	cgtgatcact	ctttactgta	agcgcggctc	gaagaagctg		1800
ctgtacatct	ttaagcaacc	cttcatgagg	cctgtgcaga	ctactcaaga	ggaggacggc		1860
tgttcatgcc	ggttcccaga	ggaggaggaa	ggcggctgcg	aactgcgcgt	gaaattcagc		1920
cgcagcgag	atgctccagc	ctacaagcag	gggcagaacc	agctctacaa	cgaactcaat		1980
cttggtcggg	gagaggagta	cgacgtgctg	gacaagcgga	gaggacggga	cccagaaatg		2040
ggcgggaagc	cgcgcagaaa	gaatccccaa	gagggcctgt	acaacgagct	ccaaaaggat		2100

aagatggcag aagcctatag cgagattggt atgaaagggg aacgcagaag aggcaaagggc 2160
 cacgacggac tgtaccaggg actcagcacc gccaccaagg acacctatga cgctcttcac 2220
 atgcaggccc tgccgcctcg g 2241

<210> 105
 <211> 747
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 105
 Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
 1 5 10 15

His Ala Ala Arg Pro Arg Ser Ser Leu Ala Leu Ser Leu Thr Ala Asp
 20 25 30

Gln Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser
 35 40 45

Glu Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu
 50 55 60

Leu Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala
 65 70 75 80

Lys Arg Val Pro Gly Phe Val Asp Leu Ala Leu His Asp Gln Val His
 85 90 95

Leu Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp
 100 105 110

Arg Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu
 115 120 125

Leu Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe
 130 135 140

Asp Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln
 145 150 155 160

Gly Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly
 165 170 175

Val Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp
 180 185 190

His Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu
 195 200 205

_SL

Met Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala
210 215 220

Gln Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Ser Lys Arg
225 230 235 240

Met Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Ser
245 250 255

Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu Gly Thr Gly Ala
260 265 270

Glu Asp Pro Arg Pro Ser Arg Lys Arg Arg Glu Ile Val Met Thr Gln
275 280 285

Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser
290 295 300

Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr Leu Asn Trp Tyr Gln Gln
305 310 315 320

Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr His Thr Ser Arg Leu
325 330 335

His Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
340 345 350

Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Val Tyr
355 360 365

Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gln Gly Thr
370 375 380

Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
385 390 395 400

Gly Gly Gly Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val
405 410 415

Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Val Ser
420 425 430

Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly
435 440 445

Leu Glu Trp Ile Gly Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Ser
450 455 460

Ser Ser Leu Lys Ser Arg Val Thr Ile Ser Lys Asp Asn Ser Lys Asn
465 470 475 480

_SL

Gln Val Ser Leu Lys₄₈₅ Leu Ser Ser Val Thr₄₉₀ Ala Ala Asp Thr Ala₄₉₅ Val
Tyr Tyr Cys Ala₅₀₀ Lys His Tyr Tyr Tyr₅₀₅ Gly Gly Ser Tyr Ala₅₁₀ Met Asp
Tyr Trp Gly₅₁₅ Gln Gly Thr Leu Val₅₂₀ Thr Val Ser Ser Thr₅₂₅ Thr Thr Pro
Ala Pro₅₃₀ Arg Pro Pro Thr Pro₅₃₅ Ala Pro Thr Ile Ala₅₄₀ Ser Gln Pro Leu
Ser₅₄₅ Leu Arg Pro Glu Ala₅₅₀ Cys Arg Pro Ala Ala₅₅₅ Gly Gly Ala Val His₅₆₀
Thr Arg Gly Leu Asp₅₆₅ Phe Ala Cys Asp Ile₅₇₀ Tyr Ile Trp Ala Pro₅₇₅ Leu
Ala Gly Thr Cys₅₈₀ Gly Val Leu Leu Leu₅₈₅ Ser Leu Val Ile Thr₅₉₀ Leu Tyr
Cys Lys Arg₅₉₅ Gly Arg Lys Lys Leu₆₀₀ Leu Tyr Ile Phe Lys₆₀₅ Gln Pro Phe
Met Arg₆₁₀ Pro Val Gln Thr Thr₆₁₅ Gln Glu Glu Asp Gly₆₂₀ Cys Ser Cys Arg
Phe₆₂₅ Pro Glu Glu Glu Glu₆₃₀ Gly Gly Cys Glu Leu₆₃₅ Arg Val Lys Phe Ser₆₄₀
Arg Ser Ala Asp Ala₆₄₅ Pro Ala Tyr Lys Gln₆₅₀ Gly Gln Asn Gln Leu₆₅₅ Tyr
Asn Glu Leu Asn₆₆₀ Leu Gly Arg Arg Glu₆₆₅ Glu Tyr Asp Val Leu₆₇₀ Asp Lys
Arg Arg Gly₆₇₅ Arg Asp Pro Glu Met₆₈₀ Gly Gly Lys Pro Arg₆₈₅ Arg Lys Asn
Pro Gln Glu Gly Leu Tyr Asn₆₉₅ Glu Leu Gln Lys Asp₇₀₀ Lys Met Ala Glu
Ala₇₀₅ Tyr Ser Glu Ile Gly₇₁₀ Met Lys Gly Glu Arg₇₁₅ Arg Arg Gly Lys Gly₇₂₀
His Asp Gly Leu Tyr₇₂₅ Gln Gly Leu Ser Thr₇₃₀ Ala Thr Lys Asp Thr₇₃₅ Tyr
Asp Ala Leu His₇₄₀ Met Gln Ala Leu Pro₇₄₅ Pro Arg

_SL

<210> 106
<211> 2241
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 106
atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60
ccccggtcgt cgttggcact ttccctgact gccgaccaga tgggtgtccgc ctttctggac 120
gccgagcctc caattctgta ctcggagtac gatccgactc gcccgttctc cgaagccagc 180
atgatgggcc tgttgactaa cctggcggac cgcgagttgg tgcacatgat taactgggct 240
aagcgggtgc cgggcttcgt ggacctggcc ctgcacgacc aagtgcacct cctggaatgc 300
gcctggatgg aaatcctcat gatcggcctc gtgtggagat ccatggagca tcccggaaag 360
ctcctgtttg cacccaacct cctgcttgat cgcaaccagg gaaaatgcgt ggaaggggggt 420
gtcgagattt tcgacatgct gctcgccacc tcttcccgggt tccggatgat gaatctgcag 480
ggagaagagt tcgtgtgtct gaagtcaatc atcctgctga actccgggggt ctataccttc 540
ctgagctcga ccctcaagtc actggaggaa aaagaccaca tccatcgcgt gctcgataag 600
atcaccgaca cccttatcca tctcatggcg aaggctggac tgaccctgca acagcagcac 660
cagaggctgg cccagttgct gctgattctg agccacatcc ggcacatgtc gtccaagagg 720
atggaacacc tgtacagcat gaagtgaag aacgtcgtgc ctctgtccga tctgctcctg 780
gaaatgctgg acgcgcacag actcgggacg ggagctgagg atccacgacc cagcagaaag 840
cgacgggaaa ttgtgatgac ccagtcaccc gccactctta gcctttcacc cggtgagcgc 900
gcaaccctgt cttgcagagc ctccaagac atctcaaaat accttaattg gtatcaacag 960
aagcccggac aggtcctcgt ctttctgac taccacacca gccggctcca ttctggaatc 1020
cctgccaggt tcagcggtag cggatctggg accgactaca ccctcactat cagctcactg 1080
cagccagagg acttcgctgt ctatttctgt cagcaaggga acaccctgcc ctacaccttt 1140
ggacagggca ccaagctcga gattaaagg ggaggtggca gcggaggagg tgggtccggc 1200
ggtggaggaa gccaggtcca actccaagaa agcggaccgg gtcttgtgaa gccatcagaa 1260
actctttcac tgacttgtac tgtgagcgga gtgtctctcc ccgattacgg ggtgtcttgg 1320
atcagacagc caccggggaa gggctctggaa tggattggag tgatttgggg ctctgagact 1380
acttactact cttcatccct caagtcacgc gtcaccatct caaaggacaa ctctaagaat 1440
caggtgtcac tgaaactgtc atctgtgacc gcagccgaca ccgccgtgta ctattgcgct 1500
aagcattact attatggcgg gagctacgca atggattact ggggacaggg tactctggtc 1560
accgtgtcca gcaccactac ccagcaccg aggccacca ccccggtcc taccatcgcc 1620
tcccagcctc tgtccctgcg tccggaggca tgtagaccg cagctgggtg ggccgtgcat 1680

_SL

accggttc ttgacttcgc ctgcgatatac tacatttggg cccctctggc tgggtacttgc 1740
gggttcctgc tgctttcact cgtgatcact ctttactgta agcgcggtcg gaagaagctg 1800
ctgtacatct ttaagcaacc cttcatgagg cctgtgcaga ctactcaaga ggaggacggc 1860
tgttcatgcc gggtcccaga ggaggaggaa ggcggctgcg aactgcgcgt gaaattcagc 1920
cgcagcgcag atgctccagc ctacaagcag gggcagaacc agctctacaa cgaactcaat 1980
cttggtcggg gagaggagta cgacgtgctg gacaagcgga gaggacggga cccagaaatg 2040
ggcggaagc cgcgcagaaa gaatcccaa gagggcctgt acaacgagct ccaaaaggat 2100
aagatggcag aagcctatag cgagattggt atgaaagggg aacgcagaag aggcaaaggc 2160
cacgacggac tgtaccaggg actcagcacc gccaccaagg acacctatga cgctcttcac 2220
atgcaggccc tgccgcctcg g 2241

<210> 107

<211> 747

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 107

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Arg Ser Ser Leu Ala Leu Ser Leu Thr Ala Asp
20 25 30

Gln Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser
35 40 45

Glu Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu
50 55 60

Leu Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala
65 70 75 80

Lys Arg Val Pro Gly Phe Val Asp Leu Ala Leu His Asp Gln Val His
85 90 95

Leu Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp
100 105 110

Arg Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu
115 120 125

Leu Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe
130 135 140

_SL

Asp Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln
145 150 155 160

Gly Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly
165 170 175

Val Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp
180 185 190

His Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu
195 200 205

Met Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala
210 215 220

Gln Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Ser Lys Arg
225 230 235 240

Met Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Ser
245 250 255

Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu Cys Lys Ile Asn
260 265 270

Gly Tyr Pro Lys Arg Gly Arg Lys Arg Arg Glu Ile Val Met Thr Gln
275 280 285

Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser
290 295 300

Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr Leu Asn Trp Tyr Gln Gln
305 310 315 320

Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr His Thr Ser Arg Leu
325 330 335

His Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
340 345 350

Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Val Tyr
355 360 365

Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gln Gly Thr
370 375 380

Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
385 390 395 400

Gly Gly Gly Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val
405 410 415

_SL

Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Val Ser
420 425 430

Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly
435 440 445

Leu Glu Trp Ile Gly Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Ser
450 455 460

Ser Ser Leu Lys Ser Arg Val Thr Ile Ser Lys Asp Asn Ser Lys Asn
465 470 475 480

Gln Val Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val
485 490 495

Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met Asp
500 505 510

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Thr Thr Thr Pro
515 520 525

Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu
530 535 540

Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His
545 550 555 560

Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu
565 570 575

Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr
580 585 590

Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe
595 600 605

Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg
610 615 620

Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser
625 630 635 640

Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr
645 650 655

Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys
660 665 670

Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn
675 680 685

_SL

Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu
690 695 700

Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly
705 710 715 720

His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr
725 730 735

Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
740 745

<210> 108

<211> 2241

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 108

```
atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg      60
ccccggtcgt cgttggcact ttccctgact gccgaccaga tgggtgtccgc ctttctggac      120
gccgagcctc caattctgta ctcgaggtac gatccgactc gcccgttctc cgaagccagc      180
atgatggggc tggtgactaa cctggcggac cgcgagttgg tgcacatgat taactgggct      240
aagcgggtgc cgggcttcgt ggacctggcc ctgcacgacc aagtgcacct cctggaatgc      300
gcctggatgg aaatcctcat gatcggcctc gtgtggagat ccatggagca tcccggaaag      360
ctcctgtttg cacccaacct cctgcttgat cgcaaccagg gaaaatgcgt ggaagggggg      420
gtcgagattt tcgacatgct gctcgccacc tcttcccggg tccggatgat gaatctgcag      480
ggagaagagt tcgtgtgtct gaagtcaatc atcctgctga actccggggg ctataccttc      540
ctgagctcga ccctcaagtc actggaggaa aaagaccaca tccatcgcgt gctcgataag      600
atcaccgaca cccttatcca tctcatggcg aaggctggac tgaccctgca acagcagcac      660
cagaggctgg ccagttgct gctgattctg agccacatcc ggcacatgtc gtccaagagg      720
atggaacacc tgtacagcat gaagtgcaag aacgtcgtgc ctctgtccga tctgctcctg      780
gaaatgctgg acgcgcacag actctgcaag atcaacggct accctaagag gggcagaaag      840
cggcgggaaa ttgtgatgac ccagtcaccc gccactctta gcctttcacc cgggtgagcgc      900
gcaaccctgt cttgcagagc ctccaagac atctcaaaat accttaattg gtatcaacag      960
aagcccggac aggctcctcg ctttctgata taccacacca gccggctcca ttctggaatc     1020
cctgccaggt tcagcggtag cggatctggg accgactaca ccctcactat cagctcactg     1080
cagccagagg acttcgctgt ctatttctgt cagcaaggga acaccctgcc ctacaccttt     1140
ggacagggca ccaagctcga gattaaagg ggaggtggca gcggaggagg tgggtccggc     1200
```

_SL

```

ggtggaggaa gccaggtcca actccaagaa agcggaccgg gtcttgtgaa gccatcagaa 1260
actctttcac tgacttgtac tgtgagcgga gtgtctctcc ccgattacgg ggtgtcttgg 1320
atcagacagc caccggggaa gggctctggaa tggattggag tgatttgggg ctctgagact 1380
acttactact cttcatccct caagtcacgc gtcaccatct caaaggacaa ctctaagaat 1440
cagggtgtcac tgaaactgtc atctgtgacc gcagccgaca ccgccgtgta ctattgcgct 1500
aagcattact attatggcgg gagctacgca atggattact ggggacaggg tactctggtc 1560
accgtgtcca gcaccactac cccagcaccg aggccaccca ccccggtctc taccatcgcc 1620
tcccagcctc tgtccctgcg tccggaggca tgtagaccgg cagctgggtg ggccgtgcat 1680
acccgggggtc ttgacttcgc ctgcgatatc tacatttggg cccctctggc tgggtacttgc 1740
ggggtcctgc tgctttcact cgtgatcact ctttactgta agcgcggtcg gaagaagctg 1800
ctgtacatct ttaagcaacc cttcatgagg cctgtgcaga ctactcaaga ggaggacggc 1860
tgttcatgcc gggtcccaga ggaggaggaa ggcggctgcg aactgcgcgt gaaattcagc 1920
cgcagcgag atgctccagc ctacaagcag ggcagaacc agctctacaa cgaactcaat 1980
cttggtcgga gagaggagta cgacgtgctg gacaagcgga gaggacggga cccagaaatg 2040
ggcggaagc cgcgcagaaa gaatcccaa gagggcctgt acaacgagct ccaaaggat 2100
aagatggcag aagcctatag cgagattggt atgaaagggg aacgcagaag aggcaaaggc 2160
cacgacggac tgtaccaggg actcagcacc gccaccaagg acacctatga cgctcttcac 2220
atgcaggccc tgccgcctcg g 2241

```

<210> 109
 <211> 748
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 109
 Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
 1 5 10 15

His Ala Ala Arg Pro Arg Ser Ser Leu Ala Leu Ser Leu Thr Ala Asp
 20 25 30

Gln Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser
 35 40 45

Glu Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu
 50 55 60

Leu Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala
 65 70 75 80

Lys Arg Val Pro Gly Phe Val Asp Leu Ala^{-SL} Leu His Asp Gln Val His
 85 90 95
 Leu Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp
 100 105 110
 Arg Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu
 115 120 125
 Leu Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe
 130 135 140
 Asp Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln
 145 150 155 160
 Gly Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly
 165 170 175
 Val Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp
 180 185 190
 His Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu
 195 200 205
 Met Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala
 210 215 220
 Gln Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Ser Lys Arg
 225 230 235 240
 Met Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Ser
 245 250 255
 Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu Leu Gln Trp Leu
 260 265 270
 Glu Gln Gln Val Ala Lys Arg Arg Thr Lys Arg Glu Ile Val Met Thr
 275 280 285
 Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu
 290 295 300
 Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr Leu Asn Trp Tyr Gln
 305 310 315 320
 Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr His Thr Ser Arg
 325 330 335
 Leu His Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr
 340 345 350

Asp Tyr Thr₃₅₅ Leu Thr Ile Ser Ser₃₆₀ Leu Gln^{-SL} Pro Glu Asp₃₆₅ Phe Ala Val
 Tyr Phe₃₇₀ Cys Gln Gln Gly Asn₃₇₅ Thr Leu Pro Tyr Thr₃₈₀ Phe Gly Gln Gly
 Thr₃₈₅ Lys Leu Glu Ile Lys₃₉₀ Gly Gly Gly Gly Ser₃₉₅ Gly Gly Gly Gly Ser₄₀₀
 Gly Gly Gly Gly Ser₄₀₅ Gln Val Gln Leu Gln₄₁₀ Glu Ser Gly Pro Gly₄₁₅ Leu
 Val Lys Pro Ser₄₂₀ Glu Thr Leu Ser Leu₄₂₅ Thr Cys Thr Val Ser₄₃₀ Gly Val
 Ser Leu Pro₄₃₅ Asp Tyr Gly Val Ser₄₄₀ Trp Ile Arg Gln Pro₄₄₅ Pro Gly Lys
 Gly Leu₄₅₀ Glu Trp Ile Gly Val₄₅₅ Ile Trp Gly Ser Glu₄₆₀ Thr Thr Tyr Tyr
 Ser₄₆₅ Ser Ser Leu Lys Ser₄₇₀ Arg Val Thr Ile Ser₄₇₅ Lys Asp Asn Ser Lys₄₈₀
 Asn Gln Val Ser₄₈₅ Leu Lys Leu Ser Ser Val₄₉₀ Thr Ala Ala Asp Thr₄₉₅ Ala
 Val Tyr Tyr Cys₅₀₀ Ala Lys His Tyr Tyr₅₀₅ Tyr Gly Gly Ser Tyr₅₁₀ Ala Met
 Asp Tyr Trp₅₁₅ Gly Gln Gly Thr Leu₅₂₀ Val Thr Val Ser Ser₅₂₅ Thr Thr Thr
 Pro Ala₅₃₀ Pro Arg Pro Pro Thr₅₃₅ Pro Ala Pro Thr Ile₅₄₀ Ala Ser Gln Pro
 Leu₅₄₅ Ser Leu Arg Pro Glu₅₅₀ Ala Cys Arg Pro Ala₅₅₅ Ala Gly Gly Ala Val₅₆₀
 His Thr Arg Gly Leu₅₆₅ Asp Phe Ala Cys Asp₅₇₀ Ile Tyr Ile Trp Ala₅₇₅ Pro
 Leu Ala Gly Thr₅₈₀ Cys Gly Val Leu Leu₅₈₅ Leu Ser Leu Val Ile₅₉₀ Thr Leu
 Tyr Cys Lys₅₉₅ Arg Gly Arg Lys Lys₆₀₀ Leu Leu Tyr Ile Phe₆₀₅ Lys Gln Pro
 Phe Met₆₁₀ Arg Pro Val Gln Thr₆₁₅ Thr Gln Glu Glu Asp₆₂₀ Gly Cys Ser Cys

Arg Phe Pro Glu Glu Glu Gly Gly Cys^{-SL} Glu Leu Arg Val Lys Phe
 625 630 635 640
 Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu
 645 650 655
 Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp
 660 665 670
 Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys
 675 680 685
 Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala
 690 695 700
 Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
 705 710 715 720
 Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
 725 730 735
 Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
 740 745

<210> 110
 <211> 2244
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 110
 atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60
 ccccggtcgt cgttggcact ttccctgact gccgaccaga tgggtgtccgc ctttctggac 120
 gccgagcctc caattctgta ctcggagtac gatccgactc gcccgttctc cgaagccagc 180
 atgatggggc tgttgactaa cctggcggac cgcgagttgg tgcacatgat taactgggct 240
 aagcgggtgc cgggcttcgt ggacctggcc ctgcacgacc aagtgcacct cctggaatgc 300
 gcctggatgg aaatcctcat gatcggcctc gtgtggagat ccatggagca tcccggaaag 360
 ctctgttttg cacccaacct cctgcttgat cgcaaccagg gaaaatgcgt ggaaggggggt 420
 gtcgagattt tcgacatgct gctcgccacc tcttcccgggt tccggatgat gaatctgcag 480
 ggagaagagt tcgtgtgtct gaagtcaatc atcctgctga actccgggggt ctataccttc 540
 ctgagctcga ccctcaagtc actggaggaa aaagaccaca tccatcgcgt gctcgataag 600
 atcaccgaca cccttatcca tctcatggcg aaggctggac tgaccctgca acagcagcac 660
 cagaggctgg cccagttgct gctgattctg agccacatcc ggcacatgtc gtccaagagg 720
 atggaacacc tgtacagcat gaagtgaag aacgtcgtgc ctctgtccga tctgtcctg 780

_SL

gaaatgctgg acgcgcacag actcctgcaa tggctggagc agcaggtggc gaagcggaga 840
actaagcggg aaattgtgat gaccagtc cccgccactc ttagcctttc acccgggtgag 900
cgcgcaaccc tgtcttgag agcctcccaa gacatctcaa aataccttaa ttggtatcaa 960
cagaagccc gacaggctcc tcgccttctg atctaccaca ccagccggct ccattctgga 1020
atccctgcca gggtcagcgg tagcggatct gggaccgact acaccctcac tatcagctca 1080
ctgcagccag aggacttcgc tgtctatttc tgtcagcaag ggaacaccct gccctacacc 1140
tttggacagg gcaccaagct cgagattaaa ggtggaggtg gcagcggagg aggtgggtcc 1200
ggcgggtggag gaagccaggt ccaactccaa gaaagcggac cgggtcttgt gaagccatca 1260
gaaactcttt cactgacttg tactgtgagc ggagtgtctc tccccgatta cggggtgtct 1320
tggatcagac agccaccggg gaagggctct gaatggattg gagtgatttg gggctctgag 1380
actacttact actcttcac cctcaagtca cgcgtcacca tctcaaagga caactctaag 1440
aatcaggtgt cactgaaact gtcattctgt accgcagccg acaccgccgt gtactattgc 1500
gctaagcatt actattatgg cgggagctac gcaatggatt actggggaca gggactctg 1560
gtcaccgtgt ccagcaccac taccagca ccgaggccac ccacccggc tcctaccatc 1620
gcctcccagc ctctgtccct gcgtccggag gcatgtagac ccgcagctgg tggggccgtg 1680
cataccggg gtcttgactt cgctgcgat atctacattt gggcccctct ggctgggtact 1740
tgcggggtcc tgctgctttc actcgtgatc actctttact gtaagcgcgg tcggaagaag 1800
ctgctgtaca tctttaagca acccttcatg aggctgtgc agactactca agaggaggac 1860
ggctgttcat gccggttccc agaggaggag gaaggcggct gcgaactgcg cgtgaaattc 1920
agccgcagc cagatgtctc agcctacaag caggggcaga accagctcta caacgaactc 1980
aatcttggc ggagagagga gtacgacgtg ctggacaagc ggagaggacg ggaccagaa 2040
atgggcggga agccgcgag aaagaatccc caagagggcc tgtacaacga gtcctaaaag 2100
gataagatgg cagaagccta tagcgagatt ggtatgaaag ggaacgcag aagaggcaaa 2160
ggccacgac gactgtacca gggactcagc accgccacca aggacaccta tgacgtcttt 2220
cacatgcagg ccctgccgcc tcgg 2244

<210> 111

<211> 753

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 111

Met Ala Leu Pro Val Thr Ala Leu Leu Pro Leu Ala Leu Leu
1 5 10 15

His Ala Ala Arg Pro Arg Ser Ser Leu Ala Leu Ser Leu Thr Ala Asp

																_SL															
20								25								30															
Gln	Met	Val 35	Ser	Ala	Leu	Leu	Asp 40	Ala	Glu	Pro	Pro	Ile 45	Leu	Tyr	Ser																
Glu	Tyr 50	Asp	Pro	Thr	Arg	Pro 55	Phe	Ser	Glu	Ala	Ser 60	Met	Met	Gly	Leu																
Leu 65	Thr	Asn	Leu	Ala	Asp 70	Arg	Glu	Leu	Val	His 75	Met	Ile	Asn	Trp	Ala 80																
Lys	Arg	Val	Pro	Gly 85	Phe	Val	Asp	Leu	Ala 90	Leu	His	Asp	Gln	Val 95	His																
Leu	Leu	Glu	Cys 100	Ala	Trp	Met	Glu	Ile 105	Leu	Met	Ile	Gly	Leu 110	Val	Trp																
Arg	Ser	Met 115	Glu	His	Pro	Gly	Lys 120	Leu	Leu	Phe	Ala	Pro 125	Asn	Leu	Leu																
Leu	Asp 130	Arg	Asn	Gln	Gly	Lys 135	Cys	Val	Glu	Gly	Gly 140	Val	Glu	Ile	Phe																
Asp 145	Met	Leu	Leu	Ala	Thr 150	Ser	Ser	Arg	Phe	Arg 155	Met	Met	Asn	Leu	Gln 160																
Gly	Glu	Glu	Phe	Val 165	Cys	Leu	Lys	Ser	Ile 170	Ile	Leu	Leu	Asn	Ser 175	Gly																
Val	Tyr	Thr	Phe 180	Leu	Ser	Ser	Thr	Leu 185	Lys	Ser	Leu	Glu	Glu 190	Lys	Asp																
His	Ile	His 195	Arg	Val	Leu	Asp	Lys 200	Ile	Thr	Asp	Thr	Leu 205	Ile	His	Leu																
Met	Ala 210	Lys	Ala	Gly	Leu	Thr 215	Leu	Gln	Gln	Gln	His 220	Gln	Arg	Leu	Ala																
Gln 225	Leu	Leu	Leu	Ile	Leu 230	Ser	His	Ile	Arg	His 235	Met	Ser	Ser	Lys	Arg 240																
Met	Glu	His	Leu	Tyr 245	Ser	Met	Lys	Cys	Lys 250	Asn	Val	Val	Pro	Leu 255	Ser																
Asp	Leu	Leu	Leu 260	Glu	Met	Leu	Asp	Ala 265	His	Arg	Leu	Gly	Thr 270	Gly	Ala																
Glu	Asp	Pro 275	Arg	Pro	Ser	Arg	Lys 280	Arg	Arg	Ser	Leu	Gly 285	Asp	Val	Gly																
Glu	Ile	Val	Met	Thr	Gln	Ser	Pro	Ala	Thr	Leu	Ser	Leu	Ser	Pro	Gly																

_SL

290		295		300											
Glu 305	Arg	Ala	Thr	Leu	Ser 310	Cys	Arg	Ala	Ser	Gln 315	Asp	Ile	Ser	Lys	Tyr 320
Leu	Asn	Trp	Tyr	Gln 325	Gln	Lys	Pro	Gly	Gln 330	Ala	Pro	Arg	Leu	Leu 335	Ile
Tyr	His	Thr	Ser 340	Arg	Leu	His	Ser	Gly 345	Ile	Pro	Ala	Arg	Phe 350	Ser	Gly
Ser	Gly	Ser 355	Gly	Thr	Asp	Tyr	Thr 360	Leu	Thr	Ile	Ser	Ser 365	Leu	Gln	Pro
Glu 370	Asp	Phe	Ala	Val	Tyr	Phe 375	Cys	Gln	Gln	Gly	Asn 380	Thr	Leu	Pro	Tyr
Thr 385	Phe	Gly	Gln	Gly	Thr 390	Lys	Leu	Glu	Ile	Lys 395	Gly	Gly	Gly	Gly	Ser 400
Gly	Gly	Gly	Gly	Ser 405	Gly	Gly	Gly	Gly	Ser 410	Gln	Val	Gln	Leu	Gln 415	Glu
Ser	Gly	Pro	Gly 420	Leu	Val	Lys	Pro	Ser 425	Glu	Thr	Leu	Ser	Leu 430	Thr	Cys
Thr	Val	Ser 435	Gly	Val	Ser	Leu	Pro 440	Asp	Tyr	Gly	Val	Ser 445	Trp	Ile	Arg
Gln 450	Pro	Pro	Gly	Lys	Gly	Leu 455	Glu	Trp	Ile	Gly	Val 460	Ile	Trp	Gly	Ser
Glu 465	Thr	Thr	Tyr	Tyr	Ser 470	Ser	Ser	Leu	Lys	Ser 475	Arg	Val	Thr	Ile	Ser 480
Lys	Asp	Asn	Ser	Lys 485	Asn	Gln	Val	Ser	Leu 490	Lys	Leu	Ser	Ser	Val 495	Thr
Ala	Ala	Asp	Thr 500	Ala	Val	Tyr	Tyr	Cys 505	Ala	Lys	His	Tyr	Tyr 510	Tyr	Gly
Gly	Ser	Tyr 515	Ala	Met	Asp	Tyr	Trp 520	Gly	Gln	Gly	Thr	Leu 525	Val	Thr	Val
Ser 530	Ser	Thr	Thr	Thr	Pro	Ala 535	Pro	Arg	Pro	Pro	Thr 540	Pro	Ala	Pro	Thr
Ile 545	Ala	Ser	Gln	Pro	Leu 550	Ser	Leu	Arg	Pro	Glu 555	Ala	Cys	Arg	Pro	Ala 560
Ala	Gly	Gly	Ala	Val	His	Thr	Arg	Gly	Leu	Asp	Phe	Ala	Cys	Asp	Ile

565 570^{-SL} 575

Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser
 580 585 590

Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr
 595 600 605

Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu
 610 615 620

Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Gly Gly Cys Glu
 625 630 635 640

Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln
 645 650 655

Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu
 660 665 670

Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly
 675 680 685

Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln
 690 695 700

Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu
 705 710 715 720

Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr
 725 730 735

Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro
 740 745 750

Arg

<210> 112
 <211> 2259
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polynucleotide"

<400> 112
 atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60
 ccccggtcgt cgttggcact ttccctgact gccgaccaga tgggtgtccgc ctttctggac 120
 gccgagcctc caattctgta ctcggagtac gatccgactc gcccgttctc cgaagccagc 180

						_SL	
atgatgggcc	tgttgactaa	cctggcggac	cgcgagttgg	tgcacatgat	taactgggct		240
aagcgggtgc	cgggcttcgt	ggacctggcc	ctgcacgacc	aagtgcacct	cctggaatgc		300
gcctggatgg	aaatcctcat	gatcggcctc	gtgtggagat	ccatggagca	tcccggaaag		360
ctcctgtttg	cacccaacct	cctgcttgat	cgcaaccagg	gaaaatgcgt	ggaagggggg		420
gtcgagattt	tcgacatgct	gctcgccacc	tcttcccggg	tccggatgat	gaatctgcag		480
ggagaagagt	tcgtgtgtct	gaagtcaatc	atcctgtctga	actccggggg	ctataaccttc		540
ctgagctcga	ccctcaagtc	actggaggaa	aaagaccaca	tccatcgcg	gctcgataag		600
atcaccgaca	cccttatcca	tctcatggcg	aaggctggac	tgaccctgca	acagcagcac		660
cagaggctgg	cccagttgct	gctgattctg	agccacatcc	ggcacatgtc	gtccaagagg		720
atggaacacc	tgtacagcat	gaagtgcaag	aacgtcgtgc	ctctgtccga	tctgtctctg		780
gaaatgctgg	acgcgcacag	actcggaacc	ggcgcggaag	acccccggcc	ctccaggaag		840
cgaaggtccc	tcggagacgt	gggtgaaatt	gtgatgacct	agtcaccgcg	cactcttagc		900
ctttcaccgg	gtgagcgcgc	aaccctgtct	tgcagagcct	ccaagacat	ctcaaaatac		960
cttaattggg	atcaacagaa	gcccggacag	gctcctcgcc	ttctgatcta	ccacaccagc		1020
cggctccatt	ctggaatccc	tgccaggttc	agcggtagcg	gatctgggac	cgactacacc		1080
ctcactatca	gctcactgca	gccagaggac	ttcgtgtctt	atttctgtca	gcaagggaac		1140
accctgccct	acacctttgg	acagggcacc	aagctcgaga	ttaaagggtg	aggtggcagc		1200
ggaggaggtg	ggtccggcgg	tggaggaagc	caggtccaac	tccaagaaag	cggaccgggt		1260
cttgtgaagc	catcagaaac	tctttcactg	acttgtactg	tgagcggagt	gtctctcccc		1320
gattacgggg	tgtcttggat	cagacagcca	ccgggggaag	gtctggaatg	gattggagtg		1380
atttggggct	ctgagactac	ttactactct	tcatccctca	agtcacgcgt	caccatctca		1440
aaggacaact	ctaagaatca	ggtgtcactg	aaactgtcat	ctgtgaccgc	agccgacacc		1500
gccgtgtact	attgcgctaa	gcattactat	tatggcggga	gctacgcaat	ggattactgg		1560
ggacagggta	ctctggtcac	cgtgtccagc	accactaccc	cagcaccgag	gccaccacc		1620
ccggctccta	ccatcgctc	ccagcctctg	tccctgcgtc	cggaggcatg	tagaccgcga		1680
gctgggtggg	ccgtgcatac	ccgggggtctt	gacttcgcct	gcgatatcta	catttggggc		1740
cctctggctg	gtacttgctg	ggtcctgctg	ctttcactcg	tgatcactct	ttactgtaag		1800
cgcggtcgg	agaagctgct	gtacatcttt	aagcaaccct	tcatgaggcc	tgtgcagact		1860
actcaagagg	aggacggctg	ttcatgccgg	ttcccagagg	aggaggaagg	cggctgcgaa		1920
ctgcgcgtga	aattcagccg	cagcgcagat	gctccagcct	acaagcaggg	gcagaaccag		1980
ctctacaacg	aactcaatct	tggtcggaga	gaggagtacg	acgtgctgga	caagcggaga		2040
ggacgggacc	cagaaatggg	cgggaagccg	cgcagaaaga	atccccaaga	gggcctgtac		2100
aacgagctcc	aaaaggataa	gatggcagaa	gcctatagcg	agattgggtat	gaaaggggaa		2160
cgcagaagag	gcaaaggcca	cgacggactg	taccagggac	tcagcaccgc	caccaaggac		2220

acctatgacg ctcttcacat gcaggccctg ccgcctcgg

_SL

2259

<210> 113
<211> 751
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 113
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Arg Ser Ser Leu Ala Leu Ser Leu Thr Ala Asp
20 25 30

Gln Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser
35 40 45

Glu Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu
50 55 60

Leu Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala
65 70 75 80

Lys Arg Val Pro Gly Phe Val Asp Leu Ala Leu His Asp Gln Val His
85 90 95

Leu Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp
100 105 110

Arg Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu
115 120 125

Leu Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe
130 135 140

Asp Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln
145 150 155 160

Gly Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly
165 170 175

Val Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp
180 185 190

His Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu
195 200 205

Met Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala
210 215 220

_SL

Gln Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Ser Lys Arg
225 230 235 240

Met Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Ser
245 250 255

Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu Gly Thr Gly Ala
260 265 270

Glu Asp Pro Arg Pro Ser Arg Lys Arg Arg Ser Leu Gly Gly Glu Ile
275 280 285

Val Met Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg
290 295 300

Ala Thr Leu Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr Leu Asn
305 310 315 320

Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr His
325 330 335

Thr Ser Arg Leu His Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly
340 345 350

Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
355 360 365

Phe Ala Val Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr Phe
370 375 380

Gly Gln Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly
385 390 395 400

Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Glu Ser Gly
405 410 415

Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val
420 425 430

Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln Pro
435 440 445

Pro Gly Lys Gly Leu Glu Trp Ile Gly Val Ile Trp Gly Ser Glu Thr
450 455 460

Thr Tyr Tyr Ser Ser Ser Leu Lys Ser Arg Val Thr Ile Ser Lys Asp
465 470 475 480

Asn Ser Lys Asn Gln Val Ser Leu Lys Leu Ser Ser Val Thr Ala Ala
485 490 495

_SL

Asp Thr Ala Val Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly Ser
500 505 510

Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
515 520 525

Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala
530 535 540

Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly
545 550 555 560

Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile
565 570 575

Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val
580 585 590

Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe
595 600 605

Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly
610 615 620

Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg
625 630 635 640

Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln
645 650 655

Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp
660 665 670

Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro
675 680 685

Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp
690 695 700

Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg
705 710 715 720

Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr
725 730 735

Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
740 745 750

<210> 114
<211> 2253

<212> DNA
<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 114

atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg	60
ccccggtcgt cgttggcact ttccctgact gccgaccaga tgggtgtccgc ctttctggac	120
gccgagcctc caattctgta ctcggagtac gatccgactc gcccgttctc cgaagccagc	180
atgatggggc tgttgactaa cctggcggac cgcgagttgg tgcacatgat taactgggct	240
aagcgggtgc cgggcttcgt ggacctggcc ctgcacgacc aagtgcacct cctggaatgc	300
gcctggatgg aaatcctcat gatcggcctc gtgtggagat ccatggagca tcccggaaag	360
ctcctgtttg caccacacct cctgcttgat cgcaaccagg gaaaatgcgt ggaaggggggt	420
gtcgagattt tcgacatgct gctcgccacc tcttcccggg tccggatgat gaatctgcag	480
ggagaagagt tcgtgtgtct gaagtcaatc atcctgctga actccggggg ctataccttc	540
ctgagctcga ccctcaagtc actggaggaa aaagaccaca tccatcgcgt gctcgataag	600
atcaccgaca cccttatcca tctcatggcg aaggctggac tgaccctgca acagcagcac	660
cagaggctgg ccagttgct gctgattctg agccacatcc ggcacatgtc gtccaagagg	720
atggaacacc tgtacagcat gaagtgaag aacgtcgtgc ctctgtccga tctgtcctg	780
gaaatgctgg acgcgcacag actcggcaca ggtgccgagg accctcggcc aagccgcaaa	840
aggaggtcac ttggcggcga aattgtgatg acccagtcac ccgccactct tagcctttca	900
cccggtgagc gcgcaaccct gtcttgaga gcctcccaag acatctcaaa ataccttaat	960
tggtatcaac agaagcccgg acaggctcct cgccttctga tctaccacac cagccggctc	1020
cattctggaa tccctgccag gttcagcggg agcggatctg ggaccgacta caccctcact	1080
atcagctcac tgcagccaga ggacttcgct gtctatttct gtcagcaagg gaacaccctg	1140
ccctacacct ttggacaggg caccaagctc gagattaaag gtggaggtgg cagcggagga	1200
ggtgggtccg gcggtggagg aagccaggtc caactccaag aaagcggacc gggctcttg	1260
aagccatcag aaactctttc actgacttgt actgtgagcg gagtgtctct ccccgattac	1320
ggggtgtctt ggatcagaca gccaccgggg aagggctctg aatggattgg agtgatttgg	1380
ggctctgaga ctacttacta ctcttcatcc ctcaagtcac gcgtcaccat ctcaaaggac	1440
aactctaaga atcaggtgtc actgaaactg tcatctgtga ccgcagccga caccgccgtg	1500
tactattgcg ctaagcatta ctattatggc gggagctacg caatggatta ctggggacag	1560
ggtactctgg tcaccgtgtc cagcaccact accccagcac cgaggccacc caccgccgct	1620
cctaccatcg cctcccagcc tctgtccctg cgtccggagg catgtagacc cgcagctggt	1680
ggggccgtgc ataccgggg tcttgacttc gcctgcgata tctacatttg ggcccctctg	1740
gctgggtactt gcggggctct gctgctttca ctctgtatca ctctttactg taagcgcggg	1800

_SL

cggaagaagc tgctgtacat ctttaagcaa cccttcacga ggcctgtgca gactactcaa 1860
gaggaggacg gctgttcacg ccggttccca gaggaggagg aaggcggtg cgaactgcgc 1920
gtgaaattca gccgcagcgc agatgctcca gcctacaagc aggggcagaa ccagctctac 1980
aacgaactca atcttggtcg gagagaggag tacgacgtgc tggacaagcg gagaggacgg 2040
gacccagaaa tgggcgggaa gccgcgcaga aagaatcccc aagagggcct gtacaacgag 2100
ctccaaaagg ataagatggc agaagcctat agcgagattg gtatgaaagg ggaacgcaga 2160
agaggcaaag gccacgacgg actgtaccag ggactcagca ccgccaccaa ggacacctat 2220
gacgctcttc acatgcaggc cctgccgcct cg 2253

<210> 115

<211> 750

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 115

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Arg Ser Ser Leu Ala Leu Ser Leu Thr Ala Asp
20 25 30

Gln Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser
35 40 45

Glu Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu
50 55 60

Leu Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala
65 70 75 80

Lys Arg Val Pro Gly Phe Val Asp Leu Ala Leu His Asp Gln Val His
85 90 95

Leu Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp
100 105 110

Arg Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu
115 120 125

Leu Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe
130 135 140

Asp Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln
145 150 155 160

_SL

Gly Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly
165 170 175

Val Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp
180 185 190

His Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu
195 200 205

Met Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala
210 215 220

Gln Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Ser Lys Arg
225 230 235 240

Met Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Ser
245 250 255

Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu Gly Thr Gly Ala
260 265 270

Glu Asp Pro Arg Pro Ser Arg Lys Arg Arg Ser Leu Gly Glu Ile Val
275 280 285

Met Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala
290 295 300

Thr Leu Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr Leu Asn Trp
305 310 315 320

Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr His Thr
325 330 335

Ser Arg Leu His Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser
340 345 350

Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe
355 360 365

Ala Val Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr Phe Gly
370 375 380

Gln Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly
385 390 395 400

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Glu Ser Gly Pro
405 410 415

Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser
420 425 430

_SL

Gly Val Ser₄₃₅ Leu Pro Asp Tyr Gly₄₄₀ Val Ser Trp Ile Arg₄₄₅ Gln Pro Pro

Gly Lys₄₅₀ Gly Leu Glu Trp Ile₄₅₅ Gly Val Ile Trp Gly₄₆₀ Ser Glu Thr Thr

Tyr₄₆₅ Tyr Ser Ser Ser Leu₄₇₀ Lys Ser Arg Val Thr₄₇₅ Ile Ser Lys Asp Asn₄₈₀

Ser Lys Asn Gln Val₄₈₅ Ser Leu Lys Leu Ser₄₉₀ Ser Val Thr Ala Ala₄₉₅ Asp

Thr Ala Val Tyr₅₀₀ Tyr Cys Ala Lys His₅₀₅ Tyr Tyr Tyr Gly Gly₅₁₀ Ser Tyr

Ala Met Asp₅₁₅ Tyr Trp Gly Gln Gly₅₂₀ Thr Leu Val Thr Val₅₂₅ Ser Ser Thr

Thr Thr₅₃₀ Pro Ala Pro Arg Pro₅₃₅ Pro Thr Pro Ala Pro₅₄₀ Thr Ile Ala Ser

Gln₅₄₅ Pro Leu Ser Leu Arg₅₅₀ Pro Glu Ala Cys Arg₅₅₅ Pro Ala Ala Gly Gly₅₆₀

Ala Val His Thr Arg₅₆₅ Gly Leu Asp Phe Ala₅₇₀ Cys Asp Ile Tyr Ile₅₇₅ Trp

Ala Pro Leu Ala₅₈₀ Gly Thr Cys Gly Val₅₈₅ Leu Leu Leu Ser Leu₅₉₀ Val Ile

Thr Leu Tyr₅₉₅ Cys Lys Arg Gly Arg₆₀₀ Lys Lys Leu Leu Tyr₆₀₅ Ile Phe Lys

Gln₆₁₀ Pro Phe Met Arg Pro Val₆₁₅ Gln Thr Thr Gln Glu₆₂₀ Glu Asp Gly Cys

Ser₆₂₅ Cys Arg Phe Pro Glu₆₃₀ Glu Glu Glu Gly Gly₆₃₅ Cys Glu Leu Arg Val₆₄₀

Lys Phe Ser Arg Ser₆₄₅ Ala Asp Ala Pro Ala₆₅₀ Tyr Lys Gln Gly Gln₆₅₅ Asn

Gln Leu Tyr Asn₆₆₀ Glu Leu Asn Leu Gly₆₆₅ Arg Arg Glu Glu Tyr₆₇₀ Asp Val

Leu Asp Lys₆₇₅ Arg Arg Gly Arg Asp₆₈₀ Pro Glu Met Gly Gly₆₈₅ Lys Pro Arg

Arg Lys₆₉₀ Asn Pro Gln Glu Gly₆₉₅ Leu Tyr Asn Glu Leu₇₀₀ Gln Lys Asp Lys

_SL

Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg
705 710 715 720

Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys
725 730 735

Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
740 745 750

<210> 116
<211> 2250
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 116
atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60
ccccggtcgt cgttggcact ttccctgact gccgaccaga tgggtgtccgc ctttctggac 120
gccgagcctc caattctgta ctcggagtac gatccgactc gcccgttctc cgaagccagc 180
atgatgggccc tgttgactaa cctggcggac cgcgagttgg tgcacatgat taactgggct 240
aagcgggtgc cgggcttcgt ggacctggcc ctgcacgacc aagtgcacct cctggaatgc 300
gcctggatgg aaatcctcat gatcggcctc gtgtggagat ccatggagca tcccggaaag 360
ctcctgtttg cacccaacct cctgcttgat cgcaaccagg gaaaatgcgt ggaaggggggt 420
gtcgagattt tgcacatgct gctcgccacc tcttcccgggt tccggatgat gaatctgcag 480
ggagaagagt tcgtgtgtct gaagtcaatc atcctgctga actccgggggt ctataccttc 540
ctgagctcga ccctcaagtc actggaggaa aaagaccaca tccatcgcgt gctcgataag 600
atcaccgaca cccttatcca tctcatggcg aaggctggac tgaccctgca acagcagcac 660
cagaggctgg cccagttgct gctgattctg agccacatcc ggcacatgtc gtccaagagg 720
atggaacacc tgtacagcat gaagtgaag aacgtcgtgc ctctgtccga tctgtcctg 780
gaaatgctgg acgcgcacag actcggaaac ggagcagaag atcccagacc aagccggaaa 840
aggcgggtccc tgggtgaaat tgtgatgacc cagtcacccg ccactcttag cttttcacc 900
ggtgagcgcg caaccctgtc ttgcagagcc tccaagaca tctcaaaata ctttaattgg 960
tatcaacaga agcccggaca ggctcctcgc cttctgatct accacaccag cgggtccat 1020
tctggaatcc ctgccagggt cagcggtagc ggatctggga ccgactacac ctcactatc 1080
agctcactgc agccagagga cttcgtgtc tatttctgtc agcaaggga caccctgccc 1140
tacacctttg gacagggcac caagctcgag attaaaggtg gaggtggcag cggaggagg 1200
gggtccggcg gtggaggaag ccaggtccaa ctccaagaaa gcggaccggg tcttgtgaag 1260
ccatcagaaa ctctttcact gacttgact gtgagcggag tgtctctccc cgattacggg 1320

_SL

gtgtcttggg	tcagacagcc	accggggaag	ggtctggaat	ggattggagt	gatttggggc	1380
tctgagacta	cttactactc	ttcatccctc	aagtcacgcg	tcaccatctc	aaaggacaac	1440
tctaagaatc	aggtgtcact	gaaactgtca	tctgtgaccg	cagccgacac	cgccgtgtac	1500
tattgcgcta	agcattacta	ttatggcggg	agctacgcaa	tggattactg	gggacagggg	1560
actctgggtc	ccgtgtccag	caccactacc	ccagcaccga	ggccaccac	cccggctcct	1620
accatcgcct	cccagcctct	gtccctgcgt	ccggaggcat	gtagaccgcg	agctgggtggg	1680
gccgtgcata	cccgggggtct	tgacttcgcc	tgcgatatct	acatttgggc	ccctctggct	1740
ggtacttgcg	gggtcctgct	gctttcactc	gtgatcactc	tttactgtaa	gcgcgggtcgg	1800
aagaagctgc	tgtacatctt	taagcaacct	ttcatgaggc	ctgtgcagac	tactcaagag	1860
gaggacggct	gttcatgccg	gttcccagag	gaggaggaag	gcggctgcga	actgcgcgtg	1920
aaattcagcc	gcagcgcaga	tgctccagcc	tacaagcagg	ggcagaacca	gctctacaac	1980
gaactcaatc	ttggtcggag	agaggagtac	gacgtgctgg	acaagcggag	aggacgggac	2040
ccagaaatgg	gcgggaagcc	gcgcagaaag	aatccccaag	agggcctgta	caacgagctc	2100
caaaaggata	agatggcaga	agcctatagc	gagattggta	tgaaagggga	acgcagaaga	2160
ggcaaaggcc	acgacggact	gtaccaggga	ctcagcaccg	ccaccaagga	cacctatgac	2220
gctcttcaca	tgcaggccct	gccgcctcgg				2250

<210> 117

<400> 117
000

<210> 118

<211> 126

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 118

aagcgcggtc	ggaagaagct	gctgtacatc	tttaagcaac	ccttcatgag	gcctgtgcag	60
------------	------------	------------	------------	------------	------------	----

actactcaag	aggaggacgg	ctgttcatgc	cggttccag	aggaggagga	aggcggctgc	120
------------	------------	------------	-----------	------------	------------	-----

gaactg						126
--------	--	--	--	--	--	-----

<210> 119

<211> 336

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 119

_SL

cgcgtgaaat tcagccgcag cgcagatgct ccagcctaca agcaggggca gaaccagctc	60
tacaacgaac tcaatcttgg tcggagagag gactacgacg tgctggacaa gcggagagga	120
cgggaccag aaatgggagg gaagccgcgc agaaagaatc cccaagaggg cctgtacaac	180
gagctccaaa aggataagat ggcagaagcc tatagcgaga ttggtatgaa aggggaacgc	240
agaagaggca aaggccacga cggactgtac cagggactca gcaccgccac caaggacacc	300
tatgacgctc ttcacatgca ggcctgccc cctcgg	336

<210> 120
 <211> 35
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 120
 Thr Lys Lys Lys Tyr Ser Ser Ser Val His Asp Pro Asn Gly Glu Tyr
 1 5 10 15

Met Phe Met Arg Ala Val Asn Thr Ala Lys Lys Ser Arg Leu Thr Asp
 20 25 30

Val Thr Leu
 35

<210> 121
 <211> 245
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 121
 Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln Met Val Ser Ala Leu Leu
 1 5 10 15

Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu Tyr Asp Pro Thr Arg Pro
 20 25 30

Phe Ser Glu Ala Ser Met Met Gly Leu Leu Thr Asn Leu Ala Asp Arg
 35 40 45

Glu Leu Val His Met Ile Asn Trp Ala Lys Arg Val Pro Gly Phe Val
 50 55 60

Asp Leu Thr Leu His Asp Gln Val His Leu Leu Glu Cys Ala Trp Met
 65 70 75 80

Glu Ile Leu Met Ile Gly Leu Val Trp Arg Ser Met Glu His Pro Gly
 Page 105

[illegible]

_SL
 ttcgtgtgtc tgaagtcaat catcctgctg aactccgggg tctatacctt cctgagctcg 480
 accctcaagt cactggagga aaaagaccac atccatcgcg tgctcgataa gatcaccgac 540
 acccttatcc atctcatggc gaaggctgga ctgaccctgc aacagcagca ccagaggctg 600
 gccagttgc tgctgattct gagccacatc cggcacatgt cgaacaagag gatggaacac 660
 ctgtacagca tgaagtgcaa gaacgtcgtg cctctgtccg atctgctcct ggaaatgctg 720
 gacgcgcaca gactc 735

<210> 123
 <211> 4
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 123
 Arg Thr Lys Arg
 1

<210> 124
 <211> 41
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 124
 Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr
 1 5 10 15

Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro
 20 25 30

Pro Arg Asp Phe Ala Ala Tyr Arg Ser
 35 40

<210> 125
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 125
 Gly Thr Gly Ala Glu Asp Pro Arg Pro Ser Arg Lys Arg Arg Ser Leu
 1 5 10 15

Gly Asp Val Gly
 20

<210> 126
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 126
ggaaccggcg cggaagaccc ccggccctcc aggaagcgaa ggtccctcgg agacgtgggt 60

<210> 127
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 127
Gly Thr Gly Ala Glu Asp Pro Arg Pro Ser Arg Lys Arg Arg
1 5 10

<210> 128
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 128
ggaaccggcg cggaagaccc ccggccctcc aggaagcgaa gg 42

<210> 129
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 129
Leu Gln Trp Leu Glu Gln Gln Val Ala Lys Arg Arg Thr Lys Arg
1 5 10 15

<210> 130
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

oligonucleotide" _SL

<400> 130
ctgcaatggc tggagcagca ggtggcgaag cggagaacta agcgg

45

<210> 131
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 131
Gly Thr Gly Ala Glu Asp Pro Arg Pro Ser Arg Lys Arg Arg Ser Leu
1 5 10 15

Gly Gly

<210> 132
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic oligonucleotide"

<400> 132
ggcacaggtg ccgaggaccc tcggccaagc cgcaaaagga ggtcacttgg cggc

54

<210> 133
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 133
Gly Thr Gly Ala Glu Asp Pro Arg Pro Ser Arg Lys Arg Arg Ser Leu
1 5 10 15

Gly

<210> 134
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic oligonucleotide"

<400> 134
ggaaccggag cagaagatcc cagaccaagc cggaaaaggc ggtccctggg t 51

<210> 135
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 135
Ser Leu Asn Leu Thr Glu Ser His Asn Ser Arg Lys Lys Arg
1 5 10

<210> 136
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic oligonucleotide"

<400> 136
agtctcaatt tgactgagtc acacaattcc aggaagaaaa gg 42

<210> 137
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 137
Cys Lys Ile Asn Gly Tyr Pro Lys Arg Gly Arg Lys Arg Arg
1 5 10

<210> 138
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic oligonucleotide"

<400> 138
tgcaagatca acggctaccc taagaggggc agaaagcggc gg 42

<210> 139
<211> 21
<212> PRT
<213> Artificial Sequence

<220>

_SL

<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 139
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro
20

<210> 140
<211> 63
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic oligonucleotide"

<400> 140
atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60
ccc 63

<210> 141
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 141
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Arg Ser Ser Leu Ala Leu Ser Leu Thr Ala Asp
20 25 30

Gln Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser
35 40 45

Glu Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu
50 55 60

Leu Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala
65 70 75 80

Lys Arg Val Pro Gly Phe Val Asp Leu Ala Leu His Asp Gln Val His
85 90 95

Leu Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp
100 105 110

Arg Ser Met Glu His Pro Gly Lys Leu Leu ^{-SL}Phe Ala Pro Asn Leu Leu
 115 120 125
 Leu Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe
 130 135 140
 Asp Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln
 145 150 155 160
 Gly Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly
 165 170 175
 Val Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp
 180 185 190
 His Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu
 195 200 205
 Met Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala
 210 215 220
 Gln Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Ser Lys Arg
 225 230 235 240
 Met Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Ser
 245 250 255
 Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu Arg Thr Lys Arg
 260 265 270
 Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 275 280 285
 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr
 290 295 300
 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
 305 310 315 320
 Tyr His Thr Ser Arg Leu His Ser Gly Ile Pro Ala Arg Phe Ser Gly
 325 330 335
 Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
 340 345 350
 Glu Asp Phe Ala Val Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr
 355 360 365
 Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser
 370 375 380

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser^{-SL} Gln Val Gln Leu Gln Glu
 385 390 395 400
 Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys
 405 410 415
 Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg
 420 425 430
 Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Val Ile Trp Gly Ser
 435 440 445
 Glu Thr Thr Tyr Tyr Ser Ser Ser Leu Lys Ser Arg Val Thr Ile Ser
 450 455 460
 Lys Asp Asn Ser Lys Asn Gln Val Ser Leu Lys Leu Ser Ser Val Thr
 465 470 475 480
 Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly
 485 490 495
 Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
 500 505 510
 Ser Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr
 515 520 525
 Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala
 530 535 540
 Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile
 545 550 555 560
 Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser
 565 570 575
 Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr
 580 585 590
 Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu
 595 600 605
 Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu
 610 615 620
 Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln
 625 630 635 640
 Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu
 645 650 655

Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg^{-SL} Asp Pro Glu Met Gly Gly
660 665 670

Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln
675 680 685

Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu
690 695 700

Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr
705 710 715 720

Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro
725 730 735

Arg

<210> 142
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 142
atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60
ccccggtcgt cgttggcact ttccctgact gccgaccaga tgggtgtccgc ctttctggac 120
gccgagcctc caattctgta ctcggagtac gatccgactc gcccgttctc cgaagccagc 180
atgatggggc tgttgactaa cctggcggac cgcgagttgg tgcacatgat taactgggct 240
aagcgggtgc cgggcttcgt ggacctggcc ctgcacgacc aagtgcacct cctggaatgc 300
gcctggatgg aaatcctcat gatcggcctc gtgtggagat ccatggagca tcccggaaag 360
ctcctgtttg caccacacct cctgcttgat cgcaaccagg gaaaatgcgt ggaaggggggt 420
gtcgagattt tcgacatgct gtcgccacc tcttcccgggt tccggatgat gaatctgcag 480
ggagaagagt tcgtgtgtct gaagtcaatc atcctgctga actccgggggt ctataccttc 540
ctgagctcga ccctcaagtc actggaggaa aaagaccaca tccatcgcgt gctcgataag 600
atcaccgaca cccttatcca tctcatggcg aaggctggac tgaccctgca acagcagcac 660
cagaggctgg ccagttgct gctgattctg agccacatcc ggcacatgtc gtccaagagg 720
atggaacacc tgtacagcat gaagtgaag aacgtcgtgc ctctgtccga tctgctcctg 780
gaaatgctgg acgcgcacag actccgtact aaaagagaaa ttgtgatgac ccagtcaccc 840
gccactctta gcctttcacc cggtagcgc gcaaccctgt cttgcagagc ctcccaagac 900
atctcaaaat accttaattg gtatcaacag aagcccggac aggtcctcgt ctttctgatac 960
taccacacca gccggctcca ttctggaatc cctgccaggt tcagcggtag cggatctggg 1020

_SL

accgactaca ccctcactat cagctcactg cagccagagg acttcgctgt ctatttctgt 1080
cagcaagggga acaccctgcc ctacaccttt ggacagggga ccaagctcga gattaaaggt 1140
ggaggtggga gcggaggagg tgggtccggc ggtggaggaa gccaggtcca actccaagaa 1200
agcggaccgg gtcttgtgaa gccatcagaa actctttcac tgacttgtag tgtgagcgga 1260
gtgtctctcc ccgattacgg ggtgtcttgg atcagacagc caccggggaa ggggtctggaa 1320
tggattggag tgatttgggg ctctgagact acttactact cttcatccct caagtcacgc 1380
gtcaccatct caaaggacaa ctctaagaat caggtgtcac tgaaactgtc atctgtgacc 1440
gcagccgaca ccgccgtgta ctattgcgct aagcattact attatggcgg gagctacgca 1500
atggattact ggggacaggg tactctggtc accgtgtcca gcaccactac cccagcaccg 1560
aggccacca ccccggtcc taccatcgcc tcccagcctc tgtccctgcg tccggaggga 1620
tgtagaccgg cagctggtgg ggccgtgcat acccggggtc ttgacttcgc ctgcatatc 1680
tacatttggg cccctctggc tgggtacttc ggggtcctgc tgctttcact cgtgatcact 1740
ctttactgta agcgcggtcg gaagaagctg ctgtacatct ttaagcaacc cttcatgagg 1800
cctgtgcaga ctactcaaga ggaggacggc tgttcatgcc ggttcccaga ggaggaggaa 1860
ggcggctgcg aactgcgctg gaaattcagc cgcagcgcag atgctccagc ctacaagcag 1920
gggcagaacc agctctacaa cgaactcaat cttggtcgga gagaggagta cgacgtgctg 1980
gacaagcgga gaggacggga cccagaaatg ggcgggaagc cgcgcagaaa gaatcccaa 2040
gagggcctgt acaacgagct ccaaaggat aagatggcag aagcctatag cgagattggt 2100
atgaaagggg aacgcagaag aggcaaaggc cagcagggac tgtaccaggg actcagcacc 2160
gccaccaagg acacctatga cgctcttcac atgcaggccc tgccgcctcg g 2211

<210> 143

<211> 753

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 143

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Arg Ser Ser Leu Ala Leu Ser Leu Thr Ala Asp
20 25 30

Gln Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser
35 40 45

Glu Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu
50 55 60

_SL

Leu Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala
65 70 75 80

Lys Arg Val Pro Gly Phe Val Asp Leu Ala Leu His Asp Gln Val His
85 90 95

Leu Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp
100 105 110

Arg Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu
115 120 125

Leu Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe
130 135 140

Asp Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln
145 150 155 160

Gly Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly
165 170 175

Val Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp
180 185 190

His Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu
195 200 205

Met Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala
210 215 220

Gln Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Ser Lys Arg
225 230 235 240

Met Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Ser
245 250 255

Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu Gly Thr Gly Ala
260 265 270

Glu Asp Pro Arg Pro Ser Arg Lys Arg Arg Ser Leu Gly Asp Val Gly
275 280 285

Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
290 295 300

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr
305 310 315 320

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
325 330 335

_SL

Tyr His Thr Ser Arg Leu His Ser Gly Ile Pro Ala Arg Phe Ser Gly
340 345 350

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
355 360 365

Glu Asp Phe Ala Val Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr
370 375 380

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser
385 390 395 400

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Glu
405 410 415

Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys
420 425 430

Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg
435 440 445

Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Val Ile Trp Gly Ser
450 455 460

Glu Thr Thr Tyr Tyr Ser Ser Ser Leu Lys Ser Arg Val Thr Ile Ser
465 470 475 480

Lys Asp Asn Ser Lys Asn Gln Val Ser Leu Lys Leu Ser Ser Val Thr
485 490 495

Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly
500 505 510

Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
515 520 525

Ser Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr
530 535 540

Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala
545 550 555 560

Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile
565 570 575

Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser
580 585 590

Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr
595 600 605

_SL

Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu
610 615 620

Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu
625 630 635 640

Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln
645 650 655

Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu
660 665 670

Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly
675 680 685

Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln
690 695 700

Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu
705 710 715 720

Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr
725 730 735

Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro
740 745 750

Arg

<210> 144

<211> 2259

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 144

atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60

ccccggtcgt cgttggcact ttccctgact gccgaccaga tgggtgtccgc ccttctggac 120

gccgagcctc caattctgta ctcggagtac gatccgactc gcccgttctc cgaagccagc 180

atgatggggc tgttgactaa cctggcggac cgcgagttgg tgcacatgat taactgggct 240

aagcgggtgc cgggcttcgt ggacctggcc ctgcacgacc aagtgcacct cctggaatgc 300

gcctggatgg aaatcctcat gatcggcctc gtgtggagat ccatggagca tcccggaaag 360

ctcctgtttg cacccaacct cctgcttgat cgcaaccagg gaaaatgcgt ggaaggggggt 420

gtcgagattt tcgacatgct gctcgccacc tcttcccgggt tccggatgat gaatctgcag 480

	_SL	
ggagaagagt	tcgtgtgtct	gaagtcaatc
ctgagctcga	ccctcaagtc	actggaggaa
atcaccgaca	cccttatcca	tctcatggcg
cagaggctgg	cccagttgct	gctgattctg
atggaacacc	tgtacagcat	gaagtgcaag
gaaatgctgg	acgcgcacag	actcggaacc
cgaaggtccc	tcggagacgt	gggtgaaatt
ctttcaccgg	gtgagcgcgc	aaccctgtct
cttaattggt	atcaacagaa	gcccggacag
cggctccatt	ctggaatccc	tgccaggttc
ctcactatca	gctcactgca	gccagaggac
accctgccct	acacctttgg	acagggcacc
ggaggaggtg	ggtccggcgg	tggaggaagc
cttgtgaagc	catcagaaac	tctttcactg
gattacgggg	tgtcttggat	cagacagcca
atttggggct	ctgagactac	ttactactct
aaggacaact	ctaagaatca	ggtgtcactg
gccgtgtact	attgcgctaa	gcattactat
ggacagggta	ctctggtcac	cgtgtccagc
ccggctccta	ccatcgcttc	ccagcctctg
gctggtgggg	ccgtgcatac	ccgggggtctt
cctctggctg	gtacttgctg	ggtcctgctg
cgcggtcggg	agaagctgct	gtacatcttt
actcaagagg	aggacggctg	ttcatgccgg
ctgcgcgtga	aattcagccg	cagcgcagat
ctctacaacg	aactcaatct	tggtcggaga
ggacgggacc	cagaaatggg	cggaagccg
aacgagctcc	aaaaggataa	gatggcagaa
cgcagaagag	gcaaaggcca	cgacggactg
acctatgacg	ctcttcacat	gcaggccctg

540
600
660
720
780
840
900
960
1020
1080
1140
1200
1260
1320
1380
1440
1500
1560
1620
1680
1740
1800
1860
1920
1980
2040
2100
2160
2220
2259

<210> 145
<211> 753
<212> PRT
<213> Artificial Sequence

<220>
<221> source

_SL

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 145

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Arg Ser Ser Leu Ala Leu Ser Leu Thr Ala Asp
20 25 30

Gln Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser
35 40 45

Glu Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu
50 55 60

Leu Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala
65 70 75 80

Lys Arg Val Pro Gly Phe Val Asp Leu Ala Leu His Asp Gln Val His
85 90 95

Leu Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp
100 105 110

Arg Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu
115 120 125

Leu Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe
130 135 140

Asp Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln
145 150 155 160

Gly Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly
165 170 175

Val Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp
180 185 190

His Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu
195 200 205

Met Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala
210 215 220

Gln Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Ser Lys Arg
225 230 235 240

Met Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Ser
245 250 255

Asp Leu Leu Leu₂₆₀ Glu Met Leu Asp Ala₂₆₅ His^{-SL} Arg Leu Gly Thr₂₇₀ Gly Ala
 Glu Asp Pro₂₇₅ Arg Pro Ser Arg Lys₂₈₀ Arg Arg Ser Leu Gly₂₈₅ Asp Val Gly
 Glu Ile₂₉₀ Val Met Thr Gln Ser₂₉₅ Pro Ala Thr Leu Ser₃₀₀ Leu Ser Pro Gly
 Glu₃₀₅ Arg Ala Thr Leu Ser₃₁₀ Cys Arg Ala Ser Gln₃₁₅ Asp Ile Ser Lys Tyr₃₂₀
 Leu Asn Trp Tyr Gln₃₂₅ Gln Lys Pro Gly Gln₃₃₀ Ala Pro Arg Leu Leu₃₃₅ Ile
 Tyr His Thr Ser₃₄₀ Arg Leu His Ser Gly₃₄₅ Ile Pro Ala Arg Phe₃₅₀ Ser Gly
 Ser Gly Ser₃₅₅ Gly Thr Asp Tyr Thr₃₆₀ Leu Thr Ile Ser Ser₃₆₅ Leu Gln Pro
 Glu Asp₃₇₀ Phe Ala Val Tyr Phe₃₇₅ Cys Gln Gln Gly Asn₃₈₀ Thr Leu Pro Tyr
 Thr₃₈₅ Phe Gly Gln Gly Thr₃₉₀ Lys Leu Glu Ile Lys₃₉₅ Gly Gly Gly Gly Ser₄₀₀
 Gly Gly Gly Gly Ser₄₀₅ Gly Gly Gly Gly Ser₄₁₀ Gln Val Gln Leu Gln₄₁₅ Glu
 Ser Gly Pro Gly₄₂₀ Leu Val Lys Pro Ser₄₂₅ Glu Thr Leu Ser Leu₄₃₀ Thr Cys
 Thr Val Ser₄₃₅ Gly Val Ser Leu Pro₄₄₀ Asp Tyr Gly Val Ser₄₄₅ Trp Ile Arg
 Gln Pro Pro Gly Lys Gly Leu₄₅₅ Glu Trp Ile Gly Val₄₆₀ Ile Trp Gly Ser
 Glu₄₆₅ Thr Thr Tyr Tyr Ser₄₇₀ Ser Ser Leu Lys Ser₄₇₅ Arg Val Thr Ile Ser₄₈₀
 Lys Asp Asn Ser Lys₄₈₅ Asn Gln Val Ser Leu₄₉₀ Lys Leu Ser Ser Val₄₉₅ Thr
 Ala Ala Asp Thr₅₀₀ Ala Val Tyr Tyr Cys₅₀₅ Ala Lys His Tyr Tyr₅₁₀ Tyr Gly
 Gly Ser Tyr₅₁₅ Ala Met Asp Tyr Trp₅₂₀ Gly Gln Gly Thr Leu₅₂₅ Val Thr Val

Ser Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr
 530 535 540
 Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala
 545 550 555 560
 Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile
 565 570 575
 Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Ser
 580 585 590
 Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr
 595 600 605
 Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu
 610 615 620
 Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu
 625 630 635 640
 Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln
 645 650 655
 Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu
 660 665 670
 Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly
 675 680 685
 Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln
 690 695 700
 Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu
 705 710 715 720
 Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr
 725 730 735
 Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro
 740 745 750

Arg

<210> 146
 <211> 2259
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 Page 122

polynucleotide" _SL

```

<400> 146
atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgtcca cgccgctcgg      60
ccccggtcgt cgttggcact ttccctgact gccgaccaga tgggtgtccgc ctttctggac      120
gccgagcctc caattctgta ctcggagtac gatccgactc gcccgttctc cgaagccagc      180
atgatggggc tgttgactaa cctggcggac cgcgagttgg tgcacatgat taactgggct      240
aagcgggtgc cgggcttcgt ggacctggcc ctgcacgacc aagtgcacct cctggaatgc      300
gcctggatgg aaatcctcat gatcggcctc gtgtggagat ccatggagca tcccggaaag      360
ctcctgtttg caccacacct cctgcttgat cgcaaccagg gaaaatgcgt ggaaggggggt      420
gtcgagattt tcgacatgct gctcgccacc tcttcccggg tccggatgat gaatctgcag      480
ggagaagagt tcgtgtgtct gaagtcaatc atcctgctga actccggggg ctataccttc      540
ctgagctcga ccctcaagtc actggaggaa aaagaccaca tccatcgcgt gctcgataag      600
atcaccgaca cccttatcca tctcatggcg aaggctggac tgaccctgca acagcagcac      660
cagaggctgg ccagttgct gctgattctg agccacatcc ggcacatgtc gtccaagagg      720
atggaacacc tgtacagcat gaagtgaag aacgtcgtgc ctctgtccga tctgctcctg      780
gaaatgctgg acgcgcacag actcggaaac ggcgcggaag acccccggcc ctccaggaag      840
cgaagggtccc tcggagacgt gggtgaaatt gtgatgacct agtcacccgc cactcttagc      900
ctttcacccg gtgagcgcgc aaccctgtct tgcagagcct cccaagacat ctcaaaatac      960
cttaattggg atcaacagaa gcccggacag gctcctcgcc ttctgatcta ccacaccagc     1020
cggctccatt ctggaatccc tgccagggtc agcggtagcg gatctgggac cgactacacc     1080
ctcactatca gtcactgca gccagaggac ttcgctgtct atttctgtca gcaagggaac     1140
accctgccct acacctttgg acagggcacc aagctcgaga ttaaagggtg aggtggcagc     1200
ggaggagggtg ggtccggcgg tggaggaagc caggtccaac tccaagaaag cggaccgggt     1260
cttgtgaagc catcagaaac tctttcactg acttgtactg tgagcggagt gtctctcccc     1320
gattacgggg tgtcttggat cagacagcca ccggggaagg gtctggaatg gattggagtg     1380
atttggggct ctgagactac ttactactct tcatccctca agtcacgcgt caccatctca     1440
aaggacaact ctaagaatca ggtgtcactg aaactgtcat ctgtgaccgc agccgacacc     1500
gccgtgtact attgcgctaa gcattactat tatggcggga gctacgcaat ggattactgg     1560
ggacagggtg ctctggtcac cgtgtccagc accactaccc cagcaccgag gccacccacc     1620
ccggctccta ccatcgcctc ccagcctctg tccctgcgtc cggaggcatg tagacccgca     1680
gctggtgggg ccgtgcatac ccggggtctt gacttcgcct gcgatatcta catttggggc     1740
cctctggctg gtacttgagg ggtcctgctg ctttctactg tgatcactct ttactgtaag     1800
cgcggtcgga agaagctgct gtacatcttt aagcaaccct tcatgaggcc tgtgcagact     1860
actcaagagg aggacggctg ttcatgccgg ttcccagagg aggaggaagg cggctgcgaa     1920
ctgcgcgtga aattcagccg cagcgcagat gctccagcct accagcaggg gcagaaccag     1980

```

_SL

ctctacaacg aactcaatct tggtcggaga gaggagtacg acgtgctgga caagcggaga 2040
ggacggggacc cagaaatggg cgggaagccg cgcagaaaga atccccaaga gggcctgtac 2100
aacgagctcc aaaaggataa gatggcagaa gcctatagcg agattggtat gaaaggggaa 2160
cgcagaagag gcaaaggcca cgacggactg taccagggac tcagcaccgc caccaaggac 2220
acctatgacg ctcttcacat gcaggccctg cgcctcgg 2259

<210> 147

<211> 747

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 147

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Arg Ser Ser Leu Ala Leu Ser Leu Thr Ala Asp
20 25 30

Gln Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser
35 40 45

Glu Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu
50 55 60

Leu Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala
65 70 75 80

Lys Arg Val Pro Gly Phe Val Asp Leu Ala Leu His Asp Gln Val His
85 90 95

Leu Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp
100 105 110

Arg Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu
115 120 125

Leu Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe
130 135 140

Asp Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln
145 150 155 160

Gly Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly
165 170 175

Val Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp

_SL

180		185		190											
His	Ile	His	Arg	Val	Leu	Asp	Lys	Ile	Thr	Asp	Thr	Leu	Ile	His	Leu
		195					200					205			
Met	Ala	Lys	Ala	Gly	Leu	Thr	Leu	Gln	Gln	Gln	His	Gln	Arg	Leu	Ala
	210					215					220				
Gln	Leu	Leu	Leu	Ile	Leu	Ser	His	Ile	Arg	His	Met	Ser	Ser	Lys	Arg
225					230					235					240
Met	Glu	His	Leu	Tyr	Ser	Met	Lys	Cys	Lys	Asn	Val	Val	Pro	Leu	Ser
				245					250					255	
Asp	Leu	Leu	Leu	Glu	Met	Leu	Asp	Ala	His	Arg	Leu	Gly	Thr	Gly	Ala
				260				265					270		
Glu	Asp	Pro	Arg	Pro	Ser	Arg	Lys	Arg	Arg	Glu	Ile	Val	Met	Thr	Gln
		275					280					285			
Ser	Pro	Ala	Thr	Leu	Ser	Leu	Ser	Pro	Gly	Glu	Arg	Ala	Thr	Leu	Ser
	290					295					300				
Cys	Arg	Ala	Ser	Gln	Asp	Ile	Ser	Lys	Tyr	Leu	Asn	Trp	Tyr	Gln	Gln
305					310					315					320
Lys	Pro	Gly	Gln	Ala	Pro	Arg	Leu	Leu	Ile	Tyr	His	Thr	Ser	Arg	Leu
				325					330					335	
His	Ser	Gly	Ile	Pro	Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp
			340					345					350		
Tyr	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp	Phe	Ala	Val	Tyr
		355					360					365			
Phe	Cys	Gln	Gln	Gly	Asn	Thr	Leu	Pro	Tyr	Thr	Phe	Gly	Gln	Gly	Thr
	370					375					380				
Lys	Leu	Glu	Ile	Lys	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly
385					390					395					400
Gly	Gly	Gly	Ser	Gln	Val	Gln	Leu	Gln	Glu	Ser	Gly	Pro	Gly	Leu	Val
				405					410					415	
Lys	Pro	Ser	Glu	Thr	Leu	Ser	Leu	Thr	Cys	Thr	Val	Ser	Gly	Val	Ser
			420					425					430		
Leu	Pro	Asp	Tyr	Gly	Val	Ser	Trp	Ile	Arg	Gln	Pro	Pro	Gly	Lys	Gly
		435					440					445			
Leu	Glu	Trp	Ile	Gly	Val	Ile	Trp	Gly	Ser	Glu	Thr	Thr	Tyr	Tyr	Ser

_SL

450		455		460											
Ser 465	Ser	Leu	Lys	Ser	Arg 470	Val	Thr	Ile	Ser	Lys 475	Asp	Asn	Ser	Lys	Asn 480
Gln	Val	Ser	Leu	Lys 485	Leu	Ser	Ser	Val	Thr 490	Ala	Ala	Asp	Thr	Ala 495	Val
Tyr	Tyr	Cys	Ala 500	Lys	His	Tyr	Tyr	Tyr 505	Gly	Gly	Ser	Tyr	Ala 510	Met	Asp
Tyr	Trp	Gly 515	Gln	Gly	Thr	Leu	Val 520	Thr	Val	Ser	Ser	Thr 525	Thr	Thr	Pro
Ala	Pro 530	Arg	Pro	Pro	Thr	Pro 535	Ala	Pro	Thr	Ile	Ala 540	Ser	Gln	Pro	Leu
Ser 545	Leu	Arg	Pro	Glu	Ala 550	Cys	Arg	Pro	Ala	Ala 555	Gly	Gly	Ala	Val	His 560
Thr	Arg	Gly	Leu	Asp 565	Phe	Ala	Cys	Asp	Ile 570	Tyr	Ile	Trp	Ala	Pro 575	Leu
Ala	Gly	Thr	Cys 580	Gly	Val	Leu	Leu	Leu 585	Ser	Leu	Val	Ile	Thr 590	Leu	Tyr
Cys	Lys	Arg 595	Gly	Arg	Lys	Lys	Leu 600	Leu	Tyr	Ile	Phe	Lys 605	Gln	Pro	Phe
Met 610	Arg	Pro	Val	Gln	Thr	Thr 615	Gln	Glu	Glu	Asp	Gly 620	Cys	Ser	Cys	Arg
Phe 625	Pro	Glu	Glu	Glu	Glu 630	Gly	Gly	Cys	Glu	Leu 635	Arg	Val	Lys	Phe	Ser 640
Arg	Ser	Ala	Asp	Ala 645	Pro	Ala	Tyr	Lys	Gln 650	Gly	Gln	Asn	Gln	Leu 655	Tyr
Asn	Glu	Leu	Asn 660	Leu	Gly	Arg	Arg	Glu 665	Glu	Tyr	Asp	Val	Leu 670	Asp	Lys
Arg	Arg	Gly 675	Arg	Asp	Pro	Glu	Met 680	Gly	Gly	Lys	Pro	Arg 685	Arg	Lys	Asn
Pro	Gln 690	Glu	Gly	Leu	Tyr	Asn 695	Glu	Leu	Gln	Lys	Asp 700	Lys	Met	Ala	Glu
Ala 705	Tyr	Ser	Glu	Ile	Gly 710	Met	Lys	Gly	Glu	Arg 715	Arg	Arg	Gly	Lys	Gly 720
His	Asp	Gly	Leu	Tyr	Gln	Gly	Leu	Ser	Thr	Ala	Thr	Lys	Asp	Thr	Tyr

Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
 740 745

<210> 148
 <211> 2241
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 148
 atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60
 ccccggctcgt cgttggcact ttccctgact gccgaccaga tgggtgtccgc ctttctggac 120
 gccgagcctc caattctgta ctcggagtac gatccgactc gcccgttctc cgaagccagc 180
 atgatggggc tgttgactaa cctggcggac cgcgagttgg tgcacatgat taactgggct 240
 aagcgggtgc cgggcttcgt ggacctggcc ctgcacgacc aagtgcacct cctggaatgc 300
 gcctggatgg aaatcctcat gatcggcctc gtgtggagat ccatggagca tcccggaaag 360
 ctctgtttg caccacacct cctgcttgat cgcaaccagg gaaaatgcgt ggaagggggt 420
 gtcgagattt tcgacatgct gctcgccacc tcttcccgtt tccggatgat gaatctgcag 480
 ggagaagagt tcgtgtgtct gaagtcaatc atcctgctga actccggggt ctataccttc 540
 ctgagctcga ccctcaagtc actggaggaa aaagaccaca tccatcgcgt gctcgataag 600
 atcaccgaca cccttatcca tctcatggcg aaggctggac tgaccctgca acagcagcac 660
 cagaggctgg ccagttgct gctgattctg agccacatcc ggcacatgtc gtccaagagg 720
 atggaacacc tgtacagcat gaagtgaag aacgtcgtgc ctctgtccga tctgtcctg 780
 gaaatgctgg acgcgcacag actcgggacg ggagctgaag atccacgacc cagcagaaag 840
 cgacgggaaa ttgtgatgac ccagtcaccc gccactctta gcctttcacc cggtgagcgc 900
 gcaaccctgt cttgcagagc ctccaagac atctcaaat accttaattg gtatcaacag 960
 aagcccggac aggtcctcg ccttctgac taccacacca gccggctcca ttctggaatc 1020
 cctgccaggt tcagcggtag cggatctggg accgactaca ccctcactat cagctcactg 1080
 cagccagagg acttcgctgt ctatttctgt cagcaaggga acaccctgcc ctacaccttt 1140
 ggacagggca ccaagctcga gattaaagg ggaggtggca gcggaggagg tgggtccggc 1200
 ggtggaggaa gccaggtcca actccaagaa agcggaccgg gtcttgtgaa gccatcagaa 1260
 actctttcac tgacttgtag tgtgagcggg gtgtctctcc ccgattacgg ggtgtcttgg 1320
 atcagacagc caccggggaa gggctctggaa tggattggag tgatttgggg ctctgagact 1380
 acttactact cttcatccct caagtcacgc gtcaccatct caaaggacaa ctctaagaat 1440
 caggtgtcac tgaaactgtc atctgtgacc gcagccgaca ccgccgtgta ctattgcgct 1500

_SL

```

aagcattact attatggcgg gagctacgca atggattact ggggacaggg tactctggtc      1560
accgtgtcca gcaccactac ccagcaccg aggccacca ccccggtcc taccatcgcc      1620
tcccagctc tgtccctgcg tccggaggca tgtagaccg cagctggtgg ggccgtgcat      1680
acccggggtc ttgacttcgc ctgcgatatc tacatttggg cccctctggc tgggtacttgc      1740
ggggtcctgc tgctttcact cgtgatcact ctttactgta agcgcggtcg gaagaagctg      1800
ctgtacatct ttaagcaacc cttcatgagg cctgtgcaga ctactcaaga ggaggacggc      1860
tgttcatgcc ggttcccaga ggaggaggaa ggcggctgcg aactgcgctg gaaattcagc      1920
cgcagcgcag atgctccagc ctacaagcag gggcagaacc agctctacaa cgaactcaat      1980
cttggtcggg gagaggagta cgacgtgctg gacaagcgga gaggacggga cccagaaatg      2040
ggcggaagc cgcgcagaaa gaatcccaa gagggcctgt acaacgagct ccaaaggat      2100
aagatggcag aagcctatag cgagattggt atgaaagggg aacgcagaag aggcaaaggc      2160
cacgacggac tgtaccaggg actcagcacc gccaccaagg acacctatga cgctcttcac      2220
atgcaggccc tgccgcctcg g                                     2241

```

<210> 149

<211> 747

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 149

```

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1           5           10           15

```

```

His Ala Ala Arg Pro Arg Ser Ser Leu Ala Leu Ser Leu Thr Ala Asp
          20           25           30

```

```

Gln Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser
          35           40           45

```

```

Glu Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu
          50           55           60

```

```

Leu Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala
65           70           75           80

```

```

Lys Arg Val Pro Gly Phe Val Asp Leu Ala Leu His Asp Gln Val His
          85           90           95

```

```

Leu Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp
          100          105          110

```

```

Arg Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu
          115          120          125

```

_SL

Leu Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe
130 135 140

Asp Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln
145 150 155 160

Gly Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly
165 170 175

Val Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp
180 185 190

His Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu
195 200 205

Met Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala
210 215 220

Gln Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Ser Lys Arg
225 230 235 240

Met Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Ser
245 250 255

Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu Gly Thr Gly Ala
260 265 270

Glu Asp Pro Arg Pro Ser Arg Lys Arg Arg Glu Ile Val Met Thr Gln
275 280 285

Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser
290 295 300

Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr Leu Asn Trp Tyr Gln Gln
305 310 315 320

Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr His Thr Ser Arg Leu
325 330 335

His Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
340 345 350

Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Val Tyr
355 360 365

Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gln Gly Thr
370 375 380

Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
385 390 395 400

_SL

Gly Gly Gly Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val
405 410 415

Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Val Ser
420 425 430

Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly
435 440 445

Leu Glu Trp Ile Gly Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Ser
450 455 460

Ser Ser Leu Lys Ser Arg Val Thr Ile Ser Lys Asp Asn Ser Lys Asn
465 470 475 480

Gln Val Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val
485 490 495

Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met Asp
500 505 510

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Thr Thr Thr Pro
515 520 525

Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu
530 535 540

Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His
545 550 555 560

Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu
565 570 575

Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr
580 585 590

Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe
595 600 605

Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg
610 615 620

Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser
625 630 635 640

Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr
645 650 655

Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys
660 665 670

_SL

Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn
675 680 685

Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu
690 695 700

Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly
705 710 715 720

His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr
725 730 735

Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
740 745

<210> 150
<211> 2241
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 150
atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60
ccccggtcgt cgttggcact ttccctgact gccgaccaga tgggtgtccgc ctttctggac 120
gccgagcctc caattctgta ctcggagtac gatccgactc gcccgttctc cgaagccagc 180
atgatgggcc tgttgactaa cctggcggac cgcgagttgg tgcacatgat taactgggct 240
aagcgggtgc cgggcttcgt ggacctggcc ctgcacgacc aagtgcacct cctggaatgc 300
gcctggatgg aaatcctcat gatcggcctc gtgtggagat ccatggagca tcccggaaag 360
ctcctgtttg cacccaacct cctgcttgat cgcaaccagg gaaaatgcgt ggaaggggggt 420
gtcgagattt tcgacatgct gctcgccacc tcttcccggg tccggatgat gaatctgcag 480
ggagaagagt tcgtgtgtct gaagtcaatc atcctgctga actccgggggt ctataccttc 540
ctgagctcga ccctcaagtc actggaggaa aaagaccaca tccatcgcgt gctcgataag 600
atcaccgaca cccttatcca tctcatggcg aaggctggac tgaccctgca acagcagcac 660
cagaggctgg ccagttgct gctgattctg agccacatcc ggcacatgtc gtccaagagg 720
atggaacacc tgtacagcat gaagtgaag aacgtcgtgc ctctgtccga tctgctcctg 780
gaaatgctgg acgcgcacag actcgggacg ggagctgaag atccacgacc cagcagaaag 840
cgacgggaaa ttgtgatgac ccagtcaccc gccactctta gcctttcacc cggtgagcgc 900
gcaaccctgt cttgcagagc ctccaagac atctcaaaat accttaattg gtatcaacag 960
aagcccggac aggctcctcg ctttctgata taccacacca gccggctcca ttctggaatc 1020
cctgccaggt tcagcggtag cggatctggg accgactaca ccctcactat cagctcactg 1080

_SL

cagccagagg acttcgctgt ctatttctgt cagcaagggga acaccctgcc ctacaccttt 1140
ggacaggggca ccaagctcga gattaaaggt ggaggtggca gcgaggaggagg tgggtccggc 1200
ggtggaggaa gccaggtcca actccaagaa agcggaccgg gtcttgtgaa gccatcagaa 1260
actctttcac tgacttgtac tgtgagcgga gtgtctctcc ccgattacgg ggtgtcttgg 1320
atcagacagc caccggggaa ggggtctggaa tggattggag tgatttgggg ctctgagact 1380
acttactact cttcatccct caagtcacgc gtcaccatct caaaggacaa ctctaagaat 1440
caggtgtcac tgaaactgtc atctgtgacc gcagccgaca ccgccgtgta ctattgcgct 1500
aagcattact attatggcgg gagctacgca atggattact ggggacaggg tactctggtc 1560
accgtgtcca gcaccactac cccagcaccg aggccaccca ccccggtctc taccatcgcc 1620
tcccagcctc tgtccctgcg tccggaggca tgtagaccgg cagctgggtg ggccgtgcat 1680
acccgggggtc ttgacttcgc ctgcgatatc tacatttggg cccctctggc tgggtacttgc 1740
ggggtcctgc tgctttcact cgtgatcact ctttactgta agcgcgggtcg gaagaagctg 1800
ctgtacatct ttaagcaacc cttcatgagg cctgtgcaga ctactcaaga ggaggacggc 1860
tgttcatgcc gggtcccaga ggaggaggaa ggcggctgcg aactgcgcgt gaaattcagc 1920
cgcagcgcag atgctccagc ctaccagcag gggcagaacc agctctacaa cgaactcaat 1980
cttggtcgga gagaggagta cgacgtgctg gacaagcgga gaggacggga cccagaaatg 2040
ggcggaagc cgcgcagaaa gaatcccaa gagggcctgt acaacgagct ccaaaggat 2100
aagatggcag aagcctatag cgagattggt atgaaagggg aacgcagaag aggcaaaggc 2160
cacgacggac tgtaccaggg actcagcacc gccaccaagg acacctatga cgctcttcac 2220
atgcaggccc tgccgcctcg g 2241

<210> 151

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 151

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Arg Ser Ser Leu Ala Leu Ser Leu Thr Ala Asp
20 25 30

Gln Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser
35 40 45

Glu Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu
50 55 60

_SL

Leu Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala
65 70 75 80

Lys Arg Val Pro Gly Phe Val Asp Leu Thr Leu His Asp Gln Val His
85 90 95

Leu Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp
100 105 110

Arg Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu
115 120 125

Leu Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe
130 135 140

Asp Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln
145 150 155 160

Gly Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly
165 170 175

Val Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp
180 185 190

His Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu
195 200 205

Met Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala
210 215 220

Gln Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Asn Lys Arg
225 230 235 240

Met Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Ser
245 250 255

Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu Arg Thr Lys Arg
260 265 270

Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
275 280 285

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr
290 295 300

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
305 310 315 320

Tyr His Thr Ser Arg Leu His Ser Gly Ile Pro Ala Arg Phe Ser Gly
325 330 335

_SL

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
340 345 350

Glu Asp Phe Ala Val Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr
355 360 365

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser
370 375 380

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Glu
385 390 395 400

Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys
405 410 415

Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg
420 425 430

Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Val Ile Trp Gly Ser
435 440 445

Glu Thr Thr Tyr Tyr Ser Ser Ser Leu Lys Ser Arg Val Thr Ile Ser
450 455 460

Lys Asp Asn Ser Lys Asn Gln Val Ser Leu Lys Leu Ser Ser Val Thr
465 470 475 480

Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly
485 490 495

Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
500 505 510

Ser Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr
515 520 525

Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala
530 535 540

Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile
545 550 555 560

Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser
565 570 575

Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr
580 585 590

Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu
595 600 605

_SL

Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu
610 615 620

Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln
625 630 635 640

Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu
645 650 655

Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly
660 665 670

Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln
675 680 685

Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu
690 695 700

Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr
705 710 715 720

Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro
725 730 735

Arg

<210> 152
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 152
atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60
ccccggctcg cgttggcact ttccctgact gccgaccaga tgggtgtccgc ctttctggac 120
gccgagcctc caattctgta ctcggagtac gatccgactc gcccgttctc cgaagccagc 180
atgatgggccc tgttgactaa cctggcggac cgcgagttgg tgcacatgat taactgggct 240
aagcgggtgc cgggcttcgt ggacctgacc ctgcacgacc aagtgcacct cctggaatgc 300
gcctggatgg aaatcctcat gatcggcctc gtgtggagat ccatggagca tcccggaaag 360
ctcctgtttg cacccaacct cctgcttgat cgcaaccagg gaaaatgcgt ggaaggggggt 420
gtcgagattt tcgacatgct gctcgccacc tcttcccgggt tccggatgat gaatctgcag 480
ggagaagagt tcgtgtgtct gaagtcaatc atcctgctga actccgggggt ctataccttc 540
ctgagctcga ccctcaagtc actggaggaa aaagaccaca tccatcgcgt gctcgataag 600

_SL

atcaccgaca	cccttatcca	tctcatggcg	aaggctggac	tgaccctgca	acagcagcac	660
cagaggctgg	cccagttgct	gctgattctg	agccacatcc	ggcacatgtc	gaacaagagg	720
atggaacacc	tgtacagcat	gaagtgcaag	aacgtcgtgc	ctctgtccga	tctgtctctg	780
gaaatgctgg	acgcgcacag	actccgtact	aaaagagaaa	ttgtgatgac	ccagtcaccc	840
gccactctta	gcctttcacc	cggtgagcgc	gcaaccctgt	cttgagagc	ctcccaagac	900
atctcaaaat	accttaattg	gtatcaacag	aagcccggac	aggctcctcg	ccttctgata	960
taccacacca	gccgggtcca	ttctggaatc	cctgccaggt	tcagcggtag	cggatctggg	1020
accgactaca	ccctcactat	cagctcactg	cagccagagg	acttcgctgt	ctatttctgt	1080
cagcaaggga	acaccctgcc	ctacaccttt	ggacagggca	ccaagctcga	gattaaaggt	1140
ggaggtggca	gcggaggagg	tgggtccggc	ggtggaggaa	gccaggtcca	actccaagaa	1200
agcggaccgg	gtcttgtgaa	gccatcagaa	actctttcac	tgacttgtac	tgtgagcgga	1260
gtgtctctcc	ccgattacgg	ggtgtcttgg	atcagacagc	caccggggaa	gggtctggaa	1320
tggattggag	tgatttgggg	ctctgagact	acttactact	cttcatccct	caagtcacgc	1380
gtcaccatct	caaaggacaa	ctctaagaat	caggtgtcac	tgaaactgtc	atctgtgacc	1440
gcagccgaca	ccgccgtgta	ctattgcgct	aagcattact	attatggcgg	gagctacgca	1500
atggattact	ggggacaggg	tactctggtc	accgtgtcca	gcaccactac	cccagcaccg	1560
aggccacca	ccccgggtcc	taccatcgcc	tcccagcctc	tgtccctgcg	tccggaggca	1620
tgtagaccgg	cagctggtgg	ggccgtgcat	acccggggtc	ttgacttcgc	ctgcatatc	1680
tacatttggg	cccctctggc	tggctacttc	gggtcctgc	tgctttcact	cgtgatcact	1740
ctttactgta	agcgcggtcg	gaagaagctg	ctgtacatct	ttaagcaacc	cttcatgagg	1800
cctgtgcaga	ctactcaaga	ggaggacggc	tgttcatgcc	ggttcccaga	ggaggaggaa	1860
ggcggctgcg	aactgcgcgt	gaaattcagc	cgcagcgcag	atgctccagc	ctacaagcag	1920
gggcagaacc	agctctacaa	cgaactcaat	cttggtcgga	gagaggagta	cgacgtgctg	1980
gacaagcggg	gaggacggga	cccagaaatg	ggcgggaagc	cgcgcagaaa	gaatccccaa	2040
gagggcctgt	acaacgagct	ccaaaaggat	aagatggcag	aagcctatag	cgagattggt	2100
atgaaagggg	aacgcagaag	aggcaaaggc	cacgacggac	tgtaccaggg	actcagcacc	2160
gccaccaagg	acacctatga	cgctcttcac	atgcaggccc	tgccgcctcg	g	2211

<210> 153

<211> 753

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 153

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

_SL

His Ala Ala Arg Pro Arg Ser Ser Leu Ala Leu Ser Leu Thr Ala Asp
20 25 30

Gln Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser
35 40 45

Glu Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu
50 55 60

Leu Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala
65 70 75 80

Lys Arg Val Pro Gly Phe Val Asp Leu Thr Leu His Asp Gln Val His
85 90 95

Leu Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp
100 105 110

Arg Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu
115 120 125

Leu Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe
130 135 140

Asp Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln
145 150 155 160

Gly Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly
165 170 175

Val Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp
180 185 190

His Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu
195 200 205

Met Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala
210 215 220

Gln Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Asn Lys Arg
225 230 235 240

Met Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Ser
245 250 255

Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu Gly Thr Gly Ala
260 265 270

Glu Asp Pro Arg Pro Ser Arg Lys Arg Arg Ser Leu Gly Asp Val Gly
275 280 285

_SL

Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
290 295 300

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr
305 310 315 320

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
325 330 335

Tyr His Thr Ser Arg Leu His Ser Gly Ile Pro Ala Arg Phe Ser Gly
340 345 350

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
355 360 365

Glu Asp Phe Ala Val Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr
370 375 380

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser
385 390 395 400

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Glu
405 410 415

Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys
420 425 430

Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg
435 440 445

Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Val Ile Trp Gly Ser
450 455 460

Glu Thr Thr Tyr Tyr Ser Ser Ser Leu Lys Ser Arg Val Thr Ile Ser
465 470 475 480

Lys Asp Asn Ser Lys Asn Gln Val Ser Leu Lys Leu Ser Ser Val Thr
485 490 495

Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly
500 505 510

Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
515 520 525

Ser Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr
530 535 540

Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala
545 550 555 560

_SL

Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile
565 570 575

Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Ser
580 585 590

Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr
595 600 605

Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu
610 615 620

Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Gly Gly Cys Glu
625 630 635 640

Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln
645 650 655

Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu
660 665 670

Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly
675 680 685

Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln
690 695 700

Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu
705 710 715 720

Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr
725 730 735

Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro
740 745 750

Arg

<210> 154
<211> 2259
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 154
atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60

ccccggtcgt cgttggcact ttccctgact gccgaccaga tgggtgtccgc ccttctggac 120
Page 139

_SL

gccgagcctc	caattctgta	ctcggagtac	gatccgactc	gcccgtttctc	cgaagccagc	180
atgatggggc	tgttgactaa	cctggcggac	cgcgagttgg	tgcacatgat	taactgggct	240
aagcgggtgc	cgggcttcgt	ggacctgacc	ctgcacgacc	aagtgcacct	cctggaatgc	300
gcctggatgg	aaatcctcat	gatcggcctc	gtgtggagat	ccatggagca	tcccggaaag	360
ctcctgtttg	cacccaacct	cctgcttgat	cgcaaccagg	gaaaatgcgt	ggaagggggg	420
gtcgagattt	tcgacatgct	gctcgccacc	tcttcccggg	tccggatgat	gaatctgcag	480
ggagaagagt	tcgtgtgtct	gaagtcaatc	atcctgctga	actccggggg	ctataccttc	540
ctgagctcga	ccctcaagtc	actggaggaa	aaagaccaca	tccatcgcg	gctcgataag	600
atcaccgaca	cccttatcca	tctcatggcg	aaggctggac	tgaccctgca	acagcagcac	660
cagaggctgg	cccagttgct	gctgattctg	agccacatcc	ggcacatgtc	gaacaagagg	720
atggaacacc	tgtacagcat	gaagtgaag	aacgtcgtgc	ctctgtccga	tctgtctctg	780
gaaatgctgg	acgcgcacag	actcggaacc	ggcgcggaag	acccccggcc	ctccaggaag	840
cgaagggtccc	tcggagacgt	gggtgaaatt	gtgatgacct	agtcacccgc	cactcttagc	900
ctttcacccg	gtgagcgcgc	aaccctgtct	tgcagagcct	cccaagacat	ctcaaaatac	960
cttaattggg	atcaacagaa	gcccggacag	gctcctcgcc	ttctgatcta	ccacaccagc	1020
cgggtccatt	ctggaatccc	tgccagggtc	agcggtagcg	gatctgggac	cgactacacc	1080
ctcactatca	gctcactgca	gccagaggac	ttcgtgtgtc	atttctgtca	gcaagggaac	1140
accctgccct	acacctttgg	acagggcacc	aagctcgaga	ttaaagggtg	aggtggcagc	1200
ggaggagggtg	ggtccggcgg	tggaggaagc	caggtccaac	tccaagaaag	cggaccgggt	1260
cttggaagc	catcagaaac	tctttcactg	acttgtagct	tgagcggagt	gtctctcccc	1320
gattacgggg	tgtcttggat	cagacagcca	ccggggaagg	gtctggaatg	gattggagtg	1380
atttggggct	ctgagactac	ttactactct	tcatccctca	agtcacgcgt	caccatctca	1440
aaggacaact	ctaagaatca	ggtgtcactg	aaactgtcat	ctgtgaccgc	agccgacacc	1500
gccgtgtact	attgcgctaa	gcattactat	tatggcggga	gctacgcaat	ggattactgg	1560
ggacagggta	ctctggtcac	cgtgtccagc	accactaccc	cagcaccgag	gccacccacc	1620
ccggctccta	ccatcgctc	ccagcctctg	tccctgcgtc	cggaggcatg	tagacccgca	1680
gctgggtggg	ccgtgcatac	ccggggtctt	gacttcgcct	gcgatatcta	catttggggc	1740
cctctggctg	gtacttgctg	ggtcctgctg	ctttcactcg	tgatcactct	ttactgtaag	1800
cgcggtcgga	agaagctgct	gtacatcttt	aagcaaccct	tcatgaggcc	tgtgcagact	1860
actcaagagg	aggacggctg	ttcatgccgg	ttcccagagg	aggaggaagg	cggctgcgaa	1920
ctgcgcgtga	aattcagccg	cagcgcagat	gctccagcct	acaagcaggg	gcagaaccag	1980
ctctacaacg	aactcaatct	tggtcggaga	gaggagtacg	acgtgctgga	caagcggaga	2040
ggacgggacc	cagaaatggg	cgggaagccg	cgcagaaaga	atccccaaga	gggcctgtac	2100
aacgagctcc	aaaaggataa	gatggcagaa	gcctatagcg	agattgggtat	gaaaggggaa	2160

_SL

cgcagaagag gcaaaggcca cgacggactg taccagggac tcagcaccgc caccaaggac 2220
acctatgacg ctcttcacat gcaggccctg cgcctcgg 2259

<210> 155
<211> 753
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 155
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Arg Ser Ser Leu Ala Leu Ser Leu Thr Ala Asp
20 25 30

Gln Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser
35 40 45

Glu Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu
50 55 60

Leu Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala
65 70 75 80

Lys Arg Val Pro Gly Phe Val Asp Leu Thr Leu His Asp Gln Val His
85 90 95

Leu Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp
100 105 110

Arg Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu
115 120 125

Leu Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe
130 135 140

Asp Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln
145 150 155 160

Gly Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly
165 170 175

Val Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp
180 185 190

His Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu
195 200 205

_SL

Met Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala
210 215 220

Gln Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Asn Lys Arg
225 230 235 240

Met Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Ser
245 250 255

Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu Gly Thr Gly Ala
260 265 270

Glu Asp Pro Arg Pro Ser Arg Lys Arg Arg Ser Leu Gly Asp Val Gly
275 280 285

Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
290 295 300

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr
305 310 315 320

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
325 330 335

Tyr His Thr Ser Arg Leu His Ser Gly Ile Pro Ala Arg Phe Ser Gly
340 345 350

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
355 360 365

Glu Asp Phe Ala Val Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr
370 375 380

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser
385 390 395 400

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Glu
405 410 415

Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys
420 425 430

Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg
435 440 445

Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Val Ile Trp Gly Ser
450 455 460

Glu Thr Thr Tyr Tyr Ser Ser Ser Leu Lys Ser Arg Val Thr Ile Ser
465 470 475 480

_SL

Lys Asp Asn Ser Lys Asn Gln Val Ser Leu Lys Leu Ser Ser Val Thr
485 490 495

Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly
500 505 510

Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
515 520 525

Ser Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr
530 535 540

Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala
545 550 555 560

Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile
565 570 575

Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser
580 585 590

Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr
595 600 605

Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu
610 615 620

Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Gly Gly Cys Glu
625 630 635 640

Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln
645 650 655

Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu
660 665 670

Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly
675 680 685

Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln
690 695 700

Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu
705 710 715 720

Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr
725 730 735

Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro
740 745 750

Arg

<210> 156
<211> 2259
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 156
atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60
ccccggctcgt cgttggcact ttccctgact gccgaccaga tgggtgtccgc ctttctggac 120
gccgagcctc caattctgta ctcggagtac gatccgactc gcccgttctc cgaagccagc 180
atgatggggc tggtgactaa cctggcggac cgcgagttgg tgcacatgat taactgggct 240
aagcgggtgc cgggcttcgt ggacctgacc ctgcacgacc aagtgcacct cctggaatgc 300
gcctggatgg aaatcctcat gatcggcctc gtgtggagat ccatggagca tcccggaaag 360
ctcctgtttg cacccaacct cctgcttgat cgcaaccagg gaaaatgcgt ggaagggggt 420
gtcgagattt tcgacatgct gctcgccacc tcttcccggg tccggatgat gaatctgcag 480
ggagaagagt tcgtgtgtct gaagtcaatc atcctgctga actccggggg ctataccttc 540
ctgagctcga ccctcaagtc actggaggaa aaagaccaca tccatcgcgt gctcgataag 600
atcaccgaca cccttatcca tctcatggcg aaggctggac tgaccctgca acagcagcac 660
cagaggctgg ccagttgct gctgattctg agccacatcc ggcacatgtc gaacaagagg 720
atggaacacc tgtacagcat gaagtgaag aacgtcgtgc ctctgtccga tctgctcctg 780
gaaatgctgg acgcgcacag actcggaaac ggcgcggaag acccccggcc ctccaggaag 840
cgaaggtccc tcggagacgt ggggtgaaatt gtgatgacct agtcacccgc cactcttagc 900
ctttcacccg gtgagcgcgc aaccctgtct tgcagagcct cccaagacat ctcaaaatac 960
cttaattggg atcaacagaa gcccgacag gtcctcgcc ttctgatcta ccacaccagc 1020
cgggtccatt ctggaatccc tgccaggttc agcggtagcg gatctgggac cgactacacc 1080
ctcactatca gtcactgca gccagaggac ttcgctgtct atttctgtca gcaagggaac 1140
accctgccct acacctttgg acagggcacc aagctcgaga ttaaagggtg aggtggcagc 1200
ggaggaggtg ggtccggcgg tggaggaagc caggtccaac tccaagaaag cggaccgggt 1260
cttgtgaagc catcagaaac tctttcactg acttgactg tgagcggagt gtctctcccc 1320
gattacgggg tgtcttgat cagacagcca ccggggaagg gtctggaatg gattggagtg 1380
atttggggct ctgagactac ttactactct tcatccctca agtcacgcgt caccatctca 1440
aaggacaact ctaagaatca ggtgtcactg aaactgtcat ctgtgaccgc agccgacacc 1500
gccgtgtact attgcgctaa gcattactat tatggcggga gctacgcaat ggattactgg 1560

_SL

```

ggacagggta ctctggtcac cgtgtccagc accactaccc cagcaccgag gccacccacc      1620
ccggctccta ccatcgctc ccagcctctg tccctgcgtc cggaggcatg tagacccgca      1680
gctgggtggg ccgtgcatac ccgggtctt gacttcgctt gcgatatcta catttgggcc      1740
cctctggctg gtacttgctg ggtcctgctg ctttcactcg tgatcactct ttactgtaag      1800
cgcggtcggg agaagctgct gtacatcttt aagcaaccct tcatgaggcc tgtgcagact      1860
actcaagagg aggacggctg ttcatgccgg ttcccagagg aggaggaagg cggctgcgaa      1920
ctgcgcgtga aattcagccg cagcgcagat gtcccagcct accagcaggg gcagaaccag      1980
ctctacaacg aactcaatct tggtcggaga gaggagtacg acgtgctgga caagcggaga      2040
ggacgggacc cagaaatggg cggaagccg cgcagaaaga atccccaaga gggcctgtac      2100
aacgagctcc aaaaggataa gatggcagaa gcctatagcg agattggtat gaaaggggaa      2160
cgcagaagag gcaaaggcca cgacggactg taccagggac tcagcaccgc caccaaggac      2220
acctatgacg ctcttcacat gcaggccctg ccgcctcgg      2259

```

<210> 157
 <211> 747
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 157
 Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
 1 5 10 15

His Ala Ala Arg Pro Arg Ser Ser Leu Ala Leu Ser Leu Thr Ala Asp
 20 25 30

Gln Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser
 35 40 45

Glu Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu
 50 55 60

Leu Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala
 65 70 75 80

Lys Arg Val Pro Gly Phe Val Asp Leu Thr Leu His Asp Gln Val His
 85 90 95

Leu Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp
 100 105 110

Arg Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu
 115 120 125

Leu Asp Arg Asn Gln Gly Lys Cys Val Glu ^{SL}Gly Gly Val Glu Ile Phe
 130 135 140
 Asp Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln
 145 150 155 160
 Gly Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly
 165 170 175
 Val Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp
 180 185 190
 His Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu
 195 200 205
 Met Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala
 210 215 220
 Gln Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Asn Lys Arg
 225 230 235 240
 Met Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Ser
 245 250 255
 Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu Gly Thr Gly Ala
 260 265 270
 Glu Asp Pro Arg Pro Ser Arg Lys Arg Arg Glu Ile Val Met Thr Gln
 275 280 285
 Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser
 290 295 300
 Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr Leu Asn Trp Tyr Gln Gln
 305 310 315 320
 Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr His Thr Ser Arg Leu
 325 330 335
 His Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
 340 345 350
 Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Val Tyr
 355 360 365
 Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gln Gly Thr
 370 375 380
 Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 385 390 395 400

Gly Gly Gly Ser Gln Val Gln Leu Gln Glu^{-SL} Ser Gly Pro Gly Leu Val
 405 410 415
 Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Val Ser
 420 425 430
 Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly
 435 440 445
 Leu Glu Trp Ile Gly Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Ser
 450 455 460
 Ser Ser Leu Lys Ser Arg Val Thr Ile Ser Lys Asp Asn Ser Lys Asn
 465 470 475 480
 Gln Val Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val
 485 490 495
 Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met Asp
 500 505 510
 Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Thr Thr Thr Pro
 515 520 525
 Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu
 530 535 540
 Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His
 545 550 555 560
 Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu
 565 570 575
 Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr
 580 585 590
 Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe
 595 600 605
 Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg
 610 615 620
 Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser
 625 630 635 640
 Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr
 645 650 655
 Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys
 660 665 670

Arg Arg Gly Arg Asp Pro Glu Met Gly Gly ^{_SL}Lys Pro Arg Arg Lys Asn
675 680 685

Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu
690 695 700

Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly
705 710 715 720

His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr
725 730 735

Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
740 745

<210> 158
<211> 2241
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 158
atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60
ccccggtcgt cgttggcact ttccctgact gccgaccaga tgggtgtccgc ctttctggac 120
gccgagcctc caattctgta ctcggagtac gatccgactc gcccgttctc cgaagccagc 180
atgatggggc tgttgactaa cctggcggac cgcgagttgg tgcacatgat taactgggct 240
aagcgggtgc cgggcttcgt ggacctgacc ctgcacgacc aagtgcacct cctggaatgc 300
gcctggatgg aaatcctcat gatcggcctc gtgtggagat ccatggagca tcccggaaag 360
ctcctgtttg cacccaacct cctgcttgat cgcaaccagg gaaaatgcgt ggaaggggggt 420
gtcgagattt tcgacatgct gctcgccacc tcttcccgggt tccggatgat gaatctgcag 480
ggagaagagt tcgtgtgtct gaagtcaatc atcctgctga actccgggggt ctataccttc 540
ctgagctcga ccctcaagtc actggaggaa aaagaccaca tccatcgcgt gctcgataag 600
atcaccgaca cccttatcca tctcatggcg aaggctggac tgaccctgca acagcagcac 660
cagaggctgg cccagttgct gctgattctg agccacatcc ggcacatgtc gaacaagagg 720
atggaacacc tgtacagcat gaagtgcaag aacgtcgtgc ctctgtccga tctgctcctg 780
gaaatgctgg acgcgcacag actcgggacg ggagctgaag atccacgacc cagcagaaag 840
cgacgggaaa ttgtgatgac ccagtcaccc gccactctta gcctttcacc cggtgagcgc 900
gcaaccctgt cttgcagagc ctccaagac atctcaaaat accttaattg gtatcaacag 960
aagcccggac aggctcctcg ctttctgata taccacacca gccggctcca ttctggaatc 1020
cctgccaggt tcagcggtag cggatctggg accgactaca ccctcactat cagctcactg 1080
cagccagagg acttcgctgt ctatttctgt cagcaaggga acaccctgcc ctacaccttt 1140

_SL

ggacagggca ccaagctcga gattaaaggt ggaggtggca gcgaggagg tgggtccggc 1200
ggtggaggaa gccaggtcca actccaagaa agcggaccgg gtcttgtgaa gccatcagaa 1260
actctttcac tgacttgtac tgtgagcgga gtgtctctcc ccgattacgg ggtgtcttgg 1320
atcagacagc caccggggaa gggctctgga tggattggag tgatttgggg ctctgagact 1380
acttactact cttcatccct caagtcacgc gtcaccatct caaaggacaa ctctaagaat 1440
caggtgtcac tgaaactgtc atctgtgacc gcagccgaca ccgccgtgta ctattgcgct 1500
aagcattact attatggcgg gagctacgca atggattact ggggacaggg tactctggtc 1560
accgtgtcca gcaccactac ccagcaccg aggccacca ccccggtcc taccatcgcc 1620
tcccagcctc tgtccctgcg tccggaggca tgtagaccgg cagctgggtg ggccgtgcat 1680
acccggggtc ttgacttcgc ctgcgatatc tacatttggg cccctctggc tggacttgc 1740
ggggctctgc tgctttcact cgtgatcact ctttactgta agcgcggtcg gaagaagctg 1800
ctgtacatct ttaagcaacc cttcatgagg cctgtgcaga ctactcaaga ggaggacggc 1860
tgttcatgcc gggtcccaga ggaggaggaa ggcggctgcg aactgcgcgt gaaattcagc 1920
cgcagcgag atgtccagc ctacaagcag ggcagaacc agctctacaa cgaactcaat 1980
cttggtcgga gagaggagta cgacgtgctg gacaagcgga gaggacggga ccagaaaatg 2040
ggcgggaagc cgcgcagaaa gaatcccaa gagggcctgt acaacgagct ccaaaggat 2100
aagatggcag aagcctatag cgagattggt atgaaagggg aacgcagaag agggaaaggc 2160
cacgacggac tgtaccaggg actcagcacc gccaccaagg acacctatga cgctcttcac 2220
atgcaggccc tgccgcctcg g 2241

<210> 159

<211> 747

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 159

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Arg Ser Ser Leu Ala Leu Ser Leu Thr Ala Asp
20 25 30

Gln Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser
35 40 45

Glu Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu
50 55 60

Leu Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala
Page 149

65				70				-SL 75				80			
Lys	Arg	Val	Pro	Gly 85	Phe	Val	Asp	Leu	Thr 90	Leu	His	Asp	Gln	Val 95	His
Leu	Leu	Glu	Cys 100	Ala	Trp	Met	Glu	Ile 105	Leu	Met	Ile	Gly	Leu 110	Val	Trp
Arg	Ser	Met 115	Glu	His	Pro	Gly	Lys 120	Leu	Leu	Phe	Ala	Pro 125	Asn	Leu	Leu
Leu	Asp 130	Arg	Asn	Gln	Gly	Lys 135	Cys	Val	Glu	Gly	Gly 140	Val	Glu	Ile	Phe
Asp 145	Met	Leu	Leu	Ala	Thr 150	Ser	Ser	Arg	Phe	Arg 155	Met	Met	Asn	Leu	Gln 160
Gly	Glu	Glu	Phe	Val 165	Cys	Leu	Lys	Ser	Ile 170	Ile	Leu	Leu	Asn	Ser 175	Gly
Val	Tyr	Thr	Phe 180	Leu	Ser	Ser	Thr	Leu 185	Lys	Ser	Leu	Glu	Glu 190	Lys	Asp
His	Ile	His 195	Arg	Val	Leu	Asp	Lys 200	Ile	Thr	Asp	Thr	Leu 205	Ile	His	Leu
Met	Ala 210	Lys	Ala	Gly	Leu	Thr 215	Leu	Gln	Gln	Gln	His 220	Gln	Arg	Leu	Ala
Gln 225	Leu	Leu	Leu	Ile	Leu 230	Ser	His	Ile	Arg	His 235	Met	Ser	Asn	Lys	Arg 240
Met	Glu	His	Leu	Tyr 245	Ser	Met	Lys	Cys	Lys 250	Asn	Val	Val	Pro	Leu 255	Ser
Asp	Leu	Leu	Leu 260	Glu	Met	Leu	Asp	Ala 265	His	Arg	Leu	Gly	Thr 270	Gly	Ala
Glu	Asp	Pro 275	Arg	Pro	Ser	Arg	Lys 280	Arg	Arg	Glu	Ile	Val 285	Met	Thr	Gln
Ser	Pro 290	Ala	Thr	Leu	Ser	Leu 295	Ser	Pro	Gly	Glu	Arg 300	Ala	Thr	Leu	Ser
Cys 305	Arg	Ala	Ser	Gln	Asp 310	Ile	Ser	Lys	Tyr	Leu 315	Asn	Trp	Tyr	Gln	Gln 320
Lys	Pro	Gly	Gln	Ala 325	Pro	Arg	Leu	Leu	Ile 330	Tyr	His	Thr	Ser	Arg 335	Leu
His	Ser	Gly	Ile	Pro	Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp

_SL

340 345 350

Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Val Tyr
355 360 365

Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gln Gly Thr
370 375 380

Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
385 390 395 400

Gly Gly Gly Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val
405 410 415

Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Val Ser
420 425 430

Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly
435 440 445

Leu Glu Trp Ile Gly Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Ser
450 455 460

Ser Ser Leu Lys Ser Arg Val Thr Ile Ser Lys Asp Asn Ser Lys Asn
465 470 475 480

Gln Val Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val
485 490 495

Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met Asp
500 505 510

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Thr Thr Thr Pro
515 520 525

Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu
530 535 540

Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His
545 550 555 560

Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu
565 570 575

Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr
580 585 590

Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe
595 600 605

Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg

_SL

610		615		620											
Phe	Pro	Glu	Glu	Glu	Glu	Gly	Gly	Cys	Glu	Leu	Arg	Val	Lys	Phe	Ser
625				630						635					640
Arg	Ser	Ala	Asp	Ala	Pro	Ala	Tyr	Gln	Gln	Gly	Gln	Asn	Gln	Leu	Tyr
				645					650					655	
Asn	Glu	Leu	Asn	Leu	Gly	Arg	Arg	Glu	Glu	Tyr	Asp	Val	Leu	Asp	Lys
			660					665					670		
Arg	Arg	Gly	Arg	Asp	Pro	Glu	Met	Gly	Gly	Lys	Pro	Arg	Arg	Lys	Asn
		675					680					685			
Pro	Gln	Glu	Gly	Leu	Tyr	Asn	Glu	Leu	Gln	Lys	Asp	Lys	Met	Ala	Glu
		690				695					700				
Ala	Tyr	Ser	Glu	Ile	Gly	Met	Lys	Gly	Glu	Arg	Arg	Arg	Gly	Lys	Gly
705					710					715					720
His	Asp	Gly	Leu	Tyr	Gln	Gly	Leu	Ser	Thr	Ala	Thr	Lys	Asp	Thr	Tyr
				725					730					735	
Asp	Ala	Leu	His	Met	Gln	Ala	Leu	Pro	Pro	Arg					
			740					745							

<210> 160
 <211> 2241
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 160	
atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg	60
ccccggtcgt cgttggcact ttccctgact gccgaccaga tgggtgtccgc ccttctggac	120
gccgagcctc caattctgta ctcggagtac gatccgactc gcccgttctc cgaagccagc	180
atgatggggc tgttgactaa cctggcggac cgcgagttgg tgcacatgat taactgggct	240
aagcgggtgc cgggcttcgt ggacctgacc ctgcacgacc aagtgcacct cctggaatgc	300
gcctggatgg aaatcctcat gatcggcctc gtgtggagat ccatggagca tcccggaaag	360
ctcctgtttg cacccaacct cctgcttgat cgcaaccagg gaaaatgcgt ggaaggggggt	420
gtcgagattt tcgacatgct gctcgccacc tcttcccgggt tccggatgat gaatctgcag	480
ggagaagagt tcgtgtgtct gaagtcaatc atcctgctga actccgggggt ctataccttc	540
ctgagctcga ccctcaagtc actggaggaa aaagaccaca tccatcgcgt gctcgataag	600
atcaccgaca cccttatcca tctcatggcg aaggctggac tgaccctgca acagcagcac	660

```

                                _SL
cagaggctgg cccagttgct gctgattctg agccacatcc ggcacatgtc gaacaagagg      720
atggaacacc tgtacagcat gaagtgcaag aacgtcgtgc ctctgtccga tctgtcctg      780
gaaatgctgg acgcgcacag actcgggacg ggagctgaag atccacgacc cagcagaaag      840
cgacgggaaa ttgtgatgac ccagtcaccc gccactctta gcctttcacc cggtgagcgc      900
gcaaccctgt cttgcagagc ctcccaagac atctcaaaat accttaattg gtatcaacag      960
aagcccggac aggtcctctg ctttctgac taccacacca gccggctcca ttctggaatc     1020
cctgccaggt tcagcggtag cggatctggg accgactaca ccctcactat cagctcactg     1080
cagccagagg acttcgctgt ctatttctgt cagcaaggga acaccctgcc ctacaccttt     1140
ggacagggca ccaagctcga gattaaaggt ggaggtggca gcgaggagg tgggtccggc     1200
ggtggaggaa gccaggtcca actccaagaa agcggaccgg gtcttgtgaa gccatcagaa     1260
actctttcac tgacttgtac tgtgagcggg gtgtctctcc ccgattacgg ggtgtcttgg     1320
atcagacagc caccggggaa gggctctggaa tggattggag tgatttgggg ctctgagact     1380
acttactact cttcatccct caagtcacgc gtcaccatct caaaggacaa ctctaagaat     1440
caggtgtcac tgaaactgtc atctgtgacc gcagccgaca ccgccgtgta ctattgcgt     1500
aagcattact attatggcgg gagctacgca atggattact ggggacaggg tactctggtc     1560
accgtgtcca gcaccactac ccagcaccg aggccacca ccccggtcc taccatcgcc     1620
tcccagctc tgtccctgcg tccggaggca tgtagaccg cagctgggtg ggccgtgcat     1680
acccggggtc ttgacttcgc ctgcgatatc tacatttggg cccctctggc tgg tacttgc     1740
ggggtcctgc tgctttcact cgtgatcact ctttactgta agcgcggtcg gaagaagctg     1800
ctgtacatct ttaagcaacc cttcatgagg cctgtgcaga ctactcaaga ggaggacggc     1860
tgttcatgcc ggttcccaga ggaggaggaa ggcggctgcg aactgcgcgt gaaattcagc     1920
cgcagcgag atgctccagc ctaccagcag ggcagaacc agctctacaa cgaactcaat     1980
cttggtcggg gagaggagta cgacgtgctg gacaagcgga gaggacggga ccagaaatg     2040
ggcgggaagc cgcgcagaaa gaatcccaa gagggcctgt acaacgagct ccaaaggat     2100
aagatggcag aagcctatag cgagattggg atgaaagggg aacgcagaag aggcaaaggc     2160
cacgacggac tgtaccaggg actcagcacc gccaccaagg acacctatga cgctcttcac     2220
atgcaggccc tgccgcctcg g                                     2241

```

<210> 161

<211> 738

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 161

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

_SL

His Ala Ala Arg Pro Arg Ser Ser Leu Ala Leu Ser Leu Thr Ala Asp
20 25 30

Gln Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser
35 40 45

Glu Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu
50 55 60

Leu Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala
65 70 75 80

Lys Arg Val Pro Gly Phe Val Asp Leu Ala Leu His Asp Gln Val His
85 90 95

Leu Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp
100 105 110

Arg Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu
115 120 125

Leu Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe
130 135 140

Asp Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln
145 150 155 160

Gly Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly
165 170 175

Val Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp
180 185 190

His Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu
195 200 205

Met Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala
210 215 220

Gln Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Ser Lys Arg
225 230 235 240

Met Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Ser
245 250 255

Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu Arg Thr Lys Arg
260 265 270

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
275 280 285

_SL

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
290 295 300

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
305 310 315 320

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
325 330 335

Gln Gly Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Ser Thr Val Tyr
340 345 350

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
355 360 365

Ala Arg Asp Met Asn Ile Leu Ala Thr Val Pro Phe Asp Ile Trp Gly
370 375 380

Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
385 390 395 400

Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro
405 410 415

Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg
420 425 430

Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro
435 440 445

Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser
450 455 460

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
465 470 475 480

Leu Thr Val Asn Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
485 490 495

Gln Gln Gly Asp Ser Val Pro Leu Thr Phe Gly Gly Gly Thr Arg Leu
500 505 510

Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro
515 520 525

Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro
530 535 540

Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp
545 550 555 560

_SL

Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu
565 570 575

Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu
580 585 590

Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu
595 600 605

Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys
610 615 620

Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln
625 630 635 640

Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu
645 650 655

Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly
660 665 670

Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu
675 680 685

Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly
690 695 700

Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser
705 710 715 720

Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro
725 730 735

Pro Arg

<210> 162

<211> 2214

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 162

atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgtcca cgccgctcgg 60

ccccggtcgt cgttggcact ttccctgact gccgaccaga tgggtgtccgc ctttctggac 120

gccgagcctc caattctgta ctcggagtac gatccgactc gcccgttctc cgaagccagc 180

atgatggggc tgttgactaa cctggcggac cgcgagttgg tgcacatgat taactgggct 240

_SL

aagcgggtgc	cgggcttcgt	ggacctggcc	ctgcacgacc	aagtgcacct	cctggaatgc	300
gcctggatgg	aaatcctcat	gatcggcctc	gtgtggagat	ccatggagca	tcccggaaag	360
ctcctgtttg	cacccaacct	cctgcttgat	cgcaaccagg	gaaaatgcgt	ggaagggggt	420
gtcgagattt	tcgacatgct	gctcgccacc	tcttcccggg	tccggatgat	gaatctgcag	480
ggagaagagt	tcgtgtgtct	gaagtcaatc	atcctgctga	actccggggg	ctataccttc	540
ctgagctcga	ccctcaagtc	actggaggaa	aaagaccaca	tccatcgcg	gctcgataag	600
atcaccgaca	cccttatcca	tctcatggcg	aaggctggac	tgaccctgca	acagcagcac	660
cagaggctgg	cccagttgct	gctgattctg	agccacatcc	ggcacatgtc	gtccaagagg	720
atggaacacc	tgtacagcat	gaagtgcaag	aacgtcgtgc	ctctgtccga	tctgctcctg	780
gaaatgctgg	acgcgcacag	actccgtact	aaaagacaag	tgcaactcgt	caaagcgga	840
gcggaagtca	agaaacccgg	agcgagcgtg	aaagtgtcct	gcaaagcctc	cggctacacc	900
tttacgggct	actacatgca	ctgggtgctc	caggcaccag	gacaggggtc	tgaatggatg	960
ggatggatca	accctaattc	gggcggaact	aactacgcac	agaagttcca	ggggagagt	1020
actctgactc	gggatacctc	catctcaact	gtctacatgg	aactctcccg	cttgcggtca	1080
gatgatacgg	cagtgtacta	ctgcgcccgc	gacatgaata	tcctggctac	cgtgccgttc	1140
gacatctggg	gacaggggac	tatggttact	gtctcatcgg	gcggtggagg	ttcaggagga	1200
ggcggctcgg	gaggcggagg	ttcggacatt	cagatgaccc	agtccccatc	ctctctgtcg	1260
gccagcgtcg	gagatagggg	gaccattacc	tgctgggcct	cgcaaagcat	ctcctcgtac	1320
ctcaactggg	atcagcaaaa	gccgggaaag	gcgcctaagc	tgctgatcta	cgccgcttcg	1380
agcttgcaaa	gcgggggtgc	atccagattc	tcgggatcag	gctcagggaac	cgacttcacc	1440
ctgaccgtga	acagcctcca	gccggaggac	tttgccactt	actactgcca	gcagggagac	1500
tccgtgccgc	ttactttcgg	gggggggtacc	cgcttgagga	tcaagaccac	tacccagca	1560
ccgaggccac	ccaccccggc	tcctaccatc	gcctcccagc	ctctgtccct	gcgtccggag	1620
gcatgtagac	ccgcagctgg	tggggccgtg	catacccggg	gtcttgactt	cgctgcgat	1680
atctacattt	gggcccctct	ggctggtact	tgcggggtcc	tgctgctttc	actcgtgac	1740
actctttact	gtaagcgcg	tcggaagaag	ctgctgtaca	tctttaagca	acccttcac	1800
aggcctgtgc	agactactca	agaggaggac	ggctgttcat	gccggttccc	agaggaggag	1860
gaaggcggct	gcgaactgcg	cgtgaaattc	agccgcagcg	cagatgctcc	agcctaccag	1920
caggggcaga	accagctcta	caacgaactc	aatcttggtc	ggagagagga	gtacgacgtg	1980
ctggacaagc	ggagaggacg	ggaccagaa	atgggcggga	agccgcgcag	aaagaatccc	2040
caagagggcc	tgtacaacga	gctccaaaag	gataagatgg	cagaagccta	tagcgagatt	2100
ggtatgaaag	gggaacgcag	aagaggcaaa	ggccacgacg	gactgtacca	gggactcagc	2160
accgccacca	aggacaccta	tgacgtcttt	cacatgcagg	ccctgccgcc	tcgg	2214

_SL

<210> 163
<211> 754
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 163
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Arg Ser Ser Leu Ala Leu Ser Leu Thr Ala Asp
20 25 30

Gln Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser
35 40 45

Glu Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu
50 55 60

Leu Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala
65 70 75 80

Lys Arg Val Pro Gly Phe Val Asp Leu Ala Leu His Asp Gln Val His
85 90 95

Leu Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp
100 105 110

Arg Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu
115 120 125

Leu Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe
130 135 140

Asp Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln
145 150 155 160

Gly Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly
165 170 175

Val Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp
180 185 190

His Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu
195 200 205

Met Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala
210 215 220

Gln Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Ser Lys Arg
Page 158

225					230					-SL 235					240
Met	Glu	His	Leu	Tyr 245	Ser	Met	Lys	Cys	Lys 250	Asn	Val	Val	Pro	Leu 255	Ser
Asp	Leu	Leu	Leu 260	Glu	Met	Leu	Asp	Ala 265	His	Arg	Leu	Gly	Thr 270	Gly	Ala
Glu	Asp	Pro 275	Arg	Pro	Ser	Arg	Lys 280	Arg	Arg	Ser	Leu	Gly 285	Asp	Val	Gly
Gln	Val 290	Gln	Leu	Val	Gln	Ser 295	Gly	Ala	Glu	Val	Lys 300	Lys	Pro	Gly	Ala
Ser 305	Val	Lys	Val	Ser	Cys 310	Lys	Ala	Ser	Gly	Tyr 315	Thr	Phe	Thr	Gly	Tyr 320
Tyr	Met	His	Trp	Val 325	Arg	Gln	Ala	Pro	Gly 330	Gln	Gly	Leu	Glu	Trp 335	Met
Gly	Trp	Ile	Asn 340	Pro	Asn	Ser	Gly	Gly 345	Thr	Asn	Tyr	Ala	Gln 350	Lys	Phe
Gln	Gly	Arg 355	Val	Thr	Leu	Thr	Arg 360	Asp	Thr	Ser	Ile	Ser 365	Thr	Val	Tyr
Met	Glu 370	Leu	Ser	Arg	Leu	Arg 375	Ser	Asp	Asp	Thr	Ala 380	Val	Tyr	Tyr	Cys
Ala 385	Arg	Asp	Met	Asn	Ile 390	Leu	Ala	Thr	Val	Pro 395	Phe	Asp	Ile	Trp	Gly 400
Gln	Gly	Thr	Met	Val 405	Thr	Val	Ser	Ser	Gly 410	Gly	Gly	Gly	Ser	Gly 415	Gly
Gly	Gly	Ser	Gly 420	Gly	Gly	Gly	Ser	Asp 425	Ile	Gln	Met	Thr	Gln 430	Ser	Pro
Ser	Ser	Leu 435	Ser	Ala	Ser	Val	Gly 440	Asp	Arg	Val	Thr	Ile 445	Thr	Cys	Arg
Ala 450	Ser	Gln	Ser	Ile	Ser	Ser 455	Tyr	Leu	Asn	Trp	Tyr 460	Gln	Gln	Lys	Pro
Gly 465	Lys	Ala	Pro	Lys	Leu 470	Leu	Ile	Tyr	Ala	Ala 475	Ser	Ser	Leu	Gln	Ser 480
Gly	Val	Pro	Ser	Arg 485	Phe	Ser	Gly	Ser	Gly 490	Ser	Gly	Thr	Asp	Phe 495	Thr
Leu	Thr	Val	Asn	Ser	Leu	Gln	Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys

<211> 2262
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 164
atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60
ccccggtcgt cgttggcact ttccctgact gccgaccaga tgggtgtccgc ctttctggac 120
gccgagcctc caattctgta ctcggagtac gatccgactc gcccgttctc cgaagccagc 180
atgatgggcc tgttgactaa cctggcggac cgcgagttgg tgcacatgat taactgggct 240
aagcgggtgc cgggcttcgt ggacctggcc ctgcacgacc aagtgcacct cctggaatgc 300
gcctggatgg aaatcctcat gatcggcctc gtgtggagat ccatggagca tcccggaaag 360
ctcctgtttg caccacacct cctgcttgat cgcaaccagg gaaaatgcgt ggaaggggggt 420
gtcgagattt tcgacatgct gctcgccacc tcttcccggg tccggatgat gaatctgcag 480
ggagaagagt tcgtgtgtct gaagtcaatc atcctgctga actccggggg ctataccttc 540
ctgagctcga ccctcaagtc actggaggaa aaagaccaca tccatcgcgt gctcgataag 600
atcaccgaca cccttatcca tctcatggcg aaggctggac tgaccctgca acagcagcac 660
cagaggctgg ccagttgct gctgattctg agccacatcc ggcacatgtc gtccaagagg 720
atggaacacc tgtacagcat gaagtgaag aacgtcgtgc ctctgtccga tctgctcctg 780
gaaatgctgg acgcgcacag actcggaaac ggcgcggaag acccccggcc ctccaggaag 840
cgaaggtccc tcggagacgt ggggtcaagt caactcgtcc aaagcggagc ggaagtcaag 900
aaaccgggag cgagcgtgaa agtgtcctgc aaagcctccg gctacacctt tacgggctac 960
tacatgcact ggggtgcgca ggcaccagga cagggtcttg aatggatggg atggatcaac 1020
cctaattcgg gcggaactaa ctacgcacag aagttccagg ggagagtgaac tctgactcgg 1080
gatacctcca tctcaactgt ctacatggaa ctctcccgtt tgcggtcaga tgatacggca 1140
gtgtactact gcgcccgcga catgaatata ctggctaccg tgccgttcga catctgggga 1200
caggggacta tggttactgt ctcatcgggc ggtggaggtt caggaggagg cggctcggga 1260
ggcggaggtt cggacattca gatgaccag tccccatcct ctctgtcggc cagcgtcggga 1320
gatagggtga ccattacctg tcgggcctcg caaagcatct cctcgtacct caactggtat 1380
cagcaaaagc cgggaaaggc gcctaagctg ctgatctacg ccgcttcgag cttgcaaagc 1440
ggggtgccat ccagattctc gggatcaggc tcaggaaccg acttcaccct gaccgtgaac 1500
agcctccagc cggaggactt tgccacttac tactgccagc agggagactc cgtgccgctt 1560
actttcgggg ggggtaccgg cctggagatc aagaccacta cccagcacc gaggccaccc 1620
accccggtc ctaccatcgc ctcccagcct ctgtccctgc gtccggaggc atgtagaccc 1680
gcagctggtg gggccgtgca taccgggggt cttgacttcg cctgcgatat ctacatttgg 1740

_SL

```

ccccctctgg ctggtacttg cggggtcctg ctgctttcac tcgtgatcac tctttactgt      1800
aagcgcggtc ggaagaagct gctgtacatc ttttaagcaac ccttcatgag gcctgtgcag      1860
actactcaag aggaggacgg ctgttcatgc cggttcccgaggaggagga aggcggctgc      1920
gaactgcgcg tgaaattcag ccgcagcgca gatgctccag cctaccagca ggggcagAAC      1980
cagctctaca acgaactcaa tcttggtcgg agagaggagt acgacgtgct ggacaagcgg      2040
agaggacggg acccagaaat gggcggaag ccgcgcagaa agaattccca agagggcctg      2100
tacaacgagc tccaaaagga taagatggca gaagcctata gcgagattgg tatgaaaggg      2160
gaacgcagaa gaggcaaagg ccacgacgga ctgtaccagg gactcagcac cgccaccaag      2220
gacacctatg acgctcttca catgcaggcc ctgccgcctc gg                        2262

```

<210> 165
 <211> 748
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 165
 Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
 1 5 10 15

His Ala Ala Arg Pro Arg Ser Ser Leu Ala Leu Ser Leu Thr Ala Asp
 20 25 30

Gln Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser
 35 40 45

Glu Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu
 50 55 60

Leu Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala
 65 70 75 80

Lys Arg Val Pro Gly Phe Val Asp Leu Ala Leu His Asp Gln Val His
 85 90 95

Leu Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp
 100 105 110

Arg Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu
 115 120 125

Leu Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe
 130 135 140

Asp Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln
 145 150 155 160

_SL

Gly Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly
165 170 175

Val Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp
180 185 190

His Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu
195 200 205

Met Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala
210 215 220

Gln Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Ser Lys Arg
225 230 235 240

Met Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Ser
245 250 255

Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu Gly Thr Gly Ala
260 265 270

Glu Asp Pro Arg Pro Ser Arg Lys Arg Arg Gln Val Gln Leu Val Gln
275 280 285

Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys
290 295 300

Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr Tyr Met His Trp Val Arg
305 310 315 320

Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Trp Ile Asn Pro Asn
325 330 335

Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Leu
340 345 350

Thr Arg Asp Thr Ser Ile Ser Thr Val Tyr Met Glu Leu Ser Arg Leu
355 360 365

Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Met Asn Ile
370 375 380

Leu Ala Thr Val Pro Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr
385 390 395 400

Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
405 410 415

Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
420 425 430

_SL

Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser
435 440 445

Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu
450 455 460

Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe
465 470 475 480

Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Val Asn Ser Leu
485 490 495

Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Gly Asp Ser Val
500 510

Pro Leu Thr Phe Gly Gly Gly Thr Arg Leu Glu Ile Lys Thr Thr Thr
515 520 525

Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro
530 535 540

Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val
545 550 555 560

His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro
565 570 575

Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu
580 585 590

Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro
595 600 605

Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys
610 615 620

Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe
625 630 635 640

Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu
645 650 655

Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp
660 665 670

Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys
675 680 685

Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala
690 695 700

_SL

Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
705 710 715 720

Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
725 730 735

Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
740 745

<210> 166
<211> 2244
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 166
atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60
ccccggtcgt cgttggcact ttccctgact gccgaccaga tgggtgtccgc ctttctggac 120
gccgagcctc caattctgta ctcggagtac gatccgactc gcccgttctc cgaagccagc 180
atgatgggcc tgttgactaa cctggcggac cgcgagttgg tgcacatgat taactgggct 240
aagcgggtgc cgggcttcgt ggacctggcc ctgcacgacc aagtgcacct cctggaatgc 300
gcctggatgg aaatcctcat gatcggcctc gtgtggagat ccatggagca tcccggaaag 360
ctcctgtttg cacccaacct cctgcttgat cgcaaccagg gaaaatgcgt ggaagggggt 420
gtcgagattt tcgacatgct gctcgccacc tcttcccgtt tccggatgat gaatctgcag 480
ggagaagagt tcgtgtgtct gaagtcaatc atcctgctga actccggggt ctataccttc 540
ctgagctcga ccctcaagtc actggaggaa aaagaccaca tccatcgcgt gctcgataag 600
atcaccgaca cccttatcca tctcatggcg aaggctggac tgaccctgca acagcagcac 660
cagaggctgg cccagttgct gctgattctg agccacatcc ggcacatgtc gtccaagagg 720
atggaacacc tgtacagcat gaagtgaag aacgtcgtgc ctctgtccga tctgctcctg 780
gaaatgctgg acgcgcacag actcgggaacc ggcgcggaag acccccggcc ctccaggaag 840
cgaaggcaag tgcaactcgt ccaaagcgga gcggaagtca agaaacccgg agcgagcgtg 900
aaagtgtcct gcaaagcctc cggctacacc tttacgggct actacatgca ctgggtgcgc 960
caggcaccag gacagggtct tgaatggatg ggatggatca accctaattc gggcggaact 1020
aactacgcac agaagttcca ggggagagtg actctgactc gggatacctc catctcaact 1080
gtctacatgg aactctcccg cttgcgggtca gatgatacgg cagtgtacta ctgcgcccgc 1140
gacatgaata tcctggctac cgtgccgttc gacatctggg gacaggggac tatggttact 1200
gtctcatcgg gcggtggagg ttcaggagga ggcggctcgg gaggcggagg ttcggacatt 1260
cagatgaccc agtccccatc ctctctgtcg gccagcgtcg gagatagggt gaccattacc 1320

_SL

tgtcgggcct cgcaaagcat ctctcgtac ctcaactggt atcagcaaaa gccgggaaag 1380
gcgcctaagc tgctgatcta cgccgcttcg agcttgcaaa gcgggggtgcc atccagattc 1440
tcgggatcag gtcaggaac cgacttcacc ctgaccgtga acagcctcca gccggaggac 1500
tttgccactt actactgcca gcaggagac tccgtgccgc ttactttcgg ggggggtacc 1560
cgcttgaga tcaagaccac taccagca ccgaggccac ccacccggc tcctaccatc 1620
gcctcccagc ctctgtccct gcgtccggag gcatgtagac ccgcagctgg tggggccgtg 1680
cataccggg gtcttgactt cgctgcgat atctacattt gggcccctct ggctggtact 1740
tgcggggtcc tgctgcttc actcgtgatc actctttact gtaagcgcg tcggaagaag 1800
ctgctgtaca tctttaagca acccttcatt aggctgtgc agactactca agaggaggac 1860
ggctgttcat gccggttccc agaggaggag gaaggcggt gcgaactgcg cgtgaaattc 1920
agccgcagc agatgctcc agcctaccag caggggcaga accagctcta caacgaactc 1980
aatcttggtc ggagagagga gtacgacgtg ctggacaagc ggagaggacg ggaccagaa 2040
atgggcggga agccgcgag aaagaatccc caagagggcc tgtacaacga gtcctaaaag 2100
gataagatgg cagaagccta tagcgagatt ggtatgaaag gggaacgcag aagaggcaaa 2160
ggccacgacg gactgtacca gggactcagc accgccacca aggacaccta tgacgtcttt 2220
cacatgcagg ccctgccgcc tcgg 2244

<210> 167

<211> 738

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 167

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Arg Ser Ser Leu Ala Leu Ser Leu Thr Ala Asp
20 25 30

Gln Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser
35 40 45

Glu Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu
50 55 60

Leu Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala
65 70 75 80

Lys Arg Val Pro Gly Phe Val Asp Leu Thr Leu His Asp Gln Val His
85 90 95

_SL

Leu Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp
100 105 110

Arg Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu
115 120 125

Leu Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe
130 135 140

Asp Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln
145 150 155 160

Gly Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly
165 170 175

Val Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp
180 185 190

His Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu
195 200 205

Met Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala
210 215 220

Gln Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Asn Lys Arg
225 230 235 240

Met Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Ser
245 250 255

Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu Arg Thr Lys Arg
260 265 270

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
275 280 285

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
290 295 300

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
305 310 315 320

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
325 330 335

Gln Gly Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Ser Thr Val Tyr
340 345 350

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
355 360 365

_SL

Ala Arg Asp Met Asn Ile Leu Ala Thr Val Pro Phe Asp Ile Trp Gly
370 375 380

Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
385 390 395 400

Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro
405 410 415

Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg
420 425 430

Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro
435 440 445

Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser
450 455 460

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
465 470 475 480

Leu Thr Val Asn Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
485 490 495

Gln Gln Gly Asp Ser Val Pro Leu Thr Phe Gly Gly Gly Thr Arg Leu
500 505 510

Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro
515 520 525

Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro
530 535 540

Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp
545 550 555 560

Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu
565 570 575

Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu
580 585 590

Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu
595 600 605

Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys
610 615 620

Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln
625 630 635 640

_SL

Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu
645 650 655

Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly
660 665 670

Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu
675 680 685

Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly
690 695 700

Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser
705 710 715 720

Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro
725 730 735

Pro Arg

<210> 168

<211> 2214

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 168

atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg	60
ccccggtcgt cgttggcact ttccctgact gccgaccaga tgggtgtccgc ccttctggac	120
gccgagcctc caattctgta ctcggtgact gatccgactc gcccgttctc cgaagccagc	180
atgatgggcc tgttgactaa cctggcggac cgcgagttgg tgcacatgat taactgggct	240
aagcgggtgc cgggcttcgt ggacctgacc ctgcacgacc aagtgcacct cctggaatgc	300
gcctggatgg aaatcctcat gatcggcctc gtgtggagat ccatggagca tcccggaaag	360
ctcctgtttg cacccaacct cctgcttgat cgcaaccagg gaaaatgcgt ggaaggggggt	420
gtcgagattt tcgacatgct gctcgccacc tcttcccgggt tccggatgat gaatctgcag	480
ggagaagagt tcgtgtgtct gaagtcaatc atcctgctga actccgggggt ctataccttc	540
ctgagctcga ccctcaagtc actggaggaa aaagaccaca tccatcgcgt gctcgataag	600
atcaccgaca cccttatcca tctcatggcg aaggctggac tgaccctgca acagcagcac	660
cagaggctgg ccagttgct gctgattctg agccacatcc ggcacatgtc gaacaagagg	720
atggaacacc tgtacagcat gaagtgcaag aacgtcgtgc ctctgtccga tctgtcctg	780
gaaatgctgg acgcgcacag actccgtact aaaagacaag tgcaactcgt ccaaagcgga	840

_SL

gcggaagtca agaaacccgg agcgagcgtg aaagtgtcct gcaaagcctc cggctacacc	900
tttacgggct actacatgca ctgggtgctg caggcaccag gacaggggtct tgaatggatg	960
ggatggatca accctaattc gggcggaact aactacgcac agaagttcca ggggagagtg	1020
actctgactc gggatacctc catctcaact gtctacatgg aactctcccg cttgcggtca	1080
gatgatacgg cagtgtacta ctgcgcccgc gacatgaata tcctggctac cgtgccgttc	1140
gacatctggg gacaggggac tatggttact gtctcatcgg gcggtggagg ttcaggagga	1200
ggcggctcgg gaggcggagg ttcggacatt cagatgaccc agtccccatc ctctctgtcg	1260
gccagcgtcg gagatagggg gaccattacc tgtcgggcct cgcaaagcat ctcctcgtac	1320
ctcaactggg atcagcaaaa gccgggaaag gcgcctaagc tgctgatcta cgccgcttcg	1380
agcttgcaaa gcgggggtgcc atccagattc tcgggatcag gctcaggaac cgacttcacc	1440
ctgaccgtga acagcctcca gccggaggac tttgccactt actactgcca gcagggagac	1500
tccgtgccgc ttactttcgg ggggggtacc cgcctggaga tcaagaccac taccacagca	1560
ccgaggccac ccaccccgcc tcctaccatc gcctcccagc ctctgtccct gcgtccggag	1620
gcatgtagac ccgcagctgg tggggccgtg catacccggg gtcttgactt cgcttgcgat	1680
atctacattt gggcccctct ggctgggtact tgcgggggtcc tgctgctttc actcgtgac	1740
actctttact gtaagcgcgg tcggaagaag ctgctgtaca tctttaagca acccttcatg	1800
aggcctgtgc agactactca agaggaggac ggctgttcac gccgggttccc agaggaggag	1860
gaaggcggct gcgaactgcg cgtgaaattc agccgcagcg cagatgctcc agcctaccag	1920
caggggcaga accagctcta caacgaactc aatcttggtc ggagagagga gtacgacgtg	1980
ctggacaagc ggagaggacg ggaccagaa atgggcggga agccgcgcag aaagaatccc	2040
caagagggcc tgtacaacga gctccaaaag gataagatgg cagaagccta tagcgagatt	2100
ggtatgaaag gggaacgcag aagaggcaaa ggccacgacg gactgtacca gggactcagc	2160
accgccacca aggacaccta tgacgtctt cacatgcagg ccctgccgcc tcgg	2214

<210> 169

<211> 754

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 169

Met	Ala	Leu	Pro	Val	Thr	Ala	Leu	Leu	Pro	Leu	Ala	Leu	Leu	Leu
1				5				10					15	

His	Ala	Ala	Arg	Pro	Arg	Ser	Ser	Leu	Ala	Leu	Ser	Leu	Thr	Ala	Asp
			20					25					30		

Gln	Met	Val	Ser	Ala	Leu	Leu	Asp	Ala	Glu	Pro	Pro	Ile	Leu	Tyr	Ser
		35					40					45			

_SL

Glu Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu
50 55 60

Leu Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala
65 70 75 80

Lys Arg Val Pro Gly Phe Val Asp Leu Thr Leu His Asp Gln Val His
85 90 95

Leu Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp
100 105 110

Arg Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu
115 120 125

Leu Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe
130 135 140

Asp Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln
145 150 155 160

Gly Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly
165 170 175

Val Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp
180 185 190

His Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu
195 200 205

Met Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala
210 215 220

Gln Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Asn Lys Arg
225 230 235 240

Met Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Ser
245 250 255

Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu Gly Thr Gly Ala
260 265 270

Glu Asp Pro Arg Pro Ser Arg Lys Arg Arg Ser Leu Gly Asp Val Gly
275 280 285

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
290 295 300

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
305 310 315 320

_SL

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
325 330 335

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
340 345 350

Gln Gly Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Ser Thr Val Tyr
355 360 365

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
370 375 380

Ala Arg Asp Met Asn Ile Leu Ala Thr Val Pro Phe Asp Ile Trp Gly
385 390 395 400

Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
405 410 415

Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro
420 425 430

Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg
435 440 445

Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro
450 455 460

Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser
465 470 475 480

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
485 490 495

Leu Thr Val Asn Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
500 505 510

Gln Gln Gly Asp Ser Val Pro Leu Thr Phe Gly Gly Gly Thr Arg Leu
515 520 525

Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro
530 535 540

Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro
545 550 555 560

Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp
565 570 575

Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu
580 585 590

_SL

Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu
595 600 605

Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu
610 615 620

Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys
625 630 635 640

Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln
645 650 655

Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu
660 665 670

Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly
675 680 685

Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu
690 695 700

Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly
705 710 715 720

Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser
725 730 735

Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro
740 745 750

Pro Arg

<210> 170

<211> 2262

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 170

atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60

ccccggctcgt cgttggcact ttccctgact gccgaccaga tgggtgtccgc ctttctggac 120

gccgagcctc caattctgta ctcggtgact gatccgactc gcccgttctc cgaagccagc 180

atgatggggc tggtgactaa cctggcggac cgcgagttgg tgcacatgat taactgggct 240

aagcgggtgc cgggcttcgt ggacctgacc ctgcacgacc aagtgcacct cctggaatgc 300

gcctggatgg aaatcctcat gatcggcctc gtgtggagat ccatggagca tcccggaaag 360

_SL

ctcctgtttg	cacccaacct	cctgcttgat	cgcaaccagg	gaaaatgcgt	ggaagggggt	420
gtcgagattt	tcgacatgct	gctcgccacc	tcttcccgggt	tccggatgat	gaatctgcag	480
ggagaagagt	tcgtgtgtct	gaagtcaatc	atcctgctga	actccgggggt	ctataccttc	540
ctgagctcga	ccctcaagtc	actggaggaa	aaagaccaca	tccatcgcgt	gctcgataag	600
atcaccgaca	cccttatcca	tctcatggcg	aaggctggac	tgaccctgca	acagcagcac	660
cagaggctgg	cccagttgct	gctgattctg	agccacatcc	ggcacatgtc	gaacaagagg	720
atggaacacc	tgtacagcat	gaagtgaag	aacgtcgtgc	ctctgtccga	tctgctcctg	780
gaaatgctgg	acgcgcacag	actcggaacc	ggcgcggaag	acccccggcc	ctccaggaag	840
cgaagggtccc	tcggagacgt	gggtcaagtg	caactcgtcc	aaagcggagc	ggaagtcaag	900
aaacccggag	cgagcgtgaa	agtgtcctgc	aaagcctccg	gctacacctt	tacgggctac	960
tacatgcact	gggtgcgcca	ggcaccagga	caggggtcttg	aatggatggg	atggatcaac	1020
cctaattcgg	gcggaactaa	ctacgcacag	aagttccagg	ggagagtgc	tctgactcgg	1080
gatacctcca	tctcaactgt	ctacatggaa	ctctcccgt	tgcggtcaga	tgatacggca	1140
gtgtactact	gcgcccgcga	catgaatatc	ctggctaccg	tgccgttcga	catctgggga	1200
caggggacta	tgggttactgt	ctcatcgggc	ggtggagggt	caggaggagg	cggctcggga	1260
ggcggagggt	cggacattca	gatgaccag	tccccatcct	ctctgtcggc	cagcgtcggga	1320
gataggggtga	ccattacctg	tcgggcctcg	caaagcatct	cctcgtacct	caactggtat	1380
cagcaaaagc	cgggaaaggc	gcctaagctg	ctgatctacg	ccgcttcgag	cttgcaaagc	1440
ggggtgccat	ccagattctc	gggatcaggc	tcaggaaccg	acttcaccct	gaccgtgaac	1500
agcctccagc	cggaggactt	tgccacttac	tactgccagc	agggagactc	cgtgccgctt	1560
actttcgggg	ggggtacccg	cctggagatc	aagaccacta	ccccagcacc	gaggccaccc	1620
accccggctc	ctaccatcgc	ctcccagcct	ctgtccctgc	gtccggaggc	atgtagaccc	1680
gcagctggtg	gggccgtgca	tacccgggggt	cttgacttcg	cctgcgatat	ctacattttg	1740
gcccctctgg	ctggtacttg	cggggtcctg	ctgctttcac	tcgtgatcac	tctttactgt	1800
aagcgcggtc	ggaagaagct	gctgtacatc	tttaagcaac	ccttcatgag	gcctgtgcag	1860
actactcaag	aggaggacgg	ctgttcatgc	cggttccag	aggaggagga	aggcggctgc	1920
gaactgcgcg	tgaaattcag	ccgcagcgca	gatgctccag	cctaccagca	ggggcagaac	1980
cagctctaca	acgaactcaa	tcttggtcgg	agagaggagt	acgacgtgct	ggacaagcgg	2040
agaggacggg	accagaaaat	gggcgggaag	ccgcgcagaa	agaatcccca	agagggcctg	2100
tacaacgagc	tccaaaagga	taagatggca	gaagcctata	gcgagattgg	tatgaaaggg	2160
gaacgcagaa	gaggcaaagg	ccacgacgga	ctgtaccagg	gactcagcac	cgccaccaag	2220
gacacctatg	acgctcttca	catgcaggcc	ctgccgcctc	gg		2262

<210> 171

<211> 748

_SL

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 171

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Arg Ser Ser Leu Ala Leu Ser Leu Thr Ala Asp
20 25 30

Gln Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser
35 40 45

Glu Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu
50 55 60

Leu Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala
65 70 75 80

Lys Arg Val Pro Gly Phe Val Asp Leu Thr Leu His Asp Gln Val His
85 90 95

Leu Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp
100 105 110

Arg Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu
115 120 125

Leu Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe
130 135 140

Asp Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln
145 150 155 160

Gly Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly
165 170 175

Val Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp
180 185 190

His Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu
195 200 205

Met Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala
210 215 220

Gln Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Asn Lys Arg
225 230 235 240

_SL

Met Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Ser
245 250 255

Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu Gly Thr Gly Ala
260 265 270

Glu Asp Pro Arg Pro Ser Arg Lys Arg Arg Gln Val Gln Leu Val Gln
275 280 285

Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys
290 295 300

Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr Tyr Met His Trp Val Arg
305 310 315 320

Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Trp Ile Asn Pro Asn
325 330 335

Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Leu
340 345 350

Thr Arg Asp Thr Ser Ile Ser Thr Val Tyr Met Glu Leu Ser Arg Leu
355 360 365

Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Met Asn Ile
370 375 380

Leu Ala Thr Val Pro Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr
385 390 395 400

Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
405 410 415

Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
420 425 430

Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser
435 440 445

Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu
450 455 460

Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe
465 470 475 480

Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Val Asn Ser Leu
485 490 495

Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Gly Asp Ser Val
500 505 510

_SL

Pro Leu Thr Phe Gly Gly Gly Thr Arg Leu Glu Ile Lys Thr Thr Thr
515 520 525

Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro
530 535 540

Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val
545 550 555 560

His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro
565 570 575

Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu
580 585 590

Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro
595 600 605

Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys
610 615 620

Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe
625 630 635 640

Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu
645 650 655

Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp
660 665 670

Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys
675 680 685

Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala
690 695 700

Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
705 710 715 720

Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
725 730 735

Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
740 745

<210> 172

<211> 2244

<212> DNA

<213> Artificial Sequence

<220>

<221> source

_SL

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 172
atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgtcca cgccgctcgg 60
ccccggctcgt cgttggcact ttccctgact gccgaccaga tgggtgtccgc ctttctggac 120
gccgagcctc caattctgta ctcggagtag gatccgactc gcccgttctc cgaagccagc 180
atgatggggc tggtgactaa cctggcggac cgcgagttgg tgcacatgat taactgggct 240
aagcgggtgc cgggcttcgt ggacctgacc ctgcacgacc aagtgcacct cctggaatgc 300
gcctggatgg aaatcctcat gatcggcctc gtgtggagat ccatggagca tcccggaaag 360
ctcctgtttg cacccaacct cctgcttgat cgcaaccagg gaaaatgcgt ggaaggggggt 420
gtcgagattt tcgacatgct gctcgccacc tcttcccggg tccggatgat gaatctgcag 480
ggagaagagt tcgtgtgtct gaagtcaatc atcctgtcta actccggggg ctataccttc 540
ctgagctcga ccctcaagtc actggaggaa aaagaccaca tccatcgcgt gctcgataag 600
atcaccgaca cccttatcca tctcatggcg aaggctggac tgaccctgca acagcagcac 660
cagaggctgg ccagttgct gctgattctg agccacatcc ggcacatgtc gaacaagagg 720
atggaacacc tgtacagcat gaagtgaag aacgtcgtgc ctctgtccga tctgtcctg 780
gaaatgctgg acgcgcacag actcgggacg ggagctgaag atccacgacc cagcagaaag 840
cgacggcaag tgcaactcgt ccaaagcgga gcggaagtca agaaaccggg agcgagcgtg 900
aaagtgtcct gcaaagcctc cggctacacc tttacgggct actacatgca ctgggtgcgc 960
caggcaccag gacaggtct tgaatggatg ggatggatca accctaattc gggcggaact 1020
aactacgcac agaagttcca ggggagagtg actctgactc gggatacctc catctcaact 1080
gtctacatgg aactctcccg cttgcgggtc gatgatacgg cagtgtacta ctgcgcccgc 1140
gacatgaata tcctggctac cgtgccgttc gacatctggg gacaggggac tatggttact 1200
gtctcatcgg gcggtggagg ttcaggagga ggcggctcgg gaggcggagg ttcggacatt 1260
cagatgacct agtccccatc ctctctgtcg gccagcgtcg gagatagggt gaccattacc 1320
tgtcgggcct cgcaaagcat ctctcgtac ctcaactggg atcagcaaaa gccgggaaag 1380
gcgcctaagc tgctgatcta cgccgcttcg agcttgcaaa gcgggggtgcc atccagattc 1440
tcgggatcag gctcaggaac cgacttcacc ctgaccgtga acagcctcca gccggaggac 1500
tttgccactt actactgcca gcaggagac tccgtgccgc ttactttcgg ggggggtacc 1560
cgctggaga tcaagaccac taccagca ccgaggccac ccacccggc tcctaccatc 1620
gcctcccagc ctctgtccct gcgtccggag gcatgtagac ccgcagctgg tggggccgtg 1680
cataccggg gtcttgactt cgctgcgat atctacattt gggcccctct ggctggtact 1740
tgcggggtcc tgctgcttc actcgtgatc actctttact gtaagcgcg tccgaagaag 1800
ctgctgtaca tctttaagca acccttcatg aggcctgtgc agactactca agaggaggac 1860
ggctgttcat gccggttccc agaggaggag gaaggcggct gcgaactgcg cgtgaaattc 1920

_SL

agccgcagcg cagatgctcc agcctaccag caggggcaga accagctcta caacgaactc	1980
aatcttgggtc ggagagagga gtacgacgtg ctggacaagc ggagaggacg ggaccagaa	2040
atgggcggga agccgcgag aaagaatccc caagagggcc tgtacaacga gtcctaaaag	2100
gataagatgg cagaagccta tagcgagatt ggtatgaaag gggaacgcag aagaggcaaa	2160
ggccacgacg gactgtacca gggactcagc accgccacca aggacaccta tgacgctctt	2220
cacatgcagg ccctgccgcc tcgg	2244

<210> 173
 <211> 734
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 173
 Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
 1 5 10 15

His Ala Ala Arg Pro Arg Ser Ser Leu Ala Leu Ser Leu Thr Ala Asp
 20 25 30

Gln Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser
 35 40 45

Glu Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu
 50 55 60

Leu Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala
 65 70 75 80

Lys Arg Val Pro Gly Phe Val Asp Leu Ala Leu His Asp Gln Val His
 85 90 95

Leu Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp
 100 105 110

Arg Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu
 115 120 125

Leu Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe
 130 135 140

Asp Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln
 145 150 155 160

Gly Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly
 165 170 175

Val Tyr Thr Phe₁₈₀ Leu Ser Ser Thr Leu₁₈₅ Lys^{-SL} Ser Leu Glu Glu₁₉₀ Lys Asp
 His Ile His₁₉₅ Arg Val Leu Asp Lys₂₀₀ Ile Thr Asp Thr Leu₂₀₅ Ile His Leu
 Met Ala₂₁₀ Lys Ala Gly Leu Thr₂₁₅ Leu Gln Gln Gln His₂₂₀ Gln Arg Leu Ala
 Gln₂₂₅ Leu Leu Leu Ile Leu₂₃₀ Ser His Ile Arg His₂₃₅ Met Ser Ser Lys Arg₂₄₀
 Met Glu His Leu Tyr₂₄₅ Ser Met Lys Cys Lys₂₅₀ Asn Val Val Pro Leu₂₅₅ Ser
 Asp Leu Leu Leu₂₆₀ Glu Met Leu Asp Ala₂₆₅ His Arg Leu Arg Thr₂₇₀ Lys Arg
 Glu Val Gln₂₇₅ Leu Val Glu Ser Gly₂₈₀ Gly Gly Leu Val Gln₂₈₅ Pro Gly Gly
 Ser Leu₂₉₀ Arg Leu Ser Cys Ala₂₉₅ Val Ser Gly Phe Ala₃₀₀ Leu Ser Asn His
 Gly₃₀₅ Met Ser Trp Val Arg₃₁₀ Arg Ala Pro Gly Lys₃₁₅ Gly Leu Glu Trp Val₃₂₀
 Ser Gly Ile Val Tyr₃₂₅ Ser Gly Ser Thr Tyr₃₃₀ Tyr Ala Ala Ser Val₃₃₅ Lys
 Gly Arg Phe Thr₃₄₀ Ile Ser Arg Asp Asn₃₄₅ Ser Arg Asn Thr Leu₃₅₀ Tyr Leu
 Gln Met Asn₃₅₅ Ser Leu Arg Pro Glu₃₆₀ Asp Thr Ala Ile Tyr₃₆₅ Tyr Cys Ser
 Ala His₃₇₀ Gly Gly Glu Ser Asp₃₇₅ Val Trp Gly Gln Gly₃₈₀ Thr Thr Val Thr
 Val₃₈₅ Ser Ser Ala Ser Gly₃₉₀ Gly Gly Gly Ser Gly₃₉₅ Gly Arg Ala Ser Gly₄₀₀
 Gly Gly Gly Ser Asp₄₀₅ Ile Gln Leu Thr Gln₄₁₀ Ser Pro Ser Ser Leu₄₁₅ Ser
 Ala Ser Val Gly₄₂₀ Asp Arg Val Thr Ile₄₂₅ Thr Cys Arg Ala Ser₄₃₀ Gln Ser
 Ile Ser Ser₄₃₅ Tyr Leu Asn Trp Tyr₄₄₀ Gln Gln Lys Pro Gly₄₄₅ Lys Ala Pro

Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu^{-SL} Gln Ser Gly Val Pro Ser
 450 455 460
 Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
 465 470 475 480
 Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr
 485 490 495
 Ser Thr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Thr
 500 505 510
 Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser
 515 520 525
 Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly
 530 535 540
 Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp
 545 550 555 560
 Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile
 565 570 575
 Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys
 580 585 590
 Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys
 595 600 605
 Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val
 610 615 620
 Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn
 625 630 635 640
 Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val
 645 650 655
 Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg
 660 665 670
 Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys
 675 680 685
 Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg
 690 695 700
 Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys
 705 710 715 720

Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
 725 ^{-SL} 730

<210> 174
 <211> 2202
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 174
 atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60
 ccccggtcgt cgttggcact ttccctgact gccgaccaga tgggtgtccgc ctttctggac 120
 gccgagcctc caattctgta ctcggagtag gatccgactc gcccgttctc cgaagccagc 180
 atgatggggc tgttgactaa cctggcggac cgcgagttgg tgcacatgat taactgggct 240
 aagcgggtgc cgggcttcgt ggacctggcc ctgcacgacc aagtgcacct cctggaatgc 300
 gcctggatgg aaatcctcat gatcggcctc gtgtggagat ccatggagca tcccggaaag 360
 ctctgttttg caccacacct cctgcttgat cgcaaccagg gaaaatgcgt ggaaggggggt 420
 gtcgagattt tcgacatgct gctcgccacc tcttcccggg tccggatgat gaatctgcag 480
 ggagaagagt tcgtgtgtct gaagtcaatc atcctgctga actccggggg ctataccttc 540
 ctgagctcga ccctcaagtc actggaggaa aaagaccaca tccatcgcgt gctcgataag 600
 atcaccgaca cccttatcca tctcatggcg aaggctggac tgaccctgca acagcagcac 660
 cagaggctgg ccagttgct gctgattctg agccacatcc ggcacatgct gtccaagagg 720
 atggaacacc tgtacagcat gaagtgaag aacgtcgtgc ctctgtccga tctgctcctg 780
 gaaatgctgg acgcgcacag actccgtact aaaagagaag tgcaattggg ggaatcaggg 840
 ggaggacttg tgcagcctgg aggatcgtg agactgtcat gtgccgtgtc cggctttgcc 900
 ctgtccaacc acgggatgtc ctgggtccgc cgcgcgctg gaaagggcct cgaatgggtg 960
 tcgggtattg tgtacagcgg tagcacctac tatgccgcat ccgtgaaggg gagattcacc 1020
 atcagccggg acaactccag gaacactctg tacctccaaa tgaattcgct gaggccagag 1080
 gacactgcca tctactactg ctccgcgcat ggcggagagt ccgacgtctg gggacagggg 1140
 accaccgtga ccgtgtctag cgcgtccggc ggaggcggca gcggggggtc ggcacagggg 1200
 ggcggcggat cggacatcca gtcacccag tcccagagct cgctgtccgc ctccgtggga 1260
 gatcgggtca ccatcacgtg ccgcgccagc cagtcgattt cctcctacct gaactggtac 1320
 caacagaagc ccggaagc cccgaagctt ctcatctacg ccgcctcgag cctgcagtca 1380
 ggagtgccct cacggttctc cggctccggg tccggtactg atttcaccct gaccatttcc 1440
 tccctgcaac cggaggactt cgctacttac tactgccagc agtcgtactc caccacctac 1500
 actttcggac aaggcaccaa ggtcgaaatc aagaccata cccagcacc gaggccaccc 1560
 accccggctc ctaccatcgc ctccagcct ctgtccctgc gtccggaggc atgtagaccc 1620

_SL

gcagctggtg gggccgtgca taccggtt cttgacttcg cctgcatat ctacatttgg 1680
gcccctcttg ctggtacttg cggggtcctg ctgctttcac tcgtgatcac tctttactgt 1740
aagcgcggtc ggaagaagct gctgtacatc ttttaagcaac ccttcatgag gcctgtgcag 1800
actactcaag aggaggacgg ctgttcatgc cggttcccag aggaggagga aggcggctgc 1860
gaactgcgcg tgaaattcag ccgcagcgca gatgctccag cctaccagca ggggcagaac 1920
cagctctaca acgaactcaa tcttggtcgg agagaggagt acgacgtgct ggacaagcgg 1980
agaggacggg acccagaaat gggcggaag ccgcgcagaa agaattccca agagggcctg 2040
tacaacgagc tccaaaagga taagatggca gaagcctata gcgagattgg tatgaaaggg 2100
gaacgcagaa gaggcaaagg ccacgacgga ctgtaccagg gactcagcac cgccaccaag 2160
gacacctatg acgctcttca catgcaggcc ctgccgcctc gg 2202

<210> 175

<211> 750

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 175

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Arg Ser Ser Leu Ala Leu Ser Leu Thr Ala Asp
20 25 30

Gln Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser
35 40 45

Glu Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu
50 55 60

Leu Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala
65 70 75 80

Lys Arg Val Pro Gly Phe Val Asp Leu Ala Leu His Asp Gln Val His
85 90 95

Leu Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp
100 105 110

Arg Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu
115 120 125

Leu Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe
130 135 140

_SL

Asp Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln
145 150 155 160

Gly Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly
165 170 175

Val Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp
180 185 190

His Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu
195 200 205

Met Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala
210 215 220

Gln Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Ser Lys Arg
225 230 235 240

Met Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Ser
245 250 255

Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu Gly Thr Gly Ala
260 265 270

Glu Asp Pro Arg Pro Ser Arg Lys Arg Arg Ser Leu Gly Asp Val Gly
275 280 285

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
290 295 300

Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Phe Ala Leu Ser Asn His
305 310 315 320

Gly Met Ser Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Trp Val
325 330 335

Ser Gly Ile Val Tyr Ser Gly Ser Thr Tyr Tyr Ala Ala Ser Val Lys
340 345 350

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr Leu
355 360 365

Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Ile Tyr Tyr Cys Ser
370 375 380

Ala His Gly Gly Glu Ser Asp Val Trp Gly Gln Gly Thr Thr Val Thr
385 390 395 400

Val Ser Ser Ala Ser Gly Gly Gly Gly Ser Gly Gly Arg Ala Ser Gly
405 410 415

_SL

Gly Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser
420 425 430

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser
435 440 445

Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
450 455 460

Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser
465 470 475 480

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
485 490 495

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr
500 505 510

Ser Thr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Thr
515 520 525

Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser
530 535 540

Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly
545 550 555 560

Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp
565 570 575

Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile
580 585 590

Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys
595 600 605

Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys
610 615 620

Ser Cys Arg Phe Pro Glu Glu Glu Gly Gly Cys Glu Leu Arg Val
625 630 635 640

Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn
645 650 655

Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val
660 665 670

Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg
675 680 685

_SL

Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys
690 695 700

Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg
705 710 715 720

Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys
725 730 735

Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
740 745 750

<210> 176

<211> 2250

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 176

```
atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg      60
ccccggtcgt cgttggcact ttccctgact gccgaccaga tgggtgtccgc ctttctggac      120
gccgagcctc caattctgta ctcggtgact gatccgactc gcccgttctc cgaagccagc      180
atgatggggc tgttgactaa cctggcggac cgcgagttgg tgcacatgat taactgggct      240
aagcgggtgc cgggcttcgt ggacctggcc ctgcacgacc aagtgcacct cctggaatgc      300
gcctggatgg aaatcctcat gatcggcctc gtgtggagat ccatggagca tcccggaaag      360
ctcctgtttg cacccaacct cctgcttgat cgcaaccagg gaaaatgcgt ggaagggggg      420
gtcgagattt tcgacatgct gctcgccacc tcttcccggg tccggatgat gaatctgcag      480
ggagaagagt tcgtgtgtct gaagtcaatc atcctgctga actccggggg ctataccttc      540
ctgagctcga ccctcaagtc actggaggaa aaagaccaca tccatcgcgt gtcgataag      600
atcaccgaca cccttatcca tctcatggcg aaggctggac tgaccctgca acagcagcac      660
cagaggctgg ccagttgct gctgattctg agccacatcc ggcacatgtc gtccaagagg      720
atggaacacc tgtacagcat gaagtgcaag aacgtcgtgc ctctgtccga tctgctcctg      780
gaaatgctgg acgcgcacag actcggaaac ggcgcggaag acccccggcc ctccaggaag      840
cgaaggtccc tcggagacgt ggggtgaagtg caattgggtg aatcaggggg aggacttggtg      900
cagcctggag gatcgctgag actgtcatgt gccgtgtccg gctttgccct gtccaaccac      960
gggatgtcct ggggtccgccg cgcgcctgga aagggcctcg aatgggtgtc gggattgtg      1020
tacagcggtg gcacctacta tgccgcatcc gtgaagggga gattcaccat cagccgggac      1080
aactccagga acactctgta cctccaaatg aattcgtgta ggccagagga cactgccatc      1140
tactactgct ccgcgcatgg cggagagtcc gacgtctggg gacaggggac caccgtgacc      1200
```

_SL

```

gtgtctagcg cgtccggcgg aggcggcagc gggggtcggg catcaggggg cggcggatcg      1260
gacatccagc tcaccagtc cccgagctcg ctgtccgcct ccgtgggaga tcgggtcacc      1320
atcacgtgcc gcgccagcca gtcgatttcc tcctacctga actggtacca acagaagccc      1380
ggaaaagccc cgaagcttct catctacgcc gcctcgagcc tgcagtcagg agtgcctca      1440
cggttctccg gctccggttc cgggtactgat ttcacctga ccatttcctc cctgcaaccg      1500
gaggacttcg ctacttacta ctgccagcag tcgtactcca cccctacac tttcggacaa      1560
ggcaccaagg tcgaaatcaa gaccactacc ccagcaccga ggccaccac cccggctcct      1620
accatcgcct cccagcctct gtccctgcgt ccggaggcat gtagaccgc agctggtggg      1680
gccgtgcata cccgggtct tgaattcgcc tgcgatattc acatttgggc ccctctggct      1740
ggtacttgcg gggtcctgct gctttcactc gtgatcactc tttactgtaa gcgcggtcgg      1800
aagaagctgc tgtacatctt taagcaacc ttcatgaggc ctgtgcagac tactcaagag      1860
gaggacggct gttcatgccg gttcccagag gaggaggaag gcggctgcga actgcgcgtg      1920
aaattcagcc gcagcgcaga tgctccagcc taccagcagg ggcagaacca gctctacaac      1980
gaactcaatc ttggtcggag agaggagtag gacgtgctgg acaagcggag aggacgggac      2040
ccagaaatgg gcgggaagcc gcgcagaaag aatccccaag agggcctgta caacgagctc      2100
caaaaggata agatggcaga agcctatagc gagattggta tgaaagggga acgcagaaga      2160
ggcaaaggcc acgacggact gtaccaggga ctcagcaccg ccaccaagga cacctatgac      2220
gctcttcaca tgcaggccct gccgcctcgg      2250

```

<210> 177
 <211> 744
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 177
 Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
 1 5 10 15

His Ala Ala Arg Pro Arg Ser Ser Leu Ala Leu Ser Leu Thr Ala Asp
 20 25 30

Gln Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser
 35 40 45

Glu Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu
 50 55 60

Leu Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala
 65 70 75 80

Lys Arg Val Pro Gly Phe Val Asp Leu Ala^{-SL} Leu His Asp Gln Val His
 85 90 95
 Leu Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp
 100 105 110
 Arg Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu
 115 120 125
 Leu Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe
 130 135 140
 Asp Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln
 145 150 155 160
 Gly Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly
 165 170 175
 Val Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp
 180 185 190
 His Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu
 195 200 205
 Met Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala
 210 215 220
 Gln Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Ser Lys Arg
 225 230 235 240
 Met Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Ser
 245 250 255
 Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu Gly Thr Gly Ala
 260 265 270
 Glu Asp Pro Arg Pro Ser Arg Lys Arg Arg Glu Val Gln Leu Val Glu
 275 280 285
 Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys
 290 295 300
 Ala Val Ser Gly Phe Ala Leu Ser Asn His Gly Met Ser Trp Val Arg
 305 310 315 320
 Arg Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Gly Ile Val Tyr Ser
 325 330 335
 Gly Ser Thr Tyr Tyr Ala Ala Ser Val Lys Gly Arg Phe Thr Ile Ser
 340 345 350

Arg Asp Asn Ser Arg Asn Thr Leu Tyr Leu ^{SL}Gln Met Asn Ser Leu Arg
 355 360 365
 Pro Glu Asp Thr Ala Ile Tyr Tyr Cys Ser Ala His Gly Gly Glu Ser
 370 375 380
 Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Gly
 385 390 395 400
 Gly Gly Gly Ser Gly Gly Arg Ala Ser Gly Gly Gly Gly Ser Asp Ile
 405 410 415
 Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
 420 425 430
 Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn
 435 440 445
 Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala
 450 455 460
 Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
 465 470 475 480
 Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
 485 490 495
 Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Tyr Thr Phe
 500 505 510
 Gly Gln Gly Thr Lys Val Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg
 515 520 525
 Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg
 530 535 540
 Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly
 545 550 555 560
 Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr
 565 570 575
 Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg
 580 585 590
 Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro
 595 600 605
 Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu
 610 615 620

Glu Glu Glu Gly Gly Cys Glu Leu Arg Val^{SL} Lys Phe Ser Arg Ser Ala
 625 630 635 640
 Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu
 645 650 655
 Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly
 660 665 670
 Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu
 675 680 685
 Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser
 690 695 700
 Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly
 705 710 715 720
 Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu
 725 730 735
 His Met Gln Ala Leu Pro Pro Arg
 740

<210> 178
 <211> 2232
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 178
 atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60
 ccccggtcgt cgttggcact ttccctgact gccgaccaga tgggtgtccgc ctttctggac 120
 gccgagcctc caattctgta ctcggagtac gatccgactc gcccgttctc cgaagccagc 180
 atgatgggccc tgttgactaa cctggcggac cgcgagttgg tgcacatgat taactgggct 240
 aagcgggtgc cgggcttcgt ggacctggcc ctgcacgacc aagtgcacct cctggaatgc 300
 gcctggatgg aaatcctcat gatcggcctc gtgtggagat ccatggagca tcccggaaag 360
 ctctgttttg cacccaacct cctgcttgat cgcaaccagg gaaaatgcgt ggaaggggggt 420
 gtcgagattt tcgacatgct gctcgccacc tcttcccgggt tccggatgat gaatctgcag 480
 ggagaagagt tcgtgtgtct gaagtcaatc atcctgctga actccgggggt ctataccttc 540
 ctgagctcga ccctcaagtc actggaggaa aaagaccaca tccatcgcgt gctcgataag 600
 atcaccgaca cccttatcca tctcatggcg aaggctggac tgaccctgca acagcagcac 660
 cagaggctgg cccagttgct gctgattctg agccacatcc ggcacatgtc gtccaagagg 720
 atggaacacc tgtacagcat gaagtgaag aacgtcgtgc ctctgtccga tctgtcctg 780

_SL

gaaatgctgg acgcgcacag actcgggacg ggagctgaag atccacgacc cagcagaaag 840
cgacgggaag tgcaattggt ggaatcaggg ggaggacttg tgcagcctgg aggatcgctg 900
agactgtcat gtgccgtgtc cggctttgcc ctgtccaacc acgggatgtc ctgggtccgc 960
cgcgcgctg gaaagggcct cgaatgggtg tcgggtattg tgtacagcg tagcacctac 1020
tatgccgcat ccgtgaaggg gagattcacc atcagccggg acaactccag gaacactctg 1080
tacctccaaa tgaattcgct gaggccagag gacactgcca tctactactg ctccgcat 1140
ggcggagagt ccgacgtctg gggacagggg accaccgtga ccgtgtctag cgcgctccggc 1200
ggaggcggca gcgggggtcg ggcatcaggg ggcgccggat cggacatcca gctcaccag 1260
tccccgagct cgctgtccgc ctccgtggga gatcgggtca ccatcacgtg ccgcgccagc 1320
cagtcgattt cctcctacct gaactggtac caacagaagc ccgaaaagc cccgaagctt 1380
ctcatctacg ccgcctcgag cctgcagtca ggagtgcct caccggttctc cggctccggt 1440
tccggtactg atttcaccct gaccatttcc tccctgcaac cggaggactt cgctacttac 1500
tactgccagc agtcgtactc caccctctac actttcggac aaggcaccaa ggtcgaaatc 1560
aagaccacta cccagcacc gaggccacc acccggctc ctaccatcg ctccagcct 1620
ctgtccctgc gtccggaggc atgtagacc gcagctggtg gggccgtgca taccgggggt 1680
cttgacttcg cctgcgatat ctacatttg gccctcttg ctggtacttg cggggtcctg 1740
ctgctttcac tcgtgatcac tctttactgt aagcgcggtc ggaagaagct gctgtacatc 1800
ttaaagcaac cttcatgag gcctgtgcag actactcaag aggaggacgg ctgttcatgc 1860
cggttcccag aggaggagga aggcggctgc gaactgcgcg tgaaattcag ccgcagcgca 1920
gatgtccag cctaccagca ggggcagaac cagctctaca acgaactcaa tcttggtcgg 1980
agagaggagt acgacgtgct ggacaagcg agaggacggg acccagaaat gggcggaag 2040
ccgcgcagaa agaatcccca agaggcctg tacaacgagc tccaaaagga taagatggca 2100
gaagcctata gcgagattgg tatgaaagg gaacgcagaa gaggcaaagg ccacgacgga 2160
ctgtaccagg gactcagcac cgccaccaag gacacctatg acgctcttca catgcaggcc 2220
ctgccgcctc gg 2232

<210> 179

<211> 734

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 179

Met Ala Leu Pro Val Thr Ala Leu Leu Pro Leu Ala Leu Leu
1 5 10 15

His Ala Ala Arg Pro Arg Ser Ser Leu Ala Leu Ser Leu Thr Ala Asp
Page 191

_SL

20	25	30
Gln Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser		
35	40	45
Glu Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu		
50	55	60
Leu Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala		
65	70	75
Lys Arg Val Pro Gly Phe Val Asp Leu Thr Leu His Asp Gln Val His		
85	90	95
Leu Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp		
100	105	110
Arg Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu		
115	120	125
Leu Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe		
130	135	140
Asp Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln		
145	150	155
Gly Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly		
165	170	175
Val Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp		
180	185	190
His Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu		
195	200	205
Met Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala		
210	215	220
Gln Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Asn Lys Arg		
225	230	235
Met Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Ser		
245	250	255
Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu Arg Thr Lys Arg		
260	265	270
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly		
275	280	285
Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Phe Ala Leu Ser Asn His		

_SL

290		295		300											
Gly 305	Met	Ser	Trp	Val	Arg 310	Arg	Ala	Pro	Gly	Lys 315	Gly	Leu	Glu	Trp	Val 320
Ser	Gly	Ile	Val	Tyr 325	Ser	Gly	Ser	Thr	Tyr 330	Tyr	Ala	Ala	Ser	Val 335	Lys
Gly	Arg	Phe	Thr 340	Ile	Ser	Arg	Asp	Asn 345	Ser	Arg	Asn	Thr	Leu 350	Tyr	Leu
Gln	Met	Asn 355	Ser	Leu	Arg	Pro	Glu 360	Asp	Thr	Ala	Ile	Tyr 365	Tyr	Cys	Ser
Ala	His 370	Gly	Gly	Glu	Ser	Asp 375	Val	Trp	Gly	Gln	Gly 380	Thr	Thr	Val	Thr
Val 385	Ser	Ser	Ala	Ser	Gly 390	Gly	Gly	Gly	Ser	Gly 395	Gly	Arg	Ala	Ser	Gly 400
Gly	Gly	Gly	Ser	Asp 405	Ile	Gln	Leu	Thr	Gln 410	Ser	Pro	Ser	Ser	Leu 415	Ser
Ala	Ser	Val	Gly 420	Asp	Arg	Val	Thr	Ile 425	Thr	Cys	Arg	Ala	Ser 430	Gln	Ser
Ile	Ser	Ser 435	Tyr	Leu	Asn	Trp	Tyr 440	Gln	Gln	Lys	Pro	Gly 445	Lys	Ala	Pro
Lys	Leu 450	Leu	Ile	Tyr	Ala	Ala 455	Ser	Ser	Leu	Gln	Ser 460	Gly	Val	Pro	Ser
Arg 465	Phe	Ser	Gly	Ser	Gly 470	Ser	Gly	Thr	Asp	Phe 475	Thr	Leu	Thr	Ile	Ser 480
Ser	Leu	Gln	Pro	Glu 485	Asp	Phe	Ala	Thr	Tyr 490	Tyr	Cys	Gln	Gln	Ser 495	Tyr
Ser	Thr	Pro	Tyr 500	Thr	Phe	Gly	Gln	Gly 505	Thr	Lys	Val	Glu	Ile 510	Lys	Thr
Thr	Thr	Pro 515	Ala	Pro	Arg	Pro	Pro 520	Thr	Pro	Ala	Pro	Thr 525	Ile	Ala	Ser
Gln	Pro 530	Leu	Ser	Leu	Arg	Pro 535	Glu	Ala	Cys	Arg	Pro 540	Ala	Ala	Gly	Gly
Ala 545	Val	His	Thr	Arg	Gly 550	Leu	Asp	Phe	Ala	Cys 555	Asp	Ile	Tyr	Ile	Trp 560
Ala	Pro	Leu	Ala	Gly	Thr	Cys	Gly	Val	Leu	Leu	Leu	Ser	Leu	Val	Ile

565 570^{-SL} 575

Thr Leu Tyr Cys₅₈₀ Lys Arg Gly Arg Lys₅₈₅ Lys Leu Leu Tyr Ile Phe Lys₅₉₀

Gln Pro Phe₅₉₅ Met Arg Pro Val Gln₆₀₀ Thr Thr Gln Glu Glu₆₀₅ Asp Gly Cys

Ser Cys₆₁₀ Arg Phe Pro Glu Glu₆₁₅ Glu Glu Gly Gly Cys₆₂₀ Glu Leu Arg Val

Lys Phe Ser Arg Ser Ala₆₃₀ Asp Ala Pro Ala Tyr₆₃₅ Gln Gln Gly Gln Asn₆₄₀

Gln Leu Tyr Asn Glu₆₄₅ Leu Asn Leu Gly Arg₆₅₀ Arg Glu Glu Tyr Asp Val₆₅₅

Leu Asp Lys Arg₆₆₀ Arg Gly Arg Asp Pro₆₆₅ Glu Met Gly Gly Lys₆₇₀ Pro Arg

Arg Lys Asn₆₇₅ Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln₆₈₅ Lys Asp Lys

Met Ala Glu Ala Tyr Ser Glu₆₉₅ Ile Gly Met Lys Gly₇₀₀ Glu Arg Arg Arg

Gly Lys Gly His Asp Glu₇₁₀ Leu Tyr Gln Gly Leu₇₁₅ Ser Thr Ala Thr Lys₇₂₀

Asp Thr Tyr Asp Ala₇₂₅ Leu His Met Gln Ala Leu Pro Pro Arg₇₃₀

<210> 180
 <211> 2202
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 180
 atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60
 ccccggtcgt cgttggcact ttccctgact gccgaccaga tgggtgtccgc ctttctggac 120
 gccgagcctc caattctgta ctcggagtac gatccgactc gcccgttctc cgaagccagc 180
 atgatgggcc tgttgactaa cctggcggac cgcgagttgg tgcacatgat taactgggct 240
 aagcgggtgc cgggcttcgt ggacctgacc ctgcacgacc aagtgcacct cctggaatgc 300
 gcctggatgg aaatcctcat gatcggcctc gtgtggagat ccatggagca tcccggaaag 360
 ctctgttttg cacccaacct cctgcttgat cgcaaccagg gaaaatgcgt ggaaggggggt 420

	_SL	
gtcgagattt	tcgacatgct	gctcgccacc
ggagaagagt	tcgtgtgtct	gaagtcaatc
ctgagctcga	ccctcaagtc	actggaggaa
atcaccgaca	cccttatcca	tctcatggcg
cagaggctgg	cccagttgct	gctgattctg
atggaacacc	tgtacagcat	gaagtgaag
gaaatgctgg	acgcgcacag	actccgtact
ggaggacttg	tgcagcctgg	aggatcgctg
ctgtccaacc	acgggatgtc	ctgggtccgc
tcgggtattg	tgtacagcgg	tagcacctac
atcagccggg	acaactccag	gaacactctg
gacactgcca	tctactactg	ctccgcgcgc
accaccgtga	ccgtgtctag	cgcggtccggc
ggcggcggat	cggacatcca	gctcaccag
gatcgggtca	ccatcacgtg	ccgcgccagc
caacagaagc	ccggaaaagc	cccgaagctt
ggagtgccct	cacggttctc	cggctccggg
tccctgcaac	cggaggactt	cgctacttac
actttcggac	aaggcaccaa	ggtcgaaatc
accccggtc	ctaccatcgc	ctcccagcct
gcagctggtg	gggccgtgca	tacccggggg
gcccctctgg	ctggtacttg	cggggtcctg
aagcgcggtc	ggaagaagct	gctgtacatc
actactcaag	aggaggacgg	ctgttcatgc
gaactgcgcg	tgaattcag	ccgcagcgca
cagctctaca	acgaactcaa	tcttggtcgg
agaggacggg	accagaaat	gggcgggaag
tacaacgagc	tccaaaagga	taagatggca
gaacgcagaa	gaggcaaagg	ccacgacgga
gacacctatg	acgctcttca	catgcaggcc

480
540
600
660
720
780
840
900
960
1020
1080
1140
1200
1260
1320
1380
1440
1500
1560
1620
1680
1740
1800
1860
1920
1980
2040
2100
2160
2202

<210> 181
 <211> 750
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source

_SL

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 181

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Arg Ser Ser Leu Ala Leu Ser Leu Thr Ala Asp
20 25 30

Gln Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser
35 40 45

Glu Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu
50 55 60

Leu Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala
65 70 75 80

Lys Arg Val Pro Gly Phe Val Asp Leu Thr Leu His Asp Gln Val His
85 90 95

Leu Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp
100 105 110

Arg Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu
115 120 125

Leu Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe
130 135 140

Asp Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln
145 150 155 160

Gly Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly
165 170 175

Val Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp
180 185 190

His Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu
195 200 205

Met Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala
210 215 220

Gln Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Asn Lys Arg
225 230 235 240

Met Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Ser
245 250 255

Asp Leu Leu Leu₂₆₀ Glu Met Leu Asp Ala₂₆₅ His^{-SL} Arg Leu Gly Thr₂₇₀ Gly Ala
 Glu Asp Pro₂₇₅ Arg Pro Ser Arg Lys₂₈₀ Arg Arg Ser Leu Gly₂₈₅ Asp Val Gly
 Glu Val₂₉₀ Gln Leu Val Glu Ser₂₉₅ Gly Gly Gly Leu Val₃₀₀ Gln Pro Gly Gly
 Ser₃₀₅ Leu Arg Leu Ser Cys₃₁₀ Ala Val Ser Gly Phe₃₁₅ Ala Leu Ser Asn His₃₂₀
 Gly Met Ser Trp Val₃₂₅ Arg Arg Ala Pro Gly₃₃₀ Lys Gly Leu Glu Trp₃₃₅ Val
 Ser Gly Ile Val₃₄₀ Tyr Ser Gly Ser Thr₃₄₅ Tyr Tyr Ala Ala Ser₃₅₀ Val Lys
 Gly Arg Phe₃₅₅ Thr Ile Ser Arg Asp₃₆₀ Asn Ser Arg Asn Thr₃₆₅ Leu Tyr Leu
 Gln Met₃₇₀ Asn Ser Leu Arg Pro₃₇₅ Glu Asp Thr Ala Ile₃₈₀ Tyr Tyr Cys Ser
 Ala₃₈₅ His Gly Gly Glu Ser₃₉₀ Asp Val Trp Gly Gln₃₉₅ Gly Thr Thr Val Thr₄₀₀
 Val Ser Ser Ala₄₀₅ Ser Gly Gly Gly Gly Ser₄₁₀ Gly Gly Arg Ala Ser₄₁₅ Gly
 Gly Gly Gly Ser₄₂₀ Asp Ile Gln Leu Thr₄₂₅ Gln Ser Pro Ser Ser₄₃₀ Leu Ser
 Ala Ser Val₄₃₅ Gly Asp Arg Val Thr₄₄₀ Ile Thr Cys Arg Ala₄₄₅ Ser Gln Ser
 Ile Ser₄₅₀ Ser Tyr Leu Asn Trp₄₅₅ Tyr Gln Gln Lys Pro₄₆₀ Gly Lys Ala Pro
 Lys₄₆₅ Leu Leu Ile Tyr Ala₄₇₀ Ala Ser Ser Leu Gln₄₇₅ Ser Gly Val Pro Ser₄₈₀
 Arg Phe Ser Gly Ser₄₈₅ Gly Ser Gly Thr Asp₄₉₀ Phe Thr Leu Thr Ile Ser₄₉₅
 Ser Leu Gln Pro₅₀₀ Glu Asp Phe Ala Thr₅₀₅ Tyr Tyr Cys Gln Gln₅₁₀ Ser Tyr
 Ser Thr Pro₅₁₅ Tyr Thr Phe Gly Gln₅₂₀ Gly Thr Lys Val Glu₅₂₅ Ile Lys Thr

Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro ^{-SL} Ala Pro Thr Ile Ala Ser
 530 535 540
 Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly
 545 550 555 560
 Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp
 565 570 575
 Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile
 580 585 590
 Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys
 595 600 605
 Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys
 610 615 620
 Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val
 625 630 635 640
 Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn
 645 650 655
 Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val
 660 665 670
 Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg
 675 680 685
 Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys
 690 695 700
 Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg
 705 710 715 720
 Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys
 725 730 735
 Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
 740 745 750

<210> 182
 <211> 2250
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 182
 atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg

_SL

ccccggtcgt	cgttggcact	ttccctgact	gccgaccaga	tgggtgtccgc	ccttctggac	120
gccgagcctc	caattctgta	ctcggagtac	gatccgactc	gcccgttctc	cgaagccagc	180
atgatgggcc	tgttgactaa	cctggcggac	cgcgagttgg	tgcacatgat	taactgggct	240
aagcgggtgc	cggttctcgt	ggacctgacc	ctgcacgacc	aagtgcacct	cctggaatgc	300
gcctggatgg	aaatcctcat	gatcggcctc	gtgtggagat	ccatggagca	tcccggaaag	360
ctcctgtttg	cacccaacct	cctgcttgat	cgcaaccagg	gaaaatgcgt	ggaagggggg	420
gtcgagattt	tcgacatgct	gctcgccacc	tcttcccggg	tccggatgat	gaatctgcag	480
ggagaagagt	tcgtgtgtct	gaagtcaatc	atcctgtctga	actccggggg	ctataccttc	540
ctgagctcga	ccctcaagtc	actggaggaa	aaagaccaca	tccatcgcgt	gctcgataag	600
atcaccgaca	cccttatcca	tctcatggcg	aaggctggac	tgaccctgca	acagcagcac	660
cagaggctgg	cccagttgct	gctgattctg	agccacatcc	ggcacatgtc	gaacaagagg	720
atggaacacc	tgtacagcat	gaagtgcaag	aacgtcgtgc	ctctgtccga	tctgtctcctg	780
gaaatgctgg	acgcgcacag	actcggaacc	ggcgcggaag	acccccggcc	ctccaggaag	840
cgaaggtccc	tcggagacgt	gggtgaagtg	caattggtgg	aatcaggggg	aggacttggtg	900
cagcctggag	gatcgctgag	actgtcatgt	gccgtgtccg	gctttgccct	gtccaaccac	960
gggatgtcct	gggtccgccg	cgcgccctgga	aagggcctcg	aatgggtgtc	gggtattgtg	1020
tacagcggtg	gcacctacta	tgccgcatcc	gtgaagggga	gattcaccat	cagccgggac	1080
aactccagga	acactctgta	cctccaaatg	aattcgctga	ggccagagga	cactgccatc	1140
tactactgct	ccgcgcatgg	cggagagtcc	gacgtctggg	gacagggggac	caccgtgacc	1200
gtgtctagcg	cgtccggcgg	aggcggcagc	gggggtcggg	catcaggggg	cggcggatcg	1260
gacatccagc	tcacccagtc	cccagagctcg	ctgtccgcct	ccgtgggaga	tcgggtcacc	1320
atcacgtgcc	gcgccagcca	gtcgatttcc	tcctacctga	actggtacca	acagaagccc	1380
ggaaaagccc	cgaagcttct	catctacgcc	gcctcgagcc	tgcagtcagg	agtgccctca	1440
cggttctccg	gtcctgggtc	cgggtactgat	ttcaccttga	ccatttcttc	cctgcaaccg	1500
gaggacttcg	ctacttacta	ctgccagcag	tcgtactcca	ccccctacac	tttcggacaa	1560
ggcaccaagg	tcgaaatcaa	gaccactacc	ccagcaccga	ggccaccac	cccggctcct	1620
accatcgctt	cccagcctct	gtccctgcgt	ccggaggcat	gtagaccgcg	agctggtggg	1680
gccgtgcata	ccgggggtct	tgacttcgcc	tgcgatatct	acatttgggc	ccctctggct	1740
ggtacttgcg	gggtcctgct	gctttcactc	gtgatcactc	tttactgtaa	gcgcggctcg	1800
aagaagctgc	tgtacatctt	taagcaaccc	ttcatgaggc	ctgtgcagac	tactcaagag	1860
gaggacggct	gttcatgccg	gttcccagag	gaggaggaag	gcggctgcga	actgcgcgtg	1920
aaattcagcc	gcagcgcaga	tgctccagcc	taccagcagg	ggcagaacca	gctctacaac	1980
gaactcaatc	ttggtcggag	agaggagtac	gacgtgctgg	acaagcggag	aggacgggac	2040
ccagaaatgg	gcgggaagcc	gcgcagaaa	aatccccaag	agggcctgta	caacgagctc	2100

_SL

caaaaggata agatggcaga agcctatagc gagattggta tgaaagggga acgcagaaga 2160
ggcaaaggcc acgacggact gtaccaggga ctcagcaccg ccaccaagga cacctatgac 2220
gctcttcaca tgcaggccct gccgcctcgg 2250

<210> 183
<211> 744
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 183
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Arg Ser Ser Leu Ala Leu Ser Leu Thr Ala Asp
20 25 30

Gln Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser
35 40 45

Glu Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu
50 55 60

Leu Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala
65 70 75 80

Lys Arg Val Pro Gly Phe Val Asp Leu Thr Leu His Asp Gln Val His
85 90 95

Leu Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp
100 105 110

Arg Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu
115 120 125

Leu Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe
130 135 140

Asp Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln
145 150 155 160

Gly Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly
165 170 175

Val Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp
180 185 190

His Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu
Page 200

_SL

195		200		205											
Met	Ala 210	Lys	Ala	Gly	Leu	Thr 215	Leu	Gln	Gln	Gln	His 220	Gln	Arg	Leu	Ala
Gln 225	Leu	Leu	Leu	Ile	Leu 230	Ser	His	Ile	Arg	His 235	Met	Ser	Asn	Lys	Arg 240
Met	Glu	His	Leu	Tyr 245	Ser	Met	Lys	Cys	Lys 250	Asn	Val	Val	Pro	Leu 255	Ser
Asp	Leu	Leu	Leu	Glu 260	Met	Leu	Asp	Ala 265	His	Arg	Leu	Gly	Thr 270	Gly	Ala
Glu	Asp	Pro 275	Arg	Pro	Ser	Arg	Lys 280	Arg	Arg	Glu	Val	Gln 285	Leu	Val	Glu
Ser	Gly 290	Gly	Gly	Leu	Val	Gln 295	Pro	Gly	Gly	Ser	Leu 300	Arg	Leu	Ser	Cys
Ala 305	Val	Ser	Gly	Phe	Ala 310	Leu	Ser	Asn	His	Gly 315	Met	Ser	Trp	Val	Arg 320
Arg	Ala	Pro	Gly	Lys 325	Gly	Leu	Glu	Trp	Val 330	Ser	Gly	Ile	Val	Tyr 335	Ser
Gly	Ser	Thr	Tyr 340	Tyr	Ala	Ala	Ser	Val 345	Lys	Gly	Arg	Phe	Thr 350	Ile	Ser
Arg	Asp	Asn 355	Ser	Arg	Asn	Thr	Leu 360	Tyr	Leu	Gln	Met	Asn 365	Ser	Leu	Arg
Pro	Glu 370	Asp	Thr	Ala	Ile	Tyr 375	Tyr	Cys	Ser	Ala	His 380	Gly	Gly	Glu	Ser
Asp 385	Val	Trp	Gly	Gln	Gly 390	Thr	Thr	Val	Thr	Val 395	Ser	Ser	Ala	Ser	Gly 400
Gly	Gly	Gly	Ser	Gly 405	Gly	Arg	Ala	Ser	Gly 410	Gly	Gly	Gly	Ser	Asp 415	Ile
Gln	Leu	Thr	Gln 420	Ser	Pro	Ser	Ser	Leu 425	Ser	Ala	Ser	Val	Gly 430	Asp	Arg
Val	Thr	Ile 435	Thr	Cys	Arg	Ala	Ser 440	Gln	Ser	Ile	Ser	Ser 445	Tyr	Leu	Asn
Trp	Tyr 450	Gln	Gln	Lys	Pro	Gly 455	Lys	Ala	Pro	Lys	Leu 460	Leu	Ile	Tyr	Ala
Ala	Ser	Ser	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly

465			470						SL 475			480			
Ser	Gly	Thr	Asp	Phe 485	Thr	Leu	Thr	Ile	Ser 490	Ser	Leu	Gln	Pro	Glu 495	Asp
Phe	Ala	Thr	Tyr 500	Tyr	Cys	Gln	Gln	Ser 505	Tyr	Ser	Thr	Pro	Tyr 510	Thr	Phe
Gly	Gln	Gly 515	Thr	Lys	Val	Glu	Ile 520	Lys	Thr	Thr	Thr	Pro 525	Ala	Pro	Arg
Pro	Pro 530	Thr	Pro	Ala	Pro	Thr 535	Ile	Ala	Ser	Gln	Pro 540	Leu	Ser	Leu	Arg
Pro 545	Glu	Ala	Cys	Arg	Pro 550	Ala	Ala	Gly	Gly	Ala 555	Val	His	Thr	Arg	Gly 560
Leu	Asp	Phe	Ala	Cys 565	Asp	Ile	Tyr	Ile	Trp 570	Ala	Pro	Leu	Ala	Gly 575	Thr
Cys	Gly	Val	Leu 580	Leu	Leu	Ser	Leu	Val 585	Ile	Thr	Leu	Tyr	Cys 590	Lys	Arg
Gly	Arg	Lys 595	Lys	Leu	Leu	Tyr	Ile 600	Phe	Lys	Gln	Pro	Phe 605	Met	Arg	Pro
Val	Gln 610	Thr	Thr	Gln	Glu	Glu 615	Asp	Gly	Cys	Ser	Cys 620	Arg	Phe	Pro	Glu
Glu 625	Glu	Glu	Gly	Gly	Cys 630	Glu	Leu	Arg	Val	Lys 635	Phe	Ser	Arg	Ser	Ala 640
Asp	Ala	Pro	Ala	Tyr 645	Gln	Gln	Gly	Gln	Asn 650	Gln	Leu	Tyr	Asn	Glu 655	Leu
Asn	Leu	Gly	Arg 660	Arg	Glu	Glu	Tyr	Asp 665	Val	Leu	Asp	Lys	Arg 670	Arg	Gly
Arg	Asp	Pro 675	Glu	Met	Gly	Gly	Lys 680	Pro	Arg	Arg	Lys	Asn 685	Pro	Gln	Glu
Gly	Leu 690	Tyr	Asn	Glu	Leu	Gln 695	Lys	Asp	Lys	Met	Ala 700	Glu	Ala	Tyr	Ser
Glu 705	Ile	Gly	Met	Lys	Gly 710	Glu	Arg	Arg	Arg	Gly 715	Lys	Gly	His	Asp	Gly 720
Leu	Tyr	Gln	Gly	Leu 725	Ser	Thr	Ala	Thr	Lys 730	Asp	Thr	Tyr	Asp	Ala 735	Leu
His	Met	Gln	Ala	Leu	Pro	Pro	Arg								

<210> 184
 <211> 2232
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 184
 atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60
 ccccggtcgt cgttggcact ttccctgact gccgaccaga tgggtgtccgc ctttctggac 120
 gccgagcctc caattctgta ctcggagtac gatccgactc gcccgttctc cgaagccagc 180
 atgatggggc tgttgactaa cctggcggac cgcgagttgg tgcacatgat taactgggct 240
 aagcgggtgc cgggcttcgt ggacctgacc ctgcacgacc aagtgcacct cctggaatgc 300
 gcctggatgg aaatcctcat gatcggcctc gtgtggagat ccatggagca tcccggaaag 360
 ctctgttttg caccacacct cctgcttgat cgcaaccagg gaaaatgcgt ggaaggggggt 420
 gtcgagattt tcgacatgct gctcgccacc tcttcccgggt tccggatgat gaatctgcag 480
 ggagaagagt tcgtgtgtct gaagtcaatc atcctgctga actccgggggt ctataccttc 540
 ctgagctcga ccctcaagtc actggaggaa aaagaccaca tccatcgcgt gctcgataag 600
 atcaccgaca cccttatcca tctcatggcg aaggctggac tgaccctgca acagcagcac 660
 cagaggctgg cccagttgct gctgattctg agccacatcc ggcacatgtc gaacaagagg 720
 atggaacacc tgtacagcat gaagtgaag aacgtcgtgc ctctgtccga tctgctcctg 780
 gaaatgctgg acgcgcacag actcgggacg ggagctgaag atccacgacc cagcagaaag 840
 cgacgggaag tgcaattggt ggaatcaggg ggaggacttg tgcagcctgg aggatcgctg 900
 agactgtcat gtgccgtgtc cggctttgcc ctgtccaacc acgggatgtc ctgggtccgc 960
 cgcgcgcctg gaaagggcct cgaatgggtg tcgggtattg tgtacagcgg tagcacctac 1020
 tatgccgcat ccgtgaaggg gagattcacc atcagccggg acaactccag gaacactctg 1080
 tacctccaaa tgaattcgct gaggccagag gacactgcca tctactactg ctccgcgcat 1140
 ggcggagagt ccgacgtctg gggacagggg accaccgtga ccgtgtctag cgcgtccggc 1200
 ggaggcggca gcgggggtcg ggcatcaggg ggcggcggat cggacatcca gctcaccag 1260
 tccccgagct cgctgtccgc ctccgtggga gatcgggtca ccatcacgtg ccgcgccagc 1320
 cagtcgattt cctcctacct gaactggtac caacagaagc ccgaaaaagc cccgaagctt 1380
 ctcatctacg ccgcctcgag cctgcagtca ggagtgcctt cacggttctc cggctccggt 1440
 tccggtactg atttcacct gaccatttcc tccttgaac cggaggactt cgctacttac 1500
 tactgccagc agtcgtactc cacccttac actttcggac aaggcaccaa ggtcgaaatc 1560
 aagaccacta cccagcacc gaggccacc accccggctc ctaccatcgc ctcccagcct 1620

_SL

ctgtccctgc gtccggaggc atgtagacct gcagctgggtg gggccgtgca taccgggggt	1680
cttgacttcg cctgcgatat ctacatttgg gccctcttgg ctggtacttg cggggtcctg	1740
ctgctttcac tcgtgatcac tctttactgt aagcgcggtc ggaagaagct gctgtacatc	1800
tttaagcaac ctttcatgag gcctgtgcag actactcaag aggaggacgg ctgttcatgc	1860
cggttcccag aggaggagga aggcggctgc gaactgcgcg tgaaattcag ccgcagcgca	1920
gatgtccag cctaccagca ggggcagaac cagctctaca acgaactcaa tcttggtcgg	1980
agagaggagt acgacgtgct ggacaagcgg agaggacggg acccagaaat gggcgggaag	2040
ccgcgcagaa agaatcccca agagggcctg tacaacgagc tccaaaagga taagatggca	2100
gaagcctata gcgagattgg tatgaaagg gaacgcagaa gaggcaaagg ccacgacgga	2160
ctgtaccagg gactcagcac cgccaccaag gacacctatg acgctcttca catgcaggcc	2220
ctgccgcctc gg	2232

<210> 185
 <211> 521
 <212> DNA
 <213> Unknown

<220>
 <221> source
 <223> /note="Description of Unknown:
 Wildtype PGK promoter"

<400> 185	
acccctctct ccagccacta agccagttgc tccctcggct gacggctgca cgcgaggcct	60
ccgaacgtct tacgccttgt ggcgcgcccc tccttgtccc ggggtgtgatg gcgggggtgtg	120
ggcgaggagg cgtggcgggg aagggccggc gacgagagcc gcgcgggacg actcgtcggc	180
gataaccggt gtcgggtagc gccagccgcg cgacggtaac gagggaccgc gacaggcaga	240
cgctcccatg atcactctgc acgccgaagg caaatagtgc aggccgtgcg gcgcttggcg	300
ttccttggaa gggctgaatc cccgcctcgt ccttcgcagc ggccccccgg gtgttcccat	360
cgccgcttct agggccactg cgacgcttgc ctgcatttct tacacgctct ggggtcccagc	420
cgcggcgacg caaagggcct tgggtcgggt ctcgtcggcg cagggacgcg tttgggtccc	480
gacggaacct tttccgcgtt ggggttgggg caccataagc t	521

<210> 186
 <211> 118
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polynucleotide"

<400> 186	
acccctctct ccagccacta agccagttgc tccctcggct gacggctgca cgcgaggcct	60
ccgaacgtct tacgccttgt ggcgcgcccc tccttgtccc ggggtgtgatg gcgggggtg	118

<210> 187
<211> 221
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 187
accctctct ccagccacta agccagttgc tccctcggct gacggctgca cgcgaggcct 60
ccgaacgtct tacgccttgt ggcgcgcccc tccttgtccc ggggtgtgatg gcgggggtgtg 120
gggcggaggg cgtggcgggg aagggccggc gacgagagcc gcgcgggacg actcgtcggc 180
gataaccggt gtcgggtagc gccagccgcg cgacggtaac g 221

<210> 188
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 188
accctctct ccagccacta agccagttgc tccctcggct gacggctgca cgcgaggcct 60
ccgaacgtct tacgccttgt ggcgcgcccc tccttgtccc ggggtgtgatg gcgggggtgtg 120
gggcggaggg cgtggcgggg aagggccggc gacgagagcc gcgcgggacg actcgtcggc 180
gataaccggt gtcgggtagc gccagccgcg cgacggtaac gagggaccgc gacaggcaga 240
cgctcccatg atcactctgc acgccgaagg caaatagtgc aggccgtgcg gcgcttggcg 300
ttccttgga gggctgaatc cccg 324

<210> 189
<211> 422
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 189
accctctct ccagccacta agccagttgc tccctcggct gacggctgca cgcgaggcct 60
ccgaacgtct tacgccttgt ggcgcgcccc tccttgtccc ggggtgtgatg gcgggggtgtg 120
gggcggaggg cgtggcgggg aagggccggc gacgagagcc gcgcgggacg actcgtcggc 180
gataaccggt gtcgggtagc gccagccgcg cgacggtaac gagggaccgc gacaggcaga 240
cgctcccatg atcactctgc acgccgaagg caaatagtgc aggccgtgcg gcgcttggcg 300
ttccttgga gggctgaatc cccgcctcgt ccttcgcagc ggccccccgg gtgttcccat 360

cgccgcttct aggccactg cgacgcttgc ctgcacttct tacacgctct ggggccagc 420
cg 422

<210> 190
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
<221> VARIANT
<222> (1)..(3)
<223> /replace=" "

<220>
<221> misc_feature
<222> (1)..(21)
<223> /note="Variant residues given in the sequence have no preference with respect to those in the annotations for variant positions"

<400> 190
Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu
1 5 10 15

Glu Asn Pro Gly Pro
20

<210> 191
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
<221> VARIANT
<222> (1)..(3)
<223> /replace=" "

<220>
<221> misc_feature
<222> (1)..(22)
<223> /note="Variant residues given in the sequence have no preference with respect to those in the annotations for variant positions"

<400> 191
Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val
1 5 10 15

Glu Glu Asn Pro Gly Pro
20

_SL

<210> 192
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
<221> VARIANT
<222> (1)..(3)
<223> /replace=" "

<220>
<221> misc_feature
<222> (1)..(23)
<223> /note="Variant residues given in the sequence have no preference with respect to those in the annotations for variant positions"

<400> 192
Gly Ser Gly Gln Cys Thr Asn Tyr Ala Leu Leu Lys Leu Ala Gly Asp
1 5 10 15

Val Glu Ser Asn Pro Gly Pro
20

<210> 193
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
<221> VARIANT
<222> (1)..(3)
<223> /replace=" "

<220>
<221> misc_feature
<222> (1)..(25)
<223> /note="Variant residues given in the sequence have no preference with respect to those in the annotations for variant positions"

<400> 193
Gly Ser Gly Val Lys Gln Thr Leu Asn Phe Asp Leu Leu Lys Leu Ala
1 5 10 15

Gly Asp Val Glu Ser Asn Pro Gly Pro
20 25

<210> 194

<400> 194

_SL

000

<210> 195

<400> 195
000

<210> 196

<400> 196
000

<210> 197

<400> 197
000

<210> 198

<400> 198
000

<210> 199

<400> 199
000

<210> 200

<400> 200
000

<210> 201

<211> 241

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 201

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Glu Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

_SL

Met Glu Leu Ser Arg₈₅ Leu Arg Ser Asp₉₀ Thr Ala Val Tyr Tyr Cys₉₅

Ala Ser Gly Trp₁₀₀ Asp Phe Asp Tyr Trp₁₀₅ Gly Gln Gly Thr Leu₁₁₀ Val Thr

Val Ser Ser₁₁₅ Gly Gly Gly Gly Ser₁₂₀ Gly Gly Gly Gly Ser₁₂₅ Gly Gly Gly

Gly Ser₁₃₀ Gly Gly Gly Gly Ser₁₃₅ Asp Ile Val Met Thr₁₄₀ Gln Ser Pro Ser

Ser₁₄₅ Leu Ser Ala Ser Val₁₅₀ Gly Asp Arg Val Thr₁₅₅ Ile Thr Cys Arg Ala₁₆₀

Ser Gln Ser Ile Arg₁₆₅ Tyr Tyr Leu Ser Trp₁₇₀ Tyr Gln Gln Lys Pro Gly₁₇₅

Lys Ala Pro Lys₁₈₀ Leu Leu Ile Tyr Thr₁₈₅ Ala Ser Ile Leu Gln Asn Gly₁₉₀

Val Pro Ser₁₉₅ Arg Phe Ser Gly Ser₂₀₀ Gly Ser Gly Thr Asp₂₀₅ Phe Thr Leu

Thr Ile₂₁₀ Ser Ser Leu Gln Pro₂₁₅ Glu Asp Phe Ala Thr₂₂₀ Tyr Tyr Cys Leu

Gln Thr Tyr Thr Thr Pro₂₃₀ Asp Phe Gly Pro Gly₂₃₅ Thr Lys Val Glu Ile₂₄₀

Lys

<210> 202

<211> 241

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 202

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

_SL

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Asn Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Arg Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Ser Gly Trp Asp Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Arg Met Thr Gln Ser Pro Ser
130 135 140

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala
145 150 155 160

Ser Gln Ser Ile Arg Tyr Tyr Leu Ser Trp Tyr Gln Gln Lys Pro Gly
165 170 175

Lys Ala Pro Lys Leu Leu Ile Tyr Thr Ala Ser Ile Leu Gln Asn Gly
180 185 190

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
195 200 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu
210 215 220

Gln Thr Tyr Thr Thr Pro Asp Phe Gly Pro Gly Thr Lys Val Glu Ile
225 230 235 240

Lys

<210> 203

<211> 239

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 203

Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Glu Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Gly Tyr
 20 25 30
 Thr Met Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
 35 40 45
 Gly Leu Ile Thr Pro Tyr Asn Gly Ala Ser Ser Tyr Asn Gln Lys Phe
 50 55 60
 Arg Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
 65 70 75 80
 Met Asp Leu Leu Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 85 90 95
 Ala Arg Gly Gly Tyr Asp Gly Arg Gly Phe Asp Tyr Trp Gly Gln Gly
 100 105 110
 Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 115 120 125
 Ser Gly Gly Gly Gly Ser Asp Ile Glu Leu Thr Gln Ser Pro Ala Ile
 130 135 140
 Met Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Ser Ala Ser
 145 150 155 160
 Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Ser Gly Thr Ser
 165 170 175
 Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val Pro
 180 185 190
 Gly Arg Phe Ser Gly Ser Gly Ser Gly Asn Ser Tyr Ser Leu Thr Ile
 195 200 205
 Ser Ser Val Glu Ala Glu Asp Asp Ala Thr Tyr Tyr Cys Gln Gln Trp
 210 215 220
 Ser Gly Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile
 225 230 235

<210> 204

<211> 244

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 204

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 Page 211

_SL

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 205

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Leu Arg Arg Thr Val Val Thr Pro Arg Ala Tyr Tyr Gly
100 105 110

Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly
115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
130 135 140

Gly Ser Asp Ile Gln Leu Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser
145 150 155 160

Val Gly Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser
165 170 175

Asn Ser Leu Asn Trp Tyr Gln Gln Lys Ala Gly Lys Ala Pro Lys Leu
180 185 190

Leu Ile Tyr Asp Ala Ser Thr Leu Glu Thr Gly Val Pro Ser Arg Phe
195 200 205

Ser Gly Ser Gly Ser Gly Thr Asp Phe Ser Phe Thr Ile Ser Ser Leu
210 215 220

Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln His Asp Asn Leu
225 230 235 240

Pro Leu Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
245 250

_SL

<210> 206
<211> 246
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 206
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Pro Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Glu Trp Asp Gly Ser Tyr Tyr Tyr Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val Leu
130 135 140

Thr Gln Thr Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr
145 150 155 160

Ile Thr Cys Arg Ala Ser Gln Ser Ile Asn Thr Tyr Leu Asn Trp Tyr
165 170 175

Gln His Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser
180 185 190

Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
195 200 205

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
210 215 220

_SL

Thr Tyr Tyr Cys Gln Gln Ser Phe Ser Pro Leu Thr Phe Gly Gly Gly
225 230 235 240

Thr Lys Leu Glu Ile Lys
245

<210> 207

<211> 242

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 207

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Trp Met His Trp Val Arg Gln Val Pro Gly Lys Gly Leu Val Trp Val
35 40 45

Ser Arg Ile Asn Thr Asp Gly Ser Thr Thr Thr Tyr Ala Asp Ser Val
50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Asp Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Val Gly Gly His Trp Ala Val Trp Gly Gln Gly Thr Thr Val Thr Val
100 105 110

Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Thr
130 135 140

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
145 150 155 160

Gln Ser Ile Ser Asp Arg Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys
165 170 175

Ala Pro Lys Leu Leu Ile Tyr Lys Ala Ser Ser Leu Glu Ser Gly Val
180 185 190

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr
195 200 205

Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Val Tyr Tyr Cys Gln Gln
210 215 220

Tyr Gly His Leu Pro Met Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu
225 230 235 240

Ile Lys

<210> 208

<211> 252

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 208

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Gly Gly Ser Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Tyr Arg Leu Ile Ala Val Ala Gly Asp Tyr Tyr Tyr Tyr Gly
100 105 110

Met Asp Val Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly
115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
130 135 140

Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ala Ser Val
145 150 155 160

Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Val Gly Arg
Page 216

SL															
165						170						175			
Trp	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Thr	Ala	Pro	Lys	Leu	Leu
			180					185					190		
Ile	Tyr	Ala	Ala	Ser	Thr	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser
		195					200					205			
Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Asn	Asn	Leu	Gln
	210					215					220				
Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Ala	Asn	Ser	Phe	Pro
225					230					235					240
Leu	Thr	Phe	Gly	Gly	Gly	Thr	Arg	Leu	Glu	Ile	Lys				
				245					250						

_SL

Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala
145 150 155 160

Ile Leu Ser Cys Arg Ala Ser Gln Ser Val Tyr Thr Lys Tyr Leu Gly
165 170 175

Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Asp
180 185 190

Ala Ser Thr Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly
195 200 205

Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Arg Leu Glu Pro Glu Asp
210 215 220

Phe Ala Val Tyr Tyr Cys Gln His Tyr Gly Gly Ser Pro Leu Ile Thr
225 230 235 240

Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
245 250

<210> 210
<211> 246
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 210
Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Thr Ser Gly Tyr Pro Phe Thr Gly Tyr
20 25 30

Ser Leu His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp His Tyr Gly Gly Asn Ser Leu Phe Tyr Trp Gly Gln Gly
100 105 110

_SL

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr
130 135 140

Gln Ser Pro Ser Ser Ile Ser Ala Ser Val Gly Asp Thr Val Ser Ile
145 150 155 160

Thr Cys Arg Ala Ser Gln Asp Ser Gly Thr Trp Leu Ala Trp Tyr Gln
165 170 175

Gln Lys Pro Gly Lys Ala Pro Asn Leu Leu Met Tyr Asp Ala Ser Thr
180 185 190

Leu Glu Asp Gly Val Pro Ser Arg Phe Ser Gly Ser Ala Ser Gly Thr
195 200 205

Glu Phe Thr Leu Thr Val Asn Arg Leu Gln Pro Glu Asp Ser Ala Thr
210 215 220

Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly
225 230 235 240

Thr Lys Val Asp Ile Lys
245

<210> 211

<211> 248

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 211

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Glu Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Gly Gly Ser Thr Gly Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val His
65 70 75 80

Met Glu Leu Ser Ser₈₅ Leu Arg Ser Glu Asp^{-SL}₉₀ Thr Ala Val Tyr Tyr₉₅ Cys

Ala Arg Gly Gly₁₀₀ Tyr Ser Ser Ser₁₀₅ Asp Ala Phe Asp Ile₁₁₀ Trp Gly

Gln Gly Thr₁₁₅ Met Val Thr Val₁₂₀ Ser Ser Gly Gly Gly₁₂₅ Ser Gly Gly

Gly Gly₁₃₀ Ser Gly Gly Gly₁₃₅ Ser Gly Gly Gly₁₄₀ Ser Asp Ile Gln

Met Thr Gln Ser Pro₁₅₀ Pro Ser Leu Ser Ala Ser₁₅₅ Val Gly Asp Arg Val₁₆₀

Thr Ile Thr Cys Arg₁₆₅ Ala Ser Gln Asp Ile₁₇₀ Ser Ser Ala Leu Ala₁₇₅ Trp

Tyr Gln Gln Lys₁₈₀ Pro Gly Thr Pro₁₈₅ Lys Leu Leu Ile Tyr₁₉₀ Asp Ala

Ser Ser Leu₁₉₅ Glu Ser Gly Val₂₀₀ Ser Arg Phe Ser Gly₂₀₅ Ser Gly Ser

Gly Thr₂₁₀ Asp Phe Thr Leu Thr₂₁₅ Ile Ser Ser Leu Gln₂₂₀ Pro Glu Asp Phe

Ala Thr Tyr Tyr Cys Gln₂₃₀ Gln Phe Ser Ser Tyr₂₃₅ Pro Leu Thr Phe Gly₂₄₀

Gly Gly Thr Arg Leu₂₄₅ Glu Ile Lys

<210> 212
 <211> 255
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 212
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

Gly Trp Ile Ser Ala Tyr Asn Gly Asn Thr Asn Tyr Ala Gln Lys Leu
 Page 220

50					55					_SL		60				
Gln 65	Gly	Arg	Val	Thr	Met 70	Thr	Thr	Asp	Thr	Ser 75	Thr	Ser	Thr	Ala	Tyr 80	
Met	Glu	Leu	Arg	Ser 85	Leu	Arg	Ser	Asp	Asp 90	Thr	Ala	Val	Tyr	Tyr 95	Cys	
Ala	Arg	Val	Ala 100	Gly	Gly	Ile	Tyr	Tyr 105	Tyr	Tyr	Gly	Met	Asp 110	Val	Trp	
Gly	Gln	Gly 115	Thr	Thr	Ile	Thr	Val 120	Ser	Ser	Gly	Gly	Gly 125	Gly	Ser	Gly	
Gly	Gly 130	Gly	Ser	Gly	Gly	Gly 135	Gly	Ser	Gly	Gly	Gly 140	Gly	Ser	Asp	Ile	
Val 145	Met	Thr	Gln	Thr	Pro 150	Asp	Ser	Leu	Ala	Val 155	Ser	Leu	Gly	Glu	Arg 160	
Ala	Thr	Ile	Ser	Cys 165	Lys	Ser	Ser	His	Ser 170	Val	Leu	Tyr	Asn	Arg 175	Asn	
Asn	Lys	Asn	Tyr 180	Leu	Ala	Trp	Tyr	Gln 185	Gln	Lys	Pro	Gly	Gln 190	Pro	Pro	
Lys	Leu	Leu 195	Phe	Tyr	Trp	Ala	Ser 200	Thr	Arg	Lys	Ser	Gly 205	Val	Pro	Asp	
Arg	Phe 210	Ser	Gly	Ser	Gly	Ser 215	Gly	Thr	Asp	Phe	Thr 220	Leu	Thr	Ile	Ser	
Ser 225	Leu	Gln	Pro	Glu	Asp 230	Phe	Ala	Thr	Tyr	Phe 235	Cys	Gln	Gln	Thr	Gln 240	
Thr	Phe	Pro	Leu	Thr 245	Phe	Gly	Gln	Gly	Thr 250	Arg	Leu	Glu	Ile	Asn 255		

_SL

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Arg Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Thr Thr Thr Ser Tyr Ala Phe Asp Ile Trp Gly Gln Gly Thr
100 105 110

Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr Gln
130 135 140

Ser Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
145 150 155 160

Cys Arg Ala Ser Gln Ser Ile Ser Thr Trp Leu Ala Trp Tyr Gln Gln
165 170 175

Lys Pro Gly Lys Ala Pro Asn Leu Leu Ile Tyr Lys Ala Ser Thr Leu
180 185 190

Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu
195 200 205

Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr
210 215 220

Tyr Cys Gln Gln Tyr Asn Thr Tyr Ser Pro Tyr Thr Phe Gly Gln Gly
225 230 235 240

Thr Lys Leu Glu Ile Lys
245

<210> 214

<211> 249

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

_SL

<400> 214

Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Ile Phe Ser Asp Tyr
20 25 30

Tyr Met Gly Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Tyr Ile Gly Arg Ser Gly Ser Ser Met Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Phe Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Ala Ser Pro Val Val Ala Ala Thr Glu Asp Phe Gln His Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val
130 135 140

Met Thr Gln Thr Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala
145 150 155 160

Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Thr Ser Asn Tyr Leu Ala
165 170 175

Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Leu Phe Gly
180 185 190

Ala Ser Thr Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly
195 200 205

Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Arg Leu Glu Pro Glu Asp
210 215 220

Phe Ala Met Tyr Tyr Cys Gln Gln Tyr Gly Ser Ala Pro Val Thr Phe
225 230 235 240

Gly Gln Gly Thr Lys Leu Glu Ile Lys
245

<210> 215

<211> 249

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 215

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Arg Ala Pro Gly Ala
 1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Phe Thr Phe Arg Gly Tyr
 20 25 30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

Gly Ile Ile Asn Pro Ser Gly Gly Ser Arg Ala Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Asp Asp Thr Ala Met Tyr Tyr Cys
 85 90 95

Ala Arg Thr Ala Ser Cys Gly Gly Asp Cys Tyr Tyr Leu Asp Tyr Trp
 100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
 115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile
 130 135 140

Gln Met Thr Gln Ser Pro Pro Thr Leu Ser Ala Ser Val Gly Asp Arg
 145 150 155 160

Val Thr Ile Thr Cys Arg Ala Ser Glu Asn Val Asn Ile Trp Leu Ala
 165 170 175

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Lys
 180 185 190

Ser Ser Ser Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
 195 200 205

Ser Gly Ala Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp
 210 215 220

Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Gln Ser Tyr Pro Leu Thr Phe
 225 230 235 240

Gly Gly Gly Thr Lys Val Asp Ile Lys
245 _SL

```
<210> 216
<211> 244
<212> PRT
<213> Artificial Sequence
```

$\langle 211 \rangle$ 244

<212> PRT

<213> Artificial Sequence

$\langle 220 \rangle$

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 216

Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Ser Trp Asn Ser Gly Ser Ile Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Asp Gly Ser Ser Ser Trp Ser Trp Gly Tyr Phe Asp Tyr Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Ser Glu Leu Thr Gln Asp
130 135 140

Pro Ala Val Ser Val Ala Leu Gly Gln Thr Val Arg Thr Thr Cys Gln
145 150 155 160

Gly Asp Ala Leu Arg Ser Tyr Tyr Ala Ser Trp Tyr Gln Gln Lys Pro
165 170 175

Gly Gln Ala Pro Met Leu Val Ile Tyr Gly Lys Asn Asn Arg Pro Ser
180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Asp Ser Gly Asp Thr Ala Ser
195 200 205

Leu Thr Ile Thr Gly Ala Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys
Page 225

210 215 _SL 220

Asn Ser Arg Asp Ser Ser Gly Tyr Pro Val Phe Gly Thr Gly Thr Lys
225 230 235 240

Val Thr Val Leu

```
<210> 217
<211> 246
<212> PRT
<213> Artificial Sequence
```

```
<220>  
<221> source  
<223> /note="Description of Artificial Sequence: Synthetic  
polypeptide"
```

<400> 217
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Ser Trp Asn Ser Gly Ser Thr Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Asp Ser Ser Ser Trp Tyr Gly Gly Gly Ser Ala Phe Asp Ile
100 105 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Ser Glu Leu Thr Gln
130 135 140

Glu Pro Ala Val Ser Val Ala Leu Gly Gln Thr Val Arg Ile Thr Cys
145 150 155 160

Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser Trp Tyr Gln Gln Lys
165 170 175

Pro Gly Gln Ala Pro Val Leu Val Ile Phe Gly Arg Ser Arg Arg Pro
180 185 190

_SL

Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Ser Ser Gly Asn Thr Ala
195 200 205

Ser Leu Ile Ile Thr Gly Ala Gln Ala Glu Asp Glu Ala Asp Tyr Tyr
210 215 220

Cys Asn Ser Arg Asp Asn Thr Ala Asn His Tyr Val Phe Gly Thr Gly
225 230 235 240

Thr Lys Leu Thr Val Leu
245

<210> 218
<211> 246
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 218
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Ser Trp Asn Ser Gly Ser Thr Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Asp Ser Ser Ser Trp Tyr Gly Gly Gly Ser Ala Phe Asp Ile
100 105 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Ser Glu Leu Thr Gln
130 135 140

Asp Pro Ala Val Ser Val Ala Leu Gly Gln Thr Val Arg Ile Thr Cys
145 150 155 160

_SL

Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser Trp Tyr Gln Gln Lys
165 170 175

Pro Gly Gln Ala Pro Val Leu Val Ile Tyr Gly Lys Asn Asn Arg Pro
180 185 190

Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Ser Ser Gly Asn Thr Ala
195 200 205

Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu Asp Glu Ala Asp Tyr Tyr
210 215 220

Cys Asn Ser Arg Gly Ser Ser Gly Asn His Tyr Val Phe Gly Thr Gly
225 230 235 240

Thr Lys Val Thr Val Leu
245

<210> 219
<211> 251
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 219
Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Trp Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Val Trp Val
35 40 45

Ser Arg Ile Asn Ser Asp Gly Ser Ser Thr Ser Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Val Arg Thr Gly Trp Val Gly Ser Tyr Tyr Tyr Tyr Met Asp Val Trp
100 105 110

Gly Lys Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly^{-SL} Gly Gly Gly Ser Glu Ile
 130 135 140
 Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg
 145 150 155 160
 Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Asn Tyr Leu
 165 170 175
 Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Arg Leu Leu Ile Tyr
 180 185 190
 Asp Val Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly Gly
 195 200 205
 Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu
 210 215 220
 Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Pro Trp
 225 230 235 240
 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 245 250

<210> 220
 <211> 250
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 220
 Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Gly Tyr Ser Arg Tyr Tyr Tyr Tyr Gly Met Asp Val Trp Gly
 Page 229

_SL

100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val
130 135 140

Met Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala
145 150 155 160

Ile Leu Ser Cys Arg Ala Ser Gln Ser Val Tyr Thr Lys Tyr Leu Gly
165 170 175

Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Asp
180 185 190

Ala Ser Thr Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly
195 200 205

Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Arg Leu Glu Pro Glu Asp
210 215 220

Phe Ala Val Tyr Tyr Cys Gln His Tyr Gly Gly Ser Pro Leu Ile Thr
225 230 235 240

Phe Gly Gln Gly Thr Lys Val Asp Ile Lys
245 250

<210> 221
<211> 249
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 221
Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

_SL

Leu Gln Met Asn Ser₈₅ Leu Arg Ala Glu Asp₉₀ Thr Ala Val Tyr Tyr₉₅ Cys

Ala Lys Arg Glu₁₀₀ Ala Ala Ala Gly His₁₀₅ Asp Trp Tyr Phe Asp₁₁₀ Leu Trp

Gly Arg Gly₁₁₅ Thr Leu Val Thr Val₁₂₀ Ser Ser Gly Gly₁₂₅ Gly Ser Gly

Gly Gly₁₃₀ Gly Ser Gly Gly₁₃₅ Gly Ser Gly Gly₁₄₀ Gly Ser Asp Ile

Arg Val Thr Gln Ser₁₅₀ Ser Ser Leu Ser₁₅₅ Ala Ser Val Gly Asp Arg₁₆₀

Val Thr Ile Thr Cys₁₆₅ Arg Ala Ser Gln Ser₁₇₀ Ile Ser Ser Tyr Leu₁₇₅ Asn

Trp Tyr Gln Gln₁₈₀ Lys Pro Gly Lys Ala₁₈₅ Pro Lys Leu Leu₁₉₀ Ile Tyr Ala

Ala Ser Ser₁₉₅ Leu Gln Ser Gly Val₂₀₀ Pro Ser Arg Phe Ser₂₀₅ Gly Ser Gly

Ser Gly₂₁₀ Thr Asp Phe Thr Leu₂₁₅ Thr Ile Ser Ser₂₂₀ Leu Gln Pro Glu Asp

Phe Ala Thr Tyr Tyr Cys₂₃₀ Gln Gln Ser Tyr Ser₂₃₅ Ile Pro Leu Thr Phe₂₄₀

Gly Gln Gly Thr Lys₂₄₅ Val Glu Ile Lys

<210> 222

<211> 247

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 222

Gln Val Gln Leu Val₅ Gln Ser Trp Ala Glu₁₀ Val Lys Lys Pro Gly₁₅ Ala

Ser Val Lys Val₂₀ Ser Cys Lys Ala Ser₂₅ Gly Tyr Thr Phe Thr₃₀ Ser Tyr

Tyr Met His₃₅ Trp Val Arg Gln Ala₄₀ Pro Gly Gln Gly Leu₄₅ Glu Trp Met

_SL

Gly Ile Ile Asn Pro Ser Gly Gly Ser Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Asn Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser Pro Arg Val Thr Thr Gly Tyr Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu
130 135 140

Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val Thr
145 150 155 160

Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Trp Leu Ala Trp Tyr
165 170 175

Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Lys Ala Ser
180 185 190

Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
195 200 205

Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala
210 215 220

Thr Tyr Tyr Cys Gln Gln Tyr Ser Ser Tyr Pro Leu Thr Phe Gly Gly
225 230 235 240

Gly Thr Arg Leu Glu Ile Lys
245

<210> 223

<211> 253

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 223

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Arg Arg Pro Gly Ala
1 5 10 15

Ser Val Lys Ile Ser Cys Arg Ala Ser Gly^{SL} Asp Thr Ser Thr Arg His
 20 25 30
 Tyr Ile His Trp Leu Arg Gln Ala Pro Gly Gln Gly Pro Glu Trp Met
 35 40 45
 Gly Val Ile Asn Pro Thr Thr Gly Pro Ala Thr Gly Ser Pro Ala Tyr
 50 55 60
 Ala Gln Met Leu Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr
 65 70 75 80
 Arg Thr Val Tyr Met Glu Leu Arg Ser Leu Arg Phe Glu Asp Thr Ala
 85 90 95
 Val Tyr Tyr Cys Ala Arg Ser Val Val Gly Arg Ser Ala Pro Tyr Tyr
 100 105 110
 Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly
 115 120 125
 Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
 130 135 140
 Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
 145 150 155 160
 Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser
 165 170 175
 Asp Tyr Ser Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu
 180 185 190
 Leu Ile Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe
 195 200 205
 Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Tyr Leu
 210 215 220
 Gln Ser Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Tyr Ser Tyr
 225 230 235 240
 Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Asp Ile Lys
 245 250

<210> 224

<211> 249

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic

_SL
polypeptide"

<400> 224

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Gly Gly Tyr Thr Thr Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Leu Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ile Arg Ser Cys Gly Gly Asp Cys Tyr Tyr Phe Asp Asn Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile
130 135 140

Gln Leu Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg
145 150 155 160

Val Thr Ile Thr Cys Arg Ala Ser Glu Asn Val Asn Ile Trp Leu Ala
165 170 175

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Lys
180 185 190

Ser Ser Ser Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
195 200 205

Ser Gly Ala Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp
210 215 220

Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Gln Ser Tyr Pro Leu Thr Phe
225 230 235 240

Gly Gly Gly Thr Lys Val Asp Ile Lys
245

<210> 225

_SL

<211> 246

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 225

Gln Ile Thr Leu Lys Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ala
20 25 30

Gly Val His Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala Leu Ile Ser Trp Ala Asp Asp Lys Arg Tyr Arg Pro Ser
50 55 60

Leu Arg Ser Arg Leu Asp Ile Thr Arg Val Thr Ser Lys Asp Gln Val
65 70 75 80

Val Leu Ser Met Thr Asn Met Gln Pro Glu Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Leu Gln Gly Phe Asp Gly Tyr Glu Ala Asn Trp Gly Pro Gly
100 105 110

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val Met Thr
130 135 140

Gln Ser Pro Ser Ser Leu Ser Ala Ser Ala Gly Asp Arg Val Thr Ile
145 150 155 160

Thr Cys Arg Ala Ser Arg Gly Ile Ser Ser Ala Leu Ala Trp Tyr Gln
165 170 175

Gln Lys Pro Gly Lys Pro Pro Lys Leu Leu Ile Tyr Asp Ala Ser Ser
180 185 190

Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205

Asp Phe Thr Leu Thr Ile Asp Ser Leu Glu Pro Glu Asp Phe Ala Thr
210 215 220

Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Trp Thr Phe Gly Gln Gly
225 230 235 240

_SL

Thr Lys Val Asp Ile Lys
245

<210> 226
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 226
Gly Tyr Thr Phe Thr Asp Tyr Tyr Met His
1 5 10

<210> 227
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 227
Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 228
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 228
Gly Trp Asp Phe Asp Tyr
1 5

<210> 229
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 229
Gly Tyr Thr Phe Thr Gly Tyr Tyr Met His
1 5 10

_SL

<210> 230
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 230
Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Asn Phe Gln
1 5 10 15

Gly

<210> 231
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 231
Gly Tyr Ser Phe Thr Gly Tyr Thr Met Asn
1 5 10

<210> 232
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 232
Leu Ile Thr Pro Tyr Asn Gly Ala Ser Ser Tyr Asn Gln Lys Phe Arg
1 5 10 15

Gly

<210> 233
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 233
Gly Gly Tyr Asp Gly Arg Gly Phe Asp Tyr
1 5 10

_SL

<210> 234
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 234
Arg Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 235
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 235
Gly Arg Tyr Tyr Gly Met Asp Val
1 5

<210> 236
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 236
Asp Leu Arg Arg Thr Val Val Thr Pro Arg Ala Tyr Tyr Gly Met Asp
1 5 10 15

Val

<210> 237
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 237
Gly Glu Trp Asp Gly Ser Tyr Tyr Tyr Asp Tyr
1 5 10

_SL

<210> 238
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 238
Gly Phe Thr Phe Ser Ser Tyr Trp Met His
1 5 10

<210> 239
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 239
Arg Ile Asn Thr Asp Gly Ser Thr Thr Thr Tyr Ala Asp Ser Val Glu
1 5 10 15

Gly

<210> 240
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 240
Gly His Trp Ala Val
1 5

<210> 241
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 241
Gly Tyr Thr Phe Thr Ser Tyr Tyr Met His
1 5 10

<210> 242
<211> 16

_SL

<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 242
Ile Ile Asn Pro Ser Gly Gly Ser Thr Ser Tyr Ala Gln Lys Phe Gln
1 5 10 15

<210> 243
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 243
Tyr Arg Leu Ile Ala Val Ala Gly Asp Tyr Tyr Tyr Tyr Gly Met Asp
1 5 10 15

Val

<210> 244
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 244
Gly Phe Thr Phe Ser Ser Tyr Ala Met His
1 5 10

<210> 245
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 245
Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 246
<211> 12

_SL

<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 246
Trp Lys Val Ser Ser Ser Ser Pro Ala Phe Asp Tyr
1 5 10

<210> 247
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 247
Gly Tyr Pro Phe Thr Gly Tyr Ser Leu His
1 5 10

<210> 248
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 248
Asp His Tyr Gly Gly Asn Ser Leu Phe Tyr
1 5 10

<210> 249
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 249
Ile Ile Asn Pro Ser Gly Gly Ser Thr Gly Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 250
<211> 12
<212> PRT
<213> Artificial Sequence

<220>

_SL

<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 250
Gly Gly Tyr Ser Ser Ser Ser Asp Ala Phe Asp Ile
1 5 10

<210> 251
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 251
Gly Tyr Thr Phe Thr Ser Tyr Gly Ile Ser
1 5 10

<210> 252
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 252
Trp Ile Ser Ala Tyr Asn Gly Asn Thr Asn Tyr Ala Gln Lys Leu Gln
1 5 10 15

<210> 253
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 253
Val Ala Gly Gly Ile Tyr Tyr Tyr Tyr Gly Met Asp Val
1 5 10

<210> 254
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 254
Thr Thr Thr Ser Tyr Ala Phe Asp Ile
1 5

_SL

<210> 255
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 255
Gly Phe Ile Phe Ser Asp Tyr Tyr Met Gly
1 5 10

<210> 256
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 256
Tyr Ile Gly Arg Ser Gly Ser Ser Met Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 257
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 257
Ser Pro Val Val Ala Ala Thr Glu Asp Phe Gln His
1 5 10

<210> 258
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 258
Gly Phe Thr Phe Arg Gly Tyr Tyr Ile His
1 5 10

<210> 259
<211> 17
<212> PRT

_SL

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 259

Ile Ile Asn Pro Ser Gly Gly Ser Arg Ala Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 260

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 260

Thr Ala Ser Cys Gly Gly Asp Cys Tyr Tyr Leu Asp Tyr
1 5 10

<210> 261

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 261

Gly Phe Thr Phe Asp Asp Tyr Ala Met His
1 5 10

<210> 262

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 262

Gly Ile Ser Trp Asn Ser Gly Ser Ile Gly Tyr Ala Asp Ser Val Lys
1 5 10 15

<210> 263

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide" ^{_SL}

<400> 263

Asp Gly Ser Ser Ser Trp Ser Trp Gly Tyr Phe Asp Tyr
1 5 10

<210> 264

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 264

Gly Ile Ser Trp Asn Ser Gly Ser Thr Gly Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 265

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 265

Asp Ser Ser Ser Trp Tyr Gly Gly Gly Ser Ala Phe Asp Ile
1 5 10

<210> 266

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 266

Arg Ile Asn Ser Asp Gly Ser Ser Thr Ser Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 267

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"
 <400> 267
 Thr Gly Trp Val Gly Ser Tyr Tyr Tyr Tyr Met Asp Val
 1 5 10

<210> 268
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic peptide"
 <400> 268
 Gly Phe Thr Phe Ser Ser Tyr Gly Met His
 1 5 10

<210> 269
 <211> 12
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic peptide"
 <400> 269
 Gly Tyr Ser Arg Tyr Tyr Tyr Tyr Gly Met Asp Val
 1 5 10

<210> 270
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic peptide"
 <400> 270
 Gly Phe Thr Phe Ser Ser Tyr Ala Met Ser
 1 5 10

<210> 271
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic peptide"
 <400> 271
 Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
 1 5 10 15

Gly

<210> 272
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 272
Arg Glu Ala Ala Ala Gly His Asp Trp Tyr Phe Asp Leu
1 5 10

<210> 273
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 273
Ile Ile Asn Pro Ser Gly Gly Ser Thr Ser Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 274
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 274
Ser Pro Arg Val Thr Thr Gly Tyr Phe Asp Tyr
1 5 10

<210> 275
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 275
Gly Asp Thr Ser Thr Arg His Tyr Ile His
1 5 10

_SL

<210> 276
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 276
Val Ile Asn Pro Thr Thr Gly Pro Ala Thr Gly Ser Pro Ala Tyr Ala
1 5 10 15

Gln Met Leu Gln Gly
20

<210> 277
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 277
Ser Val Val Gly Arg Ser Ala Pro Tyr Tyr Phe Asp Tyr
1 5 10

<210> 278
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 278
Gly Tyr Thr Phe Thr Asn Tyr Tyr Met His
1 5 10

<210> 279
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 279
Ile Ile Asn Pro Ser Gly Gly Tyr Thr Thr Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

_SL

<210> 280
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 280
Ile Arg Ser Cys Gly Gly Asp Cys Tyr Tyr Phe Asp Asn
1 5 10

<210> 281
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 281
Gly Phe Ser Leu Ser Thr Ala Gly Val His Val Gly
1 5 10

<210> 282
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 282
Leu Ile Ser Trp Ala Asp Asp Lys Arg Tyr Arg Pro Ser Leu Arg Ser
1 5 10 15

<210> 283
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 283
Gln Gly Phe Asp Gly Tyr Glu Ala Asn
1 5

<210> 284
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

_SL

peptide"

<400> 284
Arg Ala Ser Gln Ser Ile Arg Tyr Tyr Leu Ser
1 5 10

<210> 285
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 285
Thr Ala Ser Ile Leu Gln Asn
1 5

<210> 286
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 286
Leu Gln Thr Tyr Thr Thr Pro Asp
1 5

<210> 287
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 287
Ser Ala Ser Ser Ser Val Ser Tyr Met His
1 5 10

<210> 288
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 288
Asp Thr Ser Lys Leu Ala Ser
1 5

<210> 289

_SL

<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 289
Gln Gln Trp Ser Gly Tyr Pro Leu Thr
1 5

<210> 290
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 290
Arg Ala Ser Gln Ser Val Ser Ser Asn Phe Ala
1 5 10

<210> 291
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 291
Asp Ala Ser Asn Arg Ala Thr
1 5

<210> 292
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 292
His Gln Arg Ser Asn Trp Leu Tyr Thr
1 5

<210> 293
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

_SL

<400> 293
Gln Ala Ser Gln Asp Ile Ser Asn Ser Leu Asn
1 5 10

<210> 294
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 294
Asp Ala Ser Thr Leu Glu Thr
1 5

<210> 295
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 295
Gln Gln His Asp Asn Leu Pro Leu Thr
1 5

<210> 296
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 296
Arg Ala Ser Gln Ser Ile Asn Thr Tyr Leu Asn
1 5 10

<210> 297
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 297
Ala Ala Ser Ser Leu Gln Ser
1 5

<210> 298
<211> 8

_SL

<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 298
Gln Gln Ser Phe Ser Pro Leu Thr
1 5

<210> 299
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 299
Arg Ala Ser Gln Ser Ile Ser Asp Arg Leu Ala
1 5 10

<210> 300
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 300
Lys Ala Ser Ser Leu Glu Ser
1 5

<210> 301
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 301
Gln Gln Tyr Gly His Leu Pro Met Tyr Thr
1 5 10

<210> 302
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

_SL

<400> 302
Arg Ala Ser Gln Gly Val Gly Arg Trp Leu Ala
1 5 10

<210> 303
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 303
Ala Ala Ser Thr Leu Gln Ser
1 5

<210> 304
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 304
Gln Gln Ala Asn Ser Phe Pro Leu Thr
1 5

<210> 305
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 305
Arg Ala Ser Gln Ser Val Tyr Thr Lys Tyr Leu Gly
1 5 10

<210> 306
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 306
Asp Ala Ser Thr Arg Ala Thr
1 5

<210> 307
<211> 10
<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 307

Gln His Tyr Gly Gly Ser Pro Leu Ile Thr
1 5 10

<210> 308

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 308

Arg Ala Ser Gln Asp Ser Gly Thr Trp Leu Ala
1 5 10

<210> 309

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 309

Asp Ala Ser Thr Leu Glu Asp
1 5

<210> 310

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 310

Gln Gln Tyr Asn Ser Tyr Pro Leu Thr
1 5

<210> 311

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 311

Arg Ala Ser Gln Asp Ile Ser Ser Ala Leu^{-SL} Ala
1 5 10

<210> 312
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 312
Asp Ala Ser Ser Leu Glu Ser
1 5

<210> 313
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 313
Gln Gln Phe Ser Ser Tyr Pro Leu Thr
1 5

<210> 314
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 314
Lys Ser Ser His Ser Val Leu Tyr Asn Arg Asn Asn Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 315
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 315
Trp Ala Ser Thr Arg Lys Ser
1 5

_SL

<210> 316
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 316
Gln Gln Thr Gln Thr Phe Pro Leu Thr
1 5

<210> 317
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 317
Arg Ala Ser Gln Ser Ile Ser Thr Trp Leu Ala
1 5 10

<210> 318
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 318
Lys Ala Ser Thr Leu Glu Ser
1 5

<210> 319
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 319
Gln Gln Tyr Asn Thr Tyr Ser Pro Tyr Thr
1 5 10

<210> 320
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

_SL

peptide"

<400> 320

Arg Ala Ser Gln Ser Val Thr Ser Asn Tyr Leu Ala
1 5 10

<210> 321

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 321

Gly Ala Ser Thr Arg Ala Thr
1 5

<210> 322

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 322

Gln Gln Tyr Gly Ser Ala Pro Val Thr
1 5

<210> 323

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 323

Arg Ala Ser Glu Asn Val Asn Ile Trp Leu Ala
1 5 10

<210> 324

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 324

Lys Ser Ser Ser Leu Ala Ser
1 5

<210> 325

_SL

<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 325
Gln Gln Tyr Gln Ser Tyr Pro Leu Thr
1 5

<210> 326
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 326
Gln Gly Asp Ala Leu Arg Ser Tyr Tyr Ala Ser
1 5 10

<210> 327
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 327
Gly Lys Asn Asn Arg Pro Ser
1 5

<210> 328
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 328
Asn Ser Arg Asp Ser Ser Gly Tyr Pro Val
1 5 10

<210> 329
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

_SL

<400> 329
Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser
1 5 10

<210> 330
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 330
Gly Arg Ser Arg Arg Pro Ser
1 5

<210> 331
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 331
Asn Ser Arg Asp Asn Thr Ala Asn His Tyr Val
1 5 10

<210> 332
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 332
Asn Ser Arg Gly Ser Ser Gly Asn His Tyr Val
1 5 10

<210> 333
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 333
Arg Ala Ser Gln Ser Val Ser Ser Asn Tyr Leu Ala
1 5 10

<210> 334
<211> 7

_SL

<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 334
Asp Val Ser Thr Arg Ala Thr
1 5

<210> 335
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 335
Gln Gln Arg Ser Asn Trp Pro Pro Trp Thr
1 5 10

<210> 336
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 336
Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn
1 5 10

<210> 337
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 337
Gln Gln Ser Tyr Ser Ile Pro Leu Thr
1 5

<210> 338
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

_SL

<400> 338
Arg Ala Ser Gln Ser Ile Ser Ser Trp Leu Ala
1 5 10

<210> 339
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 339
Gln Gln Tyr Ser Ser Tyr Pro Leu Thr
1 5

<210> 340
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 340
Arg Ala Ser Gln Gly Ile Ser Asp Tyr Ser
1 5 10

<210> 341
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 341
Gln Gln Tyr Tyr Ser Tyr Pro Leu Thr
1 5

<210> 342
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 342
Arg Ala Ser Arg Gly Ile Ser Ser Ala Leu Ala
1 5 10

<210> 343
<211> 9
<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 343

Gln Gln Ser Tyr Ser Thr Pro Trp Thr
1 5

<210> 344

<211> 246

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 344

Glu Ile Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Thr Val Lys Ile Ser Cys Lys Gly Ser Gly Phe Asn Ile Glu Asp Tyr
20 25 30

Tyr Ile His Trp Val Gln Gln Ala Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Arg Ile Asp Pro Glu Asn Asp Glu Thr Lys Tyr Gly Pro Ile Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Thr Ser Thr Asn Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Phe Arg Gly Gly Val Tyr Trp Gly Gln Gly Thr Thr Val Thr Val
100 105 110

Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln Ser Pro Asp Ser
130 135 140

Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser
145 150 155 160

Gln Ser Leu Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Gln
165 170 175

Gln Lys Pro Gly Gln Pro Pro Lys Arg Leu Ile Ser Leu Val Ser Lys
Page 263

[illegible]

```
<210> 345
<211> 246
<212> PRT
<213> Artificial Sequence
```

$\langle 211 \rangle$ 246

<212> PRT

<213> Artificial Sequence

$\langle 220 \rangle$

<221> source

```
<221> SOURCE
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"
```

$\langle 400 \rangle$ 345

Asp Val Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser
20 25 30

Asp Gly Lys Thr Tyr Leu Asn Trp Leu Gln Gln Lys Pro Gly Gln Pro
35 40 45

Pro Lys Arg Leu Ile Ser Leu Val Ser Lys Leu Asp Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
65 70 75 80

Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Trp Gln Gly
85 90 95

Thr His Phe Pro Gly Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly

Gly Gly Gly Ser Glu Ile Gln Leu Val Gln Ser Gly Ala Glu Val Lys
130 135 140

Lys Pro Gly Ala Thr Val Lys Ile Ser Cys Lys Gly Ser Gly Phe Asn
145 150 155 160

_SL

Ile Glu Asp Tyr Tyr Ile His Trp Val Gln Gln Ala Pro Gly Lys Gly
165 170 175

Leu Glu Trp Met Gly Arg Ile Asp Pro Glu Asn Asp Glu Thr Lys Tyr
180 185 190

Gly Pro Ile Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Thr Ser Thr
195 200 205

Asn Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala
210 215 220

Val Tyr Tyr Cys Ala Phe Arg Gly Gly Val Tyr Trp Gly Gln Gly Thr
225 230 235 240

Thr Val Thr Val Ser Ser
245

<210> 346
<211> 246
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 346
Glu Ile Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Phe Asn Ile Glu Asp Tyr
20 25 30

Tyr Ile His Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Arg Ile Asp Pro Glu Asn Asp Glu Thr Lys Tyr Gly Pro Ile Phe
50 55 60

Gln Gly His Val Thr Ile Ser Ala Asp Thr Ser Ile Asn Thr Val Tyr
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Phe Arg Gly Gly Val Tyr Trp Gly Gln Gly Thr Thr Val Thr Val
100 105 110

Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120 125

_SL

Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln Ser Pro Leu Ser
130 135 140

Leu Pro Val Thr Leu Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser
145 150 155 160

Gln Ser Leu Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Gln
165 170 175

Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile Ser Leu Val Ser Lys
180 185 190

Leu Asp Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205

Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val
210 215 220

Tyr Tyr Cys Trp Gln Gly Thr His Phe Pro Gly Thr Phe Gly Gly Gly
225 230 235 240

Thr Lys Val Glu Ile Lys
245

<210> 347

<211> 246

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 347

Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser
20 25 30

Asp Gly Lys Thr Tyr Leu Asn Trp Leu Gln Gln Arg Pro Gly Gln Ser
35 40 45

Pro Arg Arg Leu Ile Ser Leu Val Ser Lys Leu Asp Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Trp Gln Gly
85 90 95

Thr His Phe Pro Gly Thr Phe Gly Gly Gly^{-SL} Thr Lys Val Glu Ile Lys
 100 105 110
 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 115 120 125
 Gly Gly Gly Ser Glu Ile Gln Leu Val Gln Ser Gly Ala Glu Val Lys
 130 135 140
 Lys Pro Gly Glu Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Phe Asn
 145 150 155 160
 Ile Glu Asp Tyr Tyr Ile His Trp Val Arg Gln Met Pro Gly Lys Gly
 165 170 175
 Leu Glu Trp Met Gly Arg Ile Asp Pro Glu Asn Asp Glu Thr Lys Tyr
 180 185 190
 Gly Pro Ile Phe Gln Gly His Val Thr Ile Ser Ala Asp Thr Ser Ile
 195 200 205
 Asn Thr Val Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala
 210 215 220
 Met Tyr Tyr Cys Ala Phe Arg Gly Gly Val Tyr Trp Gly Gln Gly Thr
 225 230 235 240
 Thr Val Thr Val Ser Ser
 245

<210> 348
 <211> 246
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 348
 Glu Ile Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Thr Val Lys Ile Ser Cys Lys Gly Ser Gly Phe Asn Ile Glu Asp Tyr
 20 25 30

Tyr Ile His Trp Val Gln Gln Ala Pro Gly Lys Gly Leu Glu Trp Met
 35 40 45

Gly Arg Ile Asp Pro Glu Asn Asp Glu Thr Lys Tyr Gly Pro Ile Phe
 50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Thr Ser Thr Asn Thr Val Tyr
 Page 267

_SL

Gly Arg Ile Asp Pro Glu Asn Asp Glu Thr Lys Tyr Gly Pro Ile Phe
50 55 60

Gln Gly His Val Thr Ile Ser Ala Asp Thr Ser Ile Asn Thr Val Tyr
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Phe Arg Gly Gly Val Tyr Trp Gly Gln Gly Thr Thr Val Thr Val
100 105 110

Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln Ser Pro Asp Ser
130 135 140

Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser
145 150 155 160

Gln Ser Leu Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Gln
165 170 175

Gln Lys Pro Gly Gln Pro Pro Lys Arg Leu Ile Ser Leu Val Ser Lys
180 185 190

Leu Asp Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val
210 215 220

Tyr Tyr Cys Trp Gln Gly Thr His Phe Pro Gly Thr Phe Gly Gly Gly
225 230 235 240

Thr Lys Val Glu Ile Lys
245

<210> 350

<211> 246

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 350

Asp Val Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

_SL

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser
20 25 30

Asp Gly Lys Thr Tyr Leu Asn Trp Leu Gln Gln Lys Pro Gly Gln Pro
35 40 45

Pro Lys Arg Leu Ile Ser Leu Val Ser Lys Leu Asp Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
65 70 75 80

Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Trp Gln Gly
85 90 95

Thr His Phe Pro Gly Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
115 120 125

Gly Gly Gly Ser Glu Ile Gln Leu Val Gln Ser Gly Ala Glu Val Lys
130 135 140

Lys Pro Gly Glu Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Phe Asn
145 150 155 160

Ile Glu Asp Tyr Tyr Ile His Trp Val Arg Gln Met Pro Gly Lys Gly
165 170 175

Leu Glu Trp Met Gly Arg Ile Asp Pro Glu Asn Asp Glu Thr Lys Tyr
180 185 190

Gly Pro Ile Phe Gln Gly His Val Thr Ile Ser Ala Asp Thr Ser Ile
195 200 205

Asn Thr Val Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala
210 215 220

Met Tyr Tyr Cys Ala Phe Arg Gly Gly Val Tyr Trp Gly Gln Gly Thr
225 230 235 240

Thr Val Thr Val Ser Ser
245

<210> 351

<211> 246

<212> PRT

<213> Artificial Sequence

<220>

<221> source

_SL

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 351

Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser
20 25 30

Asp Gly Lys Thr Tyr Leu Asn Trp Leu Gln Gln Arg Pro Gly Gln Ser
35 40 45

Pro Arg Arg Leu Ile Ser Leu Val Ser Lys Leu Asp Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Trp Gln Gly
85 90 95

Thr His Phe Pro Gly Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
115 120 125

Gly Gly Gly Ser Glu Ile Gln Leu Val Gln Ser Gly Ala Glu Val Lys
130 135 140

Lys Pro Gly Ala Thr Val Lys Ile Ser Cys Lys Gly Ser Gly Phe Asn
145 150 155 160

Ile Glu Asp Tyr Tyr Ile His Trp Val Gln Gln Ala Pro Gly Lys Gly
165 170 175

Leu Glu Trp Met Gly Arg Ile Asp Pro Glu Asn Asp Glu Thr Lys Tyr
180 185 190

Gly Pro Ile Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Thr Ser Thr
195 200 205

Asn Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala
210 215 220

Val Tyr Tyr Cys Ala Phe Arg Gly Gly Val Tyr Trp Gly Gln Gly Thr
225 230 235 240

Thr Val Thr Val Ser Ser
245

_SL

<210> 352
<211> 243
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 352
Glu Ile Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Leu Ser Cys Thr Gly Ser Gly Phe Asn Ile Glu Asp Tyr
20 25 30

Tyr Ile His Trp Val Lys Gln Arg Thr Glu Gln Gly Leu Glu Trp Ile
35 40 45

Gly Arg Ile Asp Pro Glu Asn Asp Glu Thr Lys Tyr Gly Pro Ile Phe
50 55 60

Gln Gly Arg Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Val Tyr
65 70 75 80

Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Phe Arg Gly Gly Val Tyr Trp Gly Pro Gly Thr Thr Leu Thr Val
100 105 110

Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120 125

Ser His Met Asp Val Val Met Thr Gln Ser Pro Leu Thr Leu Ser Val
130 135 140

Ala Ile Gly Gln Ser Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu
145 150 155 160

Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg Pro
165 170 175

Gly Gln Ser Pro Lys Arg Leu Ile Ser Leu Val Ser Lys Leu Asp Ser
180 185 190

Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr
195 200 205

Leu Arg Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Ile Tyr Tyr Cys
210 215 220

Trp Gln Gly Thr His Phe Pro Gly Thr Phe Gly Gly Gly Thr Lys Leu
Page 272

_SL
235

225 230 240

Glu Ile Lys

```
<220>  
<221> source  
<223> /note="Description of Artificial Sequence: Synthetic  
polypeptide"
```

<400> 353
Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Met Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Gly Tyr
20 25 30

Thr Met Asn Trp Val Lys Gln Ser His Gly Lys Asn Leu Glu Trp Ile
35 40 45

Gly Leu Ile Asn Pro Tyr Asn Gly Gly Thr Ile Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Leu Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Tyr Gly Phe Val Leu Asp Tyr Trp Gly Gln Gly Thr Thr
100 105 110

Leu Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ile Val Leu Thr Gln Ser
130 135 140

Pro Ser Ile Met Ser Val Ser Pro Gly Glu Lys Val Thr Ile Thr Cys
145 150 155 160

Ser Ala Ser Ser Ser Val Ser Tyr Met His Trp Phe Gln Gln Lys Pro
165 170 175

Gly Thr Ser Pro Lys Leu Cys Ile Tyr Ser Thr Ser Asn Leu Ala Ser
180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Arg Gly Ser Gly Thr Ser Tyr Ser
195 200 205

_SL

Leu Thr Ile Ser Arg Val Ala Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
210 215 220

Gln Gln Arg Ser Asn Tyr Pro Pro Trp Thr Phe Gly Gly Gly Thr Lys
225 230 235 240

Leu Glu Ile Lys

<210> 354

<211> 244

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 354

Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Met Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Gly Tyr
20 25 30

Thr Met Asn Trp Val Lys Gln Ser His Gly Lys Asn Leu Glu Trp Ile
35 40 45

Gly Leu Ile Asn Pro Tyr Asn Gly Gly Thr Ile Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Leu Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Tyr Gly Phe Val Leu Asp Tyr Trp Gly Gln Gly Thr Thr
100 105 110

Leu Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ile Val Leu Thr Gln Ser
130 135 140

Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys
145 150 155 160

Ser Ala Ser Ser Ser Val Ser Tyr Leu His Trp Phe Gln Gln Lys Pro
165 170 175

_SL

Gly Thr Ser Pro Lys Leu Trp Val Tyr Ser Thr Ser Asn Leu Pro Ser
180 185 190

Gly Val Pro Ala Arg Phe Gly Gly Ser Gly Ser Gly Thr Ser Tyr Ser
195 200 205

Leu Thr Ile Ser Arg Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
210 215 220

Gln Gln Arg Ser Ile Tyr Pro Pro Trp Thr Phe Gly Gly Gly Thr Lys
225 230 235 240

Leu Glu Ile Lys

<210> 355

<211> 244

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 355

Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Met Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Gly Tyr
20 25 30

Thr Met Asn Trp Val Lys Gln Ser His Gly Lys Asn Leu Glu Trp Ile
35 40 45

Gly Leu Ile Asn Pro Tyr Asn Gly Gly Thr Ile Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Leu Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Tyr Gly Phe Val Leu Asp Tyr Trp Gly Gln Gly Thr Thr
100 105 110

Leu Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ile Val Leu Thr Gln Ser
130 135 140

Pro Ser Ile Met Ser Val Ser Pro Gly Glu^{SL} Lys Val Thr Ile Thr Cys
 145 150 155 160
 Ser Ala Ser Ser Ser Val Ser Tyr Met His Trp Phe Gln Gln Lys Pro
 165 170 175
 Gly Thr Ser Pro Lys Leu Gly Ile Tyr Ser Thr Ser Asn Leu Ala Ser
 180 185 190
 Gly Val Pro Ala Arg Phe Ser Gly Arg Gly Ser Gly Thr Ser Tyr Ser
 195 200 205
 Leu Thr Ile Ser Arg Val Ala Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
 210 215 220
 Gln Gln Arg Ser Asn Tyr Pro Pro Trp Thr Phe Gly Gly Gly Thr Lys
 225 230 235 240

Leu Glu Ile Lys

<210> 356
 <211> 242
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 356
 Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
 1 5 10 15

Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
 35 40 45

Tyr His Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
 65 70 75 80

Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr
 85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr Gly Gly Gly Gly Ser
 100 105 110

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Lys Leu Gln Glu
 Page 276

115 120 _SL 125
 Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser Val Thr Cys
 130 135 140
 Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg
 145 150 155 160
 Gln Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Gly Ser
 165 170 175
 Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser Arg Leu Thr Ile Ile
 180 185 190
 Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn Ser Leu Gln
 195 200 205
 Thr Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly
 210 215 220
 Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val
 225 230 235 240
 Ser Ser

<210> 357
 <211> 242
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 357
 Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
 35 40 45

Tyr His Thr Ser Arg Leu His Ser Gly Ile Pro Ala Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Val Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr
 85 90 95

_SL

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser
100 105 110

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Glu
115 120 125

Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys
130 135 140

Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg
145 150 155 160

Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Val Ile Trp Gly Ser
165 170 175

Glu Thr Thr Tyr Tyr Ser Ser Ser Leu Lys Ser Arg Val Thr Ile Ser
180 185 190

Lys Asp Asn Ser Lys Asn Gln Val Ser Leu Lys Leu Ser Ser Val Thr
195 200 205

Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly
210 215 220

Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
225 230 235 240

Ser Ser

<210> 358
<211> 242
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 358
Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr His Thr Ser Arg Leu His Ser Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

_SL

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser
100 105 110

Gly Gly Gly Gly Ser Gly Gly Gly Ser Gln Val Gln Leu Gln Glu
115 120 125

Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys
130 135 140

Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg
145 150 155 160

Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Val Ile Trp Gly Ser
165 170 175

Glu Thr Thr Tyr Tyr Gln Ser Ser Leu Lys Ser Arg Val Thr Ile Ser
180 185 190

Lys Asp Asn Ser Lys Asn Gln Val Ser Leu Lys Leu Ser Ser Val Thr
195 200 205

Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly
210 215 220

Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
225 230 235 240

Ser Ser

<210> 359

<211> 242

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 359

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr
20 25 30

_SL

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 361

Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr His Thr Ser Arg Leu His Ser Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser
100 105 110

Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln
115 120 125

Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr
130 135 140

Leu Ser Leu Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly
145 150 155 160

Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly
165 170 175

Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Ser Ser Ser Leu Lys Ser
180 185 190

Arg Val Thr Ile Ser Lys Asp Asn Ser Lys Asn Gln Val Ser Leu Lys
195 200 205

Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Lys
210 215 220

His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly
225 230 235 240

Thr Leu Val Thr Val Ser Ser
245

_SL

<210> 362
<211> 247
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 362
Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr His Thr Ser Arg Leu His Ser Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser
100 105 110

Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln
115 120 125

Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr
130 135 140

Leu Ser Leu Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly
145 150 155 160

Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly
165 170 175

Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Gln Ser Ser Leu Lys Ser
180 185 190

Arg Val Thr Ile Ser Lys Asp Asn Ser Lys Asn Gln Val Ser Leu Lys
195 200 205

Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Lys
210 215 220

_SL

His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly
225 230 235 240

Thr Leu Val Thr Val Ser Ser
245

<210> 363

<211> 247

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 363

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr
20 25 30

Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45

Gly Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Ser Ser Ser Leu Lys
50 55 60

Ser Arg Val Thr Ile Ser Lys Asp Asn Ser Lys Asn Gln Val Ser Leu
65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Met
130 135 140

Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr
145 150 155 160

Leu Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr Leu Asn Trp Tyr
165 170 175

Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr His Thr Ser
180 185 190

Arg Leu His Ser Gly Ile Pro Ala Arg Phe ^{-SL} Ser Gly Ser Gly
195 200 205

Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
210 215 220

Val Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gln
225 230 235 240

Gly Thr Lys Leu Glu Ile Lys
245

<210> 364
<211> 247
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 364
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr
20 25 30

Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45

Gly Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Gln Ser Ser Leu Lys
50 55 60

Ser Arg Val Thr Ile Ser Lys Asp Asn Ser Lys Asn Gln Val Ser Leu
65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Met
130 135 140

Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr
145 150 155 160

Leu Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr Leu Asn Trp Tyr
Page 285

165 170 175
_SL

Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr His Thr Ser
180 185 190

Arg Leu His Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly
195 200 205

Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
210 215 220

Val Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gln
225 230 235 240

Gly Thr Lys Leu Glu Ile Lys
245

<210> 365
<211> 247
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 365
Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr His Thr Ser Arg Leu His Ser Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser
100 105 110

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln
115 120 125

Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr
130 135 140

_SL

Leu Ser Leu Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly
145 150 155 160

Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly
165 170 175

Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ser Leu Lys Ser
180 185 190

Arg Val Thr Ile Ser Lys Asp Asn Ser Lys Asn Gln Val Ser Leu Lys
195 200 205

Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Lys
210 215 220

His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly
225 230 235 240

Thr Leu Val Thr Val Ser Ser
245

<210> 366
<211> 247
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 366
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr
20 25 30

Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45

Gly Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ser Leu Lys
50 55 60

Ser Arg Val Thr Ile Ser Lys Asp Asn Ser Lys Asn Gln Val Ser Leu
65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln
100 105 110

_SL

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Met
130 135 140

Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr
145 150 155 160

Leu Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr Leu Asn Trp Tyr
165 170 175

Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr His Thr Ser
180 185 190

Arg Leu His Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly
195 200 205

Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
210 215 220

Val Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gln
225 230 235 240

Gly Thr Lys Leu Glu Ile Lys
245

<210> 367

<211> 242

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 367

Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr His Thr Ser Arg Leu His Ser Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Phe Cys Gln Gln^{-SL} Gly Asn Thr Leu Pro Tyr
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser
 100 105 110
 Gly Gly Gly Gly Ser Gly Gly Gly Ser Gln Val Gln Leu Gln Glu
 115 120 125
 Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys
 130 135 140
 Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg
 145 150 155 160
 Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Val Ile Trp Gly Ser
 165 170 175
 Glu Thr Thr Tyr Tyr Asn Ser Ser Leu Lys Ser Arg Val Thr Ile Ser
 180 185 190
 Lys Asp Asn Ser Lys Asn Gln Val Ser Leu Lys Leu Ser Ser Val Thr
 195 200 205
 Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly
 210 215 220
 Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
 225 230 235 240

Ser Ser

<210> 368

<211> 242

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 368

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
 1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr
 20 25 30

Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
 35 40 45

Gly Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ser Leu Lys
 Page 289

_SL

<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 370
Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser
1 5 10 15

<210> 371
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 371
His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr
1 5 10

<210> 372
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 372
Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Ser Ser Ser Leu Lys Ser
1 5 10 15

<210> 373
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 373
Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Gln Ser Ser Leu Lys Ser
1 5 10 15

<210> 374
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

_SL

<400> 374
Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ser Leu Lys Ser
1 5 10 15

<210> 375
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 375
Arg Ala Ser Gln Asp Ile Ser Lys Tyr Leu Asn
1 5 10

<210> 376
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 376
His Thr Ser Arg Leu His Ser
1 5

<210> 377
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 377
Gln Gln Gly Asn Thr Leu Pro Tyr Thr
1 5

<210> 378
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 378
Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr
1 5 10 15

Lys Gly

_SL

<210> 379
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 379
Gln Val Gln Leu Leu Glu Ser Gly Ala Glu Leu Val Arg Pro Gly Ser
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr
20 25 30

Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Gln Ile Tyr Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe
50 55 60

Lys Gly Gln Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Gln Leu Ser Gly Leu Thr Ser Glu Asp Ser Ala Val Tyr Ser Cys
85 90 95

Ala Arg Lys Thr Ile Ser Ser Val Val Asp Phe Tyr Phe Asp Tyr Trp
100 105 110

Gly Gln Gly Thr Thr Val Thr
115

<210> 380
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 380
Glu Leu Val Leu Thr Gln Ser Pro Lys Phe Met Ser Thr Ser Val Gly
1 5 10 15

Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Pro Leu Ile
35 40 45

Tyr Ser Ala Thr Tyr Arg Asn Ser Gly Val Pro Asp Arg Phe Thr Gly
Page 293

50 55 60 65 70 75 80 85 90 95 100 105 110															
Ser ₆₅	Gly	Ser	Gly	Thr	Asp ₇₀	Phe	Thr	Leu	Thr	Ile ₇₅	Thr	Asn	Val	Gln	Ser ₈₀
Lys	Asp	Leu	Ala	Asp ₈₅	Tyr	Phe	Tyr	Phe	Cys ₉₀	Gln	Tyr	Asn	Arg	Tyr ₉₅	Pro
Tyr	Thr	Ser	Gly ₁₀₀	Gly	Gly	Thr	Lys	Leu ₁₀₅	Glu	Ile	Lys	Arg	Arg ₁₁₀	Ser	

_SL

Pro Gly Gln Ser Pro Lys Pro Leu Ile Tyr Ser Ala Thr Tyr Arg Asn
180 185 190

Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe
195 200 205

Thr Leu Thr Ile Thr Asn Val Gln Ser Lys Asp Leu Ala Asp Tyr Phe
210 215 220

Tyr Phe Cys Gln Tyr Asn Arg Tyr Pro Tyr Thr Ser Gly Gly Gly Thr
225 230 235 240

Lys Leu Glu Ile Lys Arg Arg Ser
245

<210> 382

<211> 239

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 382

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Phe Ala Leu Ser Asn His
20 25 30

Gly Met Ser Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Val Tyr Ser Gly Ser Thr Tyr Tyr Ala Ala Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Ile Tyr Tyr Cys Ser
85 90 95

Ala His Gly Gly Glu Ser Asp Val Trp Gly Gln Gly Thr Thr Val Thr
100 105 110

Val Ser Ser Ala Ser Gly Gly Gly Gly Ser Gly Gly Arg Ala Ser Gly
115 120 125

Gly Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser
130 135 140

_SL

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser
145 150 155 160

Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
165 170 175

Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser
180 185 190

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
195 200 205

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr
210 215 220

Ser Thr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
225 230 235

<210> 383
<211> 717
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 383
gaagtgcaat tgggtggaatc agggggagga cttgtgcagc ctggaggatc gctgagactg 60
tcatgtgccg tgtccggcctt tgccctgtcc aaccacggga tgtcctgggt ccgccgcgcg 120
cctggaaagg gcctcgaatg ggtgtcgggt attgtgtaca gcggtagcac ctactatgcc 180
gcatccgtga aggggagatt caccatcagc cgggacaact ccaggaacac tctgtacctc 240
caaatgaatt cgctgaggcc agaggacact gccatctact actgctccgc gcatggcgga 300
gagtcgcgacg tctggggaca ggggaccacc gtgaccgtgt ctagcgcgtc cggcggaggc 360
ggcagcgggg gtcgggcatc agggggcggc ggatcggaca tccagctcac ccagtccccg 420
agctcgctgt ccgcctccgt gggagatcgg gtcaccatca cgtgccgcgc cagccagtcg 480
atttcctcct acctgaactg gtaccaacag aagcccggaa aagccccgaa gcttctcatc 540
tacgccgcct cgagcctgca gtcaggagtg ccctcacggt tctccggctc cggttccggt 600
actgatttca ccctgacatc ttcctccctg caaccggagg acttcgctac ttactactgc 660
cagcagtcgt actccacccc ctacactttc ggacaaggca ccaaggtcga aatcaag 717

<210> 384
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<221> source

_SL

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 384
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Phe Ala Leu Ser Asn His
 20 25 30

Gly Met Ser Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Gly Ile Val Tyr Ser Gly Ser Thr Tyr Tyr Ala Ala Ser Val Lys
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr Leu
 65 70 75 80

Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Ile Tyr Tyr Cys Ser
 85 90 95

Ala His Gly Gly Glu Ser Asp Val Trp Gly Gln Gly Thr Thr Val Thr
 100 105 110

Val Ser Ser
 115

<210> 385
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 385
 Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Tyr

85 90 _SL 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 386
<211> 246
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 386
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Gly Trp Val
35 40 45

Ser Gly Ile Ser Arg Ser Gly Glu Asn Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Asp Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser Pro Ala His Tyr Tyr Gly Gly Met Asp Val Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser Ala Ser Gly Gly Gly Gly Ser Gly
115 120 125

Gly Arg Ala Ser Gly Gly Gly Gly Ser Asp Ile Val Leu Thr Gln Ser
130 135 140

Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
145 150 155 160

Arg Ala Ser Gln Ser Ile Ser Ser Ser Phe Leu Ala Trp Tyr Gln Gln
165 170 175

Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Arg Arg
180 185 190

Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
195 200 205

_SL

Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Ser Ala Val Tyr
210 215 220

Tyr Cys Gln Gln Tyr His Ser Ser Pro Ser Trp Thr Phe Gly Gln Gly
225 230 235 240

Thr Lys Leu Glu Ile Lys
245

<210> 387
<211> 738
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 387
caagtgaac tcgtggaatc tgggtggagga ctcgtgcaac ccggaagatc gcttagactg 60
tcgtgtgccg ccagcgggtt cactttctcg aactacgcga tgtcctgggt ccgccaggca 120
cccggaaagg gactcggttg ggtgtccggc atttcccgtt ccggcgaaaa tacctactac 180
gccgactccg tgaagggccg cttcaccatc tcaagggaca acagcaaaaa caccctgtac 240
ttgcaaatga actccctgcg ggatgaagat acagccgtgt actattgcgc ccggtcgcct 300
gcccattact acggcggaat ggacgtctgg ggacagggaa ccactgtgac tgtcagcagc 360
gcgtcgggtg gcggcggctc aggggggtcgg gcctccgggg ggggagggtc cgacatcgtg 420
ctgaccagcgt ccccggaac cctgagcctg agcccgggag agcgcgcgac cctgtcatgc 480
cgggcatccc agagcattag ctctccttt ctcgcctggt atcagcagaa gcccgacag 540
gccccgaggc tgctgatcta cggcgctagc agaagggcta ccggaatccc agaccggttc 600
tccggctccg gttccgggac cgatttcacc ctactatct cgcgcctgga acctgaggac 660
tccgccgtct actactgcca gcagtaccac tcatccccgt cgtggacggt cggacagggc 720
accaagctgg agattaag 738

<210> 388
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 388
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
Page 299

20 25 _SL 30															
Ala	Met	Ser ₃₅	Trp	Val	Arg	Gln	Ala ₄₀	Pro	Gly	Lys	Gly	Leu ₄₅	Gly	Trp	Val
Ser	Gly ₅₀	Ile	Ser	Arg	Ser	Gly ₅₅	Glu	Asn	Thr	Tyr	Tyr ₆₀	Ala	Asp	Ser	Val
Lys ₆₅	Gly	Arg	Phe	Thr	Ile ₇₀	Ser	Arg	Asp	Asn	Ser ₇₅	Lys	Asn	Thr	Leu ₈₀	Tyr
Leu	Gln	Met	Asn	Ser ₈₅	Leu	Arg	Asp	Glu	Asp ₉₀	Thr	Ala	Val	Tyr	Tyr ₉₅	Cys
Ala	Arg	Ser	Pro ₁₀₀	Ala	His	Tyr	Tyr	Gly ₁₀₅	Gly	Met	Asp	Val	Trp ₁₁₀	Gly	Gln
Gly	Thr	Thr ₁₁₅	Val	Thr	Val	Ser	Ser ₁₂₀								

$$\begin{array}{ll} \langle 210 \rangle & 390 \\ \langle 211 \rangle & 244 \end{array}$$

_SL

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 390

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Ser Trp Asn Ser Gly Ser Ile Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ser Val His Ser Phe Leu Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser Ala Ser Gly Gly Gly Gly Ser Gly Gly Arg Ala Ser Gly
115 120 125

Gly Gly Gly Ser Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Pro
130 135 140

Val Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser
145 150 155 160

Leu Leu His Ser Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys
165 170 175

Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala
180 185 190

Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
195 200 205

Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
210 215 220

Cys Met Gln Ala Leu Gln Thr Pro Tyr Thr Phe Gly Gln Gly Thr Lys
225 230 235 240

Val Glu Ile Lys

<210> 391
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 391
caagtgaac tcgtcgaatc cgggtggaggt ctggtccaac ctggtagaag cctgagactg 60
tcgtgtgcgg ccagcggatt cacctttgat gactatgcta tgcactgggt gcggcaggcc 120
ccaggaaagg gcctggaatg ggtgtcggga attagctgga actccgggtc cattggctac 180
gccgactccg tgaagggccg cttcaccatc tcccgcgaca acgcaaagaa ctccctgtac 240
ttgcaaatga actcgctcag ggctgaggat accgcgctgt actactgctc cgtgcattcc 300
ttcctggcct actgggggaca gggaactctg gtcaccgtgt cgagcgcctc cggcggcggg 360
ggctcgggtg gacgggcctc gggcggaggg ggggtccgaca tcgtgatgac ccagaccccg 420
ctgagcttgc ccgtgactcc cggagagcct gcatccatct cctgccggtc atcccagtcc 480
cttctccact ccaacggata caactacctc gactggtacc tccagaagcc gggacagagc 540
cctcagcttc tgatctacct ggggtcaaat agagcctcag gagtgccgga tcggttcagc 600
ggatctggtt cgggaactga tttcactctg aagatttccc gcgtggaagc cgaggacgtg 660
ggcgtctact actgtatgca ggcgctgcag accccctata ccttcggcca agggacgaaa 720
gtggagatca ag 732

<210> 392
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 392
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg 15
1 5 10
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr 30
20 25 30
Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 45
35 40 45
Ser Gly Ile Ser Trp Asn Ser Gly Ser Ile Gly Tyr Ala Asp Ser Val 60
50 55 60

_SL

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ser Val His Ser Phe Leu Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser
115

<210> 393
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 393
Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Thr Pro Gly
1 5 10 15

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser
20 25 30

Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala
85 90 95

Leu Gln Thr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 394
<211> 243
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 394

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly^{-SL} Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Phe Ala Leu Ser Asn His
 20 25 30
 Gly Met Ser Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Gly Ile Val Tyr Ser Gly Ser Thr Tyr Tyr Ala Ala Ser Val Lys
 50 55 60
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr Leu
 65 70 75 80
 Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Ile Tyr Tyr Cys Ser
 85 90 95
 Ala His Gly Gly Glu Ser Asp Val Trp Gly Gln Gly Thr Thr Val Thr
 100 105 110
 Val Ser Ser Ala Ser Gly Gly Gly Gly Ser Gly Gly Arg Ala Ser Gly
 115 120 125
 Gly Gly Gly Ser Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Ser
 130 135 140
 Val Thr Pro Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser
 145 150 155 160
 Leu Leu Arg Asn Asp Gly Lys Thr Pro Leu Tyr Trp Tyr Leu Gln Lys
 165 170 175
 Ala Gly Gln Pro Pro Gln Leu Leu Ile Tyr Glu Val Ser Asn Arg Phe
 180 185 190
 Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
 195 200 205
 Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Ala Tyr Tyr
 210 215 220
 Cys Met Gln Asn Ile Gln Phe Pro Ser Phe Gly Gly Gly Thr Lys Leu
 225 230 235 240
 Glu Ile Lys

<210> 395

<211> 729

<212> DNA

<213> Artificial Sequence

_SL

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 395

```
gaagtgcaat tgttggaatc tggaggagga cttgtgcagc ctggaggatc actgagactt      60
tcgtgtgcgg tgtcaggctt cgccctgagc aaccacggca tgagctgggt gcggagagcc      120
ccggggaagg gtctggaatg ggtgtccggg atcgtctact ccggttcaac ttactacgcc      180
gcaagcgtga agggtcgctt caccatttcc cgcgataact cccggaacac cctgtacctc      240
caaatgaact ccctgcggcc cgaggacacc gccatctact actgttccgc gcatggagga      300
gagtccgatg tctggggaca gggcactacc gtgaccgtgt cgagcgcctc ggggggagga      360
ggctccggcg gtcgcgcctc cggggggggg ggcagcgaca ttgtgatgac gcagactcca      420
ctctcgtgt ccgtgacccc gggacagccc gcgtccatct cgtgcaagag ctcccagagc      480
ctgctgagga acgacggaaa gactcctctg tatttggtacc tccagaaggc tggacagccc      540
ccgcaactgc tcatctacga agtgtcaaat cgcttctccg gggtgccgga tcggttttcc      600
ggctcgggat cgggcaccga cttcacctg aaaatctcca gggtcgaggc cgaggacgtg      660
ggagcctact actgcatgca aaacatccag ttcccttctt tcggcggcgg cacaaagctg      720
gagattaag                                     729
```

<210> 396

<211> 115

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 396

```
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1           5           10           15
```

```
Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Phe Ala Leu Ser Asn His
          20          25          30
```

```
Gly Met Ser Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Trp Val
          35          40          45
```

```
Ser Gly Ile Val Tyr Ser Gly Ser Thr Tyr Tyr Ala Ala Ser Val Lys
50          55          60
```

```
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr Leu
65          70          75          80
```

```
Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Ile Tyr Tyr Cys Ser
          85          90          95
```

_SL

Ala His Gly Gly Glu Ser Asp Val Trp Gly Gln Gly Thr Thr Val Thr
100 105 110

Val Ser Ser
115

<210> 397
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 397
Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Arg Asn
20 25 30

Asp Gly Lys Thr Pro Leu Tyr Trp Tyr Leu Gln Lys Ala Gly Gln Pro
35 40 45

Pro Gln Leu Leu Ile Tyr Glu Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Ala Tyr Tyr Cys Met Gln Asn
85 90 95

Ile Gln Phe Pro Ser Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 398
<211> 249
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 398
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Arg Lys Thr Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ile Phe Asp Asn Phe
20 25 30

Gly Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
Page 306

_SL

tcctgcaagg cctccggcta cattttcgat aacttcggaa tcaactgggt cagacaggcc	120
ccggggccagg ggctggaatg gatgggatgg atcaacccca agaacaacaa caccaactac	180
gcacagaagt tccagggccg cgtgactatc accgccgatg aatcgaccaa taccgcctac	240
atggaggtgt cctccctgcg gtcggaggac actgccgtgt attactgcgc gaggggcccc	300
tactactacc aaagctacat ggacgtctgg ggacagggaa ccatggtgac cgtgtcatcc	360
gcctccggtg gtggaggctc cggggggcgg gcttcaggag gcggaggaag cgatattgtg	420
atgaccaga ctccgcttag cctgcccgtg actcctggag aaccggcctc catttcctgc	480
cggtcctcgc aatcactcct gcattccaac ggttacaact acctgaattg gtacctccag	540
aagcctggcc agtcgcccc gttgctgac tatctgggct cgaagcgcg ctcgggggtg	600
cctgaccggt ttagcggatc tgggagcggc acggacttca ctctccacat caccgcgctg	660
ggagcggagg acgtgggagt gtactactgt atgcaggcgc tgcagactcc gtacacattc	720
ggacagggca ccaagctgga gatcaag	747

<210> 400
 <211> 120
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 400
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Arg Lys Thr Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ile Phe Asp Asn Phe
 20 25 30

Gly Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

Gly Trp Ile Asn Pro Lys Asn Asn Asn Thr Asn Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Asn Thr Ala Tyr
 65 70 75 80

Met Glu Val Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Gly Pro Tyr Tyr Tyr Gln Ser Tyr Met Asp Val Trp Gly Gln
 100 105 110

Gly Thr Met Val Thr Val Ser Ser
 115 120

_SL

<210> 401
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 401
Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Thr Pro Gly
1 5 10 15

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser
20 25 30

Asn Gly Tyr Asn Tyr Leu Asn Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Gln Leu Leu Ile Tyr Leu Gly Ser Lys Arg Ala Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu His Ile
65 70 75 80

Thr Arg Val Gly Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala
85 90 95

Leu Gln Thr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 402
<211> 246
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 402
Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Asp
20 25 30

Ala Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Val Ile Ser Gly Ser Gly Gly Thr Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

_SL

Leu Gln Met Asn Ser₈₅ Leu Arg Ala Glu Asp₉₀ Thr Ala Val Tyr Tyr₉₅ Cys

Ala Lys Leu Asp₁₀₀ Ser Ser Gly Tyr Tyr₁₀₅ Tyr Ala Arg Gly₁₁₀ Pro Arg Tyr

Trp Gly Gln₁₁₅ Gly Thr Leu Val Thr₁₂₀ Val Ser Ser Ala Ser₁₂₅ Gly Gly Gly

Gly Ser₁₃₀ Gly Gly Arg Ala Ser₁₃₅ Gly Gly Gly Gly Ser₁₄₀ Asp Ile Gln Leu

Thr₁₄₅ Gln Ser Pro Ser₁₅₀ Ser Leu Ser Ala Ser₁₅₅ Val Gly Asp Arg Val Thr₁₆₀

Ile Thr Cys Arg Ala₁₆₅ Ser Gln Ser Ile Ser₁₇₀ Ser Tyr Leu Asn Trp₁₇₅ Tyr

Gln Gln Lys Pro₁₈₀ Gly Lys Ala Pro Lys₁₈₅ Leu Leu Ile Tyr Gly₁₉₀ Ala Ser

Thr Leu Ala₁₉₅ Ser Gly Val Pro Ala₂₀₀ Arg Phe Ser Gly₂₀₅ Ser Gly Ser Gly

Thr His₂₁₀ Phe Thr Leu Thr Ile₂₁₅ Asn Ser Leu Gln Ser₂₂₀ Glu Asp Ser Ala

Thr₂₂₅ Tyr Tyr Cys Gln Gln₂₃₀ Ser Tyr Lys Arg Ala₂₃₅ Ser Phe Gly Gln Gly₂₄₀

Thr Lys Val Glu Ile Lys₂₄₅

<210> 403

<211> 738

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 403

caagtgaac ttcaagaatc aggcggagga ctcgtgcagc ccgaggatc attgcggctc 60

tcgtgcgccg cctcgggctt caccttctcg agcgacgcca tgacctgggt ccgccaggcc 120

ccggggaagg ggctggaatg ggtgtctgtg atttcggct ccgggggaac tacgtactac 180

gccgattccg tgaaaggctc cttactatc tcccgggaca acagcaagaa caccctttat 240

ctgcaaatga attccctccg cgccgaggac accgccgtgt actactgcg caagctggac 300

tcctcgggct actactatgc ccgggggtccg agatactggg gacaggggaac cctcgtgacc 360

_SL

gtgtcctccg cgtccggcgg aggagggtcg ggagggcggg cctccggcgg cggcggttcg 420
gacatccagc tgaccagtc cccatcctca ctgagcgcaa gcgtgggcga cagagtcacc 480
attacatgca gggcgtccca gagcatcagc tcctacctga actggtacca acagaagcct 540
ggaaaggctc ctaagctgtt gatctacggg gcttcgaccc tggcatccgg ggtgcccgcg 600
aggtttagcg gaagcggtag cggcactcac ttcactctga ccattaacag cctccagtcc 660
gaggattcag ccacttacta ctgtcagcag tcctacaagc gggccagctt cggacagggc 720
actaaggtcg agatcaag 738

<210> 404
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 404
Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Asp
20 25 30

Ala Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Val Ile Ser Gly Ser Gly Gly Thr Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Leu Asp Ser Ser Gly Tyr Tyr Tyr Ala Arg Gly Pro Arg Tyr
100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 405
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

_SL

<400> 405

Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Gly Ala Ser Thr Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr His Phe Thr Leu Thr Ile Asn Ser Leu Gln Ser
65 70 75 80

Glu Asp Ser Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Lys Arg Ala Ser
85 90 95

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 406

<211> 247

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 406

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Asn Tyr
20 25 30

Gly Ile Thr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Ser Ala Tyr Asn Gly Asn Thr Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asn Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Pro Tyr Tyr Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr
100 105 110

_SL

Met Val Thr Val Ser Ser Ala Ser Gly Gly Gly Gly Ser Gly Gly Arg
115 120 125

Ala Ser Gly Gly Gly Gly Ser Glu Ile Val Met Thr Gln Ser Pro Leu
130 135 140

Ser Leu Pro Val Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Arg Ser
145 150 155 160

Ser Gln Ser Leu Leu Tyr Ser Asn Gly Tyr Asn Tyr Val Asp Trp Tyr
165 170 175

Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Leu Gly Ser
180 185 190

Asn Arg Ala Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly
195 200 205

Thr Asp Phe Lys Leu Gln Ile Ser Arg Val Glu Ala Glu Asp Val Gly
210 215 220

Ile Tyr Tyr Cys Met Gln Gly Arg Gln Phe Pro Tyr Ser Phe Gly Gln
225 230 235 240

Gly Thr Lys Val Glu Ile Lys
245

<210> 407

<211> 741

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 407

caagtccaac tgggtccagag cgggtgcagaa gtgaagaagc ccggagcagag cgtgaaagtg 60

tcctgcaagg cttccgggta caccttctcc aactacggca tcacttgggt gcgccaggcc 120

ccgggacagg gcctggaatg gatgggggtg atttccgcgt acaacggcaa tacgaactac 180

gctcagaagt tccagggtag agtgaccatg actaggaaca cctccatttc caccgcctac 240

atggaactgt cctccctgcg gagcgaggac accgccgtgt actattgcgc ccggggacca 300

tactactact acatggatgt ctgggggaag gggactatgg tcaccgtgtc atccgcctcg 360

ggaggcggcg gatcaggagg acgcgcctct ggtggtggag gatcggagat cgtgatgacc 420

cagagccctc tctccttgcc cgtgactcct ggggagcccg catccatttc atgccggagc 480

tccagtcac ttcttactc caacggctat aactacgtgg attggtacct ccaaaagccg 540

ggccagagcc cgcagctgct gatctacctg ggctcgaaca gggccagcgg agtgcctgac 600

cggttctccg ggtcgggaag cgggaccgac ttcaagctgc aaatctcgag agtggaggcc 660
gaggacgtgg gaatctacta ctgtatgcag ggccgccagt ttccgtactc gttcggacag 720
ggcaccaaag tggaatcaa g 741

<210> 408
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 408
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Asn Tyr
20 25 30

Gly Ile Thr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Ser Ala Tyr Asn Gly Asn Thr Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asn Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Pro Tyr Tyr Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr
100 105 110

Met Val Thr Val Ser Ser
115

<210> 409
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 409
Glu Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
1 5 10 15

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu Tyr Ser
20 25 30

_SL

Asn Gly Tyr Asn Tyr Val Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Lys Leu Gln Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Ile Tyr Tyr Cys Met Gln Gly
85 90 95

Arg Gln Phe Pro Tyr Ser Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 410

<211> 238

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 410

Glu Val Gln Leu Leu Glu Thr Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Phe Ala Leu Ser Asn His
20 25 30

Gly Met Ser Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Val Tyr Ser Gly Ser Thr Tyr Tyr Ala Ala Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Ile Tyr Tyr Cys Ser
85 90 95

Ala His Gly Gly Glu Ser Asp Val Trp Gly Gln Gly Thr Thr Val Thr
100 105 110

Val Ser Ser Ala Ser Gly Gly Gly Gly Ser Gly Gly Arg Ala Ser Gly
115 120 125

Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
130 135 140

Val Ser Pro Gly Glu Ser Ala Thr Leu Ser ^{-SL} Cys Arg Ala Ser Gln Ser
 145 150 155 160

Val Ser Ser Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
 165 170 175

Arg Leu Leu Ile Tyr Gly Ala Ser Thr Arg Ala Ser Gly Ile Pro Asp
 180 185 190

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
 195 200 205

Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Tyr Gly
 210 215 220

Ser Ser Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 225 230 235

<210> 411
 <211> 714
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 411
 gaagtgcaat tgctcgaaac tggaggaggt ctggtgcaac ctggaggatc acttcgcctg 60
 tcctgcgccg tgtcgggctt tgccctgtcc aaccatggaa tgagctgggt ccgccgcgcg 120
 ccggggaagg gcctcgaatg ggtgtccggc atcgtctact ccggctccac ctactacgcc 180
 gcgtccgtga agggccggtt cacgatttca cgggacaact cgcggaacac cctgtacctc 240
 caaatgaatt cccttcggcc ggaggatact gccatctact actgctccgc ccacgggtggc 300
 gaatccgacg tctggggcca gggaaccacc gtgaccgtgt ccagcgcgtc cgggggagga 360
 ggaagcgggg gtagagcatc ggggtggaggc ggatcagaga tcgtgctgac ccagtcccc 420
 gccaccttga gcgtgtcacc aggagagtcc gccaccctgt catgccgcgc cagccagtcc 480
 gtgtcctcca acctggcttg gtaccagcag aagccggggc aggcccctag actcctgata 540
 tatggggcgt cgaccgggc atctggaatt cccgataggt tcagcggatc gggctcgggc 600
 actgacttca ctctgacat ctctcgctg caagccgagg acgtggctgt gtactactgt 660
 cagcagtacg gaagctccct gactttcggt ggcgggacca aagtcgagat taag 714

<210> 412
 <211> 115
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 Page 316

_SL

polypeptide"

<400> 412

Glu Val Gln Leu Leu Glu Thr Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Phe Ala Leu Ser Asn His
20 25 30

Gly Met Ser Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Val Tyr Ser Gly Ser Thr Tyr Tyr Ala Ala Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Ile Tyr Tyr Cys Ser
85 90 95

Ala His Gly Gly Glu Ser Asp Val Trp Gly Gln Gly Thr Thr Val Thr
100 105 110

Val Ser Ser
115

<210> 413

<211> 106

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 413

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly
1 5 10 15

Glu Ser Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Asn
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Gly Ala Ser Thr Arg Ala Ser Gly Ile Pro Asp Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala
65 70 75 80

Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Leu Thr
85 90 95

_SL

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 414

<211> 239

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 414

Glu Val Gln Leu Val Glu Thr Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Phe Ala Leu Ser Asn His
20 25 30

Gly Met Ser Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Val Tyr Ser Gly Ser Thr Tyr Tyr Ala Ala Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Ile Tyr Tyr Cys Ser
85 90 95

Ala His Gly Gly Glu Ser Asp Val Trp Gly Gln Gly Thr Thr Val Thr
100 105 110

Val Ser Ser Ala Ser Gly Gly Gly Gly Ser Gly Gly Arg Ala Ser Gly
115 120 125

Gly Gly Gly Ser Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser
130 135 140

Val Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
145 150 155 160

Val Ser Ser Lys Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
165 170 175

Arg Leu Leu Met Tyr Gly Ala Ser Ile Arg Ala Thr Gly Ile Pro Asp
180 185 190

Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser
195 200 205

_SL

Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly
210 215 220

Ser Ser Ser Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
225 230 235

<210> 415
<211> 717
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 415
gaagtgcaat tgggtggaac tggaggagga cttgtgcaac ctggaggatc attgagactg 60
agctgcgcag tgtcgggatt cgccctgagc aaccatggaa tgtcctgggt cagaagggcc 120
cctggaaaag gcctcgaatg ggtgtcaggg atcgtgtact ccggttcac ttactacgcc 180
gcctccgtga aggggcgctt cactatctca cgggataact cccgcaatac cctgtacctc 240
caaatgaaca gcctgcggcc ggaggatacc gccatctact actgttccgc ccacgggtgga 300
gagtctgacg tctggggcca gggaactacc gtgaccgtgt cctccgcgtc cggcgggtgga 360
gggagcggcg gccgcgccag cggcggcgga ggctccgaga tcgtgatgac ccagagcccc 420
gctactctgt cgggtgtcgcc cggagaaagg gcgaccctgt cctgccgggc gtcgcagtcc 480
gtgagcagca agctggcttg gtaccagcag aagccgggcc aggcaccacg cctgcttatg 540
tacgggtgcct ccattcgggc caccggaatc ccggaccggt tctcggggtc ggggtccggt 600
accgagttca cactgacatc ttcctcgctc gagcccgagg actttgccgt ctattactgc 660
cagcagtacg gtcctcctc atggacgttc ggccagggga ccaaggtcga aatcaag 717

<210> 416
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 416
Glu Val Gln Leu Val Glu Thr Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Phe Ala Leu Ser Asn His
20 25 30

Gly Met Ser Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Val Tyr Ser Gly Ser Thr Tyr Tyr^{-SL} Ala Ala Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Ile Tyr Tyr Cys Ser
85 90 95

Ala His Gly Gly Glu Ser Asp Val Trp Gly Gln Gly Thr Thr Val Thr
100 105 110

Val Ser Ser
115

<210> 417
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 417
Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Lys
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Met
35 40 45

Tyr Gly Ala Ser Ile Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Ser Trp
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 418
<211> 241
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

_SL

<400> 418

Glu Val Gln Leu Val Glu Thr Gly Gly Gly Val Val Gln Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Phe Ala Leu Ser Asn His
20 25 30
Gly Met Ser Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ser Gly Ile Val Tyr Ser Gly Ser Thr Tyr Tyr Ala Ala Ser Val Lys
50 55 60
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr Leu
65 70 75 80
Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Ile Tyr Tyr Cys Ser
85 90 95
Ala His Gly Gly Glu Ser Asp Val Trp Gly Gln Gly Thr Thr Val Thr
100 105 110
Val Ser Ser Ala Ser Gly Gly Gly Gly Ser Gly Gly Arg Ala Ser Gly
115 120 125
Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser
130 135 140
Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
145 150 155 160
Val Gly Ser Thr Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala
165 170 175
Pro Arg Leu Leu Ile Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro
180 185 190
Asp Arg Phe Ser Gly Gly Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
195 200 205
Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr
210 215 220
Gly Ser Ser Pro Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
225 230 235 240

Lys

<210> 419

<211> 723

<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 419
gaagtgcaat tgggtggagac tggaggagga gtggtgcaac ctggaggaag cctgagactg 60
tcatgcgcggtgtgtcgggctt cgccctctcc aaccacggaa tgtcctgggt ccgccggggcc 120
cctgggaaag gacttgaatg ggtgtccggc atcgtgtact cgggttccac ctactacgag 180
gcctcagtga agggccgggtt tactattagc cgcgacaact ccagaaacac actgtacctc 240
caaatgaact cgctgcggcc ggaagatacc gctatctact actgctccgc ccatggggga 300
gagtcggacg tctggggaca gggcaccact gtcactgtgt ccagcgcttc cggcggtggt 360
ggaagcgggg gacgggcctc aggaggcgggt ggcagcgaga ttgtgctgac ccagtcccc 420
gggaccctga gcctgtcccc gggagaaagg gccaccctct cctgtcgggc atcccagttc 480
gtgggggtcta ctaaccttgc atggtaccag cagaagcccg gccaggcccc tcgcctgctg 540
atctacgacg cgtccaatag agccaccggc atcccggtac gcttcagcgg aggcgggatcg 600
ggcaccgact tcaccctcac catttcaagg ctggaaccgg aggacttcgc cgtgtactac 660
tgccagcagt atggttcgtc cccaccctgg acgttcggcc aggggactaa ggtcgagatc 720
aag 723

<210> 420
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 420
Glu Val Gln Leu Val Glu Thr Gly Gly Gly Val Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Phe Ala Leu Ser Asn His
20 25 30

Gly Met Ser Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Val Tyr Ser Gly Ser Thr Tyr Tyr Ala Ala Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Ile Tyr Tyr Cys Ser

85 90 _SL 95

Ala His Gly Gly Glu Ser Asp Val Trp Gly Gln Gly Thr Thr Val Thr
100 105 110

Val Ser Ser
115

<210> 421
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 421
Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Thr
20 25 30

Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60

Gly Gly Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
85 90 95

Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 422
<211> 239
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 422
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
20 25 30

_SL

Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Ser Gly Asp Gly Met Asp Val Trp Gly Gln Gly Thr Thr
100 105 110

Val Thr Val Ser Ser Ala Ser Gly Gly Gly Gly Ser Gly Gly Arg Ala
115 120 125

Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
130 135 140

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
145 150 155 160

Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys
165 170 175

Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val
180 185 190

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
195 200 205

Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
210 215 220

Ser Tyr Thr Leu Ala Phe Gly Gln Gly Thr Lys Val Asp Ile Lys
225 230 235

<210> 423

<211> 717

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 423

caagtgcac tcgtggaatc tgggtggagga ctcgtgaaac ctggaggatc attgagactg 60

tcatgcgcgg cctcgggatt cacgttctcc gattactaca tgagctggat tcgccaggct 120

_SL

```

ccggggaagg gactggaatg ggtgtcctac atttcctcat ccggctccac catctactac      180
gcggactccg tgaaggggag attcaccatt agccgcgata acgccaagaa cagcctgtac      240
cttcagatga actccctgcg ggctgaagat actgccgtct actactgcgc aagggagagc      300
ggagatggga tggacgtctg gggacagggg accactgtga ccgtgtcgtc ggcctccggc      360
ggaggggggt cgggtggaag ggccagcggc ggcggaggca gcgacatcca gatgaccag      420
tccccctcat cgctgtccgc ctccgtgggc gaccgcgtca ccatcacatg ccgggcctca      480
cagtcgatct cctcctacct caattggtat cagcagaagc ccggaaaggc ccctaagctt      540
ctgatctacg cagcgtcctc cctgcaatcc ggggtcccat ctcggttctc cggctcgggc      600
agcggtagcg atttactct gaccatctcg agcctgcagc cggaggactt cgccacttac      660
tactgtcagc aaagctacac cctcgcgttt ggccagggca ccaaagtgga catcaag      717

```

```

<210> 424
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
        polypeptide"

```

```

<400> 424
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1          5          10          15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
          20          25          30

Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
          35          40          45

Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
          50          55          60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65          70          75          80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
          85          90          95

Ala Arg Glu Ser Gly Asp Gly Met Asp Val Trp Gly Gln Gly Thr Thr
          100          105          110

Val Thr Val Ser Ser
          115

```

```

<210> 425
<211> 105
<212> PRT
<213> Artificial Sequence

```


_SL

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 425

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Thr Leu Ala Phe
85 90 95

Gly Gln Gly Thr Lys Val Asp Ile Lys
100 105

<210> 426

<211> 246

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 426

Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
20 25 30

Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Tyr Ile Ser Ser Ser Gly Asn Thr Ile Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

_SL

Ala Arg Ser Thr Met Val Arg Glu Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser Ala Ser Gly Gly Gly Gly Ser Gly Gly Arg Ala
115 120 125

Ser Gly Gly Gly Gly Ser Asp Ile Val Leu Thr Gln Ser Pro Leu Ser
130 135 140

Leu Pro Val Thr Leu Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser
145 150 155 160

Glu Ser Leu Val His Asn Ser Gly Lys Thr Tyr Leu Asn Trp Phe His
165 170 175

Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile Tyr Glu Val Ser Asn
180 185 190

Arg Asp Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr
195 200 205

Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val
210 215 220

Tyr Tyr Cys Met Gln Gly Thr His Trp Pro Gly Thr Phe Gly Gln Gly
225 230 235 240

Thr Lys Leu Glu Ile Lys
245

<210> 427
<211> 738
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 427
caagtgaac tgggtcaaag cggaggagga ttggtcaaac ccggaggaag cctgagactg 60
tcatgcgcgg cctctggatt caccttctcc gattactaca tgtcatggat cagacaggcc 120
ccggggaagg gcctcgaatg ggtgtcctac atctcgtcct ccgggaacac catctactac 180
gccgacagcg tgaagggccg ctttaccatt tcccgcgaca acgcaaagaa ctcgctgtac 240
cttcagatga attccctgcg ggctgaagat accgcggtgt actattgcgc ccggtccact 300
atggtccggg aggactactg gggacagggc acactcgtga ccgtgtccag cgcgagcggg 360
ggtggaggca gcggtggacg cgcctccggc ggcggcggtt cagacatcgt gctgactcag 420
tcgcccctgt cgctgccggt caccctgggc caaccggcct caattagctg caagtcctcg 480

_SL

gagagcctgg tgcacaactc aggaaagact tacctgaact ggttccatca gcggcctgga 540
cagtccccac ggagggtcat ctatgaagtg tccaacaggg attcgggggt gcccgaccgc 600
ttcactggct ccgggtccgg caccgacttc accttgaaaa tctccagagt ggaagccgag 660
gacgtgggcg tgtactactg tatgcagggt acccactggc ctggaacctt tggacaagga 720
actaagctcg agattaag 738

<210> 428
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 428
Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
20 25 30

Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Tyr Ile Ser Ser Ser Gly Asn Thr Ile Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser Thr Met Val Arg Glu Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 429
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 429
Asp Ile Val Leu Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly
1 5 10 15

_SL

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Glu Ser Leu Val His Asn
20 25 30

Ser Gly Lys Thr Tyr Leu Asn Trp Phe His Gln Arg Pro Gly Gln Ser
35 40 45

Pro Arg Arg Leu Ile Tyr Glu Val Ser Asn Arg Asp Ser Gly Val Pro
50 55 60

Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Gly
85 90 95

Thr His Trp Pro Gly Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 430

<211> 239

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 430

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Phe Ala Leu Ser Asn His
20 25 30

Gly Met Ser Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Val Tyr Ser Gly Ser Thr Tyr Tyr Ala Ala Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Ile Tyr Tyr Cys Ser
85 90 95

Ala His Gly Gly Glu Ser Asp Val Trp Gly Gln Gly Thr Thr Val Thr
100 105 110

Val Ser Ser Ala Ser Gly Gly Gly Gly Ser Gly Gly Arg Ala Ser Gly
115 120 125

_SL

Gly Gly Gly Ser Asp Ile Arg Leu Thr Gln Ser Pro Ser Pro Leu Ser
130 135 140

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Glu Asp
145 150 155 160

Ile Asn Lys Phe Leu Asn Trp Tyr His Gln Thr Pro Gly Lys Ala Pro
165 170 175

Lys Leu Leu Ile Tyr Asp Ala Ser Thr Leu Gln Thr Gly Val Pro Ser
180 185 190

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn
195 200 205

Ser Leu Gln Pro Glu Asp Ile Gly Thr Tyr Tyr Cys Gln Gln Tyr Glu
210 215 220

Ser Leu Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
225 230 235

<210> 431

<211> 717

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 431

caagtgaac tcgtggaatc tgggtggagga ctcgtgcaac ccggtggaag ccttaggctg	60
tcgtgcgccg tcagcgggtt tgctctgagc aaccatggaa tgccttgggt ccgccgggca	120
ccgggaaaag ggctggaatg ggtgtccggc atcgtgtaca gcgggtcaac ctattacgcc	180
gcgtccgtga agggcagatt cactatctca agagacaaca gccggaacac cctgtacttg	240
caaatgaatt ccctgcgcc cgaggacacc gccatctact actgctccgc ccacggagga	300
gagtcggacg tgtggggcca gggaacgact gtgactgtgt ccagcgcac aggaggggt	360
ggttcgggcg gccgggcctc ggggggagga ggttccgaca ttcggctgac ccagtccccg	420
tccccactgt cggcctccgt cggcgaccgc gtgaccatca cttgtcaggc gtccgaggac	480
attaacaagt tcctgaactg gtaccaccag acccctggaa aggccccaa gctgctgac	540
tacgatgcct cgacccttca aactggagt cctagccggt tctccgggtc cggctccggc	600
actgatttca ctctgaccat caactcattg cagccggaag atatcgggac ctactattgc	660
cagcagtacg aatccctccc gctcacattc ggcgggggaa ccaaggtcga gattaag	717

<210> 432

<211> 115

<212> PRT

_SL

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 432

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Phe Ala Leu Ser Asn His
20 25 30

Gly Met Ser Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Val Tyr Ser Gly Ser Thr Tyr Tyr Ala Ala Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Ile Tyr Tyr Cys Ser
85 90 95

Ala His Gly Gly Glu Ser Asp Val Trp Gly Gln Gly Thr Thr Val Thr
100 105 110

Val Ser Ser
115

<210> 433

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 433

Asp Ile Arg Leu Thr Gln Ser Pro Ser Pro Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Glu Asp Ile Asn Lys Phe
20 25 30

Leu Asn Trp Tyr His Gln Thr Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Thr Leu Gln Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Gln Pro
Page 331

65		70		-SL 75		80									
Glu	Asp	Ile	Gly	Thr	Tyr	Tyr	Cys	Gln	Gln	Tyr	Glu	Ser	Leu	Pro	Leu
			85						90					95	
Thr	Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys					
			100					105							
<210> 434															
<211> 240															
<212> PRT															
<213> Artificial Sequence															
<220>															
<221> source															
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"															
<400> 434															
Glu	Val	Gln	Leu	Val	Glu	Thr	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly
1				5					10					15	
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Val	Ser	Gly	Phe	Ala	Leu	Ser	Asn	His
			20					25					30		
Gly	Met	Ser	Trp	Val	Arg	Arg	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
		35					40					45			
Ser	Gly	Ile	Val	Tyr	Ser	Gly	Ser	Thr	Tyr	Tyr	Ala	Ala	Ser	Val	Lys
	50					55					60				
Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Arg	Asn	Thr	Leu	Tyr	Leu
65					70					75					80
Gln	Met	Asn	Ser	Leu	Arg	Pro	Glu	Asp	Thr	Ala	Ile	Tyr	Tyr	Cys	Ser
				85					90					95	
Ala	His	Gly	Gly	Glu	Ser	Asp	Val	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr
			100					105					110		
Val	Ser	Ser	Ala	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Arg	Ala	Ser	Gly
		115					120					125			
Gly	Gly	Gly	Ser	Glu	Thr	Thr	Leu	Thr	Gln	Ser	Pro	Ala	Thr	Leu	Ser
	130					135					140				
Val	Ser	Pro	Gly	Glu	Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Ser
145					150					155					160
Val	Gly	Ser	Asn	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Gly	Pro
				165					170					175	
Arg	Leu	Leu	Ile	Tyr	Gly	Ala	Ser	Thr	Arg	Ala	Thr	Gly	Ile	Pro	Ala
			180					185					190		

_SL

Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser
195 200 205

Ser Leu Gln Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Asn
210 215 220

Asp Trp Leu Pro Val Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
225 230 235 240

<210> 435
<211> 720
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 435
gaagtgaat tggatgaaac tggaggagga cttgtgcaac ctggaggatc attgcggctc 60
tcattgcgtg tctccggctt cgccctgtca aatcacggga tgtcgtgggt cagacgggcc 120
ccgggaaagg gtctggaatg ggtgtcgggg attgtgtaca gcggtccac ctactacgcc 180
gcttcggtca agggccgctt cactatttca cgggacaaca gccgcaacac cctctatctg 240
caaatgaact ctctccgcc ggaggatacc gccatctact actgctccgc acacggcggc 300
gaatccgacg tgtggggaca gggaaccact gtcaccgtgt cgtccgcac cggtggcgga 360
ggatcgggtg gccgggcctc cgggggcggc ggcagcgaga ctaccctgac ccagtcccct 420
gccactctgt ccgtgagccc gggagagaga gccaccctta gctgccgggc cagccagagc 480
gtgggctcca acctggcctg gtaccagcag aagccaggac aggggccag gctgctgac 540
tacggagcct ccactcgcgc gaccggcatc cccgcgaggt tctccgggtc gggttccggg 600
accgagttca ccctgacat ctctccctc caaccggagg acttcgcggt gtactactgt 660
cagcagtaca acgattggct gcccgtaga tttggacagg ggacgaagg ggaaatcaaa 720

<210> 436
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 436
Glu Val Gln Leu Val Glu Thr Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Phe Ala Leu Ser Asn His
20 25 30

_SL

Gly Met Ser Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Val Tyr Ser Gly Ser Thr Tyr Tyr Ala Ala Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Ile Tyr Tyr Cys Ser
85 90 95

Ala His Gly Gly Glu Ser Asp Val Trp Gly Gln Gly Thr Thr Val Thr
100 105 110

Val Ser Ser
115

<210> 437
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 437
Glu Thr Thr Leu Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Asn
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Gly Pro Arg Leu Leu Ile
35 40 45

Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Asn Asp Trp Leu Pro
85 90 95

Val Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 438
<211> 241
<212> PRT
<213> Artificial Sequence

_SL

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 438

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Phe Ala Leu Ser Asn His
20 25 30

Gly Met Ser Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Val Tyr Ser Gly Ser Thr Tyr Tyr Ala Ala Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Ile Tyr Tyr Cys Ser
85 90 95

Ala His Gly Gly Glu Ser Asp Val Trp Gly Gln Gly Thr Thr Val Thr
100 105 110

Val Ser Ser Ala Ser Gly Gly Gly Gly Ser Gly Gly Arg Ala Ser Gly
115 120 125

Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser
130 135 140

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
145 150 155 160

Ile Gly Ser Ser Ser Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala
165 170 175

Pro Arg Leu Leu Met Tyr Gly Ala Ser Ser Arg Ala Ser Gly Ile Pro
180 185 190

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
195 200 205

Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr
210 215 220

Ala Gly Ser Pro Pro Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
225 230 235 240

Lys

<210> 439
<211> 723
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 439
gaagtgcaat tgggtggaatc tgggtggagga cttgtgcaac ctggaggatc actgagactg 60
tcatgcgcgg tgtccggttt tgccctgagc aatcatggga tgcgtgggt ccggcgcgcc 120
cccggaaagg gtctggaatg ggtgtcgggt atcgtctact ccgggagcac ttactacgcc 180
gcgagcgtga agggccgctt caccatttcc cgcgataact cccgcaacac cctgtacttg 240
caaatgaact cgctccggcc tgaggacact gccatctact actgctccgc acacggagga 300
gaatccgacg tgtggggcca ggaactacc gtgaccgtca gcagcgctc cggcggcggg 360
ggctcaggcg gacgggctag cggcggcggg ggctccgaga tcgtgctgac ccagtcgcct 420
ggcactctct cgctgagccc cggggaaagg gcaaccctgt cctgtcgggc cagccagtcc 480
attggatcat cctccctcgc ctggtatcag cagaaaccgg gacaggctcc gcggctgctt 540
atgtatgggg ccagctcaag agcctccggc attcccgacc ggttctccgg gtccggttcc 600
ggcaccgatt tcaccctgac tatctcgagg ctggagccag aggacttcgc cgtgtactac 660
tgccagcagt acgcggggtc cccgccgttc acgttcggac aggaaccaa ggtcgagatc 720
aag 723

<210> 440
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 440
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Phe Ala Leu Ser Asn His
20 25 30
Gly Met Ser Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ser Gly Ile Val Tyr Ser Gly Ser Thr Tyr Tyr Ala Ala Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser^{-SL} Arg Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Ile Tyr Tyr Cys Ser
85 90 95

Ala His Gly Gly Glu Ser Asp Val Trp Gly Gln Gly Thr Thr Val Thr
100 105 110

Val Ser Ser
115

<210> 441
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 441
Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Ile Gly Ser Ser
20 25 30

Ser Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Met Tyr Gly Ala Ser Ser Arg Ala Ser Gly Ile Pro Asp Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Ala Gly Ser Pro
85 90 95

Pro Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 442
<211> 243
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 442
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15

_SL

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Ser
20 25 30

Tyr Tyr Tyr Trp Gly Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
35 40 45

Trp Ile Gly Ser Ile Tyr Tyr Ser Gly Ser Ala Tyr Tyr Asn Pro Ser
50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65 70 75 80

Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Arg His Trp Gln Glu Trp Pro Asp Ala Phe Asp Ile Trp Gly
100 105 110

Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Glu Thr Thr Leu Thr Gln Ser Pro
130 135 140

Ala Phe Met Ser Ala Thr Pro Gly Asp Lys Val Ile Ile Ser Cys Lys
145 150 155 160

Ala Ser Gln Asp Ile Asp Asp Ala Met Asn Trp Tyr Gln Gln Lys Pro
165 170 175

Gly Glu Ala Pro Leu Phe Ile Ile Gln Ser Ala Thr Ser Pro Val Pro
180 185 190

Gly Ile Pro Pro Arg Phe Ser Gly Ser Gly Phe Gly Thr Asp Phe Ser
195 200 205

Leu Thr Ile Asn Asn Ile Glu Ser Glu Asp Ala Ala Tyr Tyr Phe Cys
210 215 220

Leu Gln His Asp Asn Phe Pro Leu Thr Phe Gly Gln Gly Thr Lys Leu
225 230 235 240

Glu Ile Lys

<210> 443

<211> 729

<212> DNA

<213> Artificial Sequence

<220>

_SL

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 443

```
caagtgcagc ttcaggaaag cggaccgggc ctggtcaagc catccgaaac tctctccctg      60
acttgactg tgtctggcgg ttccatctca tcgtcgtact actactgggg ctggattagg      120
cagccgcccc gaaagggact ggagtggatc ggaagcatct actattccgg ctcggcgtac      180
tacaacccta gcctcaagtc gagagtgacc atctccgtgg atacctccaa gaaccagttt      240
tccctgcgcc tgagctccgt gaccgccgct gacaccgccg tgtactactg tgctcggcat      300
tggcaggaat ggcccgatgc cttcgacatt tggggccagg gcactatggg cactgtgtca      360
tccgggggtg gaggcagcgg gggaggaggg tccggggggg gaggttcaga gacaaccttg      420
accagtcac ccgcattcat gtccgccact ccgggagaca aggtcatcat ctctgtcaaa      480
gcgtcccagg atatcgacga tgccatgaat tggtaccagc agaagcctgg cgaagcgccg      540
ctgttcatta tccaatccgc aacctcgccc gtgcctggaa tcccaccgcg gttcagcggc      600
agcggtttcg gaaccgactt ttccctgacc attaacaaca ttgagtccga ggacgccgcc      660
tactacttct gcctgcaaca cgacaattc cctctcacgt tcggccaggg aaccaagctg      720
gaaatcaag                                     729
```

<210> 444

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 444

```
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1           5           10          15
```

```
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Ser
          20          25          30
```

```
Tyr Tyr Tyr Trp Gly Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
35          40          45
```

```
Trp Ile Gly Ser Ile Tyr Tyr Ser Gly Ser Ala Tyr Tyr Asn Pro Ser
50          55          60
```

```
Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65          70          75          80
```

```
Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85          90          95
```

```
Cys Ala Arg His Trp Gln Glu Trp Pro Asp Ala Phe Asp Ile Trp Gly
```

_SL

100 105 110

Gln Gly Thr Met Val Thr Val Ser Ser
 115 120

<210> 445
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 445
 Glu Thr Thr Leu Thr Gln Ser Pro Ala Phe Met Ser Ala Thr Pro Gly
 1 5 10 15

Asp Lys Val Ile Ile Ser Cys Lys Ala Ser Gln Asp Ile Asp Asp Ala
 20 25 30

Met Asn Trp Tyr Gln Gln Lys Pro Gly Glu Ala Pro Leu Phe Ile Ile
 35 40 45

Gln Ser Ala Thr Ser Pro Val Pro Gly Ile Pro Pro Arg Phe Ser Gly
 50 55 60

Ser Gly Phe Gly Thr Asp Phe Ser Leu Thr Ile Asn Asn Ile Glu Ser
 65 70 75 80

Glu Asp Ala Ala Tyr Tyr Phe Cys Leu Gln His Asp Asn Phe Pro Leu
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
 100 105

<210> 446
 <211> 245
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 446
 Gln Val Asn Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Arg Thr Ser
 20 25 30

Gly Met Cys Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
 35 40 45

_SL

Trp Leu Ala Arg Ile Asp Trp Asp Glu Asp Lys Phe Tyr Ser Thr Ser
50 55 60

Leu Lys Thr Arg Leu Thr Ile Ser Lys Asp Thr Ser Asp Asn Gln Val
65 70 75 80

Val Leu Arg Met Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Ser Gly Ala Gly Gly Thr Ser Ala Thr Ala Phe Asp Ile
100 105 110

Trp Gly Pro Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln
130 135 140

Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
145 150 155 160

Cys Arg Ala Ser Gln Asp Ile Tyr Asn Asn Leu Ala Trp Phe Gln Leu
165 170 175

Lys Pro Gly Ser Ala Pro Arg Ser Leu Met Tyr Ala Ala Asn Lys Ser
180 185 190

Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Ala Ser Gly Thr Asp
195 200 205

Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr
210 215 220

Tyr Cys Gln His Tyr Tyr Arg Phe Pro Tyr Ser Phe Gly Gln Gly Thr
225 230 235 240

Lys Leu Glu Ile Lys
245

<210> 447

<211> 735

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 447

caagtcaatc tgcgcgaatc cggccccgcc ttggtcaagc ctaccagac ctcactctg 60

acctgtactt tctccggctt ctccctgcgg acttccggga tgtgcgtgtc ctggatcaga 120

_SL

cagcctccgg gaaagggcct ggagtggctc gctcgcattg actgggatga ggacaagttc	180
tactccacct cactcaagac caggctgacc atcagcaaag atacctctga caaccaagtg	240
gtgctccgca tgaccaacat ggaccagcc gacactgcc a ttactactg cgcgaggagc	300
ggagcgggcg gaacctccgc caccgccttc gatatttggg gcccggttac catggtcacc	360
gtgtcaagcg gaggaggggg gtccgggggc ggcggttccg ggggaggcg atcggacatt	420
cagatgactc agtcaccatc gtccctgagc gctagcgtgg gcgacagagt gacaatcact	480
tgccgggcat cccaggacat ctataacaac cttgcgtggt tccagctgaa gcctggttcc	540
gcaccgcggt cacttatgta cgccgccaac aagagccagt cgggagtgcc gtcccggttt	600
tccggttcgg cctcggaac tgacttcacc ctgacgatct ccagcctgca acccgaggat	660
ttcgccacct actactgcca gcactactac cgctttccct actcgttcgg acaggggaacc	720
aagctggaaa tcaag	735

<210> 448
 <211> 123
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 448
 Gln Val Asn Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1 5 10 15
 Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Arg Thr Ser
 20 25 30
 Gly Met Cys Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
 35 40 45
 Trp Leu Ala Arg Ile Asp Trp Asp Glu Asp Lys Phe Tyr Ser Thr Ser
 50 55 60
 Leu Lys Thr Arg Leu Thr Ile Ser Lys Asp Thr Ser Asp Asn Gln Val
 65 70 75 80
 Val Leu Arg Met Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
 85 90 95
 Cys Ala Arg Ser Gly Ala Gly Gly Thr Ser Ala Thr Ala Phe Asp Ile
 100 105 110
 Trp Gly Pro Gly Thr Met Val Thr Val Ser Ser
 115 120

<210> 449
 <211> 107

_SL

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 449

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Tyr Asn Asn
20 25 30

Leu Ala Trp Phe Gln Leu Lys Pro Gly Ser Ala Pro Arg Ser Leu Met
35 40 45

Tyr Ala Ala Asn Lys Ser Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Ala Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Tyr Tyr Arg Phe Pro Tyr
85 90 95

Ser Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 450

<211> 246

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 450

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ser Ile Ser Ser Ser Ser Tyr Ile Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser₈₅ Leu Arg Ala Glu Asp₉₀^{-SL} Thr Ala Val Tyr Tyr Cys
 Ala Lys Thr Ile₁₀₀ Ala Ala Val Tyr Ala Phe Asp Ile Trp Gly₁₁₀ Gln Gly
 Thr Thr Val₁₁₅ Thr Val Ser Ser Gly₁₂₀ Gly Gly Gly Ser Gly₁₂₅ Gly Gly Gly
 Ser Gly₁₃₀ Gly Gly Gly Ser Glu₁₃₅ Ile Val Leu Thr Gln₁₄₀ Ser Pro Leu Ser
 Leu Pro Val Thr Pro Glu₁₅₀ Glu Pro Ala Ser Ile₁₅₅ Ser Cys Arg Ser Ser₁₆₀
 Gln Ser Leu Leu His₁₆₅ Ser Asn Gly Tyr Asn₁₇₀ Tyr Leu Asp Trp Tyr₁₇₅ Leu
 Gln Lys Pro Gly₁₈₀ Gln Ser Pro Gln₁₈₅ Leu Leu Ile Tyr Leu Gly₁₉₀ Ser Asn
 Arg Ala Ser₁₉₅ Gly Val Pro Asp Arg₂₀₀ Phe Ser Gly Ser Gly₂₀₅ Ser Gly Thr
 Asp Phe₂₁₀ Thr Leu Lys Ile Ser₂₁₅ Arg Val Glu Ala Glu₂₂₀ Asp Val Gly Val
 Tyr Tyr Cys Met Gln₂₃₀ Ala Leu Gln Thr Pro Tyr₂₃₅ Thr Phe Gly Gln Gly₂₄₀
 Thr Lys Leu Glu Ile₂₄₅ Lys

<210> 451
 <211> 738
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 451
 gaagtgcagc ttgtcgaatc cgggggggga ctggtcaagc cgggcggatc actgagactg 60
 tcctgcgccg cgagcggctt cacgttctcc tcctactcca tgaactgggt ccgccaagcc 120
 cccgggaagg gactggaatg ggtgtcctct atctcctcgt cgtcgtccta catctactac 180
 gccgactccg tgaagggaag attcaccatt tccgcgcaca acgcaaagaa ctactgtac 240
 ttgcaaata actactccg ggccgaagat actgctgtgt actattgcgc caagactatt 300
 gccgccgtct acgctttcga catctggggc cagggaacca ccgtgactgt gtcgtccggt 360
 ggtggtggct cgggcggagg aggaagcggc ggcgggggt cgcagattgt gctgaccag 420

_SL

tcgccactga gcctccctgt gacccccgag gaacccgcca gcatcagctg ccggtccagc 480
cagtccttgc tccactccaa cggatacaat tacctcgatt ggtaccttca gaagcctgga 540
caaagcccg c agctgctcat ctacttggga tcaaaccg c gtcaggagt gcctgaccgg 600
ttctccggct cgggcagcgg taccgatttc accctgaaaa tctccagggt ggaggcagag 660
gacgtggggag tgtattactg tatgcaggcg ctgcagactc cgtacacatt tgggcagggc 720
accaagctgg agatcaag 738

<210> 452
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 452
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ser Ile Ser Ser Ser Ser Tyr Ile Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Thr Ile Ala Ala Val Tyr Ala Phe Asp Ile Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser
115

<210> 453
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 453

Glu Ile Val Leu Thr Gln Ser Pro Leu Ser^{-SL} Leu Pro Val Thr Pro Glu
1 5 10 15

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser
20 25 30

Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala
85 90 95

Leu Gln Thr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 454

<211> 240

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 454

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
20 25 30

Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Leu Arg Gly Ala Phe Asp Ile Trp Gly Gln Gly Thr Met
100 105 110

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
Page 346

_SL

115	120	125	
Gly Gly Gly Ser Ser Tyr Val Leu Thr Gln Ser Pro Ser Val Ser Ala			
130	135	140	
Ala Pro Gly Tyr Thr Ala Thr Ile Ser Cys Gly Gly Asn Asn Ile Gly			
145	150	155	160
Thr Lys Ser Val His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Leu			
	165	170	175
Leu Val Ile Arg Asp Asp Ser Val Arg Pro Ser Lys Ile Pro Gly Arg			
	180	185	190
Phe Ser Gly Ser Asn Ser Gly Asn Met Ala Thr Leu Thr Ile Ser Gly			
195	200	205	
Val Gln Ala Gly Asp Glu Ala Asp Phe Tyr Cys Gln Val Trp Asp Ser			
210	215	220	
Asp Ser Glu His Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu			
225	230	235	240

<210> 455
 <211> 720
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 455	
gaagtccagc tcgtggagtc cggcggaggc cttgtgaagc ctggagggtc gctgagactg	60
tcctgcgccg cctccggctt caccttctcc gactactaca tgtcctggat cagacaggcc	120
ccgggaaagg gcctggaatg ggtgtcctac atctcgatcat cgggcagcac tatctactac	180
gcggactcag tgaaggggcg gttcaccatt tcccgggata acgcgaagaa ctcgctgtat	240
ctgcaaatga actcactgag ggccgaggac accgccgtgt actactgcgc ccgcgatctc	300
cgcggggcat ttgacatctg gggacaggga accatggtca cagtgtccag cggaggggga	360
ggatcgggtg gcggagggtc cgggggtgga ggctcctcct acgtgctgac tcagagccca	420
agcgtcagcg ctgcgcccg ttacacggca accatctcct gtggcggaaa caacattggg	480
accaagtctg tgcactggta tcagcagaag ccgggccaaag ctcccctggt ggtgatccgc	540
gatgactccg tgcggcctag caaaattccg ggacggttct ccggctcaa cagcggcaat	600
atggccactc tcaccatctc gggagtgcag gccggagatg aagccgactt ctactgcaa	660
gtctgggact cagactccga gcatgtggtg ttcgggggcg gaaccaagct gactgtgctc	720

<210> 456

_SL

<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 456
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
20 25 30

Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Leu Arg Gly Ala Phe Asp Ile Trp Gly Gln Gly Thr Met
100 105 110

Val Thr Val Ser Ser
115

<210> 457
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 457
Ser Tyr Val Leu Thr Gln Ser Pro Ser Val Ser Ala Ala Pro Gly Tyr
1 5 10 15

Thr Ala Thr Ile Ser Cys Gly Gly Asn Asn Ile Gly Thr Lys Ser Val
20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Leu Leu Val Ile Arg
35 40 45

Asp Asp Ser Val Arg Pro Ser Lys Ile Pro Gly Arg Phe Ser Gly Ser
50 55 60

_SL

Asn Ser Gly Asn Met Ala Thr Leu Thr Ile Ser Gly Val Gln Ala Gly
65 70 75 80

Asp Glu Ala Asp Phe Tyr Cys Gln Val Trp Asp Ser Asp Ser Glu His
85 90 95

Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 458

<211> 241

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 458

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Pro Ser Gly Tyr Thr Val Thr Ser His
20 25 30

Tyr Ile His Trp Val Arg Arg Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Met Ile Asn Pro Ser Gly Gly Val Thr Ala Tyr Ser Gln Thr Leu
50 55 60

Gln Gly Arg Val Thr Met Thr Ser Asp Thr Ser Ser Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg Glu Gly Ser Gly Ser Gly Trp Tyr Phe Asp Phe Trp Gly Arg
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Ser Tyr Val Leu Thr Gln Pro Pro Ser
130 135 140

Val Ser Val Ser Pro Gly Gln Thr Ala Ser Ile Thr Cys Ser Gly Asp
145 150 155 160

Gly Leu Ser Lys Lys Tyr Val Ser Trp Tyr Gln Gln Lys Ala Gly Gln
165 170 175

Ser Pro Val Val Leu Ile Ser Arg Asp Lys^{-SL} Glu Arg Pro Ser Gly Ile
 180 185 190
 Pro Asp Arg Phe Ser Gly Ser Asn Ser Ala Asp Thr Ala Thr Leu Thr
 195 200 205
 Ile Ser Gly Thr Gln Ala Met Asp Glu Ala Asp Tyr Tyr Cys Gln Ala
 210 215 220
 Trp Asp Asp Thr Thr Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val
 225 230 235 240

Leu

<210> 459
 <211> 723
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 459
 caagtgcagc tgggtgcagag cggggccgaa gtcaagaagc cgggagcctc cgtgaaagtg 60
 tcctgcaagc cttcgggata caccgtgacc tcccactaca ttcattgggt ccgccgcgcc 120
 cccggccaag gactcgagtg gatgggcatg atcaacccta gcggcggagt gaccgcgtac 180
 agccagacgc tgcagggacg cgtgactatg acctcggata cctcctcctc caccgtctat 240
 atggaactgt ccagcctgcg gtccgaggat accgccatgt actactgcgc ccgggaagga 300
 tcaggctccg ggtgggtatct cgacttctgg ggaagaggca ccctcgtgac tgtgtcatct 360
 gggggagggg gttccggtgg tggcggatcg ggaggaggcg gttcatccta cgtgctgacc 420
 cagccaccct ccgtgtccgt gagccccggc cagactgcat cgattacatg tagcggcgac 480
 ggcctctcca agaaatacgt gtcgtggtac cagcagaagg ccggacagag cccggtggtg 540
 ctgatctcaa gagataagga gcggcctagc ggaatcccgg acaggttctc gggttccaac 600
 tccgcggaca ctgctactct gaccatctcg gggaccagg ctatggacga agccgattac 660
 tactgccaag cctgggacga cactactgtc gtgtttggag ggggcaccaa gttgaccgtc 720
 ctt 723

<210> 460
 <211> 120
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

_SL

<400> 460

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Pro Ser Gly Tyr Thr Val Thr Ser His
20 25 30

Tyr Ile His Trp Val Arg Arg Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Met Ile Asn Pro Ser Gly Gly Val Thr Ala Tyr Ser Gln Thr Leu
50 55 60

Gln Gly Arg Val Thr Met Thr Ser Asp Thr Ser Ser Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg Glu Gly Ser Gly Ser Gly Trp Tyr Phe Asp Phe Trp Gly Arg
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 461

<211> 106

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 461

Ser Tyr Val Leu Thr Gln Pro Pro Ser Val Ser Val Ser Pro Gly Gln
1 5 10 15

Thr Ala Ser Ile Thr Cys Ser Gly Asp Gly Leu Ser Lys Lys Tyr Val
20 25 30

Ser Trp Tyr Gln Gln Lys Ala Gly Gln Ser Pro Val Val Leu Ile Ser
35 40 45

Arg Asp Lys Glu Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser
50 55 60

Asn Ser Ala Asp Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Met
65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Gln Ala Trp Asp Asp Thr Thr Val Val
85 90 95

Phe Gly Gly Gly Thr Lys Leu Thr Val Leu^{_SL}
100 105

<210> 462

<211> 245

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 462

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
20 25 30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu
35 40 45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Arg Ala Gly Ile Ala Ala Arg Leu Arg Gly Ala Phe Asp Ile
100 105 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val Met Thr Gln
130 135 140

Ser Pro Ser Ser Val Ser Ala Ser Val Gly Asp Arg Val Ile Ile Thr
145 150 155 160

Cys Arg Ala Ser Gln Gly Ile Arg Asn Trp Leu Ala Trp Tyr Gln Gln
165 170 175

Lys Pro Gly Lys Ala Pro Asn Leu Leu Ile Tyr Ala Ala Ser Asn Leu
180 185 190

Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Ala Asp
195 200 205

Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr
Page 352

210 215 _SL 220

Tyr Cys Gln Lys Tyr Asn Ser Ala Pro Phe Thr Phe Gly Pro Gly Thr
 225 230 235 240

Lys Val Asp Ile Lys
 245

<210> 463
 <211> 735
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 463
 caagtgcagc ttcaggagag cggcccggga ctcgtgaagc cgtcccagac cctgtccctg 60
 acttgaccg tgtcgggagg aagcatctcg agcggaggct actattggtc gtggattcgg 120
 cagcaccctg gaaagggcct ggaatggatc ggctacatct actactccgg ctcgacctac 180
 tacaacccat cgctgaagtc cagagtgaaca atctcagtgg acacgtccaa gaatcagttc 240
 agcctgaagc tctcttccgt gactgcggcc gacaccgccg tgtactactg cgcacgcgct 300
 ggaattgccg cccgggtgag ggggtgccttc gacatttggg gacagggcac catggtcacc 360
 gtgtcctccg gcggcggagg ttccgggggt ggaggctcag gaggaggggg gtccgacatc 420
 gtcattgact agtcgccctc aagcgtcagc gcgtccgtcg gggacagagt gatcatcacc 480
 tgtcgggctg cccaggggaat tcgcaactgg ctggcctggg atcagcagaa gcccggaag 540
 gcccccaacc tggtgatcta cgccgcctca aacctccaat ccgggggtgcc gagccgcttc 600
 agcggctccg gttcgggtgc cgatttcact ctgaccatct cctccctgca acctgaagat 660
 gtggctacct actactgcca aaagtacaac tccgcacctt ttactttcgg accgggggacc 720
 aaagtggaca ttaag 735

<210> 464
 <211> 123
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 464
 Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
 1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
 20 25 30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln His ^{-SL} Pro Gly Lys Gly Leu Glu
 35 40 45
 Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
 50 55 60
 Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
 65 70 75 80
 Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
 85 90 95
 Cys Ala Arg Ala Gly Ile Ala Ala Arg Leu Arg Gly Ala Phe Asp Ile
 100 105 110
 Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
 115 120

<210> 465
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 465
 Asp Ile Val Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Ile Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Trp
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Asn Leu Leu Ile
 35 40 45

Tyr Ala Ala Ser Asn Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Ala Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Val Ala Thr Tyr Tyr Cys Gln Lys Tyr Asn Ser Ala Pro Phe
 85 90 95

Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
 100 105

<210> 466
 <211> 253
 <212> PRT
 <213> Artificial Sequence

_SL

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 466

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Arg Gly Gly Tyr Gln Leu Leu Arg Trp Asp Val Gly Leu Leu
100 105 110

Arg Ser Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser
115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
130 135 140

Ser Tyr Val Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln
145 150 155 160

Thr Ala Arg Ile Thr Cys Gly Gly Asn Asn Ile Gly Ser Lys Ser Val
165 170 175

His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Leu Tyr
180 185 190

Gly Lys Asn Asn Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
195 200 205

Arg Ser Gly Thr Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu
210 215 220

Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Arg Asp Ser Ser Gly Asp His
225 230 235 240

Leu Arg Val Phe Gly Thr Gly Thr Lys Val Thr Val Leu
245 250

_SL

<210> 467
<211> 759
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 467
caagtgcagc tgggtccagtc gggcgccgag gtcaagaagc cggggagctc tgtgaaagtg 60
tcctgcaagg cctccggggg caccttttagc tcctacgccca tctcctgggt ccgccaagca 120
ccgggtcaag gcctggagtg gatgggggga attatcccta tcttcggcac tgccaactac 180
gccagaagt tccagggacg cgtgaccatt accgcggacg aatccacctc caccgcttat 240
atggagctgt ccagcttgcg ctcggaagat accgccgtgt actactgcgc ccggaggggt 300
ggataccagc tgctgagatg ggacgtgggc ctcctgcggt cggcgttcga catctggggc 360
cagggcacta tggtcactgt gtccagcggg ggaggcggat cgggaggcgg cggatcaggg 420
ggaggcgggt ccagctacgt gcttactcaa ccccttcggt tgtccgtggc cccgggacag 480
accgccagaa tcacttgcgg aggaacaac attgggtcca agagcgtgca ttggtaccag 540
cagaagccag gacaggcccc tgtgctggtg ctctacggga agaacaatcg gccagcggg 600
gtgccggaca ggttctcggg ttcacgtccc ggtacaaccg cttcactgac tatcaccggg 660
gccaggcag aggatgaagc ggactactac tgttcctccc gggattcatc cggcgaccac 720
ctccgggtgt tcggaaccgg aacgaaggtc accgtgctg 759

<210> 468
<211> 129
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 468
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
Page 356

_SL

<400> 470

Glu Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Asp Ser Val Ser Ser Asn
20 25 30

Ser Ala Ala Trp Asn Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu
35 40 45

Trp Leu Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Ser Phe Tyr Ala
50 55 60

Ile Ser Leu Lys Ser Arg Ile Ile Ile Asn Pro Asp Thr Ser Lys Asn
65 70 75 80

Gln Phe Ser Leu Gln Leu Lys Ser Val Thr Pro Glu Asp Thr Ala Val
85 90 95

Tyr Tyr Cys Ala Arg Ser Ser Pro Glu Gly Leu Phe Leu Tyr Trp Phe
100 105 110

Asp Pro Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Asp
115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Ser Glu Leu
130 135 140

Thr Gln Asp Pro Ala Val Ser Val Ala Leu Gly Gln Thr Ile Arg Ile
145 150 155 160

Thr Cys Gln Gly Asp Ser Leu Gly Asn Tyr Tyr Ala Thr Trp Tyr Gln
165 170 175

Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr Gly Thr Asn Asn
180 185 190

Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Ala Ser Ser Ser Gly Asn
195 200 205

Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu Asp Glu Ala Asp
210 215 220

Tyr Tyr Cys Asn Ser Arg Asp Ser Ser Gly His His Leu Leu Phe Gly
225 230 235 240

Thr Gly Thr Lys Val Thr Val Leu
245

<210> 471

<211> 744

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 471

```
gaagtgcagc tccaacagtc aggaccgggg ctcgtgaagc catcccagac cctgtccctg      60
acttgtgcc a tctcgggaga tagcgtgtca tcgaactccg ccgcctggaa ctggattcgg      120
cagagcccgt cccgcggact ggagtggctt ggaaggacct actaccggtc caagtggtag      180
tctttctacg cgatctcgct gaagtccgcg attatcatta accctgatac ctccaagaat      240
cagttctccc tccaactgaa atccgtcacc cccgaggaca cagcagtgtg ttactgcgca      300
cggagcagcc ccgaaggact gttcctgtat tggtttgacc cctggggcca ggggactctt      360
gtgaccgtgt cgagcggcgg agatgggtcc ggtggcgggtg gttcgggggg cggcggatca      420
tcacccgaac tgaccagga cccggctgtg tccgtggcgc tgggacaaac catccgcatt      480
acgtgccagg gagactccct gggcaactac tacgccactt ggtaccagca gaagccgggc      540
caagcccctg tgttggatcat ctacgggacc aacaacagac cttccggcat ccccgaccgg      600
ttcagcgctt cgtcctccgg caacactgcc agcctgacca tctactggagc gcaggccgaa      660
gatgaggccg actactactg caacagcaga gactcctcgg gtcatcacct cttgttcgga      720
actggaacca aggtcaccgt gctg      744
```

<210> 472

<211> 125

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 472

```
Glu Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1          5          10          15
```

```
Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Asp Ser Val Ser Ser Asn
          20          25          30
```

```
Ser Ala Ala Trp Asn Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu
          35          40          45
```

```
Trp Leu Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Ser Phe Tyr Ala
          50          55          60
```

```
Ile Ser Leu Lys Ser Arg Ile Ile Ile Asn Pro Asp Thr Ser Lys Asn
65          70          75          80
```

```
Gln Phe Ser Leu Gln Leu Lys Ser Val Thr Pro Glu Asp Thr Ala Val
          85          90          95
```

_SL

Tyr Tyr Cys Ala Arg Ser Ser Pro Glu Gly Leu Phe Leu Tyr Trp Phe
100 105 110

Asp Pro Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 473
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 473
Ser Ser Glu Leu Thr Gln Asp Pro Ala Val Ser Val Ala Leu Gly Gln
1 5 10 15

Thr Ile Arg Ile Thr Cys Gln Gly Asp Ser Leu Gly Asn Tyr Tyr Ala
20 25 30

Thr Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
35 40 45

Gly Thr Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Ala Ser
50 55 60

Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu
65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Ser Gly His His
85 90 95

Leu Leu Phe Gly Thr Gly Thr Lys Val Thr Val Leu
100 105

<210> 474
<211> 246
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 474
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly^{SL} Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Lys Val Glu Gly Ser Gly Ser Leu Asp Tyr Trp Gly Gln Gly Thr
 100 105 110
 Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 115 120 125
 Gly Gly Gly Gly Ser Glu Ile Val Met Thr Gln Ser Pro Gly Thr Leu
 130 135 140
 Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln
 145 150 155 160
 Ser Val Ser Ser Ala Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
 165 170 175
 Pro Pro Arg Leu Leu Ile Ser Gly Ala Ser Thr Arg Ala Thr Gly Ile
 180 185 190
 Pro Asp Arg Phe Gly Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 195 200 205
 Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln His
 210 215 220
 Tyr Gly Ser Ser Phe Asn Gly Ser Ser Leu Phe Thr Phe Gly Gln Gly
 225 230 235 240
 Thr Arg Leu Glu Ile Lys
 245

<210> 475

<211> 738

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 475

gaagtgcagc tcgtggagtc aggaggcggc ctggtccagc cgggagggtc ccttagactg

60

_SL

tcatgcgccg caagcggatt cactttctcc tcctatgcca tgagctgggt cgcgaagcc 120
cccggaaagg gactggaatg ggtgtccgcc atctcggggt ctggaggctc aacttactac 180
gctgactccg tgaagggacg gttcaccatt agccgcgaca actccaagaa caccctctac 240
ctccaaatga actccctgcg ggccgaggat accgccgtct actactgcg caaagtggaa 300
ggttcaggat cgctggacta ctggggacag ggtactctcg tgaccgtgct atcggggcga 360
ggaggttccg gcggtggcgg ctccggcggc ggagggtcgg agatcgtgat gaccagagc 420
cctggtactc tgagcctttc gccgggagaa agggccaccc tgcctgccg cgcttcccaa 480
tccgtgtcct ccgcgtactt ggcgtggtac cagcagaagc cgggacagcc ccctcggtg 540
ctgatcagcg gggccagcac ccgggcaacc ggaatcccag acagattcgg gggttccggc 600
agcggcacag atttcaccct gactatttcg aggttggagc ccgaggactt tgcggtgtat 660
tactgtcagc actacgggtc gtcctttaat ggctccagcc tgttcacgtt cggacagggg 720
acccgcctgg aaatcaag 738

<210> 476

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 476

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Val Glu Gly Ser Gly Ser Leu Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

_SL

<210> 477
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 477
Glu Ile Val Met Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ala
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Arg Leu Leu
35 40 45

Ile Ser Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Asp Arg Phe Gly
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln His Tyr Gly Ser Ser Phe
85 90 95

Asn Gly Ser Ser Leu Phe Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile
100 105 110

Lys

<210> 478
<211> 241
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 478
Glu Val Gln Leu Val Glu Thr Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ile Thr Phe Ser Arg Tyr
20 25 30

Pro Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Ser Asp Ser Gly Val Ser Thr Tyr Tyr Ala Asp Ser Ala
Page 363

_SL

```

gccgactccg ccaagggacg cttcaccatt tcccgggaca actcgaagaa caccctgttc      240
ctccaaatga gtcacctccg ggacgaggat actgcagtgt actactgcgt gacccgcgcc      300
gggtccgagg cgtctgacat ttggggacag ggcactatgg tcaccgtgtc gtccggcgga      360
gggggctcgg gaggcggtgg cagcggagga ggagggtccg agatcgtgct gacccaatcc      420
ccggccaccc tctcgtgag ccctggagaa agggcaacct tgtcctgtcg cgcgagccag      480
tccgtgagca actccctggc ctggtaccag cagaagcccg gacaggctcc gagacttctg      540
atctacgacg cttcgagccg ggccactgga atccccgacc gcttttcggg gtccggctca      600
ggaaccgatt tcaccctgac aatctcacgg ctggagccag aggatttcgc catctattac      660
tgccagcagt tcggtacttc ctccggcctg actttcggag gcggcacgaa gtcgaaatc      720
aag                                                                    723

```

<210> 480
 <211> 118
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 480
 Glu Val Gln Leu Val Glu Thr Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ile Thr Phe Ser Arg Tyr
 20 25 30
 Pro Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Gly Ile Ser Asp Ser Gly Val Ser Thr Tyr Tyr Ala Asp Ser Ala
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe
 65 70 75 80
 Leu Gln Met Ser Ser Leu Arg Asp Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Val Thr Arg Ala Gly Ser Glu Ala Ser Asp Ile Trp Gly Gln Gly Thr
 100 105 110
 Met Val Thr Val Ser Ser
 115

<210> 481
 <211> 108
 <212> PRT
 <213> Artificial Sequence

_SL

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 481

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Asn Ser
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro
65 70 75 80

Glu Asp Phe Ala Ile Tyr Tyr Cys Gln Gln Phe Gly Thr Ser Ser Gly
85 90 95

Leu Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 482

<211> 248

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 482

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Ile Tyr Tyr Cys
85 90 95

_SL

Ala Arg Ala Thr Tyr Lys Arg Glu Leu Arg Tyr Tyr Tyr Gly Met Asp
100 105 110

Val Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Met Thr
130 135 140

Gln Ser Pro Gly Thr Val Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu
145 150 155 160

Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser Phe Leu Ala Trp Tyr
165 170 175

Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser
180 185 190

Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly
195 200 205

Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Ser Ala
210 215 220

Val Tyr Tyr Cys Gln Gln Tyr His Ser Ser Pro Ser Trp Thr Phe Gly
225 230 235 240

Gln Gly Thr Arg Leu Glu Ile Lys
245

<210> 483

<211> 744

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 483

caagtgcagc tcgtggaatc ggggtggcgga ctggtgcagc cggggggctc acttagactg 60

tcctgcgcgg ccagcggatt cactttctcc tcctacgcca tgtcctgggt cagacaggcc 120

cctggaaagg gcctggaatg ggtgtccgca atcagcggca gcggcggtc gacctattac 180

gcggattcag tgaagggcag attcaccatt tcccgggaca acgccaagaa ctccttgtac 240

cttcaaata gaactccctccg cgcggaagat accgcaatct actactgcgc tcggggccact 300

tacaagaggg aactgcgcta ctactacggg atggacgtct ggggccaggg aaccatggctc 360

accgtgtcca gcggaggagg aggatcggga ggaggcggtg gcgggggtgg agggtcggag 420

atcgtgatga cccagtcccc cggcactgtg tcgctgtccc cggcggaacg ggccaccctg 480

_SL

tcatgtcggg ccagccagtc agtgtcgtca agcttcctcg cctggtacca gcagaaaccg 540
ggacaagctc cccgcctgct gatctacgga gccagcagcc gggccaccgg tattcctgac 600
cggttctccg gttcggggtc cgggaccgac tttactctga ctatctctcg cctcgagcca 660
gaggactccg ccgtgtatta ctgccagcag taccactcct ccccgtcctg gacgttcgga 720
cagggcaciaa ggctggagat taag 744

<210> 484
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 484
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Ile Tyr Tyr Cys
85 90 95

Ala Arg Ala Thr Tyr Lys Arg Glu Leu Arg Tyr Tyr Tyr Gly Met Asp
100 105 110

Val Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 485
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 485
Glu Ile Val Met Thr Gln Ser Pro Gly Thr Val Ser Leu Ser Pro Gly
1 5 10 15

_SL

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
20 25 30

Phe Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80

Pro Glu Asp Ser Ala Val Tyr Tyr Cys Gln Gln Tyr His Ser Ser Pro
85 90 95

Ser Trp Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
100 105

<210> 486
<211> 248
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 486
Glu Val Gln Leu Val Glu Thr Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Thr Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ala Thr Tyr Lys Arg Glu Leu Arg Tyr Tyr Tyr Gly Met Asp
100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly
115 120 125

_SL

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr
130 135 140

Gln Ser Pro Ser Thr Leu Ser Leu Ser Pro Gly Glu Ser Ala Thr Leu
145 150 155 160

Ser Cys Arg Ala Ser Gln Ser Val Ser Thr Thr Phe Leu Ala Trp Tyr
165 170 175

Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ser Ser
180 185 190

Asn Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly
195 200 205

Thr Asp Phe Thr Leu Thr Ile Arg Arg Leu Glu Pro Glu Asp Phe Ala
210 215 220

Val Tyr Tyr Cys Gln Gln Tyr His Ser Ser Pro Ser Trp Thr Phe Gly
225 230 235 240

Gln Gly Thr Lys Val Glu Ile Lys
245

<210> 487

<211> 744

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 487

gaggtgcagc ttgtggaac cgggtggcga ctggtgcagc ccggaggaag cctcaggctg	60
tcctgcgccg cgtccggctt caccttctcc tcgtacgcca tgtcctgggt ccgccaggcc	120
cccggaaagg gcctggaatg ggtgtccgcc atctctggaa gcggaggttc cacgtactac	180
gcggacagcg tcaaggaag gttcacaatc tcccgcgata attcgaagaa cactctgtac	240
cttcaaataa acaccctgaa ggccgaggac actgctgtgt actactgctg acggggccacc	300
tacaagagag agctccggta ctactacgga atggacgtct ggggccaggg aactactgtg	360
accgtgtcct cgggaggggg tggctccggg gggggcggct ccggcggagg cggttccgag	420
attgtgctga ccagtcacc ttcaactctg tcgctgtccc cgggagagag cgctactctg	480
agctgccggg ccagccagtc cgtgtccacc accttcctcg cctggtatca gcagaagccg	540
gggcaggcac cagggtcttt gatctacggg tcaagcaaca gagcgaccgg aattcctgac	600
cgcttctcgg ggagcggttc aggcaccgac ttcaccctga ctatccggcg cctggaaccc	660
gaagatttcg ccgtgtatta ctgtcaacag taccactcct cgccgtcctg gacctttggc	720

caaggaacca aagtggaaat caag

<210> 488
 <211> 124
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 488
 Glu Val Gln Leu Val Glu Thr Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Thr Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Ala Thr Tyr Lys Arg Glu Leu Arg Tyr Tyr Tyr Gly Met Asp
 100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 489
 <211> 109
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 489
 Glu Ile Val Leu Thr Gln Ser Pro Ser Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15

Glu Ser Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Thr Thr
 20 25 30

Phe Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
 35 40 45

_SL

Ile Tyr Gly Ser Ser Asn Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Arg Arg Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr His Ser Ser Pro
85 90 95

Ser Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 490

<211> 239

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 490

Glu Val Gln Leu Val Glu Thr Gly Gly Gly Leu Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Ser Trp Asn Ser Gly Ser Ile Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Asp Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Val Gly Lys Ala Val Pro Asp Val Trp Gly Gln Gly Thr Thr
100 105 110

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
115 120 125

Gly Gly Gly Ser Asp Ile Val Met Thr Gln Thr Pro Ser Ser Leu Ser
130 135 140

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser
145 150 155 160

Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln^{-SL} Lys Pro Gly Lys Ala Pro
165 170 175

Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser
180 185 190

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
195 200 205

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr
210 215 220

Ser Thr Pro Tyr Ser Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
225 230 235

<210> 491
<211> 717
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 491
gaagtgcagc tcgtggaaac tggaggtgga ctcgtgcagc ctggacggtc gctgcggtcg 60
agctgcgctg catccggctt caccttcgac gattatgcca tgcactgggt cagacaggcg 120
ccaggaagg gacttgagtg ggtgtccggt atcagctgga atagcggctc aatcggatac 180
gcggactccg tgaagggaag gttcaccatt tcccgcgaca acgccaagaa ctccctgtac 240
ttgcaaatga acagcctccg ggatgaggac actgccgtgt actactgcgc ccgcgtcgga 300
aaagctgtgc ccgacgtctg gggccaggga accactgtga ccgtgtccag cggcgggggt 360
ggatcgggcg gtggagggtc cgggtggagg ggctcagata ttgtgatgac ccagaccccc 420
tcgtccctgt ccgcctcggg cggcgaccgc gtgactatca catgtagagc ctgcagagc 480
atctccagct acctgaactg gtatcagcag aagccgggga agggcccgaa gtcctgatc 540
tacgcggcat catcactgca atcgggagtg ccgagccggt tttccgggtc cggctccggc 600
accgacttca cgctgacat ttcttcctg caaccgagg acttcgccac ttactactgc 660
cagcagtcct actccacccc ttactccttc ggccaaggaa ccaggctgga aatcaag 717

<210> 492
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 492
Glu Val Gln Leu Val Glu Thr Gly Gly Gly Leu Val Gln Pro Gly Arg

1 5 10 ^{-SL} 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
 20 25 30
 Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Gly Ile Ser Trp Asn Ser Gly Ser Ile Gly Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Asp Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Val Gly Lys Ala Val Pro Asp Val Trp Gly Gln Gly Thr Thr
 100 105 110
 Val Thr Val Ser Ser
 115

<210> 493
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 493
 Asp Ile Val Met Thr Gln Thr Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Tyr
 85 90 95

Ser Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
 100 105

_SL

<210> 494
<211> 246
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 494
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30

Ala Met His Trp Val Arg Gln Arg Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Ser Ile Asn Trp Lys Gly Asn Ser Leu Ala Tyr Gly Asp Ser Val
50 55 60

Lys Gly Arg Phe Ala Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Phe
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Ser His Gln Gly Val Ala Tyr Tyr Asn Tyr Ala Met Asp Val Trp
100 105 110

Gly Arg Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser
130 135 140

Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
145 150 155 160

Arg Ala Thr Gln Ser Ile Gly Ser Ser Phe Leu Ala Trp Tyr Gln Gln
165 170 175

Arg Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Gln Arg
180 185 190

Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Arg Gly Ser Gly Thr Asp
195 200 205

Phe Thr Leu Thr Ile Ser Arg Val Glu Pro Glu Asp Ser Ala Val Tyr
210 215 220

_SL

Tyr Cys Gln His Tyr Glu Ser Ser Pro Ser Trp Thr Phe Gly Gln Gly
225 230 235 240

Thr Lys Val Glu Ile Lys
245

<210> 495
<211> 738
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 495
gaagtgcagc tcgtggagag cgggggagga ttggtgcagc ccggaaggtc cctgcggctc 60
tcctgcactg cgtctggctt caccttcgac gactacgca tgcactgggt cagacagcgc 120
ccgggaaagg gcctggaatg ggtcgcctca atcaactgga agggaaactc cctggcctat 180
ggcgacagcg tgaagggccg cttcgccatt tcgcgcgaca acgccaagaa caccgtgttt 240
ctgcaaatga attccctgcg gaccgaggat accgctgtgt actactgcg cagccaccag 300
ggcgtggcat actataacta cgccatggac gtgtggggaa gagggacgct cgtcaccgtg 360
tcctccgggg gcggtggatc ggggtggagga ggaagcgggt gcgggggcag cgaaatcgtg 420
ctgactcaga gcccgggaac tctttcactg tccccgggag aacggggccac tctctcgtgc 480
cggggcacc agtccatcgg ctctccttc cttgcctggt accagcagag gccaggacag 540
gcgccccgcc tgctgatcta cgggtgcttc caacgcgcca ctggcattcc tgaccggttc 600
agcggcagag ggtcgggaac cgatttcaca ctgaccattt cccgggtgga gccgaagat 660
tcggcagtct actactgtca gcattacgag tcctcccctt catggacctt cgggtcaaggg 720
accaaagtgg agatcaag 738

<210> 496
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 496
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30

Ala Met His Trp Val Arg Gln Arg Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

_SL

Ala Ser Ile Asn Trp Lys Gly Asn Ser Leu Ala Tyr Gly Asp Ser Val
50 55 60

Lys Gly Arg Phe Ala Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Phe
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Ser His Gln Gly Val Ala Tyr Tyr Asn Tyr Ala Met Asp Val Trp
100 105 110

Gly Arg Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 497

<211> 109

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 497

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Thr Gln Ser Ile Gly Ser Ser
20 25 30

Phe Leu Ala Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Gly Ala Ser Gln Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60

Gly Arg Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Val Glu
65 70 75 80

Pro Glu Asp Ser Ala Val Tyr Tyr Cys Gln His Tyr Glu Ser Ser Pro
85 90 95

Ser Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 498

<211> 241

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial ^{_SL}Sequence: Synthetic polypeptide"

<400> 498

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Val Val Arg Asp Gly Met Asp Val Trp Gly Gln Gly Thr Thr
100 105 110

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
115 120 125

Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
130 135 140

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
145 150 155 160

Val Ser Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala
165 170 175

Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro
180 185 190

Asp Arg Phe Ser Gly Asn Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
195 200 205

Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr
210 215 220

Gly Ser Pro Pro Arg Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile
225 230 235 240

Lys

_SL

<210> 499
<211> 723
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 499
gaggtgcagt tggtcgaaag cgggggcggt cttgtgcagc ctggcggatc actgcggtg 60
tcctgcgcgg catcaggctt cacgttttct tcctacgcca tgcctgggt ggcgcaggcc 120
cctggaaagg gactggaatg ggtgtccgag atttcgggt cggcgaggag cacctactac 180
gccgattccg tgaagggccg cttcactatc tcgcgggaca actccaagaa caccctctac 240
ctccaaatga atagcctgcg ggccgaggat accgccgtct actattgcgc taaggctgtg 300
cgcgacggaa tggacgtgtg gggacagggt accaccgtga cagtgtcctc ggggggaggc 360
ggtagcggcg gaggaggaag cgggtggtgga ggttccgaga ttgtgctgac tcaatcacc 420
gcgaccctga gcctgtccc cggcgaaagg gccactctgt cctgtcgggc cagccaatca 480
gtctcctcct cgtacctggc ctggtaccag cagaagccag gacaggctcc gagactcctt 540
atctatggcg catcctccc cgccaccgga atcccggata ggttctcggg aaacggatcg 600
gggaccgact tcactctcac catctcccgg ctggaaccgg aggacttcgc cgtgtactac 660
tgccagcagt acggcagccc gcctagattc actttcggcc cgggcaccaa agtggacatc 720
aag 723

<210> 500
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 500
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

_SL

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Val Val Arg Asp Gly Met Asp Val Trp Gly Gln Gly Thr Thr
100 105 110

Val Thr Val Ser Ser
115

<210> 501
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 501
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60

Gly Asn Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Pro Pro
85 90 95

Arg Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 502
<211> 242
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 502
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
Page 380

_SL

<400> 503
gaagtgcagc tgctggagtc cggcgggtgga ttggtgcaac cgggggggata gctcagactg 60
tcctgtgcgg cgtcaggctt caccttctcg agctacgcca tgtcatgggt cagacaggcc 120
cctggaaagg gtctggaatg ggtgtccgcc atttccggga gcgggggata tacatactac 180
gccgatagcg tgaagggccg cttcaccatt tcccgggaca actccaagaa cactctctat 240
ctgcaaatga actccctccg cgctgaggac actgccgtgt actactgcgc caaaatccct 300
cagaccggca ccttcgacta ctggggacag gggactctgg tcaccgtcag cagcgggtggc 360
ggaggttcgg ggggaggagg aagcggcggc ggagggtccg agattgtgct gaccagtgca 420
cccggcactt tgtccctgtc gcctggagaa agggccaccc tttcctgccg ggcattccaa 480
tccgtgtcct cctcgtacct ggcttggtac cagcagaggc ccggacaggc cccacggctt 540
ctgatctacg gagcaagcag ccgcgcgacc ggtatcccg accggttttc gggctcgggc 600
tcaggaactg acttcaccct caccatctcc cgcctggaac ccgaagattt cgctgtgtat 660
tactgccagc actacggcag ctccccgtcc tggacgttcg gccagggaac tcggctggag 720
atcaag 726

<210> 504
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 504
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Ile Pro Gln Thr Gly Thr Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

_SL

Leu Val Thr Val Ser Ser
115

<210> 505
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 505
Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln His Tyr Gly Ser Ser Pro
85 90 95

Ser Trp Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
100 105

<210> 506
<211> 248
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 506
Glu Val Gln Leu Val Glu Thr Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

_SL

Lys Gly Arg Phe Thr Met Ser Arg Glu Asn Asp Lys Asn Ser Val Phe
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Val Glu Asp Thr Gly Val Tyr Tyr Cys
85 90 95

Ala Arg Ala Asn Tyr Lys Arg Glu Leu Arg Tyr Tyr Tyr Gly Met Asp
100 105 110

Val Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Met Thr
130 135 140

Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Ser Ala Thr Leu
145 150 155 160

Ser Cys Arg Ala Ser Gln Arg Val Ala Ser Asn Tyr Leu Ala Trp Tyr
165 170 175

Gln His Lys Pro Gly Gln Ala Pro Ser Leu Leu Ile Ser Gly Ala Ser
180 185 190

Ser Arg Ala Thr Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly
195 200 205

Thr Asp Phe Thr Leu Ala Ile Ser Arg Leu Glu Pro Glu Asp Ser Ala
210 215 220

Val Tyr Tyr Cys Gln His Tyr Asp Ser Ser Pro Ser Trp Thr Phe Gly
225 230 235 240

Gln Gly Thr Lys Val Glu Ile Lys
245

<210> 507

<211> 744

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 507

gaagtgaac tgggtggaac cgggtggagga ctctgtcagc ctggcggcag cctccggctg 60

agctgcgccg cttcgggatt caccttttcc tcctacgcga tgtcttggtt cagacaggcc 120

cccggaaagg ggctggaatg ggtgtcagcc atctccggct cgggcggatc aacgtactac 180

gccgactccg tgaaaggccg gttcaccatg tcgcgcgaga atgacaagaa ctccgtgttc 240

_SL

ctgcaaatga actccctgag ggtggaggac accggagtgt actattgtgc gcgcgccaac 300
tacaagagag agctgcggta ctactacgga atggacgtct ggggacaggg aactatggtg 360
accgtgtcat ccggtggagg gggaagcggc ggtggaggca gcgggggcgg gggttcagaa 420
attgtcatga cccagtcccc gggaactctt tccctctccc ccggggaatc cgcgactttg 480
tcctgccggg ccagccagcg cgtggcctcg aactacctcg catggtacca gcataagcca 540
ggccaagccc cttccctgct gatttccggg gctagcagcc gcgccactgg cgtgccggat 600
aggttctcgg gaagcggctc gggtagcgat ttcaccctgg caatctcgcg gctggaaccg 660
gaggattcgg ccgtgtacta ctgccagcac tatgactcat cccctcctg gacattcgga 720
cagggcacca aggtcgagat caag 744

<210> 508

<211> 124

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 508

Glu Val Gln Leu Val Glu Thr Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Met Ser Arg Glu Asn Asp Lys Asn Ser Val Phe
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Val Glu Asp Thr Gly Val Tyr Tyr Cys
85 90 95

Ala Arg Ala Asn Tyr Lys Arg Glu Leu Arg Tyr Tyr Tyr Gly Met Asp
100 105 110

Val Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 509

<211> 109

<212> PRT

<213> Artificial Sequence

_SL

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 509

Glu Ile Val Met Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Ser Ala Thr Leu Ser Cys Arg Ala Ser Gln Arg Val Ala Ser Asn
20 25 30

Tyr Leu Ala Trp Tyr Gln His Lys Pro Gly Gln Ala Pro Ser Leu Leu
35 40 45

Ile Ser Gly Ala Ser Ser Arg Ala Thr Gly Val Pro Asp Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Ala Ile Ser Arg Leu Glu
65 70 75 80

Pro Glu Asp Ser Ala Val Tyr Tyr Cys Gln His Tyr Asp Ser Ser Pro
85 90 95

Ser Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 510

<211> 244

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 510

Glu Val Gln Leu Leu Glu Thr Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser Ser Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

_SL

Ala Lys Ala Leu Val Gly Ala Thr Gly Ala Phe Asp Ile Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly
130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala
145 150 155 160

Ser Gln Ser Leu Ser Ser Asn Phe Leu Ala Trp Tyr Gln Gln Lys Pro
165 170 175

Gly Gln Ala Pro Gly Leu Leu Ile Tyr Gly Ala Ser Asn Trp Ala Thr
180 185 190

Gly Thr Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
195 200 205

Leu Thr Ile Thr Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys
210 215 220

Gln Tyr Tyr Gly Thr Ser Pro Met Tyr Thr Phe Gly Gln Gly Thr Lys
225 230 235 240

Val Glu Ile Lys

<210> 511

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 511

gaagtgcagc tgctcgaac cgggtggaggg ctggtgcagc cagggggctc cctgaggctt 60

tcatgcgccg ctagcggatt ctccttctcc tcttacgcca tgtcgtgggt ccgccaagcc 120

cctggaaaag gcctggaatg ggtgtccgcg atttccggga gcggaggttc gacctattac 180

gccgactccg tgaagggccg ctttaccatc tcccgggata actccaagaa cactctgtac 240

ctccaaatga actcgctgag agccgaggac accgccgtgt attactgcgc gaaggcgctg 300

gtcggcgcca ctggggcatt cgacatctgg ggacagggaa ctcttgtagc cgtgtcgagc 360

ggaggcggcg gctccggcgg aggagggagc gggggcgggtg gttccgaaat cgtgttgact 420

cagtccccgg gaaccctgag cttgtcaccg ggggagcggg ccactctctc ctgtcgcgcc 480

_SL

tcccaatcgc tctcatccaa tttcctggcc tggtagaccaga	540
agaagcccgg acaggccccg	
ggcctgctca tctacggcgc ttcaaactgg gcaacgggaa cccctgacg	600
gttcagcgga	
agcggtacgg gtactgactt taccctgacc atcaccagac	660
tggaaccgga ggacttcgcc	
gtgtactact gccagtacta cggcacctcc cccatgtaca cattcggaca	720
gggtaccaag	
gtcgagatta ag	732

<210> 512
 <211> 120
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 512
 Glu Val Gln Leu Leu Glu Thr Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser Ser Tyr
 20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Ala Leu Val Gly Ala Thr Gly Ala Phe Asp Ile Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 513
 <211> 109
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 513
 Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15

_SL

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Leu Ser Ser Asn
20 25 30

Phe Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Gly Leu Leu
35 40 45

Ile Tyr Gly Ala Ser Asn Trp Ala Thr Gly Thr Pro Asp Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Thr Arg Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Tyr Tyr Gly Thr Ser Pro
85 90 95

Met Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 514
<211> 244
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 514
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Val Leu Trp Phe Gly Glu Gly Phe Asp Pro Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
115 120 125

Gly Gly Gly Ser Asp Ile Val Leu Thr Gln ^{-SL} Ser Pro Leu Ser Leu Pro
 130 135 140
 Val Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser
 145 150 155 160
 Leu Leu His Ser Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys
 165 170 175
 Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala
 180 185 190
 Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
 195 200 205
 Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
 210 215 220
 Cys Met Gln Ala Leu Gln Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys
 225 230 235 240
 Val Asp Ile Lys

<210> 515
 <211> 733
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 515
 gaagtgcagc tgcttgagag cgggtggaggt ctggtgcagc ccgggggatc actgcgcctg 60
 tcctgtgccc cgtccggttt cactttctcc tcgtacgcca tgtcgtgggt cagacaggca 120
 ccgggaaagg gactggaatg ggtgtcagcc atttcgggtt cggggggcag cacctactac 180
 gctgactccg tgaagggccg gttcaccatt tcccgcgaca actccaagaa caccttgtag 240
 ctccaaatga actccctgcg ggccgaagat accgccgtgt attactgcgt gctgtgggtc 300
 ggagagggat tcgaccctg gggacaagga aactcgtga ctgtgtcatc cggcggaggc 360
 ggagcgggtg gcggcggttc cggcgccggc ggatctgaca tcgtgttgac ccagtcccct 420
 ctgagcctgc cggtcactcc tggcgaacca gccagcatct cctgccggtc gagccagtcc 480
 ctctgcact ccaatgggta caactacctc gatttggtatc tgcaaaagcc gggccagagc 540
 cccagctgc tgatctacct tgggtcaaac cgcgcttccg ggggtgcctga tagattctcc 600
 gggtcgggga gcggaaccga ctttacctg aaaatctcga ggggtggaggc cgaggacgtc 660
 ggagtgtact actgcatgca ggcgtccag actcccctga ccttcggagg aggaacgaag 720
 gtcgacatca aga 733

_SL

<210> 516
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 516
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Val Leu Trp Phe Gly Glu Gly Phe Asp Pro Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 517
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 517
Asp Ile Val Leu Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
1 5 10 15

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser
20 25 30

Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg^{-SL} Ala Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala
85 90 95

Leu Gln Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Asp Ile Lys
100 105 110

<210> 518

<211> 251

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 518

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Val Gly Tyr Asp Ser Ser Gly Tyr Tyr Arg Asp Tyr Tyr Gly
100 105 110

Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly
115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val
130 135 140

Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala
145 150 155 160

Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser Tyr Leu Ala
Page 392

165 170^{-SL} 175

Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly
180 185 190

Thr Ser Ser Arg Ala Thr Gly Ile Ser Asp Arg Phe Ser Gly Ser Gly
195 200 205

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp
210 215 220

Phe Ala Val Tyr Tyr Cys Gln His Tyr Gly Asn Ser Pro Pro Lys Phe
225 230 235 240

Thr Phe Gly Pro Gly Thr Lys Leu Glu Ile Lys
245 250

<210> 519
<211> 753
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 519
caagtgcagc tcgtggagtc aggcggagga ctggtgcagc ccgggggctc cctgagactt 60
tcctgcgcg catcgggttt taccttctcc tcctatgcta tgtcctgggt gcgccaggcc 120
ccgggaaagg gactggaatg ggtgtccgca atcagcggta gcgggggctc aacatactac 180
gccgactccg tcaagggctc cttcactatt tcccgggaca actccaagaa taccctgtac 240
ctccaaatga acagcctcag ggccgaggat actgccgtgt actactgcg caaagtcgga 300
tacgatagct ccggttacta ccgggactac tacggaatgg acgtgtgggg acagggcacc 360
accgtgaccg tgtcaagcgg cggaggcggg tcaggagggg gaggctccgg cggaggaggg 420
tccgaaatcg tcctgactca gtcgcctggc actctgtcgt tgtccccggg ggagcgcgct 480
accctgtcgt gtcgggctc gcagtccgtg tcgagctcct acctcgctg gtaccagcag 540
aagcccggac agggccctag acttctgata tacggcactt cttcacgcgc caccgggata 600
agcgacaggt tcagcggctc cggctccggg accgacttca ccctgaccat tagccggctg 660
gagcctgaag atttcgccgt gtattactgc caacactacg gaaactcgcc gccaaagtgc 720
acgttcggac ccggaaccaa gctggaaatc aag 753

<210> 520
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<221> source

_SL

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 520
 Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Val Gly Tyr Asp Ser Ser Gly Tyr Tyr Arg Asp Tyr Tyr Gly
 100 105 110

Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

<210> 521
 <211> 110
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 521
 Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
 20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
 35 40 45

Ile Tyr Gly Thr Ser Ser Arg Ala Thr Gly Ile Ser Asp Arg Phe Ser
 50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
 65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln His Tyr Gly Asn Ser Pro

85 90 _SL 95

Pro Lys Phe Thr Phe Gly Pro Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 522
<211> 246
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 522
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Met Gly Trp Ser Ser Gly Tyr Leu Gly Ala Phe Asp Ile Trp
100 105 110

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser
130 135 140

Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
145 150 155 160

Arg Ala Ser Gln Ser Val Ala Ser Ser Phe Leu Ala Trp Tyr Gln Gln
165 170 175

Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Gly Arg
180 185 190

Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
195 200 205

_SL

Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr
210 215 220

Tyr Cys Gln His Tyr Gly Gly Ser Pro Arg Leu Thr Phe Gly Gly Gly
225 230 235 240

Thr Lys Val Asp Ile Lys
245

<210> 523
<211> 739
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 523
gaagtccaac tggtggagtc cgggggaggg ctcgtgcagc ccggaggcag ccttcggctg 60
tcgtgcgccg cctccgggtt cacgttctca tcctacgcga tgtcgtgggt cagacaggca 120
ccaggaaagg gactggaatg ggtgtccgcc attagcggct ccggcggtag cacctactat 180
gccgactcag tgaagggaag gttcactatc tcccgcgaca acagcaagaa caccctgtac 240
ctccaaatga actctctgcg ggccgaggat accgcggtgt actattgcgc caagatgggt 300
tggtccagcg gatacttggg agccttcgac atttggggac agggcactac tgtgaccgtg 360
tcctccgggg gtggcggatc gggaggcggc ggctcgggtg gaggggggtt cgaaatcgtg 420
ttgaccagcag caccgggaac cctctcgtg tccccgggag aacgggctac actgtcatgt 480
agagcgtccc agtccgtggc ttcctcgttc ctggcctggt accagcagaa gccgggacag 540
gcaccccgcc tgctcatcta cggagccagc ggccgggcga ccggcatccc tgaccgcttc 600
tccggttccg gctcgggcac cgactttact ctgaccatta gcaggcttga gcccgaggat 660
tttgccgtgt actactgcca aactacggg gggagccctc gcctgacctt cggaggcgga 720
actaaggtcg atatcaaaa 739

<210> 524
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 524
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
Page 396

20 25 _SL 30															
Ala	Met	Ser ₃₅	Trp	Val	Arg	Gln	Ala ₄₀	Pro	Gly	Lys	Gly	Leu ₄₅	Glu	Trp	Val
Ser	Ala ₅₀	Ile	Ser	Gly	Ser	Gly ₅₅	Gly	Ser	Thr	Tyr	Tyr ₆₀	Ala	Asp	Ser	Val
Lys ₆₅	Gly	Arg	Phe	Thr	Ile ₇₀	Ser	Arg	Asp	Asn	Ser ₇₅	Lys	Asn	Thr	Leu ₈₀	Tyr
Leu	Gln	Met	Asn	Ser ₈₅	Leu	Arg	Ala	Glu	Asp ₉₀	Thr	Ala	Val	Tyr	Tyr ₉₅	Cys
Ala	Lys	Met	Gly ₁₀₀	Trp	Ser	Ser	Gly	Tyr ₁₀₅	Leu	Gly	Ala	Phe	Asp ₁₁₀	Ile	Trp
Gly	Gln	Gly ₁₁₅	Thr	Thr	Val	Thr	Val ₁₂₀	Ser	Ser						

```
<210> 525
<211> 109
<212> PRT
<213> Artificial Sequence
```

```
<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"
```

<400> 525
Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ala Ser Ser
20 25 30

Phe Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Gly Ala Ser Gly Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln His Tyr Gly Gly Ser Pro
85 90 95

Arg Leu Thr Phe Gly Gly Gly Thr Lys Val Asp Ile Lys
100 105

$\langle 210 \rangle$	526
$\langle 211 \rangle$	122

_SL

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 526

Gln Ile Gln Leu Val Gln Ser Gly Pro Asp Leu Lys Lys Pro Gly Glu
1 5 10 15

Thr Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Phe
20 25 30

Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Phe Lys Trp Met
35 40 45

Ala Trp Ile Asn Thr Tyr Thr Gly Glu Ser Tyr Phe Ala Asp Asp Phe
50 55 60

Lys Gly Arg Phe Ala Phe Ser Val Glu Thr Ser Ala Thr Thr Ala Tyr
65 70 75 80

Leu Gln Ile Asn Asn Leu Lys Thr Glu Asp Thr Ala Thr Tyr Phe Cys
85 90 95

Ala Arg Gly Glu Ile Tyr Tyr Gly Tyr Asp Gly Gly Phe Ala Tyr Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ala
115 120

<210> 527

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 527

Asp Val Val Met Thr Gln Ser His Arg Phe Met Ser Thr Ser Val Gly
1 5 10 15

Asp Arg Val Ser Ile Thr Cys Arg Ala Ser Gln Asp Val Asn Thr Ala
20 25 30

Val Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
35 40 45

Phe Ser Ala Ser Tyr Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
50 55 60

Ser Gly Ser Gly Ala Asp Phe Thr Leu Thr^{-SL} Ile Ser Ser Val Gln Ala
65 70 75 80

Glu Asp Leu Ala Val Tyr Tyr Cys Gln Gln His Tyr Ser Thr Pro Trp
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Asp Ile Lys
100 105

<210> 528

<211> 244

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 528

Gln Ile Gln Leu Val Gln Ser Gly Pro Asp Leu Lys Lys Pro Gly Glu
1 5 10 15

Thr Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Phe
20 25 30

Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Phe Lys Trp Met
35 40 45

Ala Trp Ile Asn Thr Tyr Thr Gly Glu Ser Tyr Phe Ala Asp Asp Phe
50 55 60

Lys Gly Arg Phe Ala Phe Ser Val Glu Thr Ser Ala Thr Thr Ala Tyr
65 70 75 80

Leu Gln Ile Asn Asn Leu Lys Thr Glu Asp Thr Ala Thr Tyr Phe Cys
85 90 95

Ala Arg Gly Glu Ile Tyr Tyr Gly Tyr Asp Gly Gly Phe Ala Tyr Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ala Gly Gly Gly Gly Ser Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln Ser
130 135 140

His Arg Phe Met Ser Thr Ser Val Gly Asp Arg Val Ser Ile Thr Cys
145 150 155 160

Arg Ala Ser Gln Asp Val Asn Thr Ala Val Ser Trp Tyr Gln Gln Lys
165 170 175

Pro Gly Gln Ser Pro Lys Leu Leu Ile Phe Ser Ala Ser Tyr Arg Tyr
Page 399

_SL

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 530

Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Met Ser Leu Gly
1 5 10 15

Lys Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser Val Ser Val Ile
20 25 30

Gly Ala His Leu Ile His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Tyr Leu Ala Ser Asn Leu Glu Thr Gly Val Pro Ala
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asp
65 70 75 80

Pro Val Glu Glu Asp Asp Val Ala Ile Tyr Ser Cys Leu Gln Ser Arg
85 90 95

Ile Phe Pro Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 531

<211> 249

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 531

Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu
1 5 10 15

Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Ser Ile Asn Trp Val Lys Arg Ala Pro Gly Lys Gly Leu Lys Trp Met
35 40 45

Gly Trp Ile Asn Thr Glu Thr Arg Glu Pro Ala Tyr Ala Tyr Asp Phe
50 55 60

Arg Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Leu Gln Ile Asn Asn Leu Lys Tyr Glu Asp Thr Ala Thr Tyr Phe Cys
85 90 95

Ala Leu Asp Tyr Ser Tyr Ala Met Asp Tyr^{-SL} Trp Gly Gln Gly Thr Ser
 100 105 110
 Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly
 115 120 125
 Gly Gly Gly Ser Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys
 130 135 140
 Lys Pro Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr
 145 150 155 160
 Phe Thr Asp Tyr Ser Ile Asn Trp Val Lys Arg Ala Pro Gly Lys Gly
 165 170 175
 Leu Lys Trp Met Gly Trp Ile Asn Thr Glu Thr Arg Glu Pro Ala Tyr
 180 185 190
 Ala Tyr Asp Phe Arg Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala
 195 200 205
 Ser Thr Ala Tyr Leu Gln Ile Asn Asn Leu Lys Tyr Glu Asp Thr Ala
 210 215 220
 Thr Tyr Phe Cys Ala Leu Asp Tyr Ser Tyr Ala Met Asp Tyr Trp Gly
 225 230 235 240
 Gln Gly Thr Ser Val Thr Val Ser Ser
 245

<210> 532
 <211> 117
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 532
 Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu
 1 5 10 15

Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Arg His Tyr
 20 25 30

Ser Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met
 35 40 45

Gly Arg Ile Asn Thr Glu Ser Gly Val Pro Ile Tyr Ala Asp Asp Phe
 50 55 60

Lys Gly Arg Phe Ala Phe Ser Val Glu Thr Ser Ala Ser Thr Ala Tyr
 Page 402

_SL

Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Arg His Tyr
20 25 30

Ser Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met
35 40 45

Gly Arg Ile Asn Thr Glu Ser Gly Val Pro Ile Tyr Ala Asp Asp Phe
50 55 60

Lys Gly Arg Phe Ala Phe Ser Val Glu Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Leu Val Ile Asn Asn Leu Lys Asp Glu Asp Thr Ala Ser Tyr Phe Cys
85 90 95

Ser Asn Asp Tyr Leu Tyr Ser Leu Asp Phe Trp Gly Gln Gly Thr Ala
100 105 110

Leu Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly
115 120 125

Gly Gly Gly Ser Asp Ile Val Leu Thr Gln Ser Pro Pro Ser Leu Ala
130 135 140

Met Ser Leu Gly Lys Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser
145 150 155 160

Val Thr Ile Leu Gly Ser His Leu Ile Tyr Trp Tyr Gln Gln Lys Pro
165 170 175

Gly Gln Pro Pro Thr Leu Leu Ile Gln Leu Ala Ser Asn Val Gln Thr
180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Arg Thr Asp Phe Thr
195 200 205

Leu Thr Ile Asp Pro Val Glu Glu Asp Asp Val Ala Val Tyr Tyr Cys
210 215 220

Leu Gln Ser Arg Thr Ile Pro Arg Thr Phe Gly Gly Gly Thr Lys Leu
225 230 235 240

Glu Ile Lys

<210> 535

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<221> source

_SL

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 535
 Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu
 1 5 10 15

Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr His Tyr
 20 25 30

Ser Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met
 35 40 45

Gly Arg Ile Asn Thr Glu Thr Gly Glu Pro Leu Tyr Ala Asp Asp Phe
 50 55 60

Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Tyr
 65 70 75 80

Leu Val Ile Asn Asn Leu Lys Asn Glu Asp Thr Ala Thr Phe Phe Cys
 85 90 95

Ser Asn Asp Tyr Leu Tyr Ser Cys Asp Tyr Trp Gly Gln Gly Thr Thr
 100 105 110

Leu Thr Val Ser Ser
 115

<210> 536
 <211> 111
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 536
 Asp Ile Val Leu Thr Gln Ser Pro Pro Ser Leu Ala Met Ser Leu Gly
 1 5 10 15

Lys Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser Val Thr Ile Leu
 20 25 30

Gly Ser His Leu Ile Tyr Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
 35 40 45

Thr Leu Leu Ile Gln Leu Ala Ser Asn Val Gln Thr Gly Val Pro Ala
 50 55 60

Arg Phe Ser Gly Ser Gly Ser Arg Thr Asp Phe Thr Leu Thr Ile Asp
 65 70 75 80

Pro Val Glu Glu Asp Asp Val Ala Val Tyr Tyr Cys Leu Gln Ser Arg

85 90 _SL 95

Thr Ile Pro Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 537
<211> 243
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 537
Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu
1 5 10 15

Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr His Tyr
20 25 30

Ser Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met
35 40 45

Gly Arg Ile Asn Thr Glu Thr Gly Glu Pro Leu Tyr Ala Asp Asp Phe
50 55 60

Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Leu Val Ile Asn Asn Leu Lys Asn Glu Asp Thr Ala Thr Phe Phe Cys
85 90 95

Ser Asn Asp Tyr Leu Tyr Ser Cys Asp Tyr Trp Gly Gln Gly Thr Thr
100 105 110

Leu Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
115 120 125

Gly Gly Gly Ser Asp Ile Val Leu Thr Gln Ser Pro Pro Ser Leu Ala
130 135 140

Met Ser Leu Gly Lys Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser
145 150 155 160

Val Thr Ile Leu Gly Ser His Leu Ile Tyr Trp Tyr Gln Gln Lys Pro
165 170 175

Gly Gln Pro Pro Thr Leu Leu Ile Gln Leu Ala Ser Asn Val Gln Thr
180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Arg Thr Asp Phe Thr
195 200 205

_SL

Leu Thr Ile Asp Pro Val Glu Glu Asp Asp Val Ala Val Tyr Tyr Cys
210 215 220

Leu Gln Ser Arg Thr Ile Pro Arg Thr Phe Gly Gly Gly Thr Lys Leu
225 230 235 240

Glu Ile Lys

<210> 538
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 538
Asn His Gly Met Ser
1 5

<210> 539
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 539
Gly Ile Val Tyr Ser Gly Ser Thr Tyr Tyr Ala Ala Ser Val Lys Gly
1 5 10 15

<210> 540
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 540
His Gly Gly Glu Ser Asp Val
1 5

<210> 541
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

_SL

<400> 541
Asn Tyr Ala Met Ser
1 5

<210> 542
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 542
Gly Ile Ser Arg Ser Gly Glu Asn Thr Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 543
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 543
Ser Pro Ala His Tyr Tyr Gly Gly Met Asp Val
1 5 10

<210> 544
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 544
Asp Tyr Ala Met His
1 5

<210> 545
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 545
Gly Ile Ser Trp Asn Ser Gly Ser Ile Gly Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 546
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 546
His Ser Phe Leu Ala Tyr
1 5

<210> 547
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 547
Asn Phe Gly Ile Asn
1 5

<210> 548
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 548
Trp Ile Asn Pro Lys Asn Asn Asn Thr Asn Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 549
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 549
Gly Pro Tyr Tyr Gln Ser Tyr Met Asp Val
1 5 10

<210> 550
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 550
Ser Asp Ala Met Thr
1 5

<210> 551
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 551
Val Ile Ser Gly Ser Gly Gly Thr Thr Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 552
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 552
Leu Asp Ser Ser Gly Tyr Tyr Tyr Ala Arg Gly Pro Arg Tyr
1 5 10

<210> 553
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 553
Asn Tyr Gly Ile Thr
1 5

<210> 554
<211> 17

_SL

<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 554
Trp Ile Ser Ala Tyr Asn Gly Asn Thr Asn Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 555
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 555
Gly Pro Tyr Tyr Tyr Tyr Met Asp Val
1 5

<210> 556
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 556
Asp Tyr Tyr Met Ser
1 5

<210> 557
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 557
Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 558
<211> 8

_SL

<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 558
Glu Ser Gly Asp Gly Met Asp Val
1 5

<210> 559
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 559
Tyr Ile Ser Ser Ser Gly Asn Thr Ile Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 560
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 560
Ser Thr Met Val Arg Glu Asp Tyr
1 5

<210> 561
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 561
Ser Ser Tyr Tyr Tyr Trp Gly
1 5

<210> 562
<211> 16
<212> PRT
<213> Artificial Sequence

<220>

_SL

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 562

Ser Ile Tyr Tyr Ser Gly Ser Ala Tyr Tyr Asn Pro Ser Leu Lys Ser
1 5 10 15

<210> 563

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 563

His Trp Gln Glu Trp Pro Asp Ala Phe Asp Ile
1 5 10

<210> 564

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 564

Thr Ser Gly Met Cys Val Ser
1 5

<210> 565

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 565

Arg Ile Asp Trp Asp Glu Asp Lys Phe Tyr Ser Thr Ser Leu Lys Thr
1 5 10 15

<210> 566

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 566

Ser Gly Ala Gly Gly Thr Ser Ala Thr Ala Phe Asp Ile
1 5 10

_SL

<210> 567
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 567
Ser Tyr Ser Met Asn
1 5

<210> 568
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 568
Ser Ile Ser Ser Ser Ser Tyr Ile Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 569
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 569
Thr Ile Ala Ala Val Tyr Ala Phe Asp Ile
1 5 10

<210> 570
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 570
Asp Leu Arg Gly Ala Phe Asp Ile
1 5

<210> 571
<211> 5
<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 571

Ser His Tyr Ile His
1 5

<210> 572

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 572

Met Ile Asn Pro Ser Gly Gly Val Thr Ala Tyr Ser Gln Thr Leu Gln
1 5 10 15

Gly

<210> 573

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 573

Glu Gly Ser Gly Ser Gly Trp Tyr Phe Asp Phe
1 5 10

<210> 574

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 574

Ser Gly Gly Tyr Tyr Trp Ser
1 5

<210> 575

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"
 <400> 575
 Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser Leu Lys Ser
 1 5 10 15

<210> 576
 <211> 13
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 576
 Ala Gly Ile Ala Ala Arg Leu Arg Gly Ala Phe Asp Ile
 1 5 10

<210> 577
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 577
 Ser Tyr Ala Ile Ser
 1 5

<210> 578
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 578
 Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe Gln
 1 5 10 15

Gly

<210> 579
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 579

Arg Gly Gly Tyr Gln Leu Leu Arg Trp Asp^{-SL} Val Gly Leu Leu Arg Ser
1 5 10 15

Ala Phe Asp Ile
20

<210> 580
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 580
Ser Asn Ser Ala Ala Trp Asn
1 5

<210> 581
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 581
Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Ser Phe Tyr Ala Ile Ser Leu
1 5 10 15

Lys Ser

<210> 582
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 582
Ser Ser Pro Glu Gly Leu Phe Leu Tyr Trp Phe Asp Pro
1 5 10

<210> 583
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 583

_SL

Ser Tyr Ala Met Ser
1 5

<210> 584
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 584
Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 585
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 585
Val Glu Gly Ser Gly Ser Leu Asp Tyr
1 5

<210> 586
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 586
Arg Tyr Pro Met Ser
1 5

<210> 587
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 587
Gly Ile Ser Asp Ser Gly Val Ser Thr Tyr Tyr Ala Asp Ser Ala Lys
1 5 10 15

Gly

<210> 588
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 588
Arg Ala Gly Ser Glu Ala Ser Asp Ile
1 5

<210> 589
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 589
Ala Thr Tyr Lys Arg Glu Leu Arg Tyr Tyr Tyr Gly Met Asp Val
1 5 10 15

<210> 590
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 590
Val Gly Lys Ala Val Pro Asp Val
1 5

<210> 591
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 591
Ser Ile Asn Trp Lys Gly Asn Ser Leu Ala Tyr Gly Asp Ser Val Lys
1 5 10 15

Gly

_SL

<210> 592
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 592
His Gln Gly Val Ala Tyr Tyr Asn Tyr Ala Met Asp Val
1 5 10

<210> 593
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 593
Val Val Arg Asp Gly Met Asp Val
1 5

<210> 594
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 594
Ile Pro Gln Thr Gly Thr Phe Asp Tyr
1 5

<210> 595
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 595
Ala Asn Tyr Lys Arg Glu Leu Arg Tyr Tyr Tyr Gly Met Asp Val
1 5 10 15

<210> 596
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

_SL

peptide"

<400> 596

Ala Leu Val Gly Ala Thr Gly Ala Phe Asp Ile
1 5 10

<210> 597

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 597

Trp Phe Gly Glu Gly Phe Asp Pro
1 5

<210> 598

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 598

Val Gly Tyr Asp Ser Ser Gly Tyr Tyr Arg Asp Tyr Tyr Gly Met Asp
1 5 10 15

Val

<210> 599

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 599

Met Gly Trp Ser Ser Gly Tyr Leu Gly Ala Phe Asp Ile
1 5 10

<210> 600

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 600

Asn Phe Gly Met Asn

1

5

<210> 601
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 601
Trp Ile Asn Thr Tyr Thr Gly Glu Ser Tyr Phe Ala Asp Asp Phe Lys
1 5 10 15

Gly

<210> 602
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 602
Gly Glu Ile Tyr Tyr Gly Tyr Asp Gly Gly Phe Ala Tyr
1 5 10

<210> 603
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 603
Asp Tyr Ser Ile Asn
1 5

<210> 604
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 604
Trp Ile Asn Thr Glu Thr Arg Glu Pro Ala Tyr Ala Tyr Asp Phe Arg
1 5 10 15

Gly

<210> 605
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 605
Asp Tyr Ser Tyr Ala Met Asp Tyr
1 5

<210> 606
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 606
His Tyr Ser Met Asn
1 5

<210> 607
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 607
Arg Ile Asn Thr Glu Ser Gly Val Pro Ile Tyr Ala Asp Asp Phe Lys
1 5 10 15

Gly

<210> 608
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 608
Asp Tyr Leu Tyr Ser Leu Asp Phe
1 5

<210> 609

_SL

<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 609
Arg Ile Asn Thr Glu Thr Gly Glu Pro Leu Tyr Ala Asp Asp Phe Lys
1 5 10 15

Gly

<210> 610
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 610
Asp Tyr Leu Tyr Ser Cys Asp Tyr
1 5

<210> 611
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 611
Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn
1 5 10

<210> 612
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 612
Ala Ala Ser Ser Leu Gln Ser
1 5

<210> 613
<211> 9
<212> PRT
<213> Artificial Sequence

_SL

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 613
Gln Gln Ser Tyr Ser Thr Pro Tyr Thr
1 5

<210> 614
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 614
Arg Ala Ser Gln Ser Ile Ser Ser Ser Phe Leu Ala
1 5 10

<210> 615
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 615
Gly Ala Ser Arg Arg Ala Thr
1 5

<210> 616
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 616
Gln Gln Tyr His Ser Ser Pro Ser Trp Thr
1 5 10

<210> 617
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 617
Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr Asn Tyr Leu Asp
1 5 10 15

<210> 618
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 618
Leu Gly Ser Asn Arg Ala Ser
1 5

<210> 619
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 619
Met Gln Ala Leu Gln Thr Pro Tyr Thr
1 5

<210> 620
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 620
Lys Ser Ser Gln Ser Leu Leu Arg Asn Asp Gly Lys Thr Pro Leu Tyr
1 5 10 15

<210> 621
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 621
Glu Val Ser Asn Arg Phe Ser
1 5

<210> 622
<211> 8
<212> PRT
<213> Artificial Sequence

<220>

_SL

<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 622
Met Gln Asn Ile Gln Phe Pro Ser
1 5

<210> 623
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 623
Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr Asn Tyr Leu Asn
1 5 10 15

<210> 624
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 624
Leu Gly Ser Lys Arg Ala Ser
1 5

<210> 625
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 625
Gly Ala Ser Thr Leu Ala Ser
1 5

<210> 626
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 626
Gln Gln Ser Tyr Lys Arg Ala Ser
1 5

_SL

<210> 627
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 627
Arg Ser Ser Gln Ser Leu Leu Tyr Ser Asn Gly Tyr Asn Tyr Val Asp
1 5 10 15

<210> 628
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 628
Met Gln Gly Arg Gln Phe Pro Tyr Ser
1 5

<210> 629
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 629
Arg Ala Ser Gln Ser Val Ser Ser Asn Leu Ala
1 5 10

<210> 630
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 630
Gly Ala Ser Thr Arg Ala Ser
1 5

<210> 631
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide" ^{_SL}

<400> 631
Gln Gln Tyr Gly Ser Ser Leu Thr
1 5

<210> 632
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 632
Arg Ala Ser Gln Ser Val Ser Ser Lys Leu Ala
1 5 10

<210> 633

<400> 633
000

<210> 634

<400> 634
000

<210> 635

<400> 635
000

<210> 636
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 636
Gly Ala Ser Ile Arg Ala Thr
1 5

<210> 637
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 637
Gln Gln Tyr Gly Ser Ser Ser Trp Thr

1

5

<210> 638
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 638
Arg Ala Ser Gln Ser Val Gly Ser Thr Asn Leu Ala
1 5 10

<210> 639
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 639
Asp Ala Ser Asn Arg Ala Thr
1 5

<210> 640
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 640
Gln Gln Tyr Gly Ser Ser Pro Pro Trp Thr
1 5 10

<210> 641
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 641
Gln Gln Ser Tyr Thr Leu Ala
1 5

<210> 642
<211> 16
<212> PRT
<213> Artificial Sequence

_SL

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 642

Lys Ser Ser Glu Ser Leu Val His Asn Ser Gly Lys Thr Tyr Leu Asn
1 5 10 15

<210> 643

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 643

Glu Val Ser Asn Arg Asp Ser
1 5

<210> 644

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 644

Met Gln Gly Thr His Trp Pro Gly Thr
1 5

<210> 645

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 645

Gln Ala Ser Glu Asp Ile Asn Lys Phe Leu Asn
1 5 10

<210> 646

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 646

Asp Ala Ser Thr Leu Gln Thr
1 5

<210> 647
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 647
Gln Gln Tyr Glu Ser Leu Pro Leu Thr
1 5

<210> 648
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 648
Arg Ala Ser Gln Ser Val Gly Ser Asn Leu Ala
1 5 10

<210> 649
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 649
Gly Ala Ser Thr Arg Ala Thr
1 5

<210> 650
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 650
Gln Gln Tyr Asn Asp Trp Leu Pro Val Thr
1 5 10

<210> 651
<211> 12
<212> PRT
<213> Artificial Sequence

<220>

_SL

<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 651
Arg Ala Ser Gln Ser Ile Gly Ser Ser Ser Leu Ala
1 5 10

<210> 652
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 652
Gly Ala Ser Ser Arg Ala Ser
1 5

<210> 653
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 653
Gln Gln Tyr Ala Gly Ser Pro Pro Phe Thr
1 5 10

<210> 654
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 654
Lys Ala Ser Gln Asp Ile Asp Asp Ala Met Asn
1 5 10

<210> 655
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 655
Ser Ala Thr Ser Pro Val Pro
1 5

_SL

<210> 656
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 656
Leu Gln His Asp Asn Phe Pro Leu Thr
1 5

<210> 657
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 657
Arg Ala Ser Gln Asp Ile Tyr Asn Asn Leu Ala
1 5 10

<210> 658
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 658
Ala Ala Asn Lys Ser Gln Ser
1 5

<210> 659
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 659
Gln His Tyr Tyr Arg Phe Pro Tyr Ser
1 5

<210> 660
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic
peptide" _SL

<400> 660
Gly Gly Asn Asn Ile Gly Thr Lys Ser Val His
1 5 10

<210> 661
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 661
Asp Asp Ser Val Arg Pro Ser
1 5

<210> 662
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 662
Gln Val Trp Asp Ser Asp Ser Glu His Val Val
1 5 10

<210> 663
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 663
Ser Gly Asp Gly Leu Ser Lys Lys Tyr Val Ser
1 5 10

<210> 664
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 664
Arg Asp Lys Glu Arg Pro Ser
1 5

_SL

<210> 665
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 665
Gln Ala Trp Asp Asp Thr Thr Val Val
1 5

<210> 666
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 666
Arg Ala Ser Gln Gly Ile Arg Asn Trp Leu Ala
1 5 10

<210> 667
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 667
Ala Ala Ser Asn Leu Gln Ser
1 5

<210> 668
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 668
Gln Lys Tyr Asn Ser Ala Pro Phe Thr
1 5

<210> 669
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

_SL

peptide"

<400> 669

Gly Gly Asn Asn Ile Gly Ser Lys Ser Val His
1 5 10

<210> 670

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 670

Gly Lys Asn Asn Arg Pro Ser
1 5

<210> 671

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 671

Ser Ser Arg Asp Ser Ser Gly Asp His Leu Arg Val
1 5 10

<210> 672

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 672

Gln Gly Asp Ser Leu Gly Asn Tyr Tyr Ala Thr
1 5 10

<210> 673

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 673

Gly Thr Asn Asn Arg Pro Ser
1 5

<210> 674

_SL

<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 674
Asn Ser Arg Asp Ser Ser Gly His His Leu Leu
1 5 10

<210> 675
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 675
Arg Ala Ser Gln Ser Val Ser Ser Ala Tyr Leu Ala
1 5 10

<210> 676
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 676
Gln His Tyr Gly Ser Ser Phe Asn Gly Ser Ser Leu Phe Thr
1 5 10

<210> 677
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 677
Arg Ala Ser Gln Ser Val Ser Asn Ser Leu Ala
1 5 10

<210> 678
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

_SL

<400> 678
Asp Ala Ser Ser Arg Ala Thr
1 5

<210> 679
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 679
Gln Gln Phe Gly Thr Ser Ser Gly Leu Thr
1 5 10

<210> 680
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 680
Arg Ala Ser Gln Ser Val Ser Ser Ser Phe Leu Ala
1 5 10

<210> 681
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 681
Gly Ala Ser Ser Arg Ala Thr
1 5

<210> 682
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 682
Arg Ala Ser Gln Ser Val Ser Thr Thr Phe Leu Ala
1 5 10

<210> 683
<211> 7

_SL

<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 683
Gly Ser Ser Asn Arg Ala Thr
1 5

<210> 684
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 684
Gln Gln Ser Tyr Ser Thr Pro Tyr Ser
1 5

<210> 685
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 685
Arg Ala Thr Gln Ser Ile Gly Ser Ser Phe Leu Ala
1 5 10

<210> 686
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 686
Gly Ala Ser Gln Arg Ala Thr
1 5

<210> 687
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

_SL

<400> 687

Gln His Tyr Glu Ser Ser Pro Ser Trp Thr
1 5 10

<210> 688

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 688

Arg Ala Ser Gln Ser Val Ser Ser Ser Tyr Leu Ala
1 5 10

<210> 689

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 689

Gln Gln Tyr Gly Ser Pro Pro Arg Phe Thr
1 5 10

<210> 690

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 690

Gln His Tyr Gly Ser Ser Pro Ser Trp Thr
1 5 10

<210> 691

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 691

Arg Ala Ser Gln Arg Val Ala Ser Asn Tyr Leu Ala
1 5 10

<210> 692

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 692

Gln His Tyr Asp Ser Ser Pro Ser Trp Thr
1 5 10

<210> 693

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 693

Arg Ala Ser Gln Ser Leu Ser Ser Asn Phe Leu Ala
1 5 10

<210> 694

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 694

Gly Ala Ser Asn Trp Ala Thr
1 5

<210> 695

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 695

Gln Tyr Tyr Gly Thr Ser Pro Met Tyr Thr
1 5 10

<210> 696

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 696

Met Gln Ala Leu Gln Thr Pro Leu Thr _SL
1 5

<210> 697
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 697
Gly Thr Ser Ser Arg Ala Thr
1 5

<210> 698
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 698
Gln His Tyr Gly Asn Ser Pro Pro Lys Phe Thr
1 5 10

<210> 699
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 699
Arg Ala Ser Gln Ser Val Ala Ser Ser Phe Leu Ala
1 5 10

<210> 700
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 700
Gly Ala Ser Gly Arg Ala Thr
1 5

<210> 701
<211> 10
<212> PRT
<213> Artificial Sequence

_SL

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 701
Gln His Tyr Gly Gly Ser Pro Arg Leu Thr
1 5 10

<210> 702
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 702
Arg Ala Ser Gln Asp Val Asn Thr Ala Val Ser
1 5 10

<210> 703
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 703
Ser Ala Ser Tyr Arg Tyr Thr
1 5

<210> 704
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 704
Gln Gln His Tyr Ser Thr Pro Trp Thr
1 5

<210> 705
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 705
Arg Ala Ser Glu Ser Val Ser Val Ile Gly Ala His Leu Ile His
Page 444

1	5	10	15
<210> 706			
<211> 7			
<212> PRT			
<213> Artificial Sequence			
<220>			
<221> source			
<223> /note="Description of Artificial Sequence: Synthetic peptide"			
<400> 706			
Leu Ala Ser Asn Leu Glu Thr			
1	5		
<210> 707			
<211> 9			
<212> PRT			
<213> Artificial Sequence			
<220>			
<221> source			
<223> /note="Description of Artificial Sequence: Synthetic peptide"			
<400> 707			
Leu Gln Ser Arg Ile Phe Pro Arg Thr			
1	5		
<210> 708			
<211> 15			
<212> PRT			
<213> Artificial Sequence			
<220>			
<221> source			
<223> /note="Description of Artificial Sequence: Synthetic peptide"			
<400> 708			
Arg Ala Ser Glu Ser Val Thr Ile Leu Gly Ser His Leu Ile Tyr			
1	5	10	15
<210> 709			
<211> 7			
<212> PRT			
<213> Artificial Sequence			
<220>			
<221> source			
<223> /note="Description of Artificial Sequence: Synthetic peptide"			
<400> 709			
Leu Ala Ser Asn Val Gln Thr			
1	5		
<210> 710			
<211> 9			
<212> PRT			
<213> Artificial Sequence			

_SL

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 710

Leu Gln Ser Arg Thr Ile Pro Arg Thr
1 5

<210> 711

<400> 711

000

<210> 712

<400> 712

000

<210> 713

<400> 713

000

<210> 714

<400> 714

000

<210> 715

<400> 715

000

<210> 716

<400> 716

000

<210> 717

<400> 717

000

<210> 718

<400> 718

000

<210> 719

<400> 719

000

<210> 720

<400> 720

000

_SL

<210> 721

<400> 721
000

<210> 722

<400> 722
000

<210> 723

<400> 723
000

<210> 724

<211> 485

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 724

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val
20 25 30

Glu Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr
35 40 45

Thr Phe Thr Asp Tyr Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln
50 55 60

Gly Leu Glu Trp Met Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn
65 70 75 80

Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser
85 90 95

Ile Ser Thr Ala Tyr Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr
100 105 110

Ala Val Tyr Tyr Cys Ala Ser Gly Trp Asp Phe Asp Tyr Trp Gly Gln
115 120 125

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
130 135 140

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val Met
Page 447

145	150								-SL 155				160			
Thr	Gln	Ser	Pro	Ser 165	Ser	Leu	Ser	Ala	Ser 170	Val	Gly	Asp	Arg	Val 175	Thr	
Ile	Thr	Cys	Arg 180	Ala	Ser	Gln	Ser	Ile 185	Arg	Tyr	Tyr	Leu	Ser 190	Trp	Tyr	
Gln	Gln	Lys 195	Pro	Gly	Lys	Ala	Pro 200	Lys	Leu	Leu	Ile	Tyr 205	Thr	Ala	Ser	
Ile	Leu 210	Gln	Asn	Gly	Val	Pro 215	Ser	Arg	Phe	Ser	Gly 220	Ser	Gly	Ser	Gly	
Thr 225	Asp	Phe	Thr	Leu	Thr 230	Ile	Ser	Ser	Leu	Gln 235	Pro	Glu	Asp	Phe	Ala 240	
Thr	Tyr	Tyr	Cys	Leu 245	Gln	Thr	Tyr	Thr	Thr 250	Pro	Asp	Phe	Gly	Pro 255	Gly	
Thr	Lys	Val	Glu 260	Ile	Lys	Thr	Thr	Thr 265	Pro	Ala	Pro	Arg	Pro 270	Pro	Thr	
Pro	Ala	Pro 275	Thr	Ile	Ala	Ser	Gln 280	Pro	Leu	Ser	Leu	Arg 285	Pro	Glu	Ala	
Cys	Arg 290	Pro	Ala	Ala	Gly	Gly 295	Ala	Val	His	Thr	Arg 300	Gly	Leu	Asp	Phe	
Ala 305	Cys	Asp	Ile	Tyr	Ile 310	Trp	Ala	Pro	Leu	Ala 315	Gly	Thr	Cys	Gly	Val 320	
Leu	Leu	Leu	Ser	Leu 325	Val	Ile	Thr	Leu	Tyr 330	Cys	Lys	Arg	Gly	Arg 335	Lys	
Lys	Leu	Leu	Tyr 340	Ile	Phe	Lys	Gln	Pro 345	Phe	Met	Arg	Pro	Val 350	Gln	Thr	
Thr	Gln	Glu 355	Glu	Asp	Gly	Cys	Ser 360	Cys	Arg	Phe	Pro	Glu 365	Glu	Glu	Glu	
Gly	Gly 370	Cys	Glu	Leu	Arg	Val 375	Lys	Phe	Ser	Arg	Ser 380	Ala	Asp	Ala	Pro	
Ala 385	Tyr	Lys	Gln	Gly	Gln 390	Asn	Gln	Leu	Tyr	Asn 395	Glu	Leu	Asn	Leu	Gly 400	
Arg	Arg	Glu	Glu	Tyr 405	Asp	Val	Leu	Asp	Lys 410	Arg	Arg	Gly	Arg	Asp 415	Pro	
Glu	Met	Gly	Gly	Lys	Pro	Arg	Arg	Lys	Asn	Pro	Gln	Glu	Gly	Leu	Tyr	

_SL

420 425 430

Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly
 435 440 445

Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln
 450 455 460

Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln
 465 470 475 480

Ala Leu Pro Pro Arg
 485

<210> 725
 <211> 485
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 725
 Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
 1 5 10 15

His Ala Ala Arg Pro Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Val
 20 25 30

Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr
 35 40 45

Thr Phe Thr Gly Tyr Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln
 50 55 60

Gly Leu Glu Trp Met Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn
 65 70 75 80

Tyr Ala Gln Asn Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser
 85 90 95

Ile Ser Thr Ala Tyr Met Glu Leu Arg Arg Leu Arg Ser Asp Asp Thr
 100 105 110

Ala Val Tyr Tyr Cys Ala Ser Gly Trp Asp Phe Asp Tyr Trp Gly Gln
 115 120 125

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
 130 135 140

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Arg Met
 145 150 155 160

_SL

Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr
165 170 175

Ile Thr Cys Arg Ala Ser Gln Ser Ile Arg Tyr Tyr Leu Ser Trp Tyr
180 185 190

Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Thr Ala Ser
195 200 205

Ile Leu Gln Asn Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
210 215 220

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
225 230 235 240

Thr Tyr Tyr Cys Leu Gln Thr Tyr Thr Thr Pro Asp Phe Gly Pro Gly
245 250 255

Thr Lys Val Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr
260 265 270

Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala
275 280 285

Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe
290 295 300

Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val
305 310 315 320

Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys
325 330 335

Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr
340 345 350

Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu
355 360 365

Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro
370 375 380

Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly
385 390 395 400

Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro
405 410 415

Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr
420 425 430

_SL

Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly
435 440 445

Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln
450 455 460

Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln
465 470 475 480

Ala Leu Pro Pro Arg
485

<210> 726

<211> 383

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 726

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu
20 25 30

Glu Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr
35 40 45

Ser Phe Thr Gly Tyr Thr Met Asn Trp Val Lys Gln Ser His Gly Lys
50 55 60

Ser Leu Glu Trp Ile Gly Leu Ile Thr Pro Tyr Asn Gly Ala Ser Ser
65 70 75 80

Tyr Asn Gln Lys Phe Arg Gly Lys Ala Thr Leu Thr Val Asp Lys Ser
85 90 95

Ser Ser Thr Ala Tyr Met Asp Leu Leu Ser Leu Thr Ser Glu Asp Ser
100 105 110

Ala Val Tyr Phe Cys Ala Arg Gly Gly Tyr Asp Gly Arg Gly Phe Asp
115 120 125

Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly
130 135 140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Glu Leu Thr
145 150 155 160

_SL

Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr Met
165 170 175

Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln
180 185 190

Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Leu
195 200 205

Ala Ser Gly Val Pro Gly Arg Phe Ser Gly Ser Gly Ser Gly Asn Ser
210 215 220

Tyr Ser Leu Thr Ile Ser Ser Val Glu Ala Glu Asp Asp Ala Thr Tyr
225 230 235 240

Tyr Cys Gln Gln Trp Ser Gly Tyr Pro Leu Thr Phe Gly Ala Gly Thr
245 250 255

Lys Leu Glu Ile Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala
260 265 270

Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg
275 280 285

Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys
290 295 300

Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu
305 310 315 320

Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu
325 330 335

Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln
340 345 350

Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly
355 360 365

Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala
370 375 380

<210> 727

<211> 488

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 727

Met Ala Leu Pro Val Thr Ala Leu Leu ^{-SL}Leu Pro Leu Ala Leu Leu Leu
1 5 10 15
His Ala Ala Arg Pro Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Val
20 25 30
Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr
35 40 45
Thr Phe Thr Gly Tyr Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln
50 55 60
Gly Leu Glu Trp Met Gly Arg Ile Asn Pro Asn Ser Gly Gly Thr Asn
65 70 75 80
Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser
85 90 95
Ile Ser Thr Ala Tyr Met Glu Leu Ser Arg Leu Arg Ser Glu Asp Thr
100 105 110
Ala Val Tyr Tyr Cys Ala Arg Gly Arg Tyr Tyr Gly Met Asp Val Trp
115 120 125
Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
130 135 140
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile
145 150 155 160
Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg
165 170 175
Ala Thr Ile Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Asn Phe Ala
180 185 190
Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Asp
195 200 205
Ala Ser Asn Arg Ala Thr Gly Ile Pro Pro Arg Phe Ser Gly Ser Gly
210 215 220
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp
225 230 235 240
Phe Ala Ala Tyr Tyr Cys His Gln Arg Ser Asn Trp Leu Tyr Thr Phe
245 250 255
Gly Gln Gly Thr Lys Val Asp Ile Lys Thr Thr Thr Pro Ala Pro Arg
260 265 270

Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser ^{-SL}Gln Pro Leu Ser Leu Arg
 275 280 285
 Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly
 290 295 300
 Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr
 305 310 315 320
 Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg
 325 330 335
 Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro
 340 345 350
 Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu
 355 360 365
 Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala
 370 375 380
 Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu
 385 390 395 400
 Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly
 405 410 415
 Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu
 420 425 430
 Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser
 435 440 445
 Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly
 450 455 460
 Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu
 465 470 475 480
 His Met Gln Ala Leu Pro Pro Arg
 485

<210> 728

<211> 497

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 728

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu

1	5				10				15						
His	Ala	Ala	Arg 20	Pro	Gln	Val	Gln	Leu 25	Val	Gln	Ser	Gly	Ala 30	Glu	Val
Lys	Lys	Pro 35	Gly	Ala	Ser	Val	Lys 40	Val	Ser	Cys	Lys	Ala 45	Ser	Gly	Tyr
Thr	Phe 50	Thr	Gly	Tyr	Tyr	Met 55	His	Trp	Val	Arg	Gln 60	Ala	Pro	Gly	Gln
Gly 65	Leu	Glu	Trp	Met	Gly 70	Trp	Ile	Asn	Pro	Asn 75	Ser	Gly	Gly	Thr	Asn 80
Tyr	Ala	Gln	Lys	Phe 85	Gln	Gly	Arg	Val	Thr 90	Met	Thr	Arg	Asp	Thr 95	Ser
Ile	Ser	Thr	Ala 100	Tyr	Met	Glu	Leu	Ser 105	Arg	Leu	Arg	Ser	Asp 110	Asp	Thr
Ala	Val	Tyr 115	Tyr	Cys	Ala	Arg	Asp 120	Leu	Arg	Arg	Thr	Val 125	Val	Thr	Pro
Arg	Ala 130	Tyr	Tyr	Gly	Met	Asp 135	Val	Trp	Gly	Gln	Gly 140	Thr	Thr	Val	Thr
Val 145	Ser	Ser	Gly	Gly	Gly 150	Gly	Ser	Gly	Gly	Gly 155	Gly	Ser	Gly	Gly	Gly 160
Gly	Ser	Gly	Gly	Gly 165	Gly	Ser	Asp	Ile	Gln 170	Leu	Thr	Gln	Ser	Pro 175	Ser
Thr	Leu	Ser	Ala 180	Ser	Val	Gly	Asp	Arg 185	Val	Thr	Ile	Thr	Cys 190	Gln	Ala
Ser	Gln	Asp 195	Ile	Ser	Asn	Ser	Leu 200	Asn	Trp	Tyr	Gln	Gln 205	Lys	Ala	Gly
Lys	Ala 210	Pro	Lys	Leu	Leu	Ile 215	Tyr	Asp	Ala	Ser	Thr 220	Leu	Glu	Thr	Gly
Val 225	Pro	Ser	Arg	Phe	Ser 230	Gly	Ser	Gly	Ser	Gly 235	Thr	Asp	Phe	Ser	Phe 240
Thr	Ile	Ser	Ser	Leu 245	Gln	Pro	Glu	Asp	Ile 250	Ala	Thr	Tyr	Tyr	Cys 255	Gln
Gln	His	Asp	Asn 260	Leu	Pro	Leu	Thr	Phe 265	Gly	Gln	Gly	Thr	Lys 270	Val	Glu
Ile	Lys	Thr	Thr	Thr	Pro	Ala	Pro	Arg	Pro	Pro	Thr	Pro	Ala	Pro	Thr

_SL

275 280 285

Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala
 290 295 300

Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile
 305 310 315 320

Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser
 325 330 335

Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr
 340 345 350

Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu
 355 360 365

Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu
 370 375 380

Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln
 385 390 395 400

Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu
 405 410 415

Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly
 420 425 430

Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln
 435 440 445

Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu
 450 455 460

Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr
 465 470 475 480

Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro
 485 490 495

Arg

<210> 729
 <211> 490
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

_SL

<400> 729

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val
20 25 30

Lys Lys Pro Gly Ala Pro Val Lys Val Ser Cys Lys Ala Ser Gly Tyr
35 40 45

Thr Phe Thr Gly Tyr Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln
50 55 60

Gly Leu Glu Trp Met Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn
65 70 75 80

Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser
85 90 95

Ile Ser Thr Ala Tyr Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr
100 105 110

Ala Val Tyr Tyr Cys Ala Arg Gly Glu Trp Asp Gly Ser Tyr Tyr Tyr
115 120 125

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
130 135 140

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
145 150 155 160

Ser Asp Ile Val Leu Thr Gln Thr Pro Ser Ser Leu Ser Ala Ser Val
165 170 175

Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Asn Thr
180 185 190

Tyr Leu Asn Trp Tyr Gln His Lys Pro Gly Lys Ala Pro Lys Leu Leu
195 200 205

Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser
210 215 220

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln
225 230 235 240

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Phe Ser Pro Leu
245 250 255

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Thr Thr Thr Pro Ala
260 265 270

_SL

Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser
275 280 285

Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr
290 295 300

Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala
305 310 315 320

Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys
325 330 335

Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met
340 345 350

Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe
355 360 365

Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg
370 375 380

Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn
385 390 395 400

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
405 410 415

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
420 425 430

Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
435 440 445

Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
450 455 460

Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
465 470 475 480

Ala Leu His Met Gln Ala Leu Pro Pro Arg
485 490

<210> 730

<211> 486

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

_SL

<400> 730

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15
His Ala Ala Arg Pro Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu
20 25 30
Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
35 40 45
Thr Phe Ser Ser Tyr Trp Met His Trp Val Arg Gln Val Pro Gly Lys
50 55 60
Gly Leu Val Trp Val Ser Arg Ile Asn Thr Asp Gly Ser Thr Thr Thr
65 70 75 80
Tyr Ala Asp Ser Val Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
85 90 95
Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Asp Asp Asp Thr
100 105 110
Ala Val Tyr Tyr Cys Val Gly Gly His Trp Ala Val Trp Gly Gln Gly
115 120 125
Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
130 135 140
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr
145 150 155 160
Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
165 170 175
Thr Cys Arg Ala Ser Gln Ser Ile Ser Asp Arg Leu Ala Trp Tyr Gln
180 185 190
Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Lys Ala Ser Ser
195 200 205
Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
210 215 220
Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Val
225 230 235 240
Tyr Tyr Cys Gln Gln Tyr Gly His Leu Pro Met Tyr Thr Phe Gly Gln
245 250 255
Gly Thr Lys Val Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro
260 265 270

_SL

Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu
275 280 285

Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp
290 295 300

Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly
305 310 315 320

Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg
325 330 335

Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln
340 345 350

Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu
355 360 365

Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala
370 375 380

Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu
385 390 395 400

Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp
405 410 415

Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu
420 425 430

Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile
435 440 445

Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr
450 455 460

Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met
465 470 475 480

Gln Ala Leu Pro Pro Arg
485

<210> 731

<211> 497

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 731

Met Ala Leu Pro Val Thr Ala Leu Leu ^{-SL}Leu Pro Leu Ala Leu Leu Leu
 1 5 10 15
 His Ala Ala Arg Pro Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val
 20 25 30
 Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr
 35 40 45
 Thr Phe Thr Ser Tyr Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln
 50 55 60
 Gly Leu Glu Trp Met Gly Ile Ile Asn Pro Ser Gly Gly Ser Thr Ser
 65 70 75 80
 Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser
 85 90 95
 Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr
 100 105 110
 Ala Val Tyr Tyr Cys Ala Arg Tyr Arg Leu Ile Ala Val Ala Gly Asp
 115 120 125
 Tyr Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Met Val Thr
 130 135 140
 Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
 145 150 155 160
 Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser
 165 170 175
 Ser Val Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala
 180 185 190
 Ser Gln Gly Val Gly Arg Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly
 195 200 205
 Thr Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Thr Leu Gln Ser Gly
 210 215 220
 Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
 225 230 235 240
 Thr Ile Asn Asn Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln
 245 250 255
 Gln Ala Asn Ser Phe Pro Leu Thr Phe Gly Gly Gly Thr Arg Leu Glu
 260 265 270

Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro ^{-SL} Thr Pro Ala Pro Thr
 275 280 285
 Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala
 290 295 300
 Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile
 305 310 315 320
 Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser
 325 330 335
 Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr
 340 345 350
 Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu
 355 360 365
 Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu
 370 375 380
 Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln
 385 390 395
 Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu
 405 410 415
 Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly
 420 425 430
 Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln
 435 440 445
 Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu
 450 455 460
 Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr
 465 470 475 480
 Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro
 485 490 495

Arg

<210> 732
 <211> 494
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 Page 462

polypeptide" _SL

<400> 732

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val
20 25 30

Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
35 40 45

Thr Phe Ser Ser Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys
50 55 60

Gly Leu Glu Trp Val Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr
65 70 75 80

Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser
85 90 95

Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
100 105 110

Ala Val Tyr Tyr Cys Ala Arg Trp Lys Val Ser Ser Ser Pro Ala
115 120 125

Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly
130 135 140

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
145 150 155 160

Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser
165 170 175

Pro Gly Glu Arg Ala Ile Leu Ser Cys Arg Ala Ser Gln Ser Val Tyr
180 185 190

Thr Lys Tyr Leu Gly Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg
195 200 205

Leu Leu Ile Tyr Asp Ala Ser Thr Arg Ala Thr Gly Ile Pro Asp Arg
210 215 220

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Arg
225 230 235 240

Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln His Tyr Gly Gly
245 250 255

Ser Pro Leu Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Thr
Page 463

_SL

260 265 270

Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser
275 280 285

Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly
290 295 300

Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp
305 310 315 320

Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile
325 330 335

Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys
340 345 350

Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys
355 360 365

Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val
370 375 380

Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn
385 390 395 400

Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val
405 410 415

Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg
420 425 430

Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys
435 440 445

Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg
450 455 460

Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys
465 470 475 480

Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
485 490

<210> 733
<211> 490
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

_SL

<400> 733

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Val
20 25 30

Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Thr Ser Gly Tyr
35 40 45

Pro Phe Thr Gly Tyr Ser Leu His Trp Val Arg Gln Ala Pro Gly Gln
50 55 60

Gly Leu Glu Trp Met Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn
65 70 75 80

Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser
85 90 95

Ile Ser Thr Ala Tyr Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr
100 105 110

Ala Val Tyr Tyr Cys Ala Arg Asp His Tyr Gly Gly Asn Ser Leu Phe
115 120 125

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
130 135 140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
145 150 155 160

Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Ile Ser Ala Ser Val Gly
165 170 175

Asp Thr Val Ser Ile Thr Cys Arg Ala Ser Gln Asp Ser Gly Thr Trp
180 185 190

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Asn Leu Leu Met
195 200 205

Tyr Asp Ala Ser Thr Leu Glu Asp Gly Val Pro Ser Arg Phe Ser Gly
210 215 220

Ser Ala Ser Gly Thr Glu Phe Thr Leu Thr Val Asn Arg Leu Gln Pro
225 230 235 240

Glu Asp Ser Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Pro Leu
245 250 255

Thr Phe Gly Gly Gly Thr Lys Val Asp Ile Lys Thr Thr Thr Pro Ala
260 265 270

_SL

Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser
275 280 285

Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr
290 295 300

Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala
305 310 315 320

Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys
325 330 335

Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met
340 345 350

Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe
355 360 365

Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg
370 375 380

Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn
385 390 395 400

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
405 410 415

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
420 425 430

Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
435 440 445

Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
450 455 460

Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
465 470 475 480

Ala Leu His Met Gln Ala Leu Pro Pro Arg
485 490

<210> 734

<211> 492

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

_SL

<400> 734

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15
His Ala Ala Arg Pro Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val
20 25 30
Lys Lys Pro Gly Ala Ser Val Glu Val Ser Cys Lys Ala Ser Gly Tyr
35 40 45
Thr Phe Thr Ser Tyr Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln
50 55 60
Gly Leu Glu Trp Met Gly Ile Ile Asn Pro Ser Gly Gly Ser Thr Gly
65 70 75 80
Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser
85 90 95
Thr Ser Thr Val His Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr
100 105 110
Ala Val Tyr Tyr Cys Ala Arg Gly Gly Tyr Ser Ser Ser Ser Asp Ala
115 120 125
Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly
130 135 140
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly
145 150 155 160
Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Pro Ser Leu Ser Ala Ser
165 170 175
Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Ser
180 185 190
Ser Ala Leu Ala Trp Tyr Gln Gln Lys Pro Gly Thr Pro Pro Lys Leu
195 200 205
Leu Ile Tyr Asp Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe
210 215 220
Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu
225 230 235 240
Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Phe Ser Ser Tyr
245 250 255
Pro Leu Thr Phe Gly Gly Gly Thr Arg Leu Glu Ile Lys Thr Thr Thr
260 265 270

_SL

Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro
275 280 285

Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val
290 295 300

His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro
305 310 315 320

Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu
325 330 335

Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro
340 345 350

Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys
355 360 365

Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe
370 375 380

Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu
385 390 395 400

Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp
405 410 415

Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys
420 425 430

Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala
435 440 445

Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
450 455 460

Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
465 470 475 480

Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
485 490

<210> 735

<211> 499

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 735

Met Ala Leu Pro Val Thr Ala Leu Leu Leu^{-SL} Pro Leu Ala Leu Leu Leu
1 5 10 15
His Ala Ala Arg Pro Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val
20 25 30
Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr
35 40 45
Thr Phe Thr Ser Tyr Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln
50 55 60
Gly Leu Glu Trp Met Gly Trp Ile Ser Ala Tyr Asn Gly Asn Thr Asn
65 70 75 80
Tyr Ala Gln Lys Leu Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser
85 90 95
Thr Ser Thr Ala Tyr Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr
100 105 110
Ala Val Tyr Tyr Cys Ala Arg Val Ala Gly Gly Ile Tyr Tyr Tyr Tyr
115 120 125
Gly Met Asp Val Trp Gly Gln Gly Thr Thr Ile Thr Val Ser Ser Gly
130 135 140
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
145 150 155 160
Gly Gly Ser Asp Ile Val Met Thr Gln Thr Pro Asp Ser Leu Ala Val
165 170 175
Ser Leu Gly Glu Arg Ala Thr Ile Ser Cys Lys Ser Ser His Ser Val
180 185 190
Leu Tyr Asn Arg Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys
195 200 205
Pro Gly Gln Pro Pro Lys Leu Leu Phe Tyr Trp Ala Ser Thr Arg Lys
210 215 220
Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
225 230 235 240
Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Phe
245 250 255
Cys Gln Gln Thr Gln Thr Phe Pro Leu Thr Phe Gly Gln Gly Thr Arg
260 265 270

Leu Glu Ile Asn Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala
 275 280 285
 Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg
 290 295 300
 Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys
 305 310 315 320
 Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu
 325 330 335
 Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu
 340 345 350
 Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln
 355 360 365
 Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Gly Gly
 370 375 380
 Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr
 385 390 395 400
 Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg
 405 410 415
 Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met
 420 425 430
 Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu
 435 440 445
 Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys
 450 455 460
 Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu
 465 470 475 480
 Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu
 485 490 495
 Pro Pro Arg

<210> 736

<211> 490

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic

_SL
polypeptide"

<400> 736

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val
20 25 30

Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr
35 40 45

Thr Phe Thr Gly Tyr Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln
50 55 60

Gly Leu Glu Trp Met Gly Arg Ile Asn Pro Asn Ser Gly Gly Thr Asn
65 70 75 80

Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser
85 90 95

Thr Ser Thr Ala Tyr Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr
100 105 110

Ala Val Tyr Tyr Cys Ala Arg Thr Thr Thr Ser Tyr Ala Phe Asp Ile
115 120 125

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser
130 135 140

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp
145 150 155 160

Ile Gln Leu Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly Asp
165 170 175

Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Thr Trp Leu
180 185 190

Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Asn Leu Leu Ile Tyr
195 200 205

Lys Ala Ser Thr Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
210 215 220

Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
225 230 235 240

Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Thr Tyr Ser Pro Tyr
245 250 255

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Thr Thr Thr Pro Ala
Page 471

_SL

260 265 270

Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser
275 280 285

Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr
290 295 300

Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala
305 310 315 320

Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys
325 330 335

Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met
340 345 350

Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe
355 360 365

Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg
370 375 380

Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn
385 390 395 400

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
405 410 415

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
420 425 430

Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
435 440 445

Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
450 455 460

Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
465 470 475 480

Ala Leu His Met Gln Ala Leu Pro Pro Arg
485 490

<210> 737

<211> 493

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

_SL

<400> 737

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu
20 25 30

Val Lys Pro Gly Gly Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe
35 40 45

Ile Phe Ser Asp Tyr Tyr Met Gly Trp Ile Arg Gln Ala Pro Gly Lys
50 55 60

Gly Leu Glu Trp Val Ser Tyr Ile Gly Arg Ser Gly Ser Ser Met Tyr
65 70 75 80

Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Phe Ser Arg Asp Asn Ala
85 90 95

Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
100 105 110

Ala Val Tyr Tyr Cys Ala Ala Ser Pro Val Val Ala Ala Thr Glu Asp
115 120 125

Phe Gln His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly
130 135 140

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly
145 150 155 160

Gly Ser Asp Ile Val Met Thr Gln Thr Pro Ala Thr Leu Ser Leu Ser
165 170 175

Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Thr
180 185 190

Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg
195 200 205

Leu Leu Leu Phe Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Asp Arg
210 215 220

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Arg
225 230 235 240

Leu Glu Pro Glu Asp Phe Ala Met Tyr Tyr Cys Gln Gln Tyr Gly Ser
245 250 255

Ala Pro Val Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Thr Thr
260 265 270

_SL

Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln
275 280 285

Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala
290 295 300

Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala
305 310 315 320

Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr
325 330 335

Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln
340 345 350

Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser
355 360 365

Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys
370 375 380

Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln
385 390 395 400

Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
405 410 415

Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg
420 425 430

Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met
435 440 445

Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly
450 455 460

Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp
465 470 475 480

Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
485 490

<210> 738
<211> 493
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

_SL

<400> 738

```

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1      5      10     15

His Ala Ala Arg Pro Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val
      20     25     30

Arg Ala Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Phe
      35     40     45

Thr Phe Arg Gly Tyr Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln
      50     55     60

Gly Leu Glu Trp Met Gly Ile Ile Asn Pro Ser Gly Gly Ser Arg Ala
65      70      75      80

Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser
      85     90     95

Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Asp Asp Thr
      100    105    110

Ala Met Tyr Tyr Cys Ala Arg Thr Ala Ser Cys Gly Gly Asp Cys Tyr
      115    120    125

Tyr Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
      130    135    140

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
145      150    155    160

Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Pro Thr Leu Ser Ala
      165    170    175

Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Asn Val
      180    185    190

Asn Ile Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
      195    200    205

Leu Leu Ile Tyr Lys Ser Ser Ser Leu Ala Ser Gly Val Pro Ser Arg
      210    215    220

Phe Ser Gly Ser Gly Ser Gly Ala Glu Phe Thr Leu Thr Ile Ser Ser
225      230    235    240

Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Gln Ser
      245    250    255

Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Asp Ile Lys Thr Thr
      260    265    270

```

_SL

Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln
275 280 285

Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala
290 295 300

Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala
305 310 315 320

Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr
325 330 335

Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln
340 345 350

Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser
355 360 365

Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys
370 375 380

Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln
385 390 395 400

Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
405 410 415

Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg
420 425 430

Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met
435 440 445

Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly
450 455 460

Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp
465 470 475 480

Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
485 490

<210> 739

<211> 488

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 739

Met Ala Leu Pro Val Thr Ala Leu Leu ^{-SL}Leu Pro Leu Ala Leu Leu Leu
 1 5 10 15
 His Ala Ala Arg Pro Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu
 20 25 30
 Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
 35 40 45
 Thr Phe Asp Asp Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys
 50 55 60
 Gly Leu Glu Trp Val Ser Gly Ile Ser Trp Asn Ser Gly Ser Ile Gly
 65 70 75 80
 Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
 85 90 95
 Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
 100 105 110
 Ala Val Tyr Tyr Cys Ala Lys Asp Gly Ser Ser Ser Trp Ser Trp Gly
 115 120 125
 Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
 130 135 140
 Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Ser
 145 150 155 160
 Glu Leu Thr Gln Asp Pro Ala Val Ser Val Ala Leu Gly Gln Thr Val
 165 170 175
 Arg Thr Thr Cys Gln Gly Asp Ala Leu Arg Ser Tyr Tyr Ala Ser Trp
 180 185 190
 Tyr Gln Gln Lys Pro Gly Gln Ala Pro Met Leu Val Ile Tyr Gly Lys
 195 200 205
 Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Asp Ser
 210 215 220
 Gly Asp Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu Asp Glu
 225 230 235 240
 Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Ser Gly Tyr Pro Val Phe
 245 250 255
 Gly Thr Gly Thr Lys Val Thr Val Leu Thr Thr Thr Pro Ala Pro Arg
 260 265 270

Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser ^{-SL}Gln Pro Leu Ser Leu Arg
 275 280 285
 Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly
 290 295 300
 Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr
 305 310 315 320
 Cys Gly Val Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg
 325 330 335
 Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro
 340 345 350
 Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu
 355 360 365
 Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala
 370 375 380
 Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu
 385 390 395 400
 Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly
 405 410 415
 Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu
 420 425 430
 Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser
 435 440 445
 Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly
 450 455 460
 Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu
 465 470 475 480
 His Met Gln Ala Leu Pro Pro Arg
 485

<210> 740

<211> 490

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 740

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu

1	5				10				15						
His	Ala	Ala	Arg 20	Pro	Glu	Val	Gln	Leu 25	Val	Glu	Ser	Gly	Gly 30	Gly	Leu
Val	Gln	Pro 35	Gly	Arg	Ser	Leu	Arg 40	Leu	Ser	Cys	Ala	Ala 45	Ser	Gly	Phe
Thr	Phe 50	Asp	Asp	Tyr	Ala	Met 55	His	Trp	Val	Arg	Gln 60	Ala	Pro	Gly	Lys
Gly 65	Leu	Glu	Trp	Val	Ser 70	Gly	Ile	Ser	Trp	Asn 75	Ser	Gly	Ser	Thr	Gly 80
Tyr	Ala	Asp	Ser	Val 85	Lys	Gly	Arg	Phe	Thr 90	Ile	Ser	Arg	Asp	Asn 95	Ala
Lys	Asn	Ser	Leu 100	Tyr	Leu	Gln	Met	Asn 105	Ser	Leu	Arg	Ala	Glu 110	Asp	Thr
Ala	Leu	Tyr 115	Tyr	Cys	Ala	Lys	Asp 120	Ser	Ser	Ser	Trp	Tyr 125	Gly	Gly	Gly
Ser	Ala 130	Phe	Asp	Ile	Trp	Gly 135	Gln	Gly	Thr	Met	Val 140	Thr	Val	Ser	Ser
Gly 145	Gly	Gly	Gly	Ser	Gly 150	Gly	Gly	Gly	Ser	Gly 155	Gly	Gly	Gly	Ser	Ser 160
Ser	Glu	Leu	Thr	Gln 165	Glu	Pro	Ala	Val	Ser 170	Val	Ala	Leu	Gly	Gln 175	Thr
Val	Arg	Ile	Thr 180	Cys	Gln	Gly	Asp	Ser 185	Leu	Arg	Ser	Tyr	Tyr 190	Ala	Ser
Trp	Tyr	Gln 195	Gln	Lys	Pro	Gly	Gln 200	Ala	Pro	Val	Leu	Val 205	Ile	Phe	Gly
Arg	Ser 210	Arg	Arg	Pro	Ser	Gly 215	Ile	Pro	Asp	Arg	Phe 220	Ser	Gly	Ser	Ser
Ser 225	Gly	Asn	Thr	Ala	Ser 230	Leu	Ile	Ile	Thr	Gly 235	Ala	Gln	Ala	Glu	Asp 240
Glu	Ala	Asp	Tyr	Tyr 245	Cys	Asn	Ser	Arg	Asp 250	Asn	Thr	Ala	Asn	His 255	Tyr
Val	Phe	Gly	Thr 260	Gly	Thr	Lys	Leu	Thr 265	Val	Leu	Thr	Thr	Thr 270	Pro	Ala
Pro	Arg	Pro	Pro	Thr	Pro	Ala	Pro	Thr	Ile	Ala	Ser	Gln	Pro	Leu	Ser

275 280 _SL 285
 Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr
 290 295 300
 Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala
 305 310 315 320
 Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys
 325 330 335
 Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met
 340 345 350
 Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe
 355 360 365
 Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg
 370 375 380
 Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn
 385 390 395 400
 Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
 405 410 415
 Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
 420 425 430
 Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
 435 440 445
 Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
 450 455 460
 Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
 465 470 475 480
 Ala Leu His Met Gln Ala Leu Pro Pro Arg
 485 490

<210> 741
 <211> 490
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 741
 Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
 1 5 10 15

_SL

His Ala Ala Arg Pro Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
20 25 30

Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
35 40 45

Thr Phe Asp Asp Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys
50 55 60

Gly Leu Glu Trp Val Ser Gly Ile Ser Trp Asn Ser Gly Ser Thr Gly
65 70 75 80

Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
85 90 95

Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
100 105 110

Ala Leu Tyr Tyr Cys Ala Lys Asp Ser Ser Ser Trp Tyr Gly Gly Gly
115 120 125

Ser Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
130 135 140

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser
145 150 155 160

Ser Glu Leu Thr Gln Asp Pro Ala Val Ser Val Ala Leu Gly Gln Thr
165 170 175

Val Arg Ile Thr Cys Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser
180 185 190

Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr Gly
195 200 205

Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Ser
210 215 220

Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu Asp
225 230 235 240

Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Gly Ser Ser Gly Asn His Tyr
245 250 255

Val Phe Gly Thr Gly Thr Lys Val Thr Val Leu Thr Thr Thr Pro Ala
260 265 270

Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser
275 280 285

_SL

Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr
290 295 300

Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala
305 310 315 320

Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys
325 330 335

Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met
340 345 350

Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe
355 360 365

Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg
370 375 380

Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn
385 390 395 400

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
405 410 415

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
420 425 430

Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
435 440 445

Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
450 455 460

Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
465 470 475 480

Ala Leu His Met Gln Ala Leu Pro Pro Arg
485 490

<210> 742

<211> 495

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 742

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

_SL

His Ala Ala Arg Pro Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu
20 25 30

Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
35 40 45

Thr Phe Ser Ser Tyr Trp Met His Trp Val Arg Gln Ala Pro Gly Lys
50 55 60

Gly Leu Val Trp Val Ser Arg Ile Asn Ser Asp Gly Ser Ser Thr Ser
65 70 75 80

Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
85 90 95

Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
100 105 110

Ala Val Tyr Tyr Cys Val Arg Thr Gly Trp Val Gly Ser Tyr Tyr Tyr
115 120 125

Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser Gly
130 135 140

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
145 150 155 160

Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu
165 170 175

Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val
180 185 190

Ser Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
195 200 205

Arg Leu Leu Ile Tyr Asp Val Ser Thr Arg Ala Thr Gly Ile Pro Ala
210 215 220

Arg Phe Ser Gly Gly Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
225 230 235 240

Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser
245 250 255

Asn Trp Pro Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
260 265 270

Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala
275 280 285

_SL

Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly
290 295 300

Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile
305 310 315 320

Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val
325 330 335

Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe
340 345 350

Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly
355 360 365

Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg
370 375 380

Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln
385 390 395 400

Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp
405 410 415

Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro
420 425 430

Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp
435 440 445

Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg
450 455 460

Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr
465 470 475 480

Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
485 490 495

<210> 743

<211> 494

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 743

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg₂₀ Pro Gln Val Gln Leu₂₅ Val^{-SL} Gln Ser Gly₃₀ Gly Gly Val
 Val Gln Pro₃₅ Gly Arg Ser Leu₄₀ Arg Leu Ser Cys Ala₄₅ Ala Ser Gly Phe
 Thr Phe₅₀ Ser Ser Tyr Gly₅₅ Met His Trp Val Arg₆₀ Gln Ala Pro Gly Lys
 Gly₆₅ Leu Glu Trp Val₇₀ Ala Val Ile Ser Tyr₇₅ Asp Gly Ser Asn Lys₈₀ Tyr
 Tyr Ala Asp Ser₈₅ Val Lys Gly Arg Phe₉₀ Thr Ile Ser Arg Asp₉₅ Asn Ser
 Lys Asn Thr₁₀₀ Leu Tyr Leu Gln Met₁₀₅ Asn Ser Leu Arg Ala₁₁₀ Glu Asp Thr
 Ala Val Tyr₁₁₅ Tyr Cys Ala Lys₁₂₀ Gly Tyr Ser Arg Tyr₁₂₅ Tyr Tyr Tyr Gly
 Met Asp₁₃₀ Val Trp Gly Gln₁₃₅ Gly Thr Thr Val Thr₁₄₀ Val Ser Ser Gly Gly
 Gly₁₄₅ Gly Ser Gly Gly₁₅₀ Gly Gly Ser Gly₁₅₅ Gly Gly Ser Gly₁₆₀ Gly Gly
 Gly Ser Glu Ile₁₆₅ Val Met Thr Gln Ser₁₇₀ Pro Ala Thr Leu Ser₁₇₅ Leu Ser
 Pro Gly Glu₁₈₀ Arg Ala Ile Leu Ser₁₈₅ Cys Arg Ala Ser Gln₁₉₀ Ser Val Tyr
 Thr Lys Tyr₁₉₅ Leu Gly Trp Tyr₂₀₀ Gln Gln Lys Pro Gly₂₀₅ Gln Ala Pro Arg
 Leu₂₁₀ Leu Ile Tyr Asp Ala Ser₂₁₅ Thr Arg Ala Thr Gly₂₂₀ Ile Pro Asp Arg
 Phe₂₂₅ Ser Gly Ser Gly₂₃₀ Ser Gly Thr Asp Phe₂₃₅ Thr Leu Thr Ile Asn Arg₂₄₀
 Leu Glu Pro Glu₂₄₅ Asp Phe Ala Val Tyr₂₅₀ Tyr Cys Gln His Tyr Gly₂₅₅ Gly
 Ser Pro Leu₂₆₀ Ile Thr Phe Gly Gln₂₆₅ Gly Thr Lys Val Asp₂₇₀ Ile Lys Thr
 Thr Thr Pro₂₇₅ Ala Pro Arg Pro₂₈₀ Thr Pro Ala Pro₂₈₅ Thr Ile Ala Ser

Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly
 290 295 300
 Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp
 305 310 315 320
 Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile
 325 330 335
 Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys
 340 345 350
 Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys
 355 360 365
 Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val
 370 375 380
 Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn
 385 390 395 400
 Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val
 405 410 415
 Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg
 420 425 430
 Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys
 435 440 445
 Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg
 450 455 460
 Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys
 465 470 475 480
 Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
 485 490

<210> 744

<211> 493

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 744

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu
 1 5 10 15

His Ala Ala Arg Pro Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu
 Page 486

_SL

	20		25		30														
Val	Gln	Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe				
		35					40					45							
Thr	Phe	Ser	Ser	Tyr	Ala	Met	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys				
	50					55					60								
Gly	Leu	Glu	Trp	Val	Ser	Ala	Ile	Ser	Gly	Ser	Gly	Gly	Ser	Thr	Tyr				
65					70					75					80				
Tyr	Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser				
				85					90					95					
Lys	Asn	Thr	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr				
			100					105					110						
Ala	Val	Tyr	Tyr	Cys	Ala	Lys	Arg	Glu	Ala	Ala	Ala	Gly	His	Asp	Trp				
		115					120					125							
Tyr	Phe	Asp	Leu	Trp	Gly	Arg	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Gly				
	130					135					140								
Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly				
145					150					155					160				
Gly	Gly	Ser	Asp	Ile	Arg	Val	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala				
				165					170					175					
Ser	Val	Gly	Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Ser	Ile				
			180					185					190						
Ser	Ser	Tyr	Leu	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys				
		195					200					205							
Leu	Leu	Ile	Tyr	Ala	Ala	Ser	Ser	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg				
	210					215					220								
Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser				
225					230					235					240				
Leu	Gln	Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Ser	Tyr	Ser				
				245					250					255					
Ile	Pro	Leu	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Thr	Thr				
			260					265					270						
Thr	Pro	Ala	Pro	Arg	Pro	Pro	Thr	Pro	Ala	Pro	Thr	Ile	Ala	Ser	Gln				
		275					280					285							
Pro	Leu	Ser	Leu	Arg	Pro	Glu	Ala	Cys	Arg	Pro	Ala	Ala	Gly	Gly	Ala				

_SL

Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr
35 40 45

Thr Phe Thr Ser Tyr Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln
50 55 60

Gly Leu Glu Trp Met Gly Ile Ile Asn Pro Ser Gly Gly Ser Thr Ser
65 70 75 80

Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser
85 90 95

Thr Ser Thr Val Tyr Met Glu Leu Ser Asn Leu Arg Ser Glu Asp Thr
100 105 110

Ala Val Tyr Tyr Cys Ala Arg Ser Pro Arg Val Thr Thr Gly Tyr Phe
115 120 125

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
130 135 140

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
145 150 155 160

Ser Asp Ile Gln Leu Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val
165 170 175

Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser
180 185 190

Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu
195 200 205

Ile Tyr Lys Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser
210 215 220

Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln
225 230 235 240

Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Ser Tyr Pro
245 250 255

Leu Thr Phe Gly Gly Gly Thr Arg Leu Glu Ile Lys Thr Thr Thr Pro
260 265 270

Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu
275 280 285

Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His
290 295 300

_SL

Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu
305 310 315 320

Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr
325 330 335

Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe
340 345 350

Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg
355 360 365

Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser
370 375 380

Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr
385 390 395 400

Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys
405 410 415

Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn
420 425 430

Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu
435 440 445

Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly
450 455 460

His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr
465 470 475 480

Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
485 490

<210> 746

<211> 497

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 746

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val
20 25 30

_SL

Arg Arg Pro Gly Ala Ser Val Lys Ile Ser Cys Arg Ala Ser Gly Asp
35 40 45

Thr Ser Thr Arg His Tyr Ile His Trp Leu Arg Gln Ala Pro Gly Gln
50 55 60

Gly Pro Glu Trp Met Gly Val Ile Asn Pro Thr Thr Gly Pro Ala Thr
65 70 75 80

Gly Ser Pro Ala Tyr Ala Gln Met Leu Gln Gly Arg Val Thr Met Thr
85 90 95

Arg Asp Thr Ser Thr Arg Thr Val Tyr Met Glu Leu Arg Ser Leu Arg
100 105 110

Phe Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ser Val Val Gly Arg
115 120 125

Ser Ala Pro Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
130 135 140

Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
145 150 155 160

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser
165 170 175

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala
180 185 190

Ser Gln Gly Ile Ser Asp Tyr Ser Ala Trp Tyr Gln Gln Lys Pro Gly
195 200 205

Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Thr Leu Gln Ser Gly
210 215 220

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
225 230 235 240

Thr Ile Ser Tyr Leu Gln Ser Glu Asp Phe Ala Thr Tyr Tyr Cys Gln
245 250 255

Gln Tyr Tyr Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Asp
260 265 270

Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr
275 280 285

Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala
290 295 300

_SL

Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile
305 310 315 320

Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser
325 330 335

Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr
340 345 350

Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu
355 360 365

Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu
370 375 380

Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln
385 390 395 400

Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu
405 410 415

Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly
420 425 430

Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln
435 440 445

Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu
450 455 460

Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr
465 470 475 480

Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro
485 490 495

Arg

<210> 747

<211> 493

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 747

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg₂₀ Pro Gln Val Gln Leu₂₅ Gln^{-SL} Gln Ser Gly Ala₃₀ Glu Val
 Lys Lys Pro₃₅ Gly Ala Ser Val Lys₄₀ Val Ser Cys Lys Ala₄₅ Ser Gly Tyr
 Thr Phe₅₀ Thr Asn Tyr Tyr Met₅₅ His Trp Val Arg Gln₆₀ Ala Pro Gly Gln
 Gly₆₅ Leu Glu Trp Met₇₀ Gly Ile Ile Asn Pro Ser₇₅ Gly Gly Tyr Thr₈₀
 Tyr Ala Gln Lys Phe₈₅ Gln Gly Arg Leu Thr₉₀ Met Thr Arg Asp Thr₉₅ Ser
 Thr Ser Thr Val₁₀₀ Tyr Met Glu Leu Ser₁₀₅ Ser Leu Arg Ser Glu₁₁₀ Asp Thr
 Ala Val Tyr₁₁₅ Tyr Cys Ala Arg Ile₁₂₀ Arg Ser Cys Gly Gly₁₂₅ Asp Cys Tyr
 Tyr Phe₁₃₀ Asp Asn Trp Gly Gln₁₃₅ Gly Thr Leu Val Thr₁₄₀ Val Ser Ser Gly
 Gly₁₄₅ Gly Gly Ser Gly₁₅₀ Gly Gly Gly Ser Gly₁₅₅ Gly Gly Ser Gly₁₆₀
 Gly Gly Ser Asp₁₆₅ Ile Gln Leu Thr Gln₁₇₀ Ser Pro Ser Thr Leu Ser₁₇₅ Ala
 Ser Val Gly₁₈₀ Asp Arg Val Thr Ile Thr₁₈₅ Cys Arg Ala Ser Glu₁₉₀ Asn Val
 Asn Ile Trp₁₉₅ Leu Ala Trp Tyr Gln₂₀₀ Gln Lys Pro Gly Lys₂₀₅ Ala Pro Lys
 Leu Leu₂₁₀ Ile Tyr Lys Ser Ser₂₁₅ Ser Leu Ala Ser Gly₂₂₀ Val Pro Ser Arg
 Phe₂₂₅ Ser Gly Ser Gly₂₃₀ Ser Gly Ala Glu Phe Thr₂₃₅ Leu Thr Ile Ser Ser₂₄₀
 Leu Gln Pro Asp₂₄₅ Asp Phe Ala Thr Tyr Tyr₂₅₀ Cys Gln Gln Tyr Gln₂₅₅ Ser
 Tyr Pro Leu Thr₂₆₀ Phe Gly Gly Gly Thr₂₆₅ Lys Val Asp Ile Lys₂₇₀ Thr Thr
 Thr Pro Ala₂₇₅ Pro Arg Pro Pro Thr₂₈₀ Pro Ala Pro Thr Ile₂₈₅ Ala Ser Gln

Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala
 290 295 300
 Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala
 305 310 315 320
 Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Ser Leu Val Ile Thr
 325 330 335
 Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln
 340 345 350
 Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser
 355 360 365
 Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys
 370 375 380
 Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln
 385 390 395 400
 Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
 405 410 415
 Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg
 420 425 430
 Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met
 435 440 445
 Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly
 450 455 460
 Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp
 465 470 475 480
 Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
 485 490

<210> 748

<211> 490

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 748

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu
 1 5 10 15

His Ala Ala Arg Pro Gln Ile Thr Leu Lys Glu Ser Gly Pro Ala Leu
 Page 494

_SL															
20						25						30			
Val	Lys	Pro 35	Thr	Gln	Thr	Leu	Thr 40	Leu	Thr	Cys	Thr	Phe 45	Ser	Gly	Phe
Ser	Leu 50	Ser	Thr	Ala	Gly	Val 55	His	Val	Gly	Trp	Ile 60	Arg	Gln	Pro	Pro
Gly 65	Lys	Ala	Leu	Glu	Trp 70	Leu	Ala	Leu	Ile	Ser 75	Trp	Ala	Asp	Asp	Lys 80
Arg	Tyr	Arg	Pro	Ser 85	Leu	Arg	Ser	Arg	Leu 90	Asp	Ile	Thr	Arg	Val 95	Thr
Ser	Lys	Asp	Gln 100	Val	Val	Leu	Ser	Met 105	Thr	Asn	Met	Gln	Pro 110	Glu	Asp
Thr	Ala	Thr 115	Tyr	Tyr	Cys	Ala	Leu 120	Gln	Gly	Phe	Asp	Gly 125	Tyr	Glu	Ala
Asn	Trp 130	Gly	Pro	Gly	Thr	Leu 135	Val	Thr	Val	Ser	Ser 140	Gly	Gly	Gly	Gly
Ser 145	Gly	Gly	Gly	Gly	Ser 150	Gly	Gly	Gly	Gly	Ser 155	Gly	Gly	Gly	Gly	Ser 160
Asp	Ile	Val	Met	Thr 165	Gln	Ser	Pro	Ser	Ser 170	Leu	Ser	Ala	Ser	Ala 175	Gly
Asp	Arg	Val	Thr 180	Ile	Thr	Cys	Arg	Ala 185	Ser	Arg	Gly	Ile	Ser 190	Ser	Ala
Leu	Ala	Trp 195	Tyr	Gln	Gln	Lys	Pro 200	Gly	Lys	Pro	Pro	Lys 205	Leu	Leu	Ile
Tyr	Asp 210	Ala	Ser	Ser	Leu	Glu 215	Ser	Gly	Val	Pro	Ser 220	Arg	Phe	Ser	Gly
Ser 225	Gly	Ser	Gly	Thr	Asp 230	Phe	Thr	Leu	Thr	Ile 235	Asp	Ser	Leu	Glu	Pro 240
Glu	Asp	Phe	Ala	Thr 245	Tyr	Tyr	Cys	Gln	Gln 250	Ser	Tyr	Ser	Thr	Pro 255	Trp
Thr	Phe	Gly	Gln 260	Gly	Thr	Lys	Val	Asp 265	Ile	Lys	Thr	Thr	Thr 270	Pro	Ala
Pro	Arg	Pro 275	Pro	Thr	Pro	Ala	Pro 280	Thr	Ile	Ala	Ser	Gln 285	Pro	Leu	Ser
Leu	Arg	Pro	Glu	Ala	Cys	Arg	Pro	Ala	Ala	Gly	Gly	Ala	Val	His	Thr

_SL

290		295		300											
Arg	Gly	Leu	Asp	Phe	Ala	Cys	Asp	Ile	Tyr	Ile	Trp	Ala	Pro	Leu	Ala
305					310					315					320
Gly	Thr	Cys	Gly	Val	Leu	Leu	Leu	Ser	Leu	Val	Ile	Thr	Leu	Tyr	Cys
				325					330					335	
Lys	Arg	Gly	Arg	Lys	Lys	Leu	Leu	Tyr	Ile	Phe	Lys	Gln	Pro	Phe	Met
			340					345					350		
Arg	Pro	Val	Gln	Thr	Thr	Gln	Glu	Glu	Asp	Gly	Cys	Ser	Cys	Arg	Phe
		355					360					365			
Pro	Glu	Glu	Glu	Glu	Gly	Gly	Cys	Glu	Leu	Arg	Val	Lys	Phe	Ser	Arg
	370					375					380				
Ser	Ala	Asp	Ala	Pro	Ala	Tyr	Lys	Gln	Gly	Gln	Asn	Gln	Leu	Tyr	Asn
385					390					395					400
Glu	Leu	Asn	Leu	Gly	Arg	Arg	Glu	Glu	Tyr	Asp	Val	Leu	Asp	Lys	Arg
				405					410					415	
Arg	Gly	Arg	Asp	Pro	Glu	Met	Gly	Gly	Lys	Pro	Arg	Arg	Lys	Asn	Pro
			420					425					430		
Gln	Glu	Gly	Leu	Tyr	Asn	Glu	Leu	Gln	Lys	Asp	Lys	Met	Ala	Glu	Ala
		435					440					445			
Tyr	Ser	Glu	Ile	Gly	Met	Lys	Gly	Glu	Arg	Arg	Arg	Gly	Lys	Gly	His
	450					455					460				
Asp	Gly	Leu	Tyr	Gln	Gly	Leu	Ser	Thr	Ala	Thr	Lys	Asp	Thr	Tyr	Asp
465					470					475					480
Ala	Leu	His	Met	Gln	Ala	Leu	Pro	Pro	Arg						
				485					490						

<210> 749
 <211> 1461
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 749	
atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg	60
ccccaaagtgc aactcgtcca aagcggagcg gaagtcaaga aaccgggagc gagcgtgaaa	120
gtgtcctgca aagcctccgg ctacaccttt acgggctact acatgcactg ggtgcgccag	180

_SL

gcaccaggac	agggctcttga	atggatggga	tggatcaacc	ctaattcggg	cggaactaac	240
tacgcacaga	agttccaggg	gagagtgact	ctgactcggg	atacctccat	ctcaactgtc	300
tacatggaac	tctcccgtt	gcggtcagat	gatacggcag	tgtactactg	cgcccgcgac	360
atgaatatcc	tggctaccgt	gccgttcgac	atctggggac	aggggactat	ggttactgtc	420
tcatcgggcg	gtggagggttc	aggaggaggc	ggctcgggag	gcggagggttc	ggacattcag	480
atgaccaggt	ccccatcctc	tctgtcggcc	agcgtcggag	atagggtgac	cattacctgt	540
cgggcctcgc	aaagcatctc	ctcgtacctc	aactgggtatc	agcaaaagcc	gggaaaggcg	600
cctaagctgc	tgatctacgc	cgcttcgagc	ttgcaaagcg	gggtgccatc	cagattctcg	660
ggatcagggt	caggaaccga	cttcaccctg	accgtgaaca	gcctccagcc	ggaggacttt	720
gccacttact	actgccagca	gggagactcc	gtgccgctta	ctttcggggg	gggtaccgcg	780
ctggagatca	agaccactac	cccagcaccg	aggccacca	ccccggctcc	taccatcgcc	840
tcccagcctc	tgtccctgcg	tccggaggca	tgtagaccgc	cagctggtgg	ggccgtgcat	900
accggggtc	ttgacttcgc	ctgcgatatc	tacatttggg	cccctctggc	tggtacttgc	960
ggggtcctgc	tgctttcact	cgtgatcact	ctttactgta	agcgcgggtcg	gaagaagctg	1020
ctgtacatct	ttaagcaacc	cttcattgag	cctgtgcaga	ctactcaaga	ggaggacggc	1080
tggtcatgcc	ggttcccaga	ggaggaggaa	ggcggctgcg	aactgcgcgt	gaaattcagc	1140
cgcagcgcag	atgctccagc	ctacaagcag	gggcagaacc	agctctacaa	cgaactcaat	1200
cttggtcggg	gagaggagta	cgacgtgctg	gacaagcgga	gaggacggga	cccagaaatg	1260
ggcgggaagc	cgcgcagaaa	gaatcccca	gagggcctgt	acaacgagct	ccaaaaggat	1320
aagatggcag	aagcctatag	cgagattggt	atgaaagggg	aacgcagaag	aggcaaaggc	1380
cacgacggac	tgtaccaggg	actcagcacc	gccaccaagg	acacctatga	cgctcttcac	1440
atgcaggccc	tgccgcctcg	g				1461

<210> 750

<211> 487

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 750

Met	Ala	Leu	Pro	Val	Thr	Ala	Leu	Leu	Leu	Pro	Leu	Ala	Leu	Leu	Leu
1				5				10					15		

His	Ala	Ala	Arg	Pro	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val
			20					25					30		

Lys	Lys	Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr
		35					40					45			

Thr Phe Thr Gly Tyr Tyr Met His Trp Val^{SL} Arg Gln Ala Pro Gly Gln
 50 55 60
 Gly Leu Glu Trp Met Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn
 65 70 75 80
 Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Leu Thr Arg Asp Thr Ser
 85 90 95
 Ile Ser Thr Val Tyr Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr
 100 105 110
 Ala Val Tyr Tyr Cys Ala Arg Asp Met Asn Ile Leu Ala Thr Val Pro
 115 120 125
 Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly
 130 135 140
 Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Asp Ile Gln
 145 150 155 160
 Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val
 165 170 175
 Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp
 180 185 190
 Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala
 195 200 205
 Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser
 210 215 220
 Gly Thr Asp Phe Thr Leu Thr Val Asn Ser Leu Gln Pro Glu Asp Phe
 225 230 235 240
 Ala Thr Tyr Tyr Cys Gln Gln Gly Asp Ser Val Pro Leu Thr Phe Gly
 245 250 255
 Gly Gly Thr Arg Leu Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro
 260 265 270
 Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro
 275 280 285
 Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu
 290 295 300
 Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys
 305 310 315 320

Gly Val Leu Leu Leu Ser Leu Val Ile Thr^{-SL} Leu Tyr Cys Lys Arg Gly
 325 330 335
 Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val
 340 345 350
 Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu
 355 360 365
 Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp
 370 375 380
 Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn
 385 390 395 400
 Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg
 405 410 415
 Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly
 420 425 430
 Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu
 435 440 445
 Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu
 450 455 460
 Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His
 465 470 475 480
 Met Gln Ala Leu Pro Pro Arg
 485

<210> 751
 <211> 264
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 751
 Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
 1 5 10 15

His Ala Ala Arg Pro Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val
 20 25 30

Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr
 35 40 45

Thr Phe Thr Gly Tyr Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln
 Page 499

_SL

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Met Asn Ile Leu Ala Thr Val Pro Phe Asp Ile Trp Gly
100 105 110

Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 753
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 753
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Val Asn Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Gly Asp Ser Val Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Arg Leu Glu Ile Lys
100 105

_SL

<210> 754
<211> 1461
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 754
atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60
ccccaagtcc aactcgttca atccggcgca gaagtcaaga agccaggagc atcagtgaag 120
gtgtcctgca aagcctcagg ctacatcttc acgggatact acatccactg ggtgcgccag 180
gctccggggc agggccttga gtggatgggc tggatcaacc ctaactctgg gggaaccaac 240
tacgctcaga agttccaggg gagggctact atgactcgcg atacctccat ctccactgcy 300
tacatggaac tctcgggact gagatccgac gatcctgccg tgtactactg cgcccgggac 360
atgaacatct tggcgaccgt gccgtttgac atttggggac agggcaccct cgtcactgtg 420
tcgagcgggtg gaggaggctc ggggggtggc ggatcaggag ggggaggaag cgacatccag 480
ctgactcaga gcccatcgct gttgtccgcy tcggtggggg atagagtgc cattacttgc 540
cgcgccagcc agagcatctc atcatatctg aattggtacc agcagaagcc cggaaaggcc 600
ccaaaactgc tgatctacgc tgcaagcagc ctccaatcgg gagtgcgctc acggttctcc 660
gggtccggtt cggaactga ctttaccctg accgtgaatt cgctgcaacc ggaggatttc 720
gccacgtact actgtcagca aggagactcc gtgccgctga ctttcggtgg aggcaccaag 780
gtcgaatca agaccactac ccagcaccg agggcaccga ccccggtcc taccatcgcc 840
tcccagcctc tgtccctgcy tccggaggca tgtagaccg cagctggtgg ggccgtgcat 900
accgggggtc ttgacttcgc ctgcgatatc tacatttggg cccctctggc tgggtacttgc 960
ggggtcctgc tgctttcact cgtgatcact ctttactgta agcgcggtcg gaagaagctg 1020
ctgtacatct ttaagcaacc cttcatgagg cctgtgcaga ctactcaaga ggaggacggc 1080
tgttcatgcc ggttcccaga ggaggaggaa ggcggctgcy aactgcgcyt gaaattcagc 1140
cgcagcgcag atgtccagc ctacaagcag ggcagaacc agctctacaa cgaactcaat 1200
cttggtcgga gagaggagta cgacgtgctg gacaagcgga gaggacggga cccagaaatg 1260
ggcgggaagc cgcgcagaaa gaatcccaa gagggcctgt acaacgagct ccaaaggat 1320
aagatggcag aagcctatag cgagattggt atgaaagggg aacgcagaag aggcaaaggc 1380
cacgacggac tgtaccaggg actcagcacc gccaccaagg acacctatga cgctcttcac 1440
atgcaggccc tgccgcctcg g 1461

<210> 755
<211> 487
<212> PRT
<213> Artificial Sequence

_SL

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 755

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val
20 25 30

Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr
35 40 45

Ile Phe Thr Gly Tyr Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln
50 55 60

Gly Leu Glu Trp Met Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn
65 70 75 80

Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser
85 90 95

Ile Ser Thr Ala Tyr Met Glu Leu Ser Gly Leu Arg Ser Asp Asp Pro
100 105 110

Ala Val Tyr Tyr Cys Ala Arg Asp Met Asn Ile Leu Ala Thr Val Pro
115 120 125

Phe Asp Ile Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly
130 135 140

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Asp Ile Gln
145 150 155 160

Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val
165 170 175

Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp
180 185 190

Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala
195 200 205

Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser
210 215 220

Gly Thr Asp Phe Thr Leu Thr Val Asn Ser Leu Gln Pro Glu Asp Phe
225 230 235 240

Ala Thr Tyr Tyr Cys Gln Gln Gly Asp Ser Val Pro Leu Thr Phe Gly
245 250 255

_SL

Gly Gly Thr Lys Val Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro
260 265 270

Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro
275 280 285

Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu
290 295 300

Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys
305 310 315 320

Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly
325 330 335

Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val
340 345 350

Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu
355 360 365

Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp
370 375 380

Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn
385 390 395 400

Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg
405 410 415

Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly
420 425 430

Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu
435 440 445

Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu
450 455 460

Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His
465 470 475 480

Met Gln Ala Leu Pro Pro Arg
485

<210> 756
<211> 264
<212> PRT
<213> Artificial Sequence

<220>

_SL

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 756

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val
20 25 30

Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr
35 40 45

Ile Phe Thr Gly Tyr Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln
50 55 60

Gly Leu Glu Trp Met Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn
65 70 75 80

Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser
85 90 95

Ile Ser Thr Ala Tyr Met Glu Leu Ser Gly Leu Arg Ser Asp Asp Pro
100 105 110

Ala Val Tyr Tyr Cys Ala Arg Asp Met Asn Ile Leu Ala Thr Val Pro
115 120 125

Phe Asp Ile Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly
130 135 140

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Asp Ile Gln
145 150 155 160

Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val
165 170 175

Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp
180 185 190

Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala
195 200 205

Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser
210 215 220

Gly Thr Asp Phe Thr Leu Thr Val Asn Ser Leu Gln Pro Glu Asp Phe
225 230 235 240

Ala Thr Tyr Tyr Cys Gln Gln Gly Asp Ser Val Pro Leu Thr Phe Gly
245 250 255

_SL

Gly Gly Thr Lys Val Glu Ile Lys
260

<210> 757
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 757
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ile Phe Thr Gly Tyr
20 25 30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Gly Leu Arg Ser Asp Asp Pro Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Met Asn Ile Leu Ala Thr Val Pro Phe Asp Ile Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 758
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 758
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
Page 506

_SL															
35				40								45			
Tyr	Ala 50	Ala	Ser	Ser	Leu	Gln 55	Ser	Gly	Val	Pro	Ser 60	Arg	Phe	Ser	Gly
Ser 65	Gly	Ser	Gly	Thr	Asp 70	Phe	Thr	Leu	Thr	Val 75	Asn	Ser	Leu	Gln	Pro 80
Glu	Asp	Phe	Ala	Thr 85	Tyr	Tyr	Cys	Gln	Gln 90	Gly	Asp	Ser	Val	Pro 95	Leu
Thr	Phe	Gly	Gly 100	Gly	Thr	Lys	Val	Glu 105	Ile	Lys					

```
<210> 759
<211> 1467
<212> DNA
<213> Artificial Sequence
```

<211> 1467

<212> DNA

<213> Artificial Sequence

$\langle 220 \rangle$

<221> source

```
<223> /note="Description of Artificial Sequence: Synthetic  
polynucleotide"
```

<400> 759

atggccctcc	ctgtcaccgc	cctgctgctt	ccgctggctc	ttctgctcca	cgccgctcgg	60
ccccaagtcc	aactccaaca	gtcaggcgca	gaagtgaaaa	agagcggtgc	atcggtgaaa	120
gtgtcatgca	aagcctcggg	ctacaccttc	actgactact	atatgcactg	gctgcggcag	180
gcaccgggac	agggacttga	gtggatggga	tggatcaacc	cgaattcagg	ggacactaac	240
tacgcgcaga	agttccaggg	gagagtgacc	ctgacgaggg	acacctcaat	ttcgaccgtc	300
tacatggaat	tgtcgcgcct	gagatcggac	gatactgctg	tgtactactg	tgcccgcgac	360
atgaacatcc	tcgcgactgt	gcctttttgat	atctggggac	aggggactat	ggtcaccggtt	420
tcctccgctt	ccggtggcgg	aggctcggga	ggccgggcct	ccggtggagg	aggcagcgac	480
atccagatga	ctcagagccc	ttcctcgcctg	agcgcctcag	tgggagatcg	cgtgaccatc	540
acttgccggg	ccagccagtc	catttcgtcc	tacctcaatt	ggtaccagca	gaagccggga	600
aaggcgccca	agctcttgat	ctacgctgcg	agctccctgc	aaagcgggggt	gccgagccga	660
ttctcggggt	ccggctcggg	aaccgacttc	actctgacca	tctcatccct	gcaaccagag	720
gactttgcc	cctactactg	ccaacaagga	gattctgtcc	cactgacgtt	cggcggagga	780
accaaggtcg	aaatcaagac	cactacccca	gcaccgaggc	caccacccc	ggctcctacc	840
atcgctccc	agcctctgtc	cctgcgtccg	gaggcatgta	gaccgcagc	tggtggggcc	900
gtgcataccc	ggggtcttga	cttcgcctgc	gatatctaca	tttgggcccc	tctggctggt	960
acttgccggg	tcctgctgct	ttcactcgtg	atcactcttt	actgtaagcg	cggtcggaag	1020
aagctgctgt	acatctttta	gcaacccttc	atgaggcctg	tgcagactac	tcaagaggag	1080
gacggctggt	catgccgggt	cccagaggag	gaggaaggcg	gctgcgaact	gcgcgtgaaa	1140

20

80

240

300

360

420

180

540

500

560

720

790

40

1000

—

_SL

ttcagccgca ggcgagatgc tccagcctac aagcaggggc agaaccagct ctacaacgaa	1200
ctcaatcttg gtcggagaga ggagtagcac gtgctggaca agcggagagg acgggaccca	1260
gaaatgggcg ggaagccgcg cagaaagaat cccaagagg gcctgtacaa cgagctccaa	1320
aaggataaga tggcagaagc ctatagcgag attggtatga aagggaacg cagaagaggc	1380
aaaggccacg acggactgta ccagggactc agcaccgccca ccaaggacac ctatgacgct	1440
cttcacatgc aggcctgcc gcctcgg	1467

<210> 760
 <211> 336
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 760
 Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
 1 5 10 15

His Ala Ala Arg Pro Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Val
 20 25 30

Lys Lys Ser Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr
 35 40 45

Thr Phe Thr Asp Tyr Tyr Met His Trp Leu Arg Gln Ala Pro Gly Gln
 50 55 60

Gly Leu Glu Trp Met Gly Trp Ile Asn Pro Asn Ser Gly Asp Thr Asn
 65 70 75 80

Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Leu Thr Arg Asp Thr Ser
 85 90 95

Ile Ser Thr Val Tyr Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr
 100 105 110

Ala Val Tyr Tyr Cys Ala Arg Asp Met Asn Ile Leu Ala Thr Val Pro
 115 120 125

Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser
 130 135 140

Gly Gly Gly Gly Ser Gly Gly Arg Ala Ser Gly Gly Gly Gly Ser Asp
 145 150 155 160

Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp
 165 170 175

Arg Val Thr Ile Thr Cys Arg Ala Ser Gln^{-SL} Ser Ile Ser Ser Tyr Leu
 180 185 190
 Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
 195 200 205
 Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
 210 215 220
 Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
 225 230 235 240
 Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Gly Asp Ser Val Pro Leu Thr
 245 250 255
 Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Thr Thr Thr Pro Ala Pro
 260 265 270
 Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu
 275 280 285
 Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg
 290 295 300
 Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly
 305 310 315 320
 Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys
 325 330 335

<210> 761
 <211> 266
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 761
 Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
 1 5 10 15

His Ala Ala Arg Pro Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Val
 20 25 30

Lys Lys Ser Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr
 35 40 45

Thr Phe Thr Asp Tyr Tyr Met His Trp Leu Arg Gln Ala Pro Gly Gln
 50 55 60

Gly Leu Glu Trp Met Gly Trp Ile Asn Pro Asn Ser Gly Asp Thr Asn
 Page 509

65					70					-SL 75					80
Tyr	Ala	Gln	Lys	Phe 85	Gln	Gly	Arg	Val	Thr 90	Leu	Thr	Arg	Asp	Thr 95	Ser
Ile	Ser	Thr	Val 100	Tyr	Met	Glu	Leu	Ser 105	Arg	Leu	Arg	Ser	Asp 110	Asp	Thr
Ala	Val	Tyr 115	Tyr	Cys	Ala	Arg	Asp 120	Met	Asn	Ile	Leu	Ala 125	Thr	Val	Pro
Phe	Asp 130	Ile	Trp	Gly	Gln	Gly 135	Thr	Met	Val	Thr	Val 140	Ser	Ser	Ala	Ser
Gly 145	Gly	Gly	Gly	Ser	Gly 150	Gly	Arg	Ala	Ser	Gly 155	Gly	Gly	Gly	Ser	Asp 160
Ile	Gln	Met	Thr	Gln 165	Ser	Pro	Ser	Ser	Leu 170	Ser	Ala	Ser	Val	Gly 175	Asp
Arg	Val	Thr	Ile 180	Thr	Cys	Arg	Ala	Ser 185	Gln	Ser	Ile	Ser	Ser 190	Tyr	Leu
Asn	Trp	Tyr 195	Gln	Gln	Lys	Pro	Gly 200	Lys	Ala	Pro	Lys	Leu 205	Leu	Ile	Tyr
Ala	Ala 210	Ser	Ser	Leu	Gln	Ser 215	Gly	Val	Pro	Ser	Arg 220	Phe	Ser	Gly	Ser
Gly 225	Ser	Gly	Thr	Asp	Phe 230	Thr	Leu	Thr	Ile	Ser 235	Ser	Leu	Gln	Pro	Glu 240
Asp	Phe	Ala	Thr	Tyr 245	Tyr	Cys	Gln	Gln	Gly 250	Asp	Ser	Val	Pro	Leu 255	Thr
Phe	Gly	Gly	Gly 260	Thr	Lys	Val	Glu	Ile 265	Lys						

```
<210> 762
<211> 121
<212> PRT
<213> Artificial Sequence
```

```
<220>  
<221> source  
<223> /note="Description of Artificial Sequence: Synthetic  
polypeptide"
```

<400> 762
Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Val Lys Lys Ser Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

_SL

Tyr Met His Trp Leu Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Pro Asn Ser Gly Asp Thr Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Met Asn Ile Leu Ala Thr Val Pro Phe Asp Ile Trp Gly
100 105 110

Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 763

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 763

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Gly Asp Ser Val Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 764

<211> 1461

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 764

```
atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg      60
ccccaagtcc aactcgtcca gtcaggagcg gaagtcaaga agcccggagc gtcagtcaaa      120
gtgtcatgca aagcctcggg ctacactttc actgggtact acatgcactg ggtgcgccag      180
gctccaggac agggactgga atggatggga tggatcaacc cgaactccgg tggcaccaat      240
tacgcccaga agttccaggg gagggtgacc atgactcgcg acacgtcgat cagcaccgca      300
tacatggagc tgtcaagact ccggtccgac gatactgccg tgtactactg cgcacgggac      360
atgaacattc tggccaccgt gccttttgac atctggggtc agggaaactat ggttaccgtg      420
tcctctggtg gaggcggctc cggcgggggg ggaagcggag gcggtggaag cgacattcag      480
atgaccagcgt cgccttcac cctttcggcg agcgtgggag atcgcgtcac tatcatttgt      540
cgggcctcgc agtccatctc cacctacctc aattggtacc agcagaagcc agggaaaagca      600
ccgaatctgc tgatctacgc cgcgttttcc ttgcaatcgg gagtgccaag cagattcagc      660
ggatcgggat caggcactga tttcacctc accatcaact cgctgcaacc ggaggatttc      720
gctacgtact attgccaaca aggagacagc gtgccgctca ccttcggcgg agggactaag      780
ctggaaatca agaccactac ccagcaccg aggccaccca ccccggtcc taccatcgcc      840
tcccagcctc tgtccctgcg tccggaggca tntagaccg cagctggtgg ggccgtgcat      900
acccggggtc ttgacttcgc ctgcgatatc tacatttggg cccctctggc tggctacttc      960
ggggtcctgc tgctttcact cgtgatcact ctttactgta agcgcggctc gaagaagctg     1020
ctgtacatct ttaagcaacc cttcatgagg cctgtgcaga ctactcaaga ggaggacggc     1080
tgttcatgcc gggtcccaga ggaggaggaa ggcggtcgcg aactgcgcgt gaaattcagc     1140
cgcagcgcag atgctccagc ctacaagcag gggcagaacc agctctacaa cgaactcaat     1200
cttggtcggg gagaggagta cgacgtgctg gacaagcgga gaggacggga ccagaaaatg     1260
ggcgggaagc cgcgcagaaa gaatcccaa gagggcctgt acaacgagct ccaaaaggat     1320
aagatggcag aagcctatag cgagattggg atgaaagggg aacgcagaag aggcaaaggc     1380
cacgacggac tgtaccaggg actcagcacc gccaccaagg acacctatga cgctcttcac     1440
atgcaggccc tgccgcctcg g                                     1461
```

<210> 765

<211> 487

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

_SL

<400> 765

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val
20 25 30

Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr
35 40 45

Thr Phe Thr Gly Tyr Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln
50 55 60

Gly Leu Glu Trp Met Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn
65 70 75 80

Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser
85 90 95

Ile Ser Thr Ala Tyr Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr
100 105 110

Ala Val Tyr Tyr Cys Ala Arg Asp Met Asn Ile Leu Ala Thr Val Pro
115 120 125

Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly
130 135 140

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln
145 150 155 160

Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val
165 170 175

Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Thr Tyr Leu Asn Trp
180 185 190

Tyr Gln Gln Lys Pro Gly Lys Ala Pro Asn Leu Leu Ile Tyr Ala Ala
195 200 205

Phe Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser
210 215 220

Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Gln Pro Glu Asp Phe
225 230 235 240

Ala Thr Tyr Tyr Cys Gln Gln Gly Asp Ser Val Pro Leu Thr Phe Gly
245 250 255

Gly Gly Thr Lys Leu Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro
260 265 270

_SL

Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro
275 280 285

Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu
290 295 300

Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys
305 310 315 320

Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly
325 330 335

Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val
340 345 350

Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu
355 360 365

Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp
370 375 380

Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn
385 390 395 400

Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg
405 410 415

Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly
420 425 430

Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu
435 440 445

Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu
450 455 460

Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His
465 470 475 480

Met Gln Ala Leu Pro Pro Arg
485

<210> 766

<211> 264

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

_SL

<400> 766

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15
His Ala Ala Arg Pro Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val
20 25 30
Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr
35 40 45
Thr Phe Thr Gly Tyr Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln
50 55 60
Gly Leu Glu Trp Met Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn
65 70 75 80
Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser
85 90 95
Ile Ser Thr Ala Tyr Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr
100 105 110
Ala Val Tyr Tyr Cys Ala Arg Asp Met Asn Ile Leu Ala Thr Val Pro
115 120 125
Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly
130 135 140
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Asp Ile Gln
145 150 155 160
Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val
165 170 175
Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Thr Tyr Leu Asn Trp
180 185 190
Tyr Gln Gln Lys Pro Gly Lys Ala Pro Asn Leu Leu Ile Tyr Ala Ala
195 200 205
Phe Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser
210 215 220
Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Gln Pro Glu Asp Phe
225 230 235 240
Ala Thr Tyr Tyr Cys Gln Gln Gly Asp Ser Val Pro Leu Thr Phe Gly
245 250 255
Gly Gly Thr Lys Leu Glu Ile Lys
260

_SL

<210> 767
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 767
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Met Asn Ile Leu Ala Thr Val Pro Phe Asp Ile Trp Gly
100 105 110

Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 768
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 768
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Thr Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Asn Leu Leu Ile
35 40 45

Tyr Ala Ala Phe Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
Page 516

50 55 60

Ser 65 Gly Ser Gly Thr 70 Asp Phe Thr Leu Thr 75 Ile Asn Ser Leu Gln Pro 80

Glu Asp Phe Ala 85 Thr Tyr Tyr Cys Gln 90 Gln Gly Asp Ser Val Pro 95 Leu

Thr Phe Gly 100 Gly Thr Lys Leu 105 Glu Ile Lys

ccagaaatgg gcggaagcc ggcagaaag aatccccaag agggcctgta caacgagctc 1320
 caaaaggata agatggcaga agcctatagc gagatttgta tgaaagggga acgcagaaga 1380
 ggcaaaggcc acgacggact gtaccaggga ctcagaccg ccaccaagga cacctatgac 1440
 gctcttcaca tgcaggccct gccgcctcgg 1470

<210> 770
 <211> 490
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 770
 Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
 1 5 10 15

His Ala Ala Arg Pro Glu Ile Gln Leu Val Gln Ser Gly Ala Glu Val
 20 25 30

Lys Lys Pro Gly Ala Thr Val Lys Ile Ser Cys Lys Gly Ser Gly Phe
 35 40 45

Asn Ile Glu Asp Tyr Tyr Ile His Trp Val Gln Gln Ala Pro Gly Lys
 50 55 60

Gly Leu Glu Trp Met Gly Arg Ile Asp Pro Glu Asn Asp Glu Thr Lys
 65 70 75 80

Tyr Gly Pro Ile Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Thr Ser
 85 90 95

Thr Asn Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr
 100 105 110

Ala Val Tyr Tyr Cys Ala Phe Arg Gly Gly Val Tyr Trp Gly Gln Gly
 115 120 125

Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 130 135 140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr
 145 150 155 160

Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile
 165 170 175

Asn Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser Asp Gly Lys Thr Tyr
 180 185 190

Leu Asn Trp₁₉₅ Leu Gln Gln Lys Pro₂₀₀ Gly Gln^{-SL} Pro Pro Lys₂₀₅ Arg Leu Ile
 Ser Leu₂₁₀ Val Ser Lys Leu Asp₂₁₅ Ser Gly Val Pro Asp₂₂₀ Arg Phe Ser Gly
 Ser Gly₂₂₅ Ser Gly Thr Asp₂₃₀ Phe Thr Leu Thr Ile₂₃₅ Ser Ser Leu Gln Ala₂₄₀
 Glu Asp Val Ala Val₂₄₅ Tyr Tyr Cys Trp Gln₂₅₀ Gly Thr His Phe Pro₂₅₅ Gly
 Thr Phe Gly Gly₂₆₀ Gly Thr Lys Val Glu₂₆₅ Ile Lys Thr Thr Thr₂₇₀ Pro Ala
 Pro Arg Pro₂₇₅ Pro Thr Pro Ala Pro₂₈₀ Thr Ile Ala Ser Gln₂₈₅ Pro Leu Ser
 Leu Arg₂₉₀ Pro Glu Ala Cys Arg₂₉₅ Pro Ala Ala Gly Gly₃₀₀ Ala Val His Thr
 Arg Gly₃₀₅ Leu Asp Phe Ala₃₁₀ Cys Asp Ile Tyr Ile₃₁₅ Trp Ala Pro Leu Ala₃₂₀
 Gly Thr Cys Gly Val₃₂₅ Leu Leu Leu Ser Leu₃₃₀ Val Ile Thr Leu Tyr₃₃₅ Cys
 Lys Arg Gly Arg₃₄₀ Lys Lys Leu Leu Tyr₃₄₅ Ile Phe Lys Gln Pro₃₅₀ Phe Met
 Arg Pro Val₃₅₅ Gln Thr Thr Gln Glu₃₆₀ Glu Asp Gly Cys Ser₃₆₅ Cys Arg Phe
 Pro Glu₃₇₀ Glu Glu Glu Gly Gly₃₇₅ Cys Glu Leu Arg Val₃₈₀ Lys Phe Ser Arg
 Ser Ala Asp Ala Pro Ala₃₉₀ Tyr Lys Gln Gly Gln₃₉₅ Asn Gln Leu Tyr Asn₄₀₀
 Glu Leu Asn Leu Gly₄₀₅ Arg Arg Glu Glu Tyr₄₁₀ Asp Val Leu Asp Lys₄₁₅ Arg
 Arg Gly Arg Asp₄₂₀ Pro Glu Met Gly Gly₄₂₅ Lys Pro Arg Arg Lys₄₃₀ Asn Pro
 Gln Glu Gly₄₃₅ Leu Tyr Asn Glu Leu₄₄₀ Gln Lys Asp Lys Met₄₄₅ Ala Glu Ala
 Tyr Ser₄₅₀ Glu Ile Gly Met Lys₄₅₅ Gly Glu Arg Arg Arg₄₆₀ Gly Lys Gly His

Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
 465 470 475 480

Ala Leu His Met Gln Ala Leu Pro Pro Arg
 485 490

<210> 771
 <211> 1470
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 771
 atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60
 cccgacgtgg tcatgactca aagcccagat tccttggctg tctcccttgg agaaagagca 120
 acgatcaatt gcaaaagctc gcagtccctg ttggactccg atggaaaaac ctacctcaac 180
 tggctgcagc agaagccggg acaaccacca aagcggctga tttccctcgt gtccaagctg 240
 gacagcggcg tgccggatcg cttctcgggc agcggctcgg gaaccgattt tactctcact 300
 atttcgtcac tgcaagcgga ggacgtggcg gtgtattact gctggcaggg cactcacttc 360
 ccgggtactt ttggtggagg taccaaagtc gaaatcaagg gtggaggcgg gagcggagga 420
 ggcgggtcgg gaggaggagg atcgggtggc ggaggctcag aaatccagct ggtgcagtca 480
 ggtgccgaag tgaagaagcc tggggccacg gtgaagatct cgtgcaaggg gagcggattc 540
 aacatcgagg attactacat ccattgggtg caacaggccc ctggcaaagg gctggaatgg 600
 atgggaagga tcgacccga gaatgacgag actaagtacg gcccgatctt ccaaggacgg 660
 gtgaccatca ctgcagacac ttcaaccaac accgtctaca tggaactctc ctcgctgcgc 720
 tccgaggaca ccgccgtgta ctactgtgct ttcagaggag gagtctactg gggacagggg 780
 acgaccgtga ccgtcagctc aaccactacc ccagcaccga ggccaccac cccggctcct 840
 accatcgctt cccagcctct gtccctgcgt ccggaggcat gtagaccgc agctggtggg 900
 gccgtgcata cccgggggtct tgacttcgcc tgcgatatct acatttgggc ccctctggct 960
 ggtacttgcg gggctctgct gctttcactc gtgatcactc tttactgtaa gcgcggctcgg 1020
 aagaagctgc tgtacatctt taagcaacc ttcatgaggc ctgtgcagac tactcaagag 1080
 gaggacggct gttcatgccg gttcccagag gaggaggaag gcggctgcga actgcgcgtg 1140
 aaattcagcc gcagcgcaga tgctccagcc tacaagcagg ggcagaacca gctctacaac 1200
 gaactcaatc ttggtcggag agaggagtac gacgtgctgg acaagcggag aggacgggac 1260
 ccagaaatgg gcgggaagcc gcgcagaaag aatccccaag agggcctgta caacgagctc 1320
 caaaaggata agatggcaga agcctatagc gagattggta tgaaagggga acgcagaaga 1380
 ggcaaaggcc acgacggact gtaccaggga ctcagcaccg ccaccaagga cacctatgac 1440
 gctcttcaca tgcaggccct gccgcctcgg 1470

_SL

<210> 772
<211> 490
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 772
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asp Val Val Met Thr Gln Ser Pro Asp Ser Leu
20 25 30

Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln
35 40 45

Ser Leu Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Gln Gln
50 55 60

Lys Pro Gly Gln Pro Pro Lys Arg Leu Ile Ser Leu Val Ser Lys Leu
65 70 75 80

Asp Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
85 90 95

Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr
100 105 110

Tyr Cys Trp Gln Gly Thr His Phe Pro Gly Thr Phe Gly Gly Gly Thr
115 120 125

Lys Val Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
130 135 140

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Gln Leu Val Gln Ser
145 150 155 160

Gly Ala Glu Val Lys Lys Pro Gly Ala Thr Val Lys Ile Ser Cys Lys
165 170 175

Gly Ser Gly Phe Asn Ile Glu Asp Tyr Tyr Ile His Trp Val Gln Gln
180 185 190

Ala Pro Gly Lys Gly Leu Glu Trp Met Gly Arg Ile Asp Pro Glu Asn
195 200 205

Asp Glu Thr Lys Tyr Gly Pro Ile Phe Gln Gly Arg Val Thr Ile Thr
210 215 220

_SL

Ala Asp Thr Ser Thr Asn Thr Val Tyr Met Glu Leu Ser Ser Leu Arg
225 230 235 240

Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Phe Arg Gly Gly Val Tyr
245 250 255

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Thr Thr Thr Pro Ala
260 265 270

Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser
275 280 285

Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr
290 295 300

Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala
305 310 315 320

Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys
325 330 335

Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met
340 345 350

Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe
355 360 365

Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg
370 375 380

Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn
385 390 395 400

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
405 410 415

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
420 425 430

Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
435 440 445

Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
450 455 460

Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
465 470 475 480

Ala Leu His Met Gln Ala Leu Pro Pro Arg
485 490

_SL

<210> 773
<211> 1470
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 773
atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60
cccgaaatcc agctggtgca aagcggagcc gaggtgaaga agcccggaga atccctgcgc 120
atctcgtgta agggttccgg ctttaacatc gaggattact acatccactg ggtgagacag 180
atgccgggca aaggtctgga atggatgggc cgcacgacc cggagaacga cgaaacaaaa 240
tacggacca tcttccaagg acatgtgact atttccgcgg atacctccat caacactgtc 300
tacttgca gtgagctcgt caaggcgtcg gataccgcc tgtactactg cgcattcaga 360
ggaggtgtgt actggggcca gggcactacg gtcaccgtgt cctcgggagg tggaggggtca 420
ggaggcggag gtcggggcgg tggaggatca ggaggaggag gaagcgatgt ggtcatgact 480
caatccccac tgtcactgcc tgtcactctg gggcaaccgg cttccatctc atgcaagtca 540
agccaatcgc tgctcgactc cgacggaaaa acctacctca attggcttca gcagcgccca 600
ggccagtcgc ctcgagggtc gatctcactc gtgtcgaagc ttgactccgg ggtgccggat 660
cggtttagcg gaagcggatc ggggaccgac ttcacgttga agattagccg ggtggaagcc 720
gaggacgtgg gagtctatta ctgctggcag gggaccact tcccggggac tttcggagga 780
ggcaccaaaag tcgagattaa gaccactacc ccagcaccga ggccaccac cccggctcct 840
accatcgcct cccagcctct gtccctgcgt ccggaggcat gtagaccgc agctggtggg 900
gccgtgcata cccggggtct tgacttcgcc tgcgatatct acatttgggc ccctctggct 960
ggtacttgcg gggctcgtct gctttcactc gtgatcactc tttactgtaa gcgcgggtcgg 1020
aagaagctgc tgtacatctt taagcaacct ttcattgaggc ctgtgcagac tactcaagag 1080
gaggacggct gttcatgccg gttcccagag gaggaggaag gcggctgcga actgcgcgtg 1140
aaattcagcc gcagcgaga tgctccagcc tacaagcagg ggcagaacca gctctacaac 1200
gaactcaatc ttggtcggag agaggagtac gacgtgctgg acaagcggag aggacgggac 1260
ccagaaatgg gcgggaagcc gcgcagaaag aatccccaag agggcctgta caacgagctc 1320
caaaaggata agatggcaga agcctatagc gagattggta tgaaagggga acgcagaaga 1380
ggcaaaggcc acgacggact gtaccaggga ctcagcaccg ccaccaagga cacctatgac 1440
gctcttcaca tgcaggccct gccgcctcgg 1470

<210> 774
<211> 490
<212> PRT
<213> Artificial Sequence

_SL

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 774

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Glu Ile Gln Leu Val Gln Ser Gly Ala Glu Val
20 25 30

Lys Lys Pro Gly Glu Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Phe
35 40 45

Asn Ile Glu Asp Tyr Tyr Ile His Trp Val Arg Gln Met Pro Gly Lys
50 55 60

Gly Leu Glu Trp Met Gly Arg Ile Asp Pro Glu Asn Asp Glu Thr Lys
65 70 75 80

Tyr Gly Pro Ile Phe Gln Gly His Val Thr Ile Ser Ala Asp Thr Ser
85 90 95

Ile Asn Thr Val Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr
100 105 110

Ala Met Tyr Tyr Cys Ala Phe Arg Gly Gly Val Tyr Trp Gly Gln Gly
115 120 125

Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
130 135 140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr
145 150 155 160

Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly Gln Pro Ala Ser Ile
165 170 175

Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser Asp Gly Lys Thr Tyr
180 185 190

Leu Asn Trp Leu Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile
195 200 205

Ser Leu Val Ser Lys Leu Asp Ser Gly Val Pro Asp Arg Phe Ser Gly
210 215 220

Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala
225 230 235 240

Glu Asp Val Gly Val Tyr Tyr Cys Trp Gln Gly Thr His Phe Pro Gly
245 250 255

_SL

Thr Phe Gly Gly Thr Lys Val Glu Ile Lys Thr Thr Thr Pro Ala
260 265 270

Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser
275 280 285

Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr
290 295 300

Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala
305 310 315 320

Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys
325 330 335

Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met
340 345 350

Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe
355 360 365

Pro Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg
370 375 380

Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn
385 390 395 400

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
405 410 415

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
420 425 430

Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
435 440 445

Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
450 455 460

Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
465 470 475 480

Ala Leu His Met Gln Ala Leu Pro Pro Arg
485 490

<210> 775

<211> 1470

<212> DNA

<213> Artificial Sequence

<220>

_SL

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 775

```
atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg      60
cccgacgtcg tcatgacca atccctctc tccctgccgg tcaccctggg tcagccggcg      120
tcgatctcat gcaaaagctc acagtccctg ctggattcgg acggaaaaac ctacttgaac      180
tggctccaac agaggccggg tcagtcccct cgcagactga tctcgctggt gagcaagctc      240
gactcgggtg tgccggatcg gttctccggg tcaggatcgg gcaccgactt tacgctcaag      300
atttcgagag tggaggccga ggatgtggga gtgtactatt gctggcaggg cacgcatttc      360
cccgggacct ttggaggcgg gactaagggt gaaatcaagg gaggtggcgg atcaggcgga      420
ggaggcagcg gcggaggtag atcaggaggc ggagggtcag agatccagct ggtccaaagc      480
ggagcagagg tgaagaagcc aggcgagtcc cttcgcatth cgtgcaaagg gagcggcttc      540
aacattgaag attactacat ccactgggtg cggcaaatgc caggaaaggg tctggaatgg      600
atgggacgga tcgaccaga aaatgatgaa actaagtacg gaccgatctt ccaaggacac      660
gtcactatct ccgcggacac ttcgatcaac accgtgtacc tccagtggag cagcttgaaa      720
gcctccgaca ccgctatgta ctactgtgcc ttccgcggag gagtctactg gggacagggg      780
actactgtga ccgtgtcgtc caccactacc ccagcaccga ggccaccac cccggctcct      840
accatcgctt cccagcctct gtccctgcgt ccggaggcat gtagaccgc agctgggtgg      900
gccgtgcata cccgggtctt tgacttcgcc tgcgatatct acatttgggc ccctctggct      960
ggtacttgcg gggctctgct gctttcactc gtgatcactc tttactgtaa gcgcggctcg      1020
aagaagctgc tgtacatctt taagcaacc ttcatgaggc ctgtgcagac tactcaagag      1080
gaggacggct gttcatgccg gttcccagag gaggaggaag gcggctgcga actgcgcgtg      1140
aaattcagcc gcagcgcaga tgctccagcc tacaagcagg ggcagaacca gctctacaac      1200
gaactcaatc ttggtcggag agaggagtac gacgtgctgg acaagcggag aggacgggac      1260
ccagaaatgg gcgggaagcc gcgcagaaag aatccccaag agggcctgta caacgagctc      1320
caaaaggata agatggcaga agcctatagc gagattggta tgaaagggga acgcagaaga      1380
ggcaaaggcc acgacggact gtaccaggga ctcagaccg ccaccaagga cacctatgac      1440
gctcttcaca tgcaggccct gccgcctcgg      1470
```

<210> 776

<211> 490

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 776

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu

1 5 10 ^{-SL} 15

His Ala Ala Arg Pro Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu
20 25 30

Pro Val Thr Leu Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln
35 40 45

Ser Leu Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Gln Gln
50 55 60

Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile Ser Leu Val Ser Lys Leu
65 70 75 80

Asp Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
85 90 95

Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr
100 105 110

Tyr Cys Trp Gln Gly Thr His Phe Pro Gly Thr Phe Gly Gly Gly Thr
115 120 125

Lys Val Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
130 135 140

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Gln Leu Val Gln Ser
145 150 155 160

Gly Ala Glu Val Lys Lys Pro Gly Glu Ser Leu Arg Ile Ser Cys Lys
165 170 175

Gly Ser Gly Phe Asn Ile Glu Asp Tyr Tyr Ile His Trp Val Arg Gln
180 185 190

Met Pro Gly Lys Gly Leu Glu Trp Met Gly Arg Ile Asp Pro Glu Asn
195 200 205

Asp Glu Thr Lys Tyr Gly Pro Ile Phe Gln Gly His Val Thr Ile Ser
210 215 220

Ala Asp Thr Ser Ile Asn Thr Val Tyr Leu Gln Trp Ser Ser Leu Lys
225 230 235 240

Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala Phe Arg Gly Gly Val Tyr
245 250 255

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Thr Thr Thr Pro Ala
260 265 270

Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser

_SL

275 280 285

Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr
 290 295 300

Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala
 305 310 315 320

Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys
 325 330 335

Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met
 340 345 350

Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe
 355 360 365

Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg
 370 375 380

Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn
 385 390 395 400

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
 405 410 415

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
 420 425 430

Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
 435 440 445

Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
 450 455 460

Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
 465 470 475 480

Ala Leu His Met Gln Ala Leu Pro Pro Arg
 485 490

<210> 777
 <211> 1470
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polynucleotide"

<400> 777
 atggcctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg

60

_SL

cccgaaatcc agctcgtgca gagcggagcc gaggtcaaga aaccgggtgc taccgtgaag	120
atttcatgca agggatcggg cttcaacatc gaggattact acatccactg ggtgcagcag	180
gcaccaggaa aaggacttga atggatgggc cggatcgacc cggaaaatga cgagactaag	240
tacggcccta tcttccaagg acgggtgacg atcaccgcag aactagcac caacaccgtc	300
tatatggaac tctcgtccct gaggtccgaa gatactgccg tgtactactg tgcgtttcgc	360
ggaggtgtgt actggggaca ggggtaccacc gtcaccgtgt catcgggcgg tggaggctcc	420
ggtggaggag ggtcaggagg cgggtggaagc ggaggaggcg gcagcgacgt ggtcatgact	480
caatcgccgc tgtcgtgcc cgtcactctg ggacaaccgc cgtccatcag ctgcaaatcc	540
tcgcagtcac tgcttgactc cgatggaaag acctacctca actggctgca gcaacgccc	600
ggccaatccc caagacgcct gatctcgttg gtgtcaaagc tggactcagg ggtgccggac	660
cggttctccg ggagcgggtc gggcacggat ttcactctca agatctccag agtggaaagcc	720
gaggatgtgg gagtctacta ctgctggcag ggaaccatt tccctggaac ttttggcgga	780
ggaactaagg tcgagattaa aaccactacc ccagcaccga ggccaccac cccggctcct	840
accatcgctt cccagcctct gtccctgcgt ccggaggcat gtagaccgc agctggtggg	900
gccgtgcata cccggggtct tgacttcgcc tgcgatatct acatttgggc ccctctggct	960
ggtacttgcg gggtcctgct gctttcactc gtgatcactc tttactgtaa gcgcggctcg	1020
aagaagctgc tgtacatctt taagcaacc ttcattgaggc ctgtgcagac tactcaagag	1080
gaggacggct gttcatgccg gttcccagag gaggaggaag gcggctgcga actgcgcgtg	1140
aaattcagcc gcagcgaga tgctccagcc tacaagcagg ggcagaacca gctctacaac	1200
gaactcaatc ttggtcggag agaggagtac gacgtgctgg acaagcggag aggacgggac	1260
ccagaaatgg gcgggaagcc gcgcagaaag aatccccaag agggcctgta caacgagctc	1320
caaaaggata agatggcaga agcctatagc gagattggta tgaaagggga acgcagaaga	1380
ggcaaaggcc acgacggact gtaccaggga ctcagaccgc ccaccaagga cacctatgac	1440
gctcttcaca tgcaggccct gccgcctcgg	1470

<210> 778

<211> 490

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 778

Met	Ala	Leu	Pro	Val	Thr	Ala	Leu	Leu	Leu	Pro	Leu	Ala	Leu	Leu	Leu
1				5				10						15	

His	Ala	Ala	Arg	Pro	Glu	Ile	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val
			20					25					30		

Lys Lys Pro Gly Ala Thr Val Lys Ile Ser ^{-SL}Cys Lys Gly Ser Gly Phe
 35 40 45
 Asn Ile Glu Asp Tyr Tyr Ile His Trp Val Gln Gln Ala Pro Gly Lys
 50 55 60
 Gly Leu Glu Trp Met Gly Arg Ile Asp Pro Glu Asn Asp Glu Thr Lys
 65 70 75 80
 Tyr Gly Pro Ile Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Thr Ser
 85 90 95
 Thr Asn Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr
 100 105 110
 Ala Val Tyr Tyr Cys Ala Phe Arg Gly Gly Val Tyr Trp Gly Gln Gly
 115 120 125
 Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 130 135 140
 Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr
 145 150 155 160
 Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly Gln Pro Ala Ser Ile
 165 170 175
 Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser Asp Gly Lys Thr Tyr
 180 185 190
 Leu Asn Trp Leu Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile
 195 200 205
 Ser Leu Val Ser Lys Leu Asp Ser Gly Val Pro Asp Arg Phe Ser Gly
 210 215 220
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala
 225 230 235 240
 Glu Asp Val Gly Val Tyr Tyr Cys Trp Gln Gly Thr His Phe Pro Gly
 245 250 255
 Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Thr Thr Thr Pro Ala
 260 265 270
 Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser
 275 280 285
 Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr
 290 295 300

Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr^{-SL} Ile Trp Ala Pro Leu Ala
 305 310 315 320
 Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys
 325 330 335
 Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met
 340 345 350
 Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe
 355 360 365
 Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg
 370 375 380
 Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn
 385 390 395 400
 Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
 405 410 415
 Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
 420 425 430
 Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
 435 440 445
 Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
 450 455 460
 Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
 465 470 475 480
 Ala Leu His Met Gln Ala Leu Pro Pro Arg
 485 490

<210> 779
 <211> 1470
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 779
 atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60
 cccgagattc agctcgtgca atcgaggagcg gaagtcaaga agccaggaga gtccttgctg 120
 atctcatgca agggtagcgg cttaacatc gaggattact acatccactg ggtgaggcag 180
 atgccgggga agggactcga atggatggga cggatcgacc cagaaaacga cgaaactaag 240
 tacggtccga tcttccaagg ccatgtgact attagcgccg atacttcaat caataccgtg 300

_SL

tatctgcaat ggtcctcatt gaaagcctca gataccgcga tgtactactg tgctttcaga 360
ggaggggtct actggggaca gggaactacc gtgactgtct cgtccggcgg aggcgggtca 420
ggaggtggcg gcagcggagg aggaggggtcc ggcggaggtg ggtccgacgt cgtgatgacc 480
cagagccctg acagcctggc agtgagcctg ggcgaaagag ctaccattaa ctgcaaatcg 540
tcgcagagcc tgctggactc ggacggaaaa acgtacctca attggctgca gcaaaagcct 600
ggccagccac cgaagcgcct tatctcactg gtgtcgaagc tggattcggg agtgcccgat 660
cgcttctccg gctcgggatc gggactgac ttcacctca ctatctctc gcttcaagca 720
gaggacgtgg ccgtctacta ctgctggcag ggaaccact ttccgggaac cttcggcgga 780
gggacgaaag tggagatcaa gaccactacc ccagcaccga ggccaccac cccggctcct 840
accatgcct cccagcctct gtccctgcgt ccggaggcat gtagaccgc agctggtggg 900
gccgtgcata cccgggtct tgacttcgcc tgcgatatct acatttgggc ccctctggct 960
ggtacttgcg gggtcctgct gctttcactc gtgatcactc tttactgtaa gcgcggtcgg 1020
aagaagctgc tgtacatctt taagcaacc ttcatgaggc ctgtgcagac tactcaagag 1080
gaggacggct gttcatgccg gttcccagag gaggaggaag gcggctgcga actgcgcgtg 1140
aaattcagcc gcagcgcaga tgctccagcc tacaagcagg ggcagaacca gctctacaac 1200
gaactcaatc ttggtcggag agaggagtac gacgtgctgg acaagcggag aggacgggac 1260
ccagaaatgg gcgggaagcc gcgcagaaag aatccccaag agggcctgta caacgagctc 1320
caaaaggata agatggcaga agcctatagc gagattggta tgaaagggga acgcagaaga 1380
ggcaaaggcc acgacggact gtaccagga ctcagcaccg ccaccaagga cacctatgac 1440
gctcttcaca tgcaggccct gccgcctcgg 1470

<210> 780

<211> 490

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 780

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Glu Ile Gln Leu Val Gln Ser Gly Ala Glu Val
20 25 30

Lys Lys Pro Gly Glu Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Phe
35 40 45

Asn Ile Glu Asp Tyr Tyr Ile His Trp Val Arg Gln Met Pro Gly Lys
50 55 60

_SL

Gly Leu Glu Trp Met Gly Arg Ile Asp Pro Glu Asn Asp Glu Thr Lys
65 70 75 80

Tyr Gly Pro Ile Phe Gln Gly His Val Thr Ile Ser Ala Asp Thr Ser
85 90 95

Ile Asn Thr Val Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr
100 105 110

Ala Met Tyr Tyr Cys Ala Phe Arg Gly Gly Val Tyr Trp Gly Gln Gly
115 120 125

Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
130 135 140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr
145 150 155 160

Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile
165 170 175

Asn Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser Asp Gly Lys Thr Tyr
180 185 190

Leu Asn Trp Leu Gln Gln Lys Pro Gly Gln Pro Pro Lys Arg Leu Ile
195 200 205

Ser Leu Val Ser Lys Leu Asp Ser Gly Val Pro Asp Arg Phe Ser Gly
210 215 220

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala
225 230 235 240

Glu Asp Val Ala Val Tyr Tyr Cys Trp Gln Gly Thr His Phe Pro Gly
245 250 255

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Thr Thr Thr Pro Ala
260 265 270

Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser
275 280 285

Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr
290 295 300

Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala
305 310 315 320

Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys
325 330 335

_SL

Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met
340 345 350

Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe
355 360 365

Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg
370 375 380

Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn
385 390 395 400

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
405 410 415

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
420 425 430

Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
435 440 445

Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
450 455 460

Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
465 470 475 480

Ala Leu His Met Gln Ala Leu Pro Pro Arg
485 490

<210> 781

<211> 1470

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 781

atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60

cccgacgtgg tgatgactca gtcgcctgac tcgctggctg tgtcccttgg agagcgggcc 120

actatcaatt gcaagtcac ccagtcgctg ctggattccg acgggaaaac ctacctcaat 180

tggctgcagc aaaaaccggg acagcctcca aagcggctca tcagcctggt gtccaagttg 240

gacagcggcg tgccagaccg cttctccggt tcgggaagcg gtactgattt cagcgtgacc 300

atctcatccc tccaagcgga ggatgtggca gtctactact gttggcaggg cagcatttt 360

ccgggcactt ttggaggagg gaccaaggtc gaaatcaagg gaggaggtgg ctcgggcgga 420

ggaggctcgg gaggaggagg atcaggaggc ggtggaagcg agattcaact ggtccagagc 480

_SL

ggcgcagaag tcaagaagcc ggggtgaatcg ctcagaatct cgtgcaaagg atcgggattc	540
aacatcgagg actactacat tctactgggtc agacaaatgc cgggcaaagg gctggaatgg	600
atgggggagga tcgaccccgaa aaacgatgaa accaagtacg gaccaatctt ccaagggcac	660
gtgaccattt cggcggacac ctcaatcaac actgtgtacc tccagtggag ctcacttaag	720
gccagcgata ccgccatgta ctattgcgct ttccgcggag ggggtgtactg gggacagggc	780
actactgtga ccgtgtcatc caccactacc ccagcaccga ggccaccac cccggctcct	840
accatcgctt cccagcctct gtccctgcgt ccggaggcat gtagaccgc agctgggtggg	900
gccgtgcata cccgggggtct tgacttcgcc tgcgatatct acatttgggc ccctctggct	960
gggtactgtcg ggggtcctgct gctttcactc gtgatcactc tttactgtaa gcgcggtcgg	1020
aagaagctgc tgtacatctt taagcaacc ttcatgaggc ctgtgcagac tactcaagag	1080
gaggacggct gttcatgccg gttcccagag gaggaggaag gcggctgcga actgcgcgtg	1140
aaattcagcc gcagcgcaga tgctccagcc tacaagcagg ggcagaacca gctctacaac	1200
gaactcaatc ttggtcggag agaggagtac gacgtgctgg acaagcggag aggacgggac	1260
ccagaaatgg gcgggaagcc gcgcagaaag aatccccaag agggcctgta caacgagctc	1320
caaaaggata agatggcaga agcctatagc gagattggta tgaaagggga acgcagaaga	1380
ggcaaaggcc acgacggact gtaccagga ctcagcaccg ccaccaagga cacctatgac	1440
gctcttcaca tgcaggccct gccgcctcgg	1470

<210> 782

<211> 490

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 782

Met	Ala	Leu	Pro	Val	Thr	Ala	Leu	Leu	Leu	Pro	Leu	Ala	Leu	Leu	Leu
1				5				10					15		

His	Ala	Ala	Arg	Pro	Asp	Val	Val	Met	Thr	Gln	Ser	Pro	Asp	Ser	Leu
			20					25					30		

Ala	Val	Ser	Leu	Gly	Glu	Arg	Ala	Thr	Ile	Asn	Cys	Lys	Ser	Ser	Gln
		35					40					45			

Ser	Leu	Leu	Asp	Ser	Asp	Gly	Lys	Thr	Tyr	Leu	Asn	Trp	Leu	Gln	Gln
	50					55					60				

Lys	Pro	Gly	Gln	Pro	Pro	Lys	Arg	Leu	Ile	Ser	Leu	Val	Ser	Lys	Leu
65					70					75					80

Asp	Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp
				85					90					95	

_SL

Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr
100 105 110

Tyr Cys Trp Gln Gly Thr His Phe Pro Gly Thr Phe Gly Gly Gly Thr
115 120 125

Lys Val Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
130 135 140

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Gln Leu Val Gln Ser
145 150 155 160

Gly Ala Glu Val Lys Lys Pro Gly Glu Ser Leu Arg Ile Ser Cys Lys
165 170 175

Gly Ser Gly Phe Asn Ile Glu Asp Tyr Tyr Ile His Trp Val Arg Gln
180 185 190

Met Pro Gly Lys Gly Leu Glu Trp Met Gly Arg Ile Asp Pro Glu Asn
195 200 205

Asp Glu Thr Lys Tyr Gly Pro Ile Phe Gln Gly His Val Thr Ile Ser
210 215 220

Ala Asp Thr Ser Ile Asn Thr Val Tyr Leu Gln Trp Ser Ser Leu Lys
225 230 235 240

Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala Phe Arg Gly Gly Val Tyr
245 250 255

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Thr Thr Thr Pro Ala
260 265 270

Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser
275 280 285

Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr
290 295 300

Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala
305 310 315 320

Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys
325 330 335

Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met
340 345 350

Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe
355 360 365

_SL

Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg
370 375 380

Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn
385 390 395 400

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
405 410 415

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
420 425 430

Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
435 440 445

Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
450 455 460

Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
465 470 475 480

Ala Leu His Met Gln Ala Leu Pro Pro Arg
485 490

<210> 783

<211> 1470

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 783

atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60

cccgatgtgg tcatgacgca gtcaccactg tccctccccg tgacccttgg acagccagcg 120

tcgattagct gcaagtcac ccaatccctg ctcgattcgg atggaaagac ctatctcaac 180

tggctgcagc aaagaccggt tcagagccct aggagactca tctcgttggt gtcaaagctg 240

gacagcggag tgccggaccg gttttccggt tcgggatcgg ggacggactt cactctgaag 300

atttcacggg tggaagctga ggatgtggga gtgtactact gctggcaggg aaccatttc 360

cctggcactt ttggcggagg aactaaggtc gaaatcaagg gaggaggtgg ctcgggagga 420

ggcggatcgg gcggaggcgg gagcggcgga ggagggtccg aaatccaact tgtccagtca 480

ggagccgaag tgaagaaacc gggagccacc gtcaaaatca gctgtaaggg atcgggatcc 540

aatatcgagg actactacat cactgggtg cagcaagctc cgggcaaagg actggagtgg 600

atggggcgca tcgaccaga gaacgacgaa accaaatag gcccgatctt ccaagggcgg 660

gtgaccatca ccgcgacac ctcaactaac actgtgtaca tggagctgag ctccctgcgc 720

_SL

```
tccgaagata ctgcagtcta ctactgcgcc ttccgcggtg gtgtgtactg gggacagggc 780
accactgtga ctgtcagctc gaccactacc ccagcaccga ggccaccac cccggctcct 840
accatcgctt cccagcctct gtccctgcgt ccggaggcat gtagaccgc agctggtggg 900
gccgtgcata cccggggtct tgacttcgcc tgcgatatct acatttgggc ccctctggct 960
gggtacttgcg ggggtcctgct gctttcactc gtgatcactc tttactgtaa gcgcggtcgg 1020
aagaagctgc tgtacatctt taagcaaccc ttcattgaggc ctgtgcagac tactcaagag 1080
gaggacggct gttcatgccg gttcccagag gaggaggaag gcggctgcga actgcgcgtg 1140
aaattcagcc gcagcgcaga tgctccagcc tacaagcagg ggcagaacca gctctacaac 1200
gaactcaatc ttggtcggag agaggagtac gacgtgctgg acaagcggag aggacgggac 1260
ccagaaatgg gcgggaagcc gcgcagaaag aatccccaag agggcctgta caacgagctc 1320
caaaaggata agatggcaga agcctatagc gagattggta tgaaagggga acgcagaaga 1380
ggcaaaggcc acgacggact gtaccaggga ctcagcaccg ccaccaagga cacctatgac 1440
gctcttcaca tgcaggccct gccgcctcgg 1470
```

<210> 784

<211> 490

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 784

```
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1          5          10          15
```

```
His Ala Ala Arg Pro Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu
          20          25          30
```

```
Pro Val Thr Leu Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln
          35          40          45
```

```
Ser Leu Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Gln Gln
50          55          60
```

```
Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile Ser Leu Val Ser Lys Leu
65          70          75          80
```

```
Asp Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
          85          90          95
```

```
Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr
100          105          110
```

```
Tyr Cys Trp Gln Gly Thr His Phe Pro Gly Thr Phe Gly Gly Gly Thr
Page 538
```

115					120					_SL					125				
Lys	Val	Glu	Ile	Lys	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly				
	130					135					140								
Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Glu	Ile	Gln	Leu	Val	Gln	Ser				
145					150					155					160				
Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ala	Thr	Val	Lys	Ile	Ser	Cys	Lys				
				165					170					175					
Gly	Ser	Gly	Phe	Asn	Ile	Glu	Asp	Tyr	Tyr	Ile	His	Trp	Val	Gln	Gln				
			180					185					190						
Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Met	Gly	Arg	Ile	Asp	Pro	Glu	Asn				
		195					200					205							
Asp	Glu	Thr	Lys	Tyr	Gly	Pro	Ile	Phe	Gln	Gly	Arg	Val	Thr	Ile	Thr				
	210					215					220								
Ala	Asp	Thr	Ser	Thr	Asn	Thr	Val	Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg				
225					230					235					240				
Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Phe	Arg	Gly	Gly	Val	Tyr				
				245					250					255					
Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Thr	Thr	Thr	Pro	Ala				
			260					265						270					
Pro	Arg	Pro	Pro	Thr	Pro	Ala	Pro	Thr	Ile	Ala	Ser	Gln	Pro	Leu	Ser				
		275					280					285							
Leu	Arg	Pro	Glu	Ala	Cys	Arg	Pro	Ala	Ala	Gly	Gly	Ala	Val	His	Thr				
	290					295					300								
Arg	Gly	Leu	Asp	Phe	Ala	Cys	Asp	Ile	Tyr	Ile	Trp	Ala	Pro	Leu	Ala				
305					310					315					320				
Gly	Thr	Cys	Gly	Val	Leu	Leu	Leu	Ser	Leu	Val	Ile	Thr	Leu	Tyr	Cys				
				325					330					335					
Lys	Arg	Gly	Arg	Lys	Lys	Leu	Leu	Tyr	Ile	Phe	Lys	Gln	Pro	Phe	Met				
			340					345					350						
Arg	Pro	Val	Gln	Thr	Thr	Gln	Glu	Glu	Asp	Gly	Cys	Ser	Cys	Arg	Phe				
		355					360					365							
Pro	Glu	Glu	Glu	Glu	Gly	Gly	Cys	Glu	Leu	Arg	Val	Lys	Phe	Ser	Arg				
	370					375					380								
Ser	Ala	Asp	Ala	Pro	Ala	Tyr	Lys	Gln	Gly	Gln	Asn	Gln	Leu	Tyr	Asn				

385 390 395 400															
Glu	Leu	Asn	Leu	Gly ₄₀₅	Arg	Arg	Glu	Glu	Tyr ₄₁₀	Asp	Val	Leu	Asp	Lys ₄₁₅	Arg
Arg	Gly	Arg	Asp ₄₂₀	Pro	Glu	Met	Gly	Gly ₄₂₅	Lys	Pro	Arg	Arg	Lys ₄₃₀	Asn	Pro
Gln	Glu	Gly ₄₃₅	Leu	Tyr	Asn	Glu	Leu ₄₄₀	Gln	Lys	Asp	Lys	Met ₄₄₅	Ala	Glu	Ala
Tyr	Ser ₄₅₀	Glu	Ile	Gly	Met	Lys ₄₅₅	Gly	Glu	Arg	Arg	Arg ₄₆₀	Gly	Lys	Gly	His
Asp ₄₆₅	Gly	Leu	Tyr	Gln	Gly ₄₇₀	Leu	Ser	Thr	Ala	Thr ₄₇₅	Lys	Asp	Thr	Tyr	Asp ₄₈₀
Ala	Leu	His	Met	Gln ₄₈₅	Ala	Leu	Pro	Pro	Arg ₄₉₀						

```
<210> 785
<211> 1461
<212> DNA
<213> Artificial Sequence
```

```
<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"
```

<400> 785						
atggccctcc	ctgtcaccgc	cctgctgctt	ccgctggctc	ttctgctcca	cgccgctcgg	60
cccgagatcc	agctccaaca	gagcgggagcc	gaactgggtca	aaccggggagc	gtcgggtgaag	120
ttgtcatgca	ctggatcggg	cttcaacatc	gaggattact	acatccactg	ggtcaagcaa	180
cgcaccgagc	aggggctgga	atggatcgga	cggatcgacc	ccgaaaacga	tgaaccaag	240
tacgggccta	tcttccaagg	acggggccacc	attacggctg	acacgtcaag	caataccgtc	300
tacctccagc	tttccagcct	gacctccgag	gacactgccg	tgtactactg	cgccttcaga	360
ggaggcgtgt	actggggacc	aggaaccact	ttgaccgtgt	ccagcggagg	cgggtggatca	420
ggaggaggag	gctcaggcgg	tggcggctcg	cacatggacg	tggtcatgac	tcagtccccg	480
ctgaccctgt	cgggtggcaat	tggacagagc	gcatccatct	cgtgcaagag	ctcacagtcg	540
ctgctggatt	ccgacggaaa	gacttatctg	aactggctgc	tccaaagacc	agggcaatca	600
ccgaaacgcc	ttatctccct	ggtgtcgaaa	ctcgactcgg	gtgtgccgga	tcggtttacc	660
ggtagcgggt	ccggcacgga	cttcaactctc	cgcatttcga	gggtggaagc	ggaggatctc	720
gggatctact	actgttggca	gggaaccac	ttccctggga	cttttgagg	cggaactaag	780
ctggaaatca	agaccactac	cccagcaccg	aggccacca	ccccggctcc	taccatcgcc	840
tcccagcctc	tgtccctgcg	tccggaggca	tgtagaccg	cagctggtgg	ggccgtgcat	900

_SL

```

acccgggggtc ttgacttcgc ctgcgatatc tacatttggg cccctctggc tgggtacttgc      960
gggggtcctgc tgctttcact cgtgatcact ctttactgta agcgcgggtcg gaagaagctg      1020
ctgtacatct ttaagcaacc cttcatgagg cctgtgcaga ctactcaaga ggaggacggc      1080
tgttcatgcc ggttcccaga ggaggaggaa ggcggctgcg aactgcgcgt gaaattcagc      1140
cgcagcgcag atgctccagc ctacaagcag gggcagaacc agctctacaa cgaactcaat      1200
cttggtcgga gagaggagta cgacgtgctg gacaagcgga gaggacggga cccagaaatg      1260
ggcggggaagc cgcgcagaaa gaatcccca gagggcctgt acaacgagct ccaaaaggat      1320
aagatggcag aagcctatag cgagattggg atgaaagggg aacgcagaag aggcaaaggc      1380
cacgacggac tgtaccaggg actcagcacc gccaccaagg acacctatga cgctcttcac      1440
atgcaggccc tgccgcctcg g                                     1461

```

<210> 786

<211> 487

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 786

```

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1           5           10          15

```

```

His Ala Ala Arg Pro Glu Ile Gln Leu Gln Gln Ser Gly Ala Glu Leu
          20          25          30

```

```

Val Lys Pro Gly Ala Ser Val Lys Leu Ser Cys Thr Gly Ser Gly Phe
          35          40          45

```

```

Asn Ile Glu Asp Tyr Tyr Ile His Trp Val Lys Gln Arg Thr Glu Gln
50          55          60

```

```

Gly Leu Glu Trp Ile Gly Arg Ile Asp Pro Glu Asn Asp Glu Thr Lys
65          70          75          80

```

```

Tyr Gly Pro Ile Phe Gln Gly Arg Ala Thr Ile Thr Ala Asp Thr Ser
          85          90          95

```

```

Ser Asn Thr Val Tyr Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr
          100          105          110

```

```

Ala Val Tyr Tyr Cys Ala Phe Arg Gly Gly Val Tyr Trp Gly Pro Gly
          115          120          125

```

```

Thr Thr Leu Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
          130          135          140

```


Ser Gly Gly Gly Gly Ser His Met Asp Val^{SL} Val Met Thr Gln Ser Pro
 145 150 155 160
 Leu Thr Leu Ser Val Ala Ile Gly Gln Ser Ala Ser Ile Ser Cys Lys
 165 170 175
 Ser Ser Gln Ser Leu Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn Trp
 180 185 190
 Leu Leu Gln Arg Pro Gly Gln Ser Pro Lys Arg Leu Ile Ser Leu Val
 195 200 205
 Ser Lys Leu Asp Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser
 210 215 220
 Gly Thr Asp Phe Thr Leu Arg Ile Ser Arg Val Glu Ala Glu Asp Leu
 225 230 235 240
 Gly Ile Tyr Tyr Cys Trp Gln Gly Thr His Phe Pro Gly Thr Phe Gly
 245 250 255
 Gly Gly Thr Lys Leu Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro
 260 265 270
 Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro
 275 280 285
 Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu
 290 295 300
 Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys
 305 310 315 320
 Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly
 325 330 335
 Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val
 340 345 350
 Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu
 355 360 365
 Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp
 370 375 380
 Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn
 385 390 395 400
 Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg
 405 410 415

Asp Pro Glu Met Gly Gly Lys Pro Arg Arg ^{-SL} Lys Asn Pro Gln Glu Gly
 420 425 430
 Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu
 435 440 445
 Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu
 450 455 460
 Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His
 465 470 475 480
 Met Gln Ala Leu Pro Pro Arg
 485

<210> 787
 <211> 1452
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 787
 atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60
 cccgatatcc aaatgactca gagcccttca tccctgagcg ccagcgctcg agacaggggtg 120
 accatcacgt gccgggcatc ccaaggcatt agaaataact tggcggtggta tcagcaaaaa 180
 ccaggaaagg ccccgaagcg cctgatctac gcggcctcca accttcagtc aggagtgccc 240
 tcgcgcttca ccgggagcgg tagcggaact gagtttacct ttatcgtgtc gtccctgcag 300
 ccagaggact tcgcgaccta ctactgcctc cagcatcact cgtaccggtt gacttcggga 360
 ggcggaacca aggtcgaaat caaacgcact ggctcgacgt caggggtccgg taaaccggga 420
 tcgggagaag gatcggaagt ccaagtgtg gagagcggag gcggactcgt gcaacctggc 480
 gggtcgctgc ggctcagctg tgccgcgtcg ggttttactt tcagctcgta cgctatgtca 540
 tgggtgcggc aggctccggg aaaggggctg gaatgggtgt ccgctatttc cggctcgggt 600
 ggaagcacca attacccga ctccgtgaag ggacgcttca ccatctcac ggataactcc 660
 aagaatactc tgtacctcca gatgaactcg ctgagagccg aggacaccgc agtgtactac 720
 tgcgcagggt caagcggctg gtccgaatac tggggacagg gcaccctcgt cactgtcagc 780
 tccaccacta ccccgacc gaggccacc acccggctc ctaccatcgc ctccagcct 840
 ctgtccctgc gtccggaggc atgtagacct gcagctggtg gggccgtgca taccgggggt 900
 cttgacttcg cctgcgatat ctacatttgg gccctcttgg ctggtacttg cggggtcctg 960
 ctgctttcac tcgtgatcac tctttactgt aagcgcgggtc ggaagaagct gctgtacatc 1020
 tttaagcaac cttcatgag gcctgtgcag actactcaag aggaggacgg ctgttcatgc 1080
 cggttcccag aggaggagga aggcggctgc gaactgcgcg tgaaattcag ccgcagcgca 1140

_SL

gatgctccag cctacaagca ggggcagaac cagctctaca acgaactcaa tcttggtcgg 1200
agagaggagt acgacgtgct ggacaagcgg agaggacggg acccagaaat gggcggggaag 1260
ccgcgagaa agaatcccca agagggcctg tacaacgagc tccaaaagga taagatggca 1320
gaagcctata gcgagattgg tatgaaagg gaacgcagaa gaggcaaagg ccacgacgga 1380
ctgtaccagg gactcagcac cgccaccaag gacacctatg acgctcttca catgcaggcc 1440
ctgccgcctc gg 1452

<210> 788
<211> 484
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 788
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu
20 25 30

Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln
35 40 45

Gly Ile Arg Asn Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala
50 55 60

Pro Lys Arg Leu Ile Tyr Ala Ala Ser Asn Leu Gln Ser Gly Val Pro
65 70 75 80

Ser Arg Phe Thr Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Ile Val
85 90 95

Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His
100 105 110

His Ser Tyr Pro Leu Thr Ser Gly Gly Gly Thr Lys Val Glu Ile Lys
115 120 125

Arg Thr Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly
130 135 140

Ser Glu Val Gln Val Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
145 150 155 160

Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser
165 170 175

_SL

Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
180 185 190

Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Asn Tyr Ala Asp Ser
195 200 205

Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu
210 215 220

Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
225 230 235 240

Cys Ala Gly Ser Ser Gly Trp Ser Glu Tyr Trp Gly Gln Gly Thr Leu
245 250 255

Val Thr Val Ser Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro
260 265 270

Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys
275 280 285

Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala
290 295 300

Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu
305 310 315 320

Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys
325 330 335

Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr
340 345 350

Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Gly
355 360 365

Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala
370 375 380

Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg
385 390 395 400

Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu
405 410 415

Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn
420 425 430

Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met
435 440 445

_SL

Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly
450 455 460

Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala
465 470 475 480

Leu Pro Pro Arg

<210> 789

<211> 483

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 789

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
20 25 30

Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Phe
35 40 45

Ala Leu Ser Asn His Gly Met Ser Trp Val Arg Arg Ala Pro Gly Lys
50 55 60

Gly Leu Glu Trp Val Ser Gly Ile Val Tyr Ser Gly Ser Thr Tyr Tyr
65 70 75 80

Ala Ala Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg
85 90 95

Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala
100 105 110

Ile Tyr Tyr Cys Ser Ala His Gly Gly Glu Ser Asp Val Trp Gly Gln
115 120 125

Gly Thr Thr Val Thr Val Ser Ser Ala Ser Gly Gly Gly Gly Ser Gly
130 135 140

Gly Arg Ala Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser
145 150 155 160

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
165 170 175

Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu ^{-SL} Asn Trp Tyr Gln Gln Lys
 180 185 190
 Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln
 195 200 205
 Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
 210 215 220
 Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
 225 230 235 240
 Cys Gln Gln Ser Tyr Ser Thr Pro Tyr Thr Phe Gly Gln Gly Thr Lys
 245 250 255
 Val Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala
 260 265 270
 Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg
 275 280 285
 Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys
 290 295 300
 Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu
 305 310 315 320
 Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu
 325 330 335
 Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln
 340 345 350
 Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly
 355 360 365
 Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr
 370 375 380
 Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg
 385 390 395 400
 Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met
 405 410 415
 Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu
 420 425 430
 Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys
 435 440 445

Gly Glu Arg Arg Arg Gly Lys Gly His Asp^{-SL} Gly Leu Tyr Gln Gly Leu
 450 455 460

Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu
 465 470 475 480

Pro Pro Arg

<210> 790
 <211> 1449
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 790
 atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60
 cccgaagtgc aattggtgga atcaggggga ggacttgctc agcctggagg atcgtgaga 120
 ctgtcatgtg ccgtgtccgg ctttgccctg tccaaccacg ggatgtcctg ggtccgccgc 180
 gcgcctggaa agggcctcga atgggtgtcg ggtatttgtt acagcggtag cacctactat 240
 gccgcatccg tgaaggggag attcaccatc agccgggaca actccaggaa cactctgtac 300
 ctccaaatga attcgtgag gccagaggac actgccatct actactgctc cgcgcatggc 360
 ggagagtccg acgtctgggg acaggggacc accgtgaccg tgtctagcgc gtccggcgga 420
 ggcggcagcg ggggtcgggc atcagggggc ggcggatcgg acatccagct caccagttcc 480
 ccgagctcgc tgtccgcctc cgtgggagat cgggtcacca tcacgtgccg cgccagccag 540
 tcgatttcct cctacctgaa ctggtaccaa cagaagcccc gaaaagcccc gaagcttctc 600
 atctacgccg cctcgagcct gcagtcagga gtgccctcac ggttctccgg ctccggttcc 660
 ggtactgatt tcaccctgac catttcctcc ctgcaaccgg aggacttcgc tacttactac 720
 tgccagcagt cgtactccac cccctacact ttccgacaag gcaccaaggt cgaaatcaag 780
 accactaccc cagcaccgag gccaccacc ccggctccta ccatcgctc ccagcctctg 840
 tccctgcgtc cggaggcatg tagaccgca gctggtgggg ccgtgcatac ccgggggtctt 900
 gacttcgcct gcgatatcta catttgggcc cctctggctg gtacttgccg ggtcctgctg 960
 ctttcaactc tgatcactct ttactgtaag cgcggtcggg agaagctgct gtacatcttt 1020
 aagcaaccct tcatgaggcc tgtgcagact actcaagagg aggacggctg ttcattgccg 1080
 ttcccagagg aggaggaagg cggctgcgaa ctgcgcgtga aattcagccg cagcgcagat 1140
 gctccagcct acaagcaggg gcagaaccag ctctacaacg aactcaatct tggtcggaga 1200
 gaggagtacg acgtgctgga caagcggaga ggacgggacc cagaaatggg cgggaagccg 1260
 cgagaaaaga atccccaaga gggcctgtac aacgagctcc aaaaggataa gatggcagaa 1320
 gcctatagcg agattggtat gaaaggggaa cgcagaagag gcaaaggcca cgacggactg 1380

_SL

taccagggac tcagcaccgc caccaaggac acctatgacg ctcttcacat gcaggccctg 1440
ccgcctcgg 1449

<210> 791
<211> 490
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 791
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu
20 25 30

Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
35 40 45

Thr Phe Ser Asn Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys
50 55 60

Gly Leu Gly Trp Val Ser Gly Ile Ser Arg Ser Gly Glu Asn Thr Tyr
65 70 75 80

Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser
85 90 95

Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Asp Glu Asp Thr
100 105 110

Ala Val Tyr Tyr Cys Ala Arg Ser Pro Ala His Tyr Tyr Gly Gly Met
115 120 125

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Gly
130 135 140

Gly Gly Gly Ser Gly Gly Arg Ala Ser Gly Gly Gly Gly Ser Asp Ile
145 150 155 160

Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg
165 170 175

Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Ile Ser Ser Ser Phe Leu
180 185 190

Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
195 200 205

_SL

Gly Ala Ser Arg Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser
210 215 220

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
225 230 235 240

Asp Ser Ala Val Tyr Tyr Cys Gln Gln Tyr His Ser Ser Pro Ser Trp
245 250 255

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Thr Thr Thr Pro Ala
260 265 270

Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser
275 280 285

Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr
290 295 300

Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala
305 310 315 320

Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys
325 330 335

Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met
340 345 350

Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe
355 360 365

Pro Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg
370 375 380

Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn
385 390 395 400

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
405 410 415

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
420 425 430

Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
435 440 445

Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
450 455 460

Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
465 470 475 480

_SL

Ala Leu His Met Gln Ala Leu Pro Pro Arg
485 490

<210> 792
<211> 1470
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 792
atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60
ccccaagtgc aactcgtgga atctggtgga ggactcgtgc aacccggaag atcgtttaga 120
ctgtcgtgtg ccgccagcgg gttcactttc tcgaactacg cgatgtcctg ggtccgccag 180
gcacccggaa agggactcgg ttgggtgtcc ggcatttccc ggtccggcga aaatacctac 240
tacgccgact ccgtgaaggg ccgcttcacc atctcaaggg acaacagcaa aaacaccctg 300
tacttgcaaa tgaactccct gcgggatgaa gatacagccg tgtactattg cgcccggctc 360
cctgcccatt actacggcgg aatggacgtc tggggacagg gaaccactgt gactgtcagc 420
agcgcgtcgg gtggcggcgg ctcagggggg cgggcctccg gggggggagg gtccgacatc 480
gtgctgaccc agtccccggg aaccctgagc ctgagcccgg gagagcgcgc gaccctgtca 540
tgccgggcat ccagagcat tagctcctcc tttctcgcct ggtatcagca gaagcccgga 600
caggccccga ggctgctgat ctacggcgct agcagaaggg ctaccggaat ccagaccgg 660
ttctccggct ccggttcggg gaccgatttc acccttacta tctcgcgcct ggaacctgag 720
gactccgccg tctactactg ccagcagtac cactcatccc cgtcgtggac gttcggacag 780
ggcaccaagc tggagattaa gaccactacc ccagcaccga ggccaccac cccggctcct 840
accatcgcct ccagcctct gtccctgctt ccggaggcat gtagaccgc agctggtggg 900
gccgtgcata cccggggtct tgacttcgcc tgcgatatct acatttgggc ccctctggct 960
gggtacttgcg gggctctgct gctttcactc gtgatcactc ttactgtaa gcgcggctcg 1020
aagaagctgc tgtacatctt taagcaacct ttcagaggc ctgtgcagac tactcaagag 1080
gaggacggct gttcatgccg gttcccagag gaggaggaag gcggctgcga actgcgcgtg 1140
aaattcagcc gcagcgcaga tgctccagcc tacaagcagg ggcagaacca gctctacaac 1200
gaactcaatc ttggtcggag agaggagtac gacgtgctgg acaagcggag aggacgggac 1260
ccagaaatgg gcgggaagcc gcgcagaaag aatccccaag agggcctgta caacgagctc 1320
caaaaggata agatggcaga agcctatagc gagatttgta tgaaagggga acgcagaaga 1380
ggcaaaggcc acgacggact gtaccaggga ctcagaccg ccaccaagga cacctatgac 1440
gctcttcaca tgcaggccct gccgcctcgg 1470

<210> 793

_SL

<211> 488

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 793

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu
20 25 30

Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
35 40 45

Thr Phe Asp Asp Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys
50 55 60

Gly Leu Glu Trp Val Ser Gly Ile Ser Trp Asn Ser Gly Ser Ile Gly
65 70 75 80

Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
85 90 95

Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
100 105 110

Ala Leu Tyr Tyr Cys Ser Val His Ser Phe Leu Ala Tyr Trp Gly Gln
115 120 125

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Gly Gly Gly Gly Ser Gly
130 135 140

Gly Arg Ala Ser Gly Gly Gly Gly Ser Asp Ile Val Met Thr Gln Thr
145 150 155 160

Pro Leu Ser Leu Pro Val Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys
165 170 175

Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr Asn Tyr Leu Asp
180 185 190

Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Leu
195 200 205

Gly Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly
210 215 220

Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp
225 230 235 240

_SL

Val Gly Val Tyr Tyr Cys Met Gln Ala Leu Gln Thr Pro Tyr Thr Phe
245 250 255

Gly Gln Gly Thr Lys Val Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg
260 265 270

Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg
275 280 285

Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly
290 295 300

Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr
305 310 315 320

Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg
325 330 335

Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro
340 345 350

Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu
355 360 365

Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala
370 375 380

Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu
385 390 395 400

Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly
405 410 415

Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu
420 425 430

Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser
435 440 445

Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly
450 455 460

Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu
465 470 475 480

His Met Gln Ala Leu Pro Pro Arg
485

<210> 794
<211> 1464

<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 794
atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgtcca cgccgctcgg 60
ccccaagtgc aactcgtcga atccggtgga ggtctggtcc aacctggtag aagcctgaga 120
ctgtcgtgtg cggccagcgg attcaccttt gatgactatg ctatgactg ggtgcggcag 180
gccccaggaa agggcctgga atgggtgtcg ggaattagct ggaactccgg gtccattggc 240
tacgccgact ccgtgaaggg ccgcttcacc atctcccgcg acaacgcaaa gaactccctg 300
tacttgcaaa tgaactcgtc cagggctgag gataccgcgc tgtactactg ctccgtgcat 360
tccttcctgg cctactgggg acagggaaact ctggtcaccg tgtcgagcgc ctccggcggc 420
gggggctcgg gtggacgggc ctccggcgga ggggggtccg acatcgtgat gaccagacc 480
ccgctgagct tgcccgtgac tcccggagag cctgcatcca tctcctgccg gtcacccag 540
tcccttctcc actccaacgg atacaactac ctgactggtt acctccagaa gccgggacag 600
agccctcagc ttctgatcta cctgggggtca aatagagcct caggagtgcc ggatcggttc 660
agcggatctg gttcggaac tgatttact ctgaagattt cccgcgtgga agccgaggac 720
gtgggcgtct actactgtat gcaggcgtg cagacccctt ataccttcgg ccaagggacg 780
aaagtggaga tcaagaccac taccacagca ccgaggccac ccacccggc tcctaccatc 840
gcctcccagc ctctgtccct gcgtccggag gcatgtagac ccgcagctgg tggggccgtg 900
catacccggt gtcttgactt cgctgcgat atctacattt gggcccctct ggctgggtact 960
tgccgggtcc tgctgctttc actcgtgatc actctttact gtaagcgcg tgggaagaag 1020
ctgctgtaca tctttaagca acccttcatg aggcctgtgc agactactca agaggaggac 1080
ggctgttcat gccggttccc agaggaggag gaaggcggct gcgaactgcg cgtgaaattc 1140
agccgcagcg cagatgtctc agcctacaag caggggcaga accagctcta caacgaactc 1200
aatcttggtc ggagagagga gtacgacgtg ctggacaagc ggagaggacg ggaccagaaa 1260
atgggcggga agccgcgag aaagaatccc caagagggcc tgtacaacga gtcctaaaag 1320
gataagatgg cagaagccta tagcgagatt ggtatgaaag gggaacgcag aagaggcaaa 1380
ggccacgacg gactgtacca gggactcagc accgccacca aggacaccta tgacgctctt 1440
cacatgcagg ccctgccgcc tcgg 1464

<210> 795
<211> 487
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

_SL
polypeptide"

<400> 795

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu
20 25 30

Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Phe
35 40 45

Ala Leu Ser Asn His Gly Met Ser Trp Val Arg Arg Ala Pro Gly Lys
50 55 60

Gly Leu Glu Trp Val Ser Gly Ile Val Tyr Ser Gly Ser Thr Tyr Tyr
65 70 75 80

Ala Ala Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg
85 90 95

Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala
100 105 110

Ile Tyr Tyr Cys Ser Ala His Gly Gly Glu Ser Asp Val Trp Gly Gln
115 120 125

Gly Thr Thr Val Thr Val Ser Ser Ala Ser Gly Gly Gly Gly Ser Gly
130 135 140

Gly Arg Ala Ser Gly Gly Gly Gly Ser Asp Ile Val Met Thr Gln Thr
145 150 155 160

Pro Leu Ser Leu Ser Val Thr Pro Gly Gln Pro Ala Ser Ile Ser Cys
165 170 175

Lys Ser Ser Gln Ser Leu Leu Arg Asn Asp Gly Lys Thr Pro Leu Tyr
180 185 190

Trp Tyr Leu Gln Lys Ala Gly Gln Pro Pro Gln Leu Leu Ile Tyr Glu
195 200 205

Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly
210 215 220

Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp
225 230 235 240

Val Gly Ala Tyr Tyr Cys Met Gln Asn Ile Gln Phe Pro Ser Phe Gly
245 250 255

Gly Gly Thr Lys Leu Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro
Page 555

_SL

260 265 270

Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro
275 280 285

Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu
290 295 300

Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys
305 310 315 320

Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly
325 330 335

Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val
340 345 350

Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu
355 360 365

Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp
370 375 380

Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn
385 390 395 400

Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg
405 410 415

Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly
420 425 430

Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu
435 440 445

Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu
450 455 460

Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His
465 470 475 480

Met Gln Ala Leu Pro Pro Arg
485

<210> 796
<211> 1461
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

_SL

<400> 796
atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60
cccgaagtgc aattgttgga atctggagga ggacttgtgc agcctggagg atcactgaga 120
ctttcgtgtg cgggtgtcagg cttcgccctg agcaaccacg gcatgagctg ggtgctggaga 180
gccccgggga aggggtctgga atgggtgtcc gggatcgtct actccggttc aacttactac 240
gccgcaagcg tgaagggtcg cttcaccatt tcccgcgata actcccggaa caccctgtac 300
ctccaaatga actccctgcg gcccgaggac accgccatct actactgttc cgcgcatgga 360
ggagagtccg atgtctgggg acagggcact accgtgaccg tgtcgagcgc ctcgggggga 420
ggaggctccg gcggtcgcgc ctccgggggg ggtggcagcg acatttgtat gacgcagact 480
ccactctcgc tgtccgtgac cccgggacag cccgcgtcca tctcgtgcaa gagctcccag 540
agcctgctga ggaacgacgg aaagactcct ctgtattggt acctccagaa ggctggacag 600
ccccgcaac tgctcatcta cgaagtgtca aatcgcttct ccgggggtgcc ggatcggttt 660
tccggctcgg gatcgggcac cgacttcacc ctgaaaatct ccagggtcga ggccgaggac 720
gtgggagcct actactgcat gcaaaacatc cagttccctt ccttcggcgg cggcacaaag 780
ctggagatta agaccactac ccagcaccg aggccacca ccccggtcc taccatcgcc 840
tcccagcctc tgtccctgcg tccggaggca tgtagaccg cagctggtgg ggccgtgcat 900
acccggggtc ttgacttcgc ctgcgatatc tacatttggg cccctctggc tggttacttg 960
ggggtcctgc tgctttcact cgtgatcact ctttactgta agcgcggtcg gaagaagctg 1020
ctgtacatct ttaagcaacc cttcatgagg cctgtgcaga ctactcaaga ggaggacggc 1080
tgttcatgcc ggttcccaga ggaggaggaa ggcggctgcg aactgcgctg gaaattcagc 1140
cgcagcgcag atgtccagc ctacaagcag gggcagaacc agctctacaa cgaactcaat 1200
cttggtcgga gagaggagta cgacgtgctg gacaagcggg gaggacggga cccagaaatg 1260
ggcgggaagc cgcgcagaaa gaatcccaa gagggcctgt acaacgagct caaaaggat 1320
aagatggcag aagcctatag cgagattggt atgaaagggg aacgcagaag aggcaaaggc 1380
cacgacggac tgtaccaggg actcagcacc gccaccaagg acacctatga cgctcttcac 1440
atgcaggccc tgccgcctcg g 1461

<210> 797

<211> 493

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 797

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg₂₀ Pro Gln Val Gln Leu₂₅ Val^{-SL} Gln Ser Gly Ala₃₀ Glu Val
 Arg Lys Thr₃₅ Gly Ala Ser Val Lys₄₀ Val Ser Cys Lys Ala₄₅ Ser Gly Tyr
 Ile Phe₅₀ Asp Asn Phe Gly Ile₅₅ Asn Trp Val Arg Gln₆₀ Ala Pro Gly Gln
 Gly₆₅ Leu Glu Trp Met Gly₇₀ Trp Ile Asn Pro Lys₇₅ Asn Asn Asn Thr Asn₈₀
 Tyr Ala Gln Lys Phe₈₅ Gln Gly Arg Val Thr₉₀ Ile Thr Ala Asp Glu₉₅ Ser
 Thr Asn Thr Ala₁₀₀ Tyr Met Glu Val Ser₁₀₅ Ser Leu Arg Ser Glu₁₁₀ Asp Thr
 Ala Val Tyr₁₁₅ Tyr Cys Ala Arg Gly₁₂₀ Pro Tyr Tyr Tyr Gln₁₂₅ Ser Tyr Met
 Asp Val₁₃₀ Trp Gly Gln Gly Thr₁₃₅ Met Val Thr Val Ser₁₄₀ Ser Ala Ser Gly
 Gly₁₄₅ Gly Gly Ser Gly Gly₁₅₀ Arg Ala Ser Gly Gly₁₅₅ Gly Gly Ser Asp Ile₁₆₀
 Val Met Thr Gln Thr₁₆₅ Pro Leu Ser Leu Pro₁₇₀ Val Thr Pro Gly Glu₁₇₅ Pro
 Ala Ser Ile Ser₁₈₀ Cys Arg Ser Ser Gln₁₈₅ Ser Leu Leu His Ser₁₉₀ Asn Gly
 Tyr Asn Tyr₁₉₅ Leu Asn Trp Tyr Leu₂₀₀ Gln Lys Pro Gly Gln₂₀₅ Ser Pro Gln
 Leu Leu₂₁₀ Ile Tyr Leu Gly Ser₂₁₅ Lys Arg Ala Ser Gly₂₂₀ Val Pro Asp Arg
 Phe₂₂₅ Ser Gly Ser Gly Ser₂₃₀ Gly Thr Asp Phe Thr₂₃₅ Leu His Ile Thr Arg₂₄₀
 Val Gly Ala Glu Asp₂₄₅ Val Gly Val Tyr Tyr₂₅₀ Cys Met Gln Ala Leu₂₅₅ Gln
 Thr Pro Tyr Thr₂₆₀ Phe Gly Gln Gly Thr₂₆₅ Lys Leu Glu Ile Lys₂₇₀ Thr Thr
 Thr Pro Ala₂₇₅ Pro Arg Pro Pro Thr₂₈₀ Pro Ala Pro Thr Ile₂₈₅ Ala Ser Gln

Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala
 290 295 300
 Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala
 305 310 315 320
 Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Ser Leu Val Ile Thr
 325 330 335
 Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln
 340 345 350
 Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser
 355 360 365
 Cys Arg Phe Pro Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys
 370 375 380
 Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln
 385 390 395 400
 Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
 405 410 415
 Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg
 420 425 430
 Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met
 435 440 445
 Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly
 450 455 460
 Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp
 465 470 475 480
 Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
 485 490

<210> 798

<211> 1479

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 798

atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60

ccccaagtcc aactcgtcca gtccggcgca gaagtcagaa aaaccggtgc tagcgtgaaa 120

gtgtcctgca aggcctccgg ctacattttc gataacttcg gaatcaactg ggtcagacag 180

_SL

gccccggggcc aggggctgga atggatggga tggatcaacc ccaagaacaa caacaccaac 240
tacgcacaga agttccaggg ccgctgact atcaccgccg atgaatcgac caataccgcc 300
tacatggagg tgtcctccct gcggtcggag gacactgccg tgtattactg cgcgaggggc 360
ccatactact accaaagcta catggacgtc tggggacagg gaaccatggt gaccgtgtca 420
tccgcctccg gtggtggagg ctccgggggg cgggcttcag gaggcggagg aagcgatatt 480
gtgatgacct agactccgct tagcctgccc gtgactcctg gagaaccggc ctccatttcc 540
tgccggtcct cgcaatcact cctgcattcc aacggttaca actacctgaa ttggtacctc 600
cagaagcctg gccagtcgcc ccagttgctg atctatctgg gctcgaagcg cgcctccggg 660
gtgcctgacc ggtttagcgg atctgggagc ggcacggact tcactctcca catcaccgcg 720
gtgggagcgg aggacgtggg agtgtactac tgtatgcagg cgctgcagac tccgtacaca 780
ttcggacagg gcaccaagct ggagatcaag accactaccc cagcaccgag gccacccacc 840
ccggctccta ccatcgcctc ccagcctctg tccctgcgtc cggaggcatg tagacccgca 900
gctggtgggg ccgtgcatac ccggggtctt gacttcgcct gcgatatcta catttgggcc 960
cctctggctg gtacttgagg ggtcctgctg ctttactcgt tgatcactct ttactgtaag 1020
cgcggtcggg agaagctgct gtacatcttt aagcaaccct tcatgaggcc tgtgcagact 1080
actcaagagg aggacggctg ttcatgccgg ttcccagagg aggaggaagg cggctgcgaa 1140
ctgcgcgtga aattcagccg cagcgcagat gctccagcct acaagcaggg gcagaaccag 1200
ctctacaacg aactcaatct tggtcggaga gaggagtacg acgtgctgga caagcggaga 1260
ggacgggacc cagaaatggg cgggaagccg cgcagaaaga atccccaaga gggcctgtac 1320
aacgagctcc aaaaggataa gatggcagaa gcctatagcg agattggtat gaaaggggaa 1380
cgcagaagag gcaaaggcca cgacggactg taccagggac tcagcaccgc caccaaggac 1440
acctatgacg ctcttcacat gcaggccctg ccgcctcgg 1479

<210> 799

<211> 490

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 799

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu
20 25 30

Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
35 40 45

_SL

Thr Phe Ser Ser Asp Ala Met Thr Trp Val Arg Gln Ala Pro Gly Lys
50 55 60

Gly Leu Glu Trp Val Ser Val Ile Ser Gly Ser Gly Gly Thr Thr Tyr
65 70 75 80

Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser
85 90 95

Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
100 105 110

Ala Val Tyr Tyr Cys Ala Lys Leu Asp Ser Ser Gly Tyr Tyr Tyr Ala
115 120 125

Arg Gly Pro Arg Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
130 135 140

Ala Ser Gly Gly Gly Gly Ser Gly Gly Arg Ala Ser Gly Gly Gly Gly
145 150 155 160

Ser Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
165 170 175

Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser
180 185 190

Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu
195 200 205

Ile Tyr Gly Ala Ser Thr Leu Ala Ser Gly Val Pro Ala Arg Phe Ser
210 215 220

Gly Ser Gly Ser Gly Thr His Phe Thr Leu Thr Ile Asn Ser Leu Gln
225 230 235 240

Ser Glu Asp Ser Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Lys Arg Ala
245 250 255

Ser Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Thr Thr Thr Pro Ala
260 265 270

Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser
275 280 285

Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr
290 295 300

Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala
305 310 315 320

_SL

Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys
325 330 335

Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met
340 345 350

Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe
355 360 365

Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg
370 375 380

Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn
385 390 395 400

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
405 410 415

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
420 425 430

Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
435 440 445

Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
450 455 460

Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
465 470 475 480

Ala Leu His Met Gln Ala Leu Pro Pro Arg
485 490

<210> 800

<211> 1470

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 800

atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60

ccccaagtgc aacttcaaga atcaggcgga ggactcgtgc agcccgagg atcattgcgg 120

ctctcgtgcg ccgcctcggg cttcaccttc tcgagcgacg ccatgacctg ggtccgccag 180

gccccgggga aggggctgga atgggtgtct gtgatttccg gctccggggg aactacgtac 240

tacgccgatt ccgtgaaagg tcgcttcact atctcccgga acaacagcaa gaacaccctt 300

tatctgcaaa tgaattccct ccgcgccgag gacaccgccg tgtactactg cgccaagctg 360

_SL

gactcctcgg gctactacta tgcccggggt ccgagatact ggggacaggg aaccctcgtg	420
accgtgtcct ccgcgtccgg cggaggaggg tcgggagggc gggcctccgg cggcggcggt	480
tcggacatcc agctgacca gtcccatcc tctactgagcg caagcgtggg cgacagagtc	540
accattacat gcagggcgtc ccagagcatc agctcctacc tgaactggta ccaacagaag	600
cctggaaagg ctcctaagct gttgatctac ggggcttcga ccctggcatc cggggtgcc	660
gcgaggttta gcggaagcgg tagcggcact cacttcactc tgaccattaa cagcctccag	720
tccgaggatt cagccactta ctactgtcag cagtcctaca agcgggccag cttcggacag	780
ggcactaagg tcgagatcaa gaccactacc ccagcaccga ggccaccac cccggctcct	840
accatcgcct cccagcctct gtccctgcgt ccggaggcat gtagaccgc agctggtggg	900
gccgtgcata cccggggtct tgacttcgcc tgcgatatct acatttgggc ccctctggct	960
ggtacttgcg gggctcctgct gctttcactc gtgatcactc ttactgtaa gcgcggtcgg	1020
aagaagctgc tgtacatctt taagcaacc ttcatgaggc ctgtgcagac tactcaagag	1080
gaggacggct gttcatgccg gttcccagag gaggaggaag gcggctgcga actgcgcgtg	1140
aaattcagcc gcagcgcaga tgctccagcc tacaagcagg ggcagaacca gctctacaac	1200
gaactcaatc ttggtcggag agaggagtac gacgtgctgg acaagcggag aggacgggac	1260
ccagaaatgg gcgggaagcc gcgcagaaag aatccccaag agggcctgta caacgagctc	1320
caaaaggata agatggcaga agcctatagc gagattggta tgaaagggga acgcagaaga	1380
ggcaaaggcc acgacggact gtaccagga ctcagcaccg ccaccaagga cacctatgac	1440
gctcttcaca tgcaggccct gccgcctcgg	1470

<210> 801
 <211> 491
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 801
 Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
 1 5 10 15

His Ala Ala Arg Pro Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val
 20 25 30

Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr
 35 40 45

Thr Phe Ser Asn Tyr Gly Ile Thr Trp Val Arg Gln Ala Pro Gly Gln
 50 55 60

Gly Leu Glu Trp Met Gly Trp Ile Ser Ala Tyr Asn Gly Asn Thr Asn
 65 70 75 80

_SL

Tyr Ala Gln Lys Phe₈₅ Gln Gly Arg Val Thr₉₀ Met Thr Arg Asn Thr₉₅ Ser
Ile Ser Thr Ala₁₀₀ Tyr Met Glu Leu Ser₁₀₅ Ser Leu Arg Ser Glu₁₁₀ Asp Thr
Ala Val Tyr₁₁₅ Tyr Cys Ala Arg Gly₁₂₀ Pro Tyr Tyr Tyr Tyr₁₂₅ Met Asp Val
Trp Gly₁₃₀ Lys Gly Thr Met Val₁₃₅ Thr Val Ser Ser Ala₁₄₀ Ser Gly Gly Gly
Gly₁₄₅ Ser Gly Gly Arg Ala₁₅₀ Ser Gly Gly Gly Gly₁₅₅ Ser Glu Ile Val Met₁₆₀
Thr Gln Ser Pro Leu₁₆₅ Ser Leu Pro Val Thr₁₇₀ Pro Gly Glu Pro Ala₁₇₅ Ser
Ile Ser Cys Arg₁₈₀ Ser Ser Gln Ser Leu₁₈₅ Leu Tyr Ser Asn Gly₁₉₀ Tyr Asn
Tyr Val Asp₁₉₅ Trp Tyr Leu Gln Lys₂₀₀ Pro Gly Gln Ser Pro₂₀₅ Gln Leu Leu
Ile Tyr₂₁₀ Leu Gly Ser Asn Arg₂₁₅ Ala Ser Gly Val Pro₂₂₀ Asp Arg Phe Ser
Gly₂₂₅ Ser Gly Ser Gly Thr₂₃₀ Asp Phe Lys Leu Gln₂₃₅ Ile Ser Arg Val Glu₂₄₀
Ala Glu Asp Val Gly₂₄₅ Ile Tyr Tyr Cys Met₂₅₀ Gln Gly Arg Gln Phe₂₅₅ Pro
Tyr Ser Phe Gly₂₆₀ Gln Gly Thr Lys Val₂₆₅ Glu Ile Lys Thr Thr₂₇₀ Thr Pro
Ala Pro Arg₂₇₅ Pro Pro Thr Pro Ala₂₈₀ Pro Thr Ile Ala Ser₂₈₅ Gln Pro Leu
Ser Leu Arg Pro Glu Ala Cys₂₉₅ Arg Pro Ala Ala Gly₃₀₀ Gly Ala Val His
Thr Arg Gly Leu Asp Phe₃₁₀ Ala Cys Asp Ile Tyr₃₁₅ Ile Trp Ala Pro Leu₃₂₀
Ala Gly Thr Cys Gly₃₂₅ Val Leu Leu Leu Ser₃₃₀ Leu Val Ile Thr Leu₃₃₅ Tyr
Cys Lys Arg Gly₃₄₀ Arg Lys Lys Leu Leu₃₄₅ Tyr Ile Phe Lys Gln₃₅₀ Pro Phe

_SL

Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg
355 360 365

Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser
370 375 380

Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr
385 390 395 400

Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys
405 410 415

Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn
420 425 430

Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu
435 440 445

Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly
450 455 460

His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr
465 470 475 480

Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
485 490

<210> 802
<211> 1473
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 802
atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60
ccccaagtcc aactggtcca gagcggtgca gaagtgaaga agcccggagc gagcgtgaaa 120
gtgtcctgca aggcttcagg gtacaccttc tccaactacg gcatcacttg ggtgcgccag 180
gccccgggac agggcctgga atggatgggg tggatttccg cgtacaacgg caatacgaac 240
tacgctcaga agttccagg tagagtacc atgactagga acacctccat ttccaccgcc 300
tacatggaac tgtcctccct gcggagcgag gacaccgccg tgtactattg cgcccgggga 360
ccatactact actacatgga tgtctggggg aaggggacta tggtcaccgt gtcacccgcc 420
tcgggaggcg gcggatcagg aggacgcgcc tctggtggtg gaggatcgga gatcgtgatg 480
accagagcc ctctctcctt gcccgtagct cctggggagc ccgcatccat ttcattgccg 540
agctcccagt cacttctcta ctccaacggc tataactacg tggattggta cctccaaaag 600

_SL

ccggggccaga gcccgagct gctgatctac ctgggctcga acagggccag cggagtgcct 660
gaccgggttct ccgggtcggg aagcgggacc gacttcaagc tgcaaattct gagagtggag 720
gccgaggacg tgggaatcta ctactgtatg cagggccgcc agtttccgta ctcgttcgga 780
cagggcacca aagtggaaat caagaccact accccagcac cgaggccacc caccgccgct 840
cctaccatcg cctcccagcc tctgtccctg cgtccggagg catgtagacc cgcagctggt 900
ggggccgtgc ataccgggg tcttgacttc gcctgcgata tctacatttg ggcccctctg 960
gctggtactt gcggggtcct gctgctttca ctcgtgatca ctctttactg taagcgcggt 1020
cggaagaagc tgctgtacat ctttaagcaa cccttcatga ggctgtgca gactactcaa 1080
gaggaggacg gctgttcatg ccggttccca gaggaggagg aaggcggctg cgaactgcgc 1140
gtgaaattca gccgcagcgc agatgctcca gcctacaagc aggggcagaa ccagctctac 1200
aacgaactca atcttggtcg gagagaggag tacgacgtgc tggacaagcg gagaggacgg 1260
gaccagaaa tgggcgggaa gccgcgcaga aagaatcccc aagagggcct gtacaacgag 1320
ctccaaaagg ataagatggc agaagcctat agcgagattg gtatgaaagg ggaacgcaga 1380
agaggcaaag gccacgacgg actgtaccag ggactcagca ccgccaccaa ggacacctat 1440
gacgctcttc acatgcaggc cctgccgcct cgg 1473

<210> 803

<211> 482

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 803

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Glu Val Gln Leu Leu Glu Thr Gly Gly Gly Leu
20 25 30

Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Phe
35 40 45

Ala Leu Ser Asn His Gly Met Ser Trp Val Arg Arg Ala Pro Gly Lys
50 55 60

Gly Leu Glu Trp Val Ser Gly Ile Val Tyr Ser Gly Ser Thr Tyr Tyr
65 70 75 80

Ala Ala Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg
85 90 95

Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala
Page 566

_SL

100		105		110											
Ile	Tyr	Tyr	Cys	Ser	Ala	His	Gly	Gly	Glu	Ser	Asp	Val	Trp	Gly	Gln
		115					120					125			
Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Ala	Ser	Gly	Gly	Gly	Gly	Ser	Gly
	130					135					140				
Gly	Arg	Ala	Ser	Gly	Gly	Gly	Gly	Ser	Glu	Ile	Val	Leu	Thr	Gln	Ser
145				150						155					160
Pro	Ala	Thr	Leu	Ser	Val	Ser	Pro	Gly	Glu	Ser	Ala	Thr	Leu	Ser	Cys
			165						170					175	
Arg	Ala	Ser	Gln	Ser	Val	Ser	Ser	Asn	Leu	Ala	Trp	Tyr	Gln	Gln	Lys
			180					185					190		
Pro	Gly	Gln	Ala	Pro	Arg	Leu	Leu	Ile	Tyr	Gly	Ala	Ser	Thr	Arg	Ala
		195					200					205			
Ser	Gly	Ile	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe
	210					215					220				
Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Ala	Glu	Asp	Val	Ala	Val	Tyr	Tyr
225					230					235					240
Cys	Gln	Gln	Tyr	Gly	Ser	Ser	Leu	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Val
				245					250					255	
Glu	Ile	Lys	Thr	Thr	Thr	Pro	Ala	Pro	Arg	Pro	Pro	Thr	Pro	Ala	Pro
			260					265					270		
Thr	Ile	Ala	Ser	Gln	Pro	Leu	Ser	Leu	Arg	Pro	Glu	Ala	Cys	Arg	Pro
		275					280					285			
Ala	Ala	Gly	Gly	Ala	Val	His	Thr	Arg	Gly	Leu	Asp	Phe	Ala	Cys	Asp
	290					295					300				
Ile	Tyr	Ile	Trp	Ala	Pro	Leu	Ala	Gly	Thr	Cys	Gly	Val	Leu	Leu	Leu
305					310					315					320
Ser	Leu	Val	Ile	Thr	Leu	Tyr	Cys	Lys	Arg	Gly	Arg	Lys	Lys	Leu	Leu
				325					330					335	
Tyr	Ile	Phe	Lys	Gln	Pro	Phe	Met	Arg	Pro	Val	Gln	Thr	Thr	Gln	Glu
			340					345					350		
Glu	Asp	Gly	Cys	Ser	Cys	Arg	Phe	Pro	Glu	Glu	Glu	Glu	Gly	Gly	Cys
		355					360					365			
Glu	Leu	Arg	Val	Lys	Phe	Ser	Arg	Ser	Ala	Asp	Ala	Pro	Ala	Tyr	Lys

_SL

```

actaccccag caccgaggcc acccaccg gtcctacca tcgcctcca gcctctgtcc      840
ctgctccgg aggcattag accgcagct ggtggggccg tgcataccg gggcttgac      900
ttgcctgcg atatctacat ttgggccct ctggctggta cttgcggggt cctgctgctt      960
tcactcgtga tcactcttta ctgtaagcgc ggtcggaaga agctgctgta catctttaag    1020
caacccttca tgaggcctgt gcagactact caagaggagg acggctgttc atgccggttc    1080
ccagaggagg aggaaggcgg ctgcgaactg cgcgtgaaat tcagccgcag cgcagatgct    1140
ccagcctaca agcaggggca gaaccagctc tacaacgaac tcaatcttgg tcggagagag    1200
gagtacgacg tgctggacaa gcggagagga cgggaccag aaatgggagg gaagccgcgc     1260
agaaagaatc cccaagaggg cctgtacaac gagctccaaa aggataagat ggcagaagcc    1320
tatagcgaga ttggtatgaa aggggaacgc agaagaggca aaggccacga cggactgtac    1380
cagggactca gcaccgccac caaggacacc tatgacgctc ttcacatgca ggccctgccg    1440
cctcgg                                     1446

```

<210> 805
 <211> 483
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 805
 Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
 1 5 10 15

His Ala Ala Arg Pro Glu Val Gln Leu Val Glu Thr Gly Gly Gly Leu
 20 25 30

Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Phe
 35 40 45

Ala Leu Ser Asn His Gly Met Ser Trp Val Arg Arg Ala Pro Gly Lys
 50 55 60

Gly Leu Glu Trp Val Ser Gly Ile Val Tyr Ser Gly Ser Thr Tyr Tyr
 65 70 75 80

Ala Ala Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg
 85 90 95

Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala
 100 105 110

Ile Tyr Tyr Cys Ser Ala His Gly Gly Glu Ser Asp Val Trp Gly Gln
 115 120 125

Gly Thr Thr Val Thr Val Ser Ser Ala Ser^{-SL} Gly Gly Gly Gly Ser Gly
 130 135 140
 Gly Arg Ala Ser Gly Gly Gly Gly Ser Glu Ile Val Met Thr Gln Ser
 145 150 155 160
 Pro Ala Thr Leu Ser Val Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
 165 170 175
 Arg Ala Ser Gln Ser Val Ser Ser Lys Leu Ala Trp Tyr Gln Gln Lys
 180 185 190
 Pro Gly Gln Ala Pro Arg Leu Leu Met Tyr Gly Ala Ser Ile Arg Ala
 195 200 205
 Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe
 210 215 220
 Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr
 225 230 235 240
 Cys Gln Gln Tyr Gly Ser Ser Ser Trp Thr Phe Gly Gln Gly Thr Lys
 245 250 255
 Val Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala
 260 265 270
 Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg
 275 280 285
 Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys
 290 295 300
 Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu
 305 310 315 320
 Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu
 325 330 335
 Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln
 340 345 350
 Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly
 355 360 365
 Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr
 370 375 380
 Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg
 385 390 395 400

Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met
 405 410 415
 Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu
 420 425 430
 Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys
 435 440 445
 Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu
 450 455 460
 Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu
 465 470 475 480
 Pro Pro Arg

<210> 806
 <211> 1449
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polynucleotide"

<400> 806
 atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60
 cccgaagtgc aattggtgga aactggagga ggacttgtgc aacctggagg atcattgaga 120
 ctgagctgcg cagtgtcggg attcgccctg agcaaccatg gaatgtcctg ggtcagaagg 180
 gcccttgga aaggcctcga atgggtgtca gggatcgtgt actccggttc cacttactac 240
 gccgcctccg tgaaggggcg cttcactatc tcacgggata actcccgcaa taccctgtac 300
 ctccaaatga acagcctgcg gccggaggat accgccatct actactgttc cgcccacggt 360
 ggagagtctg acgtctgggg ccagggaaact accgtgaccg tgtcctccgc gtccggcggt 420
 ggagggagcg gcggccgcgc cagcggcggc ggaggctccg agatcgtgat gaccagagc 480
 cccgctactc tgtcgggtgc gcccgagaa agggcgaccc tgtcctgccg ggcgtcgcag 540
 tccgtgagca gcaagctggc ttggtaccag cagaagccgg gccaggcacc acgcctgctt 600
 atgtacggtg cctccattcg ggccaccgga atcccggacc ggttctcggg gtcgggggtcc 660
 ggtaccgagt tcacactgac catttcctcg ctgagcccg aggactttgc cgtctattac 720
 tgccagcagt acggctcctc ctcatggacg ttcggccagg ggaccaaggt cgaaatcaag 780
 accactaccc cagcaccgag gccaccacc ccggctccta ccatgcctc ccagcctctg 840
 tccctgcgtc cggaggcatg tagaccgcga gctggtgggg ccgtgcatac ccgggggtctt 900
 gacttcgcct gcgatatcta catttgggcc cctctggctg gtacttgccg ggtcctgctg 960
 ctttcaactc tgatcactct ttactgtaag cgcggtcggg agaagctgct gtacatcttt 1020

_SL

aagcaaccct tcatgaggcc tgtgcagact actcaagagg aggacggctg ttcatgccgg 1080
ttcccagagg aggaggaagg cggctgcgaa ctgcgcgtga aattcagccg cagcgcagat 1140
gctccagcct acaagcaggg gcagaaccag ctctacaacg aactcaatct tggtcggaga 1200
gaggagtacg acgtgctgga caagcggaga ggacgggacc cagaaatggg cggaagccg 1260
cgcagaaaga atccccaaga gggcctgtac aacgagctcc aaaaggataa gatggcagaa 1320
gcctatagcg agattggtat gaaaggggaa cgcagaagag gcaaaggcca cgacggactg 1380
taccagggac tcagcaccgc caccaaggac acctatgacg ctcttcacat gcaggccctg 1440
ccgcctcgg 1449

<210> 807

<211> 485

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 807

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Glu Val Gln Leu Val Glu Thr Gly Gly Gly Val
20 25 30

Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Phe
35 40 45

Ala Leu Ser Asn His Gly Met Ser Trp Val Arg Arg Ala Pro Gly Lys
50 55 60

Gly Leu Glu Trp Val Ser Gly Ile Val Tyr Ser Gly Ser Thr Tyr Tyr
65 70 75 80

Ala Ala Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg
85 90 95

Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala
100 105 110

Ile Tyr Tyr Cys Ser Ala His Gly Gly Glu Ser Asp Val Trp Gly Gln
115 120 125

Gly Thr Thr Val Thr Val Ser Ser Ala Ser Gly Gly Gly Gly Ser Gly
130 135 140

Gly Arg Ala Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser
145 150 155 160

_SL

Pro Gly Thr Leu Ser₁₆₅ Leu Ser Pro Gly Glu₁₇₀ Arg Ala Thr Leu Ser₁₇₅ Cys
Arg Ala Ser Gln₁₈₀ Ser Val Gly Ser Thr₁₈₅ Asn Leu Ala Trp Tyr₁₉₀ Gln Gln
Lys Pro Gly₁₉₅ Gln Ala Pro Arg Leu₂₀₀ Leu Ile Tyr Asp Ala₂₀₅ Ser Asn Arg
Ala Thr Gly₂₁₀ Ile Pro Asp Arg₂₁₅ Phe Ser Gly Gly Gly₂₂₀ Ser Gly Thr Asp
Phe Thr Leu Thr Ile Ser₂₃₀ Arg Leu Glu Pro Glu₂₃₅ Asp Phe Ala Val Tyr₂₄₀
Tyr Cys Gln Gln Tyr₂₄₅ Gly Ser Ser Pro Pro₂₅₀ Trp Thr Phe Gly Gln₂₅₅ Gly
Thr Lys Val Glu₂₆₀ Ile Lys Thr Thr Thr₂₆₅ Pro Ala Pro Arg Pro₂₇₀ Pro Thr
Pro Ala Pro₂₇₅ Thr Ile Ala Ser Gln₂₈₀ Pro Leu Ser Leu Arg₂₈₅ Pro Glu Ala
Cys Arg₂₉₀ Pro Ala Ala Gly Gly₂₉₅ Ala Val His Thr Arg₃₀₀ Gly Leu Asp Phe
Ala Cys Asp Ile Tyr Ile₃₁₀ Trp Ala Pro Leu Ala₃₁₅ Gly Thr Cys Gly Val₃₂₀
Leu Leu Leu Ser Leu₃₂₅ Val Ile Thr Leu Tyr₃₃₀ Cys Lys Arg Gly Arg₃₃₅ Lys
Lys Leu Leu Tyr₃₄₀ Ile Phe Lys Gln Pro₃₄₅ Phe Met Arg Pro Val₃₅₀ Gln Thr
Thr Gln Glu₃₅₅ Glu Asp Gly Cys Ser₃₆₀ Cys Arg Phe Pro Glu₃₆₅ Glu Glu Glu
Gly Gly₃₇₀ Cys Glu Leu Arg Val₃₇₅ Lys Phe Ser Arg Ser₃₈₀ Ala Asp Ala Pro
Ala Tyr Lys Gln Gly Gln₃₉₀ Asn Gln Leu Tyr Asn₃₉₅ Glu Leu Asn Leu Gly₄₀₀
Arg Arg Glu Glu Tyr₄₀₅ Asp Val Leu Asp Lys₄₁₀ Arg Arg Gly Arg Asp₄₁₅ Pro
Glu Met Gly Gly₄₂₀ Lys Pro Arg Arg Lys₄₂₅ Asn Pro Gln Glu Gly₄₃₀ Leu Tyr

_SL

Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly
435 440 445

Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln
450 455 460

Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln
465 470 475 480

Ala Leu Pro Pro Arg
485

<210> 808

<211> 1455

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 808

```
atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg      60
cccgaagtgc aattggtgga gactggagga ggagtgggtgc aacctggagg aagcctgaga      120
ctgtcatgcg cgggtgtcggg cttcgccctc tccaaccacg gaatgtcctg ggtccgccgg      180
gcccctggga aaggacttga atgggtgtcc ggcacgtgtt actcgggttc cacctactac      240
gcggcctcag tgaagggccg gtttactatt agccgcgaca actccagaaa cactactgtac      300
ctccaaatga actcgtgctg gccggaagat accgctatct actactgctc cgcccatggg      360
ggagagtcgg acgtctgggg acagggcacc actgtcactg tgtccagcgc ttccggcggt      420
ggtggaagcg ggggacgggc ctcaggaggc ggtggcagcg agattgtgct gaccagtcct      480
cccgggaccc tgagcctgtc cccgggagaa agggccaccc tctcctgtcg ggcattccag      540
tccgtggggg ctactaacct tgcattgtac cagcagaagc ccggccaggc ccctcgcctg      600
ctgatctacg acgcgtccaa tagagccacc ggcattcccg atcgcttcag cggaggcgga      660
tcgggcaccg acttcaccct caccatttca aggttgaac cggaggactt cgccgtgtac      720
tactgccagc agtatggttc gtccccaccc tggacgttcg gccaggggac taaggctcag      780
atcaagacca ctacccagc accgaggcca cccaccccg ctcctaccat cgcctccag      840
cctctgtccc tgcgtccgga ggcattgtag cccgcagctg gtggggccgt gcatacccg      900
ggtcttgact tcgcctgcga tatctacatt tgggcccctc tggctggtac ttgcggggtc      960
ctgctgcttt cactcgtgat cactctttac tgtaagcgcg gtcggaagaa gctgctgtac     1020
atctttaagc aacccttcat gaggcctgtg cagactactc aagaggagga cggctgttca     1080
tgccggttcc cagaggagga ggaaggcggc tgcgaactgc gcgtgaaatt cagccgcagc     1140
gcagatgctc cagcctacaa gcaggggcag aaccagctct acaacgaact caatcttggt     1200
```

cgagagagg agtacgacgt gctggacaag cgagaggac gggaccaga aatgggcggg 1260
aagccgcgca gaaagaatcc ccaagagggc ctgtacaacg agtcctaaaa ggataagatg 1320
gcagaagcct atagcgagat tggtatgaaa ggggaacgca gaagaggcaa aggccacgac 1380
ggactgtacc agggactcag caccgccacc aaggacacct atgacgctct tcacatgcag 1440
gccctgccgc ctcgg 1455

<210> 809
<211> 483
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 809
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu
20 25 30

Val Lys Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
35 40 45

Thr Phe Ser Asp Tyr Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys
50 55 60

Gly Leu Glu Trp Val Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr
65 70 75 80

Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
85 90 95

Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
100 105 110

Ala Val Tyr Tyr Cys Ala Arg Glu Ser Gly Asp Gly Met Asp Val Trp
115 120 125

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Gly Gly Gly Gly
130 135 140

Ser Gly Gly Arg Ala Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr
145 150 155 160

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
165 170 175

Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln
180 185 190

_SL

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser
195 200 205

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
210 215 220

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
225 230 235 240

Tyr Tyr Cys Gln Gln Ser Tyr Thr Leu Ala Phe Gly Gln Gly Thr Lys
245 250 255

Val Asp Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala
260 265 270

Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg
275 280 285

Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys
290 295 300

Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu
305 310 315 320

Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu
325 330 335

Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln
340 345 350

Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Gly Gly
355 360 365

Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr
370 375 380

Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg
385 390 395 400

Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met
405 410 415

Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu
420 425 430

Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys
435 440 445

Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu
450 455 460

_SL

Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu
465 470 475 480

Pro Pro Arg

<210> 810
<211> 1449
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 810
atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60
ccccaagtgc aactcgtgga atctggtgga ggactcgtga aacctggagg atcattgaga 120
ctgtcatgcg cggcctcggg attcacgttc tccgattact acatgagctg gattcgccag 180
gctccggggga agggactgga atgggtgtcc tacatttcct catccggctc caccatctac 240
tacgcggact ccgtgaaggg gagattcacc attagccgcg ataacgcaa gaacagcctg 300
taccttcaga tgaactccct gcgggctgaa gatactgccg tctactactg cgcaaggag 360
agcggagatg ggatggacgt ctggggacag ggtaccactg tgaccgtgtc gtcggcctcc 420
ggcggagggg gttcgggtgg aagggccagc ggcggcggag gcagcgacat ccagatgacc 480
cagtccccct catcgtgtc cgcctccgtg ggcgaccgcg tcaccatcac atgccggggc 540
tcacagtca tctcctccta cctcaattgg tatcagcaga agcccgaaa ggcccctaag 600
cttctgatct acgcagcgtc ctccctgcaa tccggggtcc catctcggtt ctccggctcg 660
ggcagcggta ccgacttcac tctgaccatc tcgagcctgc agccggagga cttcgccact 720
tactactgtc agcaaagcta caccctcgcg tttggccagg gcaccaaagt ggacatcaag 780
accactacc cagcaccgag gccaccacc ccggctccta ccacgcctc ccagcctctg 840
tccctgcgtc cggaggcatg tagaccgca gctggtgggg ccgtgcatac ccgggggtctt 900
gacttcgcct gcgatatcta catttgggcc cctctggctg gtacttgcg ggctctgctg 960
ctttcactcg tgatcactct ttactgtaag cgcggtcgga agaagctgct gtacatcttt 1020
aagcaaccct tcatgaggcc tgtgcagact actcaagagg aggacggctg ttcatgccgg 1080
ttcccagagg aggaggaagg cggctgcgaa ctgcgcgtga aattcagccg cagcgcagat 1140
gctccagcct acaagcaggg gcagaaccag ctctacaacg aactcaatct tggtcggaga 1200
gaggagtacg acgtgctgga caagcggaga ggacgggacc cagaaatggg cgggaagccg 1260
cgcagaaaga atccccaaga gggcctgtac aacgagctcc aaaaggataa gatggcagaa 1320
gcctatagcg agattggtat gaaaggggaa cgcagaagag gcaaaggcca cgacggactg 1380
taccagggac tcagcaccgc caccaaggac acctatgacg ctcttcacat gcaggccctg 1440

ccgcctcgg

1449

<210> 811
<211> 490
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 811
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu
20 25 30

Val Lys Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
35 40 45

Thr Phe Ser Asp Tyr Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys
50 55 60

Gly Leu Glu Trp Val Ser Tyr Ile Ser Ser Ser Gly Asn Thr Ile Tyr
65 70 75 80

Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
85 90 95

Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
100 105 110

Ala Val Tyr Tyr Cys Ala Arg Ser Thr Met Val Arg Glu Asp Tyr Trp
115 120 125

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Gly Gly Gly Gly
130 135 140

Ser Gly Gly Arg Ala Ser Gly Gly Gly Gly Ser Asp Ile Val Leu Thr
145 150 155 160

Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly Gln Pro Ala Ser Ile
165 170 175

Ser Cys Lys Ser Ser Glu Ser Leu Val His Asn Ser Gly Lys Thr Tyr
180 185 190

Leu Asn Trp Phe His Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile
195 200 205

Tyr Glu Val Ser Asn Arg Asp Ser Gly Val Pro Asp Arg Phe Thr Gly
Page 578

_SL

210		215		220											
Ser 225	Gly	Ser	Gly	Thr	Asp 230	Phe	Thr	Leu	Lys	Ile 235	Ser	Arg	Val	Glu	Ala 240
Glu	Asp	Val	Gly	Val 245	Tyr	Tyr	Cys	Met	Gln 250	Gly	Thr	His	Trp	Pro 255	Gly
Thr	Phe	Gly	Gln 260	Gly	Thr	Lys	Leu	Glu 265	Ile	Lys	Thr	Thr	Thr 270	Pro	Ala
Pro	Arg	Pro 275	Pro	Thr	Pro	Ala	Pro 280	Thr	Ile	Ala	Ser	Gln 285	Pro	Leu	Ser
Leu	Arg 290	Pro	Glu	Ala	Cys	Arg 295	Pro	Ala	Ala	Gly	Gly 300	Ala	Val	His	Thr
Arg 305	Gly	Leu	Asp	Phe	Ala 310	Cys	Asp	Ile	Tyr	Ile 315	Trp	Ala	Pro	Leu	Ala 320
Gly	Thr	Cys	Gly	Val 325	Leu	Leu	Leu	Ser	Leu 330	Val	Ile	Thr	Leu	Tyr 335	Cys
Lys	Arg	Gly	Arg 340	Lys	Lys	Leu	Leu	Tyr 345	Ile	Phe	Lys	Gln	Pro 350	Phe	Met
Arg	Pro	Val 355	Gln	Thr	Thr	Gln	Glu 360	Glu	Asp	Gly	Cys	Ser 365	Cys	Arg	Phe
Pro	Glu 370	Glu	Glu	Glu	Gly	Gly 375	Cys	Glu	Leu	Arg	Val 380	Lys	Phe	Ser	Arg
Ser 385	Ala	Asp	Ala	Pro	Ala 390	Tyr	Lys	Gln	Gly	Gln 395	Asn	Gln	Leu	Tyr	Asn 400
Glu	Leu	Asn	Leu	Gly 405	Arg	Arg	Glu	Glu	Tyr 410	Asp	Val	Leu	Asp	Lys 415	Arg
Arg	Gly	Arg	Asp 420	Pro	Glu	Met	Gly	Gly 425	Lys	Pro	Arg	Arg	Lys 430	Asn	Pro
Gln	Glu	Gly 435	Leu	Tyr	Asn	Glu	Leu 440	Gln	Lys	Asp	Lys	Met 445	Ala	Glu	Ala
Tyr 450	Ser	Glu	Ile	Gly	Met	Lys 455	Gly	Glu	Arg	Arg	Arg 460	Gly	Lys	Gly	His
Asp 465	Gly	Leu	Tyr	Gln	Gly 470	Leu	Ser	Thr	Ala	Thr 475	Lys	Asp	Thr	Tyr	Asp 480
Ala	Leu	His	Met	Gln	Ala	Leu	Pro	Pro	Arg						

<210> 812
 <211> 1470
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 812
 atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60
 cccaagtgc aactggtgca aagcggagga ggattggtca aaccggagg aagcctgaga 120
 ctgtcatgcg cggcctctgg attcaccttc tccgattact acatgtcatg gatcagacag 180
 gccccgggga agggcctcga atgggtgtcc tacatctcgt cctccgggaa caccatctac 240
 tacgccgaca gcgtgaaggg ccgctttacc atttcccgcg acaacgcaaa gaactcgctg 300
 taccttcaga tgaattccct gcgggctgaa gataccgcgg tgtactattg cgcccggctc 360
 actatggtcc gggaggacta ctggggacag ggcacactcg tgaccgtgtc cagcgcgagc 420
 gggggtggag gcagcggtag acgcgcctcc ggcggcggcg gttcagacat cgtgctgact 480
 cagtcgcccc tgctcgtgcc ggtcaccttg ggccaaccgg cctcaattag ctgcaagtcc 540
 tcggagagcc tgggtgcaca ctcaggaaag acttacctga actgggtcca tcagcggcct 600
 ggacagtccc cacggaggct catctatgaa gtgtccaaca gggattcggg ggtgcccgcg 660
 cgcttcactg gctccgggtc cggcaccgac ttcaccttga aaatctccag agtggaagcc 720
 gaggacgtgg gcgtgtacta ctgtatgcag ggtaccact ggcttgaac ctttggacaa 780
 ggaactaagc tcgagattaa gaccactacc ccagcaccga ggccaccac cccggctcct 840
 accatcgctt cccagcctct gtccctgcgt ccggaggcat gtagaccgc agctggtggg 900
 gccgtgcata cccgggtctt tgacttcgcc tgcgatattt acatttgggc ccctctggct 960
 ggtacttgcg gggtcctgct gctttcactc gtgatcactc ttactgtaa gcgcggctcg 1020
 aagaagctgc tgtacatctt taagcaacc ttcatgaggc ctgtgcagac tactcaagag 1080
 gaggacggct gttcatgccg gttcccagag gaggaggaag gcggctgcga actgcgcgtg 1140
 aaattcagcc gcagcgcaga tgctccagcc tacaagcagg ggcagaacca gctctacaac 1200
 gaactcaatc ttggtcggag agaggagtag gacgtgctgg acaagcggag aggacgggac 1260
 ccagaaatgg gcgggaagcc gcgcagaaag aatccccaag agggcctgta caacgagctc 1320
 caaaaggata agatggcaga agcctatagc gagattggta tgaaagggga acgcagaaga 1380
 ggcaaaggcc acgacggact gtaccaggga ctcagcaccg ccaccaagga cacctatgac 1440
 gctcttcaca tgcaggccct gccgcctcgg 1470

<210> 813
 <211> 483
 <212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 813

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu
20 25 30

Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Phe
35 40 45

Ala Leu Ser Asn His Gly Met Ser Trp Val Arg Arg Ala Pro Gly Lys
50 55 60

Gly Leu Glu Trp Val Ser Gly Ile Val Tyr Ser Gly Ser Thr Tyr Tyr
65 70 75 80

Ala Ala Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg
85 90 95

Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala
100 105 110

Ile Tyr Tyr Cys Ser Ala His Gly Gly Glu Ser Asp Val Trp Gly Gln
115 120 125

Gly Thr Thr Val Thr Val Ser Ser Ala Ser Gly Gly Gly Gly Ser Gly
130 135 140

Gly Arg Ala Ser Gly Gly Gly Gly Ser Asp Ile Arg Leu Thr Gln Ser
145 150 155 160

Pro Ser Pro Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
165 170 175

Gln Ala Ser Glu Asp Ile Asn Lys Phe Leu Asn Trp Tyr His Gln Thr
180 185 190

Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser Thr Leu Gln
195 200 205

Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
210 215 220

Thr Leu Thr Ile Asn Ser Leu Gln Pro Glu Asp Ile Gly Thr Tyr Tyr
225 230 235 240

Cys Gln Gln Tyr Glu Ser Leu Pro Leu Thr^{-SL} Phe Gly Gly Gly Thr Lys
 245 250 255
 Val Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala
 260 265 270
 Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg
 275 280 285
 Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys
 290 295 300
 Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu
 305 310 315 320
 Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu
 325 330 335
 Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln
 340 345 350
 Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly
 355 360 365
 Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr
 370 375 380
 Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg
 385 390 395 400
 Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met
 405 410 415
 Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu
 420 425 430
 Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys
 435 440 445
 Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu
 450 455 460
 Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu
 465 470 475 480
 Pro Pro Arg

<210> 814

<211> 1449

<212> DNA

<213> Artificial Sequence

_SL

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 814

```
atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg      60
ccccaagtgc aactcgtgga atctggtgga ggactcgtgc aaccgggtgg aagccttagg      120
ctgtcgtgcg ccgtcagcgg gtttgctctg agcaaccatg gaatgtcctg ggtccgccgg      180
gcaccgggaa aagggtgga atgggtgtcc ggcatcgtgt acagcgggtc aacctattac      240
gccgcgtccg tgaagggcag attcactatc tcaagagaca acagccggaa caccctgtac      300
ttgcaaatga attccctgcg ccccgaggac accgccatct actactgctc cgcccacgga      360
ggagagtcgg acgtgtgggg ccagggaaac actgtgactg tgtccagcgc atcaggaggg      420
ggtggttcgg gcggccgggc ctcgggggga ggaggttcgg acattcgggt gaccagtcct      480
ccgtccccac tgtcggcctc cgtcggcgac cgctgacca tcacttgtca ggcgtccgag      540
gacattaaca agttcctgaa ctggtaccac cagaccctg gaaaggcccc caagctgctg      600
atctacgatg cctcgacct tcaaactgga gtgcctagcc ggttctccgg gtccggctcc      660
ggcactgatt tcactctgac catcaactca ttgcagccgg aagatatcgg gacctactat      720
tgccagcagt acgaatccct cccgctcaca ttcggcgggg gaaccaaggt cgagattaag      780
accactaccc cagcaccgag gccaccacc ccggctccta ccacgcctc ccagcctctg      840
tccctgcgtc cggaggcatg tagaccgca gctggtgggg ccgtgcatac ccggggtctt      900
gacttcgcct gcgatatcta catttgggcc cctctggctg gtacttgagg ggtcctgctg      960
ctttcactcg tgatcactct ttactgtaag cgcggtcggg agaagctgct gtacatcttt     1020
aagcaaccct tcatgaggcc tgtgcagact actcaagagg aggacggctg ttcattgccg     1080
ttcccagagg aggaggaagg cggctgcgaa ctgcgcgtga aattcagccg cagcgcagat     1140
gctccagcct acaagcaggg gcagaaccag ctctacaacg aactcaatct tggtcggaga     1200
gaggagtacg acgtgctgga caagcggaga ggacgggacc cagaaatggg cgggaagccg     1260
cgcagaaaaga atccccaaga gggcctgtac aacgagctcc aaaaggataa gatggcagaa     1320
gcctatagcg agattggtat gaaaggggaa cgcagaagag gcaaaggcca cgacggactg     1380
taccagggac tcagcaccgc caccaaggac acctatgacg ctcttcacat gcaggccctg     1440
ccgcctcgg                                     1449
```

<210> 815

<211> 484

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

_SL

<400> 815

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15
His Ala Ala Arg Pro Glu Val Gln Leu Val Glu Thr Gly Gly Gly Leu
20 25 30
Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Phe
35 40 45
Ala Leu Ser Asn His Gly Met Ser Trp Val Arg Arg Ala Pro Gly Lys
50 55 60
Gly Leu Glu Trp Val Ser Gly Ile Val Tyr Ser Gly Ser Thr Tyr Tyr
65 70 75 80
Ala Ala Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg
85 90 95
Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala
100 105 110
Ile Tyr Tyr Cys Ser Ala His Gly Gly Glu Ser Asp Val Trp Gly Gln
115 120 125
Gly Thr Thr Val Thr Val Ser Ser Ala Ser Gly Gly Gly Gly Ser Gly
130 135 140
Gly Arg Ala Ser Gly Gly Gly Gly Ser Glu Thr Thr Leu Thr Gln Ser
145 150 155 160
Pro Ala Thr Leu Ser Val Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
165 170 175
Arg Ala Ser Gln Ser Val Gly Ser Asn Leu Ala Trp Tyr Gln Gln Lys
180 185 190
Pro Gly Gln Gly Pro Arg Leu Leu Ile Tyr Gly Ala Ser Thr Arg Ala
195 200 205
Thr Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe
210 215 220
Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Val Tyr Tyr
225 230 235 240
Cys Gln Gln Tyr Asn Asp Trp Leu Pro Val Thr Phe Gly Gln Gly Thr
245 250 255
Lys Val Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro
260 265 270

_SL

Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys
275 280 285

Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala
290 295 300

Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu
305 310 315 320

Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys
325 330 335

Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr
340 345 350

Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly
355 360 365

Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala
370 375 380

Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg
385 390 395 400

Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu
405 410 415

Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn
420 425 430

Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met
435 440 445

Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly
450 455 460

Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala
465 470 475 480

Leu Pro Pro Arg

<210> 816

<211> 1452

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 816

_SL

atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg	60
cccgaagtgc aattggtgga aactggagga ggacttgtgc aacctggagg atcattgcgg	120
ctctcatgcg ctgtctccgg cttcgccctg tcaaatacac ggatgtcgtg ggtcagacgg	180
gccccgggaa agggctctgga atgggtgtcg gggatttgtt acagcggctc cacctactac	240
gccgcttcgg tcaagggccg cttcactatt tcacgggaca acagccgcaa caccctctat	300
ctgcaaataa actctctccg cccggaggat accgccatct actactgctc cgcacacggc	360
ggcgaatccg acgtgtgggg acaggaacc actgtcaccg tgtcgtccgc atccggtggc	420
ggaggatcgg gtggccgggc ctccgggggc ggccggcagc agactaccct gaccagttcc	480
cctgccactc tgtccgtgag cccgggagag agagccaccc ttagctgccg ggccagccag	540
agcgtgggct ccaacctggc ctggtaccag cagaagccag gacagggctc caggctgctg	600
atctacggag cctccactcg cgcgaccggc atccccgcga ggttctccgg gtcgggttcc	660
gggaccgagt tcaccctgac catctcctcc ctccaaccgg aggacttcgc ggtgtactac	720
tgtcagcagt acaacgattg gctgcccgtg acatttggac aggggacgaa ggtggaaatc	780
aaaaccacta ccccgaccg gagggcacc accccggctc ctaccatcgc ctcccagcct	840
ctgtccctgc gtccggaggc atgtagacc gcagctggtg gggccgtgca taccgggggt	900
cttgacttcg cctgcgatat ctacatttgg gccctcttgg ctggtacttg cggggtcctg	960
ctgctttcac tcgtgatcac tctttactgt aagcgcggtc ggaagaagct gctgtacatc	1020
tttaagcaac cttcatgag gcctgtgcag actactcaag aggaggacgg ctgttcatgc	1080
cggttcccag aggaggagga aggcggctgc gaactgcgcg tgaaattcag ccgcagcgca	1140
gatgtctcag cctacaagca ggggcagaac cagctctaca acgaactcaa tcttggtcgg	1200
agagaggagt acgacgtgct ggacaagcgg agaggacggg acccagaaat gggcggaag	1260
ccgcgcagaa agaatccca agagggcctg tacaacgagc tccaaaagga taagatggca	1320
gaagcctata gcgagattgg tatgaaagg gaacgcagaa gaggcaaagg ccacgacgga	1380
ctgtaccagg gactcagcac cgccaccaag gacacctatg acgctcttca catgcaggcc	1440
ctgccgcctc gg	1452

<210> 817

<211> 485

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 817

Met	Ala	Leu	Pro	Val	Thr	Ala	Leu	Leu	Leu	Pro	Leu	Ala	Leu	Leu	Leu
1				5				10					15		

His	Ala	Ala	Arg	Pro	Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu
			20					25					30		

_SL

Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Phe
35 40 45

Ala Leu Ser Asn His Gly Met Ser Trp Val Arg Arg Ala Pro Gly Lys
50 55 60

Gly Leu Glu Trp Val Ser Gly Ile Val Tyr Ser Gly Ser Thr Tyr Tyr
65 70 75 80

Ala Ala Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg
85 90 95

Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala
100 105 110

Ile Tyr Tyr Cys Ser Ala His Gly Gly Glu Ser Asp Val Trp Gly Gln
115 120 125

Gly Thr Thr Val Thr Val Ser Ser Ala Ser Gly Gly Gly Gly Ser Gly
130 135 140

Gly Arg Ala Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser
145 150 155 160

Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
165 170 175

Arg Ala Ser Gln Ser Ile Gly Ser Ser Ser Leu Ala Trp Tyr Gln Gln
180 185 190

Lys Pro Gly Gln Ala Pro Arg Leu Leu Met Tyr Gly Ala Ser Ser Arg
195 200 205

Ala Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
210 215 220

Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr
225 230 235 240

Tyr Cys Gln Gln Tyr Ala Gly Ser Pro Pro Phe Thr Phe Gly Gln Gly
245 250 255

Thr Lys Val Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr
260 265 270

Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala
275 280 285

Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe
290 295 300

_SL

Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val
305 310 315 320

Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys
325 330 335

Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr
340 345 350

Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu
355 360 365

Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro
370 375 380

Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly
385 390 395 400

Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro
405 410 415

Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr
420 425 430

Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly
435 440 445

Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln
450 455 460

Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln
465 470 475 480

Ala Leu Pro Pro Arg
485

<210> 818
<211> 1455
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 818
atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60
cccgaagtgc aattggtgga atctggtgga ggacttgctc aacctggagg atcactgaga 120
ctgtcatgcg cgggtgccgg ttttgccctg agcaatcatg ggatgtcgtg ggtccggcgc 180
gccccgggaa aggggtctgga atgggtgtcg ggtatcgtct actccgggag cacttactac 240

_SL

gccgcgagcg tgaagggccg cttcaccatt tcccgcgata actcccgcaa caccctgtac 300
ttgcaaatga actcgctccg gcctgaggac actgccatct actactgctc cgcacacgga 360
ggagaatccg acgtgtgggg ccagggaact accgtgaccg tcagcagcgc ctccggcggc 420
gggggctcag gcggacgggc tagcggcggc ggtggctccg agatcggtgt gaccagtcg 480
cctggcactc tctcgctgag ccccggggaa agggcaacc tgtcctgtcg ggccagccag 540
tccattggat catcctccct cgcctggtat cagcagaaac cgggacaggc tccgcggctg 600
cttatgtatg gggccagctc aagagcctcc ggcattccc accggttctc cgggtccggt 660
tccggcaccg atttcaccct gactatctcg aggttgagc cagaggactt cgccgtgtac 720
tactgccagc agtacgcggg gtccccgccg ttcacgttcg gacagggaa caaggtcgag 780
atcaagacca ctacccagc accgaggcca cccaccccg ctcctaccat cgcctcccag 840
cctctgtccc tgcgtccgga ggcatgtaga cccgcagctg gtggggccgt gcatacccg 900
ggtcttgact tcgcctgcga tatctacatt tgggccctc tggctggtac ttgcggggtc 960
ctgctgcttt cactcgtgat cactctttac tgtaagcgcg gtcggaagaa gctgctgtac 1020
atctttaagc aacccttcat gaggcctgtg cagactactc aagaggagga cggctgttca 1080
tgccggttcc cagaggagga ggaaggcggc tgcgaactgc gcgtgaaatt cagccgcagc 1140
gcagatgctc cagcctacaa gcaggggcag aaccagctct acaacgaact caatcttgg 1200
cggagagagg agtacgacgt gctggacaag cggagaggac gggaccaga aatgggcggg 1260
aagccgcgca gaaagaatcc ccaagagggc ctgtacaacg agtccaaaa ggataagatg 1320
gcagaagcct atagcgagat tggatatgaa ggggaacgca gaagaggcaa aggccacgac 1380
ggactgtacc aggactcag caccgccacc aaggacacct atgacgtctt tcacatgcag 1440
gccctgccgc ctcgg 1455

<210> 819

<211> 487

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 819

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu
20 25 30

Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly
35 40 45

Ser Ile Ser Ser Ser Tyr Tyr Tyr Trp Gly Trp Ile Arg Gln Pro Pro
Page 589

50					55					_SL		60				
Gly 65	Lys	Gly	Leu	Glu	Trp 70	Ile	Gly	Ser	Ile	Tyr 75	Tyr	Ser	Gly	Ser	Ala 80	
Tyr	Tyr	Asn	Pro	Ser 85	Leu	Lys	Ser	Arg	Val 90	Thr	Ile	Ser	Val	Asp 95	Thr	
Ser	Lys	Asn	Gln 100	Phe	Ser	Leu	Arg	Leu 105	Ser	Ser	Val	Thr	Ala 110	Ala	Asp	
Thr	Ala	Val 115	Tyr	Tyr	Cys	Ala	Arg 120	His	Trp	Gln	Glu	Trp 125	Pro	Asp	Ala	
Phe	Asp 130	Ile	Trp	Gly	Gln	Gly 135	Thr	Met	Val	Thr	Val 140	Ser	Ser	Gly	Gly	
Gly 145	Gly	Ser	Gly	Gly	Gly 150	Gly	Ser	Gly	Gly	Gly 155	Gly	Ser	Glu	Thr	Thr 160	
Leu	Thr	Gln	Ser	Pro 165	Ala	Phe	Met	Ser	Ala 170	Thr	Pro	Gly	Asp	Lys 175	Val	
Ile	Ile	Ser	Cys 180	Lys	Ala	Ser	Gln	Asp 185	Ile	Asp	Asp	Ala	Met 190	Asn	Trp	
Tyr	Gln	Gln 195	Lys	Pro	Gly	Glu	Ala 200	Pro	Leu	Phe	Ile	Ile 205	Gln	Ser	Ala	
Thr	Ser 210	Pro	Val	Pro	Gly	Ile 215	Pro	Pro	Arg	Phe	Ser 220	Gly	Ser	Gly	Phe	
Gly 225	Thr	Asp	Phe	Ser	Leu 230	Thr	Ile	Asn	Asn	Ile 235	Glu	Ser	Glu	Asp	Ala 240	
Ala	Tyr	Tyr	Phe	Cys 245	Leu	Gln	His	Asp	Asn 250	Phe	Pro	Leu	Thr	Phe 255	Gly	
Gln	Gly	Thr	Lys 260	Leu	Glu	Ile	Lys	Thr 265	Thr	Thr	Pro	Ala	Pro 270	Arg	Pro	
Pro	Thr	Pro 275	Ala	Pro	Thr	Ile	Ala 280	Ser	Gln	Pro	Leu	Ser 285	Leu	Arg	Pro	
Glu	Ala 290	Cys	Arg	Pro	Ala	Ala 295	Gly	Gly	Ala	Val	His 300	Thr	Arg	Gly	Leu	
Asp 305	Phe	Ala	Cys	Asp	Ile 310	Tyr	Ile	Trp	Ala	Pro 315	Leu	Ala	Gly	Thr	Cys 320	
Gly	Val	Leu	Leu	Leu	Ser	Leu	Val	Ile	Thr	Leu	Tyr	Cys	Lys	Arg	Gly	

									-	SL					
				325					330					335	
Arg	Lys	Lys	Leu 340	Leu	Tyr	Ile	Phe	Lys 345	Gln	Pro	Phe	Met	Arg 350	Pro	Val
Gln	Thr	Thr 355	Gln	Glu	Glu	Asp	Gly 360	Cys	Ser	Cys	Arg	Phe 365	Pro	Glu	Glu
Glu	Glu 370	Gly	Gly	Cys	Glu	Leu 375	Arg	Val	Lys	Phe	Ser 380	Arg	Ser	Ala	Asp
Ala 385	Pro	Ala	Tyr	Lys	Gln 390	Gly	Gln	Asn	Gln	Leu 395	Tyr	Asn	Glu	Leu	Asn 400
Leu	Gly	Arg	Arg	Glu 405	Glu	Tyr	Asp	Val	Leu 410	Asp	Lys	Arg	Arg	Gly 415	Arg
Asp	Pro	Glu	Met 420	Gly	Gly	Lys	Pro	Arg 425	Arg	Lys	Asn	Pro	Gln 430	Glu	Gly
Leu	Tyr	Asn 435	Glu	Leu	Gln	Lys	Asp 440	Lys	Met	Ala	Glu	Ala 445	Tyr	Ser	Glu
Ile	Gly 450	Met	Lys	Gly	Glu	Arg 455	Arg	Arg	Gly	Lys	Gly 460	His	Asp	Gly	Leu
Tyr 465	Gln	Gly	Leu	Ser	Thr 470	Ala	Thr	Lys	Asp	Thr 475	Tyr	Asp	Ala	Leu	His 480
Met	Gln	Ala	Leu	Pro 485	Pro	Arg									

```
<210> 820
<211> 1461
<212> DNA
<213> Artificial Sequence
```

```
<220>  
<221> source  
<223> /note="Description of Artificial Sequence: Synthetic  
polynucleotide"
```

<400> 820						
atggccctcc	ctgtcaccgc	cctgctgctt	ccgctggctc	ttctgctcca	cgccgctcgg	60
ccccaagtgc	agcttcagga	aagcggaccg	ggcctgggtca	agccatccga	aactctctcc	120
ctgacttgca	ctgtgtcttg	cggttccatc	tcatcgtcgt	actactactg	gggctggatt	180
aggcagccgc	ccggaaaggg	actggagtg	atcggaagca	tctactattc	cggtctggcg	240
tactacaacc	ctagcctcaa	gtcgagagtg	accatctccg	tggatacctc	caagaaccag	300
ttttccctgc	gcctgagctc	cgtgaccgcc	gctgacaccg	ccgtgtacta	ctgtgctcgg	360
cattggcagg	aatggcccga	tgcttgcgac	atttggggcc	agggcactat	ggtcactgtg	420

_SL

tcatccgggg	gtggaggcag	cgggggagga	gggtccgggg	ggggagggttc	agagacaacc	480
ttgaccagtc	cacccgcatt	catgtccgcc	actccgggag	acaagggtcat	catctcgtgc	540
aaagcgtccc	aggatatcga	cgatgccatg	aatttggtacc	agcagaagcc	tggcgaagcg	600
ccgctgttca	ttatccaatc	cgcaacctcg	cccgtgcctg	gaatcccacc	gcggttcagc	660
ggcagcgggt	tcggaaccga	cttttccttg	accattaaca	acattgagtc	cgaggacgcc	720
gcctactact	tctgcctgca	acacgacaac	ttccctctca	cgttcggcca	gggaaccaag	780
ctggaaatca	agaccactac	cccagcaccg	aggccaccca	ccccggctcc	taccatcgcc	840
tcccagcctc	tgtccctgcg	tccggaggca	tgtagaccgc	cagctggtgg	ggccgtgcat	900
acccgggggtc	ttgacttcgc	ctgcgatatc	tacatttggtg	cccctctggc	tggtacttgc	960
ggggtcctgc	tgctttcact	cgtgatcact	ctttactgta	agcgcggctg	gaagaagctg	1020
ctgtacatct	ttaagcaacc	cttcatgagg	cctgtgcaga	ctactcaaga	ggaggacggc	1080
tggtcatgcc	ggttcccaga	ggaggaggaa	ggcggctgcg	aactgcgcgt	gaaattcagc	1140
cgcagcgag	atgctccagc	ctacaagcag	gggcagaacc	agctctacaa	cgaactcaat	1200
cttggtcggg	gagaggagta	cgacgtgctg	gacaagcgga	gaggacggga	cccagaaatg	1260
ggcgggaagc	cgcgagaaa	gaatcccaa	gagggcctgt	acaacgagct	ccaaaaggat	1320
aagatggcag	aagcctatag	cgagattggt	atgaaagggg	aacgcagaag	aggcaaaggc	1380
cacgacggac	tgtaccaggg	actcagcacc	gccaccaagg	acacctatga	cgctcttcac	1440
atgcaggccc	tgccgcctcg	g				1461

<210> 821
 <211> 489
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 821
 Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
 1 5 10 15

His Ala Ala Arg Pro Gln Val Asn Leu Arg Glu Ser Gly Pro Ala Leu
 20 25 30

Val Lys Pro Thr Gln Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe
 35 40 45

Ser Leu Arg Thr Ser Gly Met Cys Val Ser Trp Ile Arg Gln Pro Pro
 50 55 60

Gly Lys Ala Leu Glu Trp Leu Ala Arg Ile Asp Trp Asp Glu Asp Lys
 65 70 75 80

Phe Tyr Ser Thr Ser₈₅ Leu Lys Thr Arg Leu₉₀^{-SL} Thr Ile Ser Lys Asp₉₅ Thr
 Ser Asp Asn Gln₁₀₀ Val Val Leu Arg Met₁₀₅ Thr Asn Met Asp₁₁₀ Pro Ala Asp
 Thr Ala Thr₁₁₅ Tyr Tyr Cys Ala Arg₁₂₀ Ser Gly Ala Gly₁₂₅ Gly Thr Ser Ala
 Thr Ala₁₃₀ Phe Asp Ile Trp Gly₁₃₅ Pro Gly Thr Met Val₁₄₀ Thr Val Ser Ser
 Gly₁₄₅ Gly Gly Gly Ser Gly₁₅₀ Gly Gly Gly Ser Gly₁₅₅ Gly Gly Gly Ser Asp₁₆₀
 Ile Gln Met Thr Gln₁₆₅ Ser Pro Ser Ser Leu₁₇₀ Ser Ala Ser Val Gly₁₇₅ Asp
 Arg Val Thr Ile₁₈₀ Thr Cys Arg Ala Ser₁₈₅ Gln Asp Ile Tyr Asn₁₉₀ Asn Leu
 Ala Trp Phe₁₉₅ Gln Leu Lys Pro Gly₂₀₀ Ser Ala Pro Arg Ser₂₀₅ Leu Met Tyr
 Ala Ala₂₁₀ Asn Lys Ser Gln Ser₂₁₅ Gly Val Pro Ser Arg₂₂₀ Phe Ser Gly Ser
 Ala Ser Gly Thr Asp Phe₂₃₀ Thr Leu Thr Ile Ser₂₃₅ Ser Leu Gln Pro Glu₂₄₀
 Asp Phe Ala Thr Tyr₂₄₅ Tyr Cys Gln His Tyr₂₅₀ Tyr Arg Phe Pro Tyr₂₅₅ Ser
 Phe Gly Gln Gly₂₆₀ Thr Lys Leu Glu Ile₂₆₅ Lys Thr Thr Thr Pro₂₇₀ Ala Pro
 Arg Pro Pro Thr Pro Ala Pro Thr₂₈₀ Ile Ala Ser Gln Pro₂₈₅ Leu Ser Leu
 Arg Pro₂₉₀ Glu Ala Cys Arg Pro₂₉₅ Ala Ala Gly Gly Ala₃₀₀ Val His Thr Arg
 Gly₃₀₅ Leu Asp Phe Ala Cys₃₁₀ Asp Ile Tyr Ile Trp₃₁₅ Ala Pro Leu Ala Gly₃₂₀
 Thr Cys Gly Val Leu₃₂₅ Leu Leu Ser Leu Val₃₃₀ Ile Thr Leu Tyr Cys₃₃₅ Lys
 Arg Gly Arg Lys₃₄₀ Lys Leu Leu Tyr Ile₃₄₅ Phe Lys Gln Pro Phe₃₅₀ Met Arg

Pro Val Gln Thr Thr Gln Glu Glu Asp Gly^{_SL} Cys Ser Cys Arg Phe Pro
 355 360 365
 Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser
 370 375 380
 Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu
 385 390 395 400
 Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg
 405 410 415
 Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln
 420 425 430
 Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr
 435 440 445
 Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp
 450 455 460
 Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala
 465 470 475 480
 Leu His Met Gln Ala Leu Pro Pro Arg
 485

<210> 822
 <211> 1467
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 822	
atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg	60
ccccaagtca atctgcgcga atccggcccc gccttggtca agcctaccca gaccctcact	120
ctgacctgta ctttctccgg cttctccctg cggacttccg ggatgtgcgt gtcctggatc	180
agacagcctc cgggaaaggc cctggagtgg ctcgctcgca ttgactggga tgaggacaag	240
ttctactcca ctcactcaa gaccaggctg accatcagca aagatacctc tgacaaccaa	300
gtggtgctcc gcatgaccaa catggacca gccgacactg ccacttacta ctgcgcgagg	360
agcggagcgg gcggaacctc cgccaccgcc ttcgatattt ggggcccggg taccatggtc	420
accgtgtcaa gcggaggagg ggggtccggg ggcggcgggt cggggggagg cggatcggac	480
attcagatga ctcagtcacc atcgtccctg agcgctagcg tgggcgacag agtgacaatc	540
acttgccggg catcccagga catctataac aaccttgcgt ggttccagct gaagcctggt	600
tccgcaccgc ggtcacttat gtacgccgcc aacaagagcc agtcgggagt gccgtcccgg	660

_SL

ttttccggtt cggcctcggg aactgacttc accctgacga tctccagcct gcaacccgag 720
gatttcgcca cctactactg ccagcactac taccgctttc cctactcggt cggacagggg 780
accaagctgg aaatcaagac cactacccca gcaccgaggg caccaccccc ggctcctacc 840
atcgctccc agcctctgtc cctgcgtccg gaggcattga gaccgcagc tgggtggggcc 900
gtgcataccc ggggtcttga cttgcctgc gatatttaca ttggggcccc tctggctggt 960
acttgcgggg tcctgctgct ttcactcgtg atcactcttt actgtaagcg cggtcggaag 1020
aagctgctgt acatctttaa gcaacccttc atgaggcctg tgcagactac tcaagaggag 1080
gacggctgtt catgccggtt cccagaggag gaggaaggcg gctgcgaact gcgcgtgaaa 1140
ttcagccgca gcgcagatgc tccagcctac aagcaggggg agaaccagct ctacaacgaa 1200
ctcaatcttg gtcggagaga ggagtacgac gtgctggaca agcggagagg acgggaccca 1260
gaaatgggcg ggaagccgag cagaaagaat cccaagagg gcctgtacaa cgagctccaa 1320
aaggataaga tggcagaagc ctatagcgag attggtatga aagggaacg cagaagaggc 1380
aaaggccacg acggactgta ccagggactc agcaccgcca ccaaggacac ctatgacgct 1440
cttcacatgc aggcctgccc gcctcgg 1467

<210> 823

<211> 490

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 823

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
20 25 30

Val Lys Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
35 40 45

Thr Phe Ser Ser Tyr Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys
50 55 60

Gly Leu Glu Trp Val Ser Ser Ile Ser Ser Ser Ser Tyr Ile Tyr
65 70 75 80

Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
85 90 95

Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
100 105 110

_SL

Ala Val Tyr Tyr Cys Ala Lys Thr Ile Ala Ala Val Tyr Ala Phe Asp
115 120 125

Ile Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly
130 135 140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr
145 150 155 160

Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Glu Glu Pro Ala Ser Ile
165 170 175

Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr Asn Tyr
180 185 190

Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile
195 200 205

Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe Ser Gly
210 215 220

Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala
225 230 235 240

Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala Leu Gln Thr Pro Tyr
245 250 255

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Thr Thr Thr Pro Ala
260 265 270

Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser
275 280 285

Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr
290 295 300

Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala
305 310 315 320

Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys
325 330 335

Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met
340 345 350

Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe
355 360 365

Pro Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg
370 375 380

_SL

Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn
385 390 395 400

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
405 410 415

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
420 425 430

Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
435 440 445

Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
450 455 460

Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
465 470 475 480

Ala Leu His Met Gln Ala Leu Pro Pro Arg
485 490

<210> 824

<211> 1470

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 824

```
atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg      60
cccgaagtgc agcttgtcga atccgggggg ggactggtca agccggggcgg atcactgaga      120
ctgtcctgcg ccgcgagcgg cttcacgttc tctctctact ccatgaactg ggtccgcca      180
gccccggga agggactgga atgggtgtcc tctatctcct cgtcgtcgtc ctacatctac      240
tacgccgact ccgtgaaggg aagattcacc atttccgcg acaacgcaa gaactcactg      300
tacttgcaaa tgaactcact ccggggccgaa gatactgctg tgtactattg cgccaagact      360
attgccgccg tctacgcttt cgacatctgg ggccaggga ccaccgtgac tgtgtcgtcc      420
ggtggtggtg gtcggggcgg aggaggaagc ggcggcgggg ggtccgagat tgtgtgacc      480
cagtcgccac tgagcctccc tgtgaccccc gaggaaccgc ccagcatcag ctgccggtcc      540
agccagtccc tgctccactc caacggatac aattacctcg attggtacct tcagaagcct      600
ggacaaagcc cgcagctgct catctacttg ggatcaaacc gcgcgtcagg agtgccctgac      660
cggttctccg gtcggggcag cggtagcgat ttcaccctga aaatctccag ggtggaggca      720
gaggacgtgg gagtgtatta ctgtatgcag gcgctgcaga ctccgtacac atttgggcag      780
ggcaccaagc tggagatcaa gaccactacc ccagcaccga ggccaccac cccggctcct      840
```


_SL

```

accatcgctt cccagcctct gtccttgcgt ccggaggcat gtagaccgc agctggtggg      900
gccgtgcata cccgggggtct tgacttcgcc tgcgatattct acatttgggc ccctctggct      960
ggtacttgcg ggggtcctgct gctttcactc gtgatcactc tttactgtaa gcgcggtcgg     1020
aagaagctgc tgtacatctt taagcaaccc ttcatgaggc ctgtgcagac tactcaagag     1080
gaggacggct gttcatgccg gttcccagag gaggaggaag gcggctgcga actgcgcgtg     1140
aaattcagcc gcagcgcaga tgctccagcc tacaagcagg ggcagaacca gctctacaac     1200
gaactcaatc ttggtcggag agaggagtac gacgtgctgg acaagcggag aggacgggac     1260
ccagaaatgg gcgggaagcc gcgcagaaag aatccccaag agggcctgta caacgagctc     1320
caaaaggata agatggcaga agcctatagc gagattggta tgaaagggga acgcagaaga     1380
ggcaaaggcc acgacggact gtaccagga ctcagcaccg ccaccaagga cacctatgac     1440
gctcttcaca tgcaggccct gccgcctcgg      1470

```

<210> 825
 <211> 484
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 825
 Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
 1 5 10 15

His Ala Ala Arg Pro Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
 20 25 30

Val Lys Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
 35 40 45

Thr Phe Ser Asp Tyr Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys
 50 55 60

Gly Leu Glu Trp Val Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr
 65 70 75 80

Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
 85 90 95

Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
 100 105 110

Ala Val Tyr Tyr Cys Ala Arg Asp Leu Arg Gly Ala Phe Asp Ile Trp
 115 120 125

Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
 130 135 140

_SL

Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Tyr Val Leu Thr Gln Ser
145 150 155 160

Pro Ser Val Ser Ala Ala Pro Gly Tyr Thr Ala Thr Ile Ser Cys Gly
165 170 175

Gly Asn Asn Ile Gly Thr Lys Ser Val His Trp Tyr Gln Gln Lys Pro
180 185 190

Gly Gln Ala Pro Leu Leu Val Ile Arg Asp Asp Ser Val Arg Pro Ser
195 200 205

Lys Ile Pro Gly Arg Phe Ser Gly Ser Asn Ser Gly Asn Met Ala Thr
210 215 220

Leu Thr Ile Ser Gly Val Gln Ala Gly Asp Glu Ala Asp Phe Tyr Cys
225 230 235 240

Gln Val Trp Asp Ser Asp Ser Glu His Val Val Phe Gly Gly Gly Thr
245 250 255

Lys Leu Thr Val Leu Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro
260 265 270

Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys
275 280 285

Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala
290 295 300

Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu
305 310 315 320

Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys
325 330 335

Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr
340 345 350

Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Gly
355 360 365

Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala
370 375 380

Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg
385 390 395 400

Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu
405 410 415

_SL

Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn
420 425 430

Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met
435 440 445

Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly
450 455 460

Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala
465 470 475 480

Leu Pro Pro Arg

<210> 826
<211> 1452
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 826
atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60
cccgaagtcc agctcgtgga gtccggcgga ggccttgtga agcctggagg ttgctgaga 120
ctgtcctgcg ccgcctccgg cttcaccttc tccgactact acatgtcctg gatcagacag 180
gccccgggaa agggcctgga atgggtgtcc tacatctcgt catcgggcag cactatctac 240
tacgcggact cagtgaaggg gcggttcacc atttcccggg ataacgcgaa gaactcgctg 300
tatctgcaaa tgaactcact gagggccgag gacaccgccg tgtactactg cgcccgcgat 360
ctccgcgggg catttgacat ctggggacag ggaaccatgg tcacagtgtc cagcggaggg 420
ggaggatcgg gtggcggagg ttccgggggt ggaggctcct cctacgtgct gactcagagc 480
ccaagcgtca gcgctgcgcc cggttacacg gcaaccatct cctgtggcgg aaacaacatt 540
gggaccaagt ctgtgcactg gtatcagcag aagccgggcc aagctcccct gttggtgac 600
cgcgatgact ccgtgcggcc tagcaaaatt ccgggacggt tctccggctc caacagcggc 660
aatatggcca ctctcacat ctcgggagtg caggccggag atgaagccga cttctactgc 720
caagtctggg actcagactc cgagcatgtg gtgttcgggg gcggaaccaa gctgactgtg 780
ctcaccacta cccagcacc gaggccacc accccggctc ctaccatcgc ctcccagcct 840
ctgtccctgc gtccggaggc atgtagacct gcagctggtg gggccgtgca taccgggggt 900
cttgacttcg cctgcgatat ctacatttgg gcccctctgg ctggtacttg cggggtcctg 960
ctgctttcac tcgtgatcac tctttactgt aagcgcggtc ggaagaagct gctgtacatc 1020
tttaagcaac cttcatgag gcctgtgcag actactcaag aggaggacgg ctgttcatgc 1080

_SL

cggttcccag aggaggagga aggcggctgc gaactgcgcg tgaaattcag ccgcagcgca 1140
gatgctccag cctacaagca ggggcagaac cagctctaca acgaactcaa tcttggtcgg 1200
agagaggagt acgacgtgct ggacaagcgg agaggacggg acccagaaat gggcggggaag 1260
ccgcgcagaa agaatcccca agagggcctg tacaacgagc tccaaaagga taagatggca 1320
gaagcctata gcgagattgg tatgaaaggg gaacgcagaa gaggcaaagg ccacgacgga 1380
ctgtaccagg gactcagcac cgccaccaag gacacctatg acgctcttca catgcaggcc 1440
ctgccgcctc gg 1452

<210> 827

<211> 485

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 827

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val
20 25 30

Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Pro Ser Gly Tyr
35 40 45

Thr Val Thr Ser His Tyr Ile His Trp Val Arg Arg Ala Pro Gly Gln
50 55 60

Gly Leu Glu Trp Met Gly Met Ile Asn Pro Ser Gly Gly Val Thr Ala
65 70 75 80

Tyr Ser Gln Thr Leu Gln Gly Arg Val Thr Met Thr Ser Asp Thr Ser
85 90 95

Ser Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr
100 105 110

Ala Met Tyr Tyr Cys Ala Arg Glu Gly Ser Gly Ser Gly Trp Tyr Phe
115 120 125

Asp Phe Trp Gly Arg Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
130 135 140

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Tyr Val Leu
145 150 155 160

Thr Gln Pro Pro Ser Val Ser Val Ser Pro Gly Gln Thr Ala Ser Ile

_SL

165	170	175
Thr Cys Ser Gly Asp Gly Leu Ser Lys Lys Tyr Val Ser Trp Tyr Gln	180	185
Gln Lys Ala Gly Gln Ser Pro Val Val Leu Ile Ser Arg Asp Lys Glu	195	200
Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Asn Ser Ala Asp	210	215
Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Met Asp Glu Ala Asp	225	230
Tyr Tyr Cys Gln Ala Trp Asp Asp Thr Thr Val Val Phe Gly Gly Gly	245	250
Thr Lys Leu Thr Val Leu Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr	260	265
Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala	275	280
Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe	290	295
Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val	305	310
Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys	325	330
Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr	340	345
Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu	355	360
Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro	370	375
Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly	385	390
Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro	405	410
Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr	420	425
Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly		

435 440 _SL 445

Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln
450 455 460

Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln
465 470 475 480

Ala Leu Pro Pro Arg
485

<210> 828
<211> 1455
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 828
atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60
ccccaagtgc agctggtgca gagcggggcc gaagtcaaga agccgggagc ctccgtgaaa 120
gtgtcctgca agccttcggg atacaccgtg acctcccact acattcattg ggtccgccgc 180
gccccgggcc aaggactcga gtggatgggc atgatcaacc ctagcggcgg agtgaccgcg 240
tacagccaga cgctgcaggg acgcgtgact atgacctcgg atacctcctc ctccaccgtc 300
tatatggaac tgtccagcct gcggtccgag gataccgcca tgtactactg cgcccgggaa 360
ggatcaggct ccgggttgta tttcgacttc tggggaagag gcaccctcgt gactgtgtca 420
tctgggggag ggggttccgg tgggtggcga tcgggaggag gcggttcac ctagctgctg 480
accagccac cctccgtgtc cgtgagcccc ggccagactg catcgattac atgtagcggc 540
gacggcctct ccaagaaata cgtgtcgtgg taccagcaga aggccggaca gagcccggtg 600
gtgctgatct caagagataa ggagcggcct agcggaatcc cggacagggt ctcgggttcc 660
aactccgcgg aactgctac tctgaccatc tcggggaccc aggctatgga cgaagccgat 720
tactactgcc aagcctggga cgacactact gtcgtgtttg gagggggcac caagttgacc 780
gtccttacca ctaccccagc accgaggcca cccaccccg ctcctaccat cgcctcccag 840
cctctgtccc tgcgtccgga ggcatgtaga cccgcagctg gtggggccgt gcatacccg 900
ggctctgact tcgcctgcga tatctacatt tgggccctc tggctggtac ttgcggggtc 960
ctgctgcttt cactcgtgat cactctttac tgtaagcgcg gtcggaagaa gctgctgtac 1020
atctttaagc aacccttcat gaggcctgtg cagactactc aagaggagga cggctgttca 1080
tgccggttcc cagaggagga ggaaggcggc tgcgaactgc gcgtgaaatt cagccgcagc 1140
gcagatgctc cagcctacaa gcaggggcag aaccagctct acaacgaact caatcttgg 1200
cggagagagg agtacgacgt gctggacaag cggagaggac gggaccaga aatgggcggg 1260

aagccgcgca gaaagaatcc ccaagagggc ctgtacaacg agctccaaaa ggataagatg 1320
 gcagaagcct atagcgagat tggtatgaaa ggggaacgca gaagaggcaa aggccacgac 1380
 ggactgtacc aggactcag caccgccacc aaggacacct atgacgctct tcacatgcag 1440
 gccctgccgc ctcgg 1455

<210> 829
 <211> 489
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 829
 Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
 1 5 10 15

His Ala Ala Arg Pro Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu
 20 25 30

Val Lys Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly
 35 40 45

Ser Ile Ser Ser Gly Gly Tyr Tyr Trp Ser Trp Ile Arg Gln His Pro
 50 55 60

Gly Lys Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr
 65 70 75 80

Tyr Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr
 85 90 95

Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp
 100 105 110

Thr Ala Val Tyr Tyr Cys Ala Arg Ala Gly Ile Ala Ala Arg Leu Arg
 115 120 125

Gly Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
 130 135 140

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp
 145 150 155 160

Ile Val Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly Asp
 165 170 175

Arg Val Ile Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Trp Leu
 180 185 190

Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Asn Leu Leu Ile Tyr
 195 200 205

Ala Ala Ser Asn Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
 210 215 220

Gly Ser Gly Ala Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
 225 230 235 240

Asp Val Ala Thr Tyr Tyr Cys Gln Lys Tyr Asn Ser Ala Pro Phe Thr
 245 250 255

Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Thr Thr Thr Pro Ala Pro
 260 265 270

Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu
 275 280 285

Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg
 290 295 300

Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly
 305 310 315 320

Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys
 325 330 335

Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg
 340 345 350

Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro
 355 360 365

Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser
 370 375 380

Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu
 385 390 395 400

Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg
 405 410 415

Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln
 420 425 430

Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr
 435 440 445

Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp
 450 455 460

Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr^{-SL} Lys Asp Thr Tyr Asp Ala
 465 470 475 480

Leu His Met Gln Ala Leu Pro Pro Arg
 485

<210> 830
 <211> 1467
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 830
 atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60
 cccaagtgc agcttcagga gagcgggccg ggactcgtga agccgtccca gaccctgtcc 120
 ctgacttgca ccgtgtcggg aggaagcatc tcgagcggag gctactattg gtcgtggatt 180
 cggcagcacc ctggaaaggg cctggaatgg atcggctaca tctactactc cggctcgcacc 240
 tactacaacc catcgtgtaa gtccagagtg acaatctcag tggacacgtc caagaatcag 300
 ttcagcctga agctctcttc cgtgactgcg gccgacaccg ccgtgtacta ctgcgcacgc 360
 gctggaattg ccgcccggct gaggggtgcc ttcgacattt ggggacaggg caccatggtc 420
 accgtgtcct ccggcggcgg aggttcggg ggtggaggct caggaggagg ggggtccgac 480
 atcgtcatga ctcagtcgcc ctcaagcgtc agcgcgtccg tcggggacag agtgatcatc 540
 acctgtcggg cgtcccaggg aattcgcaac tggctggcct ggtatcagca gaagcccgga 600
 aaggcccca acctgttgat ctacgccgcc tcaaacctcc aatccggggg gccgagccgc 660
 ttcagcggct ccggttcggg tgccgatttc actctgacca tctcctccct gcaacctgaa 720
 gatgtggcta cctactactg ccaaagtagt aactccgcac cttttacttt cggaccgggg 780
 accaaagtgg acattaagac cactaccca gcaccgaggc caccacccc ggctcctacc 840
 atcgctccc agcctctgtc cctgcgtccg gaggcattga gaccgcagc tgggtggggc 900
 gtgcataccc ggggtcttga cttgcctgc gatatttaca tttgggcccc tctggctggt 960
 acttgcgggg tcctgtgctt ttcactcgtg atcactcttt actgtaagcg cggtcggaag 1020
 aagctgctgt acatctttaa gcaacccttc atgaggcctg tgcagactac tcaagaggag 1080
 gacggctgtt catgccggtt ccagaggag gaggaaggcg gctgcgaact gcgcgtgaaa 1140
 ttcagccgca gcgcagatgc tccagcctac aagcaggggc agaaccagct ctacaacgaa 1200
 ctcaatcttg gtcggagaga ggagtacgac gtgctggaca agcggagagg acgggaccca 1260
 gaaatgggcg ggaagccgcg cagaaagaat cccaagagg gcctgtacaa cgagctccaa 1320
 aaggataaga tggcagaagc ctatagcgag attggtatga aaggggaacg cagaagaggc 1380
 aaaggccacg acggactgta ccagggactc agcaccgcca ccaaggacac ctatgacgct 1440
 cttcacatgc aggcctgccc gcctcgg 1467

_SL

<210> 831
<211> 497
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 831
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val
20 25 30

Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly
35 40 45

Thr Phe Ser Ser Tyr Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln
50 55 60

Gly Leu Glu Trp Met Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn
65 70 75 80

Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser
85 90 95

Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr
100 105 110

Ala Val Tyr Tyr Cys Ala Arg Arg Gly Gly Tyr Gln Leu Leu Arg Trp
115 120 125

Asp Val Gly Leu Leu Arg Ser Ala Phe Asp Ile Trp Gly Gln Gly Thr
130 135 140

Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
145 150 155 160

Gly Gly Gly Gly Ser Ser Tyr Val Leu Thr Gln Pro Pro Ser Val Ser
165 170 175

Val Ala Pro Gly Gln Thr Ala Arg Ile Thr Cys Gly Gly Asn Asn Ile
180 185 190

Gly Ser Lys Ser Val His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
195 200 205

Val Leu Val Leu Tyr Gly Lys Asn Asn Arg Pro Ser Gly Val Pro Asp
210 215 220

_SL

Arg Phe Ser Gly Ser Arg Ser Gly Thr Thr Ala Ser Leu Thr Ile Thr
225 230 235 240

Gly Ala Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Arg Asp
245 250 255

Ser Ser Gly Asp His Leu Arg Val Phe Gly Thr Gly Thr Lys Val Thr
260 265 270

Val Leu Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr
275 280 285

Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala
290 295 300

Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile
305 310 315 320

Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser
325 330 335

Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr
340 345 350

Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu
355 360 365

Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu
370 375 380

Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln
385 390 395 400

Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu
405 410 415

Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly
420 425 430

Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln
435 440 445

Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu
450 455 460

Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr
465 470 475 480

Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro
485 490 495

Arg

<210> 832
<211> 1491
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 832
atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgtcca cgccgctcgg 60
ccccaagtgc agctggtcca gtcgggcgcc gaggtcaaga agcccgggag ctctgtgaaa 120
gtgtcctgca aggcctccgg gggcaccttt agctcctacg ccatctcctg ggtccgcaa 180
gcaccgggtc aaggcctgga gtggatgggg ggaattatcc ctatcttcgg cactgccaac 240
tacgcccaga agttccaggg acgcgtgacc attaccgcgg acgaatccac ctccaccgt 300
tatatggagc tgtccagctt gcgctcgga gataccgccg tgtactactg cgcccgagg 360
ggtggatacc agctgctgag atgggacgtg ggcctcctgc ggtcggcggt cgacatctgg 420
ggccagggca ctatggtcac tgtgtccagc ggaggaggcg gatcgggagg cggcggatca 480
gggggaggcg gttccagcta cgtgcttact caacccccctt cgggtgtccgt ggccccggga 540
cagaccgcca gaatcacttg cggaggaaac aacattgggt ccaagagcgt gcattggtac 600
cagcagaagc caggacaggc ccctgtgctg gtgctctacg ggaagaacaa tcggcccagc 660
ggagtgccgg acaggttctc gggttcacgc tccggtacaa ccgcttcact gactatcacc 720
ggggcccagg cagaggatga agcggactac tactgttcct cccgggattc atccggcgac 780
cacctccggg tgttcggaac cggaacgaag gtcaccgtgc tgaccactac cccagcaccg 840
aggccacca ccccggtcc taccatcgcc tcccagcctc tgtccctgcg tccggaggca 900
tntagacccg cagctggtgg ggccgtgcat acccggggtc ttgacttcgc ctgcatatc 960
tacatttggg cccctctggc tggacttgc ggggtcctgc tgctttcact cgtgatcact 1020
ctttactgta agcgcggtcg gaagaagctg ctgtacatct ttaagcaacc cttcatgagg 1080
cctgtgcaga ctactcaaga ggaggacggc tgttcatgcc ggttcccaga ggaggaggaa 1140
ggcggctgcg aactgcgcgt gaaattcagc cgcagcgag atgctccagc ctacaagcag 1200
gggcagaacc agctctacaa cgaactcaat cttggtcgga gagaggagta cgacgtgctg 1260
gacaagcggg gaggacggga cccagaaatg ggcggaagc cgcgagaaa gaatcccaa 1320
gagggcctgt acaacgagct ccaaaaggat aagatggcag aagcctatag cgagattggt 1380
atgaaagggg aacgcagaag aggcaaaggc cagcagggac tgtaccaggg actcagcacc 1440
gccaccaagg acacctatga cgctcttcac atgcaggccc tgccgcctcg g 1491

<210> 833

_SL

<211> 492

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 833

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Glu Val Gln Leu Gln Gln Ser Gly Pro Gly Leu
20 25 30

Val Lys Pro Ser Gln Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Asp
35 40 45

Ser Val Ser Ser Asn Ser Ala Ala Trp Asn Trp Ile Arg Gln Ser Pro
50 55 60

Ser Arg Gly Leu Glu Trp Leu Gly Arg Thr Tyr Tyr Arg Ser Lys Trp
65 70 75 80

Tyr Ser Phe Tyr Ala Ile Ser Leu Lys Ser Arg Ile Ile Ile Asn Pro
85 90 95

Asp Thr Ser Lys Asn Gln Phe Ser Leu Gln Leu Lys Ser Val Thr Pro
100 105 110

Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ser Ser Pro Glu Gly Leu
115 120 125

Phe Leu Tyr Trp Phe Asp Pro Trp Gly Gln Gly Thr Leu Val Thr Val
130 135 140

Ser Ser Gly Gly Asp Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
145 150 155 160

Ser Ser Ser Glu Leu Thr Gln Asp Pro Ala Val Ser Val Ala Leu Gly
165 170 175

Gln Thr Ile Arg Ile Thr Cys Gln Gly Asp Ser Leu Gly Asn Tyr Tyr
180 185 190

Ala Thr Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile
195 200 205

Tyr Gly Thr Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Ala
210 215 220

Ser Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala
225 230 235 240

_SL

Glu Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Ser Gly His
245 250 255

His Leu Leu Phe Gly Thr Gly Thr Lys Val Thr Val Leu Thr Thr Thr
260 265 270

Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro
275 280 285

Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val
290 295 300

His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro
305 310 315 320

Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu
325 330 335

Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro
340 345 350

Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys
355 360 365

Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe
370 375 380

Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu
385 390 395 400

Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp
405 410 415

Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys
420 425 430

Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala
435 440 445

Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
450 455 460

Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
465 470 475 480

Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
485 490

<210> 834
<211> 1476

<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 834
atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgtcca cgccgctcgg 60
cccgaagtgc agctccaaca gtcaggaccg gggctcgtga agccatcca gaccctgtcc 120
ctgacttgtg ccatctcggg agatagcgtg tcatcgaact ccgccgcctg gaactggatt 180
cggcagagcc cgtcccgcgg actggagtgg cttggaagga cctactaccg gtccaagtgg 240
tactctttct acgcgatctc gctgaagtcc cgcattatca ttaaccctga tacctccaag 300
aatcagttct ccctccaact gaaatccgtc acccccgagg acacagcagt gtattactgc 360
gcacggagca gccccgaagg actgttcctg tattggtttg acccctgggg ccaggggact 420
cttgtgaccg tgtcgagcgg cggagatggg tccggtggcg gtggttcggg gggcggcgga 480
tcatcatccg aactgacca ggaccggct gtgtccgtgg cgctgggaca aaccatccgc 540
attacgtgcc agggagactc cctgggcaac tactacgcca cttggtacca gcagaagccg 600
ggccaagccc ctgtgttggg catctacggg accaacaaca gaccttcgg catccccgac 660
cggttcagcg cttcgtcctc cggcaacact gccagcctga ccatcactgg agcgcaggcc 720
gaagatgagg ccgactacta ctgcaacagc agagactcct cgggtcatca cctcttgttc 780
ggaactggaa ccaaggtcac cgtgctgacc actaccccag caccgaggcc acccaccg 840
gctcctacca tcgcctcca gcctctgtcc ctgcgtccgg aggcattgtag accgcagct 900
gggtggggccg tgcatacccg gggctctgac ttgcctgcg atatctacat ttggggccct 960
ctggctggta cttgcggggg cctgctgctt tctactcgtga tctactctta ctgtaagcgc 1020
ggtcgggaaga agctgctgta catctttaag caacccttca tgaggcctgt gcagactact 1080
caagaggagg acggctgttc atgccggttc ccagaggagg aggaaggcgg ctgcgaactg 1140
cgcgtgaaat tcagccgcag cgcagatgct ccagcctaca agcaggggca gaaccagctc 1200
tacaacgaac tcaatcttgg tcggagagag gactacgacg tgctggacaa gcggagagga 1260
cgggaccag aaatgggcgg gaagccgcgc agaaagaatc cccaagaggg cctgtacaac 1320
gagctccaaa aggataagat ggcagaagcc tatagcgaga ttggtatgaa aggggaacgc 1380
agaagaggca aaggccacga cggactgtac cagggactca gcaccgccac caaggacacc 1440
tatgacgctc ttcacatgca ggccctgccg cctcgg 1476

<210> 835
<211> 490
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

_SL
polypeptide"

<400> 835

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
20 25 30

Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
35 40 45

Thr Phe Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys
50 55 60

Gly Leu Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr
65 70 75 80

Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser
85 90 95

Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
100 105 110

Ala Val Tyr Tyr Cys Ala Lys Val Glu Gly Ser Gly Ser Leu Asp Tyr
115 120 125

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser
130 135 140

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Met Thr Gln
145 150 155 160

Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser
165 170 175

Cys Arg Ala Ser Gln Ser Val Ser Ser Ala Tyr Leu Ala Trp Tyr Gln
180 185 190

Gln Lys Pro Gly Gln Pro Pro Arg Leu Leu Ile Ser Gly Ala Ser Thr
195 200 205

Arg Ala Thr Gly Ile Pro Asp Arg Phe Gly Gly Ser Gly Ser Gly Thr
210 215 220

Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val
225 230 235 240

Tyr Tyr Cys Gln His Tyr Gly Ser Ser Phe Asn Gly Ser Ser Leu Phe
245 250 255

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Thr Thr Thr Pro Ala
Page 613

_SL

260 265 270

Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser
275 280 285

Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr
290 295 300

Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala
305 310 315 320

Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys
325 330 335

Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met
340 345 350

Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe
355 360 365

Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg
370 375 380

Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn
385 390 395 400

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
405 410 415

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
420 425 430

Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
435 440 445

Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
450 455 460

Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
465 470 475 480

Ala Leu His Met Gln Ala Leu Pro Pro Arg
485 490

<210> 836
<211> 1470
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

_SL

<400> 836
atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60
cccgaagtgc agctcgtgga gtcaggaggc ggcctggtcc agccgggagg gtcccttaga 120
ctgtcatgcg ccgcaagcgg attcactttc tcctcctatg ccatgagctg ggtccgccaa 180
gcccccgaa agggactgga atgggtgtcc gccatctcgg ggtctggagg ctcaacttac 240
tacgtgact ccgtgaaggg acggttcacc attagccgcg acaactccaa gaacaccctc 300
tacctccaaa tgaactccct gcgggccgag gataccgccg tctactactg cgccaaagtg 360
gaaggttcag gatcgctgga ctactgggga cagggtactc tcgtgaccgt gtcacggggc 420
ggaggagggt ccggcggtgg cggctccggc ggcggagggt cggagatcgt gatgaccag 480
agccctggta ctctgagcct ttcgccggga gaaagggcca ccctgtcctg ccgcgcttcc 540
caatccgtgt cctccgcgta cttggcgtgg taccagcaga agccgggaca gccccctcgg 600
ctgctgatca gcggggccag caccggggca accggaatcc cagacagatt cgggggttcc 660
ggcagcggca cagatttcac cctgactatt tcgaggttgg agcccgagga ctttgcggtg 720
tattactgtc agcactacgg gtcgtccttt aatggctcca gcctgttcac gttcggacag 780
gggacccgcc tggaaatcaa gaccactacc ccagcaccga ggccaccac cccggctcct 840
accatcgct cccagcctct gtccctgcgt ccggaggcat gtagaccgc agctggtggg 900
gccgtgcata cccgggtct tgaacttcgc tgcgatatct acatttgggc ccctctggct 960
ggtacttgcg gggtcctgct gctttcactc gtgatcactc ttactgtaa gcgcggtcgg 1020
aagaagctgc tgtacatctt taagcaacc ttcatgaggc ctgtgcagac tactcaagag 1080
gaggacggct gttcatgccg gttcccagag gaggaggaag gcggctgcga actgcgcgtg 1140
aaattcagcc gcagcgcaga tgctccagcc tacaagcagg ggcagaacca gctctacaac 1200
gaactcaatc ttggtcggag agaggagtac gacgtgctgg acaagcggag aggacgggac 1260
ccagaaatgg gcgggaagcc gcgcagaaag aatccccaag agggcctgta caacgagctc 1320
caaaaggata agatggcaga agcctatagc gagattggta tgaaagggga acgcagaaga 1380
ggcaaaggcc acgacggact gtaccaggga ctcagcaccg ccaccaagga cacctatgac 1440
gctcttcaca tgcaggccct gccgcctcgg 1470

<210> 837

<211> 485

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 837

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg₂₀ Pro Glu Val Gln Leu₂₅ Val^{SL} Glu Thr Gly Gly₃₀ Gly Leu
 Val Gln Pro₃₅ Gly Gly Ser Leu Arg₄₀ Leu Ser Cys Ala Ala Ser Gly Ile
 Thr Phe₅₀ Ser Arg Tyr Pro Met₅₅ Ser Trp Val Arg Gln₆₀ Ala Pro Gly Lys
 Gly₆₅ Leu Glu Trp Val Ser₇₀ Gly Ile Ser Asp Ser₇₅ Gly Val Ser Thr Tyr₈₀
 Tyr Ala Asp Ser Ala₈₅ Lys Gly Arg Phe Thr₉₀ Ile Ser Arg Asp Asn₉₅ Ser
 Lys Asn Thr Leu₁₀₀ Phe Leu Gln Met Ser₁₀₅ Ser Leu Arg Asp Glu₁₁₀ Asp Thr
 Ala Val Tyr₁₁₅ Tyr Cys Val Thr Arg₁₂₀ Ala Gly Ser Glu Ala₁₂₅ Ser Asp Ile
 Trp Gly₁₃₀ Gln Gly Thr Met Val₁₃₅ Thr Val Ser Ser Gly₁₄₀ Gly Gly Gly Ser
 Gly₁₄₅ Gly Gly Gly Ser Gly₁₅₀ Gly Gly Gly Ser Glu₁₅₅ Ile Val Leu Thr Gln₁₆₀
 Ser Pro Ala Thr Leu₁₆₅ Ser Leu Ser Pro Gly₁₇₀ Glu Arg Ala Thr Leu₁₇₅ Ser
 Cys Arg Ala Ser₁₈₀ Gln Ser Val Ser Asn₁₈₅ Ser Leu Ala Trp Tyr₁₉₀ Gln Gln
 Lys Pro Gly₁₉₅ Gln Ala Pro Arg Leu₂₀₀ Leu Ile Tyr Asp Ala₂₀₅ Ser Ser Arg
 Ala Thr₂₁₀ Gly Ile Pro Asp Arg₂₁₅ Phe Ser Gly Ser Gly₂₂₀ Ser Gly Thr Asp
 Phe Thr Leu Thr Ile Ser₂₃₀ Arg Leu Glu Pro Glu₂₃₅ Asp Phe Ala Ile Tyr₂₄₀
 Tyr Cys Gln Gln Phe₂₄₅ Gly Thr Ser Ser Gly₂₅₀ Leu Thr Phe Gly Gly₂₅₅ Gly
 Thr Lys Leu Glu₂₆₀ Ile Lys Thr Thr Thr₂₆₅ Pro Ala Pro Arg Pro₂₇₀ Pro Thr
 Pro Ala Pro₂₇₅ Thr Ile Ala Ser Gln₂₈₀ Pro Leu Ser Leu Arg₂₈₅ Pro Glu Ala

Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe
 290 295 300
 Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val
 305 310 315 320
 Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys
 325 330 335
 Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr
 340 345 350
 Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu
 355 360 365
 Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro
 370 375 380
 Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly
 385 390 395 400
 Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro
 405 410 415
 Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr
 420 425 430
 Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly
 435 440 445
 Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln
 450 455 460
 Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln
 465 470 475 480
 Ala Leu Pro Pro Arg
 485

<210> 838
 <211> 1455
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polynucleotide"

<400> 838
 atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60
 cccgaagtgc aactggtgga aaccggtggc ggcctggtgc agcctggagg atcattgagg 120
 ctgtcatgcg cggccagcgg tattaccttc tcccggtacc ccatgtcctg ggtcagacag 180

_SL

gccccgggga aagggcttga atgggtgtcc gggatctcgg actccggtgt cagcacttac 240
tacgccgact ccgccaaggg acgcttcacc atttcccggg acaactcgaa gaacaccctg 300
ttcctccaaa tgagctccct ccgggacgag gatactgcag tgtactactg cgtgaccgcg 360
gccgggtccg aggcgtctga catttgggga cagggcacta tggtcaccgt gtcgtccggc 420
ggaggggggct cgggaggcgg tggcagcgga ggaggaggt ccgagatcgt gctgacccaa 480
tccccggcca ccctctcgct gagccctgga gaaagggcaa ccttgtcctg tcgcgcgagc 540
cagtccgtga gcaactccct ggcctggtag cagcagaagc ccggacaggc tccgagactt 600
ctgatctacg acgcttcgag ccggggccact ggaatccccg accgcttttc ggggtccggc 660
tcaggaaccg atttcaccct gacaatctca cggctggagc cagaggattt cgccatctat 720
tactgccagc agttcggtag ttcctccggc ctgactttcg gaggcggcac gaagctcgaa 780
atcaagacca ctaccccagc accgaggcca cccaccccg ctcctaccat cgctcccgag 840
cctctgtccc tgcgtccgga ggcattgtag cccgcagctg gtggggccgt gcatacccg 900
ggctcttgact tcgcctgcga tatctacatt tgggccctc tggctggtag ttgcggggtc 960
ctgctgcttt cactcgtgat cactctttac tgtaagcgcg gtcggaagaa gctgctgtac 1020
atctttaagc aacccttcat gaggcctgtg cagactactc aagaggagga cggctgttca 1080
tgccggttcc cagaggagga ggaaggcggc tgcgaactgc gcgtgaaatt cagccgcagc 1140
gcagatgctc cagcctacaa gcaggggcag aaccagctct acaacgaact caatcttgg 1200
cggagagagg agtacgacgt gctggacaag cggagaggac gggaccaga aatgggcggg 1260
aagccgcgca gaaagaatcc ccaagagggc ctgtacaacg agtccaaaa ggataagatg 1320
gcagaagcct atagcgagat tggtatgaaa ggggaacgca gaagaggcaa aggccacgac 1380
ggactgtacc agggactcag caccgccacc aaggacacct atgacgctct tcacatgcag 1440
gccctgccgc ctcgg 1455

<210> 839

<211> 492

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 839

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu
20 25 30

Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
35 40 45

_SL

Thr Phe Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys
50 55 60

Gly Leu Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr
65 70 75 80

Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
85 90 95

Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
100 105 110

Ala Ile Tyr Tyr Cys Ala Arg Ala Thr Tyr Lys Arg Glu Leu Arg Tyr
115 120 125

Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Met Val Thr Val Ser
130 135 140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
145 150 155 160

Glu Ile Val Met Thr Gln Ser Pro Gly Thr Val Ser Leu Ser Pro Gly
165 170 175

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
180 185 190

Phe Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
195 200 205

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
210 215 220

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
225 230 235 240

Pro Glu Asp Ser Ala Val Tyr Tyr Cys Gln Gln Tyr His Ser Ser Pro
245 250 255

Ser Trp Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Thr Thr Thr
260 265 270

Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro
275 280 285

Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val
290 295 300

His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro
305 310 315 320

_SL

Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu
325 330 335

Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro
340 345 350

Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys
355 360 365

Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe
370 375 380

Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu
385 390 395 400

Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp
405 410 415

Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys
420 425 430

Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala
435 440 445

Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
450 455 460

Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
465 470 475 480

Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
485 490

<210> 840

<211> 1476

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 840

atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60

ccccaagtgc agctcgtgga atcgggtggc ggactggtgc agccgggggg ctcacttaga 120

ctgtcctgcg cggccagcgg attcactttc tcctcctacg ccatgtcctg ggtcagacag 180

gcccttgaa agggcctgga atgggtgtcc gcaatcagcg gcagcggcgg ctcgacctat 240

tacgcggatt cagtgaaggg cagattcacc atttcccggg acaacgcaa gaactccttg 300

taccttcaaa tgaactccct ccgcgcggaa gataccgcaa tctactactg cgctcggggc 360

_SL

```

acttacaaga gggaactgcg ctactactac gggatggacg tctggggcca gggaaccatg      420
gtcaccgtgt ccagcggagg aggaggatcg ggaggaggcg gtagcggggg tggagggctcg      480
gagatcgtga tgaccagtc ccccggcact gtgtcgtgtt ccccggcga acggggccacc      540
ctgtcatgtc gggccagcca gtcagtgtcg tcaagcttcc tcgcctggta ccagcagaaa      600
ccgggacaag ctccccgcct gctgatctac ggagccagca gccggggccac cggtattcct      660
gaccggttct ccggttcggg gtccgggacc gactttactc tgactatctc tcgcctcgag      720
ccagaggact ccgccgtgta ttactgccag cagtaccact cctccccgtc ctggacgttc      780
ggacagggca caaggctgga gattaagacc actacccag caccgaggcc acccaccctg      840
gctcctacca tcgcctccca gcctctgtcc ctgcgtccgg aggcattgtag acccgagct      900
ggtggggccg tgcatacccg gggctctgac ttcgcctgcg atatctacat ttggggccct      960
ctggctggta cttgctgggt cctgctgctt tcaactgtga tcaactctta ctgtaagcgc     1020
ggtcgaaga agctgctgta catctttaag caacccttca tgaggcctgt gcagactact     1080
caagaggagg acggctgttc atgccggttc ccagaggagg aggaaggcgg ctgcgaactg     1140
cgcggtgaaat tcagccgcag cgcagatgct ccagcctaca agcaggggca gaaccagctc     1200
tacaacgaac tcaatcttgg tcggagagag gactacgacg tgctggacaa gcggagagga     1260
cgggaccag aaatgggcgg gaagccgcgc agaaagaatc cccaagaggg cctgtacaac     1320
gagctccaaa aggataagat ggcagaagcc tatagcgaga ttggtatgaa aggggaacgc     1380
agaagaggca aaggccacga cggactgtac cagggactca gcaccgccac caaggacacc     1440
tatgacgctc ttcacatgca ggcctgccc cctcgg      1476

```

<210> 841
 <211> 492
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 841
 Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
 1 5 10 15

His Ala Ala Arg Pro Glu Val Gln Leu Val Glu Thr Gly Gly Gly Leu
 20 25 30

Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
 35 40 45

Thr Phe Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys
 50 55 60

Gly Leu Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr
 65 70 75 80

_SL

Tyr Ala Asp Ser Val₈₅ Lys Gly Arg Phe Thr₉₀ Ile Ser Arg Asp Asn₉₅ Ser
Lys Asn Thr Leu₁₀₀ Tyr Leu Gln Met Asn₁₀₅ Thr Leu Lys Ala Glu₁₁₀ Asp Thr
Ala Val Tyr₁₁₅ Tyr Cys Ala Arg Ala₁₂₀ Thr Tyr Lys Arg Glu₁₂₅ Leu Arg Tyr
Tyr Tyr₁₃₀ Gly Met Asp Val Trp₁₃₅ Gly Gln Gly Thr Thr₁₄₀ Val Thr Val Ser
Ser₁₄₅ Gly Gly Gly Gly Ser₁₅₀ Gly Gly Gly Gly Ser₁₅₅ Gly Gly Gly Gly Ser₁₆₀
Glu Ile Val Leu Thr₁₆₅ Gln Ser Pro Ser Thr₁₇₀ Leu Ser Leu Ser Pro₁₇₅ Gly
Glu Ser Ala Thr₁₈₀ Leu Ser Cys Arg Ala₁₈₅ Ser Gln Ser Val Ser₁₉₀ Thr Thr
Phe Leu Ala₁₉₅ Trp Tyr Gln Gln Lys₂₀₀ Pro Gly Gln Ala Pro₂₀₅ Arg Leu Leu
Ile Tyr₂₁₀ Gly Ser Ser Asn Arg₂₁₅ Ala Thr Gly Ile Pro₂₂₀ Asp Arg Phe Ser
Gly₂₂₅ Ser Gly Ser Gly Thr₂₃₀ Asp Phe Thr Leu Thr₂₃₅ Ile Arg Arg Leu Glu₂₄₀
Pro Glu Asp Phe Ala₂₄₅ Val Tyr Tyr Cys Gln₂₅₀ Gln Tyr His Ser Ser₂₅₅ Pro
Ser Trp Thr Phe₂₆₀ Gly Gln Gly Thr Lys₂₆₅ Val Glu Ile Lys Thr₂₇₀ Thr Thr
Pro Ala Pro₂₇₅ Arg Pro Pro Thr Pro₂₈₀ Ala Pro Thr Ile Ala₂₈₅ Ser Gln Pro
Leu Ser₂₉₀ Leu Arg Pro Glu Ala₂₉₅ Cys Arg Pro Ala Ala₃₀₀ Gly Gly Ala Val
His₃₀₅ Thr Arg Gly Leu Asp₃₁₀ Phe Ala Cys Asp Ile₃₁₅ Tyr Ile Trp Ala Pro₃₂₀
Leu Ala Gly Thr Cys₃₂₅ Gly Val Leu Leu Leu₃₃₀ Ser Leu Val Ile Thr₃₃₅ Leu
Tyr Cys Lys Arg₃₄₀ Gly Arg Lys Lys Leu₃₄₅ Leu Tyr Ile Phe Lys₃₅₀ Gln Pro

_SL

Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys
355 360 365

Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe
370 375 380

Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu
385 390 395 400

Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp
405 410 415

Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys
420 425 430

Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala
435 440 445

Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
450 455 460

Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
465 470 475 480

Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
485 490

<210> 842
<211> 1476
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 842
atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60
cccgaggtgc agcttgtgga aaccggtggc ggactggtgc agcccggagg aagcctcagg 120
ctgtcctgcg ccgcgtccgg cttcaccttc tcctcgtacg ccatgtcctg ggtccgccag 180
gccccggaa agggcctgga atgggtgtcc gccatctctg gaagcggagg ttccacgtac 240
tacgcggaca gcgtcaaggg aaggttcaca atctcccgcg ataattcgaa gaacactctg 300
taccttcaaa tgaacaccct gaaggccgag gacactgctg tgtactactg cgcacggggc 360
acctacaaga gagagctccg gtactactac ggaatggacg tctggggcca gggaactact 420
gtgaccgtgt cctcgggagg ggggtggctcc ggggggggcg gctccggcgg aggcggttcc 480
gagattgtgc tgaccagtc accttcaact ctgtcgtgtg ccccgggaga gagcgctact 540
ctgagctgcc gggccagcca gtccgtgtcc accaccttcc tcgcctggta tcagcagaag 600

_SL

ccggggcagg caccacggct cttgatctac gggtcagca acagagcgac cggaattcct 660
gaccgcttct cggggagcgg ttcaggcacc gacttcaccc tgactatccg gcgcctggaa 720
cccgaagatt tcgccgtgta ttactgtcaa cagtaccact cctcgccgtc ctggaccttt 780
ggccaaggaa ccaaagtga aatcaagacc actaccccag caccgaggcc acccaccctg 840
gctcctacca tcgcctccca gcctctgtcc ctgcgtccgg aggcattgtag acccgagct 900
ggtggggccg tgcatacccg gggctctgac ttcgcctgcg atatctacat ttggggccct 960
ctggctggta cttgcggggt cctgctgctt tctctgtga tctctcttta ctgtaagcgc 1020
ggtcggaaga agctgctgta catctttaag caacccttca tgaggcctgt gcagactact 1080
caagaggagg acggctgttc atgccggttc ccagaggagg aggaaggcgg ctgcgaactg 1140
cgcgtgaaat tcagccgcag cgcagatgct ccagcctaca agcaggggca gaaccagctc 1200
tacaacgaac tcaatcttgg tcggagagag gactacgacg tgctggacaa gcggagagga 1260
cgggaccag aaatgggcgg gaagccgcgc agaaagaatc cccaagaggg cctgtacaac 1320
gagctccaaa aggataagat ggcagaagcc tatagcgaga ttggtatgaa aggggaacgc 1380
agaagaggca aaggccacga cggactgtac cagggactca gcaccgccac caaggacacc 1440
tatgacgctc ttcacatgca ggccctgccg cctcgg 1476

<210> 843

<211> 483

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 843

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Glu Val Gln Leu Val Glu Thr Gly Gly Gly Leu
20 25 30

Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
35 40 45

Thr Phe Asp Asp Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys
50 55 60

Gly Leu Glu Trp Val Ser Gly Ile Ser Trp Asn Ser Gly Ser Ile Gly
65 70 75 80

Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
85 90 95

Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Asp Glu Asp Thr
Page 624

_SL

100		105		110											
Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Val	Gly	Lys	Ala	Val	Pro	Asp	Val	Trp
		115					120					125			
Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Gly
	130					135					140				
Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Asp	Ile	Val	Met	Thr	Gln	Thr
145					150					155					160
Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg	Val	Thr	Ile	Thr	Cys
				165					170					175	
Arg	Ala	Ser	Gln	Ser	Ile	Ser	Ser	Tyr	Leu	Asn	Trp	Tyr	Gln	Gln	Lys
			180					185					190		
Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile	Tyr	Ala	Ala	Ser	Ser	Leu	Gln
		195					200					205			
Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe
	210					215					220				
Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr
225					230					235					240
Cys	Gln	Gln	Ser	Tyr	Ser	Thr	Pro	Tyr	Ser	Phe	Gly	Gln	Gly	Thr	Arg
				245					250					255	
Leu	Glu	Ile	Lys	Thr	Thr	Thr	Pro	Ala	Pro	Arg	Pro	Pro	Thr	Pro	Ala
			260					265					270		
Pro	Thr	Ile	Ala	Ser	Gln	Pro	Leu	Ser	Leu	Arg	Pro	Glu	Ala	Cys	Arg
		275					280					285			
Pro	Ala	Ala	Gly	Gly	Ala	Val	His	Thr	Arg	Gly	Leu	Asp	Phe	Ala	Cys
	290					295					300				
Asp	Ile	Tyr	Ile	Trp	Ala	Pro	Leu	Ala	Gly	Thr	Cys	Gly	Val	Leu	Leu
305					310					315					320
Leu	Ser	Leu	Val	Ile	Thr	Leu	Tyr	Cys	Lys	Arg	Gly	Arg	Lys	Lys	Leu
				325					330					335	
Leu	Tyr	Ile	Phe	Lys	Gln	Pro	Phe	Met	Arg	Pro	Val	Gln	Thr	Thr	Gln
			340					345					350		
Glu	Glu	Asp	Gly	Cys	Ser	Cys	Arg	Phe	Pro	Glu	Glu	Glu	Glu	Gly	Gly
		355					360					365			
Cys	Glu	Leu	Arg	Val	Lys	Phe	Ser	Arg	Ser	Ala	Asp	Ala	Pro	Ala	Tyr

[illegible]

_SL

accactaccc cagcaccgag gccacccacc cgggtccta ccacgcctc ccagcctctg	840
tccctgcgtc cggaggcatg tagacccgca gctgggtggg cgtgcatac ccggggtctt	900
gacttcgcct gcgatatcta catttgggcc cctctggctg gtacttgcg ggtcctgctg	960
ctttcactcg tgatcactct ttactgtaag cgcggtcgga agaagctgct gtacatcttt	1020
aagcaaccct tcatgaggcc tgtgcagact actcaagagg aggacggctg ttcatgccgg	1080
ttcccagagg aggaggaagg cggctgcgaa ctgcgcgtga aattcagccg cagcgcatat	1140
gctccagcct acaagcaggg gcagaaccag ctctacaacg aactcaatct tggtcggaga	1200
gaggagtacg acgtgctgga caagcggaga ggacgggacc cagaaatggg cgggaagccg	1260
cgcagaaaga atccccaaga gggcctgtac aacgagctcc aaaaggataa gatggcagaa	1320
gcctatagcg agattggtat gaaaggggaa cgcagaagag gcaaaggcca cgacggactg	1380
taccagggac tcagcaccgc caccaaggac acctatgacg ctcttcacat gcaggccctg	1440
ccgcctcgg	1449

<210> 845
 <211> 490
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 845
 Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
 1 5 10 15

His Ala Ala Arg Pro Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
 20 25 30

Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe
 35 40 45

Thr Phe Asp Asp Tyr Ala Met His Trp Val Arg Gln Arg Pro Gly Lys
 50 55 60

Gly Leu Glu Trp Val Ala Ser Ile Asn Trp Lys Gly Asn Ser Leu Ala
 65 70 75 80

Tyr Gly Asp Ser Val Lys Gly Arg Phe Ala Ile Ser Arg Asp Asn Ala
 85 90 95

Lys Asn Thr Val Phe Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr
 100 105 110

Ala Val Tyr Tyr Cys Ala Ser His Gln Gly Val Ala Tyr Tyr Asn Tyr
 115 120 125

Ala Met Asp Val Trp Gly Arg Gly Thr Leu^{SL} Val Thr Val Ser Ser Gly
 130 135 140
 Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile
 145 150 155 160
 Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg
 165 170 175
 Ala Thr Leu Ser Cys Arg Ala Thr Gln Ser Ile Gly Ser Ser Phe Leu
 180 185 190
 Ala Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
 195 200 205
 Gly Ala Ser Gln Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Arg
 210 215 220
 Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Val Glu Pro Glu
 225 230 235 240
 Asp Ser Ala Val Tyr Tyr Cys Gln His Tyr Glu Ser Ser Pro Ser Trp
 245 250 255
 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Thr Thr Thr Pro Ala
 260 265 270
 Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser
 275 280 285
 Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr
 290 295 300
 Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala
 305 310 315 320
 Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys
 325 330 335
 Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met
 340 345 350
 Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe
 355 360 365
 Pro Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg
 370 375 380
 Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn
 385 390 395 400

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr^{-SL} Asp Val Leu Asp Lys Arg
 405 410 415
 Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
 420 425 430
 Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
 435 440 445
 Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
 450 455 460
 Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
 465 470 475 480
 Ala Leu His Met Gln Ala Leu Pro Pro Arg
 485 490

<210> 846
 <211> 1470
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 846
 atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60
 cccgaagtgc agctcgtgga gagcggggga ggattggtgc agcccggaag gtccctgcgg 120
 ctctcctgca ctgcgtctgg cttcaccttc gacgactacg cgatgcactg ggtagacag 180
 cgcccgggaa agggcctgga atgggtcgcc tcaatcaact ggaagggaaa ctccctggcc 240
 tatggcgaca gcgtgaaggg ccgcttcgcc atttcgcgcg acaacgcaa gaacaccgtg 300
 tttctgcaa tgaattccct gcggaccgag gataccgctg tgtactactg cgccagccac 360
 cagggcgtgg catactataa ctacgccatg gacgtgtggg gaagagggac gctcgtcacc 420
 gtgtcctccg ggggcggtgg atcgggtgga ggaggaagcg gtggcggggg cagcgaaatc 480
 gtgctgactc agagcccggg aactctttca ctgtccccgg gagaacgggc cactctctcg 540
 tgccgggcca ccaggtccat cggctcctcc ttccttgctt ggtaccagca gaggccagga 600
 caggcgcccc gcctgctgat ctacggtgct tccaacgcg ccactggcat tcctgaccgg 660
 ttcagcggca gagggtcggg aaccgatttc acactgacca tttcccgggt ggagcccga 720
 gattcggcag tctactactg tcagcattac gagtctctcc cttcatggac cttcgggtcaa 780
 gggaccaaag tggagatcaa gaccactacc ccagcaccga ggccaccac cccggctcct 840
 accatcgcct ccagcctct gtccctgcgt ccggaggcat gtagaccgc agctgggtgg 900
 gccgtgcata cccgggtct tgacttcgcc tgcgatatct acatttgggc ccctctggct 960
 ggtacttgcg gggctctgct gctttcactc gtgatcactc ttactgtaa gcgcggctcg 1020

_SL

aagaagctgc tgtacatctt taagcaaccc ttcatgaggc ctgtgcagac tactcaagag 1080
gaggacggct gttcatgccg gttcccagag gaggaggaag gcggtgcga actgcgcgtg 1140
aaattcagcc gcagcgcaga tgctccagcc tacaagcagg ggcagaacca gctctacaac 1200
gaactcaatc ttggtcggag agaggagtac gacgtgctgg acaagcggag aggacgggac 1260
ccagaaatgg gcgggaagcc gcgcagaaag aatccccaag agggcctgta caacgagctc 1320
caaaaggata agatggcaga agcctatagc gagattggta tgaaagggga acgcagaaga 1380
ggcaaaggcc acgacggact gtaccaggga ctcagcaccg ccaccaagga cacctatgac 1440
gctcttcaca tgcaggccct gccgcctcgg 1470

<210> 847

<211> 485

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 847

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
20 25 30

Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
35 40 45

Thr Phe Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys
50 55 60

Gly Leu Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr
65 70 75 80

Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser
85 90 95

Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
100 105 110

Ala Val Tyr Tyr Cys Ala Lys Val Val Arg Asp Gly Met Asp Val Trp
115 120 125

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
130 135 140

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser
145 150 155 160

_SL

Pro Ala Thr Leu Ser₁₆₅ Leu Ser Pro Gly Glu₁₇₀ Arg Ala Thr Leu Ser₁₇₅ Cys

Arg Ala Ser Gln₁₈₀ Ser Val Ser Ser Ser₁₈₅ Tyr Leu Ala Trp Tyr₁₉₀ Gln Gln

Lys Pro Gly₁₉₅ Gln Ala Pro Arg Leu₂₀₀ Leu Ile Tyr Gly Ala₂₀₅ Ser Ser Arg

Ala Thr Gly Ile Pro Asp Arg₂₁₅ Phe Ser Gly Asn Gly₂₂₀ Ser Gly Thr Asp

Phe Thr Leu Thr Ile Ser₂₃₀ Arg Leu Glu Pro Glu₂₃₅ Asp Phe Ala Val Tyr₂₄₀

Tyr Cys Gln Gln Tyr₂₄₅ Gly Ser Pro Pro Arg₂₅₀ Phe Thr Phe Gly Pro₂₅₅ Gly

Thr Lys Val Asp₂₆₀ Ile Lys Thr Thr Thr₂₆₅ Pro Ala Pro Arg Pro₂₇₀ Pro Thr

Pro Ala Pro₂₇₅ Thr Ile Ala Ser Gln₂₈₀ Pro Leu Ser Leu Arg₂₈₅ Pro Glu Ala

Cys Arg₂₉₀ Pro Ala Ala Gly Gly₂₉₅ Ala Val His Thr Arg₃₀₀ Gly Leu Asp Phe

Ala Cys Asp Ile Tyr Ile₃₁₀ Trp Ala Pro Leu Ala₃₁₅ Gly Thr Cys Gly Val₃₂₀

Leu Leu Leu Ser Leu₃₂₅ Val Ile Thr Leu Tyr₃₃₀ Cys Lys Arg Gly Arg₃₃₅ Lys

Lys Leu Leu Tyr₃₄₀ Ile Phe Lys Gln Pro₃₄₅ Phe Met Arg Pro Val₃₅₀ Gln Thr

Thr Gln Glu₃₅₅ Glu Asp Gly Cys Ser₃₆₀ Cys Arg Phe Pro Glu₃₆₅ Glu Glu Glu

Gly Gly₃₇₀ Cys Glu Leu Arg Val₃₇₅ Lys Phe Ser Arg Ser₃₈₀ Ala Asp Ala Pro

Ala Tyr Lys Gln Gly Gln₃₉₀ Asn Gln Leu Tyr Asn₃₉₅ Glu Leu Asn Leu Gly₄₀₀

Arg Arg Glu Glu Tyr₄₀₅ Asp Val Leu Asp Lys₄₁₀ Arg Arg Gly Arg Asp₄₁₅ Pro

Glu Met Gly Gly₄₂₀ Lys Pro Arg Arg Lys₄₂₅ Asn Pro Gln Glu Gly₄₃₀ Leu Tyr

_SL

Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly
435 440 445

Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln
450 455 460

Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln
465 470 475 480

Ala Leu Pro Pro Arg
485

<210> 848

<211> 1455

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 848

atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg	60
cccgaggtgc agttggtcga aagcgggggc gggcttgtgc agcctggcgg atcactgcgg	120
ctgtcctgcg cggcatcagg cttcacgttt tcttcctacg ccatgtcctg ggtgcgccag	180
gcccctggaa agggactgga atgggtgtcc gcgatttcgg ggtccggcgg gagcacctac	240
tacgccgatt ccgtgaaggg ccgcttcact atctcgcggg acaactccaa gaacaccctc	300
tacctcaaaa tgaatagcct gcggggccgag gataccgccg tctactattg cgctaaggtc	360
gtgcgcgacg gaatggacgt gtggggacag ggtaccaccg tgacagtgtc ctcgggggga	420
ggcggtagcg gcggaggagg aagcggtggt ggaggttccg agattgtgct gactcaatca	480
cccgcgaccc tgagcctgtc ccccggcgaa agggccactc tgtcctgtcg ggccagccaa	540
tcagtctcct cctcgtacct ggcctggtac cagcagaagc caggacaggc tccgagactc	600
cttatctatg gcgcatcctc ccgcgccacc ggaatcccgg ataggttctc gggaaacgga	660
tcggggaccg acttcactct caccatctcc cggctggaac cggaggactt cgccgtgtac	720
tactgccagc agtacggcag cccgcctaga ttcactttcg gccccggcac caaagtggac	780
atcaagacca ctacccagc accgaggcca cccaccccg ctcctaccat cgcctcccag	840
cctctgtccc tgcgtccgga ggcatgtaga cccgcagctg gtggggccgt gcatacccg	900
ggtcttgact tcgcctgcga tatctacatt tgggcccctc tggctggtac ttgcggggtc	960
ctgctgcttt cactcgtgat cactctttac tgtaagcgcg gtcggaagaa gctgctgtac	1020
atctttaagc aacccttcat gaggcctgtg cagactactc aagaggagga cggctgttca	1080
tgccggttcc cagaggagga ggaaggcggc tgcgaactgc gcgtgaaatt cagccgcagc	1140
gcagatgctc cagcctacaa gcaggggcag aaccagctct acaacgaact caatcttggt	1200

_SL
 cggagagagg agtacgacgt gctggacaag cggagaggac gggaccaga aatgggctggg 1260
 aagccgcgca gaaagaatcc ccaagagggc ctgtacaacg agctccaaaa ggataagatg 1320
 gcagaagcct atagcgagat tggtatgaaa ggggaacgca gaagaggcaa aggccacgac 1380
 ggactgtacc agggactcag caccgccacc aaggacacct atgacgtctt tcacatgcag 1440
 gccctgccgc ctcgg 1455

<210> 849
 <211> 486
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 849
 Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
 1 5 10 15

His Ala Ala Arg Pro Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu
 20 25 30

Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
 35 40 45

Thr Phe Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys
 50 55 60

Gly Leu Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr
 65 70 75 80

Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser
 85 90 95

Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
 100 105 110

Ala Val Tyr Tyr Cys Ala Lys Ile Pro Gln Thr Gly Thr Phe Asp Tyr
 115 120 125

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser
 130 135 140

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln
 145 150 155 160

Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser
 165 170 175

Cys Arg Ala Ser Gln Ser Val Ser Ser Ser Tyr Leu Ala Trp Tyr Gln
 180 185 190

_SL

Gln Arg Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser
195 200 205

Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr
210 215 220

Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val
225 230 235 240

Tyr Tyr Cys Gln His Tyr Gly Ser Ser Pro Ser Trp Thr Phe Gly Gln
245 250 255

Gly Thr Arg Leu Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro
260 265 270

Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu
275 280 285

Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp
290 295 300

Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly
305 310 315 320

Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg
325 330 335

Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln
340 345 350

Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu
355 360 365

Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala
370 375 380

Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu
385 390 395 400

Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp
405 410 415

Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu
420 425 430

Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile
435 440 445

Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr
450 455 460

_SL

Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met
465 470 475 480

Gln Ala Leu Pro Pro Arg
485

<210> 850
<211> 1458
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 850
atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60
cccgaagtgc agctgctgga gtccggcggt ggattggtgc aaccgggggg atcgtcaga 120
ctgtcctgtg cggcgtcagg cttcaccttc tcgagctacg ccatgtcatg ggtcagacag 180
gcccctggaa agggctctgga atgggtgtcc gccatttcg ggagcggggg atctacatac 240
tacgccgata gcgtgaaggg ccgcttcacc atttcccggg acaactccaa gaacactctc 300
tatctgcaaa tgaactccct ccgcgctgag gacactgccg tgtactactg cgccaaaatc 360
cctcagaccg gcaccttcga ctactgggga caggggactc tggtcaccgt cagcagcggg 420
ggcggagggt cggggggagg aggaagcggc ggcggagggt ccgagattgt gctgaccag 480
tcacccggca ctttgtccct gtcgcctgga gaaagggcca ccctttcctg ccgggcatcc 540
caatccgtgt cctcctcgta cctggcctgg taccagcaga ggcccggaca ggccccacgg 600
cttctgatct acggagcaag cagccgcgcg accggtatcc cggaccgggt ttcgggctcg 660
ggctcaggaa ctgacttcac cctcaccatc tccgcctgg aaccgaaga tttcgctgtg 720
tattactgcc agcactacgg cagctccccg tcctggacgt tcggccaggg aactcggctg 780
gagatcaaga ccactacccc agcaccgagg ccacccaccc cggctcctac catcgctcc 840
cagcctctgt ccctgcgtcc ggaggcatgt agaccgcag ctggtggggc cgtgcatacc 900
cggggtcttg acttcgcctg cgatatctac atttggggcc ctctggctgg tacttgcggg 960
gtcctgctgc tttcactcgt gatcactctt tactgtaagc gcggtcggaa gaagctgctg 1020
tacatcttta agcaaccctt catgaggcct gtgcagacta ctcaagagga ggacggctgt 1080
tcatgccggt tcccagagga ggaggaaggc ggctgcgaac tgcgcgtgaa attcagccgc 1140
agcgcagatg ctccagccta caagcagggg cagaaccagc tctacaacga actcaatctt 1200
ggtcggagag aggagtacga cgtgctggac aagcggagag gacgggaccc agaaatgggc 1260
gggaagccgc gcagaaagaa tcccaagag ggcctgtaca acgagctcca aaaggataag 1320
atggcagaag cctatagcga gattggtatg aaaggggaac gcagaagagg caaaggccac 1380
gacggactgt accagggact cagcaccgcc accaaggaca cctatgacgc tcttcacatg 1440

caggccctgc cgcctcgg

1458

<210> 851
<211> 492
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 851
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Glu Val Gln Leu Val Glu Thr Gly Gly Gly Leu
20 25 30

Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
35 40 45

Thr Phe Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys
50 55 60

Gly Leu Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr
65 70 75 80

Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Met Ser Arg Glu Asn Asp
85 90 95

Lys Asn Ser Val Phe Leu Gln Met Asn Ser Leu Arg Val Glu Asp Thr
100 105 110

Gly Val Tyr Tyr Cys Ala Arg Ala Asn Tyr Lys Arg Glu Leu Arg Tyr
115 120 125

Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Met Val Thr Val Ser
130 135 140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
145 150 155 160

Glu Ile Val Met Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
165 170 175

Glu Ser Ala Thr Leu Ser Cys Arg Ala Ser Gln Arg Val Ala Ser Asn
180 185 190

Tyr Leu Ala Trp Tyr Gln His Lys Pro Gly Gln Ala Pro Ser Leu Leu
195 200 205

Ile Ser Gly Ala Ser Ser Arg Ala Thr Gly Val Pro Asp Arg Phe Ser
Page 636

_SL

210		215		220											
Gly 225	Ser	Gly	Ser	Gly	Thr 230	Asp	Phe	Thr	Leu	Ala 235	Ile	Ser	Arg	Leu	Glu 240
Pro	Glu	Asp	Ser	Ala 245	Val	Tyr	Tyr	Cys	Gln 250	His	Tyr	Asp	Ser	Ser 255	Pro
Ser	Trp	Thr	Phe 260	Gly	Gln	Gly	Thr	Lys 265	Val	Glu	Ile	Lys	Thr 270	Thr	Thr
Pro	Ala	Pro 275	Arg	Pro	Pro	Thr	Pro 280	Ala	Pro	Thr	Ile	Ala 285	Ser	Gln	Pro
Leu	Ser 290	Leu	Arg	Pro	Glu	Ala 295	Cys	Arg	Pro	Ala	Ala 300	Gly	Gly	Ala	Val
His 305	Thr	Arg	Gly	Leu	Asp 310	Phe	Ala	Cys	Asp	Ile 315	Tyr	Ile	Trp	Ala	Pro 320
Leu	Ala	Gly	Thr	Cys 325	Gly	Val	Leu	Leu	Leu 330	Ser	Leu	Val	Ile	Thr 335	Leu
Tyr	Cys	Lys	Arg 340	Gly	Arg	Lys	Lys	Leu 345	Leu	Tyr	Ile	Phe	Lys 350	Gln	Pro
Phe	Met	Arg 355	Pro	Val	Gln	Thr	Thr 360	Gln	Glu	Glu	Asp	Gly 365	Cys	Ser	Cys
Arg	Phe 370	Pro	Glu	Glu	Glu	Glu 375	Gly	Gly	Cys	Glu	Leu 380	Arg	Val	Lys	Phe
Ser 385	Arg	Ser	Ala	Asp	Ala 390	Pro	Ala	Tyr	Lys	Gln 395	Gly	Gln	Asn	Gln	Leu 400
Tyr	Asn	Glu	Leu	Asn 405	Leu	Gly	Arg	Arg	Glu 410	Glu	Tyr	Asp	Val	Leu 415	Asp
Lys	Arg	Arg	Gly 420	Arg	Asp	Pro	Glu	Met 425	Gly	Gly	Lys	Pro	Arg 430	Arg	Lys
Asn	Pro	Gln 435	Glu	Gly	Leu	Tyr	Asn 440	Glu	Leu	Gln	Lys	Asp 445	Lys	Met	Ala
Glu 450	Ala	Tyr	Ser	Glu	Ile	Gly 455	Met	Lys	Gly	Glu	Arg 460	Arg	Arg	Gly	Lys
Gly 465	His	Asp	Gly	Leu	Tyr 470	Gln	Gly	Leu	Ser	Thr 475	Ala	Thr	Lys	Asp	Thr 480
Tyr	Asp	Ala	Leu	His	Met	Gln	Ala	Leu	Pro	Pro	Arg				

<210> 852
 <211> 1476
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

```

<400> 852
atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg      60
cccgaagtgc aactggtgga aaccggtgga ggactcgtgc agcctggcgg cagcctccgg      120
ctgagctgcg ccgcttcggg attcaccttt tcctcctacg cgatgtcttg ggtcagacag      180
gcccccggaaggagggtgga atgggtgtca gccatctccg gctccggcgg atcaacgtac      240
tacgccgact ccgtgaaagg ccggttcacc atgtcgcgcg agaatgacaa gaactccgtg      300
ttcctgcaaa tgaactccct gaggggtggag gacaccggag tgtactattg tgcgcgcgcc      360
aactacaaga gagagctgcg gtactactac ggaatggacg tctggggaca gggaactatg      420
gtgaccgtgt catccggtgg agggggaagc ggcggtggag gcagcggggg cgggggttca      480
gaaattgtca tgaccagtc cccgggaact ctttcctct ccccgggga atccgcgact      540
ttgtcctgcc gggccagcca gcgcgtggcc tcgaactacc tcgcatggta ccagcataag      600
ccaggccaag ccccttcctt gctgatttcc ggggctagca gccgcgccac tggcgtgccg      660
gataggttct cgggaagcgg ctcgggtacc gatttcaccc tggcaatctc gcggctggaa      720
ccggaggatt cggcctgtga ctactgccag cactatgact catccccctc ctggacattc      780
ggacagggca ccaaggtcga gatcaagacc actacccag caccgaggcc acccaccg      840
gctcctacca tcgcctcca gcctctgtcc ctgcgtccgg aggcattgtag accgcagct      900
gggtggggccg tgcatacccg gggctctgac ttgcctgcg atatctacat ttggggccct      960
ctggctggta cttgcggggg cctgctgctt tctactgtga tctactttta ctgtaagcgc     1020
ggtcggaaga agctgctgta catctttaag caacccttca tgaggcctgt gcagactact     1080
caagaggagg acggctgttc atgccggttc ccagaggagg aggaaggcgg ctgcgaactg     1140
cgcgtgaaat tcagccgcag cgcagatgct ccagcctaca agcaggggca gaaccagctc     1200
tacaacgaac tcaatcttgg tcggagagag gactacgacg tgctggacaa gcggagagga     1260
cgggaccag aaatgggcgg gaagccgcgc agaaagaatc ccaagaggg cctgtacaac     1320
gagctccaaa aggataagat ggcagaagcc tatagcgaga ttggtatgaa aggggaacgc     1380
agaagaggca aaggccacga cggactgtac cagggactca gcaccgccac caaggacacc     1440
tatgacgctc ttcacatgca ggcctgccc cctcgg      1476

```

<210> 853
 <211> 488
 <212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 853

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
 1 5 10 15

His Ala Ala Arg Pro Glu Val Gln Leu Leu Glu Thr Gly Gly Gly Leu
 20 25 30

Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
 35 40 45

Ser Phe Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys
 50 55 60

Gly Leu Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr
 65 70 75 80

Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser
 85 90 95

Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
 100 105 110

Ala Val Tyr Tyr Cys Ala Lys Ala Leu Val Gly Ala Thr Gly Ala Phe
 115 120 125

Asp Ile Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
 130 135 140

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu
 145 150 155 160

Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr
 165 170 175

Leu Ser Cys Arg Ala Ser Gln Ser Leu Ser Ser Asn Phe Leu Ala Trp
 180 185 190

Tyr Gln Gln Lys Pro Gly Gln Ala Pro Gly Leu Leu Ile Tyr Gly Ala
 195 200 205

Ser Asn Trp Ala Thr Gly Thr Pro Asp Arg Phe Ser Gly Ser Gly Ser
 210 215 220

Gly Thr Asp Phe Thr Leu Thr Ile Thr Arg Leu Glu Pro Glu Asp Phe
 225 230 235 240

Ala Val Tyr Tyr Cys₂₄₅ Gln Tyr Tyr Gly Thr₂₅₀^{-SL} Ser Pro Met Tyr Thr₂₅₅ Phe
 Gly Gln Gly Thr₂₆₀ Lys Val Glu Ile Lys₂₆₅ Thr Thr Thr Pro Ala₂₇₀ Pro Arg
 Pro Pro Thr₂₇₅ Pro Ala Pro Thr Ile₂₈₀ Ala Ser Gln Pro Leu₂₈₅ Ser Leu Arg
 Pro Glu₂₉₀ Ala Cys Arg Pro Ala₂₉₅ Ala Gly Gly Ala Val₃₀₀ His Thr Arg Gly
 Leu₃₀₅ Asp Phe Ala Cys Asp₃₁₀ Ile Tyr Ile Trp Ala₃₁₅ Pro Leu Ala Gly Thr₃₂₀
 Cys Gly Val Leu Leu₃₂₅ Leu Ser Leu Val Ile₃₃₀ Thr Leu Tyr Cys Lys₃₃₅ Arg
 Gly Arg Lys Lys₃₄₀ Leu Leu Tyr Ile Phe₃₄₅ Lys Gln Pro Phe Met₃₅₀ Arg Pro
 Val Gln Thr₃₅₅ Thr Gln Glu Glu Asp₃₆₀ Gly Cys Ser Cys Arg₃₆₅ Phe Pro Glu
 Glu Glu₃₇₀ Glu Gly Gly Cys Glu₃₇₅ Leu Arg Val Lys Phe₃₈₀ Ser Arg Ser Ala
 Asp₃₈₅ Ala Pro Ala Tyr Lys₃₉₀ Gln Gly Gln Asn Gln₃₉₅ Leu Tyr Asn Glu Leu₄₀₀
 Asn Leu Gly Arg Arg₄₀₅ Glu Glu Tyr Asp Val₄₁₀ Leu Asp Lys Arg Arg₄₁₅ Gly
 Arg Asp Pro Glu₄₂₀ Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu
 Gly Leu Tyr₄₃₅ Asn Glu Leu Gln Lys₄₄₀ Asp Lys Met Ala Glu₄₄₅ Ala Tyr Ser
 Glu Ile₄₅₀ Gly Met Lys Gly Glu₄₅₅ Arg Arg Arg Gly Lys₄₆₀ Gly His Asp Gly
 Leu Tyr Gln Gly Leu Ser₄₇₀ Thr Ala Thr Lys Asp₄₇₅ Thr Tyr Asp Ala Leu₄₈₀
 His Met Gln Ala Leu₄₈₅ Pro Pro Arg

<210> 854

<211> 1464

<212> DNA

<213> Artificial Sequence

_SL

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 854

atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg	60
cccgaagtgc agctgctcga aaccggtgga gggctgggtg agccaggggg ctccctgagg	120
ctttcatgcg ccgctagcgg attctccttc tcctcttacg ccatgtcgtg ggtccgccaa	180
gcccctggaa aaggcctgga atgggtgtcc gcgatttccg ggagcggagg ttcgacctat	240
tacgccgact ccgtgaaggg ccgctttacc atctcccggg ataactccaa gaacactctg	300
tacctccaaa tgaactcgct gagagccgag gacaccgccg tgtattactg cgccaaggcg	360
ctggtcggcg cgactggggc attcgacatc tggggacagg gaactcttgt gaccgtgtcg	420
agcggaggcg gcggctccgg cggaggaggg agcgggggcg gtggttccga aatcgtgttg	480
actcagtccc cgggaaccct gagcttgtca cccggggagc gggccactct ctctgtcgc	540
gcctcccaat cgctctcatc caatttcctg gcctggtacc agcagaagcc cggacaggcc	600
ccgggcctgc tcattctacg cgcttcaaac tgggcaacgg gaaccctga tcggttcagc	660
ggaagcggat cgggtactga ctttaccctg accatcacca gactggaacc ggaggacttc	720
gccgtgtact actgccagta ctacggcacc tccccatgt acacattcgg acagggtacc	780
aaggtcgaga ttaagaccac taccccagca ccgaggccac ccaccccggc tcctaccatc	840
gcctcccagc ctctgtccct gcgtccggag gcatgtagac ccgcagctgg tggggccgtg	900
catacccggg gtcttgactt cgctgcat atctacattt gggcccctct ggctggtact	960
tgcggggtcc tgctgctttc actcgtgatc actctttact gtaagcgcg tcggaagaag	1020
ctgctgtaca tctttaagca acccttcatg aggctgtgc agactactca agaggaggac	1080
ggctgttcat gccggttccc agaggaggag gaaggcggct gcgaactgcg cgtgaaattc	1140
agccgcagcg cagatgtctc agcctacaag caggggcaga accagctcta caacgaactc	1200
aatcttggtc ggagagagga gtacgacgtg ctggacaagc ggagaggacg ggaccagaa	1260
atgggcggga agccgcgcag aaagaatccc caagagggcc tgtacaacga gtcctaaaag	1320
gataagatgg cagaagccta tagcgagatt ggtatgaaag ggaacgcag aagaggcaaa	1380
ggccacgacg gactgtacca gggactcagc accgccacca aggacaccta tgacgtcttt	1440
cacatgcagg ccctgccgcc tcgg	1464

<210> 855

<211> 488

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

_SL

<400> 855

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15
His Ala Ala Arg Pro Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu
20 25 30
Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
35 40 45
Thr Phe Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys
50 55 60
Gly Leu Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr
65 70 75 80
Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser
85 90 95
Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
100 105 110
Ala Val Tyr Tyr Cys Val Leu Trp Phe Gly Glu Gly Phe Asp Pro Trp
115 120 125
Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
130 135 140
Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val Leu Thr Gln Ser
145 150 155 160
Pro Leu Ser Leu Pro Val Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys
165 170 175
Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr Asn Tyr Leu Asp
180 185 190
Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Leu
195 200 205
Gly Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly
210 215 220
Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp
225 230 235 240
Val Gly Val Tyr Tyr Cys Met Gln Ala Leu Gln Thr Pro Leu Thr Phe
245 250 255
Gly Gly Gly Thr Lys Val Asp Ile Lys Thr Thr Thr Pro Ala Pro Arg
260 265 270

_SL

Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg
275 280 285

Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly
290 295 300

Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr
305 310 315 320

Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg
325 330 335

Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro
340 345 350

Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu
355 360 365

Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala
370 375 380

Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu
385 390 395 400

Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly
405 410 415

Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu
420 425 430

Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser
435 440 445

Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly
450 455 460

Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu
465 470 475 480

His Met Gln Ala Leu Pro Pro Arg
485

<210> 856
<211> 1464
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 856

_SL

atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg	60
cccgaagtgc agctgcttga gagcgggtga ggtctggtgc agcccggggg atcactgcgc	120
ctgtcctgtg ccgcgtccgg tttcactttc tcctcgtacg ccatgtcgtg ggtcagacag	180
gcaccgggaa agggactgga atgggtgtca gccatttcgg gttcgggggg cagcacctac	240
tacgctgact ccgtgaaggg ccggttcacc atttcccgcg acaactccaa gaacaccttg	300
tacctcaaaa tgaactccct gcggggccgaa gataccgccg tgtattactg cgtgctgtgg	360
ttcggagagg gattcgacct gtggggacaa ggaacactcg tgactgtgtc atccggcgga	420
ggcggcagcg gtggcggcgg ttccggcggc ggcggatctg acatcgtgtt gaccagttcc	480
cctctgagcc tgccggtcac tcctggcgaa ccagccagca tctcctgccg gtcgagccag	540
tccctcctgc actccaatgg gtacaactac ctcgattggt atctgcaaaa gccggggccag	600
agcccccagc tgctgatcta ccttgggtca aaccgcgctt ccgggggtgcc tgatagattc	660
tccgggtccg ggagcggaac cgactttacc ctgaaaatct cgagggtgga ggccgaggac	720
gtcggagtgt actactgcat gcaggcgctc cagactcccc tgaccttcgg aggaggaacg	780
aaggctcgaca tcaagaccac taccccagca ccgaggccac ccaccccggc tcctaccatc	840
gcctcccagc ctctgtccct gcgtccggag gcatgtagac ccgcagctgg tggggccgtg	900
catacccggg gtcttgactt cgcttgcgat atctacattt gggcccctct ggctggtact	960
tgccgggtcc tgctgctttc actcgtgatc actctttact gtaagcgcgg tcggaagaag	1020
ctgctgtaca tctttaagca acccttcatg aggcctgtgc agactactca agaggaggac	1080
ggctgttcat gccggttccc agaggaggag gaaggcggtc gcgaactgcg cgtgaaattc	1140
agccgcagcg cagatgctcc agcctacaag caggggcaga accagctcta caacgaactc	1200
aatcttggtc ggagagagga gtacgacgtg ctggacaagc ggagaggacg ggaccagaa	1260
atgggcggga agccgcgag aaagaatccc caagagggcc tgtacaacga gtcctaaaag	1320
gataagatgg cagaagccta tagcgagatt ggtatgaaag gggaacgcag aagaggcaaa	1380
ggccacgacg gactgtacca gggactcagc accgccacca aggacaccta tgacgctctt	1440
cacatgcagg ccctgccgcc tcgg	1464

<210> 857

<211> 495

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 857

Met	Ala	Leu	Pro	Val	Thr	Ala	Leu	Leu	Leu	Pro	Leu	Ala	Leu	Leu	Leu
1				5					10					15	

His	Ala	Ala	Arg	Pro	Gln	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu
			20					25					30		

_SL

Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
35 40 45

Thr Phe Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys
50 55 60

Gly Leu Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr
65 70 75 80

Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser
85 90 95

Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
100 105 110

Ala Val Tyr Tyr Cys Ala Lys Val Gly Tyr Asp Ser Ser Gly Tyr Tyr
115 120 125

Arg Asp Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr
130 135 140

Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly
145 150 155 160

Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser
165 170 175

Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser
180 185 190

Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg
195 200 205

Leu Leu Ile Tyr Gly Thr Ser Ser Arg Ala Thr Gly Ile Ser Asp Arg
210 215 220

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg
225 230 235 240

Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln His Tyr Gly Asn
245 250 255

Ser Pro Pro Lys Phe Thr Phe Gly Pro Gly Thr Lys Leu Glu Ile Lys
260 265 270

Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala
275 280 285

Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly
290 295 300

_SL

Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile
305 310 315 320

Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val
325 330 335

Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe
340 345 350

Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly
355 360 365

Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg
370 375 380

Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln
385 390 395 400

Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp
405 410 415

Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro
420 425 430

Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp
435 440 445

Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg
450 455 460

Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr
465 470 475 480

Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
485 490 495

<210> 858

<211> 1485

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 858

atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60

ccccaagtgc agctcgtgga gtcaggcgga ggactgggtgc agcccggggg ctccctgaga 120

ctttcctgcg cggcatcggg ttttaccttc tcctcctatg ctatgtcctg ggtgcgccag 180

gccccgggaa agggactgga atgggtgtcc gcaatcagcg gtagcggggg ctcaacatac 240

_SL

tacgccgact ccgtcaaggg tcgcttcact atttcccggg acaactccaa gaataccctg 300
tacctccaaa tgaacagcct cagggccgag gatactgccg tgtactactg cgccaaagtc 360
ggatacgata gctccgggta ctaccgggac tactacggaa tggacgtgtg gggacagggc 420
accaccgtga ccgtgtcaag cggcggaggc gggttcaggag ggggaggctc cggcgggtgga 480
gggtccgaaa tcgtcctgac tcagtcgcct ggactctgt cgttgtcccc gggggagcgc 540
gctaccctgt cgtgtcgggc gtcgcagtcc gtgtcgagct cctacctgc gtggtaccag 600
cagaagcccg gacaggcccc tagacttctg atctacggca cttcttcacg cgccaccggg 660
atcagcgaca gggtcagcgg ctccgggtcc gggaccgact tcaccctgac cattagccgg 720
ctggagcctg aagatttcgc cgtgtattac tgccaacact acggaaactc gccgccaag 780
ttcacgttcg gacccggaac caagctggaa atcaagacca ctacccagc accgaggcca 840
cccaccccg ctcctacat cgcctcccag cctctgtccc tgcgtccgga ggcattgtaga 900
cccgcagctg gtggggccgt gcatacccg ggtcttgact tcgcctgcga tatctacatt 960
tgggcccctc tggctggtac ttgcggggc ctgctgcttt cactcgtgat cactctttac 1020
tgtaagcgcg gtcggaagaa gctgctgtac atctttaagc aacccttcac gaggcctgtg 1080
cagactactc aagaggagga cggctgttca tgccggttcc cagaggagga ggaaggcggc 1140
tgcgaaactg gcgtgaaatt cagccgcagc gcagatgctc cagcctacaa gcaggggcag 1200
aaccagctct acaacgaact caatcttggt cggagagagg agtacgacgt gctggacaag 1260
cggagaggac gggaccaga aatgggcggg aagccgcgca gaaagaatcc ccaagagggc 1320
ctgtacaacg agtccaaaa ggataagatg gcagaagcct atagcgagat tggatatgaaa 1380
ggggaacgca gaagaggcaa aggccacgac ggactgtacc agggactcag caccgccacc 1440
aaggacacct atgacgtctt tcacatgcag gccctgccgc ctcgg 1485

<210> 859

<211> 490

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 859

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
20 25 30

Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
35 40 45

Thr Phe Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys

50					55					_SL		60				
Gly 65	Leu	Glu	Trp	Val	Ser 70	Ala	Ile	Ser	Gly	Ser 75	Gly	Gly	Ser	Thr	Tyr 80	
Tyr	Ala	Asp	Ser	Val 85	Lys	Gly	Arg	Phe	Thr 90	Ile	Ser	Arg	Asp	Asn 95	Ser	
Lys	Asn	Thr	Leu 100	Tyr	Leu	Gln	Met	Asn 105	Ser	Leu	Arg	Ala	Glu 110	Asp	Thr	
Ala	Val	Tyr 115	Tyr	Cys	Ala	Lys	Met 120	Gly	Trp	Ser	Ser	Gly 125	Tyr	Leu	Gly	
Ala	Phe 130	Asp	Ile	Trp	Gly	Gln 135	Gly	Thr	Thr	Val	Thr 140	Val	Ser	Ser	Gly	
Gly 145	Gly	Gly	Ser	Gly	Gly 150	Gly	Gly	Ser	Gly	Gly 155	Gly	Gly	Ser	Glu	Ile 160	
Val	Leu	Thr	Gln	Ser 165	Pro	Gly	Thr	Leu	Ser 170	Leu	Ser	Pro	Gly	Glu 175	Arg	
Ala	Thr	Leu	Ser 180	Cys	Arg	Ala	Ser	Gln 185	Ser	Val	Ala	Ser	Ser 190	Phe	Leu	
Ala	Trp	Tyr 195	Gln	Gln	Lys	Pro	Gly 200	Gln	Ala	Pro	Arg	Leu 205	Leu	Ile	Tyr	
Gly	Ala 210	Ser	Gly	Arg	Ala	Thr 215	Gly	Ile	Pro	Asp	Arg 220	Phe	Ser	Gly	Ser	
Gly 225	Ser	Gly	Thr	Asp	Phe 230	Thr	Leu	Thr	Ile	Ser 235	Arg	Leu	Glu	Pro	Glu 240	
Asp	Phe	Ala	Val	Tyr 245	Tyr	Cys	Gln	His	Tyr 250	Gly	Gly	Ser	Pro	Arg 255	Leu	
Thr	Phe	Gly	Gly 260	Gly	Thr	Lys	Val	Asp 265	Ile	Lys	Thr	Thr	Thr 270	Pro	Ala	
Pro	Arg	Pro 275	Pro	Thr	Pro	Ala	Pro 280	Thr	Ile	Ala	Ser	Gln 285	Pro	Leu	Ser	
Leu	Arg 290	Pro	Glu	Ala	Cys	Arg 295	Pro	Ala	Ala	Gly	Gly 300	Ala	Val	His	Thr	
Arg 305	Gly	Leu	Asp	Phe	Ala 310	Cys	Asp	Ile	Tyr	Ile 315	Trp	Ala	Pro	Leu	Ala 320	
Gly	Thr	Cys	Gly	Val	Leu	Leu	Leu	Ser	Leu	Val	Ile	Thr	Leu	Tyr	Cys	

325 330 335

_SL

Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met
 340 345 350

Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe
 355 360 365

Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg
 370 375 380

Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn
 385 390 395 400

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
 405 410 415

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
 420 425 430

Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
 435 440 445

Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
 450 455 460

Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
 465 470 475 480

Ala Leu His Met Gln Ala Leu Pro Pro Arg
 485 490

<210> 860
 <211> 1470
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 860
 atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60
 cccgaagtcc aactggtgga gtccggggga gggctcgtgc agcccgagg cagccttcgg 120
 ctgtcgtgcg ccgcctccgg gttcacgttc tcacacctac cgatgtcgtg ggtcagacag 180
 gcaccaggaa aggactgga atgggtgtcc gccattagcg gtcctggcgg tagcacctac 240
 tatgccgact cagtgaaggg aaggttcact atctcccgcg acaacagcaa gaacaccctg 300
 tacctccaaa tgaactctct gcgggcccag gataccgcgg tgtactattg cgccaagatg 360
 ggttggtcca gcggatactt gggagccttc gacatttggg gacagggcac tactgtgacc 420

gtgtcctccg	ggggtggcgg	atcgggaggc	ggcgggctcg	gtggaggggg	ttccgaaatc	480
gtgttgaccc	agtcaccggg	aaccctctcg	ctgtccccgg	gagaacgggc	tacactgtca	540
tgtagagcgt	cccagtcctg	ggcttcctcg	ttcctggcct	ggtaccagca	gaagccggga	600
caggcacccc	gcctgctcat	ctacggagcc	agcggccggg	cgaccggcat	ccctgaccgc	660
ttctccggtt	ccggctcggg	caccgacttt	actctgacca	ttagcaggct	tgagcccagag	720
gattttgccg	tgtactactg	ccaacactac	ggggggagcc	ctcgcctgac	cttcggaggc	780
ggaactaagg	tcgatatcaa	aaccactacc	ccagcaccga	ggccaccac	cccggctcct	840
accatcgcct	cccagcctct	gtccctgcgt	ccggaggcat	gtagaccgc	agctgggtggg	900
gccgtgcata	cccgggtctt	tgacttcgcc	tgcgatatct	acatttgggc	ccctctggct	960
ggtacttgcg	gggtcctgct	gctttcactc	gtgatcactc	tttactgtaa	gcgcggtcgg	1020
aagaagctgc	tgtacatctt	taagcaaccc	ttcatgaggc	ctgtgcagac	tactcaagag	1080
gaggacggct	gttcatgccg	gttcccagag	gaggaggaag	gcggctgcga	actgcgcgtg	1140
aaattcagcc	gcagcgcaga	tgctccagcc	tacaagcagg	ggcagaacca	gctctacaac	1200
gaactcaatc	ttggtcggag	agaggagtag	gacgtgctgg	acaagcggag	aggacgggac	1260
ccagaaatgg	gcgggaagcc	gcgcagaaaag	aatccccaag	agggcctgta	caacgagctc	1320
caaaaggata	agatggcaga	agcctatagc	gagattggta	tgaaagggga	acgcagaaga	1380
ggcaaaggcc	acgacggact	gtaccaggga	ctcagcaccg	ccaccaagga	cacctatgac	1440
gctcttcaca	tgcaggccct	gccgcctcgg				1470

<210> 861

<400> 861
000

<210> 862

<400> 862
000

<210> 863

<400> 863
000

<210> 864

<400> 864
000

<210> 865

<400> 865
000

<210> 866

_SL

<400> 866
000

<210> 867

<400> 867
000

<210> 868

<400> 868
000

<210> 869

<400> 869
000

<210> 870

<400> 870
000

<210> 871

<400> 871
000

<210> 872

<400> 872
000

<210> 873

<400> 873
000

<210> 874

<400> 874
000

<210> 875

<400> 875
000

<210> 876

<400> 876
000

<210> 877

<400> 877

000

<210> 878

<400> 878
000

<210> 879

<400> 879
000

<210> 880

<400> 880
000

<210> 881

<400> 881
000

<210> 882

<400> 882
000

<210> 883

<400> 883
000

<210> 884

<400> 884
000

<210> 885

<400> 885
000

<210> 886

<400> 886
000

<210> 887

<400> 887
000

<210> 888

<400> 888
000

_SL

<210> 889

<400> 889
000

<210> 890

<400> 890
000

<210> 891

<211> 486

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 891

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu
20 25 30

Ser Ala Ser Leu Gly Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln
35 40 45

Asp Ile Ser Lys Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr
50 55 60

Val Lys Leu Leu Ile Tyr His Thr Ser Arg Leu His Ser Gly Val Pro
65 70 75 80

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile
85 90 95

Ser Asn Leu Glu Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly
100 105 110

Asn Thr Leu Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu
130 135 140

Val Lys Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser
145 150 155 160

Leu Ser Val Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly
165 170 175

Val Ser Trp Ile Arg Gln Pro Pro Arg Lys^{-SL} Gly Leu Glu Trp Leu Gly
 180 185 190
 Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser
 195 200 205
 Arg Leu Thr Ile Ile Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys
 210 215 220
 Met Asn Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys
 225 230 235 240
 His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly
 245 250 255
 Thr Ser Val Thr Val Ser Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro
 260 265 270
 Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu
 275 280 285
 Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp
 290 295 300
 Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly
 305 310 315 320
 Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg
 325 330 335
 Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln
 340 345 350
 Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu
 355 360 365
 Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala
 370 375 380
 Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu
 385 390 395 400
 Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp
 405 410 415
 Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu
 420 425 430
 Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile
 435 440 445

Gly Met Lys Gly Glu Arg Arg Arg Gly Lys^{SL} Gly His Asp Gly Leu Tyr
450 455 460

Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met
465 470 475 480

Gln Ala Leu Pro Pro Arg
485

<210> 892
<211> 465
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 892
Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
35 40 45

Tyr His Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
65 70 75 80

Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr Gly Gly Gly Gly Ser
100 105 110

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Lys Leu Gln Glu
115 120 125

Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser Val Thr Cys
130 135 140

Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg
145 150 155 160

Gln Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Gly Ser
165 170 175

Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser Arg Leu Thr Ile Ile
Page 655

_SL

180		185		190											
Lys	Asp	Asn 195	Ser	Lys	Ser	Gln	Val 200	Phe	Leu	Lys	Met	Asn 205	Ser	Leu	Gln
Thr	Asp 210	Asp	Thr	Ala	Ile	Tyr 215	Tyr	Cys	Ala	Lys	His 220	Tyr	Tyr	Tyr	Gly
Gly 225	Ser	Tyr	Ala	Met	Asp 230	Tyr	Trp	Gly	Gln	Gly 235	Thr	Ser	Val	Thr	Val 240
Ser	Ser	Thr	Thr	Thr 245	Pro	Ala	Pro	Arg	Pro 250	Pro	Thr	Pro	Ala	Pro 255	Thr
Ile	Ala	Ser	Gln 260	Pro	Leu	Ser	Leu	Arg 265	Pro	Glu	Ala	Cys	Arg 270	Pro	Ala
Ala	Gly	Gly 275	Ala	Val	His	Thr	Arg 280	Gly	Leu	Asp	Phe	Ala 285	Cys	Asp	Ile
Tyr	Ile 290	Trp	Ala	Pro	Leu	Ala 295	Gly	Thr	Cys	Gly	Val 300	Leu	Leu	Leu	Ser
Leu 305	Val	Ile	Thr	Leu	Tyr 310	Cys	Lys	Arg	Gly	Arg 315	Lys	Lys	Leu	Leu	Tyr 320
Ile	Phe	Lys	Gln	Pro 325	Phe	Met	Arg	Pro	Val 330	Gln	Thr	Thr	Gln	Glu 335	Glu
Asp	Gly	Cys	Ser 340	Cys	Arg	Phe	Pro	Glu 345	Glu	Glu	Glu	Gly	Gly 350	Cys	Glu
Leu	Arg	Val 355	Lys	Phe	Ser	Arg	Ser 360	Ala	Asp	Ala	Pro	Ala 365	Tyr	Lys	Gln
Gly	Gln 370	Asn	Gln	Leu	Tyr	Asn 375	Glu	Leu	Asn	Leu	Gly 380	Arg	Arg	Glu	Glu
Tyr 385	Asp	Val	Leu	Asp	Lys 390	Arg	Arg	Gly	Arg	Asp 395	Pro	Glu	Met	Gly	Gly 400
Lys	Pro	Arg	Arg	Lys 405	Asn	Pro	Gln	Glu	Gly 410	Leu	Tyr	Asn	Glu	Leu 415	Gln
Lys	Asp	Lys	Met 420	Ala	Glu	Ala	Tyr	Ser 425	Glu	Ile	Gly	Met	Lys 430	Gly	Glu
Arg	Arg	Arg 435	Gly	Lys	Gly	His	Asp 440	Gly	Leu	Tyr	Gln	Gly 445	Leu	Ser	Thr
Ala	Thr	Lys	Asp	Thr	Tyr	Asp	Ala	Leu	His	Met	Gln	Ala	Leu	Pro	Pro

_SL

```
<210> 893
<211> 242
<212> PRT
<213> Artificial Sequence
```

```
<220>  
<221> source  
<223> /note="Description of Artificial Sequence: Synthetic  
polypeptide"
```

<400> 893
Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr His Thr Ser Arg Leu His Ser Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser
100 105 110

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Glu

Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys
130 135 140

Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg
145 150 155 160

Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Val Ile Trp Gly Ser
165 170 175

Glu Thr Thr Tyr Tyr Ser Ser Ser Leu Lys Ser Arg Val Thr Ile Ser
180 185 190

Lys Asp Asn Ser Lys Asn Gln Val Ser Leu Lys Leu Ser Ser Val Thr
195 200 205

_SL

Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly
210 215 220

Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
225 230 235 240

Ser Ser

<210> 894
<211> 813
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 894
atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60
cccgaatttg tgatgaccca gtcacccgcc actcttagcc tttcaccggg tgagcgcgca 120
accctgtctt gcagagcctc ccaagacatc tcaaaatacc ttaattggta tcaacagaag 180
cccggacagg ctctcgcct tctgatctac cacaccagcc ggctccattc tggaatccct 240
gccaggttca gcggtagcgg atctgggacc gactacaccc tcactatcag ctactgcag 300
ccagaggact tcgctgtcta tttctgtcag caaggaaca ccctgcccta cacctttgga 360
cagggcacca agctcgagat taaaggtgga ggtggcagcg gaggaggtgg gtccggcggt 420
ggaggaagcc aggtccaact ccaagaaagc ggaccgggtc ttgtgaagcc atcagaaact 480
ctttcactga cttgtactgt gagcggagtg tctctccccg attacgggggt gtcttggatc 540
agacagccac cggggaaggg tctggaatgg attggagtga tttggggctc tgagactact 600
tactactctt catccctcaa gtcacgcgtc accatctcaa aggacaactc taagaatcag 660
gtgtcactga aactgtcatc tgtgaccgca gccgacaccg ccgtgtacta ttgcgctaag 720
cattactatt atggcgggag ctacgcaatg gattactggg gacaggggtac tctggtcacc 780
gtgtccagcc accacatca tcacatcac cat 813

<210> 895
<211> 271
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 895
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

_SL

His Ala Ala Arg Pro Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu
20 25 30

Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln
35 40 45

Asp Ile Ser Lys Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gln Ala
50 55 60

Pro Arg Leu Leu Ile Tyr His Thr Ser Arg Leu His Ser Gly Ile Pro
65 70 75 80

Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile
85 90 95

Ser Ser Leu Gln Pro Glu Asp Phe Ala Val Tyr Phe Cys Gln Gln Gly
100 105 110

Asn Thr Leu Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln
130 135 140

Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr
145 150 155 160

Leu Ser Leu Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly
165 170 175

Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly
180 185 190

Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Ser Ser Ser Leu Lys Ser
195 200 205

Arg Val Thr Ile Ser Lys Asp Asn Ser Lys Asn Gln Val Ser Leu Lys
210 215 220

Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Lys
225 230 235 240

His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly
245 250 255

Thr Leu Val Thr Val Ser Ser His His His His His His His His
260 265 270

<210> 896
<211> 1458
<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 896

```

atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgtcca cgccgctcgg      60
cccgaaattg tgatgacca gtcacccgcc actcttagcc tttcacccgg tgagcgcgca      120
accctgtctt gcagagcctc ccaagacatc tcaaaatacc ttaattggta tcaacagaag      180
cccggacagg ctctcgcctt tctgatctac cacaccagcc ggctccattc tggaatccct      240
gccaggttca gcggtagcgg atctgggacc gactacaccc tcactatcag ctactgcag      300
ccagaggact tcgctgtcta tttctgtcag caagggaaca ccctgcccta cacctttgga      360
cagggcacca agctcgagat taaaggtgga ggtggcagcg gaggaggtgg gtccggcggt      420
ggaggaagcc aggtccaact ccaagaaagc ggaccgggtc ttgtgaagcc atcagaaact      480
ctttcactga cttgtactgt gagcggagtg tctctccccg attacggggt gtcttggtac      540
agacagccac cggggaaggg tctggaatgg attggagtga tttggggctc tgagactact      600
tactactctt catccctcaa gtcacgcgtc accatctcaa aggacaactc taagaatcag      660
gtgtcactga aactgtcatc tgtgaccgca gccgacaccg ccgtgtacta ttgcgctaag      720
cattactatt atggcgggag ctacgcaatg gattactggg gacagggtag tctggtcacc      780
gtgtccagca ccactacccc agcaccgagg ccaccacccc cggctcctac catcgcctcc      840
cagcctctgt ccctgcgtcc ggaggcatgt agaccgcag ctggtggggc cgtgcatacc      900
cggggctctt acttcgcctg cgatatctac atttggggccc ctctggctgg tacttgcggg      960
gtcctgctgc tttcactcgt gatcactctt tactgtaagc gcggtcggaa gaagctgctg     1020
tacatcttta agcaaccctt catgaggcct gtgcagacta ctcaagagga ggacggctgt     1080
tcatgccggt tcccagagga ggaggaaggc ggctgcgaac tgcgcgtgaa attcagccgc     1140
agcgcagatg ctccagccta caagcagggg cagaaccagc tctacaacga actcaatctt     1200
ggtcggagag aggagtacga cgtgctggac aagcggagag gacgggaccc agaaatgggc     1260
gggaagccgc gcagaaagaa tccccaagag ggcctgtaca acgagctcca aaaggataag     1320
atggcagaag cctatagcga gattggtatg aaaggggaac gcagaagagg caaaggccac     1380
gacggactgt accagggact cagcaccgcc accaaggaca cctatgacgc tcttcacatg     1440
caggccctgc cgcctcgg                                     1458

```

<210> 897

<211> 486

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

_SL

<400> 897

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu
20 25 30

Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln
35 40 45

Asp Ile Ser Lys Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gln Ala
50 55 60

Pro Arg Leu Leu Ile Tyr His Thr Ser Arg Leu His Ser Gly Ile Pro
65 70 75 80

Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile
85 90 95

Ser Ser Leu Gln Pro Glu Asp Phe Ala Val Tyr Phe Cys Gln Gln Gly
100 105 110

Asn Thr Leu Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln
130 135 140

Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr
145 150 155 160

Leu Ser Leu Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly
165 170 175

Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly
180 185 190

Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Ser Ser Ser Leu Lys Ser
195 200 205

Arg Val Thr Ile Ser Lys Asp Asn Ser Lys Asn Gln Val Ser Leu Lys
210 215 220

Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Lys
225 230 235 240

His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly
245 250 255

Thr Leu Val Thr Val Ser Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro
260 265 270

_SL

Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu
275 280 285

Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp
290 295 300

Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly
305 310 315 320

Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg
325 330 335

Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln
340 345 350

Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu
355 360 365

Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala
370 375 380

Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu
385 390 395 400

Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp
405 410 415

Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu
420 425 430

Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile
435 440 445

Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr
450 455 460

Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met
465 470 475 480

Gln Ala Leu Pro Pro Arg
485

<210> 898

<211> 242

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

_SL

<400> 898

Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr His Thr Ser Arg Leu His Ser Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser
100 105 110

Gly Gly Gly Gly Ser Gly Gly Gly Ser Gln Val Gln Leu Gln Glu
115 120 125

Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys
130 135 140

Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg
145 150 155 160

Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Val Ile Trp Gly Ser
165 170 175

Glu Thr Thr Tyr Tyr Gln Ser Ser Leu Lys Ser Arg Val Thr Ile Ser
180 185 190

Lys Asp Asn Ser Lys Asn Gln Val Ser Leu Lys Leu Ser Ser Val Thr
195 200 205

Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly
210 215 220

Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
225 230 235 240

Ser Ser

<210> 899

<211> 813

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 899

```

atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg      60
cccgaaattg tgatgaccca gtcacccgcc actcttagcc tttcacccgg tgagcgcgca      120
accctgtctt gcagagcctc ccaagacatc tcaaaatacc ttaattggta tcaacagaag      180
cccggacagg ctctctgcct tctgatctac cacaccagcc ggctccattc tggaatccct      240
gccaggttca gcggtagcgg atctgggacc gactacaccc tcactatcag ctactgcag      300
ccagaggact tcgctgtcta tttctgtcag caagggaaca ccctgcccta cacctttgga      360
cagggcacca agctcgagat taaaggtgga ggtggcagcg gaggaggtgg gtccggcggt      420
ggaggaagcc aggtccaact ccaagaaagc ggaccgggtc ttgtgaagcc atcagaaact      480
ctttcactga cttgtactgt gagcggagtg tctctcccg attacggggt gtcttggatc      540
agacagccac cggggaaggg tctggaatgg attggagtga tttggggctc tgagactact      600
tactaccaat catccctcaa gtcacgcgtc accatctcaa aggacaactc taagaatcag      660
gtgtcactga aactgtcatc tgtgaccgca gccgacaccg ccgtgtacta ttgcgctaag      720
cattactatt atggcgggag ctacgcaatg gattactggg gacagggtag tctggtcacc      780
gtgtccagcc accacatca tcaccatcac cat                                     813

```

<210> 900

<211> 271

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 900

```

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1          5          10         15

His Ala Ala Arg Pro Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu
          20          25          30

Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln
          35          40          45

Asp Ile Ser Lys Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gln Ala
          50          55          60

Pro Arg Leu Leu Ile Tyr His Thr Ser Arg Leu His Ser Gly Ile Pro
65          70          75          80

```

Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr^{-SL} Asp Tyr Thr Leu Thr Ile
 85 90 95
 Ser Ser Leu Gln Pro Glu Asp Phe Ala Val Tyr Phe Cys Gln Gln Gly
 100 105 110
 Asn Thr Leu Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
 115 120 125
 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln
 130 135 140
 Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr
 145 150 155 160
 Leu Ser Leu Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly
 165 170 175
 Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly
 180 185 190
 Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Gln Ser Ser Leu Lys Ser
 195 200 205
 Arg Val Thr Ile Ser Lys Asp Asn Ser Lys Asn Gln Val Ser Leu Lys
 210 215 220
 Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Lys
 225 230 235 240
 His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly
 245 250 255
 Thr Leu Val Thr Val Ser Ser His His His His His His His His
 260 265 270

<210> 901
 <211> 1458
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 901	
atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg	60
cccgaatttg tgatgaccca gtcaccgcgc actcttagcc tttcaccggg tgagcgcgca	120
accctgtctt gcagagcctc ccaagacatc tcaaaatacc ttaattggta tcaacagaag	180
cccggacagg ctctcgcct tctgatctac cacaccagcc ggctccattc tggaatccct	240
gccagggttca gcggtagcgg atctgggacc gactacaccc tcactatcag ctactgcag	300

_SL

ccagaggact tcgctgtcta tttctgtcag caaggggaaca ccctgcccta cacctttgga 360
cagggcacca agctcgagat taaaggtgga ggtggcagcg gaggaggtgg gtccggcggt 420
ggaggaagcc aggtccaact ccaagaaagc ggaccgggtc ttgtgaagcc atcagaaact 480
ctttcactga cttgtactgt gagcggagtg tctctccccg attacggggt gtcttgatc 540
agacagccac cggggaaggg tctggaatgg attggagtga tttggggctc tgagactact 600
tactaccaat catccctcaa gtcacgcgtc accatctcaa aggacaactc taagaatcag 660
gtgtcactga aactgtcatc tgtgaccgca gccgacaccg ccgtgtacta ttgcgctaag 720
cattactatt atggcgggag ctacgcaatg gattactggg gacaggggtac tctggtcacc 780
gtgtccagca ccactacccc agcaccgagg ccaccacccc cggctcctac catcgcctcc 840
cagcctctgt ccctgcgtcc ggaggcatgt agaccgcag ctggtggggc cgtgcatacc 900
cggggctctg acttcgcctg cgatatctac atttggggccc ctctggctgg tacttgcggg 960
gtcctgctgc tttcactcgt gatcactctt tactgtaagc gcggtcggaa gaagctgctg 1020
tacatcttta agcaaccctt catgaggcct gtgcagacta ctcaagagga ggacggctgt 1080
tcatgccggt tcccagagga ggaggaaggc ggctgcgaac tgcgcgtgaa attcagccgc 1140
agcgcagatg ctccagccta caagcagggg cagaaccagc tctacaacga actcaatctt 1200
ggtcggagag aggagtacga cgtgctggac aagcggagag gacgggaccc agaaatgggc 1260
gggaagccgc gcagaaagaa tccccaagag ggcctgtaca acgagctcca aaaggataag 1320
atggcagaag cctatagcga gattggtatg aaaggggaac gcagaagagg caaaggccac 1380
gacggactgt accagggact cagcaccgcc accaaggaca cctatgacgc tcttcacatg 1440
caggccctgc cgcctcgg 1458

<210> 902

<211> 486

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 902

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu
20 25 30

Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln
35 40 45

Asp Ile Ser Lys Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gln Ala
50 55 60

_SL

Pro Arg Leu Leu Ile Tyr His Thr Ser Arg Leu His Ser Gly Ile Pro
65 70 75 80

Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile
85 90 95

Ser Ser Leu Gln Pro Glu Asp Phe Ala Val Tyr Phe Cys Gln Gln Gly
100 105 110

Asn Thr Leu Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln
130 135 140

Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr
145 150 155 160

Leu Ser Leu Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly
165 170 175

Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly
180 185 190

Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Gln Ser Ser Leu Lys Ser
195 200 205

Arg Val Thr Ile Ser Lys Asp Asn Ser Lys Asn Gln Val Ser Leu Lys
210 215 220

Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Lys
225 230 235 240

His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly
245 250 255

Thr Leu Val Thr Val Ser Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro
260 265 270

Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu
275 280 285

Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp
290 295 300

Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly
305 310 315 320

Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg
325 330 335

_SL

Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln
340 345 350

Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu
355 360 365

Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala
370 375 380

Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu
385 390 395 400

Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp
405 410 415

Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu
420 425 430

Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile
435 440 445

Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr
450 455 460

Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met
465 470 475 480

Gln Ala Leu Pro Pro Arg
485

<210> 903

<211> 242

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 903

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr
20 25 30

Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45

Gly Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Ser Ser Ser Leu Lys
50 55 60

Ser Arg Val Thr Ile Ser Lys Asp Asn Ser^{-SL} Lys Asn Gln Val Ser Leu
 65 70 75 80
 Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95
 Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln
 100 105 110
 Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
 115 120 125
 Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Met Thr Gln Ser Pro Ala
 130 135 140
 Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala
 145 150 155 160
 Ser Gln Asp Ile Ser Lys Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly
 165 170 175
 Gln Ala Pro Arg Leu Leu Ile Tyr His Thr Ser Arg Leu His Ser Gly
 180 185 190
 Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu
 195 200 205
 Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Val Tyr Phe Cys Gln
 210 215 220
 Gln Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu
 225 230 235 240
 Ile Lys

<210> 904
 <211> 813
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 904
 atggctctgc ccgtgaccgc actcctcctg ccactggctc tgctgcttca cgccgctcgc 60
 ccacaagtcc agcttcaaga atcagggcct ggtctggtga agccatctga gactctgtcc 120
 ctcacttgca ccgtgagcgg agtgtccctc ccagactacg gagtgagctg gattagacag 180
 cctcccggaa agggactgga gtggatcgga gtgatttggg gtagcgaaac cacttactat 240
 tcattttccc tgaagtcacg ggtcaccatt tcaaaggata actcaaagaa tcaagtgagc 300
 Page 669

_SL

ctcaagctct catcagtcac cgccgctgac accgccgtgt attactgtgc caagcattac 360
tactatggag ggtcctacgc catggactac tggggccagg gaactctggt cactgtgtca 420
tctggtggag gaggtagcgg aggaggcggg agcgggtggag gtggctccga aatcgtgatg 480
accagagacc ctgcaaccct gtccctttct cccggggaac gggctaccct ttcttgtcgg 540
gcatcacaag atatctcaaa atacctcaat tggatatcaac agaagccggg acaggcccct 600
aggcttctta tctaccacac ctctcgctg catagcggga ttcccgcacg ctttagcggg 660
tctggaagcg ggaccgacta cactctgacc atctcatctc tccagcccga ggacttcgcc 720
gtctacttct gccagcaggg taacaccctg ccgtacacct tcggccaggg caccaagctt 780
gagatcaaac atcaccacca tcatcaccat cac 813

<210> 905

<211> 271

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 905

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu
20 25 30

Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Val
35 40 45

Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys
50 55 60

Gly Leu Glu Trp Ile Gly Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr
65 70 75 80

Ser Ser Ser Leu Lys Ser Arg Val Thr Ile Ser Lys Asp Asn Ser Lys
85 90 95

Asn Gln Val Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala
100 105 110

Val Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met
115 120 125

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
130 135 140

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Met
Page 670

145		150		-SL 155		160									
Thr	Gln	Ser	Pro	Ala	Thr	Leu	Ser	Leu	Ser	Pro	Gly	Glu	Arg	Ala	Thr
				165					170					175	
Leu	Ser	Cys	Arg	Ala	Ser	Gln	Asp	Ile	Ser	Lys	Tyr	Leu	Asn	Trp	Tyr
			180					185					190		
Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Leu	Leu	Ile	Tyr	His	Thr	Ser
		195					200					205			
Arg	Leu	His	Ser	Gly	Ile	Pro	Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly
	210					215					220				
Thr	Asp	Tyr	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp	Phe	Ala
225					230					235					240
Val	Tyr	Phe	Cys	Gln	Gln	Gly	Asn	Thr	Leu	Pro	Tyr	Thr	Phe	Gly	Gln
				245					250					255	
Gly	Thr	Lys	Leu	Glu	Ile	Lys	His	His	His	His	His	His	His	His	His
			260					265						270	

<210> 906
 <211> 1458
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 906	
atggctctgc ccgtgaccgc actcctcctg ccactggctc tgctgcttca cgccgctcgc	60
ccacaagtcc agcttcaaga atcagggcct ggtctggtga agccatctga gactctgtcc	120
ctcacttgca ccgtgagcgg agtgtccctc ccagactacg gagtgagctg gattagacag	180
cctcccggaa agggactgga gtggatcgga gtgatttggg gtagcgaaac cacttactat	240
tcattcttccc tgaagtcacg ggtcaccatt tcaaaggata actcaaagaa tcaagtgagc	300
ctcaagctct catcagtcac cgccgctgac accgccgtgt attactgtgc caagcattac	360
tactatggag ggtcctacgc catggactac tggggccagg gaactctggt cactgtgtca	420
tctggtggag gaggtagcgg aggaggcggg agcgggtggag gtggctccga aatcgtgatg	480
accagagacc ctgcaaccct gtccctttct cccggggaac gggctaccct ttcttgtcgg	540
gcatcacaag atatctcaaa atacctcaat tggtatcaac agaagccggg acaggcccct	600
aggcttctta tctaccacac ctctcgctg catagcggga ttccgcgacg ctttagcggg	660
tctggaagcg ggaccgacta cactctgacc atctcatctc tccagcccga ggacttcgcc	720
gtctacttct gccagcaggg taacaccctg ccgtacacct tcggccaggg caccaagctt	780

_SL

gagatcaaaa ccactactcc cgctccaagg ccaccacccc ctgccccgac catcgctctt	840
cagccgcttt ccctgcgtcc ggaggcatgt agaccgcag ctggtggggc cgtgcatacc	900
cggggtcttg acttcgcctg cgatatctac atttggggccc ctctggctgg tacttgcggg	960
gtcctgctgc tttcactcgt gatcactctt tactgtaagc gcggtcggaa gaagctgctg	1020
tacatcttta agcaaccctt catgaggcct gtgcagacta ctcaagagga ggacggctgt	1080
tcatgccggt tcccagagga ggaggaaggc ggctgcgaac tgcgcgtgaa attcagccgc	1140
agcgcagatg ctccagccta caagcagggg cagaaccagc tctacaacga actcaatctt	1200
ggtcggagag aggagtacga cgtgctggac aagcggagag gacgggaccc agaaatgggc	1260
gggaagccgc gcagaaagaa tccccaagag ggcctgtaca acgagctcca aaaggataag	1320
atggcagaag cctatagcga gattggtatg aaaggggaac gcagaagagg caaaggccac	1380
gacggactgt accagggact cagcaccgcc accaaggaca cctatgacgc tcttcacatg	1440
caggccctgc cgcctcgg	1458

<210> 907
 <211> 486
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 907
 Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
 1 5 10 15

His Ala Ala Arg Pro Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu
 20 25 30

Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Val
 35 40 45

Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys
 50 55 60

Gly Leu Glu Trp Ile Gly Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr
 65 70 75 80

Ser Ser Ser Leu Lys Ser Arg Val Thr Ile Ser Lys Asp Asn Ser Lys
 85 90 95

Asn Gln Val Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala
 100 105 110

Val Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met
 115 120 125

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val^{SL} Ser Ser Gly Gly Gly
 130 135 140
 Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Met
 145 150 155 160
 Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr
 165 170 175
 Leu Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr Leu Asn Trp Tyr
 180 185 190
 Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr His Thr Ser
 195 200 205
 Arg Leu His Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly
 210 215 220
 Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
 225 230 235 240
 Val Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gln
 245 250 255
 Gly Thr Lys Leu Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro
 260 265 270
 Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu
 275 280 285
 Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp
 290 295 300
 Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly
 305 310 315 320
 Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg
 325 330 335
 Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln
 340 345 350
 Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu
 355 360 365
 Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala
 370 375 380
 Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu
 385 390 395 400

Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp^{-SL} Lys Arg Arg Gly Arg Asp
405 410 415

Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu
420 425 430

Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile
435 440 445

Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr
450 455 460

Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met
465 470 475 480

Gln Ala Leu Pro Pro Arg
485

<210> 908
<211> 242
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 908
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr
20 25 30

Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45

Gly Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Gln Ser Ser Leu Lys
50 55 60

Ser Arg Val Thr Ile Ser Lys Asp Asn Ser Lys Asn Gln Val Ser Leu
65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Met Thr Gln Ser Pro Ala
Page 674

[illegible]

gagatcaaac atcaccacca tcataccat cac _SL

813

<210> 910
<211> 271
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 910
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu
20 25 30

Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Val
35 40 45

Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln ProPro Gly Lys
50 55 60

Gly Leu Glu Trp Ile Gly Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr
65 70 75 80

Gln Ser Ser Leu Lys Ser Arg Val Thr Ile Ser Lys Asp Asn Ser Lys
85 90 95

Asn Gln Val Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala
100 105 110

Val Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met
115 120 125

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
130 135 140

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Met
145 150 155 160

Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr
165 170 175

Leu Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr Leu Asn Trp Tyr
180 185 190

Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr His Thr Ser
195 200 205

Arg Leu His Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly
210 215 220

_SL

Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
225 230 235 240

Val Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gln
245 250 255

Gly Thr Lys Leu Glu Ile Lys His His His His His His His His
260 265 270

<210> 911
<211> 1458
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 911
atggctctgc ccgtgaccgc actcctcctg ccactggctc tgctgcttca cgccgctcgc 60
ccacaagtcc agcttcaaga atcagggcct ggtctggtga agccatctga gactctgtcc 120
ctcacttgca ccgtgagcgg agtgtccctc ccagactacg gagtgagctg gattagacag 180
cctcccggaa agggactgga gtggatcgga gtgatttggg gtagcgaaac cacttactat 240
caatcttccc tgaagtcacg ggtcaccatt tcaaaggata actcaaagaa tcaagtgagc 300
ctcaagctct catcagtcac cgccgctgac accgccgtgt attactgtgc caagcattac 360
tactatggag ggtcctacgc catggactac tggggccagg gaactctggt cactgtgtca 420
tctggtggag gaggtagcgg aggaggcggg agcggtaggag gtggctccga aatcgtgatg 480
accagagacc ctgcaaccct gtccctttct cccggggaac gggctaccct ttcttgtcgg 540
gcatcacaag atatctcaaa atacctcaat tggatatcaac agaagccggg acaggcccct 600
aggcttctta tctaccacac ctctcgctg catagcggga ttccgcacg ctttagcggg 660
tctggaagcg ggaccgacta cactctgacc atctcatctc tccagcccga ggacttcgcc 720
gtctacttct gccagcaggg taacaccctg ccgtacacct tcggccaggg caccaagctt 780
gagatcaaaa ccactactcc cgctccaagg ccaccaccc ctgccccgac catcgctctt 840
cagccgcttt ccctgcgtcc ggaggcatgt agaccgcag ctggtggggc cgtgcatacc 900
cggggtcttg acttcgcctg cgatatctac atttgggccc ctctggctgg tacttgcggg 960
gtcctgctgc tttcactcgt gatcactctt tactgtaagc gcggtcggaa gaagctgctg 1020
tacatcttta agcaaccctt catgaggcct gtgcagacta ctcaagagga ggacggctgt 1080
tcatgccggt tcccagagga ggaggaaggc ggctgcgaac tgcgcgtgaa attcagccgc 1140
agcgagatg ctccagccta caagcagggg cagaaccagc tctacaacga actcaatctt 1200
ggtcggagag aggagtacga cgtgctggac aagcggagag gacgggaccc agaaatgggc 1260
gggaagccgc gcagaaagaa tccccaagag ggctgtgaca acgagctcca aaaggataag 1320

_SL

atggcagaag cctatagcga gattggtatg aaaggggaac gcagaagagg caaaggccac 1380
gacggactgt accagggact cagcaccgcc accaaggaca cctatgacgc tcttcacatg 1440
caggccctgc cgcctcgg 1458

<210> 912
<211> 486
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 912
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu
20 25 30

Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Val
35 40 45

Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys
50 55 60

Gly Leu Glu Trp Ile Gly Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr
65 70 75 80

Gln Ser Ser Leu Lys Ser Arg Val Thr Ile Ser Lys Asp Asn Ser Lys
85 90 95

Asn Gln Val Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala
100 105 110

Val Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met
115 120 125

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
130 135 140

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Met
145 150 155 160

Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr
165 170 175

Leu Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr Leu Asn Trp Tyr
180 185 190

Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr His Thr Ser
Page 678

_SL

195		200		205											
Arg	Leu ₂₁₀	His	Ser	Gly	Ile	Pro ₂₁₅	Ala	Arg	Phe	Ser	Gly ₂₂₀	Ser	Gly	Ser	Gly
Thr ₂₂₅	Asp	Tyr	Thr	Leu	Thr ₂₃₀	Ile	Ser	Ser	Leu	Gln ₂₃₅	Pro	Glu	Asp	Phe	Ala ₂₄₀
Val	Tyr	Phe	Cys	Gln ₂₄₅	Gln	Gly	Asn	Thr	Leu ₂₅₀	Pro	Tyr	Thr	Phe	Gly ₂₅₅	Gln
Gly	Thr	Lys	Leu ₂₆₀	Glu	Ile	Lys	Thr	Thr ₂₆₅	Thr	Pro	Ala	Pro	Arg ₂₇₀	Pro	Pro
Thr	Pro	Ala ₂₇₅	Pro	Thr	Ile	Ala	Ser ₂₈₀	Gln	Pro	Leu	Ser	Leu ₂₈₅	Arg	Pro	Glu
Ala	Cys ₂₉₀	Arg	Pro	Ala	Ala	Gly ₂₉₅	Gly	Ala	Val	His	Thr ₃₀₀	Arg	Gly	Leu	Asp
Phe ₃₀₅	Ala	Cys	Asp	Ile	Tyr ₃₁₀	Ile	Trp	Ala	Pro	Leu ₃₁₅	Ala	Gly	Thr	Cys	Gly ₃₂₀
Val	Leu	Leu	Leu	Ser ₃₂₅	Leu	Val	Ile	Thr	Leu ₃₃₀	Tyr	Cys	Lys	Arg	Gly ₃₃₅	Arg
Lys	Lys	Leu	Leu ₃₄₀	Tyr	Ile	Phe	Lys	Gln ₃₄₅	Pro	Phe	Met	Arg	Pro ₃₅₀	Val	Gln
Thr	Thr	Gln ₃₅₅	Glu	Glu	Asp	Gly	Cys ₃₆₀	Ser	Cys	Arg	Phe	Pro ₃₆₅	Glu	Glu	Glu
Glu	Gly ₃₇₀	Gly	Cys	Glu	Leu	Arg ₃₇₅	Val	Lys	Phe	Ser	Arg ₃₈₀	Ser	Ala	Asp	Ala
Pro ₃₈₅	Ala	Tyr	Lys	Gln	Gly ₃₉₀	Gln	Asn	Gln	Leu	Tyr ₃₉₅	Asn	Glu	Leu	Asn	Leu ₄₀₀
Gly	Arg	Arg	Glu	Glu ₄₀₅	Tyr	Asp	Val	Leu	Asp ₄₁₀	Lys	Arg	Arg	Gly	Arg ₄₁₅	Asp
Pro	Glu	Met	Gly ₄₂₀	Gly	Lys	Pro	Arg	Arg ₄₂₅	Lys	Asn	Pro	Gln	Glu ₄₃₀	Gly	Leu
Tyr	Asn	Glu ₄₃₅	Leu	Gln	Lys	Asp	Lys ₄₄₀	Met	Ala	Glu	Ala	Tyr ₄₄₅	Ser	Glu	Ile
Gly	Met ₄₅₀	Lys	Gly	Glu	Arg	Arg ₄₅₅	Arg	Gly	Lys	Gly	His ₄₆₀	Asp	Gly	Leu	Tyr
Gln	Gly	Leu	Ser	Thr	Ala	Thr	Lys	Asp	Thr	Tyr	Asp	Ala	Leu	His	Met

[illegible]

Gln Ala Leu Pro Pro Arg
485

```
<210> 913
<211> 247
<212> PRT
<213> Artificial Sequence
```

```
<220>  
<221> source  
<223> /note="Description of Artificial Sequence: Synthetic  
polypeptide"
```

<400> 913
Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr His Thr Ser Arg Leu His Ser Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser
100 105 110

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln
115 120 125

Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr
130 135 140

Leu Ser Leu Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly
145 150 155 160

Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly
165 170 175

Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Ser Ser Ser Leu Lys Ser
180 185 190

Arg Val Thr Ile Ser Lys Asp Asn Ser Lys Asn Gln Val Ser Leu Lys
195 200 205

_SL

Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Lys
210 215 220

His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly
225 230 235 240

Thr Leu Val Thr Val Ser Ser
245

<210> 914
<211> 828
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 914
atggccctcc cagtgaccgc tctgctgctg cctctcgcac ttcttctcca tgccgctcgg 60
cctgagatcg tcatgacca aagccccgct accctgtccc tgtcaccgg cgagagggca 120
accctttcat gcagggccag ccaggacatt tctaagtacc tcaactggta tcagcagaag 180
ccagggcagg ctctcgcct gctgatctac cacaccagcc gcctccacag cggtatcccc 240
gccagatttt ccgggagcgg gtctggaacc gactacaccc tcaccatctc ttctctgcag 300
cccgaggatt tcgccgtcta tttctgccag caggggaata ctctgccgta caccttcggt 360
caaggtacca agctggaaat caagggaggc ggaggatcag gcggtggcgg aagcggagga 420
gggtggctccg gaggaggagg ttcccaagtg cagcttcaag aatcaggacc cggacttgtg 480
aagccatcag aaacctctc cctgacttgt accgtgtccg gtgtgagcct ccccgactac 540
ggagtctctt ggattcgcca gcctccgggg aagggctttg aatggattgg ggtgatttgg 600
ggatcagaga ctacttacta ctcttcatca cttaagtcac gggtcaccat cagcaaagat 660
aatagcaaga accaagtgtc acttaagctg tcattctgtga ccgccgctga caccgccgtg 720
tactattgtg ccaaacatta ctattacgga gggctttatg ctatggacta ctggggacag 780
gggaccttgg tgactgtctc tagccatcac catcaccacc atcatcac 828

<210> 915
<211> 276
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 915
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

_SL

His Ala Ala Arg Pro Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu
20 25 30

Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln
35 40 45

Asp Ile Ser Lys Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gln Ala
50 55 60

Pro Arg Leu Leu Ile Tyr His Thr Ser Arg Leu His Ser Gly Ile Pro
65 70 75 80

Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile
85 90 95

Ser Ser Leu Gln Pro Glu Asp Phe Ala Val Tyr Phe Cys Gln Gln Gly
100 105 110

Asn Thr Leu Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
130 135 140

Gly Gly Gly Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val
145 150 155 160

Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Val Ser
165 170 175

Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly
180 185 190

Leu Glu Trp Ile Gly Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Ser
195 200 205

Ser Ser Leu Lys Ser Arg Val Thr Ile Ser Lys Asp Asn Ser Lys Asn
210 215 220

Gln Val Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val
225 230 235 240

Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met Asp
245 250 255

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser His His His His
260 265 270

His His His His
275

_SL

<210> 916
<211> 1473
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 916
atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60
cccgaaattg tgatgaccca gtcacccgcc actcttagcc tttcaccggg tgagcgcgca 120
accctgtctt gcagagcctc ccaagacatc tcaaaatacc ttaattggta tcaacagaag 180
cccggacagg ctctcgcctt tctgatctac cacaccagcc ggctccattc tggaatccct 240
gccaggttca gcggtagcgg atctgggacc gactacaccc tcactatcag ctactgacag 300
ccagaggact tcgctgtcta tttctgtcag caaggaaca ccctgcccta cacctttgga 360
cagggcacca agctcgagat taaaggtgga ggtggcagcg gaggagggtg gtccggcggt 420
ggaggaagcg gcggaggcgg gagccaggtc caactccaag aaagcggacc gggctcttggt 480
aagccatcag aaactctttc actgacttgt actgtgagcg gagtgtctct ccccgattac 540
ggggtgtctt ggatcagaca gccaccgggg aagggctctg aatggattgg agtgatttgg 600
ggctctgaga ctacttacta ctcttcaccc ctcaagtcac gcgtcaccat ctcaaaggac 660
aactctaaga atcaggtgtc actgaaactg tcactgtgta ccgcagccga caccgccgtg 720
tactattgcg ctaagcatta ctattatggc gggagctacg caatggatta ctggggacag 780
ggtactctgg tcaccgtgtc cagcaccact accccagcac cgaggccacc caccgccgtt 840
cctaccatcg cctcccagcc tctgtccctg cgtccggagg catgtagacc cgcagctggt 900
ggggccgtgc ataccggggg tcttgacttc gcctgcgata tctacatttg ggcccctctg 960
gctggtactt gcgggggtcct gctgctttca ctctgtatca ctctttactg taagcgcggt 1020
cggaagaagc tgctgtacat cttaagcaa cccttcatga ggcctgtgca gactactcaa 1080
gaggaggacg gctgttcatg ccggttccca gaggaggagg aaggcggctg cgaactgcgc 1140
gtgaaattca gccgcagcgc agatgctcca gcctacaagc aggggcagaa ccagctctac 1200
aacgaactca atcttggtcg gagagaggag tacgacgtgc tggacaagcg gagaggacgg 1260
gaccagaaa tgggcgggaa gccgcgcaga aagaatcccc aagagggcct gtacaacgag 1320
ctccaaaagg ataagatggc agaagcctat agcgagattg gtatgaaagg ggaacgcaga 1380
agaggcaaag gccacgacgg actgtaccag ggactcagca ccgccaccaa ggacacctat 1440
gacgctcttc acatgcaggc cctgccgcct cgg 1473

<210> 917
<211> 491
<212> PRT
<213> Artificial Sequence

_SL

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 917

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu
20 25 30

Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln
35 40 45

Asp Ile Ser Lys Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gln Ala
50 55 60

Pro Arg Leu Leu Ile Tyr His Thr Ser Arg Leu His Ser Gly Ile Pro
65 70 75 80

Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile
85 90 95

Ser Ser Leu Gln Pro Glu Asp Phe Ala Val Tyr Phe Cys Gln Gln Gly
100 105 110

Asn Thr Leu Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
130 135 140

Gly Gly Gly Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val
145 150 155 160

Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Val Ser
165 170 175

Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly
180 185 190

Leu Glu Trp Ile Gly Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Ser
195 200 205

Ser Ser Leu Lys Ser Arg Val Thr Ile Ser Lys Asp Asn Ser Lys Asn
210 215 220

Gln Val Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val
225 230 235 240

Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met Asp
245 250 255

_SL

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Thr Thr Thr Pro
260 265 270

Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu
275 280 285

Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His
290 295 300

Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu
305 310 315 320

Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr
325 330 335

Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe
340 345 350

Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg
355 360 365

Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser
370 375 380

Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr
385 390 395 400

Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys
405 410 415

Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn
420 425 430

Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu
435 440 445

Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly
450 455 460

His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr
465 470 475 480

Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
485 490

<210> 918

<211> 247

<212> PRT

<213> Artificial Sequence

<220>

_SL

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 918

Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr His Thr Ser Arg Leu His Ser Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser
100 105 110

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln
115 120 125

Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr
130 135 140

Leu Ser Leu Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly
145 150 155 160

Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly
165 170 175

Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Gln Ser Ser Leu Lys Ser
180 185 190

Arg Val Thr Ile Ser Lys Asp Asn Ser Lys Asn Gln Val Ser Leu Lys
195 200 205

Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Lys
210 215 220

His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly
225 230 235 240

Thr Leu Val Thr Val Ser Ser
245

_SL

<210> 919
<211> 828
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 919
atggccctcc cagtgaccgc tctgctgctg cctctcgac ttcttctcca tgccgctcgg 60
cctgagatcg tcatgaccca aagccccgct accctgtccc tgtcaccgg cgagagggca 120
accctttcat gcagggccag ccaggacatt tctaagtacc tcaactggta tcagcagaag 180
ccagggcagg ctctctgcct gctgatctac cacaccagcc gcctccacag cggatatccc 240
gccagatttt ccgggagcgg gtctggaacc gactacaccc tcaccatctc ttctctgcag 300
cccgaggatt tcgccgtcta tttctgccag caggggaata ctctgccgta caccttcggt 360
caaggtacca agctggaaat caagggaggc ggaggatcag gcggtggcgg aagcggagga 420
ggtggctccg gaggaggagg ttcccaagtg cagcttcaag aatcaggacc cggacttgtg 480
aagccatcag aaaccctctc cctgacttgt accgtgtccg gtgtgagcct ccccgactac 540
ggagtctctt ggattcgcca gcctccgggg aagggcttg aatggattgg ggtgatttgg 600
ggatcagaga ctacttacta ccagtcatca cttaagtcac gggtcaccat cagcaaagat 660
aatagcaaga accaagtgtc acttaagctg tcatctgtga ccgccgctga caccgccgtg 720
tactattgtg ccaaacatta ctattacgga gggctttatg ctatggacta ctggggacag 780
gggaccctgg tgactgtctc tagccatcac catcaccacc atcatcac 828

<210> 920
<211> 276
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 920
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu
20 25 30

Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln
35 40 45

Asp Ile Ser Lys Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gln Ala
50 55 60

Pro Arg Leu Leu Ile Tyr His Thr Ser Arg ^{SL}Leu His Ser Gly Ile Pro
 65 70 75 80
 Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile
 85 90 95
 Ser Ser Leu Gln Pro Glu Asp Phe Ala Val Tyr Phe Cys Gln Gln Gly
 100 105 110
 Asn Thr Leu Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
 115 120 125
 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 130 135 140
 Gly Gly Gly Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val
 145 150 155 160
 Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Val Ser
 165 170 175
 Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly
 180 185 190
 Leu Glu Trp Ile Gly Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Gln
 195 200 205
 Ser Ser Leu Lys Ser Arg Val Thr Ile Ser Lys Asp Asn Ser Lys Asn
 210 215 220
 Gln Val Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val
 225 230 235 240
 Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met Asp
 245 250 255
 Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser His His His His
 260 265 270
 His His His His
 275

<210> 921
 <211> 1473
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 921
 atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg

_SL

cccgaaattg tgatgacca gtcacccgcc actcttagcc tttcaccggt tgagcgcgca 120
accctgtctt gcagagcctc ccaagacatc tcaaaatacc ttaattggta tcaacagaag 180
cccggaacagg ctctctgcct tctgatctac cacaccagcc ggctccattc tggaatccct 240
gccaggttca gcggtagcgg atctgggacc gactacaccc tcactatcag ctactgcag 300
ccagaggact tcgctgtcta tttctgtcag caagggaaca ccctgcccta cacctttgga 360
cagggcacca agctcgagat taaaggtgga ggtggcagcg gaggaggtgg gtccggcggt 420
ggaggaagcg gaggcggagg gagccaggtc caactccaag aaagcggacc gggctctgtg 480
aagccatcag aaactctttc actgacttgt actgtgagcg gagtgtctct ccccgattac 540
ggggtgtctt ggatcagaca gccaccgggg aagggctctgg aatggattgg agtgatttgg 600
ggctctgaga ctacttacta ccaatcatcc ctcaagtcac gcgtcaccat ctcaaaggac 660
aactctaaga atcaggtgtc actgaaactg tcatctgtga ccgcagccga caccgccgtg 720
tactattgag ctaagcatta ctattatggc gggagctacg caatggatta ctggggacag 780
ggtactctgg tcaccgtgtc cagcaccact accccagcac cgaggccacc caccgccgt 840
cctaccatcg cctcccagcc tctgtccctg cgtccggagg catgtagacc cgcagctggt 900
ggggccgtgc ataccgggg tcttgacttc gcctgcgata tctacatttg ggcccctctg 960
gctggtactt gcggggctct gctgctttca ctctgtatca ctctttactg taagcgcggt 1020
cggaagaagc tgctgtacat ctttaagcaa cccttcatga ggcctgtgca gactactcaa 1080
gaggaggacg gctgttcatg ccggttccca gaggaggagg aaggcggctg cgaactgcgc 1140
gtgaaattca gccgcagcgc agatgctcca gcctacaagc aggggcagaa ccagctctac 1200
aacgaactca atcttggtcg gagagaggag tacgacgtgc tggacaagcg gagaggacgg 1260
gaccagaaa tgggcgggaa gccgcgcaga aagaatcccc aagagggcct gtacaacgag 1320
ctccaaaagg ataagatggc agaagcctat agcgagattg gtatgaaagg ggaacgcaga 1380
agaggcaaag gccacgacgg actgtaccag ggactcagca ccgccaccaa ggacacctat 1440
gacgtcttc acatgcaggc cctgccgcct cgg 1473

<210> 922

<211> 491

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 922

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu
20 25 30

_SL

Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln
35 40 45

Asp Ile Ser Lys Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gln Ala
50 55 60

Pro Arg Leu Leu Ile Tyr His Thr Ser Arg Leu His Ser Gly Ile Pro
65 70 75 80

Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile
85 90 95

Ser Ser Leu Gln Pro Glu Asp Phe Ala Val Tyr Phe Cys Gln Gln Gly
100 105 110

Asn Thr Leu Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
130 135 140

Gly Gly Gly Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val
145 150 155 160

Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Val Ser
165 170 175

Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly
180 185 190

Leu Glu Trp Ile Gly Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Gln
195 200 205

Ser Ser Leu Lys Ser Arg Val Thr Ile Ser Lys Asp Asn Ser Lys Asn
210 215 220

Gln Val Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val
225 230 235 240

Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met Asp
245 250 255

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Thr Thr Thr Pro
260 265 270

Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu
275 280 285

Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His
290 295 300

_SL

Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu
305 310 315 320

Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr
325 330 335

Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe
340 345 350

Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg
355 360 365

Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser
370 375 380

Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr
385 390 395 400

Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys
405 410 415

Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn
420 425 430

Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu
435 440 445

Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly
450 455 460

His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr
465 470 475 480

Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
485 490

<210> 923

<211> 247

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 923

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr
20 25 30

Gly Val Ser Trp Ile Arg Gln Pro Pro Gly^{SL} Lys Gly Leu Glu Trp Ile
35 40 45

Gly Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Ser Ser Ser Leu Lys
50 55 60

Ser Arg Val Thr Ile Ser Lys Asp Asn Ser Lys Asn Gln Val Ser Leu
65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Met
130 135 140

Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr
145 150 155 160

Leu Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr Leu Asn Trp Tyr
165 170 175

Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr His Thr Ser
180 185 190

Arg Leu His Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly
195 200 205

Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
210 215 220

Val Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gln
225 230 235 240

Gly Thr Lys Leu Glu Ile Lys
245

<210> 924

<211> 828

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 924

atggcactgc ctgtcactgc cctcctgctg cctctggccc tccttctgca tgccgccagg

60

_SL

ccccaagtcc agctgcaaga gtcaggaccc ggactggtga agccgtctga gactctctca 120
ctgacttgta ccgtcagcgg cgtgtccctc cccgactacg gagtgtcatg gatccgcca 180
cctcccggga aagggcttga atggattggt gtcactctggg gttctgaaac cacctactac 240
tcacttccc tgaagtccag ggtgaccatc agcaaggata attccaagaa ccaggtcagc 300
cttaagctgt catctgtgac cgctgctgac accgccgtgt attactgcgc caagcactac 360
tattacggag gaagctacgc tatggactat tggggacagg gcactctcgt gactgtgagc 420
agcggcgggtg gagggctctgg aggtggagga tccggtggtg gtgggtcagg cggaggaggg 480
agcgagattg tgatgactca gtcaccagcc accctttctc tttcaccgg cgagagagca 540
accctgagct gtagagccag ccaggacatt tctaagtacc tcaactggta tcagcaaaaa 600
ccggggcagg cccctcgcct cctgatctac catacctcac gccttcactc tggtatcccc 660
gctcggttta gcggatcagg atctggtacc gactacactc tgaccatttc cagcctgcag 720
ccagaagatt tcgcagtgt tttctgccag cagggcaata cccttcctta caccttcggt 780
cagggaaacca agctcgaaat caagcaccat caccatcatc accaccat 828

<210> 925

<211> 276

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 925

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu
20 25 30

Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Val
35 40 45

Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys
50 55 60

Gly Leu Glu Trp Ile Gly Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr
65 70 75 80

Ser Ser Ser Leu Lys Ser Arg Val Thr Ile Ser Lys Asp Asn Ser Lys
85 90 95

Asn Gln Val Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala
100 105 110

Val Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met
Page 693

_SL

115	120	125
Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly		
130	135	140
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly		
145	150	155
Ser Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro		
165	170	175
Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys		
180	185	190
Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu		
195	200	205
Ile Tyr His Thr Ser Arg Leu His Ser Gly Ile Pro Ala Arg Phe Ser		
210	215	220
Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln		
225	230	235
Pro Glu Asp Phe Ala Val Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro		
245	250	255
Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys His His His His		
260	265	270
His His His His		
275		

<210> 926
 <211> 1473
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400>	926		
	atggctctgc ccgtgaccgc actcctcctg ccaactggctc tgctgcttca cgccgctcgc		60
	ccacaagtcc agcttcaaga atcagggcct ggtctggtga agccatctga gactctgtcc		120
	ctcacttgca ccgtgagcgg agtgtccctc ccagactacg gagtgagctg gattagacag		180
	cctcccggaa agggactgga gtggatcgga gtgatttggg gtagcgaaac cacttactat		240
	tcatcttccc tgaagtcacg ggtcaccatt tcaaaggata actcaaagaa tcaagtgagc		300
	ctcaagctct catcagtcac cgccgctgac accgccgtgt attactgtgc caagcattac		360
	tactatggag ggtcctacgc catggactac tggggccagg gaactctggt cactgtgtca		420

_SL

tctggtggag gaggtagcgg aggaggcggg agcggtaggag gtggctccgg aggtggcgga	480
agcgaaatcg tgatgacca gagccctgca accctgtccc tttctcccgg ggaacgggct	540
accctttctt gtcgggcatc acaagatata tcaaaatacc tcaattggta tcaacagaag	600
ccgggacagg cccctaggct tcttatctac cacacctctc gcctgcatag cgggattccc	660
gcacgcttta gcgggtctgg aagcgggacc gactacactc tgaccatctc atctctccag	720
cccaggagact tcgccgtcta cttctgccag cagggttaaca ccctgccgta caccttcggc	780
cagggcacca agcttgagat caaaaccact actcccgctc caaggccacc caccctgcc	840
ccgaccatcg cctctcagcc gctttccctg cgtccggagg catgtagacc cgcagctggt	900
ggggccgtgc ataccgggg tcttgacttc gcctgcgata tctacatttg ggcccctctg	960
gctggtactt gcggggtcct gctgctttca ctcgtgatca ctctttactg taagcgcggt	1020
cggaagaagc tgctgtacat ctttaagcaa cccttcata ggcctgtgca gactactcaa	1080
gaggaggacg gctgttcata ccggttccca gaggaggagg aaggcggctg cgaactgcgc	1140
gtgaaattca gccgcagcgc agatgctcca gcctacaagc aggggcagaa ccagctctac	1200
aacgaactca atcttggtcg gagagaggag tacgacgtgc tggacaagcg gagaggacgg	1260
gaccagaaa tgggcgggaa gccgcgcaga aagaatcccc aagagggcct gtacaacgag	1320
ctccaaaagg ataagatggc agaagcctat agcgagattg gtatgaaagg ggaacgcaga	1380
agaggcaaag gccacgacgg actgtaccag ggactcagca ccgccaccaa ggacacctat	1440
gacgctcttc acatgcaggc cctgccgcct cgg	1473

<210> 927
 <211> 491
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 927
 Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
 1 5 10 15

His Ala Ala Arg Pro Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu
 20 25 30

Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Val
 35 40 45

Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys
 50 55 60

Gly Leu Glu Trp Ile Gly Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr
 65 70 75 80

Ser Ser Ser Leu Lys₈₅ Ser Arg Val Thr Ile₉₀^{-SL} Ser Lys Asp Asn Ser₉₅ Lys
 Asn Gln Val Ser₁₀₀ Leu Lys Leu Ser Ser₁₀₅ Val Thr Ala Ala Asp₁₁₀ Thr Ala
 Val Tyr Tyr₁₁₅ Cys Ala Lys His Tyr₁₂₀ Tyr Tyr Gly Gly Ser₁₂₅ Tyr Ala Met
 Asp Tyr₁₃₀ Trp Gly Gln Gly Thr₁₃₅ Leu Val Thr Val Ser₁₄₀ Ser Gly Gly Gly
 Gly₁₄₅ Ser Gly Gly Gly Gly₁₅₀ Ser Gly Gly Gly Gly₁₅₅ Ser Gly Gly Gly Gly₁₆₀
 Ser Glu Ile Val Met₁₆₅ Thr Gln Ser Pro Ala₁₇₀ Thr Leu Ser Leu Ser₁₇₅ Pro
 Gly Glu Arg Ala₁₈₀ Thr Leu Ser Cys Arg₁₈₅ Ala Ser Gln Asp Ile₁₉₀ Ser Lys
 Tyr Leu Asn₁₉₅ Trp Tyr Gln Gln Lys₂₀₀ Pro Gly Gln Ala Pro₂₀₅ Arg Leu Leu
 Ile Tyr₂₁₀ His Thr Ser Arg Leu₂₁₅ His Ser Gly Ile Pro₂₂₀ Ala Arg Phe Ser
 Gly₂₂₅ Ser Gly Ser Gly Thr₂₃₀ Asp Tyr Thr Leu Thr₂₃₅ Ile Ser Ser Leu Gln₂₄₀
 Pro Glu Asp Phe Ala₂₄₅ Val Tyr Phe Cys Gln₂₅₀ Gln Gly Asn Thr Leu₂₅₅ Pro
 Tyr Thr Phe Gly₂₆₀ Gln Gly Thr Lys Leu₂₆₅ Glu Ile Lys Thr Thr₂₇₀ Thr Pro
 Ala Pro Arg₂₇₅ Pro Pro Thr Pro Ala₂₈₀ Pro Thr Ile Ala Ser₂₈₅ Gln Pro Leu
 Ser Leu₂₉₀ Arg Pro Glu Ala Cys₂₉₅ Arg Pro Ala Ala Gly₃₀₀ Gly Ala Val His
 Thr Arg Gly Leu Asp Phe₃₁₀ Ala Cys Asp Ile Tyr₃₁₅ Ile Trp Ala Pro Leu₃₂₀
 Ala Gly Thr Cys Gly₃₂₅ Val Leu Leu Leu Ser₃₃₀ Leu Val Ile Thr Leu₃₃₅ Tyr
 Cys Lys Arg Gly₃₄₀ Arg Lys Lys Leu Leu₃₄₅ Tyr Ile Phe Lys Gln₃₅₀ Pro Phe

Met Arg Pro Val Gln Thr Thr Gln Glu Glu ^{-SL}Asp Gly Cys Ser Cys Arg
355 360 365

Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser
370 375 380

Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr
385 390 395 400

Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys
405 410 415

Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn
420 425 430

Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu
435 440 445

Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly
450 455 460

His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr
465 470 475 480

Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
485 490

<210> 928
<211> 247
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 928
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr
20 25 30

Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45

Gly Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Gln Ser Ser Leu Lys
50 55 60

Ser Arg Val Thr Ile Ser Lys Asp Asn Ser Lys Asn Gln Val Ser Leu
65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
Page 697

85 90 _SL 95

Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Met
130 135 140

Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr
145 150 155 160

Leu Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr Leu Asn Trp Tyr
165 170 175

Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr His Thr Ser
180 185 190

Arg Leu His Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly
195 200 205

Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
210 215 220

Val Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gln
225 230 235 240

Gly Thr Lys Leu Glu Ile Lys
245

<210> 929
<211> 828
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 929
atggcactgc ctgtcactgc cctcctgctg cctctggccc tccttctgca tgccgccagg 60
ccccaagtcc agctgcaaga gtcaggaccc ggactggtga agccgtctga gactctctca 120
ctgacttgta ccgtcagcgg cgtgtccctc cccgactacg gagtgtcatg gatccgcca 180
cctcccggga aagggcttga atggattggt gtcactctggg gttctgaaac cacctactac 240
cagtcttccc tgaagtccag ggtgaccatc agcaaggata attccaagaa ccaggtcagc 300
cttaagctgt catctgtgac cgctgctgac accgccgtgt attactgcgc caagcactac 360
tattacggag gaagctacgc tatggactat tggggacagg gcactctcgt gactgtgagc 420

_SL

```

agcggcggtg gaggggtctgg aggtggagga tccggtggtg gtgggtcagg cggaggaggg      480
agcgagattg tgatgactca gtcaccagcc accctttctc tttcaccg cgagagagca      540
accctgagct gtagagccag ccaggacatt tctaagtacc tcaactggta tcagcaaaaa      600
ccggggcagg cccctcgctt cctgatctac catacctcac gccttcactc tggtatcccc      660
gctcggttta gcggatcagg atctggtacc gactacactc tgaccatttc cagcctgcag      720
ccagaagatt tcgcagtgtg tttctgccag cagggcaata cccttcctta caccttcggt      780
cagggaaacca agctcgaaat caagcaccat caccatcatc atcaccac      828

```

<210> 930
 <211> 276
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 930
 Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
 1 5 10 15

His Ala Ala Arg Pro Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu
 20 25 30

Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Val
 35 40 45

Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys
 50 55 60

Gly Leu Glu Trp Ile Gly Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr
 65 70 75 80

Gln Ser Ser Leu Lys Ser Arg Val Thr Ile Ser Lys Asp Asn Ser Lys
 85 90 95

Asn Gln Val Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala
 100 105 110

Val Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met
 115 120 125

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
 130 135 140

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 145 150 155 160

Ser Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro
 165 170 175

_SL

Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys
180 185 190

Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
195 200 205

Ile Tyr His Thr Ser Arg Leu His Ser Gly Ile Pro Ala Arg Phe Ser
210 215 220

Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln
225 230 235 240

Pro Glu Asp Phe Ala Val Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro
245 250 255

Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys His His His His
260 265 270

His His His His
275

<210> 931
<211> 1473
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 931
atggctctgc ccgtgaccgc actcctcctg ccactggctc tgctgcttca cgccgctcgc 60
ccacaagtcc agcttcaaga atcagggcct ggtctggtga agccatctga gactctgtcc 120
ctcacttgca ccgtgagcgg agtgtccctc ccagactacg gagtgagctg gattagacag 180
cctcccggaaggaggactgga gtggatcgga gtgatttggg gtagcgaaac cacttactat 240
caatcttccc tgaagtcacg ggtcaccatt tcaaaggata actcaaagaa tcaagtgagc 300
ctcaagctct catcagtcac cgccgctgac accgccgtgt attactgtgc caagcattac 360
tactatggag ggtcctacgc catggactac tggggccagg gaactctggt cactgtgtca 420
tctggtggag gaggtagcgg aggaggcggg agcgggtggag gtggctccgg aggcgggtggg 480
tcagaaatcg tgatgacca gagccctgca accctgtccc tttctcccgg ggaacgggct 540
accctttctt gtcgggcac acaagatatc taaaatacc tcaattggta tcaacagaag 600
ccgggacagg cccctaggct tcttatctac cacacctctc gcctgcatag cgggattccc 660
gcacgcttta gcgggtctgg aagcgggacc gactacactc tgaccatctc atctctccag 720
cccgaggact tcgccgtcta cttctgccag cagggttaaca ccctgccgta caccttcggc 780
cagggcacca agctttagat caaaaccact actcccgctc caaggccacc caccctgcc 840

_SL

ccgaccatcg cctctcagcc gctttccctg cgtccggagg catgtagacc cgcagctggt 900
ggggccgtgc ataccggggg tcttgacttc gcctgcgata tctacatttg ggcccctctg 960
gctggtactt gcggggtcct gctgctttca ctcgtgatca ctctttactg taagcgcggt 1020
cggaagaagc tgctgtacat ctttaagcaa cccttcatga ggctgtgca gactactcaa 1080
gaggaggacg gctgttcacg ccggttccca gaggaggagg aaggcggtg cgaactgcgc 1140
gtgaaattca gccgcagcgc agatgctcca gcctacaagc aggggcagaa ccagctctac 1200
aacgaactca atcttggtcg gagagaggag tacgacgtgc tggacaagcg gagaggacgg 1260
gaccagaaa tgggcgggaa gccgcgcaga aagaatcccc aagagggcct gtacaacgag 1320
ctccaaaagg ataagatggc agaagcctat agcgagattg gtatgaaagg ggaacgcaga 1380
agaggcaaag gccacgacgg actgtaccag ggactcagca ccgccaccaa ggacacctat 1440
gacgctcttc acatgcaggc cctgccgcct cg 1473

<210> 932

<211> 491

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 932

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu
20 25 30

Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Val
35 40 45

Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys
50 55 60

Gly Leu Glu Trp Ile Gly Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr
65 70 75 80

Gln Ser Ser Leu Lys Ser Arg Val Thr Ile Ser Lys Asp Asn Ser Lys
85 90 95

Asn Gln Val Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala
100 105 110

Val Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met
115 120 125

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly

130					135					_SL		140				
Gly 145	Ser	Gly	Gly	Gly	Gly 150	Ser	Gly	Gly	Gly	Gly 155	Ser	Gly	Gly	Gly	Gly 160	
Ser	Glu	Ile	Val	Met 165	Thr	Gln	Ser	Pro	Ala 170	Thr	Leu	Ser	Leu	Ser 175	Pro	
Gly	Glu	Arg	Ala 180	Thr	Leu	Ser	Cys	Arg 185	Ala	Ser	Gln	Asp	Ile 190	Ser	Lys	
Tyr	Leu	Asn 195	Trp	Tyr	Gln	Gln	Lys 200	Pro	Gly	Gln	Ala	Pro 205	Arg	Leu	Leu	
Ile	Tyr 210	His	Thr	Ser	Arg	Leu 215	His	Ser	Gly	Ile	Pro 220	Ala	Arg	Phe	Ser	
Gly 225	Ser	Gly	Ser	Gly	Thr 230	Asp	Tyr	Thr	Leu	Thr 235	Ile	Ser	Ser	Leu	Gln 240	
Pro	Glu	Asp	Phe	Ala 245	Val	Tyr	Phe	Cys	Gln 250	Gln	Gly	Asn	Thr	Leu 255	Pro	
Tyr	Thr	Phe	Gly 260	Gln	Gly	Thr	Lys	Leu 265	Glu	Ile	Lys	Thr	Thr 270	Thr	Pro	
Ala	Pro	Arg 275	Pro	Pro	Thr	Pro	Ala 280	Pro	Thr	Ile	Ala	Ser 285	Gln	Pro	Leu	
Ser	Leu 290	Arg	Pro	Glu	Ala	Cys 295	Arg	Pro	Ala	Ala	Gly 300	Gly	Ala	Val	His	
Thr 305	Arg	Gly	Leu	Asp	Phe 310	Ala	Cys	Asp	Ile	Tyr 315	Ile	Trp	Ala	Pro	Leu 320	
Ala	Gly	Thr	Cys	Gly 325	Val	Leu	Leu	Leu	Ser 330	Leu	Val	Ile	Thr	Leu 335	Tyr	
Cys	Lys	Arg	Gly 340	Arg	Lys	Lys	Leu	Leu 345	Tyr	Ile	Phe	Lys	Gln 350	Pro	Phe	
Met	Arg	Pro 355	Val	Gln	Thr	Thr	Gln 360	Glu	Glu	Asp	Gly	Cys 365	Ser	Cys	Arg	
Phe	Pro 370	Glu	Glu	Glu	Glu	Gly 375	Gly	Cys	Glu	Leu	Arg 380	Val	Lys	Phe	Ser	
Arg 385	Ser	Ala	Asp	Ala	Pro 390	Ala	Tyr	Lys	Gln	Gly 395	Gln	Asn	Gln	Leu	Tyr 400	
Asn	Glu	Leu	Asn	Leu	Gly	Arg	Arg	Glu	Glu	Tyr	Asp	Val	Leu	Asp	Lys	

SL															
405								410				415			
Arg	Arg	Gly	Arg	Asp	Pro	Glu	Met	Gly	Gly	Lys	Pro	Arg	Arg	Lys	Asn
			420					425					430		
Pro	Gln	Glu	Gly	Leu	Tyr	Asn	Glu	Leu	Gln	Lys	Asp	Lys	Met	Ala	Glu
		435					440					445			
Ala	Tyr	Ser	Glu	Ile	Gly	Met	Lys	Gly	Glu	Arg	Arg	Arg	Gly	Lys	Gly
	450					455					460				
His	Asp	Gly	Leu	Tyr	Gln	Gly	Leu	Ser	Thr	Ala	Thr	Lys	Asp	Thr	Tyr
465					470					475					480
Asp	Ala	Leu	His	Met	Gln	Ala	Leu	Pro	Pro	Arg					
				485				490							

```
<210> 933
<211> 247
<212> PRT
<213> Artificial Sequence
```

```
<220>  
<221> source  
<223> /note="Description of Artificial Sequence: Synthetic  
polypeptide"
```

<400> 933
Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr His Thr Ser Arg Leu His Ser Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser
100 105 110

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln
115 120 125

Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr
130 135 140

_SL

Leu Ser Leu Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly
145 150 155 160

Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly
165 170 175

Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ser Leu Lys Ser
180 185 190

Arg Val Thr Ile Ser Lys Asp Asn Ser Lys Asn Gln Val Ser Leu Lys
195 200 205

Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Lys
210 215 220

His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly
225 230 235 240

Thr Leu Val Thr Val Ser Ser
245

<210> 934
<211> 828
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 934
atggccctcc cagtgaccgc tctgctgctg cctctcgac ttcttctcca tgccgctcgg 60
cctgagatcg tcatgaccca aagccccgct accctgtccc tgtcaccgg cgagagggca 120
accctttcat gcagggccag ccaggacatt tctaagtacc tcaactggta tcagcagaag 180
ccagggcagg ctctcgcct gctgatctac cacaccagcc gcctccacag cggatatccc 240
gccagatttt ccgggagcgg gtctggaacc gactacaccc tcaccatctc ttctctgcag 300
cccgaggatt tcgccgtcta tttctgccag caggggaata ctctgccgta caccttcggt 360
caaggtacca agctggaaat caagggaggc ggaggatcag gcggtggcgg aagcggagga 420
ggtggctccg gaggaggagg ttccaagtg cagcttcaag aatcaggacc cggacttggt 480
aagccatcag aaaccctctc cctgacttgt accgtgtccg gtgtgagcct ccccgactac 540
ggagtctctt ggattcgcca gcctccgggg aagggcttg aatggattgg ggtgatttgg 600
ggatcagaga ctacttacta caattcatca cttaagtcac gggtcaccat cagcaaagat 660
aatagcaaga accaagtgtc acttaagctg tcatctgtga ccgccgctga caccgccgtg 720
tactatttg ccaaacatta ctattacgga gggctttatg ctatggacta ctggggacag 780
gggaccctgg tgactgtctc tagccatcac catcaccacc atcatcac 828

_SL

<210> 935
<211> 276
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 935
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu
20 25 30

Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln
35 40 45

Asp Ile Ser Lys Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gln Ala
50 55 60

Pro Arg Leu Leu Ile Tyr His Thr Ser Arg Leu His Ser Gly Ile Pro
65 70 75 80

Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile
85 90 95

Ser Ser Leu Gln Pro Glu Asp Phe Ala Val Tyr Phe Cys Gln Gln Gly
100 105 110

Asn Thr Leu Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
130 135 140

Gly Gly Gly Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val
145 150 155 160

Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Val Ser
165 170 175

Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly
180 185 190

Leu Glu Trp Ile Gly Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Asn
195 200 205

Ser Ser Leu Lys Ser Arg Val Thr Ile Ser Lys Asp Asn Ser Lys Asn
210 215 220

_SL

Gln Val Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val
225 230 235 240

Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met Asp
245 250 255

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser His His His His
260 265 270

His His His His
275

<210> 936

<211> 1473

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 936

```
atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg      60
cccgaaattg tgatgacca gtcacccgcc actcttagcc tttcaccgg tgagcgcgca      120
accctgtctt gcagagcctc ccaagacatc tcaaaatacc ttaattggta tcaacagaag      180
cccgacaggg ctctctgcct tctgatctac cacaccagcc ggctccattc tggaatccct      240
gccaggttca gcggtagcgg atctgggacc gactacaccc tcactatcag ctactgcag      300
ccagaggact tcgctgtcta tttctgtcag caaggggaaca ccctgcccta cacctttgga      360
cagggcacca agctcgagat taaaggtgga ggtggcagcg gaggaggtgg gtccggcggt      420
ggaggaagcg gaggcggtgg gagccaggtc caactccaag aaagcggacc gggctctgtg      480
aagccatcag aaactctttc actgacttgt actgtgagcg gagtgtctct ccccgattac      540
ggggtgtctt ggatcagaca gccaccgggg aagggctctg aatggattgg agtgatttgg      600
ggctctgaga ctacttacta caactcatcc ctcaagtcac gcgtcaccat ctcaaaggac      660
aactctaaga atcaggtgtc actgaaactg tcatctgtga ccgcagccga caccgccgtg      720
tactattgcg ctaagcatta ctattatggc gggagctacg caatggatta ctggggacag      780
ggtactctgg tcaccgtgtc cagcaccact accccagcac cgaggccacc caccgccgt      840
cctaccatcg cctcccagcc tctgtccctg cgtccggagg catgtagacc cgcagctggt      900
ggggccgtgc ataccggggg tcttgacttc gcctgcgata tctacatttg ggcccctctg      960
gctggtactt gcggggctct gctgctttca ctctgtatca ctctttactg taagcgcggt     1020
cggaagaagc tgctgtacat ctttaagcaa cccttcatga ggcctgtgca gactactcaa     1080
gaggaggacg gctgttcatg ccggttccca gaggaggagg aaggcggctg cgaactgcgc     1140
gtgaaattca gccgcagcgc agatgctcca gcctacaagc aggggcagaa ccagctctac     1200
```

aacgaactca atcttggtcg gagagaggag tacgacgtgc tggacaagcg gagaggacgg 1260
 gaccagaaa tgggcgggaa gccgcgcaga aagaatcccc aagagggcct gtacaacgag 1320
 ctccaaaagg ataagatggc agaagcctat agcgagattg gtatgaaagg ggaacgcaga 1380
 agaggcaaag gccacgacgg actgtaccag ggactcagca ccgccaccaa ggacacctat 1440
 gacgctcttc acatgcaggc cctgccgcct cgg 1473

<210> 937
 <211> 491
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 937
 Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
 1 5 10 15

His Ala Ala Arg Pro Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu
 20 25 30

Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln
 35 40 45

Asp Ile Ser Lys Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gln Ala
 50 55 60

Pro Arg Leu Leu Ile Tyr His Thr Ser Arg Leu His Ser Gly Ile Pro
 65 70 75 80

Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile
 85 90 95

Ser Ser Leu Gln Pro Glu Asp Phe Ala Val Tyr Phe Cys Gln Gln Gly
 100 105 110

Asn Thr Leu Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
 115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 130 135 140

Gly Gly Gly Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val
 145 150 155 160

Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Val Ser
 165 170 175

Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly
 180 185 190

_SL

Leu Glu Trp Ile Gly Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Asn
195 200 205

Ser Ser Leu Lys Ser Arg Val Thr Ile Ser Lys Asp Asn Ser Lys Asn
210 215 220

Gln Val Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val
225 230 235 240

Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met Asp
245 250 255

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Thr Thr Thr Pro
260 265 270

Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu
275 280 285

Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His
290 295 300

Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu
305 310 315 320

Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr
325 330 335

Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe
340 345 350

Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg
355 360 365

Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser
370 375 380

Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr
385 390 395 400

Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys
405 410 415

Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn
420 425 430

Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu
435 440 445

Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly
450 455 460

_SL

His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr
465 470 475 480

Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
485 490

<210> 938

<211> 247

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 938

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr
20 25 30

Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45

Gly Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ser Leu Lys
50 55 60

Ser Arg Val Thr Ile Ser Lys Asp Asn Ser Lys Asn Gln Val Ser Leu
65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Met
130 135 140

Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr
145 150 155 160

Leu Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr Leu Asn Trp Tyr
165 170 175

Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr His Thr Ser
180 185 190

_SL

Arg Leu His Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly
195 200 205

Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
210 215 220

Val Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gln
225 230 235 240

Gly Thr Lys Leu Glu Ile Lys
245

<210> 939
<211> 828
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 939
atggcactgc ctgtcactgc cctcctgctg cctctggccc tccttctgca tgccgccagg 60
ccccaagtcc agctgcaaga gtcaggaccc ggactggtga agccgtctga gactctctca 120
ctgacttgta ccgtcagcgg cgtgtccctc cccgactacg gagtgtcatg gatccgccaa 180
cctcccggga aagggcttga atggattggt gtcactctggg gttctgaaac cacctactac 240
aactcttccc tgaagtccag ggtgaccatc agcaaggata attccaagaa ccaggtcagc 300
cttaagctgt catctgtgac cgctgctgac accgccgtgt attactgcgc caagcactac 360
tattacggag gaagctacgc tatggactat tggggacagg gcactctcgt gactgtgagc 420
agcggcggtg gaggtcttg aggtggagga tccggtggtg gtgggtcagg cggaggaggg 480
agcgagattg tgatgactca gtcaccagcc accctttctc tttcaccgg cgagagagca 540
accctgagct gtagagccag ccaggacatt tctaagtacc tcaactggta tcagcaaaaa 600
ccggggcagg cccctcgcct cctgatctac catacctcac gccttcactc tggtatcccc 660
gctcggttta gcggatcagg atctggtacc gactacactc tgaccatttc cagcctgcag 720
ccagaagatt tcgcagtgt tttctgccag cagggcaata cccttcctta caccttcggt 780
caggaacca agctcgaaat caagcacat caccatcatc accacat 828

<210> 940
<211> 276
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 940

Met Ala Leu Pro Val Thr Ala Leu Leu Leu^{-SL} Pro Leu Ala Leu Leu Leu
1 5 10 15
His Ala Ala Arg Pro Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu
20 25 30
Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Val
35 40 45
Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys
50 55 60
Gly Leu Glu Trp Ile Gly Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr
65 70 75 80
Asn Ser Ser Leu Lys Ser Arg Val Thr Ile Ser Lys Asp Asn Ser Lys
85 90 95
Asn Gln Val Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala
100 105 110
Val Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met
115 120 125
Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
130 135 140
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
145 150 155 160
Ser Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro
165 170 175
Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys
180 185 190
Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
195 200 205
Ile Tyr His Thr Ser Arg Leu His Ser Gly Ile Pro Ala Arg Phe Ser
210 215 220
Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln
225 230 235 240
Pro Glu Asp Phe Ala Val Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro
245 250 255
Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys His His His His
260 265 270

His His His His
275

<210> 941
<211> 1473
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

```

<400> 941
atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg      60
cccgaaattg tgatgaccca gtcacccgcc actcttagcc tttcaccggt tgagcgcgca      120
accctgtctt gcagagcctc ccaagacatc tcaaaatacc ttaattggta tcaacagaag      180
cccgacaggg ctctcgcctt tctgatctac cacaccagcc ggctccattc tggaatccct      240
gccaggttca gcggtagcgg atctgggacc gactacaccc tcactatcag ctactgcag      300
ccagaggact tcgctgtcta tttctgtcag caaggggaaca ccctgcccta cacctttgga      360
cagggcacca agctcgagat taaaggtgga ggtggcagcg gaggagggtg gtccggcggt      420
ggaggaagcg gaggcggtgg gagccaggtc caactccaag aaagcggacc gggctcttgtg      480
aagccatcag aaactctttc actgacttgt actgtgagcg gagtgtctct ccccgattac      540
ggggtgtctt ggatcagaca gccaccgggg aagggctctg aatggattgg agtgatttgg      600
ggctctgaga ctacttacta caactcatcc ctcaagtcac gcgtcaccat ctcaaaggac      660
aactctaaga atcaggtgtc actgaaactg tcatctgtga ccgcagccga caccgccgtg      720
tactattgcg ctaagcatta ctattatggc gggagctacg caatggatta ctggggacag      780
ggtactctgg tcaccgtgtc cagcaccact accccagcac cgaggccacc caccgccggt      840
cctaccatcg cctcccagcc tctgtccctg cgtccggagg catgtagacc cgcagctggt      900
ggggccgtgc ataccgggg tcttgacttc gcctgcgata tctacatttg ggcccctctg      960
gctggtactt gcggggtcct gctgctttca ctctgtatca ctctttactg taagcgcggt     1020
cggaagaagc tgctgtacat ctttaagcaa cccttcatga ggcctgtgca gactactcaa     1080
gaggaggacg gctgttcatt ccggttccca gaggaggagg aaggcggttg cgaactgcgc     1140
gtgaaattca gccgcagcgc agatgctcca gcctacaagc aggggcagaa ccagctctac     1200
aacgaactca atcttggtcg gagagaggag tacgacgtgc tggacaagcg gagaggacgg     1260
gaccagaaa tgggcgggaa gccgcgcaga aagaatcccc aagagggcct gtacaacgag     1320
ctccaaaagg ataagatggc agaagcctat agcgagattg gtatgaaagg ggaacgcaga     1380
agaggcaaag gccacgacgg actgtaccag ggactcagca ccgccaccaa ggacacctat     1440
gacgctcttc acatgcaggc cctgccgcct cgg                                     1473

```

<210> 942
<211> 491

_SL

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 942

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu
20 25 30

Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln
35 40 45

Asp Ile Ser Lys Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gln Ala
50 55 60

Pro Arg Leu Leu Ile Tyr His Thr Ser Arg Leu His Ser Gly Ile Pro
65 70 75 80

Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile
85 90 95

Ser Ser Leu Gln Pro Glu Asp Phe Ala Val Tyr Phe Cys Gln Gln Gly
100 105 110

Asn Thr Leu Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
130 135 140

Gly Gly Gly Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val
145 150 155 160

Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Val Ser
165 170 175

Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly
180 185 190

Leu Glu Trp Ile Gly Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Asn
195 200 205

Ser Ser Leu Lys Ser Arg Val Thr Ile Ser Lys Asp Asn Ser Lys Asn
210 215 220

Gln Val Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val
225 230 235 240

_SL

Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met Asp
245 250 255

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Thr Thr Thr Pro
260 265 270

Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu
275 280 285

Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His
290 295 300

Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu
305 310 315 320

Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr
325 330 335

Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe
340 345 350

Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg
355 360 365

Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser
370 375 380

Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr
385 390 395 400

Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys
405 410 415

Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn
420 425 430

Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu
435 440 445

Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly
450 455 460

His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr
465 470 475 480

Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
485 490

<210> 943

<211> 242

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 943

Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
 35 40 45

Tyr His Thr Ser Arg Leu His Ser Gly Ile Pro Ala Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Val Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser
 100 105 110

Gly Gly Gly Gly Ser Gly Gly Gly Ser Gln Val Gln Leu Gln Glu
 115 120 125

Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys
 130 135 140

Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg
 145 150 155 160

Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Val Ile Trp Gly Ser
 165 170 175

Glu Thr Thr Tyr Tyr Asn Ser Ser Leu Lys Ser Arg Val Thr Ile Ser
 180 185 190

Lys Asp Asn Ser Lys Asn Gln Val Ser Leu Lys Leu Ser Ser Val Thr
 195 200 205

Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly
 210 215 220

Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
 225 230 235 240

Ser Ser

<210> 944
<211> 813
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 944
atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60
cccgaaattg tgatgaccca gtcacccgcc actcttagcc tttcacccgg tgagcgcgca 120
accctgtctt gcagagcctc ccaagacatc tcaaaatacc ttaattggta tcaacagaag 180
cccggacagg ctctctgcct tctgatctac cacaccagcc ggctccattc tggaatccct 240
gccaggttca gcggtagcgg atctgggacc gactacaccc tcactatcag ctactgcag 300
ccagaggact tcgctgtcta tttctgtcag caaggggaaca ccctgcccta cacctttgga 360
cagggcacca agctcgagat taaaggtgga ggtggcagcg gaggaggtgg gtccggcggt 420
ggaggaagcc aggtccaact ccaagaaagc ggaccgggtc ttgtgaagcc atcagaaact 480
ctttcactga cttgtactgt gagcggagtg tctctccccg attacgggggt gtcttggatc 540
agacagccac cggggaaggg tctggaatgg attggagtga tttggggctc tgagactact 600
tactacaatt catccctcaa gtcacgcgtc accatctcaa aggacaactc taagaatcag 660
gtgtcactga aactgtcatc tgtgaccgca gccgacaccg ccgtgtacta ttgcgctaag 720
cattactatt atggcgggag ctacgcaatg gattactggg gacaggggtac tctggtcacc 780
gtgtccagcc accaccatca tcaccatcac cat 813

<210> 945
<211> 271
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 945
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu
20 25 30

Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln
35 40 45

Asp Ile Ser Lys Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gln Ala
Page 716

										_SL					
	50					55					60				
Pro 65	Arg	Leu	Leu	Ile	Tyr 70	His	Thr	Ser	Arg	Leu 75	His	Ser	Gly	Ile	Pro 80
Ala	Arg	Phe	Ser	Gly 85	Ser	Gly	Ser	Gly	Thr 90	Asp	Tyr	Thr	Leu	Thr 95	Ile
Ser	Ser	Leu	Gln 100	Pro	Glu	Asp	Phe	Ala 105	Val	Tyr	Phe	Cys	Gln 110	Gln	Gly
Asn	Thr	Leu 115	Pro	Tyr	Thr	Phe	Gly 120	Gln	Gly	Thr	Lys	Leu 125	Glu	Ile	Lys
Gly	Gly 130	Gly	Gly	Ser	Gly	Gly 135	Gly	Gly	Ser	Gly	Gly 140	Gly	Gly	Ser	Gln
Val 145	Gln	Leu	Gln	Glu	Ser 150	Gly	Pro	Gly	Leu	Val 155	Lys	Pro	Ser	Glu	Thr 160
Leu	Ser	Leu	Thr	Cys 165	Thr	Val	Ser	Gly	Val 170	Ser	Leu	Pro	Asp	Tyr 175	Gly
Val	Ser	Trp	Ile 180	Arg	Gln	Pro	Pro	Gly 185	Lys	Gly	Leu	Glu	Trp 190	Ile	Gly
Val	Ile	Trp 195	Gly	Ser	Glu	Thr	Thr 200	Tyr	Tyr	Asn	Ser	Ser 205	Leu	Lys	Ser
Arg	Val 210	Thr	Ile	Ser	Lys	Asp 215	Asn	Ser	Lys	Asn	Gln 220	Val	Ser	Leu	Lys
Leu 225	Ser	Ser	Val	Thr	Ala 230	Ala	Asp	Thr	Ala	Val 235	Tyr	Tyr	Cys	Ala	Lys 240
His	Tyr	Tyr	Tyr	Gly 245	Gly	Ser	Tyr	Ala	Met 250	Asp	Tyr	Trp	Gly	Gln 255	Gly
Thr	Leu	Val	Thr 260	Val	Ser	Ser	His	His 265	His	His	His	His	His	His 270	His

```
<210> 946
<211> 1473
<212> DNA
<213> Artificial Sequence
```

```
<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"
```

<400> 946
atggctctgc ccgtagaccgc actcctcctg ccactggctc tgctgcttca cgccgctcgc

_SL

ccacaagtcc agcttcaaga atcagggcct ggtctgtgtga agccatctga gactctgtcc	120
ctcacttgca ccgtgagcgg agtgtccctc ccagactacg gagtgagctg gattagacag	180
cctcccggaa agggactgga gtggatcgga gtgatttggg gtagcgaaac cacttactat	240
aactcttccc tgaagtcacg ggtcaccatt tcaaaggata actcaaagaa tcaagtgagc	300
ctcaagctct catcagtcac cgccgctgac accgccgtgt attactgtgc caagcattac	360
tactatggag ggtcctacgc catggactac tggggccagg gaactctggt cactgtgtca	420
tctggtggag gaggtagcgg aggagggcgg agcgggtggag gtggctccgg aggtggcgga	480
agcgaaatcg tgatgacca gagccctgca accctgtccc tttctcccgg ggaacgggct	540
accctttctt gtcgggcatc acaagatatc tcaaaatacc tcaattggta tcaacagaag	600
ccgggacagg cccctaggct tcttatctac cacacctctc gcctgcatag cgggattccc	660
gcacgcttta gcgggtcttg aagcgggacc gactacactc tgaccatctc atctctccag	720
cccaggact tcgccgtcta cttctgccag cagggtgaaca ccctgccgta caccttcggc	780
cagggcacca agcttgagat caaaaccact actcccgctc caaggccacc caccctgcc	840
ccgaccatcg cctctcagcc gctttccctg cgtccggagg catgtagacc cgcagctggt	900
ggggccgtgc ataccgggg tcttgacttc gcctgcgata tctacatttg ggcccctctg	960
gctggtactt gcggggtcct gctgctttca ctcgtgatca ctctttactg taagcgcggt	1020
cggaagaagc tgctgtacat ctttaagcaa cccttcatga ggctgtgca gactactcaa	1080
gaggaggacg gctgttcacg ccggttccca gaggaggagg aaggcggctg cgaactgcgc	1140
gtgaaattca gccgcagcgc agatgctcca gcctacaagc aggggcagaa ccagctctac	1200
aacgaactca atcttggtcg gagagaggag tacgacgtgc tggacaagcg gagaggacgg	1260
gaccagaaa tgggcgggaa gccgcgcaga aagaatcccc aagagggcct gtacaacgag	1320
ctccaaaagg ataagatggc agaagcctat agcgagattg gtatgaaagg ggaacgcaga	1380
agaggcaaag gccacgacgg actgtaccag ggactcagca ccgccaccaa ggacacctat	1440
gacgctcttc acatgcaggc cctgccgcct cgg	1473

<210> 947

<211> 491

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 947

Met	Ala	Leu	Pro	Val	Thr	Ala	Leu	Leu	Leu	Pro	Leu	Ala	Leu	Leu	Leu
1				5				10						15	

His	Ala	Ala	Arg	Pro	Gln	Val	Gln	Leu	Gln	Glu	Ser	Gly	Pro	Gly	Leu
			20					25					30		

Val Lys Pro Ser Glu Thr Leu Ser Leu Thr ^{SL}Cys Thr Val Ser Gly Val
 35 40 45
 Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys
 50 55 60
 Gly Leu Glu Trp Ile Gly Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr
 65 70 75 80
 Asn Ser Ser Leu Lys Ser Arg Val Thr Ile Ser Lys Asp Asn Ser Lys
 85 90 95
 Asn Gln Val Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala
 100 105 110
 Val Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met
 115 120 125
 Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
 130 135 140
 Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 145 150 155 160
 Ser Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro
 165 170 175
 Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys
 180 185 190
 Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
 195 200 205
 Ile Tyr His Thr Ser Arg Leu His Ser Gly Ile Pro Ala Arg Phe Ser
 210 215 220
 Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln
 225 230 235 240
 Pro Glu Asp Phe Ala Val Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro
 245 250 255
 Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Thr Thr Thr Pro
 260 265 270
 Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu
 275 280 285
 Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His
 290 295 300

Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile ^{-SL} Tyr Ile Trp Ala Pro Leu
 305 310 315 320
 Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr
 325 330 335
 Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe
 340 345 350
 Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg
 355 360 365
 Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser
 370 375 380
 Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr
 385 390 395 400
 Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys
 405 410 415
 Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn
 420 425 430
 Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu
 435 440 445
 Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly
 450 455 460
 His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr
 465 470 475 480
 Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
 485 490

<210> 948
 <211> 242
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 948
 Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
 1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr
 20 25 30

Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
 Page 720

35				40				_SL				45			
Gly	Val 50	Ile	Trp	Gly	Ser	Glu 55	Thr	Thr	Tyr	Tyr	Asn 60	Ser	Ser	Leu	Lys
Ser 65	Arg	Val	Thr	Ile	Ser 70	Lys	Asp	Asn	Ser	Lys 75	Asn	Gln	Val	Ser	Leu 80
Lys	Leu	Ser	Ser	Val 85	Thr	Ala	Ala	Asp	Thr 90	Ala	Val	Tyr	Tyr	Cys 95	Ala
Lys	His	Tyr	Tyr 100	Tyr	Gly	Gly	Ser	Tyr 105	Ala	Met	Asp	Tyr	Trp 110	Gly	Gln
Gly	Thr	Leu 115	Val	Thr	Val	Ser	Ser 120	Gly	Gly	Gly	Gly	Ser 125	Gly	Gly	Gly
Gly	Ser 130	Gly	Gly	Gly	Gly	Ser 135	Glu	Ile	Val	Met	Thr 140	Gln	Ser	Pro	Ala
Thr 145	Leu	Ser	Leu	Ser	Pro 150	Gly	Glu	Arg	Ala	Thr 155	Leu	Ser	Cys	Arg	Ala 160
Ser	Gln	Asp	Ile	Ser 165	Lys	Tyr	Leu	Asn	Trp 170	Tyr	Gln	Gln	Lys	Pro 175	Gly
Gln	Ala	Pro	Arg 180	Leu	Leu	Ile	Tyr	His 185	Thr	Ser	Arg	Leu	His 190	Ser	Gly
Ile	Pro	Ala 195	Arg	Phe	Ser	Gly	Ser 200	Gly	Ser	Gly	Thr	Asp 205	Tyr	Thr	Leu
Thr	Ile 210	Ser	Ser	Leu	Gln	Pro 215	Glu	Asp	Phe	Ala	Val 220	Tyr	Phe	Cys	Gln
Gln 225	Gly	Asn	Thr	Leu	Pro 230	Tyr	Thr	Phe	Gly	Gln 235	Gly	Thr	Lys	Leu	Glu 240
Ile	Lys														

_SL

```

ccacaagtcc agcttcaaga atcagggcct ggtctggtga agccatctga gactctgtcc      120
ctcacttgca ccgtgagcgg agtgtccctc ccagactacg gagtgagctg gattagacag      180
cctcccggaa agggactgga gtggatcgga gtgatttggg gtagcgaaac cacttactat      240
aactcttccc tgaagtcacg ggtcaccatt tcaaaggata actcaaagaa tcaagtgagc      300
ctcaagctct catcagtcac cgccgctgac accgccgtgt attactgtgc caagcattac      360
tactatggag ggtcctacgc catggactac tggggccagg gaactctggt cactgtgtca      420
tctggtggag gaggtagcgg aggaggcggg agcggtgagg gtggctccga aatcgtgatg      480
acccagagcc ctgcaaccct gtccctttct cccggggaac gggctaccct ttcttgtcgg      540
gcatcacaag atatctcaaa atacctcaat tggtatcaac agaagccggg acaggcccct      600
aggcttctta tctaccacac ctctcgctg catagcggga ttcccgcacg ctttagcggg      660
tctggaagcg ggaccgacta cactctgacc atctcatctc tccagcccga ggacttcgcc      720
gtctacttct gccagcaggg taacaccctg ccgtacacct tcggccaggg caccaagctt      780
gagatcaaac atcaccacca tcatcaccat cac                                  813

```

<210> 950
 <211> 271
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 950
 Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
 1 5 10 15

His Ala Ala Arg Pro Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu
 20 25 30

Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Val
 35 40 45

Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys
 50 55 60

Gly Leu Glu Trp Ile Gly Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr
 65 70 75 80

Asn Ser Ser Leu Lys Ser Arg Val Thr Ile Ser Lys Asp Asn Ser Lys
 85 90 95

Asn Gln Val Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala
 100 105 110

Val Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met
 115 120 125

_SL

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
130 135 140

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Met
145 150 155 160

Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr
165 170 175

Leu Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr Leu Asn Trp Tyr
180 185 190

Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr His Thr Ser
195 200 205

Arg Leu His Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly
210 215 220

Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
225 230 235 240

Val Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gln
245 250 255

Gly Thr Lys Leu Glu Ile Lys His His His His His His His His
260 265 270

<210> 951
<211> 1458
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 951
atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60
cccgaattg tgatgacca gtcacccgcc actcttagcc tttcaccgg tgagcgcgca 120
accctgtctt gcagagcctc ccaagacatc tcaaaatacc ttaattggta tcaacagaag 180
cccggacagg ctctctgcct tctgatctac cacaccagcc ggctccattc tggaatccct 240
gccaggttca gcggtagcgg atctgggacc gactacaccc tcactatcag ctactgcag 300
ccagaggact tcgctgtcta tttctgtcag caaggaaca ccctgcccta cacctttgga 360
cagggcacca agctcgagat taaaggtgga ggtggcagcg gaggaggtgg gtccggcggt 420
ggaggaagcc aggtccaact ccaagaaagc ggaccgggtc ttgtgaagcc atcagaaact 480
ctttactga cttgtactgt gagcggagtg tctctcccg attacggggt gtcttgatc 540
agacagccac cggggaaggg tctggaatgg attggagtga tttggggctc tgagactact 600

_SL

tactacaact catccctcaa gtcacgcgtc accatctcaa aggacaactc taagaatcag 660
gtgtcactga aactgtcatc tgtgaccgca gccgacaccg ccgtgtacta ttgcgctaag 720
cattactatt atggcgggag ctacgcaatg gattactggg gacagggtac tctggtcacc 780
gtgtccagca ccactacccc agcaccgagg ccacccaccc cggctcctac catcgctcc 840
cagcctctgt ccctgcgtcc ggaggcatgt agaccgcgag ctgggtggggc cgtgcatacc 900
cggggtcttg acttcgcctg cgatatctac atttggggccc ctctggctgg tacttgcggg 960
gtcctgctgc tttcactcgt gatcactctt tactgtaagc gcggtcggaa gaagctgctg 1020
tacatcttta agcaaccctt catgaggcct gtgcagacta ctcaagagga ggacggctgt 1080
tcatgccggt tcccagagga ggaggaaggc ggctgcgaac tgcgcgtgaa attcagccgc 1140
agcgcagatg ctccagccta caagcagggg cagaaccagc tctacaacga actcaatctt 1200
ggtcggagag aggagtacga cgtgctggac aagcggagag gacgggaccc agaaatgggc 1260
gggaagccgc gcagaaagaa tccccaagag ggcctgtaca acgagctcca aaaggataag 1320
atggcagaag cctatagcga gattggtatg aaaggggaac gcagaagagg caaaggccac 1380
gacggactgt accagggact cagcaccgcc accaaggaca cctatgacgc tcttcacatg 1440
caggccctgc cgcctcgg 1458

<210> 952

<211> 486

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 952

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu
20 25 30

Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln
35 40 45

Asp Ile Ser Lys Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gln Ala
50 55 60

Pro Arg Leu Leu Ile Tyr His Thr Ser Arg Leu His Ser Gly Ile Pro
65 70 75 80

Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile
85 90 95

Ser Ser Leu Gln Pro Glu Asp Phe Ala Val Tyr Phe Cys Gln Gln Gly
Page 724

_SL

100		105		110											
Asn	Thr	Leu	Pro	Tyr	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Leu	Glu	Ile	Lys
		115					120					125			
Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gln
	130					135					140				
Val	Gln	Leu	Gln	Glu	Ser	Gly	Pro	Gly	Leu	Val	Lys	Pro	Ser	Glu	Thr
145					150					155					160
Leu	Ser	Leu	Thr	Cys	Thr	Val	Ser	Gly	Val	Ser	Leu	Pro	Asp	Tyr	Gly
				165					170					175	
Val	Ser	Trp	Ile	Arg	Gln	Pro	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Ile	Gly
			180					185					190		
Val	Ile	Trp	Gly	Ser	Glu	Thr	Thr	Tyr	Tyr	Asn	Ser	Ser	Leu	Lys	Ser
		195					200					205			
Arg	Val	Thr	Ile	Ser	Lys	Asp	Asn	Ser	Lys	Asn	Gln	Val	Ser	Leu	Lys
	210					215					220				
Leu	Ser	Ser	Val	Thr	Ala	Ala	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Lys
225					230					235					240
His	Tyr	Tyr	Tyr	Gly	Gly	Ser	Tyr	Ala	Met	Asp	Tyr	Trp	Gly	Gln	Gly
				245					250					255	
Thr	Leu	Val	Thr	Val	Ser	Ser	Thr	Thr	Thr	Pro	Ala	Pro	Arg	Pro	Pro
			260					265					270		
Thr	Pro	Ala	Pro	Thr	Ile	Ala	Ser	Gln	Pro	Leu	Ser	Leu	Arg	Pro	Glu
		275					280					285			
Ala	Cys	Arg	Pro	Ala	Ala	Gly	Gly	Ala	Val	His	Thr	Arg	Gly	Leu	Asp
	290					295					300				
Phe	Ala	Cys	Asp	Ile	Tyr	Ile	Trp	Ala	Pro	Leu	Ala	Gly	Thr	Cys	Gly
305					310					315					320
Val	Leu	Leu	Leu	Ser	Leu	Val	Ile	Thr	Leu	Tyr	Cys	Lys	Arg	Gly	Arg
				325					330					335	
Lys	Lys	Leu	Leu	Tyr	Ile	Phe	Lys	Gln	Pro	Phe	Met	Arg	Pro	Val	Gln
			340					345					350		
Thr	Thr	Gln	Glu	Glu	Asp	Gly	Cys	Ser	Cys	Arg	Phe	Pro	Glu	Glu	Glu
		355					360					365			
Glu	Gly	Gly	Cys	Glu	Leu	Arg	Val	Lys	Phe	Ser	Arg	Ser	Ala	Asp	Ala

_SL

370 375 380

Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu
385 390 395 400

Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp
 405 410 415

Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu
 420 425 430

Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile
 435 440 445

Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr
 450 455 460

Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met
465 470 475 480

Gln Ala Leu Pro Pro Arg
 485

<210> 953
<211> 813
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 953
atggccctgc ccgtcaccgc tctgctgctg ccccttgctc tgcttcttca tgcagcaagg 60
ccggacatcc agatgaccca aaccacctca tccctctctg cctctcttgg agacaggggtg 120
accatttctt gtcgcgccag ccaggacatc agcaagtatc tgaactggta tcagcagaag 180
ccggacggaa ccgtgaagct cctgatctac catacctctc gcctgcatag cggcgtgccc 240
tcacgcttct ctggaagcgg atcaggaacc gattattctc tcactatttc aaatcttgag 300
caggaagata ttgccaccta tttctgccag cagggttaata ccctgcccta caccttcgga 360
ggagggacca agctcgaaat caccggtgga ggaggcagcg gcggtggagg gtctggtgga 420
ggtggttctg aggtgaagct gcaagaatca ggccctggac ttgtggcccc ttcacagtcc 480
ctgagcgtga cttgcaccgt gtccggagtc tccctgcccg actacggagt gtcattggatc 540
agacaacctc cacggaaagg actggaatgg ctcggtgtca tctggggtag cgaaactact 600
tactacaatt cagccctcaa aagcaggctg actattatca aggacaacag caagtcccaa 660
gtctttctta agatgaactc actccagact gacgacaccg caatctacta ttgtgctaag 720
cactactact acggaggatc ctacgctatg gattactggg gacaaggtag ttccgtcact 780

gtctcttcac accatcatca ccatcaccat cac _SL

813

<210> 954
<211> 271
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 954
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu
20 25 30

Ser Ala Ser Leu Gly Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln
35 40 45

Asp Ile Ser Lys Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr
50 55 60

Val Lys Leu Leu Ile Tyr His Thr Ser Arg Leu His Ser Gly Val Pro
65 70 75 80

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile
85 90 95

Ser Asn Leu Glu Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly
100 105 110

Asn Thr Leu Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu
130 135 140

Val Lys Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser
145 150 155 160

Leu Ser Val Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly
165 170 175

Val Ser Trp Ile Arg Gln Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly
180 185 190

Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser
195 200 205

Arg Leu Thr Ile Ile Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys
210 215 220

_SL

Met Asn Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys
225 230 235 240

His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly
245 250 255

Thr Ser Val Thr Val Ser Ser His His His His His His His His
260 265 270

<210> 955
<211> 1458
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 955
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60
ccggacatcc agatgacaca gactacatcc tccctgtctg cctctctggg agacagagtc 120
accatcagtt gcagggcaag tcaggacatt agtaaattatt taaattggta tcagcagaaa 180
ccagatggaa ctgttaaact cctgatctac catacatcaa gattacactc aggagtccca 240
tcaaggttca gtggcagtgg gtctggaaca gattattctc tcaccattag caacctggag 300
caagaagata ttgccactta cttttgcca cagggtaata cgcttcgta cacgttcgga 360
ggggggacca agctggagat cacaggtggc ggtggctcgg gcggtggtgg gtcgggtggc 420
ggcggatctg aggtgaaact gcaggagtca ggacctggcc tgggtggcgcc ctcacagagc 480
ctgtccgtca catgcactgt ctcaggggtc tcattaccgc actatggtgt aagctggatt 540
cgccagcctc cacgaaaggg tctggagtgg ctgggagtaa tatggggtag tgaaaccaca 600
tactataatt cagctctcaa atccagactg accatcatca aggacaactc caagagccaa 660
gttttcttaa aaatgaacag tctgcaaact gatgacacag ccatttacta ctgtgccaaa 720
cattattact acggtggtag ctatgctatg gactactggg gccaaggaac ctcagtcacc 780
gtctcctcaa ccacgacgcc agcgccgca ccaccaacac cggcgcccac catcgcgctg 840
cagcccctgt ccctgcgccc agaggcgtgc cggccagcgg cggggggcgc agtgcacacg 900
agggggctgg acttcgcctg tgatatctac atctgggcgc ccttggccgg gacttgtggg 960
gtccttctcc tgtcactggt tatcaccctt tactgcaaac ggggcagaaa gaaactcctg 1020
tatatattca aacaaccatt tatgagacca gtacaaacta ctcaagagga agatggctgt 1080
agctgccgat ttccagaaga agaagaagga ggatgtgaac tgagagtga gttcagcagg 1140
agcgagacg cccccgcgta caagcagggc cagaaccagc tctataacga gctcaatcta 1200
ggacgaagag aggagtacga tgttttggac aagagacgtg gccgggaccc tgagatgggg 1260
ggaaagccga gaaggaagaa ccctcaggaa ggctgtaca atgaactgca gaaagataag 1320

_SL

atggcggagg cctacagtga gattgggatg aaaggcgagc gccggagggg caaggggcac 1380
gatggccttt accaggtct cagtacagcc accaaggaca cctacgacgc ctttcacatg 1440
caggccctgc cccctcgc 1458

<210> 956
<211> 486
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 956
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu
20 25 30

Ser Ala Ser Leu Gly Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln
35 40 45

Asp Ile Ser Lys Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr
50 55 60

Val Lys Leu Leu Ile Tyr His Thr Ser Arg Leu His Ser Gly Val Pro
65 70 75 80

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile
85 90 95

Ser Asn Leu Glu Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly
100 105 110

Asn Thr Leu Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu
130 135 140

Val Lys Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser
145 150 155 160

Leu Ser Val Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly
165 170 175

Val Ser Trp Ile Arg Gln Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly
180 185 190

Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser
Page 729

_SL

195		200		205											
Arg	Leu 210	Thr	Ile	Ile	Lys	Asp 215	Asn	Ser	Lys	Ser	Gln 220	Val	Phe	Leu	Lys
Met 225	Asn	Ser	Leu	Gln	Thr 230	Asp	Asp	Thr	Ala	Ile 235	Tyr	Tyr	Cys	Ala	Lys 240
His	Tyr	Tyr	Tyr	Gly 245	Gly	Ser	Tyr	Ala	Met 250	Asp	Tyr	Trp	Gly	Gln 255	Gly
Thr	Ser	Val	Thr 260	Val	Ser	Ser	Thr	Thr 265	Thr	Pro	Ala	Pro	Arg 270	Pro	Pro
Thr	Pro	Ala 275	Pro	Thr	Ile	Ala	Ser 280	Gln	Pro	Leu	Ser	Leu 285	Arg	Pro	Glu
Ala	Cys 290	Arg	Pro	Ala	Ala	Gly 295	Gly	Ala	Val	His	Thr 300	Arg	Gly	Leu	Asp
Phe 305	Ala	Cys	Asp	Ile	Tyr 310	Ile	Trp	Ala	Pro	Leu 315	Ala	Gly	Thr	Cys	Gly 320
Val	Leu	Leu	Leu	Ser 325	Leu	Val	Ile	Thr	Leu 330	Tyr	Cys	Lys	Arg	Gly 335	Arg
Lys	Lys	Leu	Leu 340	Tyr	Ile	Phe	Lys	Gln 345	Pro	Phe	Met	Arg	Pro 350	Val	Gln
Thr	Thr	Gln 355	Glu	Glu	Asp	Gly	Cys 360	Ser	Cys	Arg	Phe	Pro 365	Glu	Glu	Glu
Glu	Gly 370	Gly	Cys	Glu	Leu	Arg 375	Val	Lys	Phe	Ser	Arg 380	Ser	Ala	Asp	Ala
Pro 385	Ala	Tyr	Lys	Gln	Gly 390	Gln	Asn	Gln	Leu	Tyr 395	Asn	Glu	Leu	Asn	Leu 400
Gly	Arg	Arg	Glu	Glu 405	Tyr	Asp	Val	Leu	Asp 410	Lys	Arg	Arg	Gly	Arg 415	Asp
Pro	Glu	Met	Gly 420	Gly	Lys	Pro	Arg	Arg 425	Lys	Asn	Pro	Gln	Glu 430	Gly	Leu
Tyr	Asn	Glu 435	Leu	Gln	Lys	Asp	Lys 440	Met	Ala	Glu	Ala	Tyr 445	Ser	Glu	Ile
Gly	Met 450	Lys	Gly	Glu	Arg	Arg 455	Arg	Gly	Lys	Gly	His 460	Asp	Gly	Leu	Tyr
Gln	Gly	Leu	Ser	Thr	Ala	Thr	Lys	Asp	Thr	Tyr	Asp	Ala	Leu	His	Met

[illegible]

Gln Ala Leu Pro Pro Arg
485

```
<210> 957
<211> 242
<212> PRT
<213> Artificial Sequence
```

```
<220>  
<221> source  
<223> /note="Description of Artificial Sequence: Synthetic  
polypeptide"
```

<400> 957
Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
35 40 45

Tyr His Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
65 70 75 80

Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr Gly Gly Gly Gly Ser
100 105 110

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Lys Leu Gln Glu

Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser Val Thr Cys
130 135 140

Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg
145 150 155 160

Gln Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Gly Ser
165 170 175

Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser Arg Leu Thr Ile Ile
180 185 190

Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn Ser Leu Gln
195 200 205

_SL

Thr Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly
210 215 220

Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val
225 230 235 240

Ser Ser

<210> 958
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 958
Asp Tyr Gly Val Ser
1 5

<210> 959
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 959
Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser
1 5 10 15

<210> 960
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 960
His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr
1 5 10

<210> 961
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

_SL

<400> 961
Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Ser Ser Ser Leu Lys Ser
1 5 10 15

<210> 962
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 962
Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Gln Ser Ser Leu Lys Ser
1 5 10 15

<210> 963
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 963
Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ser Leu Lys Ser
1 5 10 15

<210> 964
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 964
Arg Ala Ser Gln Asp Ile Ser Lys Tyr Leu Asn
1 5 10

<210> 965
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 965
His Thr Ser Arg Leu His Ser
1 5

<210> 966
<211> 9

_SL

<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 966
Gln Gln Gly Asn Thr Leu Pro Tyr Thr
1 5

<210> 967
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> MISC_FEATURE
<222> (1)..(30)
<223> /note="This sequence may encompass 1-6
'Gly Gly Gly Gly Ser' repeating units"

<400> 967
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
20 25 30

<210> 968
<211> 100
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 968
tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 60
tttttttttt tttttttttt tttttttttt tttttttttt 100

<210> 969
<211> 400
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<220>
<221> misc_feature

_SL

<222> (1)..(400)

<223> /note="This sequence may encompass 100-400 nucleotides"

<220>

<221> source

<223> /note="See specification as filed for detailed description of substitutions and preferred embodiments"

<400> 969

```
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa      60
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa      120
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa      180
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa      240
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa      300
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa      360
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa                                400
```

<210> 970

<211> 245

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 970

```
Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln Met Val Ser Ala Leu Leu
1           5           10          15
```

```
Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu Tyr Asp Pro Thr Arg Pro
          20          25          30
```

```
Phe Ser Glu Ala Ser Met Met Gly Leu Leu Thr Asn Leu Ala Asp Arg
          35          40          45
```

```
Glu Leu Val His Met Ile Asn Trp Ala Lys Arg Val Pro Gly Phe Val
          50          55          60
```

```
Asp Leu Thr Leu His Asp Gln Val His Leu Leu Glu Cys Ala Trp Leu
65          70          75          80
```

```
Glu Ile Leu Met Ile Gly Leu Val Trp Arg Ser Met Glu His Pro Gly
          85          90          95
```

```
Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu Asp Arg Asn Gln Gly Lys
          100         105         110
```

```
Cys Val Glu Gly Met Val Glu Ile Phe Asp Met Leu Leu Ala Thr Ser
          115         120         125
```

```
Ser Arg Phe Arg Met Met Asn Leu Gln Gly Glu Glu Phe Val Cys Leu
```

[illegible]

_SL

<210> 972
<211> 69
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 972
Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala
1 5 10 15

Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly
20 25 30

Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Phe Trp Leu
35 40 45

Pro Ile Gly Cys Ala Ala Phe Val Val Val Cys Ile Leu Gly Cys Ile
50 55 60

Leu Ile Cys Trp Leu
65

<210> 973
<211> 207
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 973
accacgacgc cagcgccgcg accaccaaca ccggcgccca ccatcgcgtc gcagcccctg 60
tccctgcgcc cagaggcgtg ccggccagcg gcggggggcg cagtgcacac gagggggcgtg 120
gacttcgcct gtgatttctg gttaccata ggatgtgcag cttttgttgt agtctgcatt 180
ttgggatgca tacttatttg ttggcctt 207

<210> 974
<211> 5000
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<220>
<221> misc_feature
<222> (1)..(5000)
<223> /note="This sequence may encompass 50-5000 nucleotides"

<220>

<221> source

<223> /note="See specification as filed for detailed description of substitutions and preferred embodiments"

<400> 974

tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	60
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	120
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	180
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	240
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	300
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	360
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	420
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	480
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	540
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	600
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	660
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	720
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	780
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	840
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	900
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	960
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	1020
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	1080
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	1140
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	1200
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	1260
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	1320
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	1380
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	1440
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	1500
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	1560
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	1620
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	1680
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	1740
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	1800
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	1860

_SL

tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	3960
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	4020
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	4080
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	4140
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	4200
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	4260
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	4320
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	4380
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	4440
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	4500
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	4560
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	4620
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	4680
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	4740
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	4800
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	4860
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	4920
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	4980
tttttttttt	tttttttttt					5000

<210> 975
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 975
 Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe Pro
 1 5 10 15

Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu Asp
 20 25 30

Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys Phe
 35 40 45

Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val Ala
 50 55 60

Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp Tyr
 65 70 75 80

_SL

Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala Thr
85 90 95

Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu
100 105

<210> 976
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 976
Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe Pro
1 5 10 15

Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu Asp
20 25 30

Gly Lys Lys Met Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys Phe
35 40 45

Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val Ala
50 55 60

Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp Tyr
65 70 75 80

Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala Thr
85 90 95

Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu
100 105

<210> 977
<211> 2817
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 977
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60
ccgggatccc ggggcgtgca ggttgagaca atttccccag gagatgggag aacgttcccc 120
aagcgcggac agacatgcgt tgtgcactac acaggaatgt tggaggacgg aaagaaaatg 180
gacagttcaa gagatcggaa caaacattc aaattcatgt tgggaaaaca ggaagtgata 240

						_SL	
cggggctggg	aagaggggtgt	agcgcaaagt	tccgttggtc	aacgagcaaa	actcacgata		300
agtcccgatt	atgcttacgg	cgcaaccggt	cacccgggca	tcataccgcc	tcatgcgact		360
ttggtctttg	atgtggagct	gttgaaactt	gaaactcgcg	gagtacaggt	tgaacaata		420
tcacccgggg	acgggcggac	ttttccgaag	agaggtcaga	cctgcgtcgt	ccattatacc		480
ggtatgctgg	aggacggaaa	gaaaatggac	agctcacggg	accgaaataa	accattcaaa		540
tttatgttgg	ggaaacaaga	ggttatcagg	ggctgggagg	aggggtgtggc	ccagatgtct		600
gtcggtcagc	gcgcgaaact	cacaatctct	ccggattatg	cgtatggggc	gacagggcat		660
ccgggaatta	tccctcccca	cgctaccttg	gttttcgatg	ttgagcttct	gaagttggag		720
accagaggag	ttcaagtgga	gacaatatct	cctgggggatg	gacggacggt	ccccaagcgc		780
ggccagacct	gtgtagtcca	ctacacaggg	atgcttgaag	acggaaaaaa	gatggatagc		840
agtagagatc	gcaacaaacc	atttaagttc	atgctgggga	agcaggaagt	aatacgcggc		900
tgggaggaag	gcgtggcaca	gatgagtgtt	ggtcaacggg	ccaaacttac	tatttctccc		960
gattatgcgt	atggagccac	cgggcaccct	ggcattatcc	caccccatgc	cacattgggt		1020
tttgacgttg	aattgcttaa	attggagacc	aggggagttc	aagtggaaac	aatatcaccg		1080
ggggatggtc	ggacttttcc	taaaaggggc	caaacctgtg	tagtccatta	taccggaatg		1140
ctcgaagacg	gaaagaaaat	ggactcttct	agagaccgca	ataagccctt	caagttcatg		1200
ttgggtaagc	aagaggtgat	ccggggctgg	gaagaggggg	tcgctcaaata	gtccgtcggg		1260
cagcgagcta	aactgactat	ttccccagac	tacgcatatg	gagcgactgg	ccaccccggt		1320
attattcctc	cccatgcgac	tctcgtgttc	gacgtagaac	tcttgaaatt	ggaaacgtca		1380
gcccgaaca	ggcggaagag	aggatccgac	atccagatga	cacagactac	atcctccctg		1440
tctgcctctc	tgggagacag	agtcaccatc	agttgcaggg	caagtcagga	cattagtaaa		1500
tatttaaatt	ggatcagca	gaaaccagat	ggaactgtta	aactcctgat	ctaccataca		1560
tcaagattac	actcaggagt	cccatcaagg	ttcagtggca	gtgggtctgg	aacagattat		1620
tctctcacca	ttagcaacct	ggagcaagaa	gatattgcca	cttacttttg	ccaacagggg		1680
aatacgcttc	cgtacacggt	cggagggggg	actaagttgg	aaataacagg	tggcgggtggc		1740
tcgggcggtg	gtgggtcggg	tggcggcgga	tctgaggtga	aactgcagga	gtcaggacct		1800
ggcctgggtg	cgccctcaca	gagcctgtcc	gtcacatgca	ctgtctcagg	ggtctcatta		1860
cccgactatg	gtgtaagctg	gattcgccag	cctccacgaa	agggctctgga	gtggctggga		1920
gtaatatggg	gtagtgaaac	cacatactat	aattcagctc	tcaaataccag	actgaccatc		1980
atcaaggaca	actccaagag	ccaagttttc	ttaaaaatga	acagtctgca	aactgatgac		2040
acagccattt	actactgtgc	caaacattat	tactacgggtg	gtagctatgc	tatggactac		2100
tggggcaag	gaacctcagt	caccgtctcc	tcagctagca	ccacgacgcc	agcgccgcga		2160
ccaccaacac	cggcgcccac	catcgcgctg	cagcccctgt	ccctgcgccc	agaggcggtgc		2220
cggccagcgg	cggggggcgc	agtgcacacg	agggggctgg	acttcgcctg	tgattccgga		2280

_SL

atctacatct gggcgccctt ggccgggact tgtgggggtcc ttctcctgtc actgggttacc	2340
accctttact gcaaacgggg cagaaagaaa ctctgtata tattcaaaca accatttatg	2400
agaccagtac aaactactca agaggaagat ggctgtagct gccgatttcc agaagaagaa	2460
gaaggaggat gtgaactgag agtgaagttc agcaggagcg cagacgcccc cgcgtaccag	2520
cagggccaga accagctcta taacgagctc aatctaggac gaagagagga gtacgatgtt	2580
ttggacaaga gacgtggccg ggaccctgag atggggggaa agccgagaag gaagaaccct	2640
caggaaggcc tgtacaatga actgcagaaa gataagatgg cggaggccta cagtgagatt	2700
gggatgaaag gcgagcgccg gaggggcaag gggcacgatg gcctttacca ggggtctcagt	2760
acagccacca aggacaccta cgacgccctt cacatgcagg cctgcccc tcgctaa	2817

<210> 978

<211> 939

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 978

Met	Ala	Leu	Pro	Val	Thr	Ala	Leu	Leu	Leu	Pro	Leu	Ala	Leu	Leu	Leu
1				5					10					15	

His	Ala	Ala	Arg	Pro	Gly	Ser	Arg	Gly	Val	Gln	Val	Glu	Thr	Ile	Ser
			20					25					30		

Pro	Gly	Asp	Gly	Arg	Thr	Phe	Pro	Lys	Arg	Gly	Gln	Thr	Cys	Val	Val
		35					40					45			

His	Tyr	Thr	Gly	Met	Leu	Glu	Asp	Gly	Lys	Lys	Met	Asp	Ser	Ser	Arg
	50					55					60				

Asp	Arg	Asn	Lys	Pro	Phe	Lys	Phe	Met	Leu	Gly	Lys	Gln	Glu	Val	Ile
65					70					75					80

Arg	Gly	Trp	Glu	Glu	Gly	Val	Ala	Gln	Met	Ser	Val	Gly	Gln	Arg	Ala
			85						90					95	

Lys	Leu	Thr	Ile	Ser	Pro	Asp	Tyr	Ala	Tyr	Gly	Ala	Thr	Gly	His	Pro
			100					105					110		

Gly	Ile	Ile	Pro	Pro	His	Ala	Thr	Leu	Val	Phe	Asp	Val	Glu	Leu	Leu
		115					120					125			

Lys	Leu	Glu	Thr	Arg	Gly	Val	Gln	Val	Glu	Thr	Ile	Ser	Pro	Gly	Asp
	130					135					140				

Gly	Arg	Thr	Phe	Pro	Lys	Arg	Gly	Gln	Thr	Cys	Val	Val	His	Tyr	Thr
145					150					155					160

_SL

Gly Met Leu Glu Asp Gly Lys Lys Met Asp Ser Ser Arg Asp Arg Asn
165 170 175

Lys Pro Phe Lys Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp
180 185 190

Glu Glu Gly Val Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr
195 200 205

Ile Ser Pro Asp Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile
210 215 220

Pro Pro His Ala Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu
225 230 235 240

Thr Arg Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr
245 250 255

Phe Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu
260 265 270

Glu Asp Gly Lys Lys Met Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe
275 280 285

Lys Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly
290 295 300

Val Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro
305 310 315 320

Asp Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His
325 330 335

Ala Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu Thr Arg Gly
340 345 350

Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe Pro Lys
355 360 365

Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu Asp Gly
370 375 380

Lys Lys Met Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys Phe Met
385 390 395 400

Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val Ala Gln
405 410 415

Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp Tyr Ala
420 425 430

_SL

Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala Thr Leu
435 440 445

Val Phe Asp Val Glu Leu Leu Lys Leu Glu Thr Ser Ala Arg Asn Arg
450 455 460

Arg Lys Arg Gly Ser Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu
465 470 475 480

Ser Ala Ser Leu Gly Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln
485 490 495

Asp Ile Ser Lys Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr
500 505 510

Val Lys Leu Leu Ile Tyr His Thr Ser Arg Leu His Ser Gly Val Pro
515 520 525

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile
530 535 540

Ser Asn Leu Glu Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly
545 550 555 560

Asn Thr Leu Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr
565 570 575

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu
580 585 590

Val Lys Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser
595 600 605

Leu Ser Val Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly
610 615 620

Val Ser Trp Ile Arg Gln Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly
625 630 635 640

Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser
645 650 655

Arg Leu Thr Ile Ile Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys
660 665 670

Met Asn Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys
675 680 685

His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly
690 695 700

_SL

Thr Ser Val Thr Val Ser Ser Ala Ser Thr Thr Thr Pro Ala Pro Arg
705 710 715 720

Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg
725 730 735

Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly
740 745 750

Leu Asp Phe Ala Cys Asp Ser Gly Ile Tyr Ile Trp Ala Pro Leu Ala
755 760 765

Gly Thr Cys Gly Val Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys
770 775 780

Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met
785 790 795 800

Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe
805 810 815

Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg
820 825 830

Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn
835 840 845

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
850 855 860

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
865 870 875 880

Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
885 890 895

Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
900 905 910

Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
915 920 925

Ala Leu His Met Gln Ala Leu Pro Pro Arg Glx
930 935

<210> 979

<211> 436

<212> PRT

<213> Artificial Sequence

<220>

_SL

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 979

Arg Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe
1 5 10 15

Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu
20 25 30

Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys
35 40 45

Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val
50 55 60

Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp
65 70 75 80

Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala
85 90 95

Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu Thr Arg Gly Val
100 105 110

Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe Pro Lys Arg
115 120 125

Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu Asp Gly Lys
130 135 140

Lys Met Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys Phe Met Leu
145 150 155 160

Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val Ala Gln Met
165 170 175

Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp Tyr Ala Tyr
180 185 190

Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala Thr Leu Val
195 200 205

Phe Asp Val Glu Leu Leu Lys Leu Glu Thr Arg Gly Val Gln Val Glu
210 215 220

Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe Pro Lys Arg Gly Gln Thr
225 230 235 240

Cys Val Val His Tyr Thr Gly Met Leu Glu Asp Gly Lys Lys Met Asp
245 250 255

_SL

Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys Phe Met Leu Gly Lys Gln
260 265 270

Glu Val Ile Arg Gly Trp Glu Glu Gly Val Ala Gln Met Ser Val Gly
275 280 285

Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp Tyr Ala Tyr Gly Ala Thr
290 295 300

Gly His Pro Gly Ile Ile Pro Pro His Ala Thr Leu Val Phe Asp Val
305 310 315 320

Glu Leu Leu Lys Leu Glu Thr Arg Gly Val Gln Val Glu Thr Ile Ser
325 330 335

Pro Gly Asp Gly Arg Thr Phe Pro Lys Arg Gly Gln Thr Cys Val Val
340 345 350

His Tyr Thr Gly Met Leu Glu Asp Gly Lys Lys Met Asp Ser Ser Arg
355 360 365

Asp Arg Asn Lys Pro Phe Lys Phe Met Leu Gly Lys Gln Glu Val Ile
370 375 380

Arg Gly Trp Glu Glu Gly Val Ala Gln Met Ser Val Gly Gln Arg Ala
385 390 400

Lys Leu Thr Ile Ser Pro Asp Tyr Ala Tyr Gly Ala Thr Gly His Pro
405 410 415

Gly Ile Ile Pro Pro His Ala Thr Leu Val Phe Asp Val Glu Leu Leu
420 425 430

Lys Leu Glu Thr
435

<210> 980

<211> 436

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 980

Arg Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe
1 5 10 15

Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu
20 25 30

Asp Gly Lys Lys Met Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys
 35 40 45

Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val
 50 55 60

Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp
 65 70 75 80

Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala
 85 90 95

Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu Thr Arg Gly Val
 100 105 110

Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe Pro Lys Arg
 115 120 125

Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu Asp Gly Lys
 130 135 140

Lys Met Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys Phe Met Leu
 145 150 155 160

Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val Ala Gln Met
 165 170 175

Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp Tyr Ala Tyr
 180 185 190

Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala Thr Leu Val
 195 200 205

Phe Asp Val Glu Leu Leu Lys Leu Glu Thr Arg Gly Val Gln Val Glu
 210 215 220

Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe Pro Lys Arg Gly Gln Thr
 225 230 235 240

Cys Val Val His Tyr Thr Gly Met Leu Glu Asp Gly Lys Lys Met Asp
 245 250 255

Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys Phe Met Leu Gly Lys Gln
 260 265 270

Glu Val Ile Arg Gly Trp Glu Glu Gly Val Ala Gln Met Ser Val Gly
 275 280 285

Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp Tyr Ala Tyr Gly Ala Thr
 290 295 300

Gly His Pro Gly Ile Ile Pro Pro His Ala Thr Leu Val Phe Asp Val
 305 310 315 320
 Glu Leu Leu Lys Leu Glu Thr Arg Gly Val Gln Val Glu Thr Ile Ser
 325 330 335
 Pro Gly Asp Gly Arg Thr Phe Pro Lys Arg Gly Gln Thr Cys Val Val
 340 345 350
 His Tyr Thr Gly Met Leu Glu Asp Gly Lys Lys Met Asp Ser Ser Arg
 355 360 365
 Asp Arg Asn Lys Pro Phe Lys Phe Met Leu Gly Lys Gln Glu Val Ile
 370 375 380
 Arg Gly Trp Glu Glu Gly Val Ala Gln Met Ser Val Gly Gln Arg Ala
 385 390 395 400
 Lys Leu Thr Ile Ser Pro Asp Tyr Ala Tyr Gly Ala Thr Gly His Pro
 405 410 415
 Gly Ile Ile Pro Pro His Ala Thr Leu Val Phe Asp Val Glu Leu Leu
 420 425 430
 Lys Leu Glu Thr
 435

<210> 981
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 981
 Ser Ala Arg Asn Arg Gln Lys Arg
 1 5

<210> 982
 <211> 4
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 982
 Arg Gly Asp Ser
 1

<210> 983
 <211> 244

_SL

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 983

Gln Val Gln Leu Leu Glu Ser Gly Ala Glu Leu Val Arg Pro Gly Ser
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr
20 25 30

Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Gln Ile Tyr Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe
50 55 60

Lys Gly Gln Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Gln Leu Ser Gly Leu Thr Ser Glu Asp Ser Ala Val Tyr Ser Cys
85 90 95

Ala Arg Lys Thr Ile Ser Ser Val Val Asp Phe Tyr Phe Asp Tyr Trp
100 105 110

Gly Gln Gly Thr Thr Val Thr Gly Gly Gly Ser Gly Gly Gly Ser Gly
115 120 125

Gly Gly Ser Gly Gly Gly Ser Glu Leu Val Leu Thr Gln Ser Pro Lys
130 135 140

Phe Met Ser Thr Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala
145 150 155 160

Ser Gln Asn Val Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly
165 170 175

Gln Ser Pro Lys Pro Leu Ile Tyr Ser Ala Thr Tyr Arg Asn Ser Gly
180 185 190

Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
195 200 205

Thr Ile Thr Asn Val Gln Ser Lys Asp Leu Ala Asp Tyr Phe Cys Gln
210 215 220

Tyr Asn Arg Tyr Pro Tyr Thr Ser Phe Phe Phe Thr Lys Leu Glu Ile
225 230 235 240

_SL

Lys Arg Arg Ser

<210> 984

<211> 464

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 984

Gln Val Gln Leu Leu Glu Ser Gly Ala Glu Leu Val Arg Pro Gly Ser
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr
20 25 30

Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Gln Ile Tyr Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe
50 55 60

Lys Gly Gln Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Gln Leu Ser Gly Leu Thr Ser Glu Asp Ser Ala Val Tyr Ser Cys
85 90 95

Ala Arg Lys Thr Ile Ser Ser Val Val Asp Phe Tyr Phe Asp Tyr Trp
100 105 110

Gly Gln Gly Thr Thr Val Thr Gly Gly Gly Ser Gly Gly Gly Ser Gly
115 120 125

Gly Gly Ser Gly Gly Gly Ser Glu Leu Val Leu Thr Gln Ser Pro Lys
130 135 140

Phe Met Ser Thr Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala
145 150 155 160

Ser Gln Asn Val Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly
165 170 175

Gln Ser Pro Lys Pro Leu Ile Tyr Ser Ala Thr Tyr Arg Asn Ser Gly
180 185 190

Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
195 200 205

Thr Ile Thr Asn Val Gln Ser Lys Asp Leu ^{-SL} Ala Asp Tyr Phe Cys Gln
 210 215 220
 Tyr Asn Arg Tyr Pro Tyr Thr Ser Phe Phe Phe Thr Lys Leu Glu Ile
 225 230 235 240
 Lys Arg Arg Ser Lys Ile Glu Val Met Tyr Pro Pro Pro Tyr Leu Asp
 245 250 255
 Asn Glu Lys Ser Asn Gly Thr Ile Ile His Val Lys Gly Lys His Leu
 260 265 270
 Cys Pro Ser Pro Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu
 275 280 285
 Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val
 290 295 300
 Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His
 305 310 315 320
 Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys
 325 330 335
 His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser
 340 345 350
 Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly
 355 360 365
 Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
 370 375 380
 Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
 385 390 395 400
 Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
 405 410 415
 Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
 420 425 430
 Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala
 435 440 445
 Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
 450 455 460

<210> 985

<211> 246

<212> PRT

<213> Artificial Sequence

_SL

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 985

Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
35 40 45

Tyr His Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
65 70 75 80

Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr Gly Ser Thr Ser Gly
100 105 110

Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Glu Val Lys
115 120 125

Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser
130 135 140

Val Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser
145 150 155 160

Trp Ile Arg Gln Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly Val Ile
165 170 175

Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser Arg Leu
180 185 190

Thr Ile Ile Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn
195 200 205

Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys His Tyr
210 215 220

Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser
225 230 235 240

Val Thr Val Ser Ser Glu

<210> 986
 <211> 439
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 986
 Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
 1 5 10 15

Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
 35 40 45

Tyr His Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
 65 70 75 80

Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr
 85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr Gly Ser Thr Ser Gly
 100 105 110

Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Glu Val Lys
 115 120 125

Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser
 130 135 140

Val Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser
 145 150 155 160

Trp Ile Arg Gln Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly Val Ile
 165 170 175

Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser Arg Leu
 180 185 190

Thr Ile Ile Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn
 195 200 205

Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys His Tyr
 210 215 220

_SL

Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser
225 230 235 240

Val Thr Val Ser Ser Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys
245 250 255

Pro Met Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr
260 265 270

Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Lys Arg Gly
275 280 285

Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val
290 295 300

Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Glu Glu Glu
305 310 315 320

Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala
325 330 335

Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu
340 345 350

Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp
355 360 365

Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu
370 375 380

Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile
385 390 395 400

Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr
405 410 415

Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met
420 425 430

Gln Ala Leu Pro Pro Arg Leu
435

<210> 987

<211> 819

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

_SL

<400> 987

Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15
Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr
20 25 30
Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
35 40 45
Tyr His Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
65 70 75 80
Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr
85 90 95
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr Gly Ser Thr Ser Gly
100 105 110
Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Glu Val Lys
115 120 125
Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser
130 135 140
Val Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser
145 150 155 160
Trp Ile Arg Gln Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly Val Ile
165 170 175
Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser Arg Leu
180 185 190
Thr Ile Ile Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn
195 200 205
Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys His Tyr
210 215 220
Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser
225 230 235 240
Val Thr Val Ser Ser Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys
245 250 255
Pro Met Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr
260 265 270

_SL

Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Lys Arg Gly
275 280 285

Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val
290 295 300

Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Glu Glu Glu
305 310 315 320

Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala
325 330 335

Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu
340 345 350

Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp
355 360 365

Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu
370 375 380

Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile
385 390 395 400

Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr
405 410 415

Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met
420 425 430

Gln Ala Leu Pro Pro Arg Leu Glu Gly Gly Gly Glu Gly Arg Gly Ser
435 440 445

Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Arg Met Leu
450 455 460

Leu Leu Val Thr Ser Leu Leu Leu Cys Glu Leu Pro His Pro Ala Phe
465 470 475 480

Leu Leu Ile Pro Arg Lys Val Cys Asn Gly Ile Gly Ile Gly Glu Phe
485 490 495

Lys Asp Ser Leu Ser Ile Asn Ala Thr Asn Ile Lys His Phe Lys Asn
500 505 510

Cys Thr Ser Ile Ser Gly Asp Leu His Ile Leu Pro Val Ala Phe Arg
515 520 525

Gly Asp Ser Phe Thr His Thr Pro Pro Leu Asp Pro Gln Glu Leu Asp
530 535 540

_SL

Ile Leu Lys Thr Val Lys Glu Ile Thr Gly Phe Leu Leu Ile Gln Ala
545 550 555 560

Trp Pro Glu Asn Arg Thr Asp Leu His Ala Phe Glu Asn Leu Glu Ile
565 570 575

Ile Arg Gly Arg Thr Lys Gln His Gly Gln Phe Ser Leu Ala Val Val
580 585 590

Ser Leu Asn Ile Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu Ile Ser
595 600 605

Asp Gly Asp Val Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr Ala Asn
610 615 620

Thr Ile Asn Trp Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys Thr Lys
625 630 635 640

Ile Ile Ser Asn Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly Gln Val
645 650 655

Cys His Ala Leu Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu Pro Arg
660 665 670

Asp Cys Val Ser Cys Arg Asn Val Ser Arg Gly Arg Glu Cys Val Asp
675 680 685

Lys Cys Asn Leu Leu Glu Gly Glu Pro Arg Glu Phe Val Glu Asn Ser
690 695 700

Glu Cys Ile Gln Cys His Pro Glu Cys Leu Pro Gln Ala Met Asn Ile
705 710 715 720

Thr Cys Thr Gly Arg Gly Pro Asp Asn Cys Ile Gln Cys Ala His Tyr
725 730 735

Ile Asp Gly Pro His Cys Val Lys Thr Cys Pro Ala Gly Val Met Gly
740 745 750

Glu Asn Asn Thr Leu Val Trp Lys Tyr Ala Asp Ala Gly His Val Cys
755 760 765

His Leu Cys His Pro Asn Cys Thr Tyr Gly Cys Thr Gly Pro Gly Leu
770 775 780

Glu Gly Cys Pro Thr Asn Gly Pro Lys Ile Pro Ser Ile Ala Thr Gly
785 790 795 800

Met Val Gly Ala Leu Leu Leu Leu Leu Val Val Ala Leu Gly Ile Gly
805 810 815

_SL

Leu Phe Met

<210> 988
<211> 245
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 988
Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
35 40 45

Tyr His Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
65 70 75 80

Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr Gly Ser Thr Ser Gly
100 105 110

Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Glu Val Lys
115 120 125

Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser
130 135 140

Val Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser
145 150 155 160

Trp Ile Arg Gln Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly Val Ile
165 170 175

Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser Arg Leu
180 185 190

Thr Ile Ile Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn
195 200 205

Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr Tyr^{SL} Cys Ala Lys His Tyr
 210 215 220

Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser
 225 230 235 240

Val Thr Val Ser Ser
 245

<210> 989
 <211> 467
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 989
 Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
 1 5 10 15

Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
 35 40 45

Tyr His Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
 65 70 75 80

Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr
 85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr Gly Ser Thr Ser Gly
 100 105 110

Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Glu Val Lys
 115 120 125

Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser
 130 135 140

Val Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser
 145 150 155 160

Trp Ile Arg Gln Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly Val Ile
 165 170 175

Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser Arg Leu
 Page 761

_SL

180		185		190											
Thr	Ile	Ile	Lys	Asp	Asn	Ser	Lys	Ser	Gln	Val	Phe	Leu	Lys	Met	Asn
		195					200					205			
Ser	Leu	Gln	Thr	Asp	Asp	Thr	Ala	Ile	Tyr	Tyr	Cys	Ala	Lys	His	Tyr
	210					215					220				
Tyr	Tyr	Gly	Gly	Ser	Tyr	Ala	Met	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Ser
225					230					235					240
Val	Thr	Val	Ser	Ser	Ala	Ala	Ala	Ile	Glu	Val	Met	Tyr	Pro	Pro	Pro
				245					250					255	
Tyr	Leu	Asp	Asn	Glu	Lys	Ser	Asn	Gly	Thr	Ile	Ile	His	Val	Lys	Gly
			260					265					270		
Lys	His	Leu	Cys	Pro	Ser	Pro	Leu	Phe	Pro	Gly	Pro	Ser	Lys	Pro	Phe
		275					280					285			
Trp	Val	Leu	Val	Val	Val	Gly	Gly	Val	Leu	Ala	Cys	Tyr	Ser	Leu	Leu
	290					295					300				
Val	Thr	Val	Ala	Phe	Ile	Ile	Phe	Trp	Val	Arg	Ser	Lys	Arg	Ser	Arg
305					310					315					320
Leu	Leu	His	Ser	Asp	Tyr	Met	Asn	Met	Thr	Pro	Arg	Arg	Pro	Gly	Pro
				325					330					335	
Thr	Arg	Lys	His	Tyr	Gln	Pro	Tyr	Ala	Pro	Pro	Arg	Asp	Phe	Ala	Ala
			340					345					350		
Tyr	Arg	Ser	Arg	Val	Lys	Phe	Ser	Arg	Ser	Ala	Asp	Ala	Pro	Ala	Tyr
		355					360					365			
Gln	Gln	Gly	Gln	Asn	Gln	Leu	Tyr	Asn	Glu	Leu	Asn	Leu	Gly	Arg	Arg
	370					375					380				
Glu	Glu	Tyr	Asp	Val	Leu	Asp	Lys	Arg	Arg	Gly	Arg	Asp	Pro	Glu	Met
385					390					395				400	
Gly	Gly	Lys	Pro	Arg	Arg	Lys	Asn	Pro	Gln	Glu	Gly	Leu	Tyr	Asn	Glu
				405					410					415	
Leu	Gln	Lys	Asp	Lys	Met	Ala	Glu	Ala	Tyr	Ser	Glu	Ile	Gly	Met	Lys
			420					425					430		
Gly	Glu	Arg	Arg	Arg	Gly	Lys	Gly	His	Asp	Gly	Leu	Tyr	Gln	Gly	Leu
		435					440					445			
Ser	Thr	Ala	Thr	Lys	Asp	Thr	Tyr	Asp	Ala	Leu	His	Met	Gln	Ala	Leu

_SL

465

<211> 751

<211> 751

<212> PRT

<213> Artificial Sequence

 $\langle 220 \rangle$

<221> source

```
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"
```

<400> 990

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln Met

Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu Tyr

Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu Thr

Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala Lys Arg

Val Pro Gly Phe Val Asp Leu Ala Leu His Asp Gln Val His Leu Leu

Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp Arg Ser

Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu Asp

Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe Asp Met

Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly Glu

Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val Tyr

Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His Ile

His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met Ala

_SL

Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala Gln Leu
210 215 220

Leu Leu Ile Leu Ser His Ile Arg His Met Ser Ser Lys Arg Met Glu
225 230 235 240

His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Ser Asp Leu
245 250 255

Leu Leu Glu Met Leu Asp Ala His Arg Leu Gly Thr Gly Ala Glu Asp
260 265 270

Pro Arg Pro Ser Arg Lys Arg Arg Ser Leu Gly Asp Val Gly Glu Ile
275 280 285

Val Met Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg
290 295 300

Ala Thr Leu Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr Leu Asn
305 310 315 320

Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr His
325 330 335

Thr Ser Arg Leu His Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly
340 345 350

Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
355 360 365

Phe Ala Val Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr Phe
370 375 380

Gly Gln Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly
385 390 395 400

Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Glu Ser Gly
405 410 415

Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val
420 425 430

Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln Pro
435 440 445

Pro Gly Lys Gly Leu Glu Trp Ile Gly Val Ile Trp Gly Ser Glu Thr
450 455 460

Thr Tyr Tyr Ser Ser Ser Leu Lys Ser Arg Val Thr Ile Ser Lys Asp
465 470 475 480

_SL

Asn Ser Lys Asn Gln Val Ser Leu Lys Leu Ser Ser Val Thr Ala Ala
485 490 495

Asp Thr Ala Val Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly Ser
500 505 510

Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
515 520 525

Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala
530 535 540

Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly
545 550 555 560

Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile
565 570 575

Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val
580 585 590

Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe
595 600 605

Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly
610 615 620

Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg
625 630 635 640

Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln
645 650 655

Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp
660 665 670

Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro
675 680 685

Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp
690 695 700

Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg
705 710 715 720

Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr
725 730 735

Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
740 745 750

_SL

<210> 991
<211> 751
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 991
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln Met
20 25 30

Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu Tyr
35 40 45

Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu Thr
50 55 60

Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala Lys Arg
65 70 75 80

Val Pro Gly Phe Val Asp Leu Thr Leu His Asp Gln Val His Leu Leu
85 90 95

Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp Arg Ser
100 105 110

Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu Asp
115 120 125

Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe Asp Met
130 135 140

Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly Glu
145 150 155 160

Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val Tyr
165 170 175

Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His Ile
180 185 190

His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met Ala
195 200 205

Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala Gln Leu
210 215 220

_SL

Leu Leu Ile Leu Ser His Ile Arg His Met Ser Asn Lys Arg Met Glu
225 230 235 240

His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Ser Asp Leu
245 250 255

Leu Leu Glu Met Leu Asp Ala His Arg Leu Gly Thr Gly Ala Glu Asp
260 265 270

Pro Arg Pro Ser Arg Lys Arg Arg Ser Leu Gly Asp Val Gly Glu Ile
275 280 285

Val Met Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg
290 295 300

Ala Thr Leu Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr Leu Asn
305 310 315 320

Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr His
325 330 335

Thr Ser Arg Leu His Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly
340 345 350

Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
355 360 365

Phe Ala Val Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr Phe
370 375 380

Gly Gln Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Ser Gly Gly
385 390 395 400

Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Glu Ser Gly
405 410 415

Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val
420 425 430

Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln Pro
435 440 445

Pro Gly Lys Gly Leu Glu Trp Ile Gly Val Ile Trp Gly Ser Glu Thr
450 455 460

Thr Tyr Tyr Ser Ser Ser Leu Lys Ser Arg Val Thr Ile Ser Lys Asp
465 470 475 480

Asn Ser Lys Asn Gln Val Ser Leu Lys Leu Ser Ser Val Thr Ala Ala
485 490 495

_SL

Asp Thr Ala Val Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly Ser
500 505 510

Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
515 520 525

Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala
530 535 540

Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly
545 550 555 560

Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile
565 570 575

Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val
580 585 590

Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe
595 600 605

Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly
610 615 620

Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg
625 630 635 640

Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln
645 650 655

Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp
660 665 670

Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro
675 680 685

Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp
690 695 700

Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg
705 710 715 720

Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr
725 730 735

Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
740 745 750

<210> 992

<211> 745

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 992

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
 1 5 10 15

His Ala Ala Arg Pro Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln Met
 20 25 30

Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu Tyr
 35 40 45

Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu Thr
 50 55 60

Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala Lys Arg
 65 70 75 80

Val Pro Gly Phe Val Asp Leu Ala Leu His Asp Gln Val His Leu Leu
 85 90 95

Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp Arg Ser
 100 105 110

Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu Asp
 115 120 125

Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe Asp Met
 130 135 140

Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly Glu
 145 150 155 160

Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val Tyr
 165 170 175

Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His Ile
 180 185 190

His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met Ala
 195 200 205

Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala Gln Leu
 210 215 220

Leu Leu Ile Leu Ser His Ile Arg His Met Ser Ser Lys Arg Met Glu
 225 230 235 240

His Leu Tyr Ser Met₂₄₅ Lys Cys Lys Asn Val₂₅₀ Val^{SL} Pro Leu Ser Asp₂₅₅ Leu
 Leu Leu Glu Met₂₆₀ Leu Asp Ala His Arg₂₆₅ Leu Gly Thr Gly Ala₂₇₀ Glu Asp
 Pro Arg Pro₂₇₅ Ser Arg Lys Arg₂₈₀ Glu Ile Val Met₂₈₅ Thr Gln Ser Pro
 Ala Thr₂₉₀ Leu Ser Leu Ser Pro₂₉₅ Gly Glu Arg Ala Thr₃₀₀ Leu Ser Cys Arg
 Ala Ser₃₀₅ Gln Asp Ile Ser₃₁₀ Lys Tyr Leu Asn Trp₃₁₅ Tyr Gln Gln Lys Pro₃₂₀
 Gly Gln Ala Pro Arg₃₂₅ Leu Leu Ile Tyr His₃₃₀ Thr Ser Arg Leu His₃₃₅ Ser
 Gly Ile Pro Ala₃₄₀ Arg Phe Ser Gly₃₄₅ Ser Gly Ser Gly Thr Asp₃₅₀ Tyr Thr
 Leu Thr Ile₃₅₅ Ser Ser Leu Gln Pro₃₆₀ Glu Asp Phe Ala Val₃₆₅ Tyr Phe Cys
 Gln Gln Gly Asn Thr Leu Pro₃₇₅ Tyr Thr Phe Gly Gln Gly Thr Lys Leu
 Glu Ile Lys Gly Gly₃₉₀ Gly Ser Gly Gly₃₉₅ Gly Ser Gly Gly₄₀₀
 Gly Ser Gln Val₄₀₅ Leu Gln Glu Ser Gly₄₁₀ Pro Gly Leu Val Lys₄₁₅ Pro
 Ser Glu Thr Leu₄₂₀ Ser Leu Thr Cys Thr₄₂₅ Val Ser Gly Val Ser₄₃₀ Leu Pro
 Asp Tyr Gly₄₃₅ Val Ser Trp Ile Arg₄₄₀ Gln Pro Pro Gly₄₄₅ Lys Gly Leu Glu
 Trp Ile₄₅₀ Gly Val Ile Trp Gly₄₅₅ Ser Glu Thr Thr Tyr₄₆₀ Tyr Ser Ser Ser
 Leu Lys Ser Arg Val₄₇₀ Thr Ile Ser Lys Asp Asn₄₇₅ Ser Lys Asn Gln Val₄₈₀
 Ser Leu Lys Leu Ser₄₈₅ Ser Val Thr Ala Ala₄₉₀ Asp Thr Ala Val Tyr₄₉₅ Tyr
 Cys Ala Lys His₅₀₀ Tyr Tyr Tyr Gly Gly₅₀₅ Ser Tyr Ala Met Asp₅₁₀ Tyr Trp

Gly Gln Gly Thr Leu Val Thr Val Ser Ser^{-SL} Thr Thr Thr Pro Ala Pro
 515 520 525
 Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu
 530 535 540
 Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg
 545 550 555 560
 Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly
 565 570 575
 Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys
 580 585 590
 Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg
 595 600 605
 Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro
 610 615 620
 Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser
 625 630 635 640
 Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu
 645 650 655
 Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg
 660 665 670
 Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln
 675 680 685
 Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr
 690 695 700
 Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp
 705 710 715 720
 Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala
 725 730 735
 Leu His Met Gln Ala Leu Pro Pro Arg
 740 745

<210> 993

<211> 745

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic

_SL
polypeptide"

<400> 993

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln Met
20 25 30

Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu Tyr
35 40 45

Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu Thr
50 55 60

Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala Lys Arg
65 70 75 80

Val Pro Gly Phe Val Asp Leu Thr Leu His Asp Gln Val His Leu Leu
85 90 95

Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp Arg Ser
100 105 110

Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu Asp
115 120 125

Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe Asp Met
130 135 140

Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly Glu
145 150 155 160

Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val Tyr
165 170 175

Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His Ile
180 185 190

His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met Ala
195 200 205

Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala Gln Leu
210 215 220

Leu Leu Ile Leu Ser His Ile Arg His Met Ser Asn Lys Arg Met Glu
225 230 235 240

His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Ser Asp Leu
245 250 255

Leu Leu Glu Met Leu Asp Ala His Arg Leu Gly Thr Gly Ala Glu Asp
Page 772

_SL

260		265		270											
Pro	Arg	Pro	Ser	Arg	Lys	Arg	Arg	Glu	Ile	Val	Met	Thr	Gln	Ser	Pro
		275					280					285			
Ala	Thr	Leu	Ser	Leu	Ser	Pro	Gly	Glu	Arg	Ala	Thr	Leu	Ser	Cys	Arg
	290					295					300				
Ala	Ser	Gln	Asp	Ile	Ser	Lys	Tyr	Leu	Asn	Trp	Tyr	Gln	Gln	Lys	Pro
305					310					315					320
Gly	Gln	Ala	Pro	Arg	Leu	Leu	Ile	Tyr	His	Thr	Ser	Arg	Leu	His	Ser
				325					330					335	
Gly	Ile	Pro	Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Tyr	Thr
			340					345					350		
Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp	Phe	Ala	Val	Tyr	Phe	Cys
		355					360					365			
Gln	Gln	Gly	Asn	Thr	Leu	Pro	Tyr	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Leu
	370					375					380				
Glu	Ile	Lys	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly
385					390					395					400
Gly	Ser	Gln	Val	Gln	Leu	Gln	Glu	Ser	Gly	Pro	Gly	Leu	Val	Lys	Pro
				405					410					415	
Ser	Glu	Thr	Leu	Ser	Leu	Thr	Cys	Thr	Val	Ser	Gly	Val	Ser	Leu	Pro
			420					425					430		
Asp	Tyr	Gly	Val	Ser	Trp	Ile	Arg	Gln	Pro	Pro	Gly	Lys	Gly	Leu	Glu
		435					440					445			
Trp	Ile	Gly	Val	Ile	Trp	Gly	Ser	Glu	Thr	Thr	Tyr	Tyr	Ser	Ser	Ser
	450					455					460				
Leu	Lys	Ser	Arg	Val	Thr	Ile	Ser	Lys	Asp	Asn	Ser	Lys	Asn	Gln	Val
465					470					475					480
Ser	Leu	Lys	Leu	Ser	Ser	Val	Thr	Ala	Ala	Asp	Thr	Ala	Val	Tyr	Tyr
				485					490					495	
Cys	Ala	Lys	His	Tyr	Tyr	Tyr	Gly	Gly	Ser	Tyr	Ala	Met	Asp	Tyr	Trp
			500					505					510		
Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Thr	Thr	Thr	Pro	Ala	Pro
		515					520					525			
Arg	Pro	Pro	Thr	Pro	Ala	Pro	Thr	Ile	Ala	Ser	Gln	Pro	Leu	Ser	Leu

_SL

His Ala Ala Arg Pro Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln Met
20 25 30

Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu Tyr
35 40 45

Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu Thr
50 55 60

Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala Lys Arg
65 70 75 80

Val Pro Gly Phe Val Asp Leu Ala Leu His Asp Gln Val His Leu Leu
85 90 95

Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp Arg Ser
100 105 110

Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu Asp
115 120 125

Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe Asp Met
130 135 140

Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly Glu
145 150 155 160

Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val Tyr
165 170 175

Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His Ile
180 185 190

His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met Ala
195 200 205

Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala Gln Leu
210 215 220

Leu Leu Ile Leu Ser His Ile Arg His Met Ser Ser Lys Arg Met Glu
225 230 235 240

His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Ser Asp Leu
245 250 255

Leu Leu Glu Met Leu Asp Ala His Arg Leu Gly Thr Gly Ala Glu Asp
260 265 270

Pro Arg Pro Ser Arg Lys Arg Arg Ser Leu Gly Asp Val Gly Gln Val
275 280 285

_SL

Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val
290 295 300

Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr Tyr Met
305 310 315 320

His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Trp
325 330 335

Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe Gln Gly
340 345 350

Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Ser Thr Val Tyr Met Glu
355 360 365

Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg
370 375 380

Asp Met Asn Ile Leu Ala Thr Val Pro Phe Asp Ile Trp Gly Gln Gly
385 390 395 400

Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
405 410 415

Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
420 425 430

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
435 440 445

Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys
450 455 460

Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val
465 470 475 480

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
485 490 495

Val Asn Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
500 505 510

Gly Asp Ser Val Pro Leu Thr Phe Gly Gly Gly Thr Arg Leu Glu Ile
515 520 525

Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile
530 535 540

Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala
545 550 555 560

_SL

Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr
565 570 575

Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu
580 585 590

Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile
595 600 605

Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp
610 615 620

Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu
625 630 635 640

Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly
645 650 655

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
660 665 670

Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
675 680 685

Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
690 695 700

Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
705 710 715 720

Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala
725 730 735

Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
740 745 750

<210> 995

<211> 752

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 995

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln Met
20 25 30

_SL

Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu Tyr
35 40 45

Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu Thr
50 55 60

Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala Lys Arg
65 70 75 80

Val Pro Gly Phe Val Asp Leu Thr Leu His Asp Gln Val His Leu Leu
85 90 95

Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp Arg Ser
100 105 110

Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu Asp
115 120 125

Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe Asp Met
130 135 140

Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly Glu
145 150 155 160

Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val Tyr
165 170 175

Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His Ile
180 185 190

His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met Ala
195 200 205

Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala Gln Leu
210 215 220

Leu Leu Ile Leu Ser His Ile Arg His Met Ser Asn Lys Arg Met Glu
225 230 235 240

His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Ser Asp Leu
245 250 255

Leu Leu Glu Met Leu Asp Ala His Arg Leu Gly Thr Gly Ala Glu Asp
260 265 270

Pro Arg Pro Ser Arg Lys Arg Arg Ser Leu Gly Asp Val Gly Gln Val
275 280 285

Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val
290 295 300

_SL

Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr Tyr Met
305 310 315 320

His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Trp
325 330 335

Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe Gln Gly
340 345 350

Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Ser Thr Val Tyr Met Glu
355 360 365

Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg
370 375 380

Asp Met Asn Ile Leu Ala Thr Val Pro Phe Asp Ile Trp Gly Gln Gly
385 390 395 400

Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
405 410 415

Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
420 425 430

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
435 440 445

Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys
450 455 460

Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val
465 470 475 480

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
485 490 495

Val Asn Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
500 505 510

Gly Asp Ser Val Pro Leu Thr Phe Gly Gly Gly Thr Arg Leu Glu Ile
515 520 525

Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile
530 535 540

Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala
545 550 555 560

Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr
565 570 575

_SL

Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu
580 585 590

Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile
595 600 605

Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp
610 615 620

Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Gly Gly Cys Glu Leu
625 630 635 640

Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly
645 650 655

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
660 665 670

Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
675 680 685

Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
690 695 700

Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
705 710 715 720

Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala
725 730 735

Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
740 745 750

<210> 996

<211> 746

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 996

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln Met
20 25 30

Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu Tyr
35 40 45

Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser ^{-SL}Met Met Gly Leu Leu Thr
 50 55 60
 Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala Lys Arg
 65 70 75 80
 Val Pro Gly Phe Val Asp Leu Ala Leu His Asp Gln Val His Leu Leu
 85 90 95
 Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp Arg Ser
 100 105 110
 Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu Asp
 115 120 125
 Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe Asp Met
 130 135 140
 Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly Glu
 145 150 155 160
 Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val Tyr
 165 170 175
 Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His Ile
 180 185 190
 His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met Ala
 195 200 205
 Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala Gln Leu
 210 215 220
 Leu Leu Ile Leu Ser His Ile Arg His Met Ser Ser Lys Arg Met Glu
 225 230 235 240
 His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Ser Asp Leu
 245 250 255
 Leu Leu Glu Met Leu Asp Ala His Arg Leu Gly Thr Gly Ala Glu Asp
 260 265 270
 Pro Arg Pro Ser Arg Lys Arg Arg Gln Val Gln Leu Val Gln Ser Gly
 275 280 285
 Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala
 290 295 300
 Ser Gly Tyr Thr Phe Thr Gly Tyr Tyr Met His Trp Val Arg Gln Ala
 305 310 315 320

Pro Gly Gln Gly Leu₃₂₅ Glu Trp Met Gly Trp₃₃₀^{-SL} Ile Asn Pro Asn Ser₃₃₅ Gly
 Gly Thr Asn Tyr₃₄₀ Ala Gln Lys Phe Gln₃₄₅ Gly Arg Val Thr Leu₃₅₀ Thr Arg
 Asp Thr Ser₃₅₅ Ile Ser Thr Val Tyr₃₆₀ Met Glu Leu Ser Arg₃₆₅ Leu Arg Ser
 Asp Asp₃₇₀ Thr Ala Val Tyr Tyr₃₇₅ Cys Ala Arg Asp Met₃₈₀ Asn Ile Leu Ala
 Thr Val Pro Phe Asp Ile₃₉₀ Trp Gly Gln Gly Thr₃₉₅ Met Val Thr Val Ser₄₀₀
 Ser Gly Gly Gly Gly₄₀₅ Ser Gly Gly Gly Gly₄₁₀ Ser Gly Gly Gly Gly₄₁₅ Ser
 Asp Ile Gln Met₄₂₀ Thr Gln Ser Pro Ser₄₂₅ Ser Leu Ser Ala Ser₄₃₀ Val Gly
 Asp Arg Val₄₃₅ Thr Ile Thr Cys Arg₄₄₀ Ala Ser Gln Ser Ile₄₄₅ Ser Ser Tyr
 Leu Asn Trp Tyr Gln Gln Lys₄₅₅ Pro Gly Lys Ala Pro₄₆₀ Lys Leu Leu Ile
 Tyr Ala Ala Ser Ser Leu₄₇₀ Gln Ser Gly Val Pro₄₇₅ Ser Arg Phe Ser Gly₄₈₀
 Ser Gly Ser Gly Thr₄₈₅ Asp Phe Thr Leu Thr₄₉₀ Val Asn Ser Leu Gln Pro₄₉₅
 Glu Asp Phe Ala₅₀₀ Thr Tyr Tyr Cys Gln₅₀₅ Gln Gly Asp Ser Val₅₁₀ Pro Leu
 Thr Phe Gly₅₁₅ Gly Gly Thr Arg Leu₅₂₀ Glu Ile Lys Thr Thr₅₂₅ Thr Pro Ala
 Pro Arg₅₃₀ Pro Pro Thr Pro Ala₅₃₅ Pro Thr Ile Ala Ser₅₄₀ Gln Pro Leu Ser
 Leu Arg Pro Glu Ala Cys₅₅₀ Arg Pro Ala Ala Gly₅₅₅ Gly Ala Val His Thr₅₆₀
 Arg Gly Leu Asp Phe₅₆₅ Ala Cys Asp Ile Tyr₅₇₀ Ile Trp Ala Pro Leu₅₇₅ Ala
 Gly Thr Cys Gly₅₈₀ Val Leu Leu Leu Ser₅₈₅ Leu Val Ile Thr Leu₅₉₀ Tyr Cys

Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile ^{-SL} Phe Lys Gln Pro Phe Met
 595 600 605
 Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe
 610 615 620
 Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg
 625 630 635 640
 Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn
 645 650 655
 Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
 660 665 670
 Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
 675 680 685
 Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
 690 695 700
 Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
 705 710 715 720
 Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
 725 730 735
 Ala Leu His Met Gln Ala Leu Pro Pro Arg
 740 745

<210> 997
 <211> 746
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 997
 Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
 1 5 10 15

His Ala Ala Arg Pro Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln Met
 20 25 30

Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu Tyr
 35 40 45

Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu Thr
 50 55 60

Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala Lys Arg
 Page 783

65					70					-SL 75				80
Val	Pro	Gly	Phe	Val	Asp	Leu	Thr	Leu	His	Asp	Gln	Val	His	Leu
				85					90					95
Glu	Cys	Ala	Trp	Met	Glu	Ile	Leu	Met	Ile	Gly	Leu	Val	Trp	Arg
			100					105					110	Ser
Met	Glu	His	Pro	Gly	Lys	Leu	Leu	Phe	Ala	Pro	Asn	Leu	Leu	Leu
		115					120					125		Asp
Arg	Asn	Gln	Gly	Lys	Cys	Val	Glu	Gly	Gly	Val	Glu	Ile	Phe	Asp
	130					135					140			Met
Leu	Leu	Ala	Thr	Ser	Ser	Arg	Phe	Arg	Met	Met	Asn	Leu	Gln	Gly
145					150					155				Glu
Glu	Phe	Val	Cys	Leu	Lys	Ser	Ile	Ile	Leu	Leu	Asn	Ser	Gly	Val
				165					170					175
Thr	Phe	Leu	Ser	Ser	Thr	Leu	Lys	Ser	Leu	Glu	Glu	Lys	Asp	His
			180					185					190	Ile
His	Arg	Val	Leu	Asp	Lys	Ile	Thr	Asp	Thr	Leu	Ile	His	Leu	Met
		195					200					205		Ala
Lys	Ala	Gly	Leu	Thr	Leu	Gln	Gln	Gln	His	Gln	Arg	Leu	Ala	Gln
	210					215					220			Leu
Leu	Leu	Ile	Leu	Ser	His	Ile	Arg	His	Met	Ser	Asn	Lys	Arg	Met
225					230					235				Glu
His	Leu	Tyr	Ser	Met	Lys	Cys	Lys	Asn	Val	Val	Pro	Leu	Ser	Asp
				245					250					255
Leu	Leu	Glu	Met	Leu	Asp	Ala	His	Arg	Leu	Gly	Thr	Gly	Ala	Glu
			260					265					270	Asp
Pro	Arg	Pro	Ser	Arg	Lys	Arg	Arg	Gln	Val	Gln	Leu	Val	Gln	Ser
		275					280					285		Gly
Ala	Glu	Val	Lys	Lys	Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys
	290					295					300			Ala
Ser	Gly	Tyr	Thr	Phe	Thr	Gly	Tyr	Tyr	Met	His	Trp	Val	Arg	Gln
305					310					315				320
Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met	Gly	Trp	Ile	Asn	Pro	Asn	Ser
				325					330					335
Gly	Thr	Asn	Tyr	Ala	Gln	Lys	Phe	Gln	Gly	Arg	Val	Thr	Leu	Thr
														Arg

_SL															
340				345				350							
Asp	Thr	Ser 355	Ile	Ser	Thr	Val	Tyr 360	Met	Glu	Leu	Ser	Arg 365	Leu	Arg	Ser
Asp	Asp 370	Thr	Ala	Val	Tyr	Tyr 375	Cys	Ala	Arg	Asp	Met 380	Asn	Ile	Leu	Ala
Thr 385	Val	Pro	Phe	Asp	Ile 390	Trp	Gly	Gln	Gly	Thr 395	Met	Val	Thr	Val	Ser 400
Ser	Gly	Gly	Gly	Gly 405	Ser	Gly	Gly	Gly	Gly 410	Ser	Gly	Gly	Gly	Gly 415	Ser
Asp	Ile	Gln	Met 420	Thr	Gln	Ser	Pro	Ser 425	Ser	Leu	Ser	Ala	Ser 430	Val	Gly
Asp	Arg	Val 435	Thr	Ile	Thr	Cys	Arg 440	Ala	Ser	Gln	Ser	Ile 445	Ser	Ser	Tyr
Leu	Asn 450	Trp	Tyr	Gln	Gln	Lys 455	Pro	Gly	Lys	Ala	Pro 460	Lys	Leu	Leu	Ile
Tyr 465	Ala	Ala	Ser	Ser	Leu 470	Gln	Ser	Gly	Val	Pro 475	Ser	Arg	Phe	Ser	Gly 480
Ser	Gly	Ser	Gly	Thr 485	Asp	Phe	Thr	Leu	Thr 490	Val	Asn	Ser	Leu	Gln 495	Pro
Glu	Asp	Phe	Ala 500	Thr	Tyr	Tyr	Cys	Gln 505	Gln	Gly	Asp	Ser	Val 510	Pro	Leu
Thr	Phe	Gly 515	Gly	Gly	Thr	Arg	Leu 520	Glu	Ile	Lys	Thr	Thr 525	Thr	Pro	Ala
Pro	Arg 530	Pro	Pro	Thr	Pro	Ala 535	Pro	Thr	Ile	Ala	Ser 540	Gln	Pro	Leu	Ser
Leu 545	Arg	Pro	Glu	Ala	Cys 550	Arg	Pro	Ala	Ala	Gly 555	Gly	Ala	Val	His	Thr 560
Arg	Gly	Leu	Asp	Phe 565	Ala	Cys	Asp	Ile	Tyr 570	Ile	Trp	Ala	Pro	Leu 575	Ala
Gly	Thr	Cys	Gly 580	Val	Leu	Leu	Leu	Ser 585	Leu	Val	Ile	Thr	Leu 590	Tyr	Cys
Lys	Arg	Gly 595	Arg	Lys	Lys	Leu	Leu 600	Tyr	Ile	Phe	Lys	Gln 605	Pro	Phe	Met
Arg	Pro	Val	Gln	Thr	Thr	Gln	Glu	Glu	Asp	Gly	Cys	Ser	Cys	Arg	Phe

_SL

610		615		620											
Pro	Glu	Glu	Glu	Glu	Gly	Gly	Cys	Glu	Leu	Arg	Val	Lys	Phe	Ser	Arg
625					630					635					640
Ser	Ala	Asp	Ala	Pro	Ala	Tyr	Gln	Gln	Gly	Gln	Asn	Gln	Leu	Tyr	Asn
				645					650					655	
Glu	Leu	Asn	Leu	Gly	Arg	Arg	Glu	Glu	Tyr	Asp	Val	Leu	Asp	Lys	Arg
			660					665					670		
Arg	Gly	Arg	Asp	Pro	Glu	Met	Gly	Gly	Lys	Pro	Arg	Arg	Lys	Asn	Pro
		675					680					685			
Gln	Glu	Gly	Leu	Tyr	Asn	Glu	Leu	Gln	Lys	Asp	Lys	Met	Ala	Glu	Ala
	690					695					700				
Tyr	Ser	Glu	Ile	Gly	Met	Lys	Gly	Glu	Arg	Arg	Arg	Gly	Lys	Gly	His
705					710					715					720
Asp	Gly	Leu	Tyr	Gln	Gly	Leu	Ser	Thr	Ala	Thr	Lys	Asp	Thr	Tyr	Asp
				725					730					735	
Ala	Leu	His	Met	Gln	Ala	Leu	Pro	Pro	Arg						
			740					745							

<210> 998
 <211> 748
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 998
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu
1 5 10 15
His Ala Ala Arg Pro Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln Met
20 25 30
Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu Tyr
35 40 45
Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu Thr
50 55 60
Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala Lys Arg
65 70 75 80
Val Pro Gly Phe Val Asp Leu Ala Leu His Asp Gln Val His Leu Leu
85 90 95

_SL

Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp Arg Ser
100 105 110

Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu Asp
115 120 125

Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe Asp Met
130 135 140

Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly Glu
145 150 155 160

Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val Tyr
165 170 175

Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His Ile
180 185 190

His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met Ala
195 200 205

Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala Gln Leu
210 215 220

Leu Leu Ile Leu Ser His Ile Arg His Met Ser Ser Lys Arg Met Glu
225 230 235 240

His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Ser Asp Leu
245 250 255

Leu Leu Glu Met Leu Asp Ala His Arg Leu Gly Thr Gly Ala Glu Asp
260 265 270

Pro Arg Pro Ser Arg Lys Arg Arg Ser Leu Gly Asp Val Gly Glu Val
275 280 285

Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu
290 295 300

Arg Leu Ser Cys Ala Val Ser Gly Phe Ala Leu Ser Asn His Gly Met
305 310 315 320

Ser Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Gly
325 330 335

Ile Val Tyr Ser Gly Ser Thr Tyr Tyr Ala Ala Ser Val Lys Gly Arg
340 345 350

Phe Thr Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr Leu Gln Met
355 360 365

_SL

Asn Ser Leu Arg Pro Glu Asp Thr Ala Ile Tyr Tyr Cys Ser Ala His
370 375 380

Gly Gly Glu Ser Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser
385 390 395 400

Ser Ala Ser Gly Gly Gly Gly Ser Gly Gly Arg Ala Ser Gly Gly Gly
405 410 415

Gly Ser Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
420 425 430

Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser
435 440 445

Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu
450 455 460

Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe
465 470 475 480

Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu
485 490 495

Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr
500 505 510

Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Thr Thr Thr
515 520 525

Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro
530 535 540

Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val
545 550 555 560

His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro
565 570 575

Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu
580 585 590

Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro
595 600 605

Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys
610 615 620

Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe
625 630 635 640

_SL

Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu
645 650 655

Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp
660 665 670

Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys
675 680 685

Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala
690 695 700

Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
705 710 715 720

Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
725 730 735

Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
740 745

<210> 999

<211> 748

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 999

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln Met
20 25 30

Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu Tyr
35 40 45

Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu Thr
50 55 60

Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala Lys Arg
65 70 75 80

Val Pro Gly Phe Val Asp Leu Thr Leu His Asp Gln Val His Leu Leu
85 90 95

Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp Arg Ser
100 105 110

_SL

Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu Asp
115 120 125

Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe Asp Met
130 135 140

Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly Glu
145 150 155 160

Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val Tyr
165 170 175

Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His Ile
180 185 190

His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met Ala
195 200 205

Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala Gln Leu
210 215 220

Leu Leu Ile Leu Ser His Ile Arg His Met Ser Asn Lys Arg Met Glu
225 230 235 240

His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Ser Asp Leu
245 250 255

Leu Leu Glu Met Leu Asp Ala His Arg Leu Gly Thr Gly Ala Glu Asp
260 265 270

Pro Arg Pro Ser Arg Lys Arg Arg Ser Leu Gly Asp Val Gly Glu Val
275 280 285

Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu
290 295 300

Arg Leu Ser Cys Ala Val Ser Gly Phe Ala Leu Ser Asn His Gly Met
305 310 315 320

Ser Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Gly
325 330 335

Ile Val Tyr Ser Gly Ser Thr Tyr Tyr Ala Ala Ser Val Lys Gly Arg
340 345 350

Phe Thr Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr Leu Gln Met
355 360 365

Asn Ser Leu Arg Pro Glu Asp Thr Ala Ile Tyr Tyr Cys Ser Ala His
370 375 380

_SL

Gly Gly Glu Ser Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser
385 390 395 400

Ser Ala Ser Gly Gly Gly Gly Ser Gly Gly Arg Ala Ser Gly Gly Gly
405 410 415

Gly Ser Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
420 425 430

Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser
435 440 445

Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu
450 455 460

Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe
465 470 475 480

Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu
485 490 495

Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr
500 505 510

Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Thr Thr Thr
515 520 525

Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro
530 535 540

Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val
545 550 555 560

His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro
565 570 575

Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu
580 585 590

Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro
595 600 605

Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys
610 615 620

Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe
625 630 635 640

Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu
645 650 655

_SL

Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp
660 665 670

Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys
675 680 685

Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala
690 695 700

Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
705 710 715 720

Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
725 730 735

Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
740 745

<210> 1000
<211> 742
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1000
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln Met
20 25 30

Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu Tyr
35 40 45

Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu Thr
50 55 60

Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala Lys Arg
65 70 75 80

Val Pro Gly Phe Val Asp Leu Ala Leu His Asp Gln Val His Leu Leu
85 90 95

Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp Arg Ser
100 105 110

Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu Asp
115 120 125

Arg Asn Gln Gly Lys Cys Val Glu Gly Gly^{-SL} Val Glu Ile Phe Asp Met
 130 135 140
 Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly Glu
 145 150 155
 Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val Tyr
 165 170 175
 Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His Ile
 180 185 190
 His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met Ala
 195 200 205
 Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala Gln Leu
 210 215 220
 Leu Leu Ile Leu Ser His Ile Arg His Met Ser Ser Lys Arg Met Glu
 225 230 235 240
 His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Ser Asp Leu
 245 250 255
 Leu Leu Glu Met Leu Asp Ala His Arg Leu Gly Thr Gly Ala Glu Asp
 260 265 270
 Pro Arg Pro Ser Arg Lys Arg Arg Glu Val Gln Leu Val Glu Ser Gly
 275 280 285
 Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Val
 290 295 300
 Ser Gly Phe Ala Leu Ser Asn His Gly Met Ser Trp Val Arg Arg Ala
 305 310 315 320
 Pro Gly Lys Gly Leu Glu Trp Val Ser Gly Ile Val Tyr Ser Gly Ser
 325 330 335
 Thr Tyr Tyr Ala Ala Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp
 340 345 350
 Asn Ser Arg Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu
 355 360 365
 Asp Thr Ala Ile Tyr Tyr Cys Ser Ala His Gly Gly Glu Ser Asp Val
 370 375 380
 Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Gly Gly Gly
 385 390 395 400

Gly Ser Gly Gly Arg₄₀₅ Ala Ser Gly Gly Gly^{-SL}₄₁₀ Gly Ser Asp Ile Gln₄₁₅ Leu
 Thr Gln Ser Pro₄₂₀ Ser Ser Leu Ser Ala₄₂₅ Ser Val Gly Asp Arg₄₃₀ Val Thr
 Ile Thr Cys₄₃₅ Arg Ala Ser Gln Ser₄₄₀ Ile Ser Ser Tyr Leu₄₄₅ Asn Trp Tyr
 Gln Gln₄₅₀ Lys Pro Gly Lys Ala₄₅₅ Pro Lys Leu Leu Ile₄₆₀ Tyr Ala Ala Ser
 Ser₄₆₅ Leu Gln Ser Gly Val₄₇₀ Pro Ser Arg Phe Ser₄₇₅ Gly Ser Gly Ser Gly₄₈₀
 Thr Asp Phe Thr Leu₄₈₅ Thr Ile Ser Ser Leu₄₉₀ Gln Pro Glu Asp Phe₄₉₅ Ala
 Thr Tyr Tyr Cys₅₀₀ Gln Gln Ser Tyr Ser₅₀₅ Thr Pro Tyr Thr Phe₅₁₀ Gly Gln
 Gly Thr Lys₅₁₅ Val Glu Ile Lys Thr₅₂₀ Thr Thr Pro Ala Pro₅₂₅ Arg Pro Pro
 Thr Pro₅₃₀ Ala Pro Thr Ile Ala₅₃₅ Ser Gln Pro Leu Ser₅₄₀ Leu Arg Pro Glu
 Ala₅₄₅ Cys Arg Pro Ala Ala₅₅₀ Gly Gly Ala Val His₅₅₅ Thr Arg Gly Leu Asp₅₆₀
 Phe Ala Cys Asp Ile₅₆₅ Tyr Ile Trp Ala Pro₅₇₀ Leu Ala Gly Thr Cys₅₇₅ Gly
 Val Leu Leu Leu₅₈₀ Ser Leu Val Ile Thr₅₈₅ Leu Tyr Cys Lys Arg₅₉₀ Gly Arg
 Lys Lys Leu₅₉₅ Leu Tyr Ile Phe Lys₆₀₀ Gln Pro Phe Met Arg₆₀₅ Pro Val Gln
 Thr Thr₆₁₀ Gln Glu Glu Asp Gly₆₁₅ Cys Ser Cys Arg Phe₆₂₀ Pro Glu Glu Glu
 Glu₆₂₅ Gly Gly Cys Glu Leu₆₃₀ Arg Val Lys Phe Ser₆₃₅ Arg Ser Ala Asp Ala₆₄₀
 Pro Ala Tyr Gln Gln₆₄₅ Gly Gln Asn Gln Leu₆₅₀ Tyr Asn Glu Leu Asn₆₅₅ Leu
 Gly Arg Arg Glu₆₆₀ Glu Tyr Asp Val Leu₆₆₅ Asp Lys Arg Arg Gly₆₇₀ Arg Asp

Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu
675 680 685

Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile
690 695 700

Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr
705 710 715 720

Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met
725 730 735

Gln Ala Leu Pro Pro Arg
740

<210> 1001
<211> 742
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1001
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln Met
20 25 30

Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu Tyr
35 40 45

Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu Thr
50 55 60

Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala Lys Arg
65 70 75 80

Val Pro Gly Phe Val Asp Leu Thr Leu His Asp Gln Val His Leu Leu
85 90 95

Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp Arg Ser
100 105 110

Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu Asp
115 120 125

Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe Asp Met
130 135 140

Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly Glu
Page 795

145		150		-SL 155		160									
Glu	Phe	Val	Cys	Leu 165	Lys	Ser	Ile	Ile	Leu 170	Leu	Asn	Ser	Gly	Val 175	Tyr
Thr	Phe	Leu	Ser 180	Ser	Thr	Leu	Lys	Ser 185	Leu	Glu	Glu	Lys	Asp 190	His	Ile
His	Arg	Val 195	Leu	Asp	Lys	Ile	Thr 200	Asp	Thr	Leu	Ile	His 205	Leu	Met	Ala
Lys	Ala 210	Gly	Leu	Thr	Leu	Gln 215	Gln	Gln	His	Gln	Arg 220	Leu	Ala	Gln	Leu
Leu 225	Leu	Ile	Leu	Ser	His 230	Ile	Arg	His	Met	Ser 235	Asn	Lys	Arg	Met	Glu 240
His	Leu	Tyr	Ser	Met 245	Lys	Cys	Lys	Asn	Val 250	Val	Pro	Leu	Ser	Asp 255	Leu
Leu	Leu	Glu	Met 260	Leu	Asp	Ala	His	Arg 265	Leu	Gly	Thr	Gly	Ala 270	Glu	Asp
Pro	Arg	Pro 275	Ser	Arg	Lys	Arg	Arg 280	Glu	Val	Gln	Leu	Val 285	Glu	Ser	Gly
Gly	Gly 290	Leu	Val	Gln	Pro	Gly 295	Gly	Ser	Leu	Arg	Leu 300	Ser	Cys	Ala	Val
Ser 305	Gly	Phe	Ala	Leu	Ser 310	Asn	His	Gly	Met	Ser 315	Trp	Val	Arg	Arg	Ala 320
Pro	Gly	Lys	Gly	Leu 325	Glu	Trp	Val	Ser	Gly 330	Ile	Val	Tyr	Ser	Gly 335	Ser
Thr	Tyr	Tyr	Ala 340	Ala	Ser	Val	Lys	Gly 345	Arg	Phe	Thr	Ile	Ser 350	Arg	Asp
Asn	Ser	Arg 355	Asn	Thr	Leu	Tyr	Leu 360	Gln	Met	Asn	Ser	Leu 365	Arg	Pro	Glu
Asp	Thr 370	Ala	Ile	Tyr	Tyr	Cys 375	Ser	Ala	His	Gly	Gly 380	Glu	Ser	Asp	Val
Trp 385	Gly	Gln	Gly	Thr	Thr 390	Val	Thr	Val	Ser	Ser 395	Ala	Ser	Gly	Gly	Gly 400
Gly	Ser	Gly	Gly	Arg 405	Ala	Ser	Gly	Gly	Gly 410	Gly	Ser	Asp	Ile	Gln 415	Leu
Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg	Val	Thr

_SL

420 425 430

Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr
 435 440 445

Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser
 450 455 460

Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
 465 470 475 480

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
 485 490 495

Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Tyr Thr Phe Gly Gln
 500 505 510

Gly Thr Lys Val Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro
 515 520 525

Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu
 530 535 540

Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp
 545 550 555 560

Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly
 565 570 575

Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg
 580 585 590

Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln
 595 600 605

Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu
 610 615 620

Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala
 625 630 635 640

Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu
 645 650 655

Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp
 660 665 670

Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu
 675 680 685

Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile

[illegible]

_SL

Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His
180 185 190

Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met
195 200 205

Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala Gln
210 215 220

Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Ser Lys Arg Met
225 230 235 240

Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Ser Asp
245 250 255

Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu Gly Thr Gly Ala Glu
260 265 270

Asp Pro Arg Pro Ser Arg Lys Arg Arg Ser Leu Gly Asp Val Gly Glu
275 280 285

Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu
290 295 300

Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr Leu
305 310 315 320

Asn Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
325 330 335

His Thr Ser Arg Leu His Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser
340 345 350

Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
355 360 365

Asp Phe Ala Val Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr
370 375 380

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly
385 390 395 400

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Glu Ser
405 410 415

Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr
420 425 430

Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln
435 440 445

_SL

Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Val Ile Trp Gly Ser Glu
450 455 460

Thr Thr Tyr Tyr Ser Ser Ser Leu Lys Ser Arg Val Thr Ile Ser Lys
465 470 475 480

Asp Asn Ser Lys Asn Gln Val Ser Leu Lys Leu Ser Ser Val Thr Ala
485 490 495

Ala Asp Thr Ala Val Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly
500 505 510

Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
515 520 525

Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile
530 535 540

Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala
545 550 555 560

Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr
565 570 575

Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu
580 585 590

Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile
595 600 605

Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp
610 615 620

Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu
625 630 635 640

Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly
645 650 655

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
660 665 670

Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
675 680 685

Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
690 695 700

Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
705 710 715 720

_SL

Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala
725 730 735

Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
740 745 750

<210> 1003
<211> 752
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1003
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asp Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln
20 25 30

Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu
35 40 45

Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu
50 55 60

Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala Lys
65 70 75 80

Arg Val Pro Gly Phe Val Asp Leu Thr Leu His Asp Gln Val His Leu
85 90 95

Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp Arg
100 105 110

Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu
115 120 125

Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe Asp
130 135 140

Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly
145 150 155 160

Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val
165 170 175

Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His
180 185 190

_SL

Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met
195 200 205

Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala Gln
210 215 220

Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Asn Lys Arg Met
225 230 235 240

Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Ser Asp
245 250 255

Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu Gly Thr Gly Ala Glu
260 265 270

Asp Pro Arg Pro Ser Arg Lys Arg Arg Ser Leu Gly Asp Val Gly Glu
275 280 285

Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu
290 295 300

Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr Leu
305 310 315 320

Asn Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
325 330 335

His Thr Ser Arg Leu His Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser
340 345 350

Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
355 360 365

Asp Phe Ala Val Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr
370 375 380

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly
385 390 395 400

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Glu Ser
405 410 415

Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr
420 425 430

Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln
435 440 445

Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Val Ile Trp Gly Ser Glu
450 455 460

_SL

Thr Thr Tyr Tyr Ser Ser Ser Leu Lys Ser Arg Val Thr Ile Ser Lys
465 470 475 480

Asp Asn Ser Lys Asn Gln Val Ser Leu Lys Leu Ser Ser Val Thr Ala
485 490 495

Ala Asp Thr Ala Val Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly
500 505 510

Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
515 520 525

Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile
530 535 540

Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala
545 550 555 560

Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr
565 570 575

Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu
580 585 590

Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile
595 600 605

Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp
610 615 620

Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu
625 630 635 640

Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly
645 650 655

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
660 665 670

Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
675 680 685

Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
690 695 700

Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
705 710 715 720

Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala
725 730 735

_SL

Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
740 745 750

<210> 1004
<211> 746
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1004
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asp Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln
20 25 30

Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu
35 40 45

Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu
50 55 60

Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala Lys
65 70 75 80

Arg Val Pro Gly Phe Val Asp Leu Ala Leu His Asp Gln Val His Leu
85 90 95

Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp Arg
100 105 110

Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu
115 120 125

Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe Asp
130 135 140

Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly
145 150 155 160

Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val
165 170 175

Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His
180 185 190

Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met
195 200 205

Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln ^{-SL} His Gln Arg Leu Ala Gln
 210 215 220
 Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Ser Lys Arg Met
 225 230 235 240
 Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Ser Asp
 245 250 255
 Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu Gly Thr Gly Ala Glu
 260 265 270
 Asp Pro Arg Pro Ser Arg Lys Arg Arg Glu Ile Val Met Thr Gln Ser
 275 280 285
 Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
 290 295 300
 Arg Ala Ser Gln Asp Ile Ser Lys Tyr Leu Asn Trp Tyr Gln Gln Lys
 305 310 315 320
 Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr His Thr Ser Arg Leu His
 325 330 335
 Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr
 340 345 350
 Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Val Tyr Phe
 355 360 365
 Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gln Gly Thr Lys
 370 375 380
 Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 385 390 395 400
 Gly Gly Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys
 405 410 415
 Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Val Ser Leu
 420 425 430
 Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu
 435 440 445
 Glu Trp Ile Gly Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Ser Ser
 450 455 460
 Ser Leu Lys Ser Arg Val Thr Ile Ser Lys Asp Asn Ser Lys Asn Gln
 465 470 475 480

Val Ser Leu Lys Leu Ser Ser Val Thr Ala^{-SL} Ala Asp Thr Ala Val Tyr
 485 490 495
 Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr
 500 505 510
 Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Thr Thr Thr Pro Ala
 515 520 525
 Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser
 530 535 540
 Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr
 545 550 555 560
 Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala
 565 570 575
 Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys
 580 585 590
 Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met
 595 600 605
 Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe
 610 615 620
 Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg
 625 630 635 640
 Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn
 645 650 655
 Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
 660 665 670
 Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
 675 680 685
 Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
 690 695 700
 Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
 705 710 715 720
 Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
 725 730 735
 Ala Leu His Met Gln Ala Leu Pro Pro Arg
 740 745

_SL

<210> 1005
<211> 746
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1005
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asp Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln
20 25 30

Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu
35 40 45

Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu
50 55 60

Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala Lys
65 70 75 80

Arg Val Pro Gly Phe Val Asp Leu Thr Leu His Asp Gln Val His Leu
85 90 95

Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp Arg
100 105 110

Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu
115 120 125

Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe Asp
130 135 140

Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly
145 150 155 160

Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val
165 170 175

Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His
180 185 190

Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met
195 200 205

Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala Gln
210 215 220

Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Asn Lys Arg Met
Page 807

				225				230				-SL 235				240			
Glu	His	Leu	Tyr	Ser 245	Met	Lys	Cys	Lys	Asn 250	Val	Val	Pro	Leu	Ser 255	Asp				
Leu	Leu	Leu	Glu 260	Met	Leu	Asp	Ala	His 265	Arg	Leu	Gly	Thr	Gly 270	Ala	Glu				
Asp	Pro	Arg 275	Pro	Ser	Arg	Lys	Arg 280	Arg	Glu	Ile	Val	Met 285	Thr	Gln	Ser				
Pro	Ala 290	Thr	Leu	Ser	Leu	Ser 295	Pro	Gly	Glu	Arg	Ala 300	Thr	Leu	Ser	Cys				
Arg 305	Ala	Ser	Gln	Asp	Ile 310	Ser	Lys	Tyr	Leu	Asn 315	Trp	Tyr	Gln	Gln	Lys 320				
Pro	Gly	Gln	Ala	Pro 325	Arg	Leu	Leu	Ile	Tyr 330	His	Thr	Ser	Arg	Leu 335	His				
Ser	Gly	Ile	Pro 340	Ala	Arg	Phe	Ser	Gly 345	Ser	Gly	Ser	Gly	Thr 350	Asp	Tyr				
Thr	Leu	Thr 355	Ile	Ser	Ser	Leu	Gln 360	Pro	Glu	Asp	Phe	Ala 365	Val	Tyr	Phe				
Cys	Gln 370	Gln	Gly	Asn	Thr	Leu 375	Pro	Tyr	Thr	Phe	Gly 380	Gln	Gly	Thr	Lys				
Leu 385	Glu	Ile	Lys	Gly	Gly 390	Gly	Gly	Ser	Gly	Gly 395	Gly	Gly	Ser	Gly	Gly 400				
Gly	Gly	Ser	Gln	Val 405	Gln	Leu	Gln	Glu	Ser 410	Gly	Pro	Gly	Leu	Val 415	Lys				
Pro	Ser	Glu	Thr 420	Leu	Ser	Leu	Thr	Cys 425	Thr	Val	Ser	Gly	Val 430	Ser	Leu				
Pro	Asp	Tyr 435	Gly	Val	Ser	Trp	Ile 440	Arg	Gln	Pro	Pro	Gly 445	Lys	Gly	Leu				
Glu	Trp 450	Ile	Gly	Val	Ile	Trp 455	Gly	Ser	Glu	Thr	Thr 460	Tyr	Tyr	Ser	Ser				
Ser 465	Leu	Lys	Ser	Arg	Val 470	Thr	Ile	Ser	Lys	Asp 475	Asn	Ser	Lys	Asn	Gln 480				
Val	Ser	Leu	Lys	Leu 485	Ser	Ser	Val	Thr	Ala 490	Ala	Asp	Thr	Ala	Val 495	Tyr				
Tyr	Cys	Ala	Lys	His	Tyr	Tyr	Tyr	Gly	Gly	Ser	Tyr	Ala	Met	Asp	Tyr				

_SL

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1006

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asp Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln
20 25 30

Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu
35 40 45

Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu
50 55 60

Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala Lys
65 70 75 80

Arg Val Pro Gly Phe Val Asp Leu Ala Leu His Asp Gln Val His Leu
85 90 95

Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp Arg
100 105 110

Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu
115 120 125

Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe Asp
130 135 140

Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly
145 150 155 160

Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val
165 170 175

Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His
180 185 190

Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met
195 200 205

Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala Gln
210 215 220

Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Ser Lys Arg Met
225 230 235 240

Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Ser Asp
245 250 255

_SL

Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu Gly Thr Gly Ala Glu
260 265 270

Asp Pro Arg Pro Ser Arg Lys Arg Arg Ser Leu Gly Asp Val Gly Gln
275 280 285

Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser
290 295 300

Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr Tyr
305 310 315 320

Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly
325 330 335

Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe Gln
340 345 350

Gly Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Ser Thr Val Tyr Met
355 360 365

Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala
370 375 380

Arg Asp Met Asn Ile Leu Ala Thr Val Pro Phe Asp Ile Trp Gly Gln
385 390 395 400

Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
405 410 415

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser
420 425 430

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala
435 440 445

Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly
450 455 460

Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly
465 470 475 480

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
485 490 495

Thr Val Asn Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln
500 505 510

Gln Gly Asp Ser Val Pro Leu Thr Phe Gly Gly Gly Thr Arg Leu Glu
515 520 525

_SL

Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr
530 535 540

Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala
545 550 555 560

Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile
565 570 575

Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser
580 585 590

Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr
595 600 605

Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu
610 615 620

Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu
625 630 635 640

Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln
645 650 655

Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu
660 665 670

Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly
675 680 685

Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln
690 695 700

Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu
705 710 715 720

Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr
725 730 735

Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro
740 745 750

Arg

<210> 1007

<211> 753

<212> PRT

<213> Artificial Sequence

<220>

_SL

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1007

```
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1          5          10          15

His Ala Ala Arg Pro Asp Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln
          20          25          30

Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu
          35          40          45

Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu
          50          55          60

Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala Lys
65          70          75          80

Arg Val Pro Gly Phe Val Asp Leu Thr Leu His Asp Gln Val His Leu
          85          90          95

Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp Arg
          100          105          110

Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu
          115          120          125

Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe Asp
          130          135          140

Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly
145          150          155          160

Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val
          165          170          175

Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His
          180          185          190

Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met
          195          200          205

Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala Gln
210          215          220

Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Asn Lys Arg Met
225          230          235          240

Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Ser Asp
          245          250          255
```


_SL

Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu Gly Thr Gly Ala Glu
260 265 270

Asp Pro Arg Pro Ser Arg Lys Arg Arg Ser Leu Gly Asp Val Gly Gln
275 280 285

Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser
290 295 300

Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr Tyr
305 310 315 320

Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly
325 330 335

Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe Gln
340 345 350

Gly Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Ser Thr Val Tyr Met
355 360 365

Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala
370 375 380

Arg Asp Met Asn Ile Leu Ala Thr Val Pro Phe Asp Ile Trp Gly Gln
385 390 395 400

Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
405 410 415

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser
420 425 430

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala
435 440 445

Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly
450 455 460

Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly
465 470 475 480

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
485 490 495

Thr Val Asn Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln
500 505 510

Gln Gly Asp Ser Val Pro Leu Thr Phe Gly Gly Gly Thr Arg Leu Glu
515 520 525

_SL

Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr
530 535 540

Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala
545 550 555 560

Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile
565 570 575

Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser
580 585 590

Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr
595 600 605

Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu
610 615 620

Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu
625 630 635 640

Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln
645 650 655

Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu
660 665 670

Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly
675 680 685

Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln
690 695 700

Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu
705 710 715 720

Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr
725 730 735

Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro
740 745 750

Arg

<210> 1008
<211> 747
<212> PRT
<213> Artificial Sequence

<220>
<221> source

_SL

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1008

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asp Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln
20 25 30

Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu
35 40 45

Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu
50 55 60

Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala Lys
65 70 75 80

Arg Val Pro Gly Phe Val Asp Leu Ala Leu His Asp Gln Val His Leu
85 90 95

Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp Arg
100 105 110

Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu
115 120 125

Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe Asp
130 135 140

Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly
145 150 155 160

Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val
165 170 175

Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His
180 185 190

Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met
195 200 205

Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala Gln
210 215 220

Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Ser Lys Arg Met
225 230 235 240

Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Ser Asp
245 250 255

Leu Leu Leu Glu Met Leu Asp Ala His Arg ^{-SL} Leu Gly Thr Gly Ala Glu
 260 265 270
 Asp Pro Arg Pro Ser Arg Lys Arg Arg Gln Val Gln Leu Val Gln Ser
 275 280 285
 Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys
 290 295 300
 Ala Ser Gly Tyr Thr Phe Thr Gly Tyr Tyr Met His Trp Val Arg Gln
 305 310 315 320
 Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Trp Ile Asn Pro Asn Ser
 325 330 335
 Gly Gly Thr Asn Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Leu Thr
 340 345 350
 Arg Asp Thr Ser Ile Ser Thr Val Tyr Met Glu Leu Ser Arg Leu Arg
 355 360 365
 Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Met Asn Ile Leu
 370 375 380
 Ala Thr Val Pro Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val
 385 390 395 400
 Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 405 410 415
 Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
 420 425 430
 Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser
 435 440 445
 Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu
 450 455 460
 Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser
 465 470 475 480
 Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Val Asn Ser Leu Gln
 485 490 495
 Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Gly Asp Ser Val Pro
 500 505 510
 Leu Thr Phe Gly Gly Gly Thr Arg Leu Glu Ile Lys Thr Thr Thr Pro
 515 520 525

Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr ^{-SL} Ile Ala Ser Gln Pro Leu
 530 535 540
 Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His
 545 550 555 560
 Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu
 565 570 575
 Ala Gly Thr Cys Gly Val Leu Leu Ser Leu Val Ile Thr Leu Tyr
 580 585 590
 Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe
 595 600 605
 Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg
 610 615 620
 Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser
 625 630 635 640
 Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr
 645 650 655
 Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys
 660 665 670
 Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn
 675 680 685
 Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu
 690 695 700
 Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly
 705 710 715 720
 His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr
 725 730 735
 Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
 740 745

<210> 1009

<211> 747

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1009

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu

1	5				10				15						
His	Ala	Ala	Arg 20	Pro	Asp	Ser	Leu	Ala 25	Leu	Ser	Leu	Thr	Ala 30	Asp	Gln
Met	Val	Ser 35	Ala	Leu	Leu	Asp	Ala 40	Glu	Pro	Pro	Ile	Leu 45	Tyr	Ser	Glu
Tyr	Asp 50	Pro	Thr	Arg	Pro	Phe 55	Ser	Glu	Ala	Ser	Met 60	Met	Gly	Leu	Leu
Thr 65	Asn	Leu	Ala	Asp	Arg 70	Glu	Leu	Val	His	Met 75	Ile	Asn	Trp	Ala	Lys 80
Arg	Val	Pro	Gly	Phe 85	Val	Asp	Leu	Thr	Leu 90	His	Asp	Gln	Val	His 95	Leu
Leu	Glu	Cys	Ala 100	Trp	Met	Glu	Ile	Leu 105	Met	Ile	Gly	Leu	Val 110	Trp	Arg
Ser	Met	Glu 115	His	Pro	Gly	Lys	Leu 120	Leu	Phe	Ala	Pro	Asn 125	Leu	Leu	Leu
Asp	Arg 130	Asn	Gln	Gly	Lys	Cys 135	Val	Glu	Gly	Gly	Val 140	Glu	Ile	Phe	Asp
Met 145	Leu	Leu	Ala	Thr	Ser 150	Ser	Arg	Phe	Arg	Met 155	Met	Asn	Leu	Gln	Gly 160
Glu	Glu	Phe	Val	Cys 165	Leu	Lys	Ser	Ile	Ile 170	Leu	Leu	Asn	Ser	Gly 175	Val
Tyr	Thr	Phe	Leu 180	Ser	Ser	Thr	Leu	Lys 185	Ser	Leu	Glu	Glu	Lys 190	Asp	His
Ile	His	Arg 195	Val	Leu	Asp	Lys	Ile 200	Thr	Asp	Thr	Leu	Ile 205	His	Leu	Met
Ala	Lys 210	Ala	Gly	Leu	Thr	Leu 215	Gln	Gln	Gln	His	Gln 220	Arg	Leu	Ala	Gln
Leu 225	Leu	Leu	Ile	Leu	Ser 230	His	Ile	Arg	His	Met 235	Ser	Asn	Lys	Arg	Met 240
Glu	His	Leu	Tyr	Ser 245	Met	Lys	Cys	Lys	Asn 250	Val	Val	Pro	Leu	Ser 255	Asp
Leu	Leu	Leu	Glu 260	Met	Leu	Asp	Ala	His 265	Arg	Leu	Gly	Thr	Gly 270	Ala	Glu
Asp	Pro	Arg	Pro	Ser	Arg	Lys	Arg	Arg	Gln	Val	Gln	Leu	Val	Gln	Ser

_SL

275		280		285											
Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys
	290					295					300				
Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Gly	Tyr	Tyr	Met	His	Trp	Val	Arg	Gln
305					310					315					320
Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met	Gly	Trp	Ile	Asn	Pro	Asn	Ser
				325					330					335	
Gly	Gly	Thr	Asn	Tyr	Ala	Gln	Lys	Phe	Gln	Gly	Arg	Val	Thr	Leu	Thr
			340					345					350		
Arg	Asp	Thr	Ser	Ile	Ser	Thr	Val	Tyr	Met	Glu	Leu	Ser	Arg	Leu	Arg
		355					360					365			
Ser	Asp	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Asp	Met	Asn	Ile	Leu
	370					375					380				
Ala	Thr	Val	Pro	Phe	Asp	Ile	Trp	Gly	Gln	Gly	Thr	Met	Val	Thr	Val
385					390					395					400
Ser	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly
				405					410					415	
Ser	Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val
			420					425					430		
Gly	Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Ser	Ile	Ser	Ser
		435					440					445			
Tyr	Leu	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu
	450					455					460				
Ile	Tyr	Ala	Ala	Ser	Ser	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser
465					470					475					480
Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Val	Asn	Ser	Leu	Gln
				485					490					495	
Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Gly	Asp	Ser	Val	Pro
			500					505					510		
Leu	Thr	Phe	Gly	Gly	Gly	Thr	Arg	Leu	Glu	Ile	Lys	Thr	Thr	Thr	Pro
		515					520					525			
Ala	Pro	Arg	Pro	Pro	Thr	Pro	Ala	Pro	Thr	Ile	Ala	Ser	Gln	Pro	Leu
	530					535					540				
Ser	Leu	Arg	Pro	Glu	Ala	Cys	Arg	Pro	Ala	Ala	Gly	Gly	Ala	Val	His

_SL

Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu
35 40 45

Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu
50 55 60

Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala Lys
65 70 75 80

Arg Val Pro Gly Phe Val Asp Leu Ala Leu His Asp Gln Val His Leu
85 90 95

Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp Arg
100 105 110

Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu
115 120 125

Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe Asp
130 135 140

Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly
145 150 155 160

Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val
165 170 175

Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His
180 185 190

Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met
195 200 205

Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala Gln
210 215 220

Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Ser Lys Arg Met
225 230 235 240

Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Ser Asp
245 250 255

Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu Gly Thr Gly Ala Glu
260 265 270

Asp Pro Arg Pro Ser Arg Lys Arg Arg Ser Leu Gly Asp Val Gly Glu
275 280 285

Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
290 295 300

_SL

Leu Arg Leu Ser Cys Ala Val Ser Gly Phe Ala Leu Ser Asn His Gly
305 310 315 320

Met Ser Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
325 330 335

Gly Ile Val Tyr Ser Gly Ser Thr Tyr Tyr Ala Ala Ser Val Lys Gly
340 345 350

Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr Leu Gln
355 360 365

Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Ile Tyr Tyr Cys Ser Ala
370 375 380

His Gly Gly Glu Ser Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val
385 390 395 400

Ser Ser Ala Ser Gly Gly Gly Gly Ser Gly Gly Arg Ala Ser Gly Gly
405 410 415

Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala
420 425 430

Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile
435 440 445

Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
450 455 460

Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg
465 470 475 480

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser
485 490 495

Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser
500 505 510

Thr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Thr Thr
515 520 525

Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln
530 535 540

Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala
545 550 555 560

Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala
565 570 575

_SL

Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr
580 585 590

Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln
595 600 605

Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser
610 615 620

Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys
625 630 635 640

Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln
645 650 655

Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
660 665 670

Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg
675 680 685

Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met
690 695 700

Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly
705 710 715 720

Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp
725 730 735

Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
740 745

<210> 1011

<211> 749

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1011

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asp Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln
20 25 30

Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu
35 40 45

_SL

Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu
50 55 60

Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala Lys
65 70 75 80

Arg Val Pro Gly Phe Val Asp Leu Thr Leu His Asp Gln Val His Leu
85 90 95

Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp Arg
100 105 110

Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu
115 120 125

Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe Asp
130 135 140

Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly
145 150 155 160

Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val
165 170 175

Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His
180 185 190

Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met
195 200 205

Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala Gln
210 215 220

Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Asn Lys Arg Met
225 230 235 240

Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Ser Asp
245 250 255

Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu Gly Thr Gly Ala Glu
260 265 270

Asp Pro Arg Pro Ser Arg Lys Arg Arg Ser Leu Gly Asp Val Gly Glu
275 280 285

Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
290 295 300

Leu Arg Leu Ser Cys Ala Val Ser Gly Phe Ala Leu Ser Asn His Gly
305 310 315 320

_SL

Met Ser Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
325 330 335

Gly Ile Val Tyr Ser Gly Ser Thr Tyr Tyr Ala Ala Ser Val Lys Gly
340 345 350

Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr Leu Gln
355 360 365

Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Ile Tyr Tyr Cys Ser Ala
370 375 380

His Gly Gly Glu Ser Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val
385 390 395 400

Ser Ser Ala Ser Gly Gly Gly Gly Ser Gly Gly Arg Ala Ser Gly Gly
405 410 415

Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala
420 425 430

Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile
435 440 445

Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
450 455 460

Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg
465 470 475 480

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser
485 490 495

Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser
500 505 510

Thr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Thr Thr
515 520 525

Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln
530 535 540

Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala
545 550 555 560

Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala
565 570 575

Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr
580 585 590

_SL

Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln
595 600 605

Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser
610 615 620

Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys
625 630 635 640

Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln
645 650 655

Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
660 665 670

Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg
675 680 685

Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met
690 695 700

Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly
705 710 715 720

Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp
725 730 735

Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
740 745

<210> 1012
<211> 743
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1012
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asp Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln
20 25 30

Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu
35 40 45

Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu
50 55 60

Thr Asn Leu Ala Asp Arg Glu Leu Val His ^{-SL} Met Ile Asn Trp Ala Lys
 65 70 75 80
 Arg Val Pro Gly Phe Val Asp Leu Ala Leu His Asp Gln Val His Leu
 85 90 95
 Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp Arg
 100 105 110
 Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu
 115 120 125
 Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe Asp
 130 135 140
 Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly
 145 150 155 160
 Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val
 165 170 175
 Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His
 180 185 190
 Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met
 195 200 205
 Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala Gln
 210 215 220
 Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Ser Lys Arg Met
 225 230 235 240
 Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Ser Asp
 245 250 255
 Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu Gly Thr Gly Ala Glu
 260 265 270
 Asp Pro Arg Pro Ser Arg Lys Arg Arg Glu Val Gln Leu Val Glu Ser
 275 280 285
 Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala
 290 295 300
 Val Ser Gly Phe Ala Leu Ser Asn His Gly Met Ser Trp Val Arg Arg
 305 310 315 320
 Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Gly Ile Val Tyr Ser Gly
 325 330 335

Ser Thr Tyr Tyr₃₄₀ Ala Ala Ser Val Lys₃₄₅ Gly^{-SL} Arg Phe Thr Ile₃₅₀ Ser Arg
 Asp Asn Ser₃₅₅ Arg Asn Thr Leu Tyr₃₆₀ Leu Gln Met Asn Ser₃₆₅ Leu Arg Pro
 Glu Asp₃₇₀ Thr Ala Ile Tyr Tyr₃₇₅ Cys Ser Ala His Gly₃₈₀ Gly Glu Ser Asp
 Val₃₈₅ Trp Gly Gln Gly Thr₃₉₀ Thr Val Thr Val₃₉₅ Ser Ala Ser Gly₄₀₀
 Gly Gly Ser Gly₄₀₅ Arg Ala Ser Gly Gly₄₁₀ Gly Gly Ser Asp Ile₄₁₅ Gln
 Leu Thr Gln Ser₄₂₀ Pro Ser Ser Leu Ser₄₂₅ Ala Ser Val Gly₄₃₀ Asp Arg Val
 Thr Ile Thr₄₃₅ Cys Arg Ala Ser Gln₄₄₀ Ser Ile Ser Ser Tyr₄₄₅ Leu Asn Trp
 Tyr Gln₄₅₀ Gln Lys Pro Gly Lys₄₅₅ Ala Pro Lys Leu Leu₄₆₀ Ile Tyr Ala Ala
 Ser₄₆₅ Ser Leu Gln Ser Gly₄₇₀ Val Pro Ser Arg Phe₄₇₅ Ser Gly Ser Gly₄₈₀
 Gly Thr Asp Phe Thr₄₈₅ Leu Thr Ile Ser Ser₄₉₀ Leu Gln Pro Glu Asp₄₉₅ Phe
 Ala Thr Tyr Tyr₅₀₀ Cys Gln Gln Ser Tyr₅₀₅ Ser Thr Pro Tyr Thr₅₁₀ Phe Gly
 Gln Gly Thr₅₁₅ Lys Val Glu Ile Lys₅₂₀ Thr Thr Thr Pro Ala₅₂₅ Pro Arg Pro
 Pro Thr₅₃₀ Pro Ala Pro Thr Ile₅₃₅ Ala Ser Gln Pro Leu₅₄₀ Ser Leu Arg Pro
 Glu₅₄₅ Ala Cys Arg Pro Ala₅₅₀ Ala Gly Gly Ala Val₅₅₅ His Thr Arg Gly Leu₅₆₀
 Asp Phe Ala Cys Asp₅₆₅ Ile Tyr Ile Trp Ala₅₇₀ Pro Leu Ala Gly Thr₅₇₅ Cys
 Gly Val Leu₅₈₀ Leu Ser Leu Val Ile₅₈₅ Thr Leu Tyr Cys Lys₅₉₀ Arg Gly
 Arg Lys Lys₅₉₅ Leu Leu Tyr Ile Phe₆₀₀ Lys Gln Pro Phe Met₆₀₅ Arg Pro Val

Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser ^{-SL}Cys Arg Phe Pro Glu Glu
 610 615 620
 Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp
 625 630 635 640
 Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn
 645 650 655
 Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg
 660 665 670
 Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly
 675 680 685
 Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu
 690 695 700
 Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu
 705 710 715 720
 Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His
 725 730 735
 Met Gln Ala Leu Pro Pro Arg
 740

<210> 1013
 <211> 743
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1013
 Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
 1 5 10 15

His Ala Ala Arg Pro Asp Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln
 20 25 30

Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu
 35 40 45

Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu
 50 55 60

Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala Lys
 65 70 75 80

Arg Val Pro Gly Phe Val Asp Leu Thr Leu His Asp Gln Val His Leu
 Page 830

_SL															
85								90				95			
Leu	Glu	Cys	Ala 100	Trp	Met	Glu	Ile	Leu 105	Met	Ile	Gly	Leu	Val 110	Trp	Arg
Ser	Met	Glu 115	His	Pro	Gly	Lys	Leu 120	Leu	Phe	Ala	Pro	Asn 125	Leu	Leu	Leu
Asp	Arg 130	Asn	Gln	Gly	Lys	Cys 135	Val	Glu	Gly	Gly	Val 140	Glu	Ile	Phe	Asp
Met 145	Leu	Leu	Ala	Thr	Ser 150	Ser	Arg	Phe	Arg	Met 155	Met	Asn	Leu	Gln	Gly 160
Glu	Glu	Phe	Val	Cys 165	Leu	Lys	Ser	Ile	Ile 170	Leu	Leu	Asn	Ser	Gly 175	Val
Tyr	Thr	Phe	Leu 180	Ser	Ser	Thr	Leu	Lys 185	Ser	Leu	Glu	Glu	Lys 190	Asp	His
Ile	His	Arg 195	Val	Leu	Asp	Lys	Ile 200	Thr	Asp	Thr	Leu	Ile 205	His	Leu	Met
Ala	Lys 210	Ala	Gly	Leu	Thr	Leu 215	Gln	Gln	Gln	His	Gln 220	Arg	Leu	Ala	Gln
Leu 225	Leu	Leu	Ile	Leu	Ser 230	His	Ile	Arg	His	Met 235	Ser	Asn	Lys	Arg	Met 240
Glu	His	Leu	Tyr	Ser 245	Met	Lys	Cys	Lys	Asn 250	Val	Val	Pro	Leu	Ser 255	Asp
Leu	Leu	Leu	Glu 260	Met	Leu	Asp	Ala	His 265	Arg	Leu	Gly	Thr	Gly 270	Ala	Glu
Asp	Pro	Arg 275	Pro	Ser	Arg	Lys	Arg 280	Arg	Glu	Val	Gln	Leu 285	Val	Glu	Ser
Gly	Gly 290	Gly	Leu	Val	Gln	Pro 295	Gly	Gly	Ser	Leu	Arg 300	Leu	Ser	Cys	Ala
Val 305	Ser	Gly	Phe	Ala	Leu 310	Ser	Asn	His	Gly	Met 315	Ser	Trp	Val	Arg	Arg 320
Ala	Pro	Gly	Lys	Gly 325	Leu	Glu	Trp	Val	Ser 330	Gly	Ile	Val	Tyr	Ser 335	Gly
Ser	Thr	Tyr	Tyr 340	Ala	Ala	Ser	Val	Lys 345	Gly	Arg	Phe	Thr	Ile 350	Ser	Arg
Asp	Asn	Ser	Arg	Asn	Thr	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Pro

_SL

355		360		365											
Glu	Asp	Thr	Ala	Ile	Tyr	Tyr	Cys	Ser	Ala	His	Gly	Gly	Glu	Ser	Asp
	370					375					380				
Val	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Ala	Ser	Gly	Gly
385					390					395					400
Gly	Gly	Ser	Gly	Gly	Arg	Ala	Ser	Gly	Gly	Gly	Gly	Ser	Asp	Ile	Gln
				405					410					415	
Leu	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg	Val
			420					425					430		
Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Ser	Ile	Ser	Ser	Tyr	Leu	Asn	Trp
		435					440					445			
Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile	Tyr	Ala	Ala
	450					455					460				
Ser	Ser	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly	Ser
465					470					475					480
Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp	Phe
				485					490					495	
Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Ser	Tyr	Ser	Thr	Pro	Tyr	Thr	Phe	Gly
			500					505					510		
Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Thr	Thr	Thr	Pro	Ala	Pro	Arg	Pro
		515					520					525			
Pro	Thr	Pro	Ala	Pro	Thr	Ile	Ala	Ser	Gln	Pro	Leu	Ser	Leu	Arg	Pro
	530					535					540				
Glu	Ala	Cys	Arg	Pro	Ala	Ala	Gly	Gly	Ala	Val	His	Thr	Arg	Gly	Leu
545					550					555					560
Asp	Phe	Ala	Cys	Asp	Ile	Tyr	Ile	Trp	Ala	Pro	Leu	Ala	Gly	Thr	Cys
				565					570					575	
Gly	Val	Leu	Leu	Leu	Ser	Leu	Val	Ile	Thr	Leu	Tyr	Cys	Lys	Arg	Gly
			580					585					590		
Arg	Lys	Lys	Leu	Leu	Tyr	Ile	Phe	Lys	Gln	Pro	Phe	Met	Arg	Pro	Val
		595					600					605			
Gln	Thr	Thr	Gln	Glu	Glu	Asp	Gly	Cys	Ser	Cys	Arg	Phe	Pro	Glu	Glu
	610					615					620				
Glu	Glu	Gly	Gly	Cys	Glu	Leu	Arg	Val	Lys	Phe	Ser	Arg	Ser	Ala	Asp

_SL

Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu
115 120 125

Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe Asp
130 135 140

Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly
145 150 155 160

Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val
165 170 175

Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His
180 185 190

Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met
195 200 205

Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala Gln
210 215 220

Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Ser Lys Arg Met
225 230 235 240

Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Ser Asp
245 250 255

Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu Gly Thr Gly Ala Glu
260 265 270

Asp Pro Arg Pro Ser Arg Lys Arg Arg Ser Leu Gly Asp Val Gly Glu
275 280 285

Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu
290 295 300

Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr Leu
305 310 315 320

Asn Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
325 330 335

His Thr Ser Arg Leu His Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser
340 345 350

Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
355 360 365

Asp Phe Ala Val Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr
370 375 380

_SL

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly
385 390 395 400

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Glu Ser
405 410 415

Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr
420 425 430

Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln
435 440 445

Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Val Ile Trp Gly Ser Glu
450 455 460

Thr Thr Tyr Tyr Ser Ser Ser Leu Lys Ser Arg Val Thr Ile Ser Lys
465 470 475 480

Asp Asn Ser Lys Asn Gln Val Ser Leu Lys Leu Ser Ser Val Thr Ala
485 490 495

Ala Asp Thr Ala Val Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly
500 505 510

Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
515 520 525

Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile
530 535 540

Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala
545 550 555 560

Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr
565 570 575

Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu
580 585 590

Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile
595 600 605

Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp
610 615 620

Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu
625 630 635 640

Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly
645 650 655

_SL

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
660 665 670

Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
675 680 685

Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
690 695 700

Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
705 710 715 720

Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala
725 730 735

Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
740 745 750

<210> 1015
<211> 752
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1015
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln
20 25 30

Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu
35 40 45

Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu
50 55 60

Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala Lys
65 70 75 80

Arg Val Pro Gly Phe Val Asp Leu Thr Leu His Asp Gln Val His Leu
85 90 95

Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp Arg
100 105 110

Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu
115 120 125

_SL

Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe Asp
130 135 140

Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly
145 150 155 160

Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val
165 170 175

Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His
180 185 190

Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met
195 200 205

Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala Gln
210 215 220

Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Asn Lys Arg Met
225 230 235 240

Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Ser Asp
245 250 255

Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu Gly Thr Gly Ala Glu
260 265 270

Asp Pro Arg Pro Ser Arg Lys Arg Arg Ser Leu Gly Asp Val Gly Glu
275 280 285

Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu
290 295 300

Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr Leu
305 310 315 320

Asn Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
325 330 335

His Thr Ser Arg Leu His Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser
340 345 350

Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
355 360 365

Asp Phe Ala Val Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr
370 375 380

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly
385 390 395 400

_SL

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Glu Ser
405 410 415

Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr
420 425 430

Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln
435 440 445

Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Val Ile Trp Gly Ser Glu
450 455 460

Thr Thr Tyr Tyr Ser Ser Ser Leu Lys Ser Arg Val Thr Ile Ser Lys
465 470 475 480

Asp Asn Ser Lys Asn Gln Val Ser Leu Lys Leu Ser Ser Val Thr Ala
485 490 495

Ala Asp Thr Ala Val Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly
500 505 510

Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
515 520 525

Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile
530 535 540

Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala
545 550 555 560

Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr
565 570 575

Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu
580 585 590

Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile
595 600 605

Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp
610 615 620

Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu
625 630 635 640

Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly
645 650 655

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
660 665 670

_SL

Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
675 680 685

Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
690 695 700

Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
705 710 715 720

Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala
725 730 735

Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
740 745 750

<210> 1016
<211> 746
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1016
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln
20 25 30

Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu
35 40 45

Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu
50 55 60

Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala Lys
65 70 75 80

Arg Val Pro Gly Phe Val Asp Leu Ala Leu His Asp Gln Val His Leu
85 90 95

Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp Arg
100 105 110

Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu
115 120 125

Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe Asp
130 135 140

Met Leu Leu Ala Thr Ser Ser Arg Phe Arg ^{SL} Met Met Asn Leu Gln Gly
 145 150 155 160
 Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val
 165 170 175
 Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His
 180 185 190
 Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met
 195 200 205
 Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala Gln
 210 215 220
 Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Ser Lys Arg Met
 225 230 235 240
 Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Ser Asp
 245 250 255
 Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu Gly Thr Gly Ala Glu
 260 265 270
 Asp Pro Arg Pro Ser Arg Lys Arg Arg Glu Ile Val Met Thr Gln Ser
 275 280 285
 Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
 290 295 300
 Arg Ala Ser Gln Asp Ile Ser Lys Tyr Leu Asn Trp Tyr Gln Gln Lys
 305 310 315 320
 Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr His Thr Ser Arg Leu His
 325 330 335
 Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr
 340 345 350
 Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Val Tyr Phe
 355 360 365
 Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gln Gly Thr Lys
 370 375 380
 Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
 385 390 395 400
 Gly Gly Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys
 405 410 415

Pro Ser Glu Thr₄₂₀ Leu Ser Leu Thr Cys₄₂₅ Thr^{-SL} Val Ser Gly Val₄₃₀ Ser Leu
 Pro Asp Tyr₄₃₅ Gly Val Ser Trp Ile₄₄₀ Arg Gln Pro Pro Gly₄₄₅ Lys Gly Leu
 Glu Trp₄₅₀ Ile Gly Val Ile Trp₄₅₅ Gly Ser Glu Thr Thr₄₆₀ Tyr Tyr Ser Ser
 Ser₄₆₅ Leu Lys Ser Arg Val₄₇₀ Thr Ile Ser Lys Asp₄₇₅ Asn Ser Lys Asn Gln₄₈₀
 Val Ser Leu Lys Leu₄₈₅ Ser Ser Val Thr Ala₄₉₀ Ala Asp Thr Ala Val₄₉₅ Tyr
 Tyr Cys Ala Lys₅₀₀ His Tyr Tyr Tyr Gly₅₀₅ Gly Ser Tyr Ala Met₅₁₀ Asp Tyr
 Trp Gly Gln₅₁₅ Gly Thr Leu Val Thr₅₂₀ Val Ser Ser Thr Thr₅₂₅ Thr Pro Ala
 Pro Arg₅₃₀ Pro Pro Thr Pro Ala₅₃₅ Pro Thr Ile Ala Ser₅₄₀ Gln Pro Leu Ser
 Leu₅₄₅ Arg Pro Glu Ala Cys₅₅₀ Arg Pro Ala Ala Gly₅₅₅ Gly Ala Val His Thr₅₆₀
 Arg Gly Leu Asp Phe₅₆₅ Ala Cys Asp Ile Tyr₅₇₀ Ile Trp Ala Pro Leu₅₇₅ Ala
 Gly Thr Cys Gly₅₈₀ Val Leu Leu Leu Ser₅₈₅ Leu Val Ile Thr Leu₅₉₀ Tyr Cys
 Lys Arg Gly₅₉₅ Arg Lys Lys Leu Leu₆₀₀ Tyr Ile Phe Lys Gln₆₀₅ Pro Phe Met
 Arg Pro Val Gln Thr Thr Gln₆₁₅ Glu Glu Asp Gly Cys₆₂₀ Ser Cys Arg Phe
 Pro₆₂₅ Glu Glu Glu Glu Gly₆₃₀ Gly Cys Glu Leu Arg₆₃₅ Val Lys Phe Ser Arg₆₄₀
 Ser Ala Asp Ala Pro₆₄₅ Ala Tyr Gln Gln Gly₆₅₀ Gln Asn Gln Leu Tyr Asn₆₅₅
 Glu Leu Asn Leu₆₆₀ Gly Arg Arg Glu Glu₆₆₅ Tyr Asp Val Leu Asp₆₇₀ Lys Arg
 Arg Gly Arg₆₇₅ Asp Pro Glu Met Gly₆₈₀ Gly Lys Pro Arg Arg₆₈₅ Lys Asn Pro

Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys^{-SL} Asp Lys Met Ala Glu Ala
690 695 700

Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
705 710 715 720

Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
725 730 735

Ala Leu His Met Gln Ala Leu Pro Pro Arg
740 745

<210> 1017

<211> 746

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1017

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln
20 25 30

Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu
35 40 45

Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu
50 55 60

Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala Lys
65 70 75 80

Arg Val Pro Gly Phe Val Asp Leu Thr Leu His Asp Gln Val His Leu
85 90 95

Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp Arg
100 105 110

Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu
115 120 125

Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe Asp
130 135 140

Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly
145 150 155 160

Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val
Page 842

SL															
165								170				175			
Tyr	Thr	Phe	Leu 180	Ser	Ser	Thr	Leu	Lys 185	Ser	Leu	Glu	Glu	Lys 190	Asp	His
Ile	His	Arg 195	Val	Leu	Asp	Lys	Ile 200	Thr	Asp	Thr	Leu	Ile 205	His	Leu	Met
Ala	Lys 210	Ala	Gly	Leu	Thr	Leu 215	Gln	Gln	Gln	His	Gln 220	Arg	Leu	Ala	Gln
Leu 225	Leu	Leu	Ile	Leu	Ser 230	His	Ile	Arg	His	Met 235	Ser	Asn	Lys	Arg	Met 240
Glu	His	Leu	Tyr	Ser 245	Met	Lys	Cys	Lys	Asn 250	Val	Val	Pro	Leu	Ser 255	Asp
Leu	Leu	Leu	Glu 260	Met	Leu	Asp	Ala	His 265	Arg	Leu	Gly	Thr	Gly 270	Ala	Glu
Asp	Pro	Arg 275	Pro	Ser	Arg	Lys	Arg 280	Arg	Glu	Ile	Val	Met 285	Thr	Gln	Ser
Pro	Ala 290	Thr	Leu	Ser	Leu	Ser 295	Pro	Gly	Glu	Arg	Ala 300	Thr	Leu	Ser	Cys
Arg 305	Ala	Ser	Gln	Asp	Ile 310	Ser	Lys	Tyr	Leu	Asn 315	Trp	Tyr	Gln	Gln	Lys 320
Pro	Gly	Gln	Ala	Pro 325	Arg	Leu	Leu	Ile	Tyr 330	His	Thr	Ser	Arg	Leu 335	His
Ser	Gly	Ile	Pro 340	Ala	Arg	Phe	Ser	Gly 345	Ser	Gly	Ser	Gly	Thr 350	Asp	Tyr
Thr	Leu	Thr 355	Ile	Ser	Ser	Leu	Gln 360	Pro	Glu	Asp	Phe	Ala 365	Val	Tyr	Phe
Cys	Gln 370	Gln	Gly	Asn	Thr	Leu 375	Pro	Tyr	Thr	Phe	Gly 380	Gln	Gly	Thr	Lys
Leu 385	Glu	Ile	Lys	Gly	Gly 390	Gly	Gly	Ser	Gly	Gly 395	Gly	Gly	Ser	Gly	Gly 400
Gly	Gly	Ser	Gln	Val 405	Gln	Leu	Gln	Glu	Ser 410	Gly	Pro	Gly	Leu	Val 415	Lys
Pro	Ser	Glu	Thr 420	Leu	Ser	Leu	Thr	Cys 425	Thr	Val	Ser	Gly	Val 430	Ser	Leu
Pro	Asp	Tyr	Gly	Val	Ser	Trp	Ile	Arg	Gln	Pro	Pro	Gly	Lys	Gly	Leu

_SL

435		440		445											
Glu	Trp	Ile	Gly	Val	Ile	Trp	Gly	Ser	Glu	Thr	Thr	Tyr	Tyr	Ser	Ser
	450					455					460				
Ser	Leu	Lys	Ser	Arg	Val	Thr	Ile	Ser	Lys	Asp	Asn	Ser	Lys	Asn	Gln
465					470					475					480
Val	Ser	Leu	Lys	Leu	Ser	Ser	Val	Thr	Ala	Ala	Asp	Thr	Ala	Val	Tyr
				485					490					495	
Tyr	Cys	Ala	Lys	His	Tyr	Tyr	Tyr	Gly	Gly	Ser	Tyr	Ala	Met	Asp	Tyr
			500					505					510		
Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Thr	Thr	Thr	Pro	Ala
		515					520					525			
Pro	Arg	Pro	Pro	Thr	Pro	Ala	Pro	Thr	Ile	Ala	Ser	Gln	Pro	Leu	Ser
	530					535					540				
Leu	Arg	Pro	Glu	Ala	Cys	Arg	Pro	Ala	Ala	Gly	Gly	Ala	Val	His	Thr
545					550					555					560
Arg	Gly	Leu	Asp	Phe	Ala	Cys	Asp	Ile	Tyr	Ile	Trp	Ala	Pro	Leu	Ala
				565					570					575	
Gly	Thr	Cys	Gly	Val	Leu	Leu	Leu	Ser	Leu	Val	Ile	Thr	Leu	Tyr	Cys
			580					585					590		
Lys	Arg	Gly	Arg	Lys	Lys	Leu	Leu	Tyr	Ile	Phe	Lys	Gln	Pro	Phe	Met
		595					600					605			
Arg	Pro	Val	Gln	Thr	Thr	Gln	Glu	Glu	Asp	Gly	Cys	Ser	Cys	Arg	Phe
	610					615					620				
Pro	Glu	Glu	Glu	Glu	Gly	Gly	Cys	Glu	Leu	Arg	Val	Lys	Phe	Ser	Arg
625					630					635					640
Ser	Ala	Asp	Ala	Pro	Ala	Tyr	Gln	Gln	Gly	Gln	Asn	Gln	Leu	Tyr	Asn
				645					650					655	
Glu	Leu	Asn	Leu	Gly	Arg	Arg	Glu	Glu	Tyr	Asp	Val	Leu	Asp	Lys	Arg
			660					665					670		
Arg	Gly	Arg	Asp	Pro	Glu	Met	Gly	Gly	Lys	Pro	Arg	Arg	Lys	Asn	Pro
		675					680					685			
Gln	Glu	Gly	Leu	Tyr	Asn	Glu	Leu	Gln	Lys	Asp	Lys	Met	Ala	Glu	Ala
	690					695					700				
Tyr	Ser	Glu	Ile	Gly	Met	Lys	Gly	Glu	Arg	Arg	Arg	Gly	Lys	Gly	His

705 710 715 720

Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp

725 730 735

Ala Leu His Met Gln Ala Leu Pro Pro Arg
740 745

```
<210> 1018
<211> 753
<212> PRT
<213> Artificial Sequence
```

```
<220>  
<221> source  
<223> /note="Description of Artificial Sequence: Synthetic  
polypeptide"
```

```
<400> 1018
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu
1           5           10          15
```

His Ala Ala Arg Pro Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln
20 25 30

Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu
35 40 45

Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu
50 55 60

Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala Lys
65 70 75 80

Arg Val Pro Gly Phe Val Asp Leu Ala Leu His Asp Gln Val His Leu
85 90 95

Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp Arg
100 105 110

Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu
115 120 125

Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe Asp
130 135 140

Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly
145 150 155 160

Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val
165 170 175

Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His
180 185 190

_SL

Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met
195 200 205

Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala Gln
210 215 220

Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Ser Lys Arg Met
225 230 235 240

Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Ser Asp
245 250 255

Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu Gly Thr Gly Ala Glu
260 265 270

Asp Pro Arg Pro Ser Arg Lys Arg Arg Ser Leu Gly Asp Val Gly Gln
275 280 285

Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser
290 295 300

Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr Tyr
305 310 315 320

Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly
325 330 335

Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe Gln
340 345 350

Gly Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Ser Thr Val Tyr Met
355 360 365

Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala
370 375 380

Arg Asp Met Asn Ile Leu Ala Thr Val Pro Phe Asp Ile Trp Gly Gln
385 390 395 400

Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
405 410 415

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser
420 425 430

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala
435 440 445

Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly
450 455 460

_SL

Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly
465 470 475 480

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
485 490 495

Thr Val Asn Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln
500 505 510

Gln Gly Asp Ser Val Pro Leu Thr Phe Gly Gly Gly Thr Arg Leu Glu
515 520 525

Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr
530 535 540

Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala
545 550 555 560

Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile
565 570 575

Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser
580 585 590

Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr
595 600 605

Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu
610 615 620

Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Gly Gly Cys Glu
625 630 635 640

Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln
645 650 655

Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu
660 665 670

Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly
675 680 685

Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln
690 695 700

Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu
705 710 715 720

Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr
725 730 735

_SL

Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro
740 745 750

Arg

<210> 1019
<211> 753
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1019
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln
20 25 30

Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu
35 40 45

Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu
50 55 60

Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala Lys
65 70 75 80

Arg Val Pro Gly Phe Val Asp Leu Thr Leu His Asp Gln Val His Leu
85 90 95

Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp Arg
100 105 110

Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu
115 120 125

Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe Asp
130 135 140

Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly
145 150 155 160

Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val
165 170 175

Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His
180 185 190

_SL

Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met
195 200 205

Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala Gln
210 215 220

Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Asn Lys Arg Met
225 230 235 240

Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Ser Asp
245 250 255

Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu Gly Thr Gly Ala Glu
260 265 270

Asp Pro Arg Pro Ser Arg Lys Arg Arg Ser Leu Gly Asp Val Gly Gln
275 280 285

Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser
290 295 300

Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr Tyr
305 310 315 320

Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly
325 330 335

Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe Gln
340 345 350

Gly Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Ser Thr Val Tyr Met
355 360 365

Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala
370 375 380

Arg Asp Met Asn Ile Leu Ala Thr Val Pro Phe Asp Ile Trp Gly Gln
385 390 395 400

Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
405 410 415

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser
420 425 430

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala
435 440 445

Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly
450 455 460

_SL

Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly
465 470 475 480

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
485 490 495

Thr Val Asn Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln
500 505 510

Gln Gly Asp Ser Val Pro Leu Thr Phe Gly Gly Gly Thr Arg Leu Glu
515 520 525

Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr
530 535 540

Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala
545 550 555 560

Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile
565 570 575

Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Ser
580 585 590

Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr
595 600 605

Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu
610 615 620

Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu
625 630 635 640

Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln
645 650 655

Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu
660 665 670

Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly
675 680 685

Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln
690 695 700

Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu
705 710 715 720

Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr
725 730 735

_SL

Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro
740 745 750

Arg

<210> 1020
<211> 747
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1020
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln
20 25 30

Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu
35 40 45

Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu
50 55 60

Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala Lys
65 70 75 80

Arg Val Pro Gly Phe Val Asp Leu Ala Leu His Asp Gln Val His Leu
85 90 95

Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp Arg
100 105 110

Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu
115 120 125

Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe Asp
130 135 140

Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly
145 150 155 160

Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val
165 170 175

Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His
180 185 190

Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr^{-SL} Leu Ile His Leu Met
 195 200 205
 Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala Gln
 210 215 220
 Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Ser Lys Arg Met
 225 230 235 240
 Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Ser Asp
 245 250 255
 Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu Gly Thr Gly Ala Glu
 260 265 270
 Asp Pro Arg Pro Ser Arg Lys Arg Arg Gln Val Gln Leu Val Gln Ser
 275 280 285
 Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys
 290 295 300
 Ala Ser Gly Tyr Thr Phe Thr Gly Tyr Tyr Met His Trp Val Arg Gln
 305 310 315 320
 Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Trp Ile Asn Pro Asn Ser
 325 330 335
 Gly Gly Thr Asn Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Leu Thr
 340 345 350
 Arg Asp Thr Ser Ile Ser Thr Val Tyr Met Glu Leu Ser Arg Leu Arg
 355 360 365
 Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Met Asn Ile Leu
 370 375 380
 Ala Thr Val Pro Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val
 385 390 395 400
 Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 405 410 415
 Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
 420 425 430
 Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser
 435 440 445
 Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu
 450 455 460

Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly^{SL} Val Pro Ser Arg Phe Ser
 465 470 475 480
 Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Val Asn Ser Leu Gln
 485 490 495
 Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Gly Asp Ser Val Pro
 500 505 510
 Leu Thr Phe Gly Gly Gly Thr Arg Leu Glu Ile Lys Thr Thr Thr Pro
 515 520 525
 Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu
 530 535 540
 Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His
 545 550 555 560
 Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu
 565 570 575
 Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr
 580 585 590
 Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe
 595 600 605
 Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg
 610 615 620
 Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser
 625 630 635 640
 Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr
 645 650 655
 Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys
 660 665 670
 Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn
 675 680 685
 Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu
 690 695 700
 Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly
 705 710 715 720
 His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr
 725 730 735

Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
740 745 SL

<210> 1021
<211> 747
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1021
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln
20 25 30

Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu
35 40 45

Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu
50 55 60

Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala Lys
65 70 75 80

Arg Val Pro Gly Phe Val Asp Leu Thr Leu His Asp Gln Val His Leu
85 90 95

Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp Arg
100 105 110

Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu
115 120 125

Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe Asp
130 135 140

Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly
145 150 155 160

Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val
165 170 175

Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His
180 185 190

Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met
195 200 205

Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala Gln
Page 854

_SL

210		215		220											
Leu 225	Leu	Leu	Ile	Leu	Ser 230	His	Ile	Arg	His	Met 235	Ser	Asn	Lys	Arg	Met 240
Glu	His	Leu	Tyr	Ser 245	Met	Lys	Cys	Lys	Asn 250	Val	Val	Pro	Leu	Ser 255	Asp
Leu	Leu	Leu	Glu 260	Met	Leu	Asp	Ala	His 265	Arg	Leu	Gly	Thr	Gly 270	Ala	Glu
Asp	Pro	Arg 275	Pro	Ser	Arg	Lys	Arg 280	Arg	Gln	Val	Gln	Leu 285	Val	Gln	Ser
Gly	Ala 290	Glu	Val	Lys	Lys	Pro 295	Gly	Ala	Ser	Val	Lys 300	Val	Ser	Cys	Lys
Ala 305	Ser	Gly	Tyr	Thr	Phe 310	Thr	Gly	Tyr	Tyr	Met 315	His	Trp	Val	Arg	Gln 320
Ala	Pro	Gly	Gln	Gly 325	Leu	Glu	Trp	Met	Gly 330	Trp	Ile	Asn	Pro	Asn 335	Ser
Gly	Gly	Thr	Asn 340	Tyr	Ala	Gln	Lys	Phe 345	Gln	Gly	Arg	Val	Thr 350	Leu	Thr
Arg	Asp	Thr 355	Ser	Ile	Ser	Thr	Val 360	Tyr	Met	Glu	Leu	Ser 365	Arg	Leu	Arg
Ser	Asp 370	Asp	Thr	Ala	Val	Tyr 375	Tyr	Cys	Ala	Arg	Asp 380	Met	Asn	Ile	Leu
Ala 385	Thr	Val	Pro	Phe	Asp 390	Ile	Trp	Gly	Gln	Gly 395	Thr	Met	Val	Thr	Val 400
Ser	Ser	Gly	Gly	Gly 405	Gly	Ser	Gly	Gly	Gly 410	Gly	Ser	Gly	Gly	Gly 415	Gly
Ser	Asp	Ile	Gln 420	Met	Thr	Gln	Ser	Pro 425	Ser	Ser	Leu	Ser	Ala 430	Ser	Val
Gly	Asp	Arg 435	Val	Thr	Ile	Thr	Cys 440	Arg	Ala	Ser	Gln	Ser 445	Ile	Ser	Ser
Tyr	Leu 450	Asn	Trp	Tyr	Gln	Gln 455	Lys	Pro	Gly	Lys	Ala 460	Pro	Lys	Leu	Leu
Ile 465	Tyr	Ala	Ala	Ser	Ser 470	Leu	Gln	Ser	Gly	Val 475	Pro	Ser	Arg	Phe	Ser 480
Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Val	Asn	Ser	Leu	Gln

485 490 _SL 495

Pro Glu Asp Phe₅₀₀ Ala Thr Tyr Tyr Cys₅₀₅ Gln Gln Gly Asp Ser₅₁₀ Val Pro

Leu Thr Phe₅₁₅ Gly Gly Gly Thr Arg₅₂₀ Leu Glu Ile Lys Thr₅₂₅ Thr Thr Pro

Ala Pro₅₃₀ Arg Pro Pro Thr Pro₅₃₅ Ala Pro Thr Ile Ala₅₄₀ Ser Gln Pro Leu

Ser₅₄₅ Leu Arg Pro Glu Ala₅₅₀ Cys Arg Pro Ala Ala₅₅₅ Gly Gly Ala Val His₅₆₀

Thr Arg Gly Leu Asp₅₆₅ Phe Ala Cys Asp Ile₅₇₀ Tyr Ile Trp Ala Pro₅₇₅ Leu

Ala Gly Thr Cys₅₈₀ Gly Val Leu Leu Leu₅₈₅ Ser Leu Val Ile Thr₅₉₀ Leu Tyr

Cys Lys Arg₅₉₅ Gly Arg Lys Lys Leu₆₀₀ Leu Tyr Ile Phe Lys₆₀₅ Gln Pro Phe

Met Arg₆₁₀ Pro Val Gln Thr Thr₆₁₅ Gln Glu Glu Asp Gly₆₂₀ Cys Ser Cys Arg

Phe₆₂₅ Pro Glu Glu Glu Glu₆₃₀ Gly Gly Cys Glu Leu₆₃₅ Arg Val Lys Phe Ser₆₄₀

Arg Ser Ala Asp Ala₆₄₅ Pro Ala Tyr Gln Gln₆₅₀ Gly Gln Asn Gln Leu₆₅₅ Tyr

Asn Glu Leu Asn₆₆₀ Leu Gly Arg Arg Glu₆₆₅ Glu Tyr Asp Val Leu₆₇₀ Asp Lys

Arg Arg Gly₆₇₅ Arg Asp Pro Glu Met₆₈₀ Gly Gly Lys Pro Arg₆₈₅ Arg Lys Asn

Pro Gln₆₉₀ Glu Gly Leu Tyr Asn₆₉₅ Glu Leu Gln Lys Asp₇₀₀ Lys Met Ala Glu

Ala Tyr Ser Glu Ile Gly₇₁₀ Met Lys Gly Glu Arg₇₁₅ Arg Arg Gly Lys Gly₇₂₀

His Asp Gly Leu Tyr₇₂₅ Gln Gly Leu Ser Thr₇₃₀ Ala Thr Lys Asp Thr₇₃₅ Tyr

Asp Ala Leu His₇₄₀ Met Gln Ala Leu Pro₇₄₅ Pro Arg

<210> 1022

_SL

<211> 749

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1022

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln
20 25 30

Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu
35 40 45

Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu
50 55 60

Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala Lys
65 70 75 80

Arg Val Pro Gly Phe Val Asp Leu Ala Leu His Asp Gln Val His Leu
85 90 95

Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp Arg
100 105 110

Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu
115 120 125

Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe Asp
130 135 140

Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly
145 150 155 160

Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val
165 170 175

Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His
180 185 190

Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met
195 200 205

Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala Gln
210 215 220

Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Ser Lys Arg Met
225 230 235 240

_SL

Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Ser Asp
245 250 255

Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu Gly Thr Gly Ala Glu
260 265 270

Asp Pro Arg Pro Ser Arg Lys Arg Arg Ser Leu Gly Asp Val Gly Glu
275 280 285

Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
290 295 300

Leu Arg Leu Ser Cys Ala Val Ser Gly Phe Ala Leu Ser Asn His Gly
305 310 315 320

Met Ser Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
325 330 335

Gly Ile Val Tyr Ser Gly Ser Thr Tyr Tyr Ala Ala Ser Val Lys Gly
340 345 350

Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr Leu Gln
355 360 365

Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Ile Tyr Tyr Cys Ser Ala
370 375 380

His Gly Gly Glu Ser Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val
385 390 395 400

Ser Ser Ala Ser Gly Gly Gly Gly Ser Gly Gly Arg Ala Ser Gly Gly
405 410 415

Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala
420 425 430

Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile
435 440 445

Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
450 455 460

Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg
465 470 475 480

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser
485 490 495

Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser
500 505 510

_SL

Thr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Thr Thr
515 520 525

Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln
530 535 540

Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala
545 550 555 560

Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala
565 570 575

Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr
580 585 590

Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln
595 600 605

Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser
610 615 620

Cys Arg Phe Pro Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys
625 630 635 640

Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln
645 650 655

Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
660 665 670

Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg
675 680 685

Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met
690 695 700

Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly
705 710 715 720

Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp
725 730 735

Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
740 745

<210> 1023

<211> 749

<212> PRT

<213> Artificial Sequence

<220>

_SL

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1023

```
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1          5          10          15

His Ala Ala Arg Pro Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln
          20          25          30

Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu
          35          40          45

Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu
          50          55          60

Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala Lys
65          70          75          80

Arg Val Pro Gly Phe Val Asp Leu Thr Leu His Asp Gln Val His Leu
          85          90          95

Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp Arg
          100          105          110

Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu
          115          120          125

Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe Asp
          130          135          140

Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly
145          150          155          160

Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val
          165          170          175

Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His
          180          185          190

Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met
          195          200          205

Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala Gln
210          215          220

Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Asn Lys Arg Met
225          230          235          240

Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Ser Asp
          245          250          255
```

_SL

Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu Gly Thr Gly Ala Glu
260 265 270

Asp Pro Arg Pro Ser Arg Lys Arg Arg Ser Leu Gly Asp Val Gly Glu
275 280 285

Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
290 295 300

Leu Arg Leu Ser Cys Ala Val Ser Gly Phe Ala Leu Ser Asn His Gly
305 310 315 320

Met Ser Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
325 330 335

Gly Ile Val Tyr Ser Gly Ser Thr Tyr Tyr Ala Ala Ser Val Lys Gly
340 345 350

Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr Leu Gln
355 360 365

Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Ile Tyr Tyr Cys Ser Ala
370 375 380

His Gly Gly Glu Ser Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val
385 390 395 400

Ser Ser Ala Ser Gly Gly Gly Gly Ser Gly Gly Arg Ala Ser Gly Gly
405 410 415

Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala
420 425 430

Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile
435 440 445

Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
450 455 460

Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg
465 470 475 480

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser
485 490 495

Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser
500 505 510

Thr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Thr Thr
515 520 525

_SL

Thr Pro Ala Pro Arg Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln
530 535 540

Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala
545 550 555 560

Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala
565 570 575

Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr
580 585 590

Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln
595 600 605

Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser
610 615 620

Cys Arg Phe Pro Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys
625 630 635 640

Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln
645 650 655

Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
660 665 670

Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg
675 680 685

Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met
690 695 700

Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly
705 710 715 720

Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp
725 730 735

Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
740 745

<210> 1024
<211> 743
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1024

Met Ala Leu Pro Val Thr Ala Leu Leu ^{-SL}Leu Pro Leu Ala Leu Leu Leu
 1 5 10 15
 His Ala Ala Arg Pro Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln
 20 25 30
 Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu
 35 40 45
 Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu
 50 55 60
 Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala Lys
 65 70 75 80
 Arg Val Pro Gly Phe Val Asp Leu Ala Leu His Asp Gln Val His Leu
 85 90 95
 Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp Arg
 100 105 110
 Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu
 115 120 125
 Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe Asp
 130 135 140
 Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly
 145 150 155 160
 Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val
 165 170 175
 Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His
 180 185 190
 Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met
 195 200 205
 Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala Gln
 210 215 220
 Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Ser Lys Arg Met
 225 230 235 240
 Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Ser Asp
 245 250 255
 Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu Gly Thr Gly Ala Glu
 260 265 270

Asp Pro Arg₂₇₅ Pro Ser Arg Lys Arg₂₈₀ Arg Glu^{-SL} Val Gln Leu₂₈₅ Val Glu Ser
 Gly Gly₂₉₀ Gly Leu Val Gln Pro₂₉₅ Gly Gly Ser Leu Arg₃₀₀ Leu Ser Cys Ala
 Val Ser Gly Phe Ala Leu₃₁₀ Ser Asn His Gly Met₃₁₅ Ser Trp Val Arg Arg₃₂₀
 Ala Pro Gly Lys Gly₃₂₅ Leu Glu Trp Val Ser₃₃₀ Gly Ile Val Tyr Ser₃₃₅ Gly
 Ser Thr Tyr Tyr₃₄₀ Ala Ala Ser Val Lys₃₄₅ Gly Arg Phe Thr Ile₃₅₀ Ser Arg
 Asp Asn Ser₃₅₅ Arg Asn Thr Leu Tyr₃₆₀ Leu Gln Met Asn Ser₃₆₅ Leu Arg Pro
 Glu Asp₃₇₀ Thr Ala Ile Tyr Tyr₃₇₅ Cys Ser Ala His Gly₃₈₀ Gly Glu Ser Asp
 Val Trp Gly Gln Gly Thr₃₉₀ Thr Val Thr Val Ser₃₉₅ Ser Ala Ser Gly Gly₄₀₀
 Gly Gly Ser Gly Gly₄₀₅ Arg Ala Ser Gly Gly₄₁₀ Gly Gly Ser Asp Ile₄₁₅ Gln
 Leu Thr Gln Ser₄₂₀ Pro Ser Ser Leu Ser₄₂₅ Ala Ser Val Gly Asp₄₃₀ Arg Val
 Thr Ile Thr₄₃₅ Cys Arg Ala Ser Gln₄₄₀ Ser Ile Ser Ser Tyr₄₄₅ Leu Asn Trp
 Tyr Gln₄₅₀ Gln Lys Pro Gly Lys₄₅₅ Ala Pro Lys Leu Leu₄₆₀ Ile Tyr Ala Ala
 Ser Ser Leu Gln Ser Gly₄₇₀ Val Pro Ser Arg Phe₄₇₅ Ser Gly Ser Gly Ser₄₈₀
 Gly Thr Asp Phe Thr₄₈₅ Leu Thr Ile Ser Ser₄₉₀ Leu Gln Pro Glu Asp₄₉₅ Phe
 Ala Thr Tyr Tyr₅₀₀ Cys Gln Gln Ser Tyr₅₀₅ Ser Thr Pro Tyr Thr₅₁₀ Phe Gly
 Gln Gly Thr₅₁₅ Lys Val Glu Ile Lys₅₂₀ Thr Thr Thr Pro Ala₅₂₅ Pro Arg Pro
 Pro Thr₅₃₀ Pro Ala Pro Thr Ile₅₃₅ Ala Ser Gln Pro Leu₅₄₀ Ser Leu Arg Pro

Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala^{-SL} Val His Thr Arg Gly Leu
 545 550 555 560
 Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys
 565 570 575
 Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly
 580 585 590
 Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val
 595 600 605
 Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu
 610 615 620
 Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp
 625 630 635 640
 Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn
 645 650 655
 Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg
 660 665 670
 Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly
 675 680 685
 Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu
 690 695 700
 Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu
 705 710 715 720
 Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His
 725 730 735
 Met Gln Ala Leu Pro Pro Arg
 740

<210> 1025
 <211> 743
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1025
 Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
 1 5 10 15

His Ala Ala Arg Pro Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln
 Page 865

_SL															
20							25					30			
Met	Val	Ser 35	Ala	Leu	Leu	Asp	Ala 40	Glu	Pro	Pro	Ile	Leu 45	Tyr	Ser	Glu
Tyr	Asp 50	Pro	Thr	Arg	Pro	Phe 55	Ser	Glu	Ala	Ser	Met 60	Met	Gly	Leu	Leu
Thr 65	Asn	Leu	Ala	Asp	Arg 70	Glu	Leu	Val	His	Met 75	Ile	Asn	Trp	Ala	Lys 80
Arg	Val	Pro	Gly	Phe 85	Val	Asp	Leu	Thr	Leu 90	His	Asp	Gln	Val	His 95	Leu
Leu	Glu	Cys	Ala 100	Trp	Met	Glu	Ile	Leu 105	Met	Ile	Gly	Leu	Val 110	Trp	Arg
Ser	Met	Glu 115	His	Pro	Gly	Lys	Leu 120	Leu	Phe	Ala	Pro	Asn 125	Leu	Leu	Leu
Asp	Arg 130	Asn	Gln	Gly	Lys	Cys 135	Val	Glu	Gly	Gly	Val 140	Glu	Ile	Phe	Asp
Met 145	Leu	Leu	Ala	Thr	Ser 150	Ser	Arg	Phe	Arg	Met 155	Met	Asn	Leu	Gln	Gly 160
Glu	Glu	Phe	Val	Cys 165	Leu	Lys	Ser	Ile	Ile 170	Leu	Leu	Asn	Ser	Gly 175	Val
Tyr	Thr	Phe	Leu 180	Ser	Ser	Thr	Leu	Lys 185	Ser	Leu	Glu	Glu	Lys 190	Asp	His
Ile	His	Arg 195	Val	Leu	Asp	Lys	Ile 200	Thr	Asp	Thr	Leu	Ile 205	His	Leu	Met
Ala	Lys 210	Ala	Gly	Leu	Thr	Leu 215	Gln	Gln	Gln	His	Gln 220	Arg	Leu	Ala	Gln
Leu 225	Leu	Leu	Ile	Leu	Ser 230	His	Ile	Arg	His	Met 235	Ser	Asn	Lys	Arg	Met 240
Glu	His	Leu	Tyr	Ser 245	Met	Lys	Cys	Lys	Asn 250	Val	Val	Pro	Leu	Ser 255	Asp
Leu	Leu	Leu	Glu 260	Met	Leu	Asp	Ala	His 265	Arg	Leu	Gly	Thr	Gly 270	Ala	Glu
Asp	Pro	Arg 275	Pro	Ser	Arg	Lys	Arg 280	Arg	Glu	Val	Gln	Leu 285	Val	Glu	Ser
Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala

_SL

290		295		300											
Val 305	Ser	Gly	Phe	Ala	Leu 310	Ser	Asn	His	Gly	Met 315	Ser	Trp	Val	Arg	Arg 320
Ala	Pro	Gly	Lys	Gly 325	Leu	Glu	Trp	Val	Ser 330	Gly	Ile	Val	Tyr	Ser 335	Gly
Ser	Thr	Tyr	Tyr 340	Ala	Ala	Ser	Val	Lys 345	Gly	Arg	Phe	Thr	Ile 350	Ser	Arg
Asp	Asn	Ser 355	Arg	Asn	Thr	Leu	Tyr 360	Leu	Gln	Met	Asn	Ser 365	Leu	Arg	Pro
Glu	Asp 370	Thr	Ala	Ile	Tyr	Tyr 375	Cys	Ser	Ala	His	Gly 380	Gly	Glu	Ser	Asp
Val 385	Trp	Gly	Gln	Gly	Thr 390	Thr	Val	Thr	Val	Ser 395	Ser	Ala	Ser	Gly	Gly 400
Gly	Gly	Ser	Gly	Gly 405	Arg	Ala	Ser	Gly	Gly 410	Gly	Gly	Ser	Asp	Ile 415	Gln
Leu	Thr	Gln	Ser 420	Pro	Ser	Ser	Leu	Ser 425	Ala	Ser	Val	Gly	Asp 430	Arg	Val
Thr	Ile	Thr 435	Cys	Arg	Ala	Ser	Gln 440	Ser	Ile	Ser	Ser	Tyr 445	Leu	Asn	Trp
Tyr	Gln 450	Gln	Lys	Pro	Gly	Lys 455	Ala	Pro	Lys	Leu	Leu 460	Ile	Tyr	Ala	Ala
Ser 465	Ser	Leu	Gln	Ser	Gly 470	Val	Pro	Ser	Arg	Phe 475	Ser	Gly	Ser	Gly	Ser 480
Gly	Thr	Asp	Phe	Thr 485	Leu	Thr	Ile	Ser	Ser 490	Leu	Gln	Pro	Glu	Asp 495	Phe
Ala	Thr	Tyr	Tyr 500	Cys	Gln	Gln	Ser	Tyr 505	Ser	Thr	Pro	Tyr	Thr 510	Phe	Gly
Gln	Gly	Thr 515	Lys	Val	Glu	Ile	Lys 520	Thr	Thr	Thr	Pro	Ala 525	Pro	Arg	Pro
Pro	Thr 530	Pro	Ala	Pro	Thr	Ile 535	Ala	Ser	Gln	Pro	Leu 540	Ser	Leu	Arg	Pro
Glu 545	Ala	Cys	Arg	Pro	Ala 550	Ala	Gly	Gly	Ala	Val 555	His	Thr	Arg	Gly	Leu 560
Asp	Phe	Ala	Cys	Asp	Ile	Tyr	Ile	Trp	Ala	Pro	Leu	Ala	Gly	Thr	Cys

_SL

Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu
50 55 60

Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala Lys
65 70 75 80

Arg Val Pro Gly Phe Val Asp Leu Ala Leu His Asp Gln Val His Leu
85 90 95

Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp Arg
100 105 110

Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu
115 120 125

Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe Asp
130 135 140

Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly
145 150 155 160

Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val
165 170 175

Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His
180 185 190

Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met
195 200 205

Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala Gln
210 215 220

Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Ser Lys Arg Met
225 230 235 240

Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Ser Asp
245 250 255

Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu Gly Thr Gly Ala Glu
260 265 270

Asp Pro Arg Pro Ser Arg Lys Arg Arg Ser Leu Gly Asp Val Gly Glu
275 280 285

Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu
290 295 300

Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr Leu
305 310 315 320

_SL

Asn Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
325 330 335

His Thr Ser Arg Leu His Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser
340 345 350

Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
355 360 365

Asp Phe Ala Val Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr
370 375 380

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly
385 390 395 400

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Glu Ser
405 410 415

Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr
420 425 430

Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln
435 440 445

Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Val Ile Trp Gly Ser Glu
450 455 460

Thr Thr Tyr Tyr Ser Ser Ser Leu Lys Ser Arg Val Thr Ile Ser Lys
465 470 475 480

Asp Asn Ser Lys Asn Gln Val Ser Leu Lys Leu Ser Ser Val Thr Ala
485 490 495

Ala Asp Thr Ala Val Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly
500 505 510

Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
515 520 525

Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile
530 535 540

Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala
545 550 555 560

Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr
565 570 575

Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu
580 585 590

_SL

Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile
595 600 605

Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp
610 615 620

Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu
625 630 635 640

Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly
645 650 655

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
660 665 670

Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
675 680 685

Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
690 695 700

Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
705 710 715 720

Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala
725 730 735

Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
740 745 750

<210> 1027
<211> 752
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1027
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Glu Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln
20 25 30

Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu
35 40 45

Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu
50 55 60

_SL

Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala Lys
65 70 75 80

Arg Val Pro Gly Phe Val Asp Leu Thr Leu His Asp Gln Val His Leu
85 90 95

Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp Arg
100 105 110

Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu
115 120 125

Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe Asp
130 135 140

Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly
145 150 155 160

Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val
165 170 175

Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His
180 185 190

Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met
195 200 205

Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala Gln
210 215 220

Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Asn Lys Arg Met
225 230 235 240

Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Ser Asp
245 250 255

Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu Gly Thr Gly Ala Glu
260 265 270

Asp Pro Arg Pro Ser Arg Lys Arg Arg Ser Leu Gly Asp Val Gly Glu
275 280 285

Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu
290 295 300

Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr Leu
305 310 315 320

Asn Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
325 330 335

_SL

His Thr Ser Arg Leu His Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser
340 345 350

Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
355 360 365

Asp Phe Ala Val Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr
370 375 380

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly
385 390 395 400

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Glu Ser
405 410 415

Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr
420 425 430

Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln
435 440 445

Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Val Ile Trp Gly Ser Glu
450 455 460

Thr Thr Tyr Tyr Ser Ser Ser Leu Lys Ser Arg Val Thr Ile Ser Lys
465 470 475 480

Asp Asn Ser Lys Asn Gln Val Ser Leu Lys Leu Ser Ser Val Thr Ala
485 490 495

Ala Asp Thr Ala Val Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly
500 505 510

Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
515 520 525

Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile
530 535 540

Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala
545 550 555 560

Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr
565 570 575

Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu
580 585 590

Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile
595 600 605

_SL

Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp
610 615 620

Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu
625 630 635 640

Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly
645 650 655

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
660 665 670

Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
675 680 685

Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
690 695 700

Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
705 710 715 720

Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala
725 730 735

Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
740 745 750

<210> 1028
<211> 746
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1028
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Glu Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln
20 25 30

Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu
35 40 45

Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu
50 55 60

Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala Lys
65 70 75 80

Arg Val Pro Gly Phe Val Asp Leu Ala Leu^{-SL} His Asp Gln Val His Leu
 85 90 95
 Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp Arg
 100 105 110
 Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu
 115 120 125
 Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe Asp
 130 135 140
 Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly
 145 150 155 160
 Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val
 165 170 175
 Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His
 180 185 190
 Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met
 195 200 205
 Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala Gln
 210 215 220
 Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Ser Lys Arg Met
 225 230 235 240
 Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Ser Asp
 245 250 255
 Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu Gly Thr Gly Ala Glu
 260 265 270
 Asp Pro Arg Pro Ser Arg Lys Arg Arg Glu Ile Val Met Thr Gln Ser
 275 280 285
 Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
 290 295 300
 Arg Ala Ser Gln Asp Ile Ser Lys Tyr Leu Asn Trp Tyr Gln Gln Lys
 305 310 315 320
 Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr His Thr Ser Arg Leu His
 325 330 335
 Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr
 340 345 350

Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu ^{-SL} Asp Phe Ala Val Tyr Phe
 355 360 365
 Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gln Gly Thr Lys
 370 375 380
 Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 385 390 400
 Gly Gly Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys
 405 410 415
 Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Val Ser Leu
 420 425 430
 Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu
 435 440 445
 Glu Trp Ile Gly Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Ser Ser
 450 455 460
 Ser Leu Lys Ser Arg Val Thr Ile Ser Lys Asp Asn Ser Lys Asn Gln
 465 470 475 480
 Val Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr
 485 490 495
 Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr
 500 505 510
 Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Thr Thr Thr Pro Ala
 515 520 525
 Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser
 530 535 540
 Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr
 545 550 555 560
 Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala
 565 570 575
 Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys
 580 585 590
 Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met
 595 600 605
 Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe
 610 615 620

Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu ^{-SL} Arg Val Lys Phe Ser Arg
 625 630 635 640
 Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn
 645 650 655
 Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
 660 665 670
 Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
 675 680 685
 Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
 690 695 700
 Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
 705 710 715 720
 Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
 725 730 735
 Ala Leu His Met Gln Ala Leu Pro Pro Arg
 740 745

<210> 1029
 <211> 746
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1029
 Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
 1 5 10 15

His Ala Ala Arg Pro Glu Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln
 20 25 30

Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu
 35 40 45

Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu
 50 55 60

Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala Lys
 65 70 75 80

Arg Val Pro Gly Phe Val Asp Leu Thr Leu His Asp Gln Val His Leu
 85 90 95

Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp Arg
 Page 877

_SL

100	105	110
Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu		
115	120	125
Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe Asp		
130	135	140
Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly		
145	150	155
Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val		
165	170	175
Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His		
180	185	190
Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met		
195	200	205
Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala Gln		
210	215	220
Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Asn Lys Arg Met		
225	230	235
Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Ser Asp		
245	250	255
Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu Gly Thr Gly Ala Glu		
260	265	270
Asp Pro Arg Pro Ser Arg Lys Arg Arg Glu Ile Val Met Thr Gln Ser		
275	280	285
Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys		
290	295	300
Arg Ala Ser Gln Asp Ile Ser Lys Tyr Leu Asn Trp Tyr Gln Gln Lys		
305	310	315
Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr His Thr Ser Arg Leu His		
325	330	335
Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr		
340	345	350
Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Val Tyr Phe		
355	360	365
Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gln Gly Thr Lys		

370					375					_SL		380				
Leu 385	Glu	Ile	Lys	Gly	Gly 390	Gly	Gly	Ser	Gly	Gly 395	Gly	Gly	Ser	Gly	Gly 400	
Gly	Gly	Ser	Gln	Val 405	Gln	Leu	Gln	Glu	Ser 410	Gly	Pro	Gly	Leu	Val 415	Lys	
Pro	Ser	Glu	Thr 420	Leu	Ser	Leu	Thr	Cys 425	Thr	Val	Ser	Gly	Val 430	Ser	Leu	
Pro	Asp	Tyr 435	Gly	Val	Ser	Trp	Ile 440	Arg	Gln	Pro	Pro	Gly 445	Lys	Gly	Leu	
Glu	Trp 450	Ile	Gly	Val	Ile	Trp 455	Gly	Ser	Glu	Thr	Thr 460	Tyr	Tyr	Ser	Ser	
Ser 465	Leu	Lys	Ser	Arg	Val 470	Thr	Ile	Ser	Lys	Asp 475	Asn	Ser	Lys	Asn	Gln 480	
Val	Ser	Leu	Lys	Leu 485	Ser	Ser	Val	Thr	Ala 490	Ala	Asp	Thr	Ala	Val 495	Tyr	
Tyr	Cys	Ala	Lys 500	His	Tyr	Tyr	Tyr	Gly 505	Gly	Ser	Tyr	Ala	Met 510	Asp	Tyr	
Trp	Gly	Gln 515	Gly	Thr	Leu	Val	Thr 520	Val	Ser	Ser	Thr	Thr 525	Thr	Pro	Ala	
Pro	Arg 530	Pro	Pro	Thr	Pro	Ala 535	Pro	Thr	Ile	Ala	Ser 540	Gln	Pro	Leu	Ser	
Leu 545	Arg	Pro	Glu	Ala	Cys 550	Arg	Pro	Ala	Ala	Gly 555	Gly	Ala	Val	His	Thr 560	
Arg	Gly	Leu	Asp	Phe 565	Ala	Cys	Asp	Ile	Tyr 570	Ile	Trp	Ala	Pro	Leu 575	Ala	
Gly	Thr	Cys	Gly 580	Val	Leu	Leu	Leu	Ser 585	Leu	Val	Ile	Thr	Leu 590	Tyr	Cys	
Lys	Arg	Gly 595	Arg	Lys	Lys	Leu	Leu 600	Tyr	Ile	Phe	Lys	Gln 605	Pro	Phe	Met	
Arg	Pro 610	Val	Gln	Thr	Thr	Gln 615	Glu	Glu	Asp	Gly	Cys 620	Ser	Cys	Arg	Phe	
Pro 625	Glu	Glu	Glu	Glu	Gly 630	Gly	Cys	Glu	Leu	Arg 635	Val	Lys	Phe	Ser	Arg 640	
Ser	Ala	Asp	Ala	Pro	Ala	Tyr	Gln	Gln	Gly	Gln	Asn	Gln	Leu	Tyr	Asn	

_SL

645 650 655

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
 660 665 670

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
 675 680 685

Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
 690 695 700

Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
 705 710 715 720

Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
 725 730 735

Ala Leu His Met Gln Ala Leu Pro Pro Arg
 740 745

<210> 1030
 <211> 753
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1030
 Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
 1 5 10 15

His Ala Ala Arg Pro Glu Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln
 20 25 30

Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu
 35 40 45

Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu
 50 55 60

Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala Lys
 65 70 75 80

Arg Val Pro Gly Phe Val Asp Leu Ala Leu His Asp Gln Val His Leu
 85 90 95

Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp Arg
 100 105 110

Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu
 115 120 125

_SL

Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe Asp
130 135 140

Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly
145 150 155 160

Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val
165 170 175

Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His
180 185 190

Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met
195 200 205

Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala Gln
210 215 220

Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Ser Lys Arg Met
225 230 235 240

Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Ser Asp
245 250 255

Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu Gly Thr Gly Ala Glu
260 265 270

Asp Pro Arg Pro Ser Arg Lys Arg Arg Ser Leu Gly Asp Val Gly Gln
275 280 285

Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser
290 295 300

Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr Tyr
305 310 315 320

Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly
325 330 335

Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe Gln
340 345 350

Gly Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Ser Thr Val Tyr Met
355 360 365

Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala
370 375 380

Arg Asp Met Asn Ile Leu Ala Thr Val Pro Phe Asp Ile Trp Gly Gln
385 390 395 400

_SL

Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
405 410 415

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser
420 425 430

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala
435 440 445

Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly
450 455 460

Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly
465 470 475 480

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
485 490 495

Thr Val Asn Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln
500 505 510

Gln Gly Asp Ser Val Pro Leu Thr Phe Gly Gly Gly Thr Arg Leu Glu
515 520 525

Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr
530 535 540

Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala
545 550 555 560

Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile
565 570 575

Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser
580 585 590

Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr
595 600 605

Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu
610 615 620

Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu
625 630 635 640

Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln
645 650 655

Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu
660 665 670

_SL

Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly
675 680 685

Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln
690 695 700

Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu
705 710 715 720

Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr
725 730 735

Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro
740 745 750

Arg

<210> 1031
<211> 753
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1031
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Glu Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln
20 25 30

Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu
35 40 45

Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu
50 55 60

Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala Lys
65 70 75 80

Arg Val Pro Gly Phe Val Asp Leu Thr Leu His Asp Gln Val His Leu
85 90 95

Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp Arg
100 105 110

Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu
115 120 125

_SL

Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe Asp
130 135 140

Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly
145 150 155 160

Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val
165 170 175

Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His
180 185 190

Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met
195 200 205

Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala Gln
210 215 220

Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Asn Lys Arg Met
225 230 235 240

Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Ser Asp
245 250 255

Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu Gly Thr Gly Ala Glu
260 265 270

Asp Pro Arg Pro Ser Arg Lys Arg Arg Ser Leu Gly Asp Val Gly Gln
275 280 285

Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser
290 295 300

Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr Tyr
305 310 315 320

Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly
325 330 335

Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe Gln
340 345 350

Gly Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Ser Thr Val Tyr Met
355 360 365

Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala
370 375 380

Arg Asp Met Asn Ile Leu Ala Thr Val Pro Phe Asp Ile Trp Gly Gln
385 390 395 400

_SL

Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
405 410 415

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser
420 425 430

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala
435 440 445

Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly
450 455 460

Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly
465 470 475 480

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
485 490 495

Thr Val Asn Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln
500 505 510

Gln Gly Asp Ser Val Pro Leu Thr Phe Gly Gly Gly Thr Arg Leu Glu
515 520 525

Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr
530 535 540

Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala
545 550 555 560

Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile
565 570 575

Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser
580 585 590

Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr
595 600 605

Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu
610 615 620

Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Gly Gly Cys Glu
625 630 635 640

Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln
645 650 655

Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu
660 665 670

_SL

Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly
675 680 685

Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln
690 695 700

Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu
705 710 715 720

Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr
725 730 735

Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro
740 745 750

Arg

<210> 1032

<211> 747

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1032

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Glu Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln
20 25 30

Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu
35 40 45

Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu
50 55 60

Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala Lys
65 70 75 80

Arg Val Pro Gly Phe Val Asp Leu Ala Leu His Asp Gln Val His Leu
85 90 95

Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp Arg
100 105 110

Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu
115 120 125

Asp Arg Asn Gln Gly Lys Cys Val Glu Gly^{-SL} Gly Val Glu Ile Phe Asp
 130 135 140
 Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly
 145 150 155 160
 Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val
 165 170 175
 Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His
 180 185 190
 Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met
 195 200 205
 Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala Gln
 210 215 220
 Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Ser Lys Arg Met
 225 230 235 240
 Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Ser Asp
 245 250 255
 Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu Gly Thr Gly Ala Glu
 260 265 270
 Asp Pro Arg Pro Ser Arg Lys Arg Arg Gln Val Gln Leu Val Gln Ser
 275 280 285
 Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys
 290 295 300
 Ala Ser Gly Tyr Thr Phe Thr Gly Tyr Tyr Met His Trp Val Arg Gln
 305 310 315 320
 Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Trp Ile Asn Pro Asn Ser
 325 330 335
 Gly Gly Thr Asn Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Leu Thr
 340 345 350
 Arg Asp Thr Ser Ile Ser Thr Val Tyr Met Glu Leu Ser Arg Leu Arg
 355 360 365
 Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Met Asn Ile Leu
 370 375 380
 Ala Thr Val Pro Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val
 385 390 395 400

Ser Ser Gly Gly Gly₄₀₅ Gly Ser Gly Gly Gly^{-SL}₄₁₀ Gly Ser Gly Gly Gly₄₁₅ Gly
 Ser Asp Ile Gln₄₂₀ Met Thr Gln Ser Pro₄₂₅ Ser Ser Leu Ser Ala₄₃₀ Ser Val
 Gly Asp Arg₄₃₅ Val Thr Ile Thr Cys₄₄₀ Arg Ala Ser Gln Ser₄₄₅ Ile Ser Ser
 Tyr Leu₄₅₀ Asn Trp Tyr Gln Gln₄₅₅ Lys Pro Gly Lys Ala₄₆₀ Pro Lys Leu Leu
 Ile Tyr Ala Ala Ser Ser₄₇₀ Leu Gln Ser Gly Val₄₇₅ Pro Ser Arg Phe Ser₄₈₀
 Gly Ser Gly Ser Gly₄₈₅ Thr Asp Phe Thr Leu₄₉₀ Thr Val Asn Ser Leu₄₉₅ Gln
 Pro Glu Asp Phe₅₀₀ Ala Thr Tyr Tyr Cys₅₀₅ Gln Gln Gly Asp Ser₅₁₀ Val Pro
 Leu Thr Phe₅₁₅ Gly Gly Gly Thr Arg₅₂₀ Leu Glu Ile Lys Thr₅₂₅ Thr Thr Pro
 Ala Pro₅₃₀ Arg Pro Pro Thr Pro₅₃₅ Ala Pro Thr Ile Ala₅₄₀ Ser Gln Pro Leu
 Ser₅₄₅ Leu Arg Pro Glu Ala₅₅₀ Cys Arg Pro Ala Ala₅₅₅ Gly Gly Ala Val His₅₆₀
 Thr Arg Gly Leu Asp₅₆₅ Phe Ala Cys Asp Ile₅₇₀ Tyr Ile Trp Ala Pro₅₇₅ Leu
 Ala Gly Thr Cys₅₈₀ Gly Val Leu Leu Leu₅₈₅ Ser Leu Val Ile Thr₅₉₀ Leu Tyr
 Cys Lys Arg₅₉₅ Gly Arg Lys Lys Leu₆₀₀ Leu Tyr Ile Phe Lys₆₀₅ Gln Pro Phe
 Met Arg₆₁₀ Pro Val Gln Thr Thr₆₁₅ Gln Glu Glu Asp Gly₆₂₀ Cys Ser Cys Arg
 Phe₆₂₅ Pro Glu Glu Glu Glu₆₃₀ Gly Gly Cys Glu Leu₆₃₅ Arg Val Lys Phe Ser₆₄₀
 Arg Ser Ala Asp Ala₆₄₅ Pro Ala Tyr Gln Gln₆₅₀ Gly Gln Asn Gln Leu₆₅₅ Tyr
 Asn Glu Leu Asn₆₆₀ Leu Gly Arg Arg Glu₆₆₅ Glu Tyr Asp Val Leu₆₇₀ Asp Lys

Arg Arg Gly Arg Asp Pro Glu Met Gly Gly^{_SL} Lys Pro Arg Arg Lys Asn
675 680 685

Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu
690 695 700

Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly
705 710 715 720

His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr
725 730 735

Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
740 745

<210> 1033
<211> 747
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1033
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Glu Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln
20 25 30

Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu
35 40 45

Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu
50 55 60

Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala Lys
65 70 75 80

Arg Val Pro Gly Phe Val Asp Leu Thr Leu His Asp Gln Val His Leu
85 90 95

Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp Arg
100 105 110

Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu
115 120 125

Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe Asp
130 135 140

Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly
Page 889

145					150					-SL 155					160
Glu	Glu	Phe	Val	Cys 165	Leu	Lys	Ser	Ile	Ile 170	Leu	Leu	Asn	Ser	Gly 175	Val
Tyr	Thr	Phe	Leu 180	Ser	Ser	Thr	Leu	Lys 185	Ser	Leu	Glu	Glu	Lys 190	Asp	His
Ile	His	Arg 195	Val	Leu	Asp	Lys	Ile 200	Thr	Asp	Thr	Leu	Ile 205	His	Leu	Met
Ala	Lys 210	Ala	Gly	Leu	Thr	Leu 215	Gln	Gln	Gln	His	Gln 220	Arg	Leu	Ala	Gln
Leu 225	Leu	Leu	Ile	Leu	Ser 230	His	Ile	Arg	His	Met 235	Ser	Asn	Lys	Arg	Met 240
Glu	His	Leu	Tyr	Ser 245	Met	Lys	Cys	Lys	Asn 250	Val	Val	Pro	Leu	Ser 255	Asp
Leu	Leu	Leu	Glu 260	Met	Leu	Asp	Ala	His 265	Arg	Leu	Gly	Thr	Gly 270	Ala	Glu
Asp	Pro	Arg 275	Pro	Ser	Arg	Lys	Arg 280	Arg	Gln	Val	Gln	Leu 285	Val	Gln	Ser
Gly	Ala 290	Glu	Val	Lys	Lys	Pro 295	Gly	Ala	Ser	Val	Lys 300	Val	Ser	Cys	Lys
Ala 305	Ser	Gly	Tyr	Thr	Phe 310	Thr	Gly	Tyr	Tyr	Met 315	His	Trp	Val	Arg	Gln 320
Ala	Pro	Gly	Gln	Gly 325	Leu	Glu	Trp	Met	Gly 330	Trp	Ile	Asn	Pro	Asn 335	Ser
Gly	Gly	Thr	Asn 340	Tyr	Ala	Gln	Lys	Phe 345	Gln	Gly	Arg	Val	Thr 350	Leu	Thr
Arg	Asp 355	Thr	Ser	Ile	Ser	Thr	Val 360	Tyr	Met	Glu	Leu	Ser 365	Arg	Leu	Arg
Ser	Asp 370	Asp	Thr	Ala	Val	Tyr 375	Tyr	Cys	Ala	Arg	Asp 380	Met	Asn	Ile	Leu
Ala 385	Thr	Val	Pro	Phe	Asp 390	Ile	Trp	Gly	Gln	Gly 395	Thr	Met	Val	Thr	Val 400
Ser	Ser	Gly	Gly	Gly 405	Gly	Ser	Gly	Gly	Gly 410	Gly	Ser	Gly	Gly	Gly 415	Gly
Ser	Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val

										_SL					
			420					425					430		
Gly	Asp	Arg 435	Val	Thr	Ile	Thr	Cys 440	Arg	Ala	Ser	Gln	Ser 445	Ile	Ser	Ser
Tyr	Leu 450	Asn	Trp	Tyr	Gln	Gln 455	Lys	Pro	Gly	Lys	Ala 460	Pro	Lys	Leu	Leu
Ile 465	Tyr	Ala	Ala	Ser	Ser 470	Leu	Gln	Ser	Gly	Val 475	Pro	Ser	Arg	Phe	Ser 480
Gly	Ser	Gly	Ser	Gly 485	Thr	Asp	Phe	Thr	Leu 490	Thr	Val	Asn	Ser	Leu 495	Gln
Pro	Glu	Asp	Phe 500	Ala	Thr	Tyr	Tyr	Cys 505	Gln	Gln	Gly	Asp	Ser 510	Val	Pro
Leu	Thr	Phe 515	Gly	Gly	Gly	Thr	Arg 520	Leu	Glu	Ile	Lys	Thr 525	Thr	Thr	Pro
Ala	Pro 530	Arg	Pro	Pro	Thr	Pro 535	Ala	Pro	Thr	Ile	Ala 540	Ser	Gln	Pro	Leu
Ser 545	Leu	Arg	Pro	Glu	Ala 550	Cys	Arg	Pro	Ala	Ala 555	Gly	Gly	Ala	Val	His 560
Thr	Arg	Gly	Leu	Asp 565	Phe	Ala	Cys	Asp	Ile 570	Tyr	Ile	Trp	Ala	Pro 575	Leu
Ala	Gly	Thr	Cys 580	Gly	Val	Leu	Leu	Leu 585	Ser	Leu	Val	Ile	Thr 590	Leu	Tyr
Cys	Lys	Arg 595	Gly	Arg	Lys	Lys	Leu 600	Leu	Tyr	Ile	Phe	Lys 605	Gln	Pro	Phe
Met	Arg 610	Pro	Val	Gln	Thr	Thr 615	Gln	Glu	Glu	Asp	Gly 620	Cys	Ser	Cys	Arg
Phe 625	Pro	Glu	Glu	Glu	Glu 630	Gly	Gly	Cys	Glu	Leu 635	Arg	Val	Lys	Phe	Ser 640
Arg	Ser	Ala	Asp	Ala 645	Pro	Ala	Tyr	Gln	Gln 650	Gly	Gln	Asn	Gln	Leu 655	Tyr
Asn	Glu	Leu	Asn 660	Leu	Gly	Arg	Arg	Glu 665	Glu	Tyr	Asp	Val	Leu 670	Asp	Lys
Arg	Arg	Gly 675	Arg	Asp	Pro	Glu	Met 680	Gly	Gly	Lys	Pro	Arg 685	Arg	Lys	Asn
Pro	Gln	Glu	Gly	Leu	Tyr	Asn	Glu	Leu	Gln	Lys	Asp	Lys	Met	Ala	Glu

690										695					_SL		700				
Ala 705	Tyr	Ser	Glu	Ile	Gly 710	Met	Lys	Gly	Glu	Arg 715	Arg	Arg	Gly	Lys	Gly 720						
His	Asp	Gly	Leu	Tyr 725	Gln	Gly	Leu	Ser	Thr 730	Ala	Thr	Lys	Asp	Thr 735	Tyr						
Asp	Ala	Leu	His 740	Met	Gln	Ala	Leu	Pro 745	Pro	Arg											

```
<210> 1034
<211> 749
<212> PRT
<213> Artificial Sequence
```

<211> 749

<212> PRT

<213> Artificial Sequence

$\langle 220 \rangle$

<221> source

```
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"
```

<400> 1034

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Glu Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln
20 25 30

Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu
35 40 45

Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu
50 55 60

Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala Lys
65 70 75 80

Arg Val Pro Gly Phe Val Asp Leu Ala Leu His Asp Gln Val His Leu
85 90 95

Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp Arg
100 105 110

Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu
115 120 125

Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe Asp
130 135 140

Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly
145 150 155 160

Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val
165 170 175

_SL

Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His
180 185 190

Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met
195 200 205

Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala Gln
210 215 220

Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Ser Lys Arg Met
225 230 235 240

Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Ser Asp
245 250 255

Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu Gly Thr Gly Ala Glu
260 265 270

Asp Pro Arg Pro Ser Arg Lys Arg Arg Ser Leu Gly Asp Val Gly Glu
275 280 285

Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
290 295 300

Leu Arg Leu Ser Cys Ala Val Ser Gly Phe Ala Leu Ser Asn His Gly
305 310 315 320

Met Ser Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
325 330 335

Gly Ile Val Tyr Ser Gly Ser Thr Tyr Tyr Ala Ala Ser Val Lys Gly
340 345 350

Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr Leu Gln
355 360 365

Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Ile Tyr Tyr Cys Ser Ala
370 375 380

His Gly Gly Glu Ser Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val
385 390 395 400

Ser Ser Ala Ser Gly Gly Gly Gly Ser Gly Gly Arg Ala Ser Gly Gly
405 410 415

Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala
420 425 430

Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile
435 440 445

_SL

Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
450 455 460

Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg
465 470 475 480

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser
485 490 495

Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser
500 505 510

Thr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Thr Thr
515 520 525

Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln
530 535 540

Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala
545 550 555 560

Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala
565 570 575

Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr
580 585 590

Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln
595 600 605

Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser
610 615 620

Cys Arg Phe Pro Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys
625 630 635 640

Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln
645 650 655

Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
660 665 670

Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg
675 680 685

Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met
690 695 700

Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly
705 710 715 720

_SL

Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp
725 730 735

Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
740 745

<210> 1035
<211> 749
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1035
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Glu Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln
20 25 30

Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu
35 40 45

Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu
50 55 60

Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala Lys
65 70 75 80

Arg Val Pro Gly Phe Val Asp Leu Thr Leu His Asp Gln Val His Leu
85 90 95

Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp Arg
100 105 110

Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu
115 120 125

Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe Asp
130 135 140

Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly
145 150 155 160

Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val
165 170 175

Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His
180 185 190

_SL

Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met
195 200 205

Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala Gln
210 215 220

Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Asn Lys Arg Met
225 230 235 240

Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Ser Asp
245 250 255

Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu Gly Thr Gly Ala Glu
260 265 270

Asp Pro Arg Pro Ser Arg Lys Arg Arg Ser Leu Gly Asp Val Gly Glu
275 280 285

Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
290 295 300

Leu Arg Leu Ser Cys Ala Val Ser Gly Phe Ala Leu Ser Asn His Gly
305 310 315 320

Met Ser Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
325 330 335

Gly Ile Val Tyr Ser Gly Ser Thr Tyr Tyr Ala Ala Ser Val Lys Gly
340 345 350

Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr Leu Gln
355 360 365

Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Ile Tyr Tyr Cys Ser Ala
370 375 380

His Gly Gly Glu Ser Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val
385 390 395 400

Ser Ser Ala Ser Gly Gly Gly Gly Ser Gly Gly Arg Ala Ser Gly Gly
405 410 415

Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala
420 425 430

Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile
435 440 445

Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
450 455 460

_SL

Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg
465 470 475 480

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser
485 490 495

Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser
500 505 510

Thr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Thr Thr
515 520 525

Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln
530 535 540

Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala
545 550 555 560

Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala
565 570 575

Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr
580 585 590

Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln
595 600 605

Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser
610 615 620

Cys Arg Phe Pro Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys
625 630 635 640

Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln
645 650 655

Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
660 665 670

Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg
675 680 685

Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met
690 695 700

Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly
705 710 715 720

Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp
725 730 735

_SL

Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
740 745

<210> 1036
<211> 743
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1036
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Glu Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln
20 25 30

Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu
35 40 45

Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu
50 55 60

Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala Lys
65 70 75 80

Arg Val Pro Gly Phe Val Asp Leu Ala Leu His Asp Gln Val His Leu
85 90 95

Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp Arg
100 105 110

Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu
115 120 125

Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe Asp
130 135 140

Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly
145 150 155 160

Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val
165 170 175

Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His
180 185 190

Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met
195 200 205

Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln ^{-SL} His Gln Arg Leu Ala Gln
 210 215 220
 Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Ser Lys Arg Met
 225 230 235 240
 Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Ser Asp
 245 250 255
 Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu Gly Thr Gly Ala Glu
 260 265 270
 Asp Pro Arg Pro Ser Arg Lys Arg Arg Glu Val Gln Leu Val Glu Ser
 275 280 285
 Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala
 290 295 300
 Val Ser Gly Phe Ala Leu Ser Asn His Gly Met Ser Trp Val Arg Arg
 305 310 315 320
 Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Gly Ile Val Tyr Ser Gly
 325 330 335
 Ser Thr Tyr Tyr Ala Ala Ser Val Lys Gly Arg Phe Thr Ile Ser Arg
 340 345 350
 Asp Asn Ser Arg Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro
 355 360 365
 Glu Asp Thr Ala Ile Tyr Tyr Cys Ser Ala His Gly Gly Glu Ser Asp
 370 375 380
 Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Gly Gly
 385 390 395 400
 Gly Gly Ser Gly Gly Arg Ala Ser Gly Gly Gly Gly Ser Asp Ile Gln
 405 410 415
 Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val
 420 425 430
 Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp
 435 440 445
 Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala
 450 455 460
 Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser
 465 470 475 480

Gly Thr Asp Phe Thr₄₈₅ Leu Thr Ile Ser Ser^{-SL}₄₉₀ Leu Gln Pro Glu Asp₄₉₅ Phe
 Ala Thr Tyr Tyr₅₀₀ Cys Gln Gln Ser Tyr₅₀₅ Ser Thr Pro Tyr Thr₅₁₀ Phe Gly
 Gln Gly Thr₅₁₅ Lys Val Glu Ile Lys₅₂₀ Thr Thr Thr Pro Ala₅₂₅ Pro Arg Pro
 Pro Thr₅₃₀ Pro Ala Pro Thr Ile₅₃₅ Ala Ser Gln Pro Leu₅₄₀ Ser Leu Arg Pro
 Glu₅₄₅ Ala Cys Arg Pro Ala₅₅₀ Ala Gly Gly Ala Val₅₅₅ His Thr Arg Gly Leu₅₆₀
 Asp Phe Ala Cys Asp₅₆₅ Ile Tyr Ile Trp Ala₅₇₀ Pro Leu Ala Gly Thr₅₇₅ Cys
 Gly Val Leu₅₈₀ Leu Ser Leu Val Ile₅₈₅ Thr Leu Tyr Cys Lys₅₉₀ Arg Gly
 Arg Lys Lys₅₉₅ Leu Leu Tyr Ile Phe₆₀₀ Lys Gln Pro Phe Met₆₀₅ Arg Pro Val
 Gln Thr₆₁₀ Thr Gln Glu Glu Asp₆₁₅ Gly Cys Ser Cys Arg₆₂₀ Phe Pro Glu Glu
 Glu₆₂₅ Glu Gly Gly Cys Glu₆₃₀ Leu Arg Val Lys Phe₆₃₅ Ser Arg Ser Ala Asp₆₄₀
 Ala Pro Ala Tyr Gln₆₄₅ Gln Gly Gln Asn Gln₆₅₀ Leu Tyr Asn Glu Leu₆₅₅ Asn
 Leu Gly Arg Arg₆₆₀ Glu Glu Tyr Asp Val₆₆₅ Leu Asp Lys Arg Arg₆₇₀ Gly Arg
 Asp Pro Glu₆₇₅ Met Gly Gly Lys Pro₆₈₀ Arg Arg Lys Asn Pro₆₈₅ Gln Glu Gly
 Leu Tyr₆₉₀ Asn Glu Leu Gln Lys₆₉₅ Asp Lys Met Ala Glu₇₀₀ Ala Tyr Ser Glu
 Ile Gly Met Lys Gly Glu₇₁₀ Arg Arg Arg Gly Lys₇₁₅ Gly His Asp Gly Leu₇₂₀
 Tyr Gln Gly Leu Ser₇₂₅ Thr Ala Thr Lys Asp₇₃₀ Thr Tyr Asp Ala Leu₇₃₅ His
 Met Gln Ala Leu₇₄₀ Pro Pro Arg

_SL

<210> 1037
<211> 743
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1037
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Glu Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln
20 25 30

Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu
35 40 45

Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu
50 55 60

Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala Lys
65 70 75 80

Arg Val Pro Gly Phe Val Asp Leu Thr Leu His Asp Gln Val His Leu
85 90 95

Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp Arg
100 105 110

Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu
115 120 125

Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe Asp
130 135 140

Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly
145 150 155 160

Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val
165 170 175

Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His
180 185 190

Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met
195 200 205

Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala Gln
210 215 220

Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Asn Lys Arg Met
Page 901

225				230				-SL 235				240			
Glu	His	Leu	Tyr	Ser 245	Met	Lys	Cys	Lys	Asn 250	Val	Val	Pro	Leu	Ser 255	Asp
Leu	Leu	Leu	Glu 260	Met	Leu	Asp	Ala	His 265	Arg	Leu	Gly	Thr	Gly 270	Ala	Glu
Asp	Pro	Arg 275	Pro	Ser	Arg	Lys	Arg 280	Arg	Glu	Val	Gln	Leu 285	Val	Glu	Ser
Gly	Gly 290	Gly	Leu	Val	Gln	Pro 295	Gly	Gly	Ser	Leu	Arg 300	Leu	Ser	Cys	Ala
Val 305	Ser	Gly	Phe	Ala	Leu 310	Ser	Asn	His	Gly	Met 315	Ser	Trp	Val	Arg	Arg 320
Ala	Pro	Gly	Lys	Gly 325	Leu	Glu	Trp	Val	Ser 330	Gly	Ile	Val	Tyr	Ser 335	Gly
Ser	Thr	Tyr	Tyr 340	Ala	Ala	Ser	Val	Lys 345	Gly	Arg	Phe	Thr	Ile 350	Ser	Arg
Asp	Asn	Ser 355	Arg	Asn	Thr	Leu	Tyr 360	Leu	Gln	Met	Asn	Ser 365	Leu	Arg	Pro
Glu	Asp 370	Thr	Ala	Ile	Tyr	Tyr 375	Cys	Ser	Ala	His	Gly 380	Gly	Glu	Ser	Asp
Val 385	Trp	Gly	Gln	Gly	Thr 390	Thr	Val	Thr	Val	Ser 395	Ser	Ala	Ser	Gly	Gly 400
Gly	Gly	Ser	Gly	Gly 405	Arg	Ala	Ser	Gly	Gly 410	Gly	Gly	Ser	Asp	Ile 415	Gln
Leu	Thr	Gln	Ser 420	Pro	Ser	Ser	Leu	Ser 425	Ala	Ser	Val	Gly	Asp 430	Arg	Val
Thr	Ile	Thr 435	Cys	Arg	Ala	Ser	Gln 440	Ser	Ile	Ser	Ser	Tyr 445	Leu	Asn	Trp
Tyr	Gln 450	Gln	Lys	Pro	Gly	Lys 455	Ala	Pro	Lys	Leu	Leu 460	Ile	Tyr	Ala	Ala
Ser 465	Ser	Leu	Gln	Ser	Gly 470	Val	Pro	Ser	Arg	Phe 475	Ser	Gly	Ser	Gly	Ser 480
Gly	Thr	Asp	Phe	Thr 485	Leu	Thr	Ile	Ser	Ser 490	Leu	Gln	Pro	Glu	Asp 495	Phe
Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Ser	Tyr	Ser	Thr	Pro	Tyr	Thr	Phe	Gly

_SL

500 505 510

Gln Gly Thr Lys Val Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro
515 520 525

Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro
530 535 540

Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu
545 550 555 560

Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys
565 570 575

Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly
580 585 590

Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val
595 600 605

Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu
610 615 620

Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp
625 630 635 640

Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn
645 650 655

Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg
660 665 670

Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly
675 680 685

Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu
690 695 700

Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu
705 710 715 720

Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His
725 730 735

Met Gln Ala Leu Pro Pro Arg
740

<210> 1038
<211> 752
<212> PRT
<213> Artificial Sequence

_SL

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1038

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gln Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln
20 25 30

Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu
35 40 45

Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu
50 55 60

Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala Lys
65 70 75 80

Arg Val Pro Gly Phe Val Asp Leu Ala Leu His Asp Gln Val His Leu
85 90 95

Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp Arg
100 105 110

Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu
115 120 125

Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe Asp
130 135 140

Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly
145 150 155 160

Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val
165 170 175

Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His
180 185 190

Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met
195 200 205

Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala Gln
210 215 220

Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Ser Lys Arg Met
225 230 235 240

Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Ser Asp
245 250 255

_SL

Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu Gly Thr Gly Ala Glu
260 265 270

Asp Pro Arg Pro Ser Arg Lys Arg Arg Ser Leu Gly Asp Val Gly Glu
275 280 285

Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu
290 295 300

Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr Leu
305 310 315 320

Asn Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
325 330 335

His Thr Ser Arg Leu His Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser
340 345 350

Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
355 360 365

Asp Phe Ala Val Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr
370 375 380

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly
385 390 395 400

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Glu Ser
405 410 415

Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr
420 425 430

Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln
435 440 445

Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Val Ile Trp Gly Ser Glu
450 455 460

Thr Thr Tyr Tyr Ser Ser Ser Leu Lys Ser Arg Val Thr Ile Ser Lys
465 470 475 480

Asp Asn Ser Lys Asn Gln Val Ser Leu Lys Leu Ser Ser Val Thr Ala
485 490 495

Ala Asp Thr Ala Val Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly
500 505 510

Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
515 520 525

_SL

Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile
530 535 540

Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala
545 550 555 560

Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr
565 570 575

Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu
580 585 590

Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile
595 600 605

Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp
610 615 620

Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu
625 630 635 640

Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly
645 650 655

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
660 665 670

Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
675 680 685

Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
690 695 700

Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
705 710 715 720

Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala
725 730 735

Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
740 745 750

<210> 1039

<211> 752

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

_SL

<400> 1039

```

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1      5      10      15

His Ala Ala Arg Pro Gln Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln
20      25      30

Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu
35      40      45

Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu
50      55      60

Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala Lys
65      70      75      80

Arg Val Pro Gly Phe Val Asp Leu Thr Leu His Asp Gln Val His Leu
85      90      95

Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp Arg
100     105     110

Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu
115     120     125

Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe Asp
130     135     140

Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly
145     150     155     160

Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val
165     170     175

Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His
180     185     190

Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met
195     200     205

Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala Gln
210     215     220

Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Asn Lys Arg Met
225     230     235     240

Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Ser Asp
245     250     255

Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu Gly Thr Gly Ala Glu
260     265     270

```

_SL

Asp Pro Arg Pro Ser Arg Lys Arg Arg Ser Leu Gly Asp Val Gly Glu
275 280 285

Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu
290 295 300

Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr Leu
305 310 315 320

Asn Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
325 330 335

His Thr Ser Arg Leu His Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser
340 345 350

Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
355 360 365

Asp Phe Ala Val Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr
370 375 380

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly
385 390 395 400

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Glu Ser
405 410 415

Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr
420 425 430

Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln
435 440 445

Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Val Ile Trp Gly Ser Glu
450 455 460

Thr Thr Tyr Tyr Ser Ser Ser Leu Lys Ser Arg Val Thr Ile Ser Lys
465 470 475 480

Asp Asn Ser Lys Asn Gln Val Ser Leu Lys Leu Ser Ser Val Thr Ala
485 490 495

Ala Asp Thr Ala Val Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly
500 505 510

Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
515 520 525

Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile
530 535 540

_SL

Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala
545 550 555 560

Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr
565 570 575

Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu
580 585 590

Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile
595 600 605

Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp
610 615 620

Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu
625 630 635 640

Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly
645 650 655

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
660 665 670

Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
675 680 685

Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
690 695 700

Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
705 710 715 720

Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala
725 730 735

Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
740 745 750

<210> 1040

<211> 746

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1040

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gln Ser Leu Ala Leu ^{-SL} Ser Leu Thr Ala Asp Gln
 20 25 30
 Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu
 35 40 45
 Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu
 50 55 60
 Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala Lys
 65 70 75 80
 Arg Val Pro Gly Phe Val Asp Leu Ala Leu His Asp Gln Val His Leu
 85 90 95
 Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp Arg
 100 105 110
 Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu
 115 120 125
 Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe Asp
 130 135 140
 Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly
 145 150 155 160
 Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val
 165 170 175
 Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His
 180 185 190
 Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met
 195 200 205
 Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala Gln
 210 215 220
 Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Ser Lys Arg Met
 225 230 235 240
 Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Ser Asp
 245 250 255
 Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu Gly Thr Gly Ala Glu
 260 265 270
 Asp Pro Arg Pro Ser Arg Lys Arg Arg Glu Ile Val Met Thr Gln Ser
 275 280 285

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu ^{-SL} Arg Ala Thr Leu Ser Cys
 290 295 300
 Arg Ala Ser Gln Asp Ile Ser Lys Tyr Leu Asn Trp Tyr Gln Gln Lys
 305 310 315 320
 Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr His Thr Ser Arg Leu His
 325 330 335
 Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr
 340 345 350
 Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Val Tyr Phe
 355 360 365
 Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gln Gly Thr Lys
 370 375 380
 Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 385 390 395 400
 Gly Gly Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys
 405 410 415
 Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Val Ser Leu
 420 425 430
 Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu
 435 440 445
 Glu Trp Ile Gly Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Ser Ser
 450 455 460
 Ser Leu Lys Ser Arg Val Thr Ile Ser Lys Asp Asn Ser Lys Asn Gln
 465 470 475 480
 Val Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr
 485 490 495
 Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr
 500 505 510
 Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Thr Thr Thr Pro Ala
 515 520 525
 Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser
 530 535 540
 Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr
 545 550 555 560

Arg Gly Leu Asp Phe₅₆₅ Ala Cys Asp Ile Tyr₅₇₀^{-SL} Ile Trp Ala Pro Leu₅₇₅ Ala
 Gly Thr Cys Gly₅₈₀ Val Leu Leu Leu Ser₅₈₅ Leu Val Ile Thr Leu₅₉₀ Tyr Cys
 Lys Arg Gly₅₉₅ Arg Lys Lys Leu₆₀₀ Leu Tyr Ile Phe Lys Gln₆₀₅ Pro Phe Met
 Arg Pro₆₁₀ Val Gln Thr Thr Gln₆₁₅ Glu Glu Asp Gly₆₂₀ Cys Ser Cys Arg Phe
 Pro₆₂₅ Glu Glu Glu Glu Gly₆₃₀ Gly Cys Glu Leu Arg₆₃₅ Val Lys Phe Ser Arg₆₄₀
 Ser Ala Asp Ala Pro₆₄₅ Ala Tyr Gln Gln Gly₆₅₀ Gln Asn Gln Leu Tyr₆₅₅ Asn
 Glu Leu Asn Leu₆₆₀ Gly Arg Arg Glu Glu₆₆₅ Tyr Asp Val Leu Asp₆₇₀ Lys Arg
 Arg Gly Arg₆₇₅ Asp Pro Glu Met Gly₆₈₀ Gly Lys Pro Arg Arg₆₈₅ Lys Asn Pro
 Gln Glu Gly Leu Tyr Asn Glu₆₉₅ Leu Gln Lys Asp Lys₇₀₀ Met Ala Glu Ala
 Tyr₇₀₅ Ser Glu Ile Gly₇₁₀ Met Lys Gly Glu Arg Arg₇₁₅ Arg Gly Lys Gly His₇₂₀
 Asp Gly Leu Tyr Gln₇₂₅ Gly Leu Ser Thr Ala₇₃₀ Thr Lys Asp Thr Tyr₇₃₅ Asp
 Ala Leu His Met₇₄₀ Gln Ala Leu Pro Pro Arg₇₄₅

<210> 1041
 <211> 746
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1041
 Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
 1 5 10 15

His Ala Ala Arg Pro Gln Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln
 20 25 30

Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu
 Page 912

_SL															
35					40					45					
Tyr	Asp 50	Pro	Thr	Arg	Pro	Phe 55	Ser	Glu	Ala	Ser	Met 60	Met	Gly	Leu	Leu
Thr 65	Asn	Leu	Ala	Asp	Arg 70	Glu	Leu	Val	His	Met 75	Ile	Asn	Trp	Ala	Lys 80
Arg	Val	Pro	Gly	Phe 85	Val	Asp	Leu	Thr	Leu 90	His	Asp	Gln	Val	His 95	Leu
Leu	Glu	Cys	Ala 100	Trp	Met	Glu	Ile	Leu 105	Met	Ile	Gly	Leu	Val 110	Trp	Arg
Ser	Met	Glu 115	His	Pro	Gly	Lys	Leu 120	Leu	Phe	Ala	Pro	Asn 125	Leu	Leu	Leu
Asp	Arg 130	Asn	Gln	Gly	Lys	Cys 135	Val	Glu	Gly	Gly	Val 140	Glu	Ile	Phe	Asp
Met 145	Leu	Leu	Ala	Thr	Ser 150	Ser	Arg	Phe	Arg	Met 155	Met	Asn	Leu	Gln	Gly 160
Glu	Glu	Phe	Val	Cys 165	Leu	Lys	Ser	Ile	Ile 170	Leu	Leu	Asn	Ser	Gly 175	Val
Tyr	Thr	Phe	Leu 180	Ser	Ser	Thr	Leu	Lys 185	Ser	Leu	Glu	Glu	Lys 190	Asp	His
Ile	His	Arg 195	Val	Leu	Asp	Lys	Ile 200	Thr	Asp	Thr	Leu	Ile 205	His	Leu	Met
Ala	Lys 210	Ala	Gly	Leu	Thr	Leu 215	Gln	Gln	Gln	His	Gln 220	Arg	Leu	Ala	Gln
Leu 225	Leu	Leu	Ile	Leu	Ser 230	His	Ile	Arg	His	Met 235	Ser	Asn	Lys	Arg	Met 240
Glu	His	Leu	Tyr	Ser 245	Met	Lys	Cys	Lys	Asn 250	Val	Val	Pro	Leu	Ser 255	Asp
Leu	Leu	Leu	Glu 260	Met	Leu	Asp	Ala	His 265	Arg	Leu	Gly	Thr	Gly 270	Ala	Glu
Asp	Pro	Arg 275	Pro	Ser	Arg	Lys	Arg 280	Arg	Glu	Ile	Val	Met 285	Thr	Gln	Ser
Pro	Ala 290	Thr	Leu	Ser	Leu	Ser 295	Pro	Gly	Glu	Arg	Ala 300	Thr	Leu	Ser	Cys
Arg	Ala	Ser	Gln	Asp	Ile	Ser	Lys	Tyr	Leu	Asn	Trp	Tyr	Gln	Gln	Lys

305					310					-SL 315					320
Pro	Gly	Gln	Ala	Pro	Arg	Leu	Leu	Ile	Tyr	His	Thr	Ser	Arg	Leu	His
				325					330					335	
Ser	Gly	Ile	Pro	Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Tyr
			340					345					350		
Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp	Phe	Ala	Val	Tyr	Phe
		355					360					365			
Cys	Gln	Gln	Gly	Asn	Thr	Leu	Pro	Tyr	Thr	Phe	Gly	Gln	Gly	Thr	Lys
	370					375					380				
Leu	Glu	Ile	Lys	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly
385					390					395					400
Gly	Gly	Ser	Gln	Val	Gln	Leu	Gln	Glu	Ser	Gly	Pro	Gly	Leu	Val	Lys
				405					410					415	
Pro	Ser	Glu	Thr	Leu	Ser	Leu	Thr	Cys	Thr	Val	Ser	Gly	Val	Ser	Leu
			420					425					430		
Pro	Asp	Tyr	Gly	Val	Ser	Trp	Ile	Arg	Gln	Pro	Pro	Gly	Lys	Gly	Leu
		435					440					445			
Glu	Trp	Ile	Gly	Val	Ile	Trp	Gly	Ser	Glu	Thr	Thr	Tyr	Tyr	Ser	Ser
	450					455					460				
Ser	Leu	Lys	Ser	Arg	Val	Thr	Ile	Ser	Lys	Asp	Asn	Ser	Lys	Asn	Gln
465					470					475					480
Val	Ser	Leu	Lys	Leu	Ser	Ser	Val	Thr	Ala	Ala	Asp	Thr	Ala	Val	Tyr
				485					490					495	
Tyr	Cys	Ala	Lys	His	Tyr	Tyr	Tyr	Gly	Gly	Ser	Tyr	Ala	Met	Asp	Tyr
			500					505					510		
Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Thr	Thr	Thr	Pro	Ala
		515					520					525			
Pro	Arg	Pro	Pro	Thr	Pro	Ala	Pro	Thr	Ile	Ala	Ser	Gln	Pro	Leu	Ser
	530					535					540				
Leu	Arg	Pro	Glu	Ala	Cys	Arg	Pro	Ala	Ala	Gly	Gly	Ala	Val	His	Thr
545					550					555					560
Arg	Gly	Leu	Asp	Phe	Ala	Cys	Asp	Ile	Tyr	Ile	Trp	Ala	Pro	Leu	Ala
				565					570					575	
Gly	Thr	Cys	Gly	Val	Leu	Leu	Leu	Ser	Leu	Val	Ile	Thr	Leu	Tyr	Cys

_SL

Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala Lys
65 70 75 80

Arg Val Pro Gly Phe Val Asp Leu Ala Leu His Asp Gln Val His Leu
85 90 95

Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp Arg
100 105 110

Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu
115 120 125

Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe Asp
130 135 140

Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly
145 150 155 160

Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val
165 170 175

Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His
180 185 190

Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met
195 200 205

Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala Gln
210 215 220

Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Ser Lys Arg Met
225 230 235 240

Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Ser Asp
245 250 255

Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu Gly Thr Gly Ala Glu
260 265 270

Asp Pro Arg Pro Ser Arg Lys Arg Arg Ser Leu Gly Asp Val Gly Gln
275 280 285

Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser
290 295 300

Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr Tyr
305 310 315 320

Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly
325 330 335

_SL

Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe Gln
340 345 350

Gly Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Ser Thr Val Tyr Met
355 360 365

Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala
370 375 380

Arg Asp Met Asn Ile Leu Ala Thr Val Pro Phe Asp Ile Trp Gly Gln
385 390 395 400

Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly
405 410 415

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser
420 425 430

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala
435 440 445

Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly
450 455 460

Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly
465 470 475 480

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
485 490 495

Thr Val Asn Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln
500 505 510

Gln Gly Asp Ser Val Pro Leu Thr Phe Gly Gly Gly Thr Arg Leu Glu
515 520 525

Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr
530 535 540

Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala
545 550 555 560

Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile
565 570 575

Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser
580 585 590

Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr
595 600 605

_SL

Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu
610 615 620

Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu
625 630 635 640

Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln
645 650 655

Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu
660 665 670

Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly
675 680 685

Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln
690 695 700

Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu
705 710 715 720

Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr
725 730 735

Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro
740 745 750

Arg

<210> 1043
<211> 753
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1043
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gln Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln
20 25 30

Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu
35 40 45

Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu
50 55 60

_SL

Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala Lys
65 70 75 80

Arg Val Pro Gly Phe Val Asp Leu Thr Leu His Asp Gln Val His Leu
85 90 95

Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp Arg
100 105 110

Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu
115 120 125

Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe Asp
130 135 140

Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly
145 150 155 160

Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val
165 170 175

Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His
180 185 190

Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met
195 200 205

Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala Gln
210 215 220

Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Asn Lys Arg Met
225 230 235 240

Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Ser Asp
245 250 255

Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu Gly Thr Gly Ala Glu
260 265 270

Asp Pro Arg Pro Ser Arg Lys Arg Arg Ser Leu Gly Asp Val Gly Gln
275 280 285

Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser
290 295 300

Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr Tyr
305 310 315 320

Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly
325 330 335

_SL

Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe Gln
340 345 350

Gly Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Ser Thr Val Tyr Met
355 360 365

Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala
370 375 380

Arg Asp Met Asn Ile Leu Ala Thr Val Pro Phe Asp Ile Trp Gly Gln
385 390 395 400

Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly
405 410 415

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser
420 425 430

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala
435 440 445

Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly
450 455 460

Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly
465 470 475 480

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
485 490 495

Thr Val Asn Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln
500 505 510

Gln Gly Asp Ser Val Pro Leu Thr Phe Gly Gly Gly Thr Arg Leu Glu
515 520 525

Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr
530 535 540

Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala
545 550 555 560

Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile
565 570 575

Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser
580 585 590

Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr
595 600 605

_SL

Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu
610 615 620

Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu
625 630 635 640

Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln
645 650 655

Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu
660 665 670

Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly
675 680 685

Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln
690 695 700

Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu
705 710 715 720

Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr
725 730 735

Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro
740 745 750

Arg

<210> 1044

<211> 747

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1044

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gln Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln
20 25 30

Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu
35 40 45

Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu
50 55 60

Thr Asn Leu Ala Asp Arg Glu Leu Val His ^{-SL}Met Ile Asn Trp Ala Lys
 65 70 75 80
 Arg Val Pro Gly Phe Val Asp Leu Ala Leu His Asp Gln Val His Leu
 85 90 95
 Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp Arg
 100 105 110
 Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu
 115 120 125
 Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe Asp
 130 135 140
 Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly
 145 150 155 160
 Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val
 165 170 175
 Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His
 180 185 190
 Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met
 195 200 205
 Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala Gln
 210 215 220
 Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Ser Lys Arg Met
 225 230 235 240
 Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Ser Asp
 245 250 255
 Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu Gly Thr Gly Ala Glu
 260 265 270
 Asp Pro Arg Pro Ser Arg Lys Arg Arg Gln Val Gln Leu Val Gln Ser
 275 280 285
 Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys
 290 295 300
 Ala Ser Gly Tyr Thr Phe Thr Gly Tyr Tyr Met His Trp Val Arg Gln
 305 310 315 320
 Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Trp Ile Asn Pro Asn Ser
 325 330 335

Gly Gly Thr Asn Tyr Ala Gln Lys Phe Gln^{-SL} Gly Arg Val Thr Leu Thr
 340 345 350
 Arg Asp Thr Ser Ile Ser Thr Val Tyr Met Glu Leu Ser Arg Leu Arg
 355 360 365
 Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Met Asn Ile Leu
 370 375 380
 Ala Thr Val Pro Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val
 385 390 395 400
 Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 405 410 415
 Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
 420 425 430
 Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser
 435 440 445
 Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu
 450 455 460
 Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser
 465 470 475 480
 Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Val Asn Ser Leu Gln
 485 490 495
 Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Gly Asp Ser Val Pro
 500 505 510
 Leu Thr Phe Gly Gly Gly Thr Arg Leu Glu Ile Lys Thr Thr Thr Pro
 515 520 525
 Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu
 530 535 540
 Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His
 545 550 555 560
 Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu
 565 570 575
 Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr
 580 585 590
 Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe
 595 600 605

Met Arg Pro Val Gln Thr Thr Gln Glu Glu ^{-SL}Asp Gly Cys Ser Cys Arg
610 615 620

Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser
625 630 635 640

Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr
645 650 655

Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys
660 665 670

Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn
675 680 685

Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu
690 695 700

Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly
705 710 715 720

His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr
725 730 735

Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
740 745

<210> 1045
<211> 747
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1045
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gln Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln
20 25 30

Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu
35 40 45

Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu
50 55 60

Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala Lys
65 70 75 80

Arg Val Pro Gly Phe Val Asp Leu Thr Leu His Asp Gln Val His Leu
Page 924

_SL

85	90	95
Leu Glu Cys Ala Trp Met Glu Ile	Leu Met Ile Gly Leu Val Trp Arg	
100	105	110
Ser Met Glu His Pro Gly Lys	Leu Leu Phe Ala Pro Asn Leu Leu Leu	
115	120	125
Asp Arg Asn Gln Gly Lys Cys	Val Glu Gly Gly Val Glu Ile Phe Asp	
130	135	140
Met Leu Leu Ala Thr Ser Ser	Arg Phe Arg Met Met Asn Leu Gln Gly	
145	150	155
Glu Glu Phe Val Cys Leu Lys	Ser Ile Ile Leu Leu Asn Ser Gly Val	
165	170	175
Tyr Thr Phe Leu Ser Ser Thr	Leu Lys Ser Leu Glu Glu Lys Asp His	
180	185	190
Ile His Arg Val Leu Asp Lys	Ile Thr Asp Thr Leu Ile His Leu Met	
195	200	205
Ala Lys Ala Gly Leu Thr Leu	Gln Gln Gln His Gln Arg Leu Ala Gln	
210	215	220
Leu Leu Leu Ile Leu Ser His	Ile Arg His Met Ser Asn Lys Arg Met	
225	230	235
Glu His Leu Tyr Ser Met Lys	Cys Lys Asn Val Val Pro Leu Ser Asp	
245	250	255
Leu Leu Leu Glu Met Leu Asp	Ala His Arg Leu Gly Thr Gly Ala Glu	
260	265	270
Asp Pro Arg Pro Ser Arg Lys	Arg Arg Gln Val Gln Leu Val Gln Ser	
275	280	285
Gly Ala Glu Val Lys Lys Pro	Gly Ala Ser Val Lys Val Ser Cys Lys	
290	295	300
Ala Ser Gly Tyr Thr Phe Thr	Gly Tyr Tyr Met His Trp Val Arg Gln	
305	310	315
Ala Pro Gly Gln Gly Leu Glu	Trp Met Gly Trp Ile Asn Pro Asn Ser	
325	330	335
Gly Gly Thr Asn Tyr Ala Gln	Lys Phe Gln Gly Arg Val Thr Leu Thr	
340	345	350
Arg Asp Thr Ser Ile Ser Thr	Val Tyr Met Glu Leu Ser Arg Leu Arg	

_SL

355	360	365	
Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Met Asn Ile Leu			
370	375	380	
Ala Thr Val Pro Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val			
385	390	395	400
Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly			
405	410	415	
Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val			
420	425	430	
Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser			
435	440	445	
Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu			
450	455	460	
Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser			
465	470	475	480
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Val Asn Ser Leu Gln			
485	490	495	
Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Gly Asp Ser Val Pro			
500	505	510	
Leu Thr Phe Gly Gly Gly Thr Arg Leu Glu Ile Lys Thr Thr Thr Pro			
515	520	525	
Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu			
530	535	540	
Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His			
545	550	555	560
Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu			
565	570	575	
Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr			
580	585	590	
Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe			
595	600	605	
Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg			
610	615	620	
Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser			

_SL

Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu
115 120 125

Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe Asp
130 135 140

Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly
145 150 155 160

Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val
165 170 175

Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His
180 185 190

Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met
195 200 205

Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala Gln
210 215 220

Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Ser Lys Arg Met
225 230 235 240

Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Ser Asp
245 250 255

Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu Gly Thr Gly Ala Glu
260 265 270

Asp Pro Arg Pro Ser Arg Lys Arg Arg Ser Leu Gly Asp Val Gly Glu
275 280 285

Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
290 295 300

Leu Arg Leu Ser Cys Ala Val Ser Gly Phe Ala Leu Ser Asn His Gly
305 310 315 320

Met Ser Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
325 330 335

Gly Ile Val Tyr Ser Gly Ser Thr Tyr Tyr Ala Ala Ser Val Lys Gly
340 345 350

Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr Leu Gln
355 360 365

Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Ile Tyr Tyr Cys Ser Ala
370 375 380

_SL

His Gly Gly Glu Ser Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val
385 390 395 400

Ser Ser Ala Ser Gly Gly Gly Gly Ser Gly Gly Arg Ala Ser Gly Gly
405 410 415

Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala
420 425 430

Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile
435 440 445

Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
450 455 460

Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg
465 470 475 480

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser
485 490 495

Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser
500 505 510

Thr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Thr Thr
515 520 525

Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln
530 535 540

Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala
545 550 555 560

Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala
565 570 575

Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr
580 585 590

Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln
595 600 605

Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser
610 615 620

Cys Arg Phe Pro Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys
625 630 635 640

Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln
645 650 655

_SL

Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
660 665 670

Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg
675 680 685

Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met
690 695 700

Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly
705 710 715 720

Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp
725 730 735

Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
740 745

<210> 1047

<211> 749

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1047

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gln Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln
20 25 30

Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu
35 40 45

Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu
50 55 60

Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala Lys
65 70 75 80

Arg Val Pro Gly Phe Val Asp Leu Thr Leu His Asp Gln Val His Leu
85 90 95

Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp Arg
100 105 110

Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu
115 120 125

_SL

Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe Asp
130 135 140

Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly
145 150 155 160

Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val
165 170 175

Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His
180 185 190

Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met
195 200 205

Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala Gln
210 215 220

Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Asn Lys Arg Met
225 230 235 240

Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Ser Asp
245 250 255

Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu Gly Thr Gly Ala Glu
260 265 270

Asp Pro Arg Pro Ser Arg Lys Arg Arg Ser Leu Gly Asp Val Gly Glu
275 280 285

Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
290 295 300

Leu Arg Leu Ser Cys Ala Val Ser Gly Phe Ala Leu Ser Asn His Gly
305 310 315 320

Met Ser Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
325 330 335

Gly Ile Val Tyr Ser Gly Ser Thr Tyr Tyr Ala Ala Ser Val Lys Gly
340 345 350

Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr Leu Gln
355 360 365

Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Ile Tyr Tyr Cys Ser Ala
370 375 380

His Gly Gly Glu Ser Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val
385 390 395 400

_SL

Ser Ser Ala Ser Gly₄₀₅ Gly Gly Gly Ser Gly₄₁₀ Gly Arg Ala Ser Gly₄₁₅ Gly
Gly Gly Ser Asp₄₂₀ Ile Gln Leu Thr Gln₄₂₅ Ser Pro Ser Ser Leu₄₃₀ Ser Ala
Ser Val Gly₄₃₅ Asp Arg Val Thr Ile₄₄₀ Thr Cys Arg Ala Ser₄₄₅ Gln Ser Ile
Ser Ser Tyr Leu Asn Trp Tyr₄₅₅ Gln Gln Lys Pro Gly₄₆₀ Lys Ala Pro Lys
Leu₄₆₅ Leu Ile Tyr Ala Ala₄₇₀ Ser Ser Leu Gln Ser₄₇₅ Gly Val Pro Ser Arg₄₈₀
Phe Ser Gly Ser Gly₄₈₅ Ser Gly Thr Asp Phe₄₉₀ Thr Leu Thr Ile Ser₄₉₅ Ser
Leu Gln Pro Glu₅₀₀ Asp Phe Ala Thr Tyr₅₀₅ Tyr Cys Gln Gln Ser₅₁₀ Tyr Ser
Thr Pro Tyr₅₁₅ Thr Phe Gly Gln Gly₅₂₀ Thr Lys Val Glu Ile₅₂₅ Lys Thr Thr
Thr Pro Ala₅₃₀ Pro Arg Pro Pro₅₃₅ Thr Pro Ala Pro Thr₅₄₀ Ile Ala Ser Gln
Pro₅₄₅ Leu Ser Leu Arg Pro₅₅₀ Glu Ala Cys Arg Pro₅₅₅ Ala Ala Gly Gly Ala₅₆₀
Val His Thr Arg Gly₅₆₅ Leu Asp Phe Ala Cys₅₇₀ Asp Ile Tyr Ile Trp₅₇₅ Ala
Pro Leu Ala Gly₅₈₀ Thr Cys Gly Val Leu₅₈₅ Leu Leu Ser Leu Val₅₉₀ Ile Thr
Leu Tyr Cys₅₉₅ Lys Arg Gly Arg Lys₆₀₀ Lys Leu Leu Tyr Ile₆₀₅ Phe Lys Gln
Pro Phe₆₁₀ Met Arg Pro Val Gln₆₁₅ Thr Thr Gln Glu Glu₆₂₀ Asp Gly Cys Ser
Cys₆₂₅ Arg Phe Pro Glu Glu₆₃₀ Glu Glu Gly Gly Cys₆₃₅ Glu Leu Arg Val Lys₆₄₀
Phe Ser Arg Ser Ala₆₄₅ Asp Ala Pro Ala Tyr₆₅₀ Gln Gln Gly Gln Asn₆₅₅ Gln
Leu Tyr Asn Glu₆₆₀ Leu Asn Leu Gly Arg₆₆₅ Arg Glu Glu Tyr Asp₆₇₀ Val Leu

_SL

Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg
675 680 685

Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met
690 695 700

Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly
705 710 715 720

Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp
725 730 735

Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
740 745

<210> 1048
<211> 743
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1048
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gln Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln
20 25 30

Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu
35 40 45

Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu
50 55 60

Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala Lys
65 70 75 80

Arg Val Pro Gly Phe Val Asp Leu Ala Leu His Asp Gln Val His Leu
85 90 95

Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp Arg
100 105 110

Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu
115 120 125

Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe Asp
130 135 140

Met Leu Leu Ala Thr Ser Ser Arg Phe Arg ^{-SL} Met Met Asn Leu Gln Gly
 145 150 155 160
 Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val
 165 170 175
 Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His
 180 185 190
 Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met
 195 200 205
 Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala Gln
 210 215 220
 Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Ser Lys Arg Met
 225 230 235 240
 Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Ser Asp
 245 250 255
 Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu Gly Thr Gly Ala Glu
 260 265 270
 Asp Pro Arg Pro Ser Arg Lys Arg Arg Glu Val Gln Leu Val Glu Ser
 275 280 285
 Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala
 290 295 300
 Val Ser Gly Phe Ala Leu Ser Asn His Gly Met Ser Trp Val Arg Arg
 305 310 315 320
 Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Gly Ile Val Tyr Ser Gly
 325 330 335
 Ser Thr Tyr Tyr Ala Ala Ser Val Lys Gly Arg Phe Thr Ile Ser Arg
 340 345 350
 Asp Asn Ser Arg Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro
 355 360 365
 Glu Asp Thr Ala Ile Tyr Tyr Cys Ser Ala His Gly Gly Glu Ser Asp
 370 375 380
 Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Gly Gly
 385 390 395 400
 Gly Gly Ser Gly Gly Arg Ala Ser Gly Gly Gly Gly Ser Asp Ile Gln
 405 410 415

Leu Thr Gln Ser₄₂₀ Pro Ser Ser Leu Ser₄₂₅ Ala^{-SL} Ser Val Gly Asp₄₃₀ Arg Val
 Thr Ile Thr₄₃₅ Cys Arg Ala Ser Gln₄₄₀ Ser Ile Ser Ser Tyr₄₄₅ Leu Asn Trp
 Tyr Gln₄₅₀ Gln Lys Pro Gly Lys₄₅₅ Ala Pro Lys Leu₄₆₀ Leu Ile Tyr Ala Ala
 Ser₄₆₅ Ser Leu Gln Ser Gly₄₇₀ Val Pro Ser Arg Phe₄₇₅ Ser Gly Ser Gly Ser₄₈₀
 Gly Thr Asp Phe Thr₄₈₅ Leu Thr Ile Ser Ser₄₉₀ Leu Gln Pro Glu Asp₄₉₅ Phe
 Ala Thr Tyr Tyr₅₀₀ Cys Gln Gln Ser Tyr₅₀₅ Ser Thr Pro Tyr Thr₅₁₀ Phe Gly
 Gln Gly Thr₅₁₅ Lys Val Glu Ile Lys₅₂₀ Thr Thr Thr Pro Ala₅₂₅ Pro Arg Pro
 Pro Thr₅₃₀ Pro Ala Pro Thr Ile₅₃₅ Ala Ser Gln Pro Leu₅₄₀ Ser Leu Arg Pro
 Glu₅₄₅ Ala Cys Arg Pro Ala₅₅₀ Ala Gly Gly Ala Val₅₅₅ His Thr Arg Gly Leu₅₆₀
 Asp Phe Ala Cys Asp₅₆₅ Ile Tyr Ile Trp Ala₅₇₀ Pro Leu Ala Gly Thr₅₇₅ Cys
 Gly Val Leu₅₈₀ Leu Ser Leu Val Ile₅₈₅ Thr Leu Tyr Cys Lys₅₉₀ Arg Gly
 Arg Lys Lys₅₉₅ Leu Leu Tyr Ile Phe₆₀₀ Lys Gln Pro Phe Met₆₀₅ Arg Pro Val
 Gln Thr Thr₆₁₀ Gln Glu Glu Asp₆₁₅ Gly Cys Ser Cys Arg₆₂₀ Phe Pro Glu Glu
 Glu₆₂₅ Glu Gly Gly Cys Glu₆₃₀ Leu Arg Val Lys Phe₆₃₅ Ser Arg Ser Ala Asp₆₄₀
 Ala Pro Ala Tyr Gln₆₄₅ Gln Gly Gln Asn Gln₆₅₀ Leu Tyr Asn Glu Leu₆₅₅ Asn
 Leu Gly Arg Arg₆₆₀ Glu Glu Tyr Asp Val₆₆₅ Leu Asp Lys Arg Arg₆₇₀ Gly Arg
 Asp Pro Glu₆₇₅ Met Gly Gly Lys Pro₆₈₀ Arg Arg Lys Asn Pro₆₈₅ Gln Glu Gly

Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met^{-SL} Ala Glu Ala Tyr Ser Glu
690 695 700

Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu
705 710 715 720

Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His
725 730 735

Met Gln Ala Leu Pro Pro Arg
740

<210> 1049

<211> 743

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1049

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gln Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln
20 25 30

Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu
35 40 45

Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu
50 55 60

Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala Lys
65 70 75 80

Arg Val Pro Gly Phe Val Asp Leu Thr Leu His Asp Gln Val His Leu
85 90 95

Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp Arg
100 105 110

Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu
115 120 125

Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe Asp
130 135 140

Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly
145 150 155 160

Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val
Page 936

_SL

165	170	175
Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His	180	185
Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met	195	200
Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala Gln	210	215
Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Asn Lys Arg Met	225	230
Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Ser Asp	245	250
Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu Gly Thr Gly Ala Glu	260	265
Asp Pro Arg Pro Ser Arg Lys Arg Arg Glu Val Gln Leu Val Glu Ser	275	280
Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala	290	295
Val Ser Gly Phe Ala Leu Ser Asn His Gly Met Ser Trp Val Arg Arg	305	310
Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Gly Ile Val Tyr Ser Gly	325	330
Ser Thr Tyr Tyr Ala Ala Ser Val Lys Gly Arg Phe Thr Ile Ser Arg	340	345
Asp Asn Ser Arg Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro	355	360
Glu Asp Thr Ala Ile Tyr Tyr Cys Ser Ala His Gly Gly Glu Ser Asp	370	375
Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Gly Gly	385	390
Gly Gly Ser Gly Gly Arg Ala Ser Gly Gly Gly Gly Ser Asp Ile Gln	405	410
Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val	420	425
Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp		

_SL

435 440 445

Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala
450 455 460

Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser
465 470 475 480

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe
485 490 495

Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Tyr Thr Phe Gly
500 505 510

Gln Gly Thr Lys Val Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro
515 520 525

Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro
530 535 540

Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu
545 550 555 560

Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys
565 570 575

Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly
580 585 590

Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val
595 600 605

Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu
610 615 620

Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp
625 630 635 640

Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn
645 650 655

Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg
660 665 670

Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly
675 680 685

Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu
690 695 700

Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu

	_SL	
ggctctgaga ctacttacta ctcttcatcc ctcaagtcac gcgtcaccat ctcaaaggac		1440
aactctaaga atcaggtgtc actgaaactg tcatctgtga ccgcagccga caccgccgtg		1500
tactattgcg ctaagcatta ctattatggc gggagctacg caatggatta ctggggacag		1560
ggtactctgg tcaccgtgtc cagcaccact accccagcac cgaggccacc caccgccgt		1620
cctaccatcg cctcccagcc tctgtccctg cgtccggagg catgtagacc cgcagctggt		1680
ggggccgtgc ataccgggg tcttgacttc gcctgcgata tctacatttg ggcccctctg		1740
gctggtactt gcggggtcct gctgctttca ctctgtatca ctctttactg taagcgcggt		1800
cggaagaagc tgctgtacat ctttaagcaa cccttcatga ggcctgtgca gactactcaa		1860
gaggaggacg gctgttcacg ccggttccca gaggaggagg aaggcggctg cgaactgcgc		1920
gtgaaattca gccgcagcgc agatgctcca gcctaccagc aggggcagaa ccagctctac		1980
aacgaactca atcttggtcg gagagaggag tacgacgtgc tggacaagcg gagaggacgg		2040
gaccagaaa tgggcgggaa gccgcgcaga aagaatcccc aagagggcct gtacaacgag		2100
ctccaaaagg ataagatggc agaagcctat agcgagattg gtatgaaagg ggaacgcaga		2160
agaggcaaag gccacgacgg actgtaccag ggactcagca ccgccaccaa ggacacctat		2220
gacgctcttc acatgcaggc cctgccgcct cgg		2253

<210> 1051

<211> 2253

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1051

atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg		60
ccctcgttgg cactttccct gactgccgac cagatggtgt ccgcccttct ggacgccgag		120
cctccaattc tgtactcgga gtacgatccg actcgcccgt tctccgaagc cagcatgatg		180
ggcctgttga ctaacctggc ggaccgcgag ttggtgcaca tgattaactg ggctaagcgg		240
gtgccgggct tcgtggacct gaccctgcac gaccaagtgc acctcctgga atgcgcctgg		300
atggaaatcc tcatgatcgg cctcgtgtgg agatccatgg agcatcccgg aaagctcctg		360
tttgaccca acctcctgct tgatcgcaac cagggaaaat gcgtggaagg ggggtgtcgag		420
attttcgaca tgctgctcgc cacctcttcc cggttccgga tgatgaatct gcaggagaaa		480
gagttcgtgt gtctgaagtc aatcatcctg ctgaactccg gggctctatac cttcctgagc		540
tcgaccctca agtactgga ggaaaaagac cacatccatc gcgtgctcga taagatcacc		600
gacaccctta tccatctcat ggcgaaggct ggactgacct tgcaacagca gcaccagagg		660
ctggcccagt tgctgctgat tctgagccac atccggcaca tgtcgaacaa gaggatggaa		720
cacctgtaca gcatgaagtg caagaacgtc gtgcctctgt ccgatctgct cctggaaatg		780

_SL

ctggacgcgc acagactcgg aaccggcgcg gaagaccccc	ggccctccag gaagcgaagg	840
tccctcggag acgtgggtga aattgtgatg acccagtcac	ccgccactct tagcctttca	900
cccggtgagc gcgcaaccct gtcttgca gaacctcaaa	ataccttaat	960
tggtatcaac agaagcccgg acaggctcct cgccttctga	tctaccacac cagccggctc	1020
cattctggaa tccctgccag gttcagcggg agcggatctg	ggaccgacta caccctcact	1080
atcagctcac tgcagccaga ggacttcgct gtctatttct	gtcagcaagg gaacaccctg	1140
ccctacacct ttggacaggg caccaagctc gagattaaag	gtggagggtg cagcggagga	1200
ggtgggtccg gcggtggagg aagccaggct caactccaag	aaagcggacc gggctttgtg	1260
aagccatcag aaactctttc actgacttgt actgtgagcg	gagtgtctct ccccgattac	1320
ggggtgtctt ggatcagaca gccaccgggg aagggctctg	aatggattgg agtgatttgg	1380
ggctctgaga ctacttacta ctcttcatcc ctcaagtcac	gcgtcaccat ctcaaaggac	1440
aactctaaga atcaggtgtc actgaaactg tcatctgtga	ccgcagccga caccgccgtg	1500
tactattgcg ctaagcatta ctattatggc gggagctacg	caatggatta ctggggacag	1560
ggtactctgg tcaccgtgtc cagcaccact accccagcac	cgaggccacc caccgccggt	1620
cctaccatcg cctcccagcc tctgtccctg cgtccggagg	catgtagacc cgcagctggt	1680
ggggccgtgc ataccgggg tcttgacttc gcctgcgata	tctacatttg ggcccctctg	1740
gctgggtactt gcggggctct gctgctttca ctctgtatca	ctctttactg taagcgcggt	1800
cggaagaagc tgctgtacat cttaagcaa cccttcatga	ggcctgtgca gactactcaa	1860
gaggaggacg gctgttcatg ccggttccca gaggaggagg	aaggcggctg cgaactgcgc	1920
gtgaaattca gccgcagcgc agatgtcca gcctaccagc	aggggcagaa ccagctctac	1980
aacgaactca atcttggtcg gagagaggag tacgacgtgc	tggacaagcg gagaggacgg	2040
gaccagaaa tgggcgggaa gccgcgcaga aagaatcccc	aagagggcct gtacaacgag	2100
ctccaaaagg ataagatggc agaagcctat agcgagattg	gtatgaaagg ggaacgcaga	2160
agaggcaaag gccacgacgg actgtaccag ggactcagca	ccgccaccaa ggacacctat	2220
gacgtcttc acatgcaggc cctgccgcct cgg		2253

<210> 1052

<211> 2235

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1052

atggccctcc ctgtcaccgc cctgctgctt ccgctggctc	ttctgctcca cgccgctcgg	60
ccctcgttgg cactttccct gactgccgac cagatggtgt	ccgcccttct ggacgccgag	120
cctccaattc tgtactcgga gtacgatccg actcgcccgt	tctccgaagc cagcatgatg	180

						_SL	
ggcctgttga	ctaacctggc	ggaccgcgag	ttgggtgcaca	tgattaactg	ggctaagcgg		240
gtgccgggct	tcgtggacct	ggccctgcac	gaccaagtgc	acctcctgga	atgcgcctgg		300
atggaaatcc	tcattgatcg	cctcgtgtgg	agatccatgg	agcatcccgg	aaagctcctg		360
tttgcaccca	acctcctgct	tgatcgcaac	cagggaaaat	gcgtggaagg	gggtgtcgag		420
attttcgaca	tgctgctcgc	cacctcttcc	cggttccgga	tgatgaatct	gcaggagaaa		480
gagttcgtgt	gtctgaagtc	aatcatcctg	ctgaactccg	gggtctatac	cttcctgagc		540
tcgacctca	agtcactgga	ggaaaaagac	cacatccatc	gcgtgctcga	taagatcacc		600
gacaccctta	tccatctcat	ggcgaaggct	ggactgacct	tgcaacagca	gcaccagagg		660
ctggcccagt	tgctgctgat	tctgagccac	atccggcaca	tgctgtccaa	gaggatggaa		720
cacctgtaca	gcatgaagtg	caagaacgtc	gtgcctctgt	ccgatctgct	cctggaaatg		780
ctggacgcgc	acagactcgg	gacgggagct	gaagatccac	gaccagcag	aaagcgacgg		840
gaaattgtga	tgaccagtc	acccgccact	cttagccttt	cacccggtga	gcgcgcaacc		900
ctgtcttgca	gagcctccca	agacatctca	aaatacctta	attggtatca	acagaagccc		960
ggacaggctc	ctgccttct	gatctaccac	accagccggc	tccattctgg	aatccctgcc		1020
aggttcagcg	gtagcggatc	tgggaccgac	tacaccctca	ctatcagctc	actgcagcca		1080
gaggacttcg	ctgtctattt	ctgtcagcaa	gggaacaccc	tgccctacac	ctttggacag		1140
ggcaccaagc	tcgagattaa	aggtggaggt	ggcagcggag	gaggtgggtc	cggcgggtgga		1200
ggaagccagg	tccaactcca	agaaagcggg	ccgggtcttg	tgaagccatc	agaaactctt		1260
tcactgactt	gtactgtgag	cggagtgtct	ctccccgatt	acggggtgtc	ttggatcaga		1320
cagccaccgg	ggaaggggtc	ggaatggatt	ggagtgattt	ggggctctga	gactacttac		1380
tactcttcat	ccctcaagtc	acgcgtcacc	atctcaaagg	acaactctaa	gaatcaggtg		1440
tcactgaaac	tgtcatctgt	gaccgcagcc	gacaccgccg	tgtactattg	cgctaagcat		1500
tactattatg	gcgggagcta	cgcaatggat	tactggggac	agggactctt	ggtcaccgtg		1560
tccagcacca	ctaccccagc	accgaggcca	cccaccccg	ctcctaccat	cgcctcccag		1620
cctctgtccc	tgcttccgga	ggcatgtaga	ccgcagctg	gtggggccgt	gcatacccgg		1680
ggctcttgact	tcgcctgcga	tatctacatt	tgggcccctc	tggctgggtac	ttgcgggggtc		1740
ctgctgcttt	cactcgtgat	cactctttac	tgtaagcgcg	gtcgggaagaa	gctgctgtac		1800
atctttaagc	aacccttcat	gaggcctgtg	cagactactc	aagaggagga	cggctgttca		1860
tgccgggtcc	cagaggagga	ggaaggcggc	tgcaactgc	gcgtgaaatt	cagccgcagc		1920
gcagatgctc	cagcctacca	gcaggggcag	aaccagctct	acaacgaact	caatcttggg		1980
cggagagagg	agtacgacgt	gctggacaag	cggagaggac	gggaccaga	aatgggcggg		2040
aagccgcgca	gaaagaatcc	ccaagagggc	ctgtacaacg	agctccaaaa	ggataagatg		2100
gcagaagcct	atagcgagat	tgggtatgaaa	ggggaacgca	gaagaggcaa	aggccacgac		2160
ggactgtacc	agggactcag	caccgccacc	aaggacacct	atgacgctct	tcacatgcag		2220

gccctgccgc ctcgg

2235

<210> 1053

<211> 2235

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1053

atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg	60
ccctcgttgg cactttccct gactgccgac cagatggtgt ccgcccttct ggacgccgag	120
cctccaattc tgtactcgga gtacgatccg actcgcccggt tctccgaagc cagcatgatg	180
ggcctgttga ctaacctggc ggaccgcgag ttggtgcaca tgattaactg ggctaagcgg	240
gtgccgggct tcgtggacct gaccctgcac gaccaagtgc acctcctgga atgcgcctgg	300
atggaaatcc tcatgatcgg cctcgtgtgg agatccatgg agcatcccgg aaagctcctg	360
tttgacacca acctcctgct tgatcgcaac cagggaaaaat gcgtggaagg ggggtgtcga	420
attttcgaca tgctgctcgc cacctcttcc cggttccgga tgatgaatct gcaggagaa	480
gagttcgtgt gtctgaagtc aatcatcctg ctgaactccg ggggtctatac cttcctgagc	540
tcgaccctca agtcaactgga ggaaaaagac cacatccatc gcgtgctcga taagatcacc	600
gacaccctta tccatctcat ggcgaaggct ggactgacct tgcaacagca gcaccagagg	660
ctggcccagt tgctgctgat tctgagccac atccggcaca tgtcgaacaa gaggatggaa	720
cacctgtaca gcatgaagtg caagaacgtc gtgcctctgt ccgatctgct cctggaaatg	780
ctggacgcgc acagactcgg gacgggagct gaagatccac gaccagcag aaagcgacgg	840
gaaattgtga tgaccagtc acccgccact cttagccttt caccgggtga gcgcgcaacc	900
ctgtcttgca gagcctccca agacatctca aaatacctta attggtatca acagaagccc	960
ggacaggctc ctgccttct gatctaccac accagccggc tccattctgg aatccctgcc	1020
aggttcagcg gtagcggatc tgggaccgac tacaccctca ctatcagctc actgcagcca	1080
gaggacttcg ctgtctatct ctgtcagcaa gggaacaccc tgcctacac ctttggacag	1140
ggcaccaagc tcgagattaa aggtggaggt ggcagcggag gaggtgggtc cggcgggtga	1200
ggaagccagg tccaactcca agaaagcggg ccgggtcttg tgaagccatc agaaactctt	1260
tcactgactt gtactgtgag cggagtgtct ctccccgatt acgggggtgtc ttggatcaga	1320
cagccaccgg ggaagggctt ggaatggatt ggagtgattt ggggctctga gactacttac	1380
tactcttcat ccctcaagtc acgcgtcacc atctcaaagg acaactctaa gaatcagggtg	1440
tcactgaaac tgtcatctgt gaccgcagcc gacaccgccg tgtactattg cgctaagcat	1500
tactattatg gcgggagcta cgcaatggat tactggggac aggggtactct ggtcaccgtg	1560
tccagcacca ctacccagc accgaggcca cccaccccg ctcctaccat cgcctcccag	1620

cctctgtccc	tgcggtccgga	ggcatgtaga	cccgcagctg	gtggggccgt	gcatacccg	1680
ggctcttgact	tcgcctgcga	tatctacatt	tgggccctc	tggttggtac	ttgcggggtc	1740
ctgctgcttt	cactcgtgat	cactctttac	tgtgaagcgcg	gtcggaagaa	gctgctgtac	1800
atctttaagc	aacccttcat	gaggcctgtg	cagactactc	aagaggagga	cggctgttca	1860
tgccggttcc	cagaggagga	ggaaggcggc	tgcaactgc	gcgtgaaatt	cagccgcagc	1920
gcagatgctc	cagcctacca	gcaggggcag	aaccagctct	acaacgaact	caatcttggt	1980
cggagagagg	agtacgacgt	gctggacaag	cggagaggac	gggaccaga	aatgggcggg	2040
aagccgcgca	gaaagaatcc	ccaagagggc	ctgtacaacg	agctccaaaa	ggataagatg	2100
gcagaagcct	atagcgagat	tggtatgaaa	ggggaacgca	gaagaggcaa	aggccacgac	2160
ggactgtacc	agggactcag	caccgccacc	aaggacacct	atgacgctct	tcacatgcag	2220
gccctgccgc	ctcgg					2235

<210> 1054

<211> 2256

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1054

atggccctcc	ctgtcaccgc	cctgctgctt	ccgctggctc	ttctgctcca	cgccgctcgg	60
ccctcgttgg	cactttccct	gactgccgac	cagatggtgt	ccgcccttct	ggacgccgag	120
cctccaattc	tgtactcgga	gtacgatccg	actcgcccg	tctccgaagc	cagcatgatg	180
ggcctgttga	ctaacctggc	ggaccgcgag	ttggtgcaca	tgattaactg	ggctaagcgg	240
gtgccgggct	tcgtggacct	ggccctgcac	gaccaagtgc	acctcctgga	atgcgcctgg	300
atggaaatcc	tcatgatcgg	cctcgtgtgg	agatccatgg	agcatcccgg	aaagctcctg	360
tttgcacca	acctcctgct	tgatcgcaac	cagggaaaat	gcgtggaagg	gggtgtcgag	420
attttcgaca	tgctgctcgc	cacctcttcc	cggttccgga	tgatgaatct	gcagggagaa	480
gagttcgtgt	gtctgaagtc	aatcatcctg	ctgaactccg	gggtctatac	cttcctgagc	540
tcgaccctca	agtcactgga	ggaaaaagac	cacatccatc	gcgtgctcga	taagatcacc	600
gacaccctta	tccatctcat	ggcgaaggct	ggactgacct	tgcaacagca	gcaccagagg	660
ctggcccagt	tgctgctgat	tctgagccac	atccggcaca	tgctgtccaa	gaggatggaa	720
cacctgtaca	gcatgaagtg	caagaacgtc	gtgcctctgt	ccgatctgct	cctggaaatg	780
ctggacgcgc	acagactcgg	aaccggcgcg	gaagaccccc	ggccctccag	gaagcgaagg	840
tccctcggag	acgtgggtca	agtgaactc	gtccaaagcg	gagcggaagt	caagaaaccc	900
ggagcgagcg	tgaagtgctc	ctgcaaagcc	tccggctaca	cctttacggg	ctactacatg	960
cactgggtgc	gccaggcacc	aggacagggt	cttgaatgga	tgggatggat	caacccta	1020

_SL						
tcgggcgga	ctaactacgc	acagaagttc	caggggagag	tgactctgac	tcgggatacc	1080
tccatctcaa	ctgtctacat	ggaactctcc	cgcttgcggt	cagatgatac	ggcagtgtac	1140
tactgcgccc	gcgacatgaa	tatcctggct	accgtgccgt	tcgacatctg	gggacagggg	1200
actatggtta	ctgtctcatc	gggcgggtgga	ggttcaggag	gaggcggctc	gggaggcgga	1260
ggttcggaca	ttcagatgac	ccagtcccca	tcctctctgt	cggccagcgt	cggagatagg	1320
gtgaccatta	cctgtcgggc	ctcgcaaagc	atctcctcgt	acctcaactg	gtatcagcaa	1380
aagccggga	aggcgcctaa	gctgctgata	tacgccgctt	cgagcttgca	aagcgggggtg	1440
ccatccagat	tctcgggata	aggctcagga	accgacttca	ccctgaccgt	gaacagcctc	1500
cagccggagg	actttgccac	ttactactgc	cagcaggggag	actccgtgcc	gcttactttc	1560
ggggggggta	ccgccttga	gatcaagacc	actaccccag	caccgaggcc	accaccccgc	1620
gctcctacca	tcgcctccca	gcctctgtcc	ctgcgtccgc	aggcatgtag	accgcagct	1680
ggtggggccg	tgcataccgc	gggtcttgac	ttcgccctgcg	atatctacat	ttggggcccct	1740
ctggctggta	cttgcggggt	cctgctgctt	tcactcgtga	tcactcttta	ctgtaagcgc	1800
ggtcggaaga	agctgctgta	catctttaag	caacccttca	tgaggcctgt	gcagactact	1860
caagaggagg	acggctgttc	atgccggttc	ccagaggagg	aggaaggcgc	ctgcgaactg	1920
cgctgaaat	tcagccgcag	cgcagatgct	ccagccctacc	agcaggggca	gaaccagctc	1980
tacaacgaac	tcaatcttgg	tcggagagag	gagtacgacg	tgctggacaa	gcggagagga	2040
cgggaccag	aaatgggcgc	gaagccgcgc	agaaagaatc	cccaagaggg	cctgtacaac	2100
gagctccaaa	aggataagat	ggcagaagcc	tatagcgaga	ttggtatgaa	aggggaacgc	2160
agaagaggca	aaggccacga	cggactgtac	cagggactca	gcaccgccac	caaggacacc	2220
tatgacgctc	ttcacatgca	ggccctgccg	cctcgg			2256

```
<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"
```

<400> 1055							
atggccctcc	ctgtcaccgc	cctgctgctt	ccgctggctc	ttctgctcca	cgccgctcgg		60
ccctcgtttg	cactttccct	gactgccgac	cagatgggtgt	ccgcccttct	ggacgccgag		120
cctccaattc	tgtactcgga	gtacgatccg	actcgcccgt	tctccgaagc	cagcatgatg		180
ggcctgttga	ctaacctggc	ggaccgcgag	ttggtgcaca	tgattaactg	ggctaagcgg		240
gtgccgggct	tcgtggacct	gaccctgcac	gaccaagtgc	acctcctgga	atgcgcctgg		300
atggaaatcc	tcatgatcgg	cctcgtgtgg	agatccatgg	agcatcccgg	aaagctcctg		360
tttgcaccca	acctcctgct	tgatcgcaac	cagggaaaat	gcgtggaagg	gggtgtcgag		420

					_SL	
attttcgaca	tgctgctcgc	cacctcttcc	cggttccgga	tgatgaatct	gcagggagaa	480
gagttcgtgt	gtctgaagtc	aatcatcctg	ctgaactccg	gggtctatac	cttcctgagc	540
tcgaccctca	agtcactgga	ggaaaaagac	cacatccatc	gcgtgctcga	taagatcacc	600
gacaccctta	tccatctcat	ggcgaaggct	ggactgaccc	tgcaacagca	gcaccagagg	660
ctggcccagt	tgctgctgat	tctgagccac	atccggcaca	tgtcgaacaa	gaggatggaa	720
cacctgtaca	gcatgaagtg	caagaacgtc	gtgcctctgt	ccgatctgct	cctggaaatg	780
ctggacgcgc	acagactcgg	aaccggcgcg	gaagaccccc	ggccctccag	gaagcgaagg	840
tccctcggag	acgtgggtca	agtgaactc	gtccaaagcg	gagcggaagt	caagaaaccc	900
ggagcgagcg	tgaaagtgtc	ctgcaaagcc	tccggctaca	cctttacggg	ctactacatg	960
cactgggtgc	gccaggcacc	aggacagggt	cttgaatgga	tgggatggat	caaccctaata	1020
tcgggcggaa	ctaactacgc	acagaagttc	caggggagag	tgactctgac	tcgggataacc	1080
tccatctcaa	ctgtctacat	ggaactctcc	cgcttgcggt	cagatgatac	ggcagtgtac	1140
tactgcgccc	gcgacatgaa	tatcctggct	accgtgccgt	tcgacatctg	gggacagggg	1200
actatggtta	ctgtctcatc	gggcgggtgga	ggttcaggag	gaggcggctc	gggaggcgga	1260
ggttcggaca	ttcagatgac	ccagtcccca	tcctctctgt	cggccagcgt	cggagatagg	1320
gtgaccatta	cctgtcgggc	ctcgcaaagc	atctcctcgt	acctcaactg	gtatcagcaa	1380
aagccgggaa	aggcgcctaa	gctgctgata	tacgccgctt	cgagcttgca	aagcgggggtg	1440
ccatccagat	tctcgggatc	aggctcagga	accgacttca	ccctgaccgt	gaacagcctc	1500
cagccggagg	actttgccac	ttactactgc	cagcagggag	actccgtgcc	gcttactttc	1560
gggggggggta	cccgcctgga	gatcaagacc	actacccag	caccgaggcc	accacccccg	1620
gctcctacca	tcgcctccca	gcctctgtcc	ctgcgtccgg	aggcatgtag	acccgcagct	1680
ggtggggccg	tgcataccgc	gggtcttgac	ttcgctgcg	atatctacat	ttgggcccct	1740
ctggctggta	cttgccgggt	cctgctgctt	tcactcgtga	tcactcttta	ctgtaagcgc	1800
ggtcgggaaga	agctgctgta	catctttaag	caacccttca	tgaggcctgt	gcagactact	1860
caagaggagg	acggctgttc	atgccggttc	ccagaggagg	aggaaggcgg	ctgcgaactg	1920
cgcgtgaaat	tcagccgcag	cgcagatgct	ccagcctacc	agcaggggca	gaaccagctc	1980
tacaacgaac	tcaatcttgg	tcggagagag	gagtacgacg	tgctggacaa	gcggagagga	2040
cgggaccag	aaatgggcgg	gaagccgcgc	agaaagaatc	cccaagaggg	cctgtacaac	2100
gagctccaaa	aggataagat	ggcagaagcc	tatagcgaga	ttggtatgaa	aggggaacgc	2160
agaagaggca	aaggccacga	cggactgtac	cagggactca	gcaccgccac	caaggacacc	2220
tatgacgctc	ttcacatgca	ggccctgccg	cctcgg			2256

<210> 1056
 <211> 2238
 <212> DNA
 <213> Artificial Sequence

_SL

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1056

atggccctcc	ctgtcaccgc	cctgctgctt	ccgctggctc	ttctgctcca	cgccgctcgg	60
ccctcgttgg	cactttccct	gactgccgac	cagatggtgt	ccgcccttct	ggacgccgag	120
cctccaattc	tgtactcgga	gtacgatccg	actcgcccgt	tctccgaagc	cagcatgatg	180
ggcctgttga	ctaacctggc	ggaccgag	ttggtgcaca	tgattaactg	ggctaagcgg	240
gtgccgggct	tcgtggacct	ggccctgcac	gaccaagtgc	acctcctgga	atgcgcctgg	300
atggaaatcc	tcatgatcgg	cctcgtgtgg	agatccatgg	agcatcccgg	aaagctcctg	360
tttgcaccca	acctcctgct	tgatcgcaac	cagggaaaat	gcgtggaagg	gggtgtcgag	420
attttcgaca	tgctgctcgc	cacctcttcc	cggttccgga	tgatgaatct	gcaggagaaa	480
gagttcgtgt	gtctgaagtc	aatcatcctg	ctgaactccg	gggtctatac	cttcctgagc	540
tcgaccctca	agtcactgga	ggaaaaagac	cacatccatc	gcgtgctcga	taagatcacc	600
gacaccctta	tccatctcat	ggcgaaggct	ggactgacct	tgcaacagca	gcaccagagg	660
ctggcccagt	tgctgctgat	tctgagccac	atccggcaca	tgctgctcaa	gaggatggaa	720
cacctgtaca	gcatgaagtg	caagaacgtc	gtgcctctgt	ccgatctgct	cctggaaatg	780
ctggacgcgc	acagactcgg	aaccggcgcg	gaagaccccc	ggccctccag	gaagcgaagg	840
caagtgaac	tcgtccaaag	cggagcggaa	gtcaagaaac	ccggagcgag	cgtgaaagtg	900
tcctgcaaag	cctccggcta	cacctttacg	ggctactaca	tgactgggt	gcgccaggca	960
ccaggacagg	gtcttgaatg	gatgggatgg	atcaacccta	attcggggcg	aactaactac	1020
gcacagaagt	tccaggggag	agtgactctg	actcgggata	cctccatctc	aactgtctac	1080
atggaactct	cccgtttgcg	gtcagatgat	acggcagtgt	actactgcgc	ccgcgacatg	1140
aatatcctgg	ctaccgtgcc	gttcgacatc	tggggacagg	ggactatggt	tactgtctca	1200
tcgggcggtg	gaggttcagg	aggaggcggc	tcgggagggc	gaggttcgga	cattcagatg	1260
accagtccc	catcctctct	gtcggccagc	gtcggagata	gggtgaccat	tacctgtcgg	1320
gcctcgcaaa	gcatctcctc	gtacctcaac	tggtatcagc	aaaagccggg	aaaggcgcct	1380
aagctgctga	tctacgccgc	ttcgagcttg	caaagcgggg	tgccatccag	attctcggga	1440
tcaggctcag	gaaccgactt	caccctgacc	gtgaacagcc	tccagccgga	ggactttgcc	1500
acttactact	gccagcaggg	agactccgtg	ccgcttactt	tcgggggggg	taccgcctg	1560
gagatcaaga	ccactacccc	agcaccgagg	ccaccacccc	cggctcctac	catgcctcc	1620
cagcctctgt	ccctgcgtcc	ggaggcatgt	agaccgcag	ctggtggggc	cgtgcatacc	1680
cggggctctt	acttcgcctg	cgatatctac	atttggggcc	ctctggctgg	tacttgccgg	1740
gtcctgctgc	tttcaactcg	gatcactctt	tactgtaagc	gcggtcggaa	gaagctgctg	1800
tacatcttta	agcaaccctt	catgaggcct	gtgcagacta	ctcaagagga	ggacggctgt	1860

tcatgccggt	tcccagagga	ggaggaaggc	ggctgcgaac	tgcgcgtaga	attcagccgc	1920
agcgcagatg	ctccagccta	ccagcagggg	cagaaccagc	tctacaacga	actcaatctt	1980
ggtcggagag	aggagtacga	cgtgctggac	aagcggagag	gacgggaccc	agaaatgggc	2040
gggaagccgc	gcagaaagaa	tccccaagag	ggcctgtaca	acgagctcca	aaaggataag	2100
atggcagaag	cctatagcga	gattggtatg	aaaggggaac	gcagaagagg	caaaggccac	2160
gacggactgt	accagggact	cagcaccgcc	accaaggaca	cctatgacgc	tcttcacatg	2220
caggccctgc	cgcctcgg					2238

<210> 1057
 <211> 2238
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1057	
atggccctcc	ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60
ccctcgttgg	cactttccct gactgccgac cagatggtgt ccgcccttct ggacgccgag 120
cctccaattc	tgtactcgga gtacgatccg actcgcccgt tctccgaagc cagcatgatg 180
ggcctgttga	ctaacctggc ggaccgagag ttggtgcaca tgattaactg ggctaagcgg 240
gtgccgggct	tcgtggacct gaccctgcac gaccaagtgc acctcctgga atgcgcctgg 300
atggaaatcc	tcatgatcgg cctcgtgtgg agatccatgg agcatcccgg aaagctcctg 360
tttgaccca	acctcctgct tgatcgcaac cagggaaaat gcgtggaagg ggggtgtcag 420
attttcgaca	tgctgctcgc cacctcttcc cggttccgga tgatgaatct gcaggagaaa 480
gagttcgtgt	gtctgaagtc aatcatcctg ctgaactccg ggggtctatac cttcctgagc 540
tcgaccctca	agtcactgga ggaaaaagac cacatccatc gcgtgctcga taagatcacc 600
gacaccctta	tccatctcat ggcaaggct ggactgaccc tgcaacagca gcaccagagg 660
ctggcccagt	tgctgctgat tctgagccac atccggcaca tgtcgaacaa gaggatggaa 720
cacctgtaca	gcatgaagtg caagaacgtc gtgcctctgt ccgatctgct cctggaaatg 780
ctggacgcgc	acagactcgg gacgggagct gaagatccac gaccagcag aaagcgacgg 840
caagtgaac	tcgtccaaag cggagcggaa gtcaagaaac ccggagcgag cgtgaaagtg 900
tcctgcaaag	cctccggcta cacctttacg ggctactaca tgcactgggt gcgccaggca 960
ccaggacagg	gtcttgaatg gatgggatgg atcaacccta attcgggcgg aactaactac 1020
gcacagaagt	tccaggggag agtgactctg actcgggata cctccatctc aactgtctac 1080
atggaactct	cccgttgcg gtcagatgat acggcagtgt actactgcgc ccgcgacatg 1140
aatatcctgg	ctaccgtgcc gttcgacatc tggggacagg ggactatggt tactgtctca 1200
tcgggcggtg	gagggtcagg aggaggcggc tcgggaggcg gaggttcgga cattcagatg 1260

	_SL	
accaggtccc catcctctct gtcggccagc gtcggagata gggtgaccat tacctgtcgg		1320
gcctcgcaaa gcatctcctc gtacctcaac tggtatcagc aaaagccggg aaaggcgcct		1380
aagctgctga tctacgccgc ttcgagcttg caaagcgggg tgccatccag attctcggga		1440
tcaggctcag gaaccgactt caccctgacc gtgaacagcc tccagccgga ggactttgcc		1500
acttactact gccagcaggg agactccgtg ccgcttactt tcgggggggg taccgcctg		1560
gagatcaaga ccactacccc agcaccgagg ccaccaccc cggtcctac catgcctcc		1620
cagcctctgt ccctgcgtcc ggaggcatgt agaccgcag ctggtggggc cgtgcatacc		1680
cggggtcttg acttcgcctg cgatatctac atttggggcc ctctggctgg tacttgccgg		1740
gtcctgctgc tttcactcgt gatcactctt tactgtaagc gcggtcggaa gaagctgctg		1800
tacatcttta agcaaccctt catgaggcct gtgcagacta ctcaagagga ggacggctgt		1860
tcatgccggt tcccagagga ggaggaaggc ggctgcgaac tgcgcgtgaa attcagccgc		1920
agcgcatatg ctccagccta ccagcagggg cagaaccagc tctacaacga actcaatctt		1980
ggtcggagag aggagtacga cgtgctggac aagcggagag gacgggacc agaaatgggc		2040
gggaagccgc gcagaaagaa tccccaagag ggcctgtaca acgagctcca aaaggataag		2100
atggcagaag cctatagcga gattggtatg aaaggggaac gcagaagagg caaaggccac		2160
gacggactgt accagggact cagcaccgcc accaaggaca cctatgacgc tcttcacatg		2220
caggccctgc cgcctcgg		2238

<210> 1058

<211> 2244

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1058

atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg		60
ccctcgttgg cactttccct gactgccgac cagatggtgt ccgcccttct ggacgccgag		120
cctccaattc tgtactcgga gtacgatccg actcgccgt tctccgaagc cagcatgatg		180
ggcctgttga ctaacctggc ggaccgcgag ttggtgcaca tgattaactg ggctaagcgg		240
gtgccgggct tcgtggacct ggccctgcac gaccaagtgc acctcctgga atgcgcctgg		300
atggaaatcc tcatgatcgg cctcgtgtgg agatccatgg agcatcccgg aaagctcctg		360
tttgcacca acctcctgct tgatcgcaac cagggaaaat gcgtggaagg ggggtgtcag		420
attttcgaca tgctgctcgc cacctcttcc cggttccgga tgatgaatct gcaggagaaa		480
gagttcgtgt gtctgaagtc aatcatcctg ctgaactccg gggctctatac cttcctgagc		540
tcgaccctca agtcactgga ggaaaaagac cacatccatc gcgtgctcga taagatcacc		600
gacaccctta tccatctcat ggcgaaggct ggactgacct tgcaacagca gcaccagagg		660

_SL

ctggcccagt	tgctgctgat	tctgagccac	atccggcaca	tgctgtccaa	gaggatggaa	720
cacctgtaca	gcatgaagtg	caagaacgtc	gtgcctctgt	ccgatctgct	cctggaaatg	780
ctggacgcgc	acagactcgg	aaccggcgcg	gaagaccccc	ggccctccag	gaagcgaagg	840
tccctcggag	acgtgggtga	agtgaattg	gtggaatcag	ggggaggact	tgtgcagcct	900
ggaggatcgc	tgagactgtc	atgtgccgtg	tccggctttg	ccctgtccaa	ccacgggatg	960
tcctgggtcc	gccgcgcgcc	tggaaggggc	ctcgaatggg	tgctgggtat	tgtgtacagc	1020
ggtagcacct	actatgccgc	atccgtgaag	gggagattca	ccatcagccg	ggacaactcc	1080
aggaacactc	tgtacctcca	aatgaattcg	ctgaggccag	aggacactgc	catctactac	1140
tgctccgcgc	atggcggaga	gtccgacgtc	tggggacagg	ggaccaccgt	gaccgtgtct	1200
agcgcgtccg	gcggaggcgg	cagcgggggt	cgggcatcag	ggggcggcgg	atcggacatc	1260
cagctacccc	agtccccgag	ctcgtgtgcc	gcctccgtgg	gagatcgggt	caccatcacg	1320
tgccgcgcca	gccagtcgat	ttcctcctac	ctgaactggg	accaacagaa	gcccggaaaa	1380
gccccgaagc	ttctcatcta	cgccgcctcg	agcctgcagt	caggagtgcc	ctcacggttc	1440
tccggctccg	gttccggtac	tgatttcacc	ctgaccattt	cctccctgca	accggaggac	1500
ttcgctactt	actactgcc	gcagtcgtac	tccaccccct	acactttcgg	acaaggcacc	1560
aaggtcgaaa	tcaagaccac	taccccagca	ccgaggccac	ccaccccggc	tcctaccatc	1620
gcctcccagc	ctctgtccct	gcgtccggag	gcatgtagac	ccgcagctgg	tggggccgtg	1680
catacccggg	gtcttgactt	cgcctgcgat	atctacattt	gggcccctct	ggctggtact	1740
tgcggggtcc	tgctgctttc	actcgtgatc	actctttact	gtaagcgcg	tcggaagaag	1800
ctgctgtaca	tctttaagca	acccttcatg	aggcctgtgc	agactactca	agaggaggac	1860
ggctgttcat	gccggttccc	agaggaggag	gaaggcggct	gcgaactgcg	cgtgaaattc	1920
agccgcagcg	cagatgtctc	agcctaccag	caggggcaga	accagctcta	caacgaactc	1980
aatcttggtc	ggagagagga	gtacgacgtg	ctggacaagc	ggagaggacg	ggaccagaaa	2040
atgggcggga	agccgcgcag	aaagaatccc	caagagggcc	tgtacaacga	gtcctaaaag	2100
gataagatgg	cagaagccta	tagcgagatt	ggtatgaaag	gggaacgcag	aagaggcaaa	2160
ggccacgacg	gactgtacca	gggactcagc	accgccacca	aggacaccta	tgacgctctt	2220
cacatgcagg	ccctgccgcc	tcgg				2244

<210> 1059

<211> 2244

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1059

atggccctcc	ctgtcaccgc	cctgctgctt	ccgctggctc	ttctgctcca	cgccgctcgg	60
------------	------------	------------	------------	------------	------------	----

						_SL	
ccctcgttgg	cactttccct	gactgccgac	cgatggtgt	ccgcccttct	ggacgccgag	120	
cctccaattc	tgtactcgga	gtacgatccg	actcgcccgt	tctccgaagc	cagcatgatg	180	
ggcctgttga	ctaacctggc	ggaccgag	ttggtgcaca	tgattaactg	ggctaagcgg	240	
gtgccgggct	tcgtggacct	gaccctgcac	gaccaagtgc	acctcctgga	atgcgcctgg	300	
atggaaatcc	tcatgatcgg	cctcgtgtgg	agatccatgg	agcatcccgg	aaagctcctg	360	
tttgacacca	acctcctgct	tgatcgcaac	cagggaaaat	gcgtggaagg	gggtgtcgag	420	
attttcgaca	tgctgctcgc	cacctcttcc	cggttccgga	tgatgaatct	gcagggagaa	480	
gagttcgtgt	gtctgaagtc	aatcatcctg	ctgaactccg	gggtctatac	cttcctgagc	540	
tcgacctca	agtcactgga	ggaaaaagac	cacatccatc	gcgtgctcga	taagatcacc	600	
gacaccctta	tccatctcat	ggcgaaggct	ggactgacct	tgcaacagca	gcaccagagg	660	
ctggcccagt	tgctgctgat	tctgagccac	atccggcaca	tgtcgaacaa	gaggatggaa	720	
cacctgtaca	gcatgaagtg	caagaacgtc	gtgcctctgt	ccgatctgct	cctggaaatg	780	
ctggacgcgc	acagactcgg	aaccggcgcg	gaagaccccc	ggccctccag	gaagcgaagg	840	
tccctcggag	acgtgggtga	agtgcattg	gtggaatcag	ggggaggact	tgtgcagcct	900	
ggaggatcgc	tgagactgtc	atgtgccgtg	tccggctttg	ccctgtccaa	ccacgggatg	960	
tcctgggtcc	gccgcgcgcc	tggaaagggc	ctcgaatggg	tgtcgggtat	tgtgtacagc	1020	
ggtagcacct	actatgccgc	atccgtgaag	gggagattca	ccatcagccg	ggacaactcc	1080	
aggaacactc	tgtacctcca	aatgaattcg	ctgaggccag	aggacactgc	catctactac	1140	
tgctccgcgc	atggcggaga	gtccgacgtc	tggggacagg	ggaccaccgt	gaccgtgtct	1200	
agcgcgtccg	gcggaggcgg	cagcgggggt	cgggcatcag	ggggcggcgg	atcggacatc	1260	
cagctcacc	agtccccgag	ctcgtgttcc	gcctccgtgg	gagatcgggt	caccatcacg	1320	
tgccgcgcca	gccagtcgat	ttcctcctac	ctgaactggg	accaacagaa	gcccggaaaa	1380	
gccccgaagc	ttctcatcta	cgccgcctcg	agcctgcagt	caggagtgcc	ctcacggttc	1440	
tccgggtccg	gttccggtac	tgatttcacc	ctgaccattt	cctccctgca	accggaggac	1500	
ttcgctactt	actactgcca	gcagtcgtac	tccacccctt	acactttcgg	acaaggcacc	1560	
aaggtcga	tcaagaccac	tacccagca	ccgaggccac	ccacccggc	tcctaccatc	1620	
gcctcccagc	ctctgtccct	gcgtccggag	gcatgtagac	ccgcagctgg	tggggccgtg	1680	
catacccggg	gtcttgactt	cgctgcgat	atctacattt	gggccctct	ggctggtact	1740	
tgccgggtcc	tgctgctttc	actcgtgatc	actctttact	gtaagcgcg	tcggaagaag	1800	
ctgctgtaca	tctttaagca	acccttcatg	aggcctgtgc	agactactca	agaggaggac	1860	
ggctgttcat	gccggttccc	agaggaggag	gaaggcggct	gcgaactgcg	cgtgaaattc	1920	
agccgcagcg	cagatgtctc	agcctaccag	caggggcaga	accagctcta	caacgaactc	1980	
aatcttggtc	ggagagagga	gtacgacgtg	ctggacaagc	ggagaggacg	ggaccagaa	2040	
atgggcggga	agccgcgcag	aaagaatccc	caagagggcc	tgtacaacga	gctccaaaag	2100	

	_SL	
gataagatgg	cagaagccta tagcgagatt ggtatgaaag gggaacgcag aagaggcaaa	2160
ggccacgacg	gactgtacca gggactcagc accgccacca aggacaccta tgacgctctt	2220
cacatgcagg	ccctgccgcc tcgg	2244

<210> 1060
 <211> 2226
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1060		
atggccctcc	ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg	60
ccctcgttgg	cactttccct gactgccgac cagatggtgt ccgcccttct ggacgccgag	120
cctccaattc	tgtactcgga gtacgatccg actcgcccgt tctccgaagc cagcatgatg	180
ggcctgttga	ctaacctggc ggaccgcgag ttggtgcaca tgattaactg ggctaagcgg	240
gtgccgggct	tcgtggacct ggccctgcac gaccaagtgc acctcctgga atgcgcctgg	300
atggaaatcc	tcatgatcgg cctcgtgtgg agatccatgg agcatcccgg aaagctcctg	360
tttgaccca	acctcctgct tgatcgcaac cagggaaaat gcgtggaagg ggggtgtcag	420
attttcgaca	tgctgctcgc cacctcttcc cggttccgga tgatgaatct gcaggagaaa	480
gagttcgtgt	gtctgaagtc aatcatcctg ctgaactccg ggggtctatac cttcctgagc	540
tcgaccctca	agtcactgga ggaaaaagac cacatccatc gcgtgctcga taagatcacc	600
gacaccctta	tccatctcat ggcgaggct ggactgacct tgcaacagca gcaccagagg	660
ctggcccagt	tgctgctgat tctgagccac atccggcaca tgtcgtccaa gaggatggaa	720
cacctgtaca	gcatgaagtg caagaacgtc gtgcctctgt ccgatctgct cctggaaatg	780
ctggacgcgc	acagactcgg gacgggagct gaagatccac gaccagcag aaagcgacgg	840
gaagtgcaat	tggtggaatc agggggagga cttgtgcagc ctggaggatc gctgagactg	900
tcatgtgccg	tgtccggctt tgccctgtcc aaccacggga tgcctgggt ccgccgcgcg	960
cctggaaagg	gcctcgaatg ggtgtcgggt attgtgtaca gcggtagcac ctactatgcc	1020
gcatccgtga	aggggagatt caccatcagc cgggacaact ccaggaacac tctgtacctc	1080
caaatgaatt	cgctgaggcc agaggacact gccatctact actgctccgc gcatggcgga	1140
gagtcgcgac	tctggggaca ggggaccacc gtgaccgtgt ctagcgcgtc cggcggaggc	1200
ggcagcgggg	gtcgggcatc agggggcggc ggatcggaca tccagctcac ccagtccccg	1260
agctcgctgt	ccgcctccgt gggagatcgg gtcacatca cgtgccgcgc cagccagtcg	1320
atttcctcct	acctgaactg gtaccaacag aagcccggaa aagccccgaa gcttctcatc	1380
tacgccgcct	cgagcctgca gtcaggagtg ccctcacggt tctccggctc cggttccggt	1440
actgatttca	ccctgacatc ttcctccctg caaccggagg acttcgctac ttactactgc	1500

	_SL	
cagcagtcgt actccacccc ctacactttc ggacaaggca ccaaggtcga aatcaagacc	1560	
actaccccag caccgaggcc acccaccocg gtcctacca tcgcctcca gcctctgtcc	1620	
ctgcgtccgg aggcattag acccgagct ggtggggccg tgcatacccg gggctttgac	1680	
ttcgctgcg atatctacat ttgggccct ctggctggta cttgcgggt cctgctgctt	1740	
tcactcgtga tcactcttta ctgtaagcgc ggtcggaaga agctgctgta catctttaag	1800	
caacccttca tgaggcctgt gcagactact caagaggagg acggctgttc atgccggttc	1860	
ccagaggagg aggaaggcgg ctgcgaactg cgcgtgaaat tcagccgcag cgcagatgct	1920	
ccagcctacc agcaggggca gaaccagctc tacaacgaac tcaatcttgg tcggagagag	1980	
gagtacgacg tgctggacaa gcggagagga cgggaccag aaatgggcgg gaagccgcgc	2040	
agaaagaatc cccaagaggg cctgtacaac gagctccaaa aggataagat ggcagaagcc	2100	
tatagcgaga ttggtatgaa aggggaacgc agaagaggca aaggccacga cggactgtac	2160	
cagggactca gcaccgccac caaggacacc tatgacgctc ttcacatgca ggccctgccg	2220	
cctcgg	2226	

<210> 1061

<211> 2226

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1061

atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgtcca cgccgctcgg	60
ccctcgttgg cactttccct gactgccgac cagatggtgt ccgcccttct ggacgccgag	120
cctccaattc tgtactcgga gtacgatccg actcgcccg tctccgaagc cagcatgatg	180
ggcctgttga ctaacctggc ggaccgcgag ttggtgcaca tgattaactg ggctaagcgg	240
gtgccgggct tcgtggacct gaccctgcac gaccaagtgc acctcctgga atgcgcctgg	300
atggaaatcc tcatgatcgg cctcgtgtgg agatccatgg agcatcccgg aaagctcctg	360
tttgaccca acctcctgct tgatcgcaac cagggaaaat gcgtggaagg ggggtgtcga	420
attttcgaca tgctgctcgc cacctcttcc cggttccgga tgatgaatct gcaggagaa	480
gagttcgtgt gtctgaagtc aatcatcctg ctgaactccg gggctctatac cttcctgagc	540
tcgaccctca agtcactgga ggaaaaagac cacatccatc gcgtgctcga taagatcacc	600
gacaccctta tccatctcat ggcgaaggct ggactgacct tgcaacagca gcaccagagg	660
ctggcccagt tgctgctgat tctgagccac atccggcaca tgtcgaacaa gaggatggaa	720
cacctgtaca gcatgaagtg caagaacgtc gtgcctctgt ccgatctgct cctggaaatg	780
ctggacgcgc acagactcgg gacgggagct gaagatccac gaccagcag aaagcgacgg	840
gaagtgcaat tgggtggaatc agggggagga cttgtgcagc ctggaggatc gctgagactg	900

	_SL	
tcatgtgccg tgtccggctt tgccctgtcc aaccacggga tgtcctgggt cgcgcgcgcg	960	
cctggaaagg gcctcgaatg ggtgtcgggt attgtgtaca gcggtagcac ctactatgcc	1020	
gcatccgtga aggggagatt caccatcagc cgggacaact ccaggaacac tctgtacctc	1080	
caaatgaatt cgctgaggcc agaggacact gccatctact actgctccgc gcatggcgga	1140	
gagtccgacg tctggggaca ggggaccacc gtgaccgtgt ctagcgcgtc cggcggaggc	1200	
ggcagcgggg gtcgggcatc agggggcggc ggatcggaca tccagctcac ccagtccccg	1260	
agctcgctgt ccgcctccgt gggagatcgg gtcacatca cgtgccgcgc cagccagtcg	1320	
atttcctcct acctgaactg gtaccaacag aagcccggaa aagccccgaa gcttctcatc	1380	
tacgccgcct cgagcctgca gtcaggagtg ccctcacggt tctccggctc cggttccggt	1440	
actgatttca ccctgacatc ttcctccctg caaccggagg acttcgctac ttactactgc	1500	
cagcagtcgt actccacccc ctacactttc ggacaaggca ccaaggtcga aatcaagacc	1560	
actaccccag caccgaggcc acccaccctg gtcctacca tcgcctcca gcctctgtcc	1620	
ctgctcccg aggcatttag acccgagct ggtggggccg tgcatacccg gggcttgac	1680	
ttcgctgcg atatctacat ttgggcccct ctggctggta cttgcggggg cctgctgctt	1740	
tcactcgtga tcactcttta ctgtaagcgc ggtcggaaga agctgctgta catctttaag	1800	
caacccttca tgaggcctgt gcagactact caagaggagg acggctgttc atgccggttc	1860	
ccagaggagg aggaaggcgg ctgcgaactg cgcgtgaaat tcagccgcag cgcagatgct	1920	
ccagcctacc agcaggggca gaaccagctc tacaacgaac tcaatcttgg tcggagagag	1980	
gagtacgacg tgctggacaa gcggagagga cgggaccag aaatgggcgg gaagccgcgc	2040	
agaaagaatc cccaagaggg cctgtacaac gagctccaaa aggataagat ggcagaagcc	2100	
tatagcgaga ttggtatgaa aggggaacgc agaagaggca aaggccacga cggactgtac	2160	
cagggactca gcaccgccac caaggacacc tatgacgctc ttcacatgca ggccctgccg	2220	
cctcgg	2226	

<210> 1062

<211> 2256

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1062

atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgcgcgtcgg	60
cccgattcgt tggcactttc cctgactgcc gaccagatgg tgtccgccct tctggacgcc	120
gagcctccaa ttctgtactc ggagtacgat ccgactcgcc cgttctccga agccagcatg	180
atgggcctgt tgactaacct ggcggaccgc gagttggtgc acatgattaa ctgggctaag	240
cgggtgccgg gcttcgtgga cctggccctg cagaccaag tgcacctcct ggaatgcgcc	300

						_SL	
tggatggaaa	tcctcatgat	cggcctcgtg	tggagatcca	tggagcatcc	cggaaagctc		360
ctgtttgcac	ccaacctcct	gcttgatcgc	aaccagggaa	aatgcgtgga	agggggtgtc		420
gagattttcg	acatgctgct	cgccacctct	tcccggttcc	ggatgatgaa	tctgcaggga		480
gaagagttcg	tgtgtctgaa	gtcaatcatc	ctgctgaact	ccggggtcta	taccttcctg		540
agctcgaccc	tcaagtcact	ggaggaaaaa	gaccacatcc	atcgctgct	cgataagatc		600
accgacaccc	ttatccatct	catggcgaag	gctggactga	ccctgcaaca	gcagcaccag		660
aggctggccc	agttgctgct	gattctgagc	cacatccggc	acatgtcgtc	caagaggatg		720
gaacacctgt	acagcatgaa	gtgcaagaac	gtcgtgcctc	tgtccgatct	gctcctggaa		780
atgctggacg	cgcacagact	cggaaaccggc	gcggaagacc	cccggccctc	caggaagcga		840
aggtccctcg	gagacgtggg	tgaattgtg	atgaccagct	caccgcccac	tcttagcctt		900
tcaccgggtg	agcgcgaac	cctgtcttgc	agagcctccc	aagacatctc	aaaatacctt		960
aattggtatc	aacagaagcc	cggacaggct	cctcgccttc	tgatctacca	caccagccgg		1020
ctccattctg	gaatccctgc	caggttcagc	ggtagcggat	ctgggaccga	ctacaccctc		1080
actatcagct	cactgcagcc	agaggacttc	gctgtctatt	tctgtcagca	agggaacacc		1140
ctgccctaca	cctttggaca	gggcaccaag	ctcgagatta	aagggtggagg	tggcagcgga		1200
ggaggtgggt	ccggcggtag	aggaagccag	gtccaactcc	aagaaagcgg	accgggtctt		1260
gtgaagccat	cagaaactct	ttcactgact	tgtactgtga	gcggagtgtc	tctccccgat		1320
tacggggtgt	cttggatcag	acagccaccg	gggaagggtc	tggaatggat	tggagtgatt		1380
tggggctctg	agactactta	ctactcttca	tccctcaagt	cacgcgtcac	catctcaaag		1440
gacaactcta	agaatcaggt	gtcactgaaa	ctgtcatctg	tgaccgcagc	cgacaccgcc		1500
gtgtactatt	gcgctaagca	ttactattat	ggcgggagct	acgcaatgga	ttactgggga		1560
cagggtactc	tggtcaccgt	gtccagcacc	actaccccag	caccgaggcc	acccaccccg		1620
gctcctacca	tcgcctccca	gcctctgtcc	ctgcgtccgg	aggcatgtag	accgcagct		1680
ggtggggccg	tgcatacccg	gggtcttgac	ttcgcctgcg	atatctacat	ttggggccct		1740
ctggctggta	cttgcggggt	cctgctgctt	tactcgtga	tcactcttta	ctgtaagcgc		1800
ggtcggaaga	agctgctgta	catctttaag	caacccttca	tgaggcctgt	gcagactact		1860
caagaggagg	acggctgttc	atgccggttc	ccagaggagg	aggaaggcgg	ctgcgaactg		1920
cgcgtgaaat	tcagccgcag	cgcagatgct	ccagcctacc	agcaggggca	gaaccagctc		1980
tacaacgaac	tcaatcttgg	tcggagagag	gagtacgacg	tgctggacaa	gcggagagga		2040
cgggacccag	aaatgggcgg	gaagccgcgc	agaaagaatc	ccaagagggg	cctgtacaac		2100
gagctccaaa	aggataagat	ggcagaagcc	tatagcgaga	ttggtatgaa	aggggaacgc		2160
agaagaggca	aaggccacga	cggactgtac	cagggactca	gcaccgccac	caaggacacc		2220
tatgacgctc	ttcacatgca	ggccctgccg	cctcgg				2256

<210> 1063

<211> 2256
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1063
atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60
cccgattcgt tggcactttc cctgactgcc gaccagatgg tgtccgccct tctggacgcc 120
gagcctccaa ttctgtactc ggagtagcat ccgactcgcc cgttctccga agccagcatg 180
atgggcctgt tgactaacct ggcggaccgc gagttggtgc acatgattaa ctgggctaag 240
cgggtgccgg gcttcgtgga cctgaccctg caccaccaag tgcacctcct ggaatgcgcc 300
tggtatgaaa tcctcatgat cggcctcgtg tggagatcca tggagcatcc cggaagctc 360
ctgtttgcac ccaacctcct gcttgatcgc aaccaggga aatgcgtgga agggggtgtc 420
gagattttcg acatgctgct cgccacctct tcccggttcc ggatgatgaa tctgcaggga 480
gaagagtctg tgtgtctgaa gtcaatcatc ctgctgaact cgggggtcta taccttcctg 540
agctcgaccc tcaagtcact ggaggaaaaa gaccacatcc atcgctgct cgataagatc 600
accgacaccc ttatccatct catggcgaag gctggactga ccctgcaaca gcagcaccag 660
aggctggccc agttgctgct gattctgagc cacatccggc acatgtcgaa caagaggatg 720
gaacacctgt acagcatgaa gtgcaagaac gtcgtgcctc tgtccgatct gtccttgaa 780
atgctggacg cgcacagact cggaaccggc gcggaagacc cccggccctc caggaagcga 840
aggtccctcg gagacgtggg tgaaattgtg atgaccagc caccgcccac tcttagcctt 900
tcaccgggtg agcgcgcaac cctgtcttgc agagcctccc aagacatctc aaaatacctt 960
aattggtatc aacagaagcc cggacaggct cctcgccttc tgatctacca caccagccgg 1020
ctccattctg gaatccctgc caggttcagc ggtagcggat ctgggaccga ctacaccctc 1080
actatcagct cactgcagcc agaggacttc gctgtctatt tctgtcagca agggaacacc 1140
ctgccctaca cctttggaca gggcaccaag ctcgagatta aagggtggagg tggcagcgga 1200
ggaggtgggt ccggcggtgg aggaagccag gtccaactcc aagaaagcgg accgggtctt 1260
gtgaagccat cagaaactct ttcactgact tgtactgtga gcggagtgtc tctccccgat 1320
tacggggtgt cttggatcag acagccaccg gggaagggtc tggaatggat tggagtgatt 1380
tggggctctg agactactta ctactcttca tccctcaagt caccgctcac catctcaaag 1440
gacaactcta agaatcaggt gtcactgaaa ctgtcatctg tgaccgcagc cgacaccgcc 1500
gtgtactatt gcgctaagca ttactattat ggcgggagct acgcaatgga ttactgggga 1560
cagggtactc tggtcaccgt gtccagcacc actacccag caccgaggcc acccaccctg 1620
gtcctacca tcgcctccca gcctctgtcc ctgcgtccgg aggcattgag accgcagct 1680
ggtggggccg tgcatacccg gggctctgac ttcgcctgcg atatctacat ttgggcccct 1740

ctggctggta cttgcggggt cctgctgctt	<u>SL</u>	tcactcgtga tcactcttta ctgtaagcgc	1800
ggtcgggaaga agctgctgta catctttaag	caacccttca tgaggcctgt gcagactact	1860	
caagaggagg acggctgttc atgccggttc	ccagaggagg aggaaggcgg ctgcgaactg	1920	
cgcgtgaaat tcagccgcag cgcagatgct	ccagcctacc agcaggggca gaaccagctc	1980	
tacaacgaac tcaatcttgg tcggagagag	gagtagcagc tgctggacaa gcggagagga	2040	
cgggaccag aaatgggcgg gaagccgcgc	agaaagaatc cccaagaggg cctgtacaac	2100	
gagctccaaa aggataagat ggcagaagcc	tatagcgaga ttggtatgaa aggggaacgc	2160	
agaagaggca aaggccacga cggactgtac	cagggactca gcaccgccac caaggacacc	2220	
tatgacgctc ttcacatgca ggccctgccg	cctcgg	2256	

<210> 1064
 <211> 2238
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1064	atggccctcc ctgtcaccgc cctgctgctt	ccgctggctc ttctgctcca cgccgctcgg	60
cccgattcgt tggcactttc cctgactgcc	gaccagatgg tgtccgccct tctggacgcc	120	
gagcctccaa ttctgtactc ggagtagcat	ccgactcgcc cgttctccga agccagcatg	180	
atgggcctgt tgactaacct ggcggaccgc	gagttggtgc acatgattaa ctgggctaag	240	
cgggtgccgg gcttcgtgga cctggccctg	cacgaccaag tgcacctcct ggaatgcgcc	300	
tggatggaaa tcctcatgat cggcctcgtg	tggagatcca tggagcatcc cggaaagctc	360	
ctgtttgcac ccaacctcct gcttgatcgc	aaccagggaa aatgcgtgga agggggtgtc	420	
gagattttcg acatgctgct cgccacctct	tcccggttcc ggatgatgaa tctgcaggga	480	
gaagagttcg tgtgtctgaa gtcaatcatc	ctgctgaact ccgggggtcta taccttcctg	540	
agctcgaccc tcaagtcact ggaggaaaaa	gaccacatcc atcgcgtgct cgataagatc	600	
accgacaccc ttatccatct catggcgaag	gctggactga ccctgcaaca gcagcaccag	660	
aggctggccc agttgctgct gattctgagc	cacatccggc acatgtcgtc caagaggatg	720	
gaacacctgt acagcatgaa gtgcaagaac	gtcgtgcctc tgtccgatct gtccttgaa	780	
atgctggacg cgcacagact cgggacggga	gctgaagatc cacgaccag cagaaagcga	840	
cgggaaattg tgatgaccca gtcacccgcc	actcttagcc tttcacccgg tgagcgcgca	900	
accctgtctt gcagagcctc ccaagacatc	tcaaaatacc ttaattggta tcaacagaag	960	
cccgacagg ctctctgcct tctgatctac	cacaccagcc ggctccattc tggaatccct	1020	
gccaggttca gcggtagcgg atctgggacc	gactacaccc tcactatcag ctactgcag	1080	
ccagaggact tcgctgtcta tttctgtcag	caagggaaca ccctgcccta cacctttgga	1140	

	_SL	
cagggcacca agctcgagat taaaggtgga ggtggcagcg gaggaggtgg gtccggcggt	1200	
ggaggaagcc aggtccaact ccaagaaagc ggaccgggtc ttgtgaagcc atcagaaact	1260	
ctttcactga cttgtactgt gagcggagtg tctctccccg attacggggt gtcttgatc	1320	
agacagccac cggggaaggg tctggaatgg attggagtga tttggggctc tgagactact	1380	
tactactctt catccctcaa gtcacgcgtc accatctcaa aggacaactc taagaatcag	1440	
gtgtcactga aactgtcatc tgtgaccgca gccgacaccg ccgtgtacta ttgcgctaag	1500	
cattactatt atggcgggag ctacgcaatg gattactggg gacagggtag tctggtcacc	1560	
gtgtccagca ccactacccc agcaccgagg ccacccaccc cggctcctac catcgcctcc	1620	
cagcctctgt ccctgcgtcc ggaggcatgt agaccgcgag ctggtggggc cgtgcatacc	1680	
cggggtcttg acttcgcctg cgatatctac atttggggcc ctctggctgg tacttgcggg	1740	
gtcctgctgc tttcactcgt gatcactctt tactgtaagc gcggtcggaa gaagctgctg	1800	
tacatcttta agcaaccctt catgaggcct gtgcagacta ctcaagagga ggacggctgt	1860	
tcatgccggt tcccagagga ggaggaaggc ggctgcgaac tgcgcgtgaa attcagccgc	1920	
agcgcagatg ctccagccta ccagcagggg cagaaccagc tctacaacga actcaatctt	1980	
ggtcggagag aggagtacga cgtgctggac aagcggagag gacgggaccc agaaatgggc	2040	
gggaagccgc gcagaaagaa tccccaagag ggcctgtaca acgagctcca aaaggataag	2100	
atggcagaag cctatagcga gattggtatg aaaggggaac gcagaagagg caaaggccac	2160	
gacggactgt accagggact cagcaccgcc accaaggaca cctatgacgc tcttcacatg	2220	
caggccctgc cgcctcgg	2238	

<210> 1065
 <211> 2238
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1065	
atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg	60
cccgattcgt tggcactttc cctgactgcc gaccagatgg tgtccgccct tctggacgcc	120
gagcctcaa ttctgtactc ggagtacgat ccgactcgcc cgttctccga agccagcatg	180
atgggcctgt tgactaacct ggcggaccgc gagttggtgc acatgattaa ctgggctaag	240
cgggtgccgg gcttcgtgga cctgaccctg cagcaccaag tgcacctcct ggaatgcgcc	300
tggatggaat tcctcatgat cggcctcgtg tggagatcca tggagcatcc cggaagctc	360
ctgtttgcac ccaacctcct gcttgatcgc aaccagggaa aatgcgtgga agggggtgtc	420
gagattttcg acatgctgct cgccacctct tcccggttcc ggatgatgaa tctgcaggga	480
gaagagttcg tgtgtctgaa gtcaatcatc ctgctgaact ccggggctta taccttcctg	540

	_SL	
agctcgaccc tcaagtcact ggaggaaaaa gaccacatcc atcgcggtgct cgataagatc	600	
accgacaccc ttatccatct catggcgaag gctggactga ccctgcaaca gcagcaccag	660	
aggctggccc agttgctgct gattctgagc cacatccggc acatgtcgaa caagaggatg	720	
gaacacctgt acagcatgaa gtgcaagaac gtcgtgcctc tgtccgatct gtccttgga	780	
atgctggacg cgcacagact cgggacggga gctgaagatc cacgaccag cagaaagcga	840	
cgggaaattg tgatgaccca gtcacccgcc actcttagcc tttcacccgg tgagcgcgca	900	
accctgtctt gcagagcctc ccaagacatc tcaaaatacc ttaattggta tcaacagaag	960	
cccggacagg ctctcgcct tctgatctac cacaccagcc ggctccattc tggaatccct	1020	
gccaggttca gcggtagcgg atctgggacc gactacaccc tcaactatcag ctactgcag	1080	
ccagaggact tcgctgtcta tttctgtcag caagggaaca ccctgcccta cacctttgga	1140	
cagggcacca agctcgagat taaaggtgga ggtggcagcg gaggagggtg gtccggcggg	1200	
ggaggaagcc aggtccaact ccaagaaagc ggaccgggtc ttgtgaagcc atcagaaact	1260	
ctttcactga cttgtactgt gagcggagtg tctctccccg attacgggggt gtcttgatc	1320	
agacagccac cggggaagg tctggaatgg attggagtga tttggggctc tgagactact	1380	
tactactctt catccctcaa gtcacgcgtc accatctcaa aggacaactc taagaatcag	1440	
gtgtcactga aactgtcatc tgtgaccgca gccgacaccg ccgtgtacta ttgcgctaag	1500	
cattactatt atggcgggag ctacgcaatg gattactggg gacaggggtac tctggtcacc	1560	
gtgtccagca ccactacccc agcaccgagg ccaccacccc cggctcctac catcgctcc	1620	
cagcctctgt ccctgcgtcc ggaggcatgt agaccgcag ctggtggggc cgtgcatacc	1680	
cggggctctt acttcgcctg cgatatctac atttggggccc ctctggctgg tacttgcggg	1740	
gtcctgctgc tttcactcgt gatcactctt tactgtaagc gcggtcggaa gaagctgctg	1800	
tacatcttta agcaaccctt catgaggcct gtgcagacta ctcaagagga ggacggctgt	1860	
tcatgccggt tcccagagga ggaggaaggc ggctgcgaac tgcgcgtgaa attcagccgc	1920	
agcgcagatg ctccagccta ccagcagggg cagaaccagc tctacaacga actcaatctt	1980	
ggtcggagag aggagtacga cgtgctggac aagcggagag gacgggaccc agaaatgggc	2040	
gggaagccgc gcagaaagaa tccccaagag ggcctgtaca acgagctcca aaaggataag	2100	
atggcagaag cctatagcga gattggtatg aaaggggaac gcagaagagg caaaggccac	2160	
gacggactgt accagggact cagcaccgcc accaaggaca cctatgacgc tcttcacatg	2220	
caggccctgc cgctcgg	2238	

<210> 1066

<211> 2259

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

_SL

<400> 1066
atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60
cccgattcgt tggcactttc cctgactgcc gaccagatgg tgtccgccct tctggacgcc 120
gagcctccaa ttctgtactc ggagtacgat ccgactcgcc cgttctccga agccagcatg 180
atgggcctgt tgactaacct ggcggaaccgc gagttggtgc acatgattaa ctgggctaag 240
cgggtgccgg gcttcgtgga cctggccctg cagcaccaag tgcacctcct ggaatgcgcc 300
tggatggaaa tcctcatgat cggcctcgtg tggagatcca tggagcatcc cggaaagctc 360
ctgtttgcac ccaacctcct gcttgatcgc aaccaggga aatgcgtgga agggggtgtc 420
gagattttcg acatgctgct cgccacctct tcccggttcc ggatgatgaa tctgcaggga 480
gaagagtctg tgtgtctgaa gtcaatcatc ctgctgaact ccgggggtcta taccttcctg 540
agctcgaccc tcaagtcact ggaggaaaaa gaccacatcc atcgctgctc cgataagatc 600
accgacaccc ttatccatct catggcgaag gctggactga ccctgcaaca gcagcaccag 660
aggctggccc agttgctgct gattctgagc cacatccggc acatgtcgtc caagaggatg 720
gaacacctgt acagcatgaa gtgcaagaac gtcgtgcctc tgtccgatct gtccttgaa 780
atgctggacg cgcacagact cggaaccggc gcggaagacc cccggccctc caggaagcga 840
aggccctcg gagacgtggg tcaagtcaa ctcgtccaaa gcggagcggg agtcaagaaa 900
cccggagcga gcgtgaaagt gtccctgcaa gcctccggct acacctttac gggctactac 960
atgactggg tgccgaggc accaggacag ggtcttgaat ggatgggatg gatcaaccct 1020
aattcgggcg gaactaacta cgcacagaag ttccaggga gagtgactct gactcgggat 1080
acctccatct caactgtcta catggaactc tcccgtttgc ggtcagatga tacggcagtg 1140
tactactgcg cccgcgacat gaatatcctg gctaccgtgc cgttcgacat ctggggacag 1200
gggactatgg ttactgtctc atcgggcggg ggagggttcag gaggaggcgg ctccggaggc 1260
ggagggttcg acattcagat gaccagtc ccacctctc tgtcggccag cgtcggagat 1320
agggtgacca ttacctgtcg ggcctcgaa agcatctcct cgtacctcaa ctggtatcag 1380
caaaagccgg gaaaggcgc taagctgctg atctacgccg cttcgagctt gcaaagcggg 1440
gtgccatcca gattctcggg atcaggctca ggaaccgact tcacctgac cgtgaacagc 1500
ctccagccgg aggactttgc cacttactac tgccagcagg gagactccgt gccgcttact 1560
ttcggggggg gtaccgcct ggagatcaag accactacc cagcaccgag gccaccacc 1620
ccggctccta ccatgcctc ccagcctctg tccttgcgtc cggaggcatg tagaccgca 1680
gctggtgggg ccgtgcatac ccggggtctt gacttcgcct gcgatata ctttggggc 1740
cctctggctg gtacttgcg ggtcctgctg ctttactcg tgatcactct ttactgtaag 1800
cgcggtcggg agaagctgct gtacatcttt aagcaaccct tcatgaggcc tgtgcagact 1860
actcaagagg aggacggctg ttcattgccg tcccagagg aggaggaagg cggctgcgaa 1920
ctgcgcgtga aattcagccg cagcgcagat gctccagcct accagcagg gcagaaccag 1980

ctctacaacg aactcaatct tggtcggaga gaggagtacg acgtgctgga caagcggaga	2040
ggacgggacc cagaaatggg cgggaagccg cgcagaaaga atccccaaga gggcctgtac	2100
aacgagctcc aaaaggataa gatggcagaa gcctatagcg agattggtat gaaaggggaa	2160
cgcagaagag gcaaaggcca cgacggactg taccagggac tcagcaccgc caccaaggac	2220
acctatgacg ctcttcacat gcaggccctg ccgcctcgg	2259

<210> 1067

<211> 2259

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1067

atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg	60
cccgattcgt tggcactttc cctgactgcc gaccagatgg tgtccgccct tctggacgcc	120
gagcctccaa ttctgtactc ggagtacgat ccgactcgcc cgttctccga agccagcatg	180
atgggcctgt tgactaacct ggcggaccgc gagttggtgc acatgattaa ctgggctaag	240
cgggtgccgg gcttcgtgga cctgaccctg caccaccaag tgcacctcct ggaatgcgcc	300
tggatggaaa tcctcatgat cggcctcgtg tggagatcca tggagcatcc cggaagctc	360
ctgtttgcac ccaacctcct gcttgatcgc aaccagggaa aatgcgtgga agggggtgtc	420
gagattttcg acatgctgct cgccacctct tcccggttcc ggatgatgaa tctgcaggga	480
gaagagtctg tgtgtctgaa gtcaatcatc ctgctgaact ccgggggtcta taccttcctg	540
agctcgaccc tcaagtcact ggaggaaaaa gaccacatcc atcgctgct cgataagatc	600
accgacaccc ttatccatct catggcgaag gctggactga ccctgcaaca gcagcaccag	660
aggctggccc agttgctgct gattctgagc cacatccggc acatgtcgaa caagaggatg	720
gaacacctgt acagcatgaa gtgcaagaac gtcgtgcctc tgtccgatct gtccttgaa	780
atgctggacg cgcacagact cggaaccggc gcggaagacc cccggccctc caggaagcga	840
aggccctcgc gagacgtggg tcaagtgcaa ctcgctccaaa gcggagcgga agtcaagaaa	900
cccggagcga gcgtgaaagt gtcctgcaaa gcctccggct acacctttac gggctactac	960
atgcactggg tgcgccaggc accaggacag ggtcttgaat ggatgggatg gatcaaccct	1020
aattcgggcg gaactaacta cgcacagaag ttccagggga gagtgactct gactcgggat	1080
acctccatct caactgtcta catggaactc tcccgcttgc ggtcagatga tacggcagtg	1140
tactactgcg cccgcgacat gaatatcctg gctaccgtgc cgttcgacat ctggggacag	1200
gggactatgg ttactgtctc atcgggcggt ggaggttcag gaggaggcgg ctcgggaggc	1260
ggaggttcgg acattcagat gaccagtc ccacacctc tgtcggccag cgtcggagat	1320
agggtgacca ttacctgtcg ggcctcgcaa agcatctcct cgtacctcaa ctggtatcag	1380

	_SL	
caaaagccgg gaaaggcgcc taagctgctg atctacgccg cttcgagctt gcaaagcggg		1440
gtgccatcca gattctcggg atcagggtca ggaaccgact tcaccctgac cgtgaacagc		1500
ctccagccgg aggactttgc cacttactac tgccagcagg gagactccgt gccgcttact		1560
ttcggggggg gtaccgcctt ggagatcaag accactaccc cagcaccgag gccacccacc		1620
ccggctccta ccatcgccctc ccagcctctg tccctgcgtc cggaggcatg tagacccgca		1680
gctggtgggg ccgtgcatac ccggggtctt gacttcgcct gcgatatcta catttgggcc		1740
cctctggctg gtacttgcg ggtcctgctg ctttcactcg tgatcactct ttactgtaag		1800
cgcggtcggg agaagctgct gtacatcttt aagcaaccct tcatgaggcc tgtgcagact		1860
actcaagagg aggacggctg ttcattgccg ttcacagagg aggaggaagg cggctgcgaa		1920
ctgcgcgtga aattcagccg cagcgcagat gctccagcct accagcaggg gcagaaccag		1980
ctctacaacg aactcaatct tggtcggaga gaggagtacg acgtgctgga caagcggaga		2040
ggacgggacc cagaaatggg cggaagccg cgcagaaaga atccccaaga gggcctgtac		2100
aacgagctcc aaaaggataa gatggcagaa gcctatagcg agattggtat gaaaggggaa		2160
cgcagaagag gcaaaggcca cgacggactg taccagggac tcagcaccgc caccaaggac		2220
acctatgacg ctcttcacat gcaggccctg ccgcctcgg		2259

<210> 1068

<211> 2241

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1068

atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgtcca cgccgctcgg	60
cccgattcgt tggcactttc cctgactgcc gaccagatgg tgtccgccct tctggacgcc	120
gagcctccaa ttctgtactc ggagtacgat ccgactcgcc cgttctccga agccagcatg	180
atgggcctgt tgactaacct ggcggaccgc gagttggtgc acatgattaa ctgggctaag	240
cgggtgccgg gcttcgtgga cctggccctg cagcaccaag tgcacctcct ggaatgcgcc	300
tggatggaat tcctcatgat cggcctcgtg tggagatcca tggagcatcc cggaaagctc	360
ctgtttgcac ccaacctcct gcttgatcgc aaccagggaa aatgcgtgga agggggtgtc	420
gagattttcg acatgctgct cgccacctct tcccggttcc ggatgatgaa tctgcaggga	480
gaagagtctg tgtgtctgaa gtcaatcatc ctgctgaact ccgggggtcta taccttcctg	540
agctcgaccc tcaagtcact ggaggaaaaa gaccacatcc atcgctgct cgataagatc	600
accgacaccc ttatccatct catggcgaag gctggactga ccctgcaaca gcagcaccag	660
aggctggccc agttgctgct gattctgagc cacatccggc acatgtcgtc caagaggatg	720
gaacacctgt acagcatgaa gtgcaagaac gtcgtgcctc tgtccgatct gtcctggaa	780

	_SL	
atgctggacg cgcacagact cggaaccggc gcggaagacc cccggccctc caggaagcga	840	
aggcaagtgc aactcgtcca aagcggagcg gaagtcaaga aaccgggagc gagcgtgaaa	900	
gtgtcctgca aagcctccgg ctacaccttt acgggctact acatgactg ggtgcgccag	960	
gcaccaggac agggctcttga atggatggga tggatcaacc ctaattcggg cggaactaac	1020	
tacgcacaga agttccaggg gagagtgact ctgactcggg atacctccat ctcaactgtc	1080	
tacatggaac tctcccgtt gcggtcagat gatacggcag tgtactactg cgcccgcgac	1140	
atgaatatcc tggctaccgt gccgttcgac atctggggac aggggactat ggttactgtc	1200	
tcatcgggcg gtggagggttc aggaggaggc ggctcgggag gcggagggttc ggacattcag	1260	
atgaccagcgt ccccatcctc tctgtcggcc agcgtcggag atagggtgac cattacctgt	1320	
cgggcctcgc aaagcatctc ctcgtacctc aactgggtatc agcaaaagcc gggaaaggcg	1380	
cctaagctgc tgatctacgc cgcttcgagc ttgcaaagcg ggggtgccatc cagattctcg	1440	
ggatcaggct caggaaccga cttcacctg accgtgaaca gcctccagcc ggaggacttt	1500	
gccacttact actgccagca gggagactcc gtgccgttta ctttcggggg gggtagccgc	1560	
ctggagatca agaccactac cccagcaccg aggccaccca cccgggtcc taccatcgcc	1620	
tcccagcctc tgtccctgcg tccggaggca tgtagaccg cagctggtgg ggccgtgcat	1680	
accgggggtc ttgacttcgc ctgcgatatc tacatttggg cccctctggc tggtagttgc	1740	
ggggtcctgc tgcttttact cgtgatcact ctttactgta agcgcgggtcg gaagaagctg	1800	
ctgtacatct ttaagcaacc cttcatgagg cctgtgcaga ctactcaaga ggaggacggc	1860	
tgttcatgcc ggttcccaga ggaggaggaa ggcggctgcg aactgcgcgt gaaattcagc	1920	
cgcagcgcag atgtccagc ctaccagcag gggcagaacc agctctacaa cgaactcaat	1980	
cttggtcggg gagaggagta cgacgtgctg gacaagcgga gaggacggga cccagaaatg	2040	
ggcgggaagc cgcgcagaaa gaatcccaa gagggcctgt acaacgagct ccaaaaggat	2100	
aagatggcag aagcctatag cgagattggt atgaaagggg aacgcagaag agggcaaaggc	2160	
cacgacggac tgtaccaggg actcagcacc gccaccaagg acacctatga cgctcttcac	2220	
atgcaggccc tgccgcctcg g	2241	

<210> 1069

<211> 2241

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1069

atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg	60
cccgattcgt tggcactttc cctgactgcc gaccagatgg tgtccgccct tctggacgcc	120
gagcctccaa ttctgtactc ggagtacgat ccgactcgcc cgttctccga agccagcatg	180

						_SL	
atgggcctgt	tgactaacct	ggcggaccgc	gagttggtgc	acatgattaa	ctgggctaag		240
cgggtgccgg	gcttcgtgga	cctgaccctg	cacgaccaag	tgcacctcct	ggaatgcgcc		300
tggatggaaa	tcctcatgat	cggcctcgtg	tggagatcca	tggagcatcc	cggaaagctc		360
ctgtttgcac	ccaacctcct	gcttgatcgc	aaccagggaa	aatgcgtgga	agggggtgtc		420
gagattttcg	acatgctgct	cgccacctct	tcccggttcc	ggatgatgaa	tctgcaggga		480
gaagagttcg	tgtgtctgaa	gtcaatcatc	ctgctgaact	cgggggtcta	taccttcctg		540
agctcgaccc	tcaagtcact	ggaggaaaaa	gaccacatcc	atcgcgtgct	cgataagatc		600
accgacaccc	ttatccatct	catggcgaag	gctggactga	ccctgcaaca	gcagcaccag		660
aggctggccc	agttgctgct	gattctgagc	cacatccggc	acatgtcgaa	caagaggatg		720
gaacacctgt	acagcatgaa	gtgcaagaac	gtcgtgcctc	tgtccgatct	gctcctggaa		780
atgctggacg	cgcacagact	cgggacggga	gctgaagatc	cacgaccag	cagaaagcga		840
cggcaagtgc	aactcgtcca	aagcggagcg	gaagtcaaga	aacccgagc	gagcgtgaaa		900
gtgtcctgca	aagcctccgg	ctacaccttt	acgggctact	acatgcactg	ggtgcgccag		960
gcaccaggac	agggctcttga	atggatggga	tggatcaacc	ctaattcggg	cggaaactaac		1020
tacgcacaga	agttccaggg	gagagtgact	ctgactcggg	ataacctcat	ctcaactgtc		1080
tacatggaac	tctcccgtt	gcggtcagat	gatacggcag	tgtactactg	cgcccgcgac		1140
atgaatatcc	tggtaccgt	gccgttcgac	atctggggac	aggggactat	ggttactgtc		1200
tcatcgggcg	gtggagggttc	aggaggaggc	ggctcgggag	gcggagggttc	ggacattcag		1260
atgaccaggt	ccccatcctc	tctgtcggcc	agcgtcggag	atagggtgac	cattacctgt		1320
cgggcctcgc	aaagcatctc	ctcgtacctc	aactggtatc	agcaaaaagcc	gggaaaggcg		1380
cctaagctgc	tgatctacgc	cgcttcgagc	ttgcaaagcg	gggtgccatc	cagattctcg		1440
ggatcaggct	caggaaccga	cttcaccctg	accgtgaaca	gcctccagcc	ggaggacttt		1500
gccacttact	actgccagca	gggagactcc	gtgccgctta	ctttcggggg	gggtaccgcg		1560
ctggagatca	agaccactac	cccagcaccg	aggccacca	ccccggctcc	taccatcgcc		1620
tcccagcctc	tgtccctgcg	tccggaggca	tgtagaccgc	cagctggtgg	ggccgtgcat		1680
acccgggggtc	ttgacttcgc	ctgcgatatc	tacatttggt	cccctctggc	tggtacttgc		1740
ggggtcctgc	tgctttcact	cgtgatcact	ctttactgta	agcgcgggtcg	gaagaagctg		1800
ctgtacatct	ttaagcaacc	cttcattgag	cctgtgcaga	ctactcaaga	ggaggacggc		1860
tgttcatgcc	ggttcccaga	ggaggaggaa	ggcggctgcg	aactgcgcgt	gaaattcagc		1920
cgcagcgcag	atgctccagc	ctaccagcag	gggcagaacc	agctctacaa	cgaactcaat		1980
cttggtcgga	gagaggagta	cgacgtgctg	gacaagcgga	gaggacggga	cccagaaatg		2040
ggcgggaagc	cgcgcagaaa	gaatccccaa	gagggcctgt	acaacgagct	ccaaaaggat		2100
aagatggcag	aagcctatag	cgagattggt	atgaaagggg	aacgcagaag	aggcaaaggc		2160
cacgacggac	tgtaccaggg	actcagcacc	gccaccaagg	acacctatga	cgctcttcac		2220

atgcaggccc tgccgcctcg g

2241

<210> 1070

<211> 2247

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1070

atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg	60
cccgattcgt tggcactttc cctgactgcc gaccagatgg tgtccgccct tctggacgcc	120
gagcctccaa ttctgtactc ggagtacgat ccgactcgcc cgttctccga agccagcatg	180
atgggcctgt tgactaacct ggcggaccgc gagttggtgc acatgattaa ctgggctaag	240
cgggtgccgg gcttcgtgga cctggccctg caccaccaag tgcacctcct ggaatgcgcc	300
tggatggaaa tcctcatgat cggcctcgtg tggagatcca tggagcatcc cggaaagctc	360
ctgtttgcac ccaacctcct gcttgatcgc aaccaggga aatgcgtgga agggggtgtc	420
gagattttcg acatgctgct cgccacctct tcccggttcc ggatgatgaa tctgcaggga	480
gaagagttcg tgtgtctgaa gtcaatcatc ctgctgaact ccgggggtcta taccttcctg	540
agctcgaccc tcaagtcact ggaggaaaaa gaccacatcc atcgctgctc cgataagatc	600
accgacaccc ttatccatct catggcgaag gctggactga ccctgcaaca gcagcaccag	660
aggctggccc agttgctgct gattctgagc cacatccggc acatgtcgtc caagaggatg	720
gaacacctgt acagcatgaa gtgcaagaac gtcgtgcctc tgtccgatct gtcctggaa	780
atgctggacg cgcacagact cggaaccggc gcggaagacc cccggccctc caggaagcga	840
aggtccctcg gagacgtggg tgaagtcaa ttggtggaat cagggggagg acttgtgcag	900
cctggaggat cgctgagact gtcattgtgc gtgtccggct ttgccctgtc caaccacggg	960
atgtcctggg tccgccgcgc gcctggaaag ggcctcgaat ggggtgtcggg tattgtgtac	1020
agcggtagca cctactatgc cgcatccgtg aaggggagat tcaccatcag ccgggacaac	1080
tccaggaaca ctctgtacct ccaaataaat tcgctgaggc cagaggacac tgccatctac	1140
tactgtccg cgcatggcgg agagtccgac gtctggggac aggggaccac cgtgaccgtg	1200
tctagcgcgt ccggcggagg cggcagcggg ggtcgggcat cagggggcg cggatcggac	1260
atccagctca ccagtcctcc gagctcgtg tccgcctccg tgggagatcg ggtcaccatc	1320
acgtgccgcg ccagccagtc gatttcctcc tacctgaact ggtaccaaca gaagcccga	1380
aaagccccga agcttctcat ctacgccgc tcgagcctgc agtcaggagt gccctcacgg	1440
ttctccggct ccggttcggg tactgatttc accctgacca ttctctcct gcaaccggag	1500
gacttcgcta cttactactg ccagcagtcg tactccaccc cctacacttt cggacaaggc	1560
accaaggtcg aaatcaagac cactacccca gcaccaggc caccacccc ggctcctacc	1620

atcgctccc	agcctctgtc	cctgcgtccg	gaggcatgta	gacccgcagc	tggtggggcc	1680
gtgcataccc	ggggtcttga	cttcgcctgc	gatatctaca	tttgggcccc	tctggctggt	1740
acttgccggg	tcctgctgct	ttcactcgtg	atcactcttt	actgtaagcg	cggtcgggaag	1800
aagctgctgt	acatctttaa	gcaacccttc	atgaggcctg	tgcagactac	tcaagaggag	1860
gacggctgtt	catgccgggt	cccagaggag	gaggaaggcg	gctgcgaact	gcgcgtgaaa	1920
ttcagccgca	gcgcagatgc	tccagcctac	cagcaggggc	agaaccagct	ctacaacgaa	1980
ctcaatcttg	gtcggagaga	ggagtacgac	gtgctggaca	agcggagagg	acgggaccca	2040
gaaatgggcg	ggaagccgcg	cagaaagaat	ccccagagg	gcctgtacaa	cgagctccaa	2100
aaggataaga	tggcagaagc	ctatagcgag	attggtatga	aaggggaacg	cagaagaggc	2160
aaaggccacg	acggactgta	ccagggactc	agcaccgcca	ccaaggacac	ctatgacgct	2220
cttcacatgc	aggccctgcc	gcctcgg				2247

<210> 1071

<211> 2247

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1071

atggccctcc	ctgtcaccgc	cctgctgctt	ccgctggctc	ttctgctcca	cgccgctcgg	60
cccgattcgt	tggcactttc	cctgactgcc	gaccagatgg	tgtccgccct	tctggacgcc	120
gagcctccaa	ttctgtactc	ggagtacgat	ccgactcgcc	cgttctccga	agccagcatg	180
atgggcctgt	tgactaacct	ggcggaccgc	gagttggtgc	acatgattaa	ctgggctaag	240
cgggtgccgg	gcttcgtgga	cctgaccctg	cacgaccaag	tgcacctcct	ggaatgcgcc	300
tggatggaaa	tcctcatgat	cggcctcgtg	tggagatcca	tggagcatcc	cggaaagctc	360
ctgtttgcac	ccaacctcct	gcttgatcgc	aaccagggaa	aatgcgtgga	agggggtgtc	420
gagattttcg	acatgctgct	cgccacctct	tcccggttcc	ggatgatgaa	tctgcaggga	480
gaagagttcg	tgtgtctgaa	gtcaatcatc	ctgctgaact	ccgggggtcta	taccttcctg	540
agctcgaccc	tcaagtcact	ggaggaaaaa	gaccacatcc	atcgctgctg	cgataagatc	600
accgacaccc	ttatccatct	catggcgaag	gctggactga	ccctgcaaca	gcagcaccag	660
aggctggccc	agttgctgct	gattctgagc	cacatccggc	acatgtcgaa	caagaggatg	720
gaacacctgt	acagcatgaa	gtgcaagaac	gtcgtgcctc	tgtccgatct	gctcctggaa	780
atgctggacg	cgcacagact	cggaaccggc	gcggaagacc	cccggccctc	caggaagcga	840
aggccctcg	gagacgtggg	tgaagtgcaa	ttggtggaat	cagggggagg	acttgtgcag	900
cctggaggat	cgctgagact	gtcatgtgcc	gtgtccggct	ttgccctgtc	caaccacggg	960
atgtcctggg	tccgccgcgc	gcctggaaaag	ggcctcgaat	gggtgtcggg	tatttgtgtac	1020

	_SL	
agcggtagca cctactatgc cgcattccgtg aaggggagat tcaccatcag ccgggacaac	1080	
tccaggaaca ctctgtacct ccaaataaat tctgtgagggc cagaggacac tgccatctac	1140	
tactgtctccg cgcattggcgg agagtccgac gtctggggac aggggaccac cgtgaccgtg	1200	
tctagcgcgt ccggcggagg cggcagcggg ggtcggggcat cagggggcgg cggatcggac	1260	
atccagctca cccagtcccc gagctcgtg tccgcctccg tgggagatcg ggtcaccatc	1320	
acgtgccgcg ccagccagtc gatttcctcc tacctgaact ggtaccaaca gaagcccgga	1380	
aaagccccga agcttctcat ctacgccgc tctgagcctgc agtcaggagt gccctcacgg	1440	
ttctccggct ccggttccgg tactgatttc accctgacca ttctctccct gcaaccggag	1500	
gacttcgcta ctactactg ccagcagtcg tactccaccc cctacacttt cggacaaggc	1560	
accaaggtcg aaatcaagac cactaccca gcaccgaggc caccacccc ggctcctacc	1620	
atgcctccc agcctctgtc cctgcgtccg gaggcattga gaccgcagc tgggtggggcc	1680	
gtgcataccc ggggtcttga cttgcctgc gatattctaca ttggggcccc tctggctggt	1740	
acttgccggg tctgtctgt ttcactcgtg atcactcttt actgtaagcg cggtcggaag	1800	
aagctgctgt acatctttaa gcaacccttc atgaggcctg tgcagactac tcaagaggag	1860	
gacggctgtt catgccggtt ccagaggag gaggaaggcg gctgcgaact gcgcgtgaaa	1920	
ttcagccgca gcgcagatgc tccagcctac cagcaggggc agaaccagct ctacaacgaa	1980	
ctcaatcttg gtcggagaga ggagtacgac gtgctggaca agcggagagg acgggaccca	2040	
gaaatgggcg ggaagccgcg cagaaagaat cccaagagg gcctgtacaa cgagctccaa	2100	
aaggataaga tggcagaagc ctatagcgag attggtatga aaggggaacg cagaagaggc	2160	
aaaggccacg acggactgta ccagggactc agcaccgcca ccaaggacac ctatgacgct	2220	
cttcacatgc aggccctgcc gcctcgg	2247	

<210> 1072

<211> 2229

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1072

atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg	60
cccgattcgt tggcactttc cctgactgcc gaccagatgg tgtccgccct tctggacgcc	120
gagcctccaa ttctgtactc ggagtacgat ccgactcgcc cgttctccga agccagcatg	180
atgggcctgt tgactaacct ggcggaccgc gagttggtgc acatgattaa ctgggctaag	240
cggttgccgg gcttcgtgga cctggccctg cagaccaag tgcacctcct ggaatgcgcc	300
tggatggaaa tcctcatgat cggcctcgtg tggagatcca tggagcatcc cggaaagctc	360
ctgtttgcac ccaacctcct gcttgatcgc aaccagggaa aatgcgtgga agggggtgtc	420

						_SL	
gagattttcg	acatgctgct	cgccacctct	tcccggttcc	ggatgatgaa	tctgcagggg		480
gaagagttcg	tgtgtctgaa	gtcaatcatc	ctgctgaact	ccgggggtcta	taccttcctg		540
agctcgaccc	tcaagtcact	ggaggaaaaa	gaccacatcc	atcgcggtgct	cgataagatc		600
accgacaccc	ttatccatct	catggcgaag	gctggactga	ccctgcaaca	gcagcaccag		660
aggctggccc	agttgctgct	gattctgagc	cacatccggc	acatgtcgtc	caagaggatg		720
gaacacctgt	acagcatgaa	gtgcaagaac	gtcgtgcctc	tgtccgatct	gctcctggaa		780
atgctggacg	cgcacagact	cgggacggga	gctgaagatc	cacgaccag	cagaaagcga		840
cgggaagtgc	aattggtgga	atcaggggga	ggacttgtgc	agcctggagg	atcgctgaga		900
ctgtcatgtg	ccgtgtccgg	ctttgccctg	tccaaccacg	ggatgtcctg	ggtccgccgc		960
gcgcctggaa	agggcctcga	atgggtgtcg	ggtatttgtt	acagcggtag	cacctactat		1020
gccgcatccg	tgaaggggag	attcaccatc	agccgggaca	actccaggaa	cactctgtac		1080
ctccaaatga	attcgctgag	gccagaggac	actgccatct	actactgctc	cgcgcatggc		1140
ggagagtccg	acgtctgggg	acaggggacc	accgtgaccg	tgtctagcgc	gtccggcgga		1200
ggcggcagcg	ggggtcgggc	atcagggggc	ggcggatcgg	acatccagct	caccaggtcc		1260
ccgagctcgc	tgtccgcctc	cgtgggagat	cgggtcacca	tcacgtgccg	cgccagccag		1320
tcgatttcct	cctacctgaa	ctggtaccaa	cagaagcccg	gaaaagcccc	gaagcttctc		1380
atctacgccg	cctcgagcct	gcagtcagga	gtgccctcac	ggttctccgg	ctccggttcc		1440
ggtactgatt	tcaccctgac	catttcctcc	ctgcaaccgg	aggacttcgc	tacttactac		1500
tgccagcagt	cgtactccac	cccctacact	ttcggacaag	gcaccaaggt	cgaaatcaag		1560
accactaccc	cagcaccgag	gccaccacc	ccggctccta	ccatcgctc	ccagcctctg		1620
tccctgcgtc	cggaggcatg	tagaccgcga	gctggtgggg	ccgtgcatac	ccgggggtctt		1680
gacttcgcct	gcgatatcta	catttgggcc	cctctggctg	gtacttgccg	ggtcctgctg		1740
ctttcactcg	tgatcactct	ttactgtaag	cgcggtcgga	agaagctgct	gtacatcttt		1800
aagcaaccct	tcattgagcc	tgtgcagact	actcaagagg	aggacggctg	ttcatgccgg		1860
ttcccagagg	aggaggaagg	cggctgcgaa	ctgcgcgtga	aattcagccg	cagcgcagat		1920
gctccagcct	accagcaggg	gcagaaccag	ctctacaacg	aactcaatct	tggtcggaga		1980
gaggagtacg	acgtgctgga	caagcggaga	ggacgggacc	cagaaatggg	cgggaagccg		2040
cgcagaaaga	atccccaaga	gggcctgtac	aacgagctcc	aaaaggataa	gatggcagaa		2100
gcctatagcg	agattggtat	gaaaggggaa	cgcagaagag	gcaaaggcca	cgacggactg		2160
taccagggac	tcagcaccgc	caccaaggac	acctatgacg	ctcttcacat	gcaggccctg		2220
ccgcctcgg							2229

<210> 1073
 <211> 2229
 <212> DNA
 <213> Artificial Sequence

_SL

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1073

atggccctcc	ctgtcaccgc	cctgctgctt	ccgctggctc	ttctgctcca	cgccgctcgg	60
cccgattcgt	tggcactttc	cctgactgcc	gaccagatgg	tgtccgccct	tctggacgcc	120
gagcctcaa	ttctgtactc	ggagtacgat	ccgactcgcc	cgttctccga	agccagcatg	180
atgggcctgt	tgactaacct	ggcggaccgc	gagttggtgc	acatgattaa	ctgggctaag	240
cggttgccgg	gcttcgtgga	cctgaccctg	cacgaccaag	tgcacctcct	ggaatgcgcc	300
tggatgaaa	tcctcatgat	cggcctcgtg	tggagatcca	tggagcatcc	cgaaaagctc	360
ctgtttgcac	ccaacctcct	gcttgatcgc	aaccagggaa	aatgcgtgga	agggggtgtc	420
gagattttcg	acatgctgct	cgccacctct	tcccggttcc	ggatgatgaa	tctgcaggga	480
gaagagttcg	tgtgtctgaa	gtcaatcatc	ctgctgaact	ccgggggtcta	taccttcctg	540
agctcgaccc	tcaagtcact	ggaggaaaaa	gaccacatcc	atcgctgct	cgataagatc	600
accgacaccc	ttatccatct	catggcgaag	gctggactga	ccctgcaaca	gcagcaccag	660
aggctggccc	agttgctgct	gattctgagc	cacatccggc	acatgtcgaa	caagaggatg	720
gaacacctgt	acagcatgaa	gtgcaagaac	gtcgtgcctc	tgtccgatct	gctcctggaa	780
atgctggacg	cgcacagact	cgggacggga	gctgaagatc	cacgaccag	cagaaagcga	840
cgggaagtgc	aattggtgga	atcaggggga	ggacttgtgc	agcctggagg	atcgctgaga	900
ctgtcatgtg	ccgtgtccgg	ctttgccctg	tccaaccacg	ggatgtcctg	ggtcgcccg	960
gcgcctggaa	agggcctcga	atgggtgtcg	ggtatttgtg	acagcggtag	cacctactat	1020
gccgcatccg	tgaaggggag	attcaccatc	agccgggaca	actccaggaa	cactctgtac	1080
ctccaaatga	attcgctgag	gccagaggac	actgccatct	actactgctc	cgcgcatggc	1140
ggagagtccg	acgtctgggg	acaggggacc	accgtgaccg	tgtctagcgc	gtccggcgga	1200
ggcggcagcg	ggggtcgggc	atcagggggc	ggcggatcgg	acatccagct	caccagctcc	1260
ccgagctcgc	tgtccgcctc	cgtgggagat	cgggtcacca	tcacgtgccg	cgccagccag	1320
tcgatttcct	cctacctgaa	ctggtaccaa	cagaagcccg	gaaaagcccc	gaagcttctc	1380
atctacgccg	cctcgagcct	gcagtcagga	gtgccctcac	ggttctccgg	ctccggttcc	1440
ggtactgatt	tcaccctgac	catttcctcc	ctgcaaccgg	aggacttcgc	tacttactac	1500
tgccagcagt	cgtactccac	cccctacact	ttcggacaag	gcaccaaggt	cgaaatcaag	1560
accactaccc	cagcaccgag	gccaccacc	ccggctccta	ccatcgctc	ccagcctctg	1620
tccctgcgtc	cggaggcatg	tagaccgca	gctggtgggg	ccgtgcatac	ccggggctct	1680
gacttcgcct	gcgatatcta	catttgggcc	cctctggctg	gtacttgccg	ggtcctgctg	1740
ctttcactcg	tgatcactct	ttactgtaag	cgcggtcgga	agaagctgct	gtacatcttt	1800
aagcaaccct	tcatgaggcc	tgtgcagact	actcaagagg	aggacggctg	ttcatgccgg	1860

ttcccagagg	aggaggaagg	cggctgcgaa	ctg ^{_SL} cgctga	aattcagccg	cagcgcagat	1920
gctccagcct	accagcaggg	gcagaaccag	ctctacaacg	aactcaatct	tggtcggaga	1980
gaggagtacg	acgtgctgga	caagcggaga	ggacggggacc	cagaaatggg	cggaagccg	2040
cgcagaaaga	atccccaaga	gggcctgtac	aacgagctcc	aaaaggataa	gatggcagaa	2100
gcctatagcg	agattggtat	gaaaggggaa	cgcagaagag	gcaaaggcca	cgacggactg	2160
taccagggac	tcagcaccgc	caccaaggac	acctatgacg	ctcttcacat	gcaggccctg	2220
ccgcctcgg						2229

<210> 1074
 <211> 2256
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1074	
atggccctcc	ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60
cccaactcgt	tggcactttc cctgactgcc gaccagatgg tgtccgccct tctggacgcc 120
gagcctccaa	ttctgtactc ggagtacgat ccgactcgcc cgttctccga agccagcatg 180
atgggcctgt	tgactaacct ggcggaccgc gagttggtgc acatgattaa ctgggctaag 240
cggtgcccgg	gcttcgtgga cctggccctg caccaccaag tgcacctcct ggaatgcgcc 300
tggatggaaa	tcctcatgat cggcctcgtg tggagatcca tggagcatcc cggaaagctc 360
ctgtttgcac	ccaacctcct gcttgatcgc aaccagggaa aatgcgtgga agggggtgtc 420
gagattttcg	acatgctgct cgccacctct tcccggttcc ggatgatgaa tctgcaggga 480
gaagagttcg	tgtgtctgaa gtcaatcatc ctgctgaact ccgggggtcta taccttcctg 540
agctcgaccc	tcaagtcact ggaggaaaaa gaccacatcc atcgcgtgct cgataagatc 600
accgacaccc	ttatccatct catggcgaag gctggactga ccctgcaaca gcagcaccag 660
aggctggccc	agttgctgct gattctgagc cacatccggc acatgtcgtc caagaggatg 720
gaacacctgt	acagcatgaa gtgcaagaac gtcgtgcctc tgtccgatct gtcctggaa 780
atgctggacg	cgcacagact cggaaccggc gcggaagacc cccggccctc caggaagcga 840
aggtccctcg	gagacgtggg tgaaattgtg atgaccagat caccgcccac tcttagcctt 900
tcaccgggtg	agcgcgcaac cctgtcttgc agagcctccc aagacatctc aaaatacctt 960
aattggtatc	aacagaagcc cggacaggct cctcgccttc tgatctacca caccagccgg 1020
ctccattctg	gaatccctgc caggttcagc ggtagcggat ctgggaccga ctacaccctc 1080
actatcagct	cactgcagcc agaggacttc gctgtctatt tctgtcagca agggaacacc 1140
ctgccctaca	cctttggaca gggcaccaag ctcgagatta aaggtggagg tggcagcgga 1200
ggaggtgggt	ccggcggtgg aggaagccag gtccaactcc aagaaagcgg accgggtcctt 1260

gtgaagccat	cagaaactct	ttcactgact	tgtactgtga	gctgagtgct	tctccccgat	1320
tacgggggtgt	cttggatcag	acagccaccg	gggaaggggtc	tggaatggat	tggagtgatt	1380
tgggggtctg	agactactta	ctactcttca	tccctcaagt	cacgcgtcac	catctcaaag	1440
gacaactcta	agaatcaggt	gtcactgaaa	ctgtcatctg	tgaccgcagc	cgacaccgcc	1500
gtgtactatt	gcgctaagca	ttactattat	ggcgggagct	acgcaatgga	ttactgggga	1560
caggggtactc	tggtcaccgt	gtccagcacc	actaccccg	caccgaggcc	acccaccccg	1620
gctcctacca	tcgcctccca	gcctctgtcc	ctgcgtccgg	aggcatgtag	acccgcagct	1680
ggtggggccg	tgcatacccg	gggtcttgac	ttcgcctgcg	atatctacat	ttggggccct	1740
ctggctggta	cttgcgggggt	cctgctgctt	tactcgtga	tcactcttta	ctgtaagcgc	1800
ggtcggaaga	agctgctgta	catctttaag	caacccttca	tgaggcctgt	gcagactact	1860
caagaggagg	acggctgttc	atgccgggtc	ccagaggagg	aggaaggcgg	ctgcgaactg	1920
cgcgtgaaat	tcagccgcag	cgcagatgct	ccagcctacc	agcaggggca	gaaccagctc	1980
tacaacgaac	tcaatcttgg	tcggagagag	gagtacgacg	tgctggacaa	gcggagagga	2040
cgggaccag	aaatgggagg	gaagccgcgc	agaaagaatc	cccaagaggg	cctgtacaac	2100
gagctccaaa	aggataagat	ggcagaagcc	tatagcgaga	ttggtatgaa	aggggaacgc	2160
agaagaggca	aaggccacga	cggactgtac	cagggactca	gcaccgccac	caaggacacc	2220
tatgacgctc	ttcacatgca	ggccctgccg	cctcgg			2256

<210> 1075

<211> 2256

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1075

atggccctcc	ctgtcaccgc	cctgctgctt	ccgctggctc	ttctgctcca	cgccgctcgg	60
cccaactcgt	tggcactttc	cctgactgcc	gaccagatgg	tgtccgccct	tctggacgcc	120
gagcctccaa	ttctgtactc	ggagtacgat	ccgactcgcc	cgttctccga	agccagcatg	180
atgggcctgt	tgactaacct	ggcggaccgc	gagttggtgc	acatgattaa	ctgggctaag	240
cgggtgccgg	gcttcgtgga	cctgaccctg	cacgaccaag	tgacctcct	ggaatgcgcc	300
tggatggaaa	tcctcatgat	cggcctcgtg	tggagatcca	tggagcatcc	cggaagctc	360
ctgtttgcac	ccaacctcct	gcttgatcgc	aaccagggaa	aatgcgtgga	agggggtgct	420
gagattttcg	acatgctgct	cgccacctct	tcccggttcc	ggatgatgaa	tctgcaggga	480
gaagagtctg	tgtgtctgaa	gtcaatcatc	ctgctgaact	ccgggggtcta	taccttcctg	540
agctcgaccc	tcaagtcact	ggaggaaaaa	gaccacatcc	atcgctgct	cgataagatc	600
accgacaccc	ttatccatct	catggcgaag	gctggactga	ccctgcaaca	gcagcaccag	660

	_SL	
aggctggccc agttgctgct gattctgagc cacatccggc acatgtcgaa caagaggatg	720	
gaacacctgt acagcatgaa gtgcaagaac gtcgtgcctc tgtccgatct gtccttgaa	780	
atgctggacg cgcacagact cggaaccggc gcggaagacc cccggccctc caggaagcga	840	
aggtccctcg gagacgtggg tgaaattgtg atgaccagc caccgcccac tcttagcctt	900	
tcacccggtg agcgcgcaac cctgtcttgc agagcctccc aagacatctc aaaatacctt	960	
aattggtatc aacagaagcc cggacaggct cctgcgcttc tgatctacca caccagccgg	1020	
ctccattctg gaatccctgc caggttcagc ggtagcggat ctgggaccga ctacaccctc	1080	
actatcagct cactgcagcc agaggacttc gctgtctatt tctgtcagca agggaacacc	1140	
ctgccctaca ctttggaca gggcaccaag ctcgagatta aagggtggagg tggcagcggg	1200	
ggaggtgggt ccggcgggtg aggaagccag gtccaactcc aagaaagcgg accgggtctt	1260	
gtgaagccat cagaaactct ttactgact tgtactgtga gcggagtgtc tctccccgat	1320	
tacggggtgt cttggatcag acagccaccg gggaagggtc tggaatggat tggagtgatt	1380	
tggggctctg agactactta ctactcttca tccctcaagt cacgcgtcac catctcaaag	1440	
gacaactcta agaatcaggt gtcactgaaa ctgtcatctg tgaccgcagc cgacaccgcc	1500	
gtgtactatt gcgctaagca ttactattat ggcgggagct acgcaatgga ttactgggga	1560	
cagggtactc tggtcaccgt gtccagcacc actaccccag caccgaggcc acccaccctg	1620	
gctcctacca tcgcctccca gcctctgtcc ctgcgtccgg aggcattgtag accgcagct	1680	
ggtggggccg tgcatacccg gggctctgac ttcgcctgcg atatctacat ttggggccct	1740	
ctggctggta cttgcggggt cctgctgctt tctactgtga tctactctta ctgtaagcgc	1800	
ggtcgggaag agctgctgta catctttaag caacccttca tgaggcctgt gcagactact	1860	
caagaggagg acggctgttc atgccggttc ccagaggagg aggaaggcgg ctgcgaactg	1920	
cgcgtgaaat tcagccgcag cgcagatgct ccagcctacc agcaggggca gaaccagctc	1980	
tacaacgaac tcaatcttgg tcggagagag gactacgacg tgctggacaa gcggagagga	2040	
cgggaccag aaatgggcgg gaagccgcgc agaaagaatc cccaagaggg cctgtacaac	2100	
gagctccaaa aggataagat ggcagaagcc tatagcgaga ttggtatgaa aggggaacgc	2160	
agaagaggca aaggccacga cggactgtac cagggactca gcaccgccac caaggacacc	2220	
tatgacgctc ttcacatgca ggccctgccg cctcgg	2256	

<210> 1076

<211> 2238

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1076

atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg	60
---	----

						_SL	
cccaactcgt	tggcactttc	cctgactgcc	gaccagatgg	tgtccgccct	tctggacgcc		120
gagcctccaa	ttctgtactc	ggagtacgat	ccgactcgcc	cgttctccga	agccagcatg		180
atgggcctgt	tgactaacct	ggcggaccgc	gagttggtgc	acatgattaa	ctgggctaag		240
cgggtgccgg	gcttcgtgga	cctggccctg	cacgaccaag	tgcacctcct	ggaatgcgcc		300
tggatggaaa	tcctcatgat	cggcctcgtg	tggagatcca	tggagcatcc	cggaaagctc		360
ctgtttgcac	ccaacctcct	gcttgatcgc	aaccagggaa	aatgcgtgga	agggggtgtc		420
gagattttcg	acatgctgct	cgccacctct	tcccggttcc	ggatgatgaa	tctgcaggga		480
gaagagttcg	tgtgtctgaa	gtcaatcatc	ctgctgaact	ccgggggtcta	taccttcctg		540
agctcgaccc	tcaagtcact	ggaggaaaaa	gaccacatcc	atcgctgct	cgataagatc		600
accgacaccc	ttatccatct	catggcgaag	gctggactga	ccctgcaaca	gcagcaccag		660
aggctggccc	agttgctgct	gattctgagc	cacatccggc	acatgtcgtc	caagaggatg		720
gaacacctgt	acagcatgaa	gtgcaagaac	gtcgtgcctc	tgtccgatct	gctcctggaa		780
atgctggacg	cgcacagact	cgggacggga	gctgaagatc	cacgaccag	cagaaagcga		840
cgggaaattg	tgatgaccca	gtcaccgcgc	actcttagcc	tttcaccggg	tgagcgcgca		900
accctgtctt	gcagagcctc	ccaagacatc	tcaaaatacc	ttaattggta	tcaacagaag		960
cccggacagg	ctcctcgcct	tctgatctac	cacaccagcc	ggctccattc	tggaatccct		1020
gccagggttca	gcggtagcgg	atctgggacc	gactacaccc	tcactatcag	ctcactgcag		1080
ccagaggact	tcgctgtcta	tttctgtcag	caagggaaca	ccctgcccta	cacctttgga		1140
cagggcacca	agctcgagat	taaaggtgga	ggtggcagcg	gaggaggtgg	gtccggcggt		1200
ggaggaagcc	aggtccaact	ccaagaaagc	ggaccgggtc	ttgtgaagcc	atcagaaaact		1260
ctttcactga	cttgtactgt	gagcggagtg	tctctccccg	attacggggg	gtcttgatc		1320
agacagccac	cggggaaggg	tctggaatgg	attggagtga	tttggggctc	tgagactact		1380
tactactctt	catccctcaa	gtcacgcgtc	accatctcaa	aggacaactc	taagaatcag		1440
gtgtcactga	aactgtcatc	tgtgaccgca	gccgacaccg	ccgtgtacta	ttgcgctaag		1500
cattactatt	atggcgggag	ctacgcaatg	gattactggg	gacagggtag	tctggtcacc		1560
gtgtccagca	ccactacccc	agcaccgagg	ccaccacccc	cggctcctac	catcgctcc		1620
cagcctctgt	ccctgcgtcc	ggaggcatgt	agaccgcgag	ctgggtggggc	cgtgcatacc		1680
cggggctctg	acttcgcctg	cgatatctac	atttggggcc	ctctggctgg	tacttgcggg		1740
gtcctgctgc	tttcactcgt	gatcactctt	tactgtaagc	gcggtcggaa	gaagctgctg		1800
tacatcttta	agcaaccctt	catgaggcct	gtgcagacta	ctcaagagga	ggacggctgt		1860
tcatgccggt	tcccagagga	ggaggaaggc	ggctgcgaac	tgcgctgaa	attcagccgc		1920
agcgcatatg	ctccagccta	ccagcagggg	cagaaccagc	tctacaacga	actcaatctt		1980
ggtcggagag	aggagtacga	cgtgctggac	aagcggagag	gacgggaccc	agaaatgggc		2040
gggaagccgc	gcagaaagaa	tccccaagag	ggcctgtaca	acgagctcca	aaaggataag		2100

atggcagaag cctatagcga gattggtatg aaaggggaac gcagaagagg caaaggccac	2160
gacggactgt accagggact cagcaccgcc accaaggaca cctatgacgc tcttcacatg	2220
caggccctgc cgcctcgg	2238

<210> 1077
 <211> 2238
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1077	
atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg	60
cccaactcgt tggcactttc cctgactgcc gaccagatgg tgtccgccct tctggacgcc	120
gagcctcaa ttctgtactc ggagtacgat ccgactcgcc cgttctccga agccagcatg	180
atgggcctgt tgactaacct ggcggaccgc gagttggtgc acatgattaa ctgggctaag	240
cgggtgccgg gcttcgtgga cctgaccctg cagcaccaag tgcacctcct ggaatgcgcc	300
tggatggaat tcctcatgat cggcctcgtg tggagatcca tggagcatcc cggaagctc	360
ctgtttgcac ccaacctcct gcttgatcgc aaccagggaa aatgcgtgga agggggtgtc	420
gagattttcg acatgctgct cgccacctct tcccggttcc ggatgatgaa tctgcaggga	480
gaagagtctg tgtgtctgaa gtcaatcatc ctgctgaact ccgggggtcta taccttcctg	540
agctcgaccc tcaagtcact ggaggaaaaa gaccacatcc atcgctgctc cgataagatc	600
accgacaccc ttatccatct catggcgaag gctggactga ccctgcaaca gcagcaccag	660
aggctggccc agttgctgct gattctgagc cacatccggc acatgtcgaa caagaggatg	720
gaacacctgt acagcatgaa gtgcaagaac gtcgtgcctc tgtccgatct gtccttgaa	780
atgctggacg cgcacagact cgggacggga gctgaagatc cagcaccag cagaaagcga	840
cgggaaattg tgatgaccca gtcacccgcc actcttagcc tttcacccgg tgagcgcgca	900
accctgtctt gcagagcctc ccaagacatc tcaaaatacc ttaattggta tcaacagaag	960
cccggacagg ctctcgcctt tctgatctac cacaccagcc ggctccattc tggaatccct	1020
gccaggttca gcggtagcgg atctgggacc gactacaccc tcactatcag ctactgcag	1080
ccagaggact tcgctgtcta tttctgtcag caagggaaca ccctgcccta cacctttgga	1140
cagggcacca agctcgagat taaaggtgga ggtggcagcg gaggaggtgg gtccggcggt	1200
ggaggaagcc aggtccaact ccaagaaagc ggaccgggtc ttgtgaagcc atcagaaact	1260
ctttcactga cttgtactgt gagcggagtg tctctccccg attacggggt gtcttgatc	1320
agacagccac cggggaaggg tctggaatgg attggagtga tttggggctc tgagactact	1380
tactactctt catccctcaa gtcacgcgtc accatctcaa aggacaactc taagaatcag	1440
gtgtcactga aactgtcatc tgtgaccgca gccgacaccg ccgtgtacta ttgcgctaag	1500

cattactatt atggcgggag ctacgcaatg gattact ^{_SL} ggg gacaggggtac tctgggtcacc	1560
gtgtccagca ccactacccc agcaccgagg ccacccaccc cggctcctac catcgcctcc	1620
cagcctctgt ccctgcgtcc ggaggcatgt agaccgcgag ctggtggggc cgtgcatacc	1680
cggggtcttg acttcgcctg cgatatctac atttggggccc ctctggctgg tacttgcggg	1740
gtcctgctgc tttcactcgt gatcactctt tactgtaagc gcggtcggaa gaagctgctg	1800
tacatcttta agcaaccctt catgaggcct gtgcagacta ctcaagagga ggacggctgt	1860
tcatgccggt tcccagagga ggaggaaggc ggctgcgaac tgcgcgtgaa attcagccgc	1920
agcgcagatg ctccagccta ccagcagggg cagaaccagc tctacaacga actcaatctt	1980
ggtcggagag aggagtacga cgtgctggac aagcggagag gacgggaccc agaaatgggc	2040
gggaagccgc gcagaaagaa tccccaagag ggcctgtaca acgagctcca aaaggataag	2100
atggcagaag cctatagcga gattggtatg aaaggggaac gcagaagagg caaaggccac	2160
gacggactgt accagggact cagcaccgcc accaaggaca cctatgacgc tcttcacatg	2220
caggccctgc cgcctcgg	2238

<210> 1078

<211> 2259

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1078

atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgtcca cgccgctcgg	60
cccaactcgt tggcactttc cctgactgcc gaccagatgg tgtccgccct tctggacgcc	120
gagcctcaa ttctgtactc ggagtacgat ccgactcgcc cgttctccga agccagcatg	180
atgggcctgt tgactaacct ggcggaccgc gagttggtgc acatgattaa ctgggctaag	240
cgggtgccgg gcttcgtgga cctggccctg caccaccaag tgcacctcct ggaatgcgcc	300
tggatggaat tcctcatgat cggcctcgtg tggagatcca tggagcatcc cggaagctc	360
ctgtttgcac ccaacctcct gcttgatcgc aaccagggaat aatgcgtgga agggggtgtc	420
gagattttcg acatgctgct cgccacctct tcccggttcc ggatgatgaa tctgcaggga	480
gaagagtctg tgtgtctgaa gtcaatcatc ctgctgaact ccgggggtcta taccttcctg	540
agctcgaccc tcaagtcact ggaggaaaaa gaccacatcc atcgcgtgct cgataagatc	600
accgacaccc ttatccatct catggcgaag gctggactga ccctgcaaca gcagcaccag	660
aggctggccc agttgctgct gattctgagc cacatccggc acatgtcgtc caagaggatg	720
gaacacctgt acagcatgaa gtgcaagaac gtcgtgcctc tgtccgatct gtccttgaa	780
atgctggacg cgcacagact cggaaccggc gcggaagacc cccggccctc caggaagcga	840
aggtccctcg gagacgtggg tcaagtgcaa ctcgtccaaa gcggagcggg agtcaagaaa	900

	_SL	
cccgagcg	gcgtgaaagt gtcctgcaaa gcctccggct acacctttac gggctactac	960
atgcactggg	tgcgccaggc accaggacag ggtcttgaat ggatgggatg gatcaaccct	1020
aattcggg	cggaactaacta cgcacagaag ttccagggga gaggtagctct gactcgggat	1080
acctccatct	caactgtcta catggaactc tcccgcttgc ggtcagatga tacggcagtg	1140
tactactg	cccgcgacat gaatatcctg gctaccgtgc cgttcgacat ctggggacag	1200
gggactatgg	ttactgtctc atcggggcgg ggaggttcag gaggaggcgg ctcgggaggc	1260
ggaggttc	acattcagat gacccagtcc ccacctctc tgtcggccag cgtcggagat	1320
agggtgacca	ttacctgtcg ggcctcgcaa agcatctcct cgtacctcaa ctggtatcag	1380
caaaagcc	gaaaggcgcc taagctgctg atctacgccg cttcgagctt gcaaagcggg	1440
gtgccatcca	gattctcggg atcaggctca ggaaccgact tcaccctgac cgtgaacagc	1500
ctccagcc	aggactttgc cacttactac tgccagcagg gagactccgt gccgcttact	1560
ttcggggg	gtaccgcct ggagatcaag accactacc cagcaccgag gccaccacc	1620
ccggctccta	ccatcgctc ccagcctctg tcctgcgtc cggaggcatg tagaccgcga	1680
gctggtgg	ccgtgcatac ccggggtctt gacttcgcct gcgatatacta catttgggcc	1740
cctctggctg	gtacttgcg ggtcctgctg ctttactcg tgatcactct ttactgtaag	1800
cgcggtcgga	agaagctgct gtacatcttt aagcaaccct tcatgaggcc tgtgcagact	1860
actcaagagg	aggacggctg ttcattgccg ttcccagagg aggaggaagg cggctgcgaa	1920
ctgcgcgtga	aattcagccg cagcgcagat gctccagcct accagcagg gcagaaccag	1980
ctctacaacg	aactcaatct tggtcggaga gaggagtacg acgtgctgga caagcggaga	2040
ggacgggacc	cagaaatggg cgggaagccg cgcagaaaga atccccaaga gggcctgtac	2100
aacgagctcc	aaaaggataa gatggcagaa gcctatagcg agattggtat gaaaggggaa	2160
cgcagaagag	gcaaaggcca cgacggactg taccagggac tcagcaccgc caccaaggac	2220
acctatgacg	ctcttcacat gcaggccctg ccgcctcgg	2259

<210> 1079

<211> 2259

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1079

atggccctcc	ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg	60
cccaactcgt	tggcactttc cctgactgcc gaccagatgg tgtccgccct tctggacgcc	120
gagcctccaa	ttctgtactc ggagtacgat ccgactcgcc cgttctccga agccagcatg	180
atgggcctgt	tgactaacct ggcggaccgc gagttggtgc acatgattaa ctgggctaag	240
cgggtgccgg	gcttcgtgga cctgaccctg cagaccaag tgcacctcct ggaatgcgcc	300

						_SL	
tggatggaaa	tcctcatgat	cggcctcgtg	tggagatcca	tggagcatcc	cggaaagctc		360
ctgtttgcac	ccaacctcct	gcttgatcgc	aaccagggaa	aatgcgtgga	agggggtgtc		420
gagattttcg	acatgctgct	cgccacctct	tcccggttcc	ggatgatgaa	tctgcaggga		480
gaagagttcg	tgtgtctgaa	gtcaatcatc	ctgctgaact	ccggggtcta	taccttcctg		540
agctcgaccc	tcaagtcact	ggaggaaaaa	gaccacatcc	atcgcgtgct	cgataagatc		600
accgacaccc	ttatccatct	catggcgaag	gctggactga	ccctgcaaca	gcagcaccag		660
aggctggccc	agttgctgct	gattctgagc	cacatccggc	acatgtcgaa	caagaggatg		720
gaacacctgt	acagcatgaa	gtgcaagaac	gtcgtgcctc	tgtccgatct	gctcctggaa		780
atgctggacg	cgcacagact	cggaaccggc	gcggaagacc	cccggccctc	caggaagcga		840
aggtccctcg	gagacgtggg	tcaagtgcaa	ctcgtccaaa	gcggagcgga	agtcaagaaa		900
cccggagcga	gcgtgaaagt	gtcctgcaaa	gcctccggct	acacctttac	gggctactac		960
atgactggg	tgccagaggc	accaggacag	ggtcttgaat	ggatgggatg	gatcaaccct		1020
aattcgggcg	gaactaacta	cgcacagaag	ttccagggga	gagtgactct	gactcgggat		1080
acctccatct	caactgtcta	catggaactc	tcccgccttg	ggtcagatga	tacggcagtg		1140
tactactgcg	cccgcgacat	gaatatcctg	gctaccgtgc	cgttcgacat	ctggggacag		1200
gggactatgg	ttactgtctc	atcgggcggg	ggaggttcag	gaggaggcgg	ctcgggaggg		1260
ggaggttcgg	acattcagat	gaccaggtcc	ccatcctctc	tgtcggccag	cgtcggagat		1320
agggtgacca	ttacctgtcg	ggcctcgcaa	agcatctcct	cgtacctcaa	ctggtatcag		1380
caaaagccgg	gaaaggcgcc	taagctgctg	atctacgccg	cttcgagctt	gcaaagcggg		1440
gtgccatcca	gattctcggg	atcagggtca	ggaaccgact	tcaccctgac	cgtgaacagc		1500
ctccagccgg	aggactttgc	cacttactac	tgccagcagg	gagactccgt	gccgcttact		1560
ttcggggggg	gtacccgcct	ggagatcaag	accactaccc	cagcaccgag	gccacccacc		1620
ccggctccta	ccatcgcttc	ccagcctctg	tccctgcgtc	cggaggcatg	tagacccgca		1680
gctggtgggg	ccgtgcatac	ccggggtctt	gacttcgcct	gcgatatcta	catttggggc		1740
cctctggctg	gtacttgcg	ggtcctgctg	ctttcactcg	tgatcactct	ttactgtaag		1800
cgcggtcggg	agaagctgct	gtacatcttt	aagcaaccct	tcagtaggcc	tgtgcagact		1860
actcaagagg	aggacggctg	ttcatgccgg	ttcccagagg	aggaggaagg	cggctgcgaa		1920
ctgcgcgtga	aattcagccg	cagcgcagat	gctccagcct	accagcaggg	gcagaaccag		1980
ctctacaacg	aactcaatct	tggtcggaga	gaggagtacg	acgtgctgga	caagcggaga		2040
ggacgggacc	cagaaatggg	cgggaagccg	cgcagaaaga	atccccaaga	gggcctgtac		2100
aacgagctcc	aaaaggataa	gatggcagaa	gcctatagcg	agattggtat	gaaaggggaa		2160
cgcagaagag	gcaaaggcca	cgacggactg	taccagggac	tcagcaccgc	caccaaggac		2220
acctatgacg	ctcttcacat	gcaggccctg	ccgcctcgg				2259

<210> 1080

<211> 2241
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1080
 atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60
 cccaactcgt tggcactttc cctgactgcc gaccagatgg tgtccgccct tctggacgcc 120
 gagcctccaa ttctgtactc ggagtagcat ccgactcgcc cgttctccga agccagcatg 180
 atgggcctgt tgactaacct ggcggaccgc gagttggtgc acatgattaa ctgggctaag 240
 cgggtgccgg gcttcgtgga cctggccctg caccaccaag tgcacctcct ggaatgcgcc 300
 tggatgga aa tcctcatgat cggcctcgtg tggagatcca tggagcatcc cggaagctc 360
 ctgtttgcac ccaacctcct gcttgatcgc aaccaggga aatgcgtgga agggggtgtc 420
 gagattttcg acatgctgct cgccacctct tcccggttcc ggatgatgaa tctgcaggga 480
 gaagagtctg tgtgtctgaa gtcaatcatc ctgctgaact cgggggtcta taccttcctg 540
 agctcgaccc tcaagtcact ggaggaaaaa gaccacatcc atcgctgct cgataagatc 600
 accgacaccc ttatccatct catggcgaag gctggactga ccctgcaaca gcagcaccag 660
 aggctggccc agttgctgct gattctgagc cacatccggc acatgtcgtc caagaggatg 720
 gaacacctgt acagcatgaa gtgcaagaac gtcgtgcctc tgtccgatct gtccttgaa 780
 atgctggacg cgcacagact cggaaccggc gcggaagacc cccggccctc caggaagcga 840
 aggcaagtgc aactcgtcca aagcggagcg gaagtcaaga aaccgggagc gagcgtgaaa 900
 gtgtcctgca aagcctccgg ctacaccttt acgggctact acatgactg ggtgcgccag 960
 gcaccaggac agggctcttg atggatggga tggatcaacc ctaattcggg cggaactaac 1020
 tacgcacaga agttccaggg gagagtgact ctgactcggg atacctccat ctcaactgtc 1080
 tacatggaac tctcccgtt gcggtcagat gatacggcag tgtactactg cgcccgcgac 1140
 atgaatatcc tggctaccgt gccgttcgac atctggggac aggggactat ggttactgtc 1200
 tcacggggcg gtggagggtc aggaggaggc ggctcgggag gcggagggtc ggacattcag 1260
 atgaccagcgt ccccatcctc tctgtcggcc agcgtcggag atagggtgac cattacctgt 1320
 cgggcctcgc aaagcatctc ctcgtacctc aactggatat agcaaaagcc gggaaaggcg 1380
 cctaagctgc tgatctacgc cgcttcgagc ttgcaaagcg gggtgccatc cagattctcg 1440
 ggatcaggct caggaaccga cttcacctg accgtgaaca gcctccagcc ggaggacttt 1500
 gccacttact actgccagca gggagactcc gtgccgctta ctttcggggg gggtaaccgc 1560
 ctggagatca agaccactac ccagcaccg aggccacca cccgggtcc taccatcgcc 1620
 tcccagcctc tgtccctgcg tccggaggca tgtagaccg cagctggtgg ggccgtgcat 1680
 acccggggtc ttgacttcgc ctgcgatatc tacatttggg cccctctggc tggtaacttg 1740

ggggtcctgc	tgctttcact	cgatgatcact	ctttactgta	agcgcggtcg	gaagaagctg	1800
ctgtacatct	ttaagcaacc	cttcatgagg	cctgtgcaga	ctactcaaga	ggaggacggc	1860
tgttcatgcc	ggttcccaga	ggaggaggaa	ggcggtctgcg	aactgcgcgt	gaaattcagc	1920
cgcagcgcag	atgctccagc	ctaccagcag	gggcagaacc	agctctacaa	cgaactcaat	1980
cttggtcggg	gagaggagta	cgacgtgctg	gacaagcgga	gaggacggga	cccagaaatg	2040
ggcggaagc	cgcgagaaa	gaatcccaa	gagggcctgt	acaacgagct	ccaaaaggat	2100
aagatggcag	aagcctatag	cgagattggt	atgaaagggg	aacgcagaag	aggcaaaggc	2160
cacgacggac	tgtaccaggg	actcagcacc	gccaccaagg	acacctatga	cgctcttcac	2220
atgcaggccc	tgccgcctcg	g				2241

<210> 1081

<211> 2241

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1081

atggccctcc	ctgtcaccgc	cctgctgctt	ccgctggctc	ttctgctcca	cgccgctcgg	60
cccaactcgt	tggcactttc	cctgactgcc	gaccagatgg	tgtccgccct	tctggacgcc	120
gagcctccaa	ttctgtactc	ggagtacgat	ccgactcgcc	cgttctccga	agccagcatg	180
atgggcctgt	tgactaacct	ggcggaccgc	gagttggtgc	acatgattaa	ctgggctaag	240
cgggtgccgg	gcttcgtgga	cctgaccctg	cacgaccaag	tgcacctcct	ggaatgcgcc	300
tggatggaaa	tcctcatgat	cggcctcgtg	tggagatcca	tggagcatcc	cgaaaagctc	360
ctgtttgcac	ccaacctcct	gcttgatcgc	aaccagggaa	aatgcgtgga	agggggtgtc	420
gagattttcg	acatgctgct	cgccacctct	tcccggttcc	ggatgatgaa	tctgcagggg	480
gaagagttcg	tgtgtctgaa	gtcaatcatc	ctgctgaact	ccgggggtcta	taccttcctg	540
agctcgaccc	tcaagtcact	ggaggaaaaa	gaccacatcc	atcgcgctgct	cgataagatc	600
accgacaccc	ttatccatct	catggcgaag	gctggactga	ccctgcaaca	gcagcaccag	660
aggctggccc	agttgctgct	gattctgagc	cacatccggc	acatgtcgaa	caagaggatg	720
gaacacctgt	acagcatgaa	gtgcaagaac	gtcgtgcctc	tgtccgatct	gctcctggaa	780
atgctggacg	cgcacagact	cgggacggga	gctgaagatc	cacgaccag	cagaaagcga	840
cggcaagtgc	aactcgtcca	aagcggagcg	gaagtcaaga	aaccgggagc	gagcgtgaaa	900
gtgtcctgca	aagcctccgg	ctacaccttt	acgggctact	acatgcactg	ggtgcgccag	960
gcaccaggac	agggtcttga	atggatggga	tggatcaacc	ctaattcggg	cggaactaac	1020
tacgcacaga	agttccaggg	gagagtgact	ctgactcggg	atacctccat	ctcaactgtc	1080
tacatggaac	tctcccgtt	gcggtcagat	gatacggcag	tgtactactg	cgcccgcgac	1140

	_SL	
atgaatatcc tggctaccgt gccgttcgac atctggggac aggggactat ggttactgtc		1200
tcatcgggcg gtggagggtc aggaggaggc ggctcgggag gcggagggtc ggacattcag		1260
atgaccagcag ccccatcctc tctgtcggcc agcgtcggag atagggtgac cattacctgt		1320
cgggcctcgc aaagcatctc ctcgtacctc aactgggtatc agcaaaagcc gggaaaggcg		1380
cctaagctgc tgatctacgc cgcttcgagc ttgcaaagcg gggtgccatc cagattctcg		1440
ggatcagggt caggaaccga cttcacctg accgtgaaca gcctccagcc ggaggacttt		1500
gccacttact actgccagca gggagactcc gtgccgctta ctttcggggg gggtagccgc		1560
ctggagatca agaccactac ccagcaccg aggccaccca cccgggtcc taccatcgcc		1620
tcccagcctc tgtccctgcg tccggaggca tgtagaccg cagctgggtg ggcgtgcat		1680
acccggggtc ttgacttcgc ctgcgatatc tacatttggg cccctctggc tggtagctgc		1740
ggggtcctgc tgctttcact cgtgatcact ctttactgta agcgcgggtc gaagaagctg		1800
ctgtacatct ttaagcaacc cttcatgagg cctgtgcaga ctactcaaga ggaggacggc		1860
tggtcatgcc ggttcccaga ggaggaggaa ggcggctgcg aactgcgcgt gaaattcagc		1920
cgcagcgcag atgctccagc ctaccagcag gggcagaacc agctctacaa cgaactcaat		1980
cttggtcgga gagaggagta cgacgtgctg gacaagcgga gaggacggga cccagaaatg		2040
ggcgggaagc cgcgcagaaa gaatcccca gagggcctgt acaacgagct ccaaaaggat		2100
aagatggcag aagcctatag cgagattggg atgaaagggg aacgcagaag aggcaaaggc		2160
cacgacggac tgtaccaggg actcagcacc gccaccaagg acacctatga cgctcttcac		2220
atgcaggccc tgccgcctcg g		2241

<210> 1082
 <211> 2247
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1082	
atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg	60
cccaactcgt tggcactttc cctgactgcc gaccagatgg tgtccgccct tctggacgcc	120
gagcctccaa ttctgtactc ggagtagcat ccgactcgcc cgttctccga agccagcatg	180
atgggcctgt tgactaacct ggcggaccgc gagttggtgc acatgattaa ctgggctaag	240
cgggtgccgg gcttcgtgga cctggccctg cacgaccaag tgcacctcct ggaatgcgcc	300
tggatggaat tcctcatgat cggcctcgtg tggagatcca tggagcatcc cggaaagctc	360
ctgtttgcac ccaacctcct gcttgatcgc aaccagggaa aatgcgtgga aggggggtgtc	420
gagattttcg acatgctgct cgccacctct tcccggttcc ggatgatgaa tctgcaggga	480
gaagagttcg tgtgtctgaa gtcaatcatc ctgctgaact ccgggggtcta taccttcctg	540

	_SL	
agctcgaccc tcaagtcact ggaggaaaaa gaccacatcc atcgcggtgct cgataagatc	600	
accgacaccc ttatccatct catggcgaag gctggactga ccctgcaaca gcagcaccag	660	
aggctggccc agttgctgct gattctgagc cacatccggc acatgtcgtc caagaggatg	720	
gaacacctgt acagcatgaa gtgcaagaac gtcgtgcctc tgtccgatct gtccttgga	780	
atgctggacg cgcacagact cggaaccggc gcggaagacc cccggccctc caggaagcga	840	
aggtccctcg gagacgtggg tgaagtgcaa ttggtggaat cagggggagg attgtgcag	900	
cctggaggat cgctgagact gtcattgtgcc gtgtccggct ttgccctgtc caaccacggg	960	
atgtcctggg tccgccgcgc gcctggaaag ggcctcgaat ggggtgtcggg tattgtgtac	1020	
agcggtagca cctactatgc cgcattccgtg aaggggagat tcaccatcag ccgggacaac	1080	
tccaggaaca ctctgtacct ccaaataaat tcgctgaggc cagaggacac tgccatctac	1140	
tactgtccg cgcattggcg agagtccgac gtctggggac aggggaccac cgtgaccgtg	1200	
tctagcgcgt ccggcggagg cggcagcggg ggtcgggcat cagggggcg cggatcggac	1260	
atccagctca cccagtcctc gagctcgtg tccgcctccg tgggagatcg ggtcaccatc	1320	
acgtgccg cccagccagtc gatttcctcc tactgaact ggtaccaaca gaagcccga	1380	
aaagccccga agcttctcat ctacgccgc tcgagcctgc agtcaggagt gccctcacgg	1440	
ttctccggct ccggttccg tactgatttc accctgacca ttctctcct gcaaccggag	1500	
gacttcgcta ctactactg ccagcagtc tactccaccc cctacacttt cggacaaggc	1560	
accaaggtcg aaatcaagac cactaccca gcaccgaggc caccacccc ggctcctacc	1620	
atgcctccc agcctctgtc cctgcgtccg gaggcattga gaccgcagc tgggtggggcc	1680	
gtgcataccc ggggtcttga cttgcctgc gatattctaca ttggggccc tctggctggt	1740	
acttgccggg tcctgctgct ttactcgtg atcactcttt actgtaagcg cggtcggaag	1800	
aagctgctgt acatctttaa gcaaccctc atgaggcctg tgcagactac tcaagaggag	1860	
gacggctgtt catgccggtt cccagaggag gaggaaggcg gctgcgaact gcgcgtgaaa	1920	
ttcagccgca gcgcagatgc tccagcctac cagcaggggc agaaccagct ctacaacgaa	1980	
ctcaatcttg gtcggagaga ggagtacgac gtgctggaca agcggagagg acgggaccca	2040	
gaaatggg cggagccgc cagaaagaat cccaagagg gcctgtacaa cgagctccaa	2100	
aaggataaga tggcagaagc ctatagcgag attggtatga aaggggaacg cagaagaggc	2160	
aaaggccacg acggactgta ccagggactc agcaccgcca ccaaggacac ctatgacgct	2220	
cttcacatgc aggcctgcc gcctcgg	2247	

<210> 1083
 <211> 2247
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

_SL

<400> 1083
atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60
cccaactcgt tggcactttc cctgactgcc gaccagatgg tgtccgccct tctggacgcc 120
gagcctccaa ttctgtactc ggagtacgat ccgactcgcc cgttctccga agccagcatg 180
atgggcctgt tgactaacct ggcggaaccgc gagttggtgc acatgattaa ctgggctaag 240
cgggtgccgg gcttcgtgga cctgaccctg cagcaccaag tgcacctcct ggaatgcgcc 300
tggatggaaa tcctcatgat cggcctcgtg tggagatcca tggagcatcc cggaaagctc 360
ctgtttgcac ccaacctcct gcttgatcgc aaccaggga aatgcgtgga agggggtgtc 420
gagattttcg acatgctgct cgccacctct tcccggttcc ggatgatgaa tctgcaggga 480
gaagagtctg tgtgtctgaa gtcaatcatc ctgctgaact ccgggggtcta taccttcctg 540
agctcgaccc tcaagtcact ggaggaaaaa gaccacatcc atcgctgct cgataagatc 600
accgacaccc ttatccatct catggcgaag gctggactga ccctgcaaca gcagcaccag 660
aggctggccc agttgctgct gattctgagc cacatccggc acatgtcgaa caagaggatg 720
gaacacctgt acagcatgaa gtgcaagaac gtcgtgcctc tgtccgatct gtcctggaa 780
atgctggacg cgcacagact cggaaccggc gcggaagacc cccggccctc caggaagcga 840
aggccctcg gagacgtggg tgaagtcaa ttggtggaat cagggggagg acttgtgcag 900
cctggaggat cgctgagact gtcattgtgc gtgtccggct ttgccctgtc caaccacggg 960
atgtcctggg tccgccgcgc gcctggaaag ggcctcgaat ggggtgtcggg tattgtgtac 1020
agcggtagca cctactatgc cgcattccgtg aaggggagat tcaccatcag ccgggacaac 1080
tccaggaaca ctctgtacct ccaaatgaat tcgctgaggc cagaggacac tgccatctac 1140
tactgtccg cgcattggcg agagtccgac gtctggggac aggggaccac cgtgaccgtg 1200
tctagcgcgt ccggcggagg cggcagcggg ggtcgggcat cagggggcg cggatcggac 1260
atccagctca ccagtcctcc gagctcgtg tccgcctccg tgggagatcg ggtcaccatc 1320
acgtgccgcg ccagccagtc gatttcctcc tacctgaact ggtaccaaca gaagcccga 1380
aaagccccga agcttctcat ctacgccgc tcgagcctgc agtcaggagt gccctcacgg 1440
ttctccggct ccggttcgg tactgatttc accctgacca ttctctccct gcaaccggag 1500
gacttcgcta ctactactg ccagcagtcg tactccaccc cctacacttt cggacaaggc 1560
accaaggtcg aaatcaagac cactaccca gcaccaggc caccacccc ggctcctacc 1620
atgcctccc agcctctgtc cctgcgtccg gaggcattga gaccgcagc tgggtggggcc 1680
gtgcataccc ggggtcttga cttgcctgc gatattctaca tttgggcccc tctggctggt 1740
acttgccggg tcctgctgct ttactcgtg atcactcttt actgtaagcg cggtcggaag 1800
aagctgctgt acatctttaa gcaaccctc atgaggcctg tgcagactac tcaagaggag 1860
gacggctgtt catgccggtt cccagaggag gaggaaggcg gctgcgaact gcgcgtgaaa 1920
ttcagccgca gcgcagatgc tccagcctac cagcaggggc agaaccagct ctacaacgaa 1980

ctcaatcttg gtcggagaga ggagtagcac	gtgctggaca agcggagagg acgggaccca	2040
gaaatgggcg ggaagccgcg cagaaagaat	ccccaagagg gcctgtacaa cgagctccaa	2100
aaggataaga tggcagaagc ctatagcgag	attggtatga aaggggaacg cagaagaggc	2160
aaaggccacg acggactgta ccagggactc	agcaccgccca ccaaggacac ctatgacgct	2220
cttcacatgc aggccctgcc gcctcgg		2247

<210> 1084
 <211> 2229
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1084		
atggccctcc ctgtcaccgc cctgctgctt	ccgctggctc ttctgtcca cgccgctcgg	60
cccaactcgt tggcactttc cctgactgcc	gaccagatgg tgtccgccct tctggacgcc	120
gagcctccaa ttctgtactc ggagtagcat	ccgactcgcc cgttctccga agccagcatg	180
atgggcctgt tgactaacct ggcggaccgc	gagttggtgc acatgattaa ctgggctaag	240
cgggtgccgg gcttcgtgga cctggccctg	cacgaccaag tgcacctcct ggaatgcgcc	300
tggatggaaa tcctcatgat cggcctcgtg	tggagatcca tggagcatcc cggaagctc	360
ctgtttgcac ccaacctcct gcttgatcgc	aaccagggaa aatgcgtgga agggggtgtc	420
gagattttcg acatgctgct cgccacctct	tcccggttcc ggatgatgaa tctgcaggga	480
gaagagtctg tgtgtctgaa gtcaatcatc	ctgctgaact ccgggggtcta taccttcctg	540
agctcgaccc tcaagtcact ggaggaaaaa	gaccacatcc atcgctgct cgataagatc	600
accgacaccc ttatccatct catggcgaag	gctggactga ccctgcaaca gcagcaccag	660
aggctggccc agttgctgct gattctgagc	cacatccggc acatgtcgtc caagaggatg	720
gaacacctgt acagcatgaa gtgcaagaac	gtcgtgcctc tgtccgatct gtccttgaa	780
atgctggacg cgcacagact cgggacggga	gctgaagatc cacgaccag cagaaagcga	840
cgggaagtgc aattggtgga atcaggggga	ggacttgtgc agcctggagg atcgtgaga	900
ctgtcatgtg ccgtgtccgg ctttgccctg	tccaaccacg ggatgtcctg ggtccgccgc	960
gcgcctggaa agggcctcga atgggtgtcg	ggtatttgtt acagcggtag cacctactat	1020
gccgcatccg tgaaggggag attcaccatc	agccgggaca actccaggaa cactctgtac	1080
ctccaaatga attcgctgag gccagaggac	actgccatct actactgtc cgcgcatggc	1140
ggagagtccg acgtctgggg acaggggacc	accgtgaccg tgtctagcgc gtccggcgga	1200
ggcggcagcg ggggtcgggc atcagggggc	ggcggatcgg acatccagct caccagtc	1260
ccgagctcgc tgtccgcctc cgtgggagat	cgggtcacca tcacgtgccg cgccagccag	1320
tcgatttcct cctacctgaa ctggtaccaa	cagaagcccc gaaaagcccc gaagcttctc	1380

atctacgccg cctcgagcct gcagtcagga gtgccc ^{_SL} ctcac ggttctccgg ctccggttcc	1440
ggtactgatt tcaccctgac catttcctcc ctgcaaccgg aggacttcgc tacttactac	1500
tgccagcagt cgtactccac cccctacact ttcggaacaag gcaccaaggt cgaaatcaag	1560
accactaccc cagcaccgag gccacccacc ccggctccta ccatcgctc ccagcctctg	1620
tccctgcgtc cggaggcatg tagaccgcga gctggtgggg ccgtgcatac ccggggtctt	1680
gacttcgcct gcgatatcta catttgggcc cctctggctg gtacttgagg ggtcctgctg	1740
ctttcactcg tgatcactct ttactgtaag cgcggtcggg agaagctgct gtacatcttt	1800
aagcaaccct tcatgaggcc tgtgcagact actcaagagg aggacggctg ttcattgccg	1860
ttcccagagg aggaggaagg cggctgcgaa ctgcgcgtga aattcagccg cagcgcagat	1920
gctccagcct accagcaggg gcagaaccag ctctacaacg aactcaatct tggtcggaga	1980
gaggagtacg acgtgctgga caagcggaga ggacgggacc cagaaatggg cgggaagccg	2040
cgcagaaaga atccccaaga gggcctgtac aacgagctcc aaaaggataa gatggcagaa	2100
gcctatagcg agattggtat gaaaggggaa cgcagaagag gcaaaggcca cgacggactg	2160
taccagggac tcagcaccgc caccaaggac acctatgacg ctcttcacat gcaggccctg	2220
ccgcctcgg	2229

<210> 1085

<211> 2229

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1085

atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgtcca cgccgctcgg	60
cccaactcgt tggcactttc cctgactgcc gaccagatgg tgtccgccct tctggacgcc	120
gagcctccaa ttctgtactc ggagtacgat ccgactcgcc cgttctccga agccagcatg	180
atgggcctgt tgactaacct ggcggaccgc gagttggtgc acatgattaa ctgggctaag	240
cgggtgccgg gcttcgtgga cctgaccctg cagcaccgag tgcacctcct ggaatgcgcc	300
tggatggaat tcctcatgat cggcctcgtg tggagatcca tggagcatcc cggaaagctc	360
ctgtttgcac ccaacctcct gcttgatcgc aaccaggga aatgcgtgga agggggtgtc	420
gagattttcg acatgctgct cgccacctct tcccggttcc ggatgatgaa tctgcaggga	480
gaagagtctg tgtgtctgaa gtcaatcatc ctgctgaact ccgggggtcta taccttcctg	540
agctcgaccc tcaagtcact ggaggaaaaa gaccacatcc atcgctgct cgataagatc	600
accgacaccc ttatccatct catggcgaag gctggactga ccctgcaaca gcagcaccag	660
aggctggccc agttgctgct gattctgagc cacatccggc acatgtcgaa caagaggatg	720
gaacacctgt acagcatgaa gtgcaagaac gtcgtgcctc tgtccgatct gtccttgaa	780

	_SL	
atgctggacg cgcacagact cgggacggga gctgaagatc cagacccag cagaaagcga	840	
cggaagtgc aattggtgga atcaggggga ggacttgtgc agcctggagg atcgtgaga	900	
ctgtcatgtg ccgtgtccgg ctttgcctg tccaaccacg ggatgtcctg ggtccgccgc	960	
gcgctggaa agggcctcga atgggtgtcg ggtatttgtt acagcggtag cacctactat	1020	
gccgcatccg tgaaggggag attcaccatc agccgggaca actccaggaa cactctgtac	1080	
ctccaaatga attcgtgag gccagaggac actgccatct actactgctc cgcgcatggc	1140	
ggagagtccg acgtctgggg acaggggacc accgtgaccg tgtctagcgc gtccggcgga	1200	
ggcggcagcg ggggtcgggc atcagggggc ggcggtatcg acatccagct caccagttcc	1260	
ccgagctcgc tgtccgcctc cgtgggagat cgggtcacca tcacgtgccg cgccagccag	1320	
tcgatttcct cctacctgaa ctggtaccaa cagaagcccg gaaaagcccc gaagcttctc	1380	
atctacgccg cctcgagcct gcagtcagga gtgccctcac ggttctccgg ctccggttcc	1440	
ggtactgatt tcaccctgac catttcctcc ctgcaaccgg aggacttcgc tacttactac	1500	
tgccagcagt cgtactccac cccctacact ttccgacaag gcaccaaggt cgaaatcaag	1560	
accactaccc cagcaccgag gccaccacc ccggctccta ccatcgctc ccagcctctg	1620	
tccctgcgtc cggaggcatg tagaccgcga gctggtgggg ccgtgcatac ccggggtctt	1680	
gacttcgcct gcgatatcta catttgggcc cctctggctg gtacttgccg ggtcctgctg	1740	
ctttcactcg tgatcactct ttactgtaag cgcggtcggga agaagctgct gtacatcttt	1800	
aagcaaccct tcatgaggcc tgtgcagact actcaagagg aggacggctg ttcattgccg	1860	
ttcccagagg aggaggaagg cggctgcgaa ctgcgcgtga aattcagccg cagcgcagat	1920	
gctccagcct accagcaggg gcagaaccag ctctacaacg aactcaatct tggtcggaga	1980	
gaggagtacg acgtgctgga caagcggaga ggacgggacc cagaaatggg cggaagccg	2040	
cgcagaaaga atcccaaga gggcctgtac aacgagctcc aaaaggataa gatggcagaa	2100	
gcctatagcg agattggtat gaaaggggaa cgcagaagag gcaaaggcca cgacggactg	2160	
taccagggac tcagcaccgc caccaaggac acctatgacg ctcttcacat gcaggccctg	2220	
ccgcctcgg	2229	

<210> 1086

<211> 2256

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1086

atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgtcca cgccgctcgg	60
cccagatcgt tggcactttc cctgactgcc gaccagatgg tgtccgccct tctggacgcc	120
gagcctccaa ttctgtactc ggagtacgat ccgactcgcc cgttctccga agccagcatg	180

						_SL	
atgggcctgt	tgactaacct	ggcggaccgc	gagttggtgc	acatgattaa	ctgggctaag		240
cgggtgccgg	gcttcgtgga	cctggccctg	cacgaccaag	tgcacctcct	ggaatgcgcc		300
tggatggaaa	tcctcatgat	cggcctcgtg	tggagatcca	tggagcatcc	cggaaagctc		360
ctgtttgcac	ccaacctcct	gcttgatcgc	aaccagggaa	aatgcgtgga	agggggtgtc		420
gagattttcg	acatgctgct	cgccacctct	tcccggttcc	ggatgatgaa	tctgcaggga		480
gaagagttcg	tgtgtctgaa	gtcaatcatc	ctgctgaact	ccgggggtcta	taccttcctg		540
agctcgaccc	tcaagtcact	ggaggaaaaa	gaccacatcc	atcgcgctgct	cgataagatc		600
accgacaccc	ttatccatct	catggcgaag	gctggactga	ccctgcaaca	gcagcaccag		660
aggctggccc	agttgctgct	gattctgagc	cacatccggc	acatgtcgtc	caagaggatg		720
gaacacctgt	acagcatgaa	gtgcaagaac	gtcgtgcctc	tgtccgatct	gctcctggaa		780
atgctggacg	cgcacagact	cgggaaccggc	gcggaagacc	cccggccctc	caggaagcga		840
aggcccctcg	gagacgtggg	tgaaattgtg	atgaccagct	caccgcgccac	tcttagcctt		900
tcacccggtg	agcgcgcaac	cctgtcttgc	agagcctccc	aagacatctc	aaaatacctt		960
aattggtatc	aacagaagcc	cggacaggct	cctcgccttc	tgatctacca	caccagccgg		1020
ctccattctg	gaatccctgc	caggttcagc	ggtagcggat	ctgggaccga	ctacaccctc		1080
actatcagct	cactgcagcc	agaggacttc	gctgtctatt	tctgtcagca	agggaacacc		1140
ctgccctaca	cctttggaca	gggcaccaag	ctcgagatta	aagggtggagg	tggcagcgga		1200
ggaggtgggt	ccggcggtgg	aggaagccag	gtccaactcc	aagaaagcgg	accgggtctt		1260
gtgaagccat	cagaaactct	ttactgact	tgtactgtga	gcggagtgtc	tctccccgat		1320
tacggggtgt	cttggatcag	acagccaccg	gggaagggtc	tggaatggat	tggagtgatt		1380
tggggctctg	agactactta	ctactcttca	tcctcaagt	cacgcgtcac	catctcaaag		1440
gacaactcta	agaatcaggt	gtcactgaaa	ctgtcatctg	tgaccgcagc	cgacaccgcc		1500
gtgtactatt	gcgctaagca	ttactattat	ggcgggagct	acgcaatgga	ttactgggga		1560
cagggtactc	tggtcaccgt	gtccagcacc	actaccccag	caccgaggcc	accaccccgc		1620
gctcctacca	tcgcctccca	gcctctgtcc	ctgcgtccgg	aggcatgtag	accgcagct		1680
ggtggggccg	tgcatacccg	gggtcttgac	ttcgcttcgc	atatctacat	ttggggccct		1740
ctggctggta	cttgcggggg	cctgctgctt	tcactcgtga	tcactcttta	ctgtaagcgc		1800
ggtcggaaga	agctgctgta	catctttaag	caacccttca	tgaggcctgt	gcagactact		1860
caagaggagg	acggctgttc	atgccggttc	ccagaggagg	aggaaggcgg	ctgcgaactg		1920
cgcgtgaaat	tcagccgcag	cgcagatgct	ccagcctacc	agcaggggca	gaaccagctc		1980
tacaacgaac	tcaatcttgg	tcggagagag	gagtacgacg	tgctggacaa	gcggagagga		2040
cgggaccag	aaatgggcgg	gaagccgcgc	agaaagaatc	ccaagagggg	cctgtacaac		2100
gagctccaaa	aggataagat	ggcagaagcc	tatagcgaga	ttggtatgaa	aggggaacgc		2160
agaagaggca	aaggccacga	cggactgtac	cagggactca	gcaccgccac	caaggacacc		2220

tatgacgctc ttcacatgca ggccctgccg cctcgg^{_SL} 2256

<210> 1087
 <211> 2256
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1087
 atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60
 cccgagtcgt tggcactttc cctgactgcc gaccagatgg tgtccgccct tctggacgcc 120
 gagcctccaa ttctgtactc ggagtacgat ccgactcgcc cgttctccga agccagcatg 180
 atgggcctgt tgactaacct ggcggaaccgc gagttggtgc acatgattaa ctgggctaag 240
 cgggtgccgg gcttcgtgga cctgaccctg caccaccaag tgcacctcct ggaatgcgcc 300
 tggatggaaa tcctcatgat cggcctcgtg tggagatcca tggagcatcc cggaaagctc 360
 ctgtttgcac ccaacctcct gcttgatcgc aaccagggaa aatgcgtgga aggggggtgtc 420
 gagattttcg acatgctgct cgccacctct tcccggttcc ggatgatgaa tctgcaggga 480
 gaagagttcg tgtgtctgaa gtcaatcatc ctgctgaact ccgggggtcta taccttcctg 540
 agctcgaccc tcaagtcact ggaggaaaaa gaccacatcc atcgcgtgct cgataagatc 600
 accgacaccc ttatccatct catggcgaag gctggactga ccctgcaaca gcagcaccag 660
 aggctggccc agttgctgct gattctgagc cacatccggc acatgtcgaa caagaggatg 720
 gaacacctgt acagcatgaa gtgcaagaac gtcgtgcctc tgtccgatct gtcctggaa 780
 atgctggacg cgcacagact cggaaccggc gcggaagacc cccggccctc caggaagcga 840
 aggtccctcg gagacgtggg tgaaattgtg atgaccagc caccgcccac tcttagcctt 900
 tcacccggtg agcgcgcaac cctgtcttgc agagcctccc aagacatctc aaaatacctt 960
 aattggtatc aacagaagcc cggacaggct cctcgccttc tgatctacca caccagccgg 1020
 ctccattctg gaatccctgc caggttcagc ggtagcggat ctgggaccga ctacaccctc 1080
 actatcagct cactgcagcc agaggacttc gctgtctatt tctgtcagca agggaaacacc 1140
 ctgccctaca cttttggaca gggcaccaag ctcgagatta aaggtggagg tggcagcgga 1200
 ggaggtgggt ccggcggtgg aggaagccag gtccaactcc aagaaagcgg accgggtcctt 1260
 gtgaagccat cagaaactct ttcactgact tgtactgtga gcggagtgtc tctccccgat 1320
 tacggggtgt cttggatcag acagccaccg gggaagggtc tggaatggat tggagtgatt 1380
 tggggctctg agactactta ctactcttca tccctcaagt cacgcgtcac catctcaaag 1440
 gacaactcta agaatcaggt gtcactgaaa ctgtcatctg tgaccgcagc cgacaccgcc 1500
 gtgtactatt gcgctaagca ttactattat ggcgggagct acgcaatgga ttactgggga 1560
 cagggtactc tggtcaccgt gtccagcacc actaccccag caccgaggcc acccaccgcc 1620

gctcctacca	tcgcctccca	gcctctgtcc	ctg ^{_SL} cggtccgg	aggcatgtag	acccgcagct	1680
ggtggggccg	tgcataccg	gggtcttgac	ttcgctgcg	atatctacat	ttgggccct	1740
ctggctggta	cttgcggggt	cctgctgctt	tcactcgtga	tcactcttta	ctgtaagcgc	1800
ggtcgggaaga	agctgctgta	catctttaag	caacccttca	tgaggcctgt	gcagactact	1860
caagaggagg	acggctgttc	atgccggttc	ccagaggagg	aggaaggcgg	ctgcgaactg	1920
cgcgtgaaat	tcagccgcag	cgcagatgct	ccagcctacc	agcaggggca	gaaccagctc	1980
tacaacgaac	tcaatcttgg	tcggagagag	gagtacgacg	tgctggacaa	gcggagagga	2040
cgggaccag	aaatgggcgg	gaagccgcgc	agaaagaatc	cccaagaggg	cctgtacaac	2100
gagctccaaa	aggataagat	ggcagaagcc	tatagcgaga	ttggtatgaa	aggggaacgc	2160
agaagaggca	aaggccacga	cggactgtac	cagggactca	gcaccgccac	caaggacacc	2220
tatgacgctc	ttcacatgca	ggccctgccg	cctcgg			2256

<210> 1088

<211> 2238

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1088

atggccctcc	ctgtcaccgc	cctgctgctt	ccgctggctc	ttctgctcca	cgccgctcgg	60
cccgagtcgt	tggcactttc	cctgactgcc	gaccagatgg	tgtccgccct	tctggacgcc	120
gagcctccaa	ttctgtactc	ggagtacgat	ccgactcgcc	cgttctccga	agccagcatg	180
atgggcctgt	tgactaacct	ggcggaccgc	gagttggtgc	acatgattaa	ctgggctaag	240
cgggtgccgg	gcttcgtgga	cctggccctg	cacgaccaag	tgcacctcct	ggaatgcgcc	300
tggatggaaa	tcctcatgat	cggcctcgtg	tggagatcca	tggagcatcc	cggaaagctc	360
ctgtttgcac	ccaacctcct	gcttgatcgc	aaccagggaa	aatgcgtgga	agggggtgtc	420
gagattttcg	acatgctgct	cgccacctct	tcccggttcc	ggatgatgaa	tctgcaggga	480
gaagagttcg	tgtgtctgaa	gtcaatcatc	ctgctgaact	ccgggggtcta	taccttcctg	540
agctcgaccc	tcaagtcact	ggaggaaaaa	gaccacatcc	atcgcgctgct	cgataagatc	600
accgacaccc	ttatccatct	catggcgaag	gctggactga	ccctgcaaca	gcagcaccag	660
aggctggccc	agttgctgct	gattctgagc	cacatccggc	acatgtcgtc	caagaggatg	720
gaacacctgt	acagcatgaa	gtgcaagaac	gtcgtgcctc	tgtccgatct	gctcctggaa	780
atgctggacg	cgcacagact	cgggacggga	gctgaagatc	cacgaccag	cagaaagcga	840
cgggaaattg	tgatgacca	gtcaccgcc	actcttagcc	tttcaccgg	tgagcgcgca	900
accctgtctt	gcagagcctc	ccaagacatc	tcaaaatacc	ttaattggta	tcaacagaag	960
cccggacagg	ctcctcgcct	tctgatctac	cacaccagcc	ggctccattc	tggaatccct	1020

	_SL	
gccaggttca gcggtagcgg atctgggacc gactacaccc tcactatcag ctactgcag	1080	
ccagaggact tcgctgtcta tttctgtcag caaggggaaca ccctgcccta cacctttgga	1140	
cagggcacca agctcgagat taaaggtgga ggtggcagcg gaggaggtgg gtccggcggg	1200	
ggaggaagcc aggtccaact ccaagaaagc ggaccgggtc ttgtgaagcc atcagaaact	1260	
ctttcactga cttgtactgt gagcggagtg tctctccccg attacggggg gtcttggatc	1320	
agacagccac cggggaaggg tctggaatgg attggagtga tttggggctc tgagactact	1380	
tactactctt catccctcaa gtcacgcgtc accatctcaa aggacaactc taagaatcag	1440	
gtgtcactga aactgtcatc tgtgaccgca gccgacaccg ccgtgtacta ttgcgctaag	1500	
cattactatt atggcgggag ctacgcaatg gattactggg gacagggtac tctggtcacc	1560	
gtgtccagca ccactacccc agcaccgagg ccacccaccc cggctcctac catcgctcc	1620	
cagcctctgt ccctgcgtcc ggaggcatgt agaccgcgag ctgggtggggc cgtgcatacc	1680	
cggggctctt acttcgcctg cgatatctac atttggggcc ctctggctgg tacttgcggg	1740	
gtcctgctgc tttcactcgt gatcactctt tactgtaagc gcggtcggaa gaagctgctg	1800	
tacatcttta agcaaccctt catgaggcct gtgcagacta ctcaagagga ggacggctgt	1860	
tcatgccggt tcccagagga ggaggaaggc ggctgcgaac tgcgcgtgaa attcagccgc	1920	
agcgcagatg ctccagccta ccagcagggg cagaaccagc tctacaacga actcaatctt	1980	
ggtcggagag aggagtacga cgtgctggac aagcggagag gacgggaccc agaaatgggc	2040	
gggaagccgc gcagaaagaa tccccaagag ggcctgtaca acgagctcca aaaggataag	2100	
atggcagaag cctatagcga gattggtatg aaaggggaac gcagaagagg caaaggccac	2160	
gacggactgt accagggact cagcaccgcc accaaggaca cctatgacgc tcttcacatg	2220	
caggccctgc cgcctcgg	2238	

<210> 1089

<211> 2238

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1089

atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg	60
cccagatcgt tggcactttc cctgactgcc gaccagatgg tgtccgccct tctggacgcc	120
gagcctccaa ttctgtactc ggagtacgat ccgactcgcc cgttctccga agccagcatg	180
atgggcctgt tgactaacct ggcggaaccgc gagttggtgc acatgattaa ctgggctaag	240
cgggtgccgg gcttcgtgga cctgaccctg cagcaccaag tgcacctcct ggaatgcgcc	300
tggatggaaa tcctcatgat cggcctcgtg tggagatcca tggagcatcc cggaaagctc	360
ctgtttgcac ccaacctcct gcttgatcgc aaccagggaa aatgcgtgga aggggggtgc	420

	_SL	
gagatttttcg	acatgctgct	cgccacctct
gaagagttcg	tgtgtctgaa	gtcaatcatc
agctcgaccc	tcaagtcact	ggaggaaaaa
accgacaccc	ttatccatct	catggcgaag
aggctggccc	agttgctgct	gattctgagc
gaacacctgt	acagcatgaa	gtgcaagaac
atgctggacg	cgcacagact	cgggacggga
cgggaaattg	tgatgaccca	gtcaccgcgc
accctgtctt	gcagagcctc	ccaagacatc
cccggacagg	ctcctcgctt	tctgatctac
gccaggttca	gcggtagcgg	atctgggacc
ccagaggact	tcgctgtcta	tttctgtcag
cagggcacca	agctcgagat	taaaggtgga
ggaggaagcc	aggtccaact	ccaagaaagc
ctttcactga	cttgtactgt	gagcggagtg
agacagccac	cggggaaggg	tctggaatgg
tactactctt	catccctcaa	gtcacgcgtc
gtgtcactga	aactgtcatc	tgtgaccgca
cattactatt	atggcgggag	ctacgcaatg
gtgtccagca	ccactacccc	agcaccgagg
cagcctctgt	ccctgcgtcc	ggaggcatgt
cggggctctg	acttcgcctg	cgatatctac
gtcctgctgc	tttcactcgt	gatcactctt
tacatcttta	agcaaccctt	catgaggcct
tcatgccggt	tcccagagga	ggaggaaggc
agcgcagatg	ctccagccta	ccagcagggg
ggtcggagag	aggagtacga	cgtgctggac
gggaagccgc	gcagaaagaa	tccccaagag
atggcagaag	cctatagcga	gattggtatg
gacggactgt	accagggact	cagcaccgcc
caggccctgc	cgctctcg	

<210> 1090
 <211> 2259
 <212> DNA
 <213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1090

atggccctcc	ctgtcaccgc	cctgctgctt	ccgctggctc	ttctgctcca	cgccgctcgg	60
cccgagtcgt	tggcactttc	cctgactgcc	gaccagatgg	tgtccgccct	tctggacgcc	120
gagcctcaa	ttctgtactc	ggagtacgat	ccgactcgcc	cgttctccga	agccagcatg	180
atgggcctgt	tgactaacct	ggcggaccgc	gagttggtgc	acatgattaa	ctgggctaag	240
cggtgcccgg	gcttcgtgga	cctggccctg	cacgaccaag	tgcacctcct	ggaatgcgcc	300
tggatgaaa	tcctcatgat	cggcctcgtg	tggagatcca	tggagcatcc	cggaagctc	360
ctgtttgcac	ccaacctcct	gcttgatcgc	aaccagggaa	aatgcgtgga	agggggtgtc	420
gagattttcg	acatgctgct	cgccacctct	tcccgtttcc	ggatgatgaa	tctgcaggga	480
gaagagtctg	tgtgtctgaa	gtcaatcatc	ctgctgaact	ccggggtcta	taccttcctg	540
agctcgaccc	tcaagtcact	ggaggaaaaa	gaccacatcc	atcgctgct	cgataagatc	600
accgacaccc	ttatccatct	catggcgaag	gctggactga	ccctgcaaca	gcagcaccag	660
aggctggccc	agttgctgct	gattctgagc	cacatccggc	acatgtcgtc	caagaggatg	720
gaacacctgt	acagcatgaa	gtgcaagaac	gtcgtgcctc	tgtccgatct	gctcctggaa	780
atgctggacg	cgcacagact	cggaaccggc	gcggaagacc	cccggccctc	caggaagcga	840
aggcccctcg	gagacgtggg	tcaagtgcaa	ctcgtccaaa	gcggagcgga	agtcaagaaa	900
cccggagcga	gcgtgaaagt	gtcctgcaaa	gcctccggct	acacctttac	gggctactac	960
atgcactggg	tgcgccaggc	accaggacag	ggtcttgaat	ggatgggatg	gatcaaccct	1020
aattcgggcg	gaactaacta	cgcacagaag	ttccagggga	gagtgactct	gactcgggat	1080
acctccatct	caactgtcta	catggaactc	tcccgtttgc	ggtcagatga	tacggcagtg	1140
tactactgcg	cccgcgacat	gaatatcctg	gctaccgtgc	cgttcgacat	ctggggacag	1200
gggactatgg	ttactgtctc	atcgggcggg	ggaggttcag	gaggaggcgg	ctcgggaggc	1260
ggaggttcgg	acattcagat	gaccagtc	ccatcctctc	tgtcggccag	cgtcggagat	1320
agggtgacca	ttacctgtcg	ggcctcgcaa	agcatctcct	cgtacctcaa	ctggtatcag	1380
caaaagccgg	gaaaggcgcc	taagctgctg	atctacgccg	cttcgagctt	gcaaagcggg	1440
gtgccatcca	gattctcggg	atcaggctca	ggaaccgact	tcaccctgac	cgtgaacagc	1500
ctccagccgg	aggactttgc	cacttactac	tgccagcagg	gagactccgt	gccgcttact	1560
ttcggggggg	gtacccgcct	ggagatcaag	accactaccc	cagcaccgag	gccaccacc	1620
ccggctccta	ccatcgctc	ccagcctctg	tccctgcgtc	cggaggcatg	tagaccgcga	1680
gctgggtggg	ccgtgcatac	ccggggtctt	gacttcgcct	gcgatattcta	catttgggcc	1740
cctctggctg	gtacttgcg	ggtcctgctg	ctttcactcg	tgatcactct	ttactgtaag	1800
cgcggtcgg	agaagctgct	gtacatcttt	aagcaaccct	tcatgaggcc	tgtgcagact	1860

	_SL	
actcaagagg	aggacggctg	ttcatgccgg
ctgcgcgtga	aattcagccg	cagcgcagat
ctctacaacg	aactcaatct	tggtcggaga
ggacgggacc	cagaaatggg	cggaagccg
aacgagctcc	aaaaggataa	gatggcagaa
cgcagaagag	gcaaaggcca	cgacggactg
acctatgacg	ctcttcacat	gcaggccctg

<210> 1091
 <211> 2259
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1091	
atggccctcc	ctgtcaccgc
cccagatcgt	tggcactttc
gagcctccaa	ttctgtactc
atgggcctgt	tgactaacct
cggtgccc	gcttcgtgga
tggatggaaa	tcctcatgat
ctgtttgcac	ccaacctcct
gagattttcg	acatgctgct
gaagagttcg	tgtgtctgaa
agctcgaccc	tcaagtcact
accgacaccc	ttatccatct
aggctggccc	agttgctgct
gaacacctgt	acagcatgaa
atgctggacg	cgcacagact
aggtccctcg	gagacgtggg
cccggagcga	gcgtgaaagt
atgcactggg	tgcgccaggc
aattcgggcg	gaactaacta
acctccatct	caactgtcta
tactactgcg	cccgcgacat
gggactatgg	ttactgtctc

ggaggttcgg	acattcagat	gaccagtc	ccatcctctc	tgctggccag	cgctggagat	1320
agggtgacca	ttacctgtcg	ggcctcgcaa	agcatctcct	cgtacctcaa	ctggtatcag	1380
caaaagccgg	gaaaggcgcc	taagctgctg	atctacgccg	cttcgagctt	gcaaagcggg	1440
gtgccatcca	gattctcggg	atcaggctca	ggaaccgact	tcaccctgac	cgtgaacagc	1500
ctccagccgg	aggactttgc	cacttactac	tgccagcagg	gagactccgt	gccgcttact	1560
ttcggggggg	gtaccgcct	ggagatcaag	accactacce	cagcaccgag	gccacccacc	1620
ccggctccta	ccatcgctc	ccagcctctg	tccttgcgtc	cggaggcatg	tagaccgcga	1680
gctggtgggg	ccgtgcatac	ccggggtctt	gacttcgcct	gcgatatcta	catttggggc	1740
cctctggctg	gtacttgctg	ggctctgctg	ctttcactcg	tgatcactct	ttactgtaag	1800
cgcggtcggg	agaagctgct	gtacatcttt	aagcaaccct	tcattgaggcc	tgtgcagact	1860
actcaagagg	aggacggctg	ttcatgccgg	ttcccagagg	aggaggaagg	cggtgcgaa	1920
ctgcgcgtga	aattcagccg	cagcgcagat	gctccagcct	accagcaggg	gcagaaccag	1980
ctctacaacg	aactcaatct	tggtcggaga	gaggagtacg	acgtgctgga	caagcggaga	2040
ggacgggacc	cagaaatggg	cggaagccg	cgcagaaaga	atccccaaga	gggcctgtac	2100
aacgagctcc	aaaaggataa	gatggcagaa	gcctatagcg	agattggtat	gaaaggggaa	2160
cgcagaagag	gcaaaggcca	cgacggactg	taccagggac	tcagcaccgc	caccaaggac	2220
acctatgacg	ctcttcacat	gcaggccctg	ccgcctcgg			2259

<210> 1092

<211> 2241

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1092

atggccctcc	ctgtcaccgc	cctgctgctt	ccgctggctc	ttctgctcca	cgccgctcgg	60
cccagatcgt	tggcactttc	cctgactgcc	gaccagatgg	tgtccgccct	tctggacgcc	120
gagcctccaa	ttctgtactc	ggagtacgat	ccgactcgcc	cgttctccga	agccagcatg	180
atgggcctgt	tgactaacct	ggcggaccgc	gagttggtgc	acatgattaa	ctgggctaag	240
cgggtgccgg	gcttcgtgga	cctggccctg	cacgaccaag	tgcacctcct	ggaatgcgcc	300
tggatggaaa	tcctcatgat	cggcctcgtg	tggagatcca	tggagcatcc	cggaagctc	360
ctgtttgcac	ccaacctcct	gcttgatcgc	aaccagggaa	aatgcgtgga	agggggtgtc	420
gagattttcg	acatgctgct	cgccacctct	tcccggttcc	ggatgatgaa	tctgcaggga	480
gaagagttcg	tgtgtctgaa	gtcaatcatc	ctgctgaact	ccggggtcta	taccttcctg	540
agctcgaccc	tcaagtcact	ggaggaaaaa	gaccacatcc	atcgctgct	cgataagatc	600
accgacaccc	ttatccatct	catggcgaag	gctggactga	ccctgcaaca	gcagcaccag	660

	_SL	
aggctggccc agttgctgct gattctgagc cacatccggc acatgtcgtc caagaggatg	720	
gaacacctgt acagcatgaa gtgcaagaac gtcgtgcctc tgtccgatct gtccttgaa	780	
atgctggacg cgcacagact cggaaccggc gcggaagacc cccggccctc caggaagcga	840	
aggcaagtgc aactcgtcca aagcggagcg gaagtcaaga aaccgggagc gagcgtgaaa	900	
gtgtcctgca aagcctccgg ctacaccttt acgggctact acatgcactg ggtgcgccag	960	
gcaccaggac agggctcttga atggatggga tggatcaacc ctaattcggg cggaactaac	1020	
tacgcacaga agttccaggg gagagtgact ctgactcggg atacctccat ctcaactgtc	1080	
tacatggaac tctcccgtt gcggtcagat gatacggcag tgtactactg cgcccgcgac	1140	
atgaatatcc tggctaccgt gccgttcgac atctggggac aggggactat ggttactgtc	1200	
tcatcgggcg gtggagggttc aggaggaggc ggctcgggag gcggagggttc ggacattcag	1260	
atgacccagt ccccatcctc tctgtcggcc agcgtcggag atagggtgac cattacctgt	1320	
cgggcctcgc aaagcatctc ctcgtacctc aactggtatc agcaaaagcc gggaaaggcg	1380	
cctaagctgc tgatctacgc cgcttcgagc ttgcaaagcg gggtgccatc cagattctcg	1440	
ggatcaggct caggaaccga cttcacctg accgtgaaca gcctccagcc ggaggacttt	1500	
gccacttact actgccagca gggagactcc gtgccgctta ctttcggggg gggtagccgc	1560	
ctggagatca agaccactac cccagcaccg aggccacca cccgggtcc taccatcgcc	1620	
tcccagcctc tgtccctgcg tccggaggca tgtagaccg cagctggtgg ggccgtgcat	1680	
acccggggtc ttgacttcgc ctgcgatatc tacatttggg cccctctggc tggtagttgc	1740	
ggggtcctgc tgctttcact cgtgatcact ctttactgta agcgcggtcg gaagaagctg	1800	
ctgtacatct ttaagcaacc cttcatgagg cctgtgcaga ctactcaaga ggaggacggc	1860	
tgttcatgcc ggttcccaga ggaggaggaa ggcggctgcg aactgcgcgt gaaattcagc	1920	
cgcagcgag atgctccagc ctaccagcag ggcagaacc agctctacaa cgaactcaat	1980	
cttggtcggga gagaggagta cgacgtgctg gacaagcgga gaggacggga cccagaaatg	2040	
ggcgggaagc cgcgcagaaa gaatcccaa gagggcctgt acaacgagct ccaaaaggat	2100	
aagatggcag aagcctatag cgagattggt atgaaagggg aacgcagaag aggcaaaggc	2160	
cacgacggac tgtaccaggg actcagcacc gccaccaagg acacctatga cgctcttcac	2220	
atgcaggccc tgccgcctcg g	2241	

<210> 1093

<211> 2241

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1093

atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg	60
---	----

						_SL	
cccgagtcgt	tggcactttc	cctgactgcc	gaccagatgg	tgtccgccct	tctggacgcc		120
gagcctccaa	ttctgtactc	ggagtacgat	ccgactcgcc	cgttctccga	agccagcatg		180
atgggcctgt	tgactaacct	ggcggaccgc	gagttggtgc	acatgattaa	ctgggctaag		240
cgggtgccgg	gcttcgtgga	cctgaccctg	cacgaccaag	tgcacctcct	ggaatgcgcc		300
tggatggaaa	tcctcatgat	cggcctcgtg	tggagatcca	tggagcatcc	cgaaaagctc		360
ctgtttgcac	ccaacctcct	gcttgatcgc	aaccagggaa	aatgcgtgga	agggggtgtc		420
gagattttcg	acatgctgct	cgccacctct	tcccggttcc	ggatgatgaa	tctgcaggga		480
gaagagttcg	tgtgtctgaa	gtcaatcatc	ctgctgaact	ccgggggtcta	taccttcctg		540
agctcgaccc	tcaagtcact	ggaggaaaaa	gaccacatcc	atcgctgct	cgataagatc		600
accgacaccc	ttatccatct	catggcgaag	gctggactga	ccctgcaaca	gcagcaccag		660
aggctggccc	agttgctgct	gattctgagc	cacatccggc	acatgtcgaa	caagaggatg		720
gaacacctgt	acagcatgaa	gtgcaagaac	gtcgtgcctc	tgtccgatct	gctcctggaa		780
atgctggacg	cgcacagact	cgggacggga	gctgaagatc	cacgaccag	cagaaagcga		840
cggcaagtgc	aactcgtcca	aagcggagcg	gaagtcaaga	aaccgggagc	gagcgtgaaa		900
gtgtcctgca	aagcctccgg	ctacaccttt	acgggctact	acatgactg	ggtgcgccag		960
gcaccaggac	agggctctga	atggatggga	tggatcaacc	ctaattcggg	cggaactaac		1020
tacgcacaga	agttccaggg	gagagtgact	ctgactcggg	atacctccat	ctcaactgtc		1080
tacatggaac	tctcccgctt	gcggtcagat	gatacggcag	tgtactactg	cgcccgcgac		1140
atgaatatcc	tggctaccgt	gccgttcgac	atctggggac	aggggactat	ggttactgtc		1200
tcacgggcg	gtggagggttc	aggaggaggc	ggctcgggag	gcggagggttc	ggacattcag		1260
atgaccaggt	ccccatcctc	tctgtcggcc	agcgtcggag	atagggtgac	cattacctgt		1320
cgggcctcgc	aaagcatctc	ctcgtacctc	aactggtatc	agcaaaagcc	gggaaaggcg		1380
cctaagctgc	tgatctacgc	cgcttcgagc	ttgcaaagcg	gggtgccatc	cagattctcg		1440
ggatcaggct	caggaaccga	cttcaccctg	accgtgaaca	gcctccagcc	ggaggacttt		1500
gccacttact	actgccagca	gggagactcc	gtgccgctta	ctttcggggg	gggtaccgcg		1560
ctggagatca	agaccactac	cccagcaccg	aggccacca	ccccggctcc	taccatcgcc		1620
tcccagcctc	tgtccctgcg	tccggaggca	tgtagaccgc	cagctggtgg	ggccgtgcat		1680
accgggggtc	ttgacttcgc	ctgcgatatc	tacatttggt	cccctctggc	tggtacttgc		1740
ggggtcctgc	tgctttcact	cgtgatcact	ctttactgta	agcgcggctc	gaagaagctg		1800
ctgtacatct	ttaagcaacc	cttcatgagg	cctgtgcaga	ctactcaaga	ggaggacggc		1860
tgttcatgcc	ggttcccaga	ggaggaggaa	ggcggctgcg	aactgcgcgt	gaaattcagc		1920
cgcagcgag	atgctccagc	ctaccagcag	gggcagaacc	agctctacaa	cgaactcaat		1980
cttggtcggg	gagaggagta	cgacgtgctg	gacaagcgga	gaggacggga	cccagaaatg		2040
ggcgggaagc	cgcgcagaaa	gaatccccaa	gagggcctgt	acaacgagct	ccaaaaggat		2100

aagatggcag aagcctatag cgagattggt atgaaagggg aacgcagaag aggcaaaggc	2160
cacgacggac tgtaccaggg actcagcacc gccaccaagg acacctatga cgctcttcac	2220
atgcaggccc tgccgcctcg g	2241

<210> 1094
 <211> 2247
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1094	
atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg	60
cccgagtcgt tggcactttc cctgactgcc gaccagatgg tgtccgccct tctggacgcc	120
gagcctccaa ttctgtactc ggagtacgat ccgactcgcc cgttctccga agccagcatg	180
atgggcctgt tgactaacct ggcggaccgc gagttggtgc acatgattaa ctgggctaag	240
cgggtgccgg gcttcgtgga cctggccctg caccaccaag tgcacctcct ggaatgcgcc	300
tggatgga aa tcctcatgat cggcctcgtg tggagatcca tggagcatcc cggaagctc	360
ctgtttgcac ccaacctcct gcttgatcgc aaccagggaa aatgcgtgga agggggtgtc	420
gagattttcg acatgctgct cgccacctct tcccggttcc ggatgatgaa tctgcaggga	480
gaagagtctg tgtgtctgaa gtcaatcatc ctgctgaact ccgggggtcta taccttcctg	540
agctcgaccc tcaagtcact ggaggaaaaa gaccacatcc atcgctgct cgataagatc	600
accgacaccc ttatccatct catggcgaag gctggactga ccctgcaaca gcagcaccag	660
aggctggccc agttgctgct gattctgagc cacatccggc acatgtcgtc caagaggatg	720
gaacacctgt acagcatgaa gtgcaagaac gtcgtgcctc tgtccgatct gtccttgaa	780
atgctggacg cgcacagact cggaaccggc gcggaagacc cccggccctc caggaagcga	840
aggcccctcg gagacgtggg tgaagtgcaa ttggtggaat cagggggagg acttggtcag	900
cctggaggat cgctgagact gtcattgtcc gtgtccggct ttgccctgtc caaccacggg	960
atgtcctggg tccgccgcgc gcctggaaag ggcctcgaat ggggtgtcggg tattgtgtac	1020
agcggtagca cctactatgc cgcattccgtg aaggggagat tcaccatcag ccgggacaac	1080
tccaggaaca ctctgtacct ccaaataaat tcgctgaggc cagaggacac tgccatctac	1140
tactgtccg cgcattggcg agagtccgac gtctggggac aggggaccac cgtgaccgtg	1200
tctagcgcgt ccggcggagg cggcagcggg ggtcgggcat cagggggcgg cggatcggac	1260
atccagctca ccagtcctcc gagctcgtg tccgcctccg tgggagatcg ggtcaccatc	1320
acgtgcccg ccagccagtc gatttcctcc tacctgaact ggtaccaaca gaagcccga	1380
aaagccccga agcttctcat ctacgccgc tcgagcctgc agtcaggagt gccctcacgg	1440
ttctccggct ccggttcgg tactgatttc accctgacca tttcctccct gcaaccggag	1500

	_SL	
gacttcgcta cttactactg ccagcagtcg tactccaccc cctacacttt cggacaaggc	1560	
accaaggtcg aaatcaagac cactacccca gcaccgaggc caccaccccc ggctcctacc	1620	
atcgctccc agcctctgtc cctgcgtccg gaggcattga gaccgcagc tgggtggggcc	1680	
gtgcataccc ggggtcttga cttcgctgc gatattctaca tttgggcccc tctggctggt	1740	
acttgcgggg tcctgctgct ttcactcgtg atcactcttt actgtaagcg cggtcggaag	1800	
aagctgctgt acatctttaa gcaacccttc atgaggcctg tgcagactac tcaagaggag	1860	
gacggctgtt catgccggtt cccagaggag gaggaaggcg gctgcgaact gcgcgtgaaa	1920	
ttcagccgca gcgcagatgc tccagcctac cagcaggggc agaaccagct ctacaacgaa	1980	
ctcaatcttg gtcggagaga ggagtacgac gtgctggaca agcggagagg acgggaccca	2040	
gaaatgggcg ggaagccgcg cagaaagaat cccaagagg gcctgtacaa cgagctccaa	2100	
aaggataaga tggcagaagc ctatagcgag attggtatga aaggggaacg cagaagaggc	2160	
aaaggccacg acggactgta ccagggactc agcaccgcc ccaaggacac ctatgacgt	2220	
cttcacatgc aggcctgcc gcctcgg	2247	

<210> 1095

<211> 2247

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1095

atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgtcca cgccgctcgg	60
cccagagtcgt tggcactttc cctgactgcc gaccagatgg tgtccgccct tctggacgcc	120
gagcctccaa ttctgtactc ggagtacgat ccgactcgcc cgttctccga agccagcatg	180
atgggcctgt tgactaacct ggcgaccgc gagttggtgc acatgattaa ctgggctaag	240
cgggtgccgg gcttcgtgga cctgaccctg cagcaccaag tgcacctcct ggaatgcgcc	300
tggatgga aa tcctcatgat cggcctcgtg tggagatcca tggagcatcc cgaaaagctc	360
ctgtttgcac ccaacctcct gcttgatcgc aaccaggga aatgcgtgga agggggtgtc	420
gagattttcg acatgctgct cgccacctct tcccggttcc ggatgatgaa tctgcaggga	480
gaagagtctg tgtgtctgaa gtcaatcatc ctgctgaact ccgggggtcta taccttcctg	540
agctcgaccc tcaagtcact ggaggaaaaa gaccacatcc atcgctgct cgataagatc	600
accgacaccc ttatccatct catggcgaag gctggactga ccctgcaaca gcagcaccag	660
aggctggccc agttgctgct gattctgagc cacatccggc acatgtcgaa caagaggatg	720
gaacacctgt acagcatgaa gtgcaagaac gtcgtgcctc tgtccgatct gtcctggaa	780
atgctggacg cgcacagact cggaaccggc gcggaagacc cccggccctc caggaagcga	840
aggtccctcg gagacgtggg tgaagtgcaa ttggtggaat cagggggagg acttgtgcag	900

	_SL	
cctggaggat cgctgagact gtcattgtgcc gtgtccggct ttgccctgtc caaccacggg	960	
atgtcctggg tccgccgcgc gcctggaaag ggcctcgaat ggggtgtcggg tatttgtgtac	1020	
agcggtagca cctactatgc cgcattccgtg aaggggagat tcaccatcag ccgggacaac	1080	
tccaggaaca ctctgtacct ccaaataaat tcgctgaggc cagaggacac tgccatctac	1140	
tactgtcccg cgcattggcg agagtccgac gtctggggac aggggaccac cgtgaccgtg	1200	
tctagcgcgt ccggcggagg cggcagcggg ggtcggggcat cagggggcg cggatcggac	1260	
atccagctca cccagtcccc gagctcgtg tccgcctccg tgggagatcg ggtcaccatc	1320	
acgtgccgcg ccagccagtc gatttcctcc tactgaact ggtaccaaca gaagcccga	1380	
aaagccccga agcttctcat ctacgccgc tcgagcctgc agtcaggagt gccctcacgg	1440	
ttctccggct ccggttccg tactgatttc accctgacca ttctctccct gcaaccggag	1500	
gacttcgcta ctactactg ccagcagtcg tactccaccc cctacacttt cggacaaggc	1560	
accaaggtcg aaatcaagac cactaccca gcaccgaggc caccacccc ggctcctacc	1620	
atgcctccc agcctctgtc cctgcgtccg gaggcattga gaccgcagc tgggtggggcc	1680	
gtgcataccc ggggtcttga cttgcctgc gatattctaca ttggggccc tctggctggt	1740	
acttgccggg tcctgtctgt ttactcgtg atcactcttt actgtaagcg cggtcggaag	1800	
aagctgctgt acatctttaa gcaaccctt atgaggcctg tgcagactac tcaagaggag	1860	
gacggctgtt catgccggtt ccagaggag gaggaaggcg gctgcgaact gcgcgtgaaa	1920	
ttcagccgca gcgcagatgc tccagcctac cagcaggggc agaaccagct ctacaacgaa	1980	
ctcaatcttg gtcggagaga ggagtacgac gtgctggaca agcggagagg acgggaccca	2040	
gaaatgggcg ggaagccgcg cagaaagaat cccaagagg gcctgtacaa cgagctccaa	2100	
aaggataaga tggcagaagc ctatagcgag attggtatga aaggggaacg cagaagaggc	2160	
aaaggccacg acggactgta ccagggactc agcaccgcca ccaaggacac ctatgacgct	2220	
cttcacatgc aggccctgcc gcctcgg	2247	

<210> 1096

<211> 2229

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1096

atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgtcca cgccgctcgg	60
cccagatcgt tggcactttc cctgactgcc gaccagatgg tgtccgccct tctggacgcc	120
gagctccaa ttctgtactc ggagtacgat ccgactcgcc cgttctccga agccagcatg	180
atgggcctgt tgactaacct ggcggaccgc gagttggtgc acatgattaa ctgggctaag	240
cgggtgccgg gcttcgtgga cctggccctg cagaccaag tgcacctcct ggaatgcgcc	300

tggatgga	aa	tcctcatgat	cggcctcgtg	tggagatcca	tggagcatcc	cggaagctc	360
ctgtttgcac	ccaacctcct	gcttgatcgc	aaccagggaa	aatgcgtgga	agggggtgtc		420
gagattttcg	acatgctgct	cgccacctct	tcccggttcc	ggatgatgaa	tctgcaggga		480
gaagagttcg	tgtgtctgaa	gtcaatcatc	ctgctgaact	ccgggggtcta	taccttcctg		540
agctcgaccc	tcaagtcact	ggaggaaaaa	gaccacatcc	atcgcgtgct	cgataagatc		600
accgacaccc	ttatccatct	catggcgaag	gctggactga	ccctgcaaca	gcagcaccag		660
aggctggccc	agttgctgct	gattctgagc	cacatccggc	acatgtcgtc	caagaggatg		720
gaacacctgt	acagcatgaa	gtgcaagaac	gtcgtgcctc	tgtccgatct	gctcctggaa		780
atgctggacg	cgcacagact	cgggacggga	gctgaagatc	cacgaccag	cagaaagcga		840
cggaagtgc	aattggtgga	atcaggggga	ggacttggtc	agcctggagg	atcgtgaga		900
ctgtcatgtg	ccgtgtccgg	ctttgccctg	tccaaccacg	ggatgtcctg	gtccgccgc		960
gcgcctggaa	agggcctcga	atgggtgtcg	ggtatttgt	acagcggtag	cacctactat		1020
gccgcatccg	tgaaggggag	attcaccatc	agccgggaca	actccaggaa	cactctgtac		1080
ctccaaatga	attcgtgag	gccagaggac	actgccatct	actactgctc	cgcgcatggc		1140
ggagagtccg	acgtctgggg	acaggggacc	accgtgaccg	tgtctagcgc	gtccggcgga		1200
ggcggcagcg	ggggctgggc	atcagggggc	ggcggatcgg	acatccagct	caccagtc		1260
ccgagctcgc	tgtccgcctc	cgtgggagat	cgggtcacca	tcacgtgccg	cgccagccag		1320
tcgatttcct	cctacctgaa	ctggtaccaa	cagaagccc	gaaaagcccc	gaagcttctc		1380
atctacgccg	cctcgagcct	gcagtcagga	gtgccctcac	ggttctccgg	ctccggttc		1440
ggtactgatt	tcacctgac	catttcctcc	ctgcaaccgg	aggacttcgc	tacttactac		1500
tgccagcagt	cgtactccac	cccctacact	ttcggacaag	gcaccaaggt	cgaaatcaag		1560
accactaccc	cagcaccgag	gccaccac	ccggctccta	ccatgcctc	ccagcctctg		1620
tccctgcgtc	cggaggcatg	tagaccgcga	gctgggtggg	ccgtgcatac	ccggggctct		1680
gacttcgcct	gcgatatcta	catttgggcc	cctctggctg	gtacttgcg	ggtcctgctg		1740
ctttcactcg	tgatcactct	ttactgtaag	cgcggtcgga	agaagctgct	gtacatcttt		1800
aagcaaccct	tcatgaggcc	tgtgcagact	actcaagagg	aggacggctg	ttcatgccgg		1860
ttcccagagg	aggaggaagg	cggctgcgaa	ctgcgcgtga	aattcagccg	cagcgcat		1920
gctccagcct	accagcagg	gcagaaccag	ctctacaacg	aactcaatct	tggctcgaga		1980
gaggagtacg	acgtgctgga	caagcggaga	ggacgggacc	cagaaatggg	cgggaagccg		2040
cgcagaaaga	atccccaaga	gggcctgtac	aacgagctcc	aaaaggataa	gatggcagaa		2100
gcctatagcg	agattggtat	gaaaggggaa	cgcagaagag	gcaaaggcca	cgacggactg		2160
taccagggac	tcagcaccgc	caccaaggac	acctatgacg	ctcttcacat	gcaggccctg		2220
ccgcctcgg							2229

<211> 2229
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1097
atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60
cccgagtcgt tggcactttc cctgactgcc gaccagatgg tgtccgccct tctggacgcc 120
gagcctccaa ttctgtactc ggagtacgat ccgactcgcc cgttctccga agccagcatg 180
atgggcctgt tgactaacct ggcggaccgc gagttggtgc acatgattaa ctgggctaag 240
cgggtgccgg gcttcgtgga cctgaccctg caccaccaag tgcacctcct ggaatgcgcc 300
tggtatgaaa tcctcatgat cggcctcgtg tggagatcca tggagcatcc cggaagctc 360
ctgtttgcac ccaacctcct gcttgatcgc aaccaggga aatgcgtgga agggggtgtc 420
gagattttcg acatgctgct cgccacctct tcccggttcc ggatgatgaa tctgcaggga 480
gaagagtctg tgtgtctgaa gtcaatcatc ctgctgaact cgggggtcta taccttcctg 540
agctcgaccc tcaagtcact ggaggaaaaa gaccacatcc atcgctgct cgataagatc 600
accgacaccc ttatccatct catggcgaag gctggactga ccctgcaaca gcagcaccag 660
aggctggccc agttgctgct gattctgagc cacatccggc acatgtcgaa caagaggatg 720
gaacacctgt acagcatgaa gtgcaagaac gtcgtgcctc tgtccgatct gtccttgaa 780
atgctggacg cgcacagact cgggacggga gctgaagatc caccgaccag cagaaagcga 840
cgggaagtgc aattggtgga atcaggggga ggacttgtgc agcctggagg atcgctgaga 900
ctgtcatgtg ccgtgtccgg ctttgccctg tccaaccacg ggatgtcctg ggtccgccgc 960
gcgcctggaa agggcctcga atgggtgtcg ggtatttgtt acagcggtag cacctactat 1020
gccgcatccg tgaaggggag attcaccatc agccgggaca actccaggaa cactctgtac 1080
ctccaaatga attcgctgag gccagaggac actgccatct actactgctc cgcgcatggc 1140
ggagagtccg acgtctgggg acaggggacc accgtgaccg tgtctagcgc gtccggcgga 1200
ggcggcagcg ggggtcgggc atcagggggc ggcggatcgg acatccagct caccagtc 1260
ccgagctcgc tgtccgcctc cgtgggagat cgggtcacca tcacgtgccg cgccagccag 1320
tcgatttcct cctacctgaa ctggtaccaa cagaagcccg gaaaagcccc gaagcttctc 1380
atctacgccg cctcagacct gcagtcagga gtgccctcac ggttctccgg ctccggttcc 1440
ggtactgatt tcacctgac catttcctcc ctgcaaccgg aggacttcgc tacttactac 1500
tgccagcagt cgtactccac cccctacact ttcggacaag gcaccaaggt cgaaatcaag 1560
accactaccc cagcaccgag gccaccacc ccggctccta ccatcgctc ccagcctctg 1620
tccctgcgtc cggaggcatg tagaccgca gctggtgggg ccgtgcatac cgggggtctt 1680
gacttcgcct gcgatatcta catttgggcc cctctggctg gtacttgccg ggtcctgctg 1740

ctttcactcg	tgatcactct	ttactgtaag	cgcggtcggg	agaagctgct	gtacatcttt	1800
aagcaaccct	tcatgaggcc	tgtgcagact	actcaagagg	aggacggctg	ttcatgccgg	1860
ttcccagagg	aggaggaagg	cggctgcgaa	ctgcgcgtga	aattcagccg	cagcgcagat	1920
gctccagcct	accagcaggg	gcagaaccag	ctctacaacg	aactcaatct	tggtcggaga	1980
gaggagtacg	acgtgctgga	caagcggaga	ggacgggacc	cagaaatggg	cggaagccg	2040
cgcagaaaga	atccccaaga	gggcctgtac	aacgagctcc	aaaaggataa	gatggcagaa	2100
gcctatagcg	agattggtat	gaaaggggaa	cgcagaagag	gcaaaggcca	cgacggactg	2160
taccagggac	tcagcaccgc	caccaaggac	acctatgacg	ctcttcacat	gcaggccctg	2220
ccgcctcgg						2229

<210> 1098

<211> 2256

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1098

atggccctcc	ctgtcaccgc	cctgctgctt	ccgctggctc	ttctgctcca	cgccgctcgg	60
ccccagtcgt	tggcactttc	cctgactgcc	gaccagatgg	tgtccgccct	tctggacgcc	120
gagcctccaa	ttctgtactc	ggagtacgat	ccgactcgcc	cgttctccga	agccagcatg	180
atgggcctgt	tgactaacct	ggcggaccgc	gagttggtgc	acatgattaa	ctgggctaag	240
cgggtgccgg	gcttcgtgga	cctggccctg	cacgaccaag	tgcacctcct	ggaatgcgcc	300
tggatggaaa	tcctcatgat	cggcctcgtg	tggagatcca	tggagcatcc	cgaaaagctc	360
ctgtttgcac	ccaacctcct	gcttgatcgc	aaccagggaa	aatgcgtgga	agggggtgtc	420
gagattttcg	acatgctgct	cgccacctct	tcccggttcc	ggatgatgaa	tctgcagggg	480
gaagagttcg	tgtgtctgaa	gtcaatcatc	ctgctgaact	ccgggggtcta	taccttcctg	540
agctcgaccc	tcaagtcact	ggaggaaaaa	gaccacatcc	atcgcgctgct	cgataagatc	600
accgacaccc	ttatccatct	catggcgaag	gctggactga	ccctgcaaca	gcagcaccag	660
aggctggccc	agttgctgct	gattctgagc	cacatccggc	acatgtcgtc	caagaggatg	720
gaacacctgt	acagcatgaa	gtgcaagaac	gtcgtgcctc	tgtccgatct	gctcctggaa	780
atgctggacg	cgcacagact	cggaaccggc	gcggaagacc	cccggccctc	caggaagcga	840
aggtccctcg	gagacgtggg	tgaaattgtg	atgaccagct	caccgcccac	tcttagcctt	900
tcaccgggtg	agcgcgaac	cctgtcttgc	agagcctccc	aagacatctc	aaaatacctt	960
aattggtatc	aacagaagcc	cggacaggct	cctcgccttc	tgatctacca	caccagccgg	1020
ctccattctg	gaatccctgc	caggttcagc	ggtagcggat	ctgggaccga	ctacaccctc	1080
actatcagct	cactgcagcc	agaggacttc	gctgtctatt	tctgtcagca	agggaacacc	1140

	_SL	
ctgccctaca cctttggaca gggcaccaag ctcgagatta aaggtggagg tggcagcgga	1200	
ggaggtgggt ccggcggtgg aggaagccag gtccaactcc aagaaagcgg accgggtcct	1260	
gtgaagccat cagaaactct ttactgact tgtactgtga gcggagtgtc tctccccgat	1320	
tacggggtgt cttggatcag acagccaccg gggaagggtc tggaatggat tggagtgatt	1380	
tggggctctg agactactta ctactcttca tccctcaagt cacgcgtcac catctcaaag	1440	
gacaactcta agaatcaggt gtcactgaaa ctgtcatctg tgaccgcagc cgacaccgcc	1500	
gtgtactatt gcgctaagca ttactattat ggcgggagct acgcaatgga ttactgggga	1560	
caggggtactc tggtcaccgt gtccagcacc actacccag caccgaggcc acccaccgcc	1620	
gctcctacca tcgcctccca gcctctgtcc ctgcgtccgg aggcatttag accgcagct	1680	
ggtggggccg tgcatacccg gggctctgac ttgcctgcg atatctacat ttggggccct	1740	
ctggctggta cttgcggggt cctgctgctt tctactgtga tctactctta ctgtaagcgc	1800	
ggtcggaaga agctgctgta catctttaag caacccttca tgaggcctgt gcagactact	1860	
caagaggagg acggctgttc atgccggttc ccagaggagg aggaaggcgg ctgcgaactg	1920	
cgctgaaaat tcagccgcag cgcagatgct ccagcctacc agcaggggca gaaccagctc	1980	
tacaacgaac tcaatcttgg tcggagagag gactacgacg tgctggacaa gcggagagga	2040	
cgggaccag aaatgggcgg gaagccgcgc agaaagaatc cccaagaggg cctgtacaac	2100	
gagctccaaa aggataagat ggcagaagcc tatagcgaga ttggtatgaa aggggaacgc	2160	
agaagaggca aaggccacga cggactgtac cagggactca gcaccgccac caaggacacc	2220	
tatgacgctc ttcacatgca ggccctgccg cctcgg	2256	

<210> 1099

<211> 2256

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1099

atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg	60
ccccagtcgt tggcactttc cctgactgcc gaccagatgg tgtccgccct tctggacgcc	120
gagcctccaa ttctgtactc ggagtacgat ccgactcgcc cgttctccga agccagcatg	180
atgggcctgt tgactaacct ggcggaccgc gagttggtgc acatgattaa ctgggctaag	240
cggttgccgg gcttcgtgga cctgaccctg cagaccaag tgcacctcct ggaatgcgcc	300
tggatggaat tcctcatgat cggcctcgtg tggagatcca tggagcatcc cggaagctc	360
ctgtttgcac ccaacctcct gcttgatcgc aaccaggga aatgcgtgga agggggtgtc	420
gagattttcg acatgctgct cgccacctct tcccggttcc ggatgatgaa tctgcaggga	480
gaagagttcg tgtgtctgaa gtcaatcatc ctgctgaact ccggggtcta taccttcctg	540

	_SL	
agctcgaccc tcaagtcact ggaggaaaaa gaccacatcc atcgcggtgct cgataagatc	600	
accgacaccc ttatccatct catggcgaag gctggactga ccctgcaaca gcagcaccag	660	
aggctggccc agttgctgct gattctgagc cacatccggc acatgtcgaa caagaggatg	720	
gaacacctgt acagcatgaa gtgcaagaac gtcgtgcctc tgtccgatct gtccttgga	780	
atgctggacg cgcacagact cggaaccggc gcggaagacc cccggccctc caggaagcga	840	
aggccctcg gagacgtggg tgaaattgtg atgaccagc caccgcccac tcttagcctt	900	
tcaccgggtg agcgcgcaac cctgtcttgc agagcctccc aagacatctc aaaatacctt	960	
aattgggtatc aacagaagcc cggacaggct cctgccttc tgatctacca caccagccgg	1020	
ctccattctg gaatccctgc caggttcagc ggtagcggat ctgggaccga ctacaccctc	1080	
actatcagct cactgcagcc agaggacttc gctgtctatt tctgtcagca agggaacacc	1140	
ctgccctaca ctttggaca gggcaccaag ctcgagatta aagggtggagg tggcagcgga	1200	
ggaggtgggt ccggcggtgg aggaagccag gtccaactcc aagaaagcgg accgggtctt	1260	
gtgaagccat cagaaactct ttcactgact tgtactgtga gcggagtgtc tctccccgat	1320	
tacgggggtgt cttggatcag acagccaccg gggaagggtc tggaatggat tggagtgatt	1380	
tggggctctg agactactta ctactcttca tccctcaagt cacgcgtcac catctcaaag	1440	
gacaactcta agaatcaggt gtcactgaaa ctgtcatctg tgaccgcagc cgacaccgcc	1500	
gtgtactatt gcgctaagca ttactattat ggcgggagct acgcaatgga ttactgggga	1560	
cagggctactc tggtcaccgt gtccagcacc actacccag caccgaggcc acccaccgcc	1620	
gctcctacca tcgcctcca gcctctgtcc ctgcgtccgg aggcattgtag acccgagct	1680	
ggtggggccg tgcatacccg gggctctgac ttcgcctgcg atatctacat ttggggccct	1740	
ctggctggta cttgcggggc cctgctgctt tctactctga tctactcttta ctgtaagcgc	1800	
ggtcggaaga agctgctgta catctttaag caacccttca tgaggcctgt gcagactact	1860	
caagaggagg acggctgttc atgccggttc ccagaggagg aggaaggcgg ctgcgaactg	1920	
cgcgtgaaat tcagccgcag cgcagatgct ccagcctacc agcaggggca gaaccagctc	1980	
tacaacgaac tcaatcttgg tcggagagag gactacgacg tgctggacaa gcggagagga	2040	
cgggaccagc aaatgggcgg gaagccgcgc agaaagaatc cccaagaggg cctgtacaac	2100	
gagctccaaa aggataagat ggcagaagcc tatagcgaga ttggtatgaa aggggaacgc	2160	
agaagaggca aaggccacga cggactgtac cagggactca gcaccgccac caaggacacc	2220	
tatgacgctc ttcacatgca ggcctgccc cctcgg	2256	

<210> 1100

<211> 2238

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

_SL

<400> 1100
atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60
ccccagtcgt tggcactttc cctgactgcc gaccagatgg tgtccgccct tctggacgcc 120
gagcctccaa ttctgtactc ggagtacgat ccgactcgcc cgttctccga agccagcatg 180
atgggcctgt tgactaacct ggcggaaccgc gagttggtgc acatgattaa ctgggctaag 240
cgggtgccgg gcttcgtgga cctggccctg caccaccaag tgcacctcct ggaatgcgcc 300
tggatggaaa tcctcatgat cggcctcgtg tggagatcca tggagcatcc cggaaagctc 360
ctgtttgcac ccaacctcct gcttgatcgc aaccaggga aatgcgtgga agggggtgtc 420
gagattttcg acatgctgct cgccacctct tcccggttcc ggatgatgaa tctgcaggga 480
gaagagttcg tgtgtctgaa gtcaatcatc ctgctgaact ccgggggtcta taccttcctg 540
agctcgaccc tcaagtcact ggaggaaaaa gaccacatcc atcgctgct cgataagatc 600
accgacaccc ttatccatct catggcgaag gctggactga ccctgcaaca gcagcaccag 660
aggctggccc agttgctgct gattctgagc cacatccggc acatgtcgtc caagaggatg 720
gaacacctgt acagcatgaa gtgcaagaac gtcgtgcctc tgtccgatct gtcctggaa 780
atgctggacg cgcacagact cgggacggga gctgaagatc caccaccag cagaaagcga 840
cgggaaattg tgatgacca gtcacccgcc actcttagcc tttcaccgg tgagcgcgca 900
accctgtctt gcagagcctc ccaagacatc tcaaaatacc ttaattggta tcaacagaag 960
cccgacagg ctctcgcct tctgatctac cacaccagcc ggctccattc tggaatccct 1020
gccaggttca gcggtagcgg atctgggacc gactacaccc tcactatcag ctactgcag 1080
ccagaggact tcgctgtcta tttctgtcag caagggaaca ccctgcccta cacctttgga 1140
cagggcacca agctcgagat taaaggtgga ggtggcagcg gaggaggtgg gtccggcggg 1200
ggaggaagcc aggtccaact ccaagaaagc ggaccgggtc ttgtgaagcc atcagaaact 1260
ctttcactga cttgtactgt gagcggagtg tctctccccg attacggggg gtcttggatc 1320
agacagccac cggggaaggg tctggaatgg attggagtga tttggggctc tgagactact 1380
tactactctt catccctcaa gtcacgcgtc accatctcaa aggacaactc taagaatcag 1440
gtgtcactga aactgtcatc tgtgaccgca gccgacaccg ccgtgtacta ttgcgctaag 1500
cattactatt atggcgggag ctacgcaatg gattactggg gacagggtac tctggtcacc 1560
gtgtccagca ccactacccc agcaccgagg ccaccacccc cggtcctac catcgcctcc 1620
cagcctctgt ccctgcgtcc ggaggcatgt agaccgcag ctggtggggc cgtgcatacc 1680
cggggctctt acttcgcctg cgatatctac atttggggcc ctctggctgg tacttgcggg 1740
gtcctgctgc tttcactcgt gatcactctt tactgtaagc gcggtcggaa gaagctgctg 1800
tacatcttta agcaaccctt catgaggcct gtgcagacta ctcaagagga ggacggctgt 1860
tcatgccggg tcccagagga ggaggaaggc ggctgcgaac tgcgcgtgaa attcagccgc 1920
agcgcagatg ctccagccta ccagcagggg cagaaccagc tctacaacga actcaatctt 1980

ggtcggagag	aggagtacga	cgtgctggac	aagcggagag	gacgggaccc	agaaatgggc	2040
gggaagccgc	gcagaaagaa	tccccaagag	ggcctgtaca	acgagctcca	aaaggataag	2100
atggcagaag	cctatagcga	gattggtatg	aaaggggaac	gcagaagagg	caaaggccac	2160
gacggactgt	accagggact	cagcaccgcc	accaaggaca	cctatgacgc	tcttcacatg	2220
caggccctgc	cgctcgg					2238

<210> 1101
 <211> 2238
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1101		
atggccctcc	ctgtcaccgc	cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60
ccccagtcgt	tggcactttc	cctgactgcc gaccagatgg tgtccgccct tctggacgcc 120
gagcctccaa	ttctgtactc	ggagtacgat ccgactcgcc cgttctccga agccagcatg 180
atgggcctgt	tgactaacct	ggcggaccgc gagttggtgc acatgattaa ctgggctaag 240
cgggtgccgg	gcttcgtgga	cctgaccctg cagcaccaag tgcacctcct ggaatgcgcc 300
tggatggaaa	tcctcatgat	cggcctcgtg tggagatcca tggagcatcc cggaagctc 360
ctgtttgcac	ccaacctcct	gcttgatcgc aaccagggaa aatgcgtgga agggggtgtc 420
gagattttcg	acatgctgct	cgccacctct tcccggttcc ggatgatgaa tctgcaggga 480
gaagagttcg	tgtgtctgaa	gtcaatcatc ctgctgaact ccgggggtcta taccttcctg 540
agctcgaccc	tcaagtcact	ggaggaaaaa gaccacatcc atcgcgtgct cgataagatc 600
accgacaccc	ttatccatct	catggcgaag gctggactga ccctgcaaca gcagcaccag 660
aggctggccc	agttgctgct	gattctgagc cacatccggc acatgtcgaa caagaggatg 720
gaacacctgt	acagcatgaa	gtgcaagaac gtcgtgcctc tgtccgatct gtccttgaa 780
atgctggacg	cgcacagact	cgggacggga gctgaagatc cacgaccag cagaaagcga 840
cgggaaattg	tgatgacca	gtcaccgcc actcttagcc tttcaccgg tgagcgcgca 900
accctgtctt	gcagagcctc	ccaagacatc tcaaaatacc ttaattggta tcaacagaag 960
cccggacagg	ctcctcgctt	tctgatctac cacaccagcc ggctccattc tggaatccct 1020
gccaggttca	gcggtagcgg	atctgggacc gactacaccc tcactatcag ctactgcag 1080
ccagaggact	tcgctgtcta	tttctgtcag caagggaaca ccctgcccta cacctttgga 1140
cagggcacca	agctcgagat	taaagggtgga ggtggcagcg gaggagggtg gtccggcgg 1200
ggaggaagcc	aggtccaact	ccaagaaagc ggaccgggtc ttgtgaagcc atcagaaact 1260
ctttcactga	cttgtactgt	gagcggagtg tctctccccg attacgggggt gtcttgatc 1320
agacagccac	cggggaaggg	tctggaatgg attggagtga tttggggctc tgagactact 1380

tactactctt catccctcaa gtcacgcgtc accatctcaa	aggacaactc taagaatcag	1440
gtgtcactga aactgtcatc tgtgaccgca gccgacaccg	ccgtgtacta ttgcgctaag	1500
cattactatt atggcgggag ctacgcaatg gattactggg	gacaggggtac tctggtcacc	1560
gtgtccagca ccactacccc agcaccgagg ccacccaccc	cggctcctac catcgctcc	1620
cagcctctgt ccctgcgtcc ggaggcatgt agaccgcgag	ctgggtggggc cgtgcatacc	1680
cggggctcttg acttcgcctg cgatatctac atttggggcc	ctctggctgg tacttgcggg	1740
gtcctgctgc tttcactcgt gatcactctt tactgtaagc	gcggtcggaa gaagctgctg	1800
tacatcttta agcaaccctt catgaggcct gtgcagacta	ctcaagagga ggacggctgt	1860
tcatgccggt tcccagagga ggaggaaggc ggctgcgaac	tgcgcgtgaa attcagccgc	1920
agcgcagatg ctccagccta ccagcagggg cagaaccagc	tctacaacga actcaatctt	1980
ggtcggagag aggagtacga cgtgctggac aagcggagag	gacgggaccc agaaatgggc	2040
gggaagccgc gcagaaagaa tccccaagag ggcctgtaca	acgagctcca aaaggataag	2100
atggcagaag cctatagcga gattggtatg aaaggggaac	gcagaagagg caaaggccac	2160
gacggactgt accagggact cagcaccgcc accaaggaca	cctatgacgc tcttcacatg	2220
caggccctgc cgcctcgg		2238

<210> 1102

<211> 2259

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1102

atggccctcc ctgtcaccgc cctgctgctt ccgctggctc	ttctgtcca cgccgctcgg	60
ccccagtcgt tggcactttc cctgactgcc gaccagatgg	tgtccgccct tctggacgcc	120
gagcctccaa ttctgtactc ggagtacgat ccgactcgcc	cgttctccga agccagcatg	180
atgggcctgt tgactaacct ggcggaccgc gagttggtgc	acatgattaa ctgggctaag	240
cgggtgccgg gcttcgtgga cctggccctg cagcaccaag	tgcacctcct ggaatgcgcc	300
tggatgga aa tcctcatgat cggcctcgtg tggagatcca	tggagcatcc cggaaagctc	360
ctgtttgcac ccaacctcct gcttgatcgc aaccagggaa	aatgcgtgga agggggtgtc	420
gagattttcg acatgctgct cgccacctct tcccggttcc	ggatgatgaa tctgcaggga	480
gaagagtctg tgtgtctgaa gtcaatcatc ctgctgaact	ccggggtcta taccttcctg	540
agctcgaccc tcaagtcact ggaggaaaaa gaccacatcc	atcgcgtgct cgataagatc	600
accgacaccc ttatccatct catggcgaag gctggactga	ccctgcaaca gcagcaccag	660
aggctggccc agttgctgct gattctgagc cacatccggc	acatgtcgtc caagaggatg	720
gaacacctgt acagcatgaa gtgcaagaac gtcgtgcctc	tgtccgatct gtcctggaa	780

	_SL	
atgctggacg cgcacagact cggaaccggc gcggaagacc cccggccctc caggaagcga	840	
aggtccctcg gagacgtggg tcaagtcaa ctcgtccaaa gcggagcggg agtcaagaaa	900	
cccggagcga gcgtgaaagt gtcctgcaaa gcctccggct acacctttac gggctactac	960	
atgcactggg tgcgccaggc accaggacag ggtcttgaat ggatgggatg gatcaaccct	1020	
aattcgggcg gaactaacta cgcacagaag ttccagggga gagtgactct gactcgggat	1080	
acctccatct caactgtcta catggaactc tcccgtttgc ggtcagatga tacggcagtg	1140	
tactactgcg cccgcgacat gaatatcctg gctaccgtgc cgttcgacat ctggggacag	1200	
gggactatgg ttactgtctc atcgggcggg ggaggttcag gaggaggcgg ctcgggaggc	1260	
ggaggttcgg acattcagat gaccagtc ccacctctc tgtcggccag cgtcggagat	1320	
agggtgacca ttacctgtcg ggcctcgcaa agcatctcct cgtacctcaa ctggtatcag	1380	
caaaagccgg gaaaggcgcc taagctgctg atctacgccg cttcgagctt gcaaagcggg	1440	
gtgccatcca gattctcggg atcaggctca ggaaccgact tcaccctgac cgtgaacagc	1500	
ctccagccgg aggactttgc cacttactac tgccagcagg gagactccgt gccgcttact	1560	
ttcggggggg gtaccgcct ggagatcaag accactacc cagcaccgag gccaccacc	1620	
ccggctccta ccatcgctc ccagcctctg tccctgcgtc cggaggcatg tagaccgcga	1680	
gctggtgggg ccgtgcatac ccggggtctt gacttcgcct gcgatattta catttgggcc	1740	
cctctggctg gtacttgcg ggtcctgctg ctttactcgt tgatcactct ttactgtaag	1800	
cgcggtcggg agaagctgct gtacatcttt aagcaaccct tcatgaggcc tgtgcagact	1860	
actcaagagg aggacggctg ttcatgccgg ttcccagagg aggaggaagg cggctgcgaa	1920	
ctgcgcgtga aattcagccg cagcgcagat gctccagcct accagcaggg gcagaaccag	1980	
ctctacaacg aactcaatct tggtcggaga gaggagtacg acgtgctgga caagcggaga	2040	
ggacgggacc cagaaatggg cggaagccg cgcagaaaga atccccaaga gggcctgtac	2100	
aacgagctcc aaaaggataa gatggcagaa gcctatagcg agattggtat gaaaggggaa	2160	
cgcagaagag gcaaaggcca cgacggactg taccagggac tcagcaccgc caccaaggac	2220	
acctatgacg ctcttcacat gcaggccctg ccgcctcgg	2259	

<210> 1103

<211> 2259

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1103

atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg	60
ccccagtcgt tggcactttc cctgactgcc gaccagatgg tgtccgccct tctggacgcc	120
gagcctccaa ttctgtactc ggagtacgat ccgactcgcc cgttctccga agccagcatg	180

						_SL	
atgggcctgt	tgactaacct	ggcggaccgc	gagttggtgc	acatgattaa	ctgggctaag		240
cgggtgccgg	gcttcgtgga	cctgaccctg	cacgaccaag	tgcacctcct	ggaatgcgcc		300
tggatggaaa	tcctcatgat	cggcctcgtg	tggagatcca	tggagcatcc	cggaaagctc		360
ctgtttgcac	ccaacctcct	gcttgatcgc	aaccagggaa	aatgcgtgga	agggggtgtc		420
gagattttcg	acatgctgct	cgccacctct	tcccggttcc	ggatgatgaa	tctgcaggga		480
gaagagttcg	tgtgtctgaa	gtcaatcatc	ctgctgaact	ccgggggtcta	taccttcctg		540
agctcgaccc	tcaagtcact	ggaggaaaaa	gaccacatcc	atcgcgtgct	cgataagatc		600
accgacaccc	ttatccatct	catggcgaag	gctggactga	ccctgcaaca	gcagcaccag		660
aggctggccc	agttgctgct	gattctgagc	cacatccggc	acatgtcgaa	caagaggatg		720
gaacacctgt	acagcatgaa	gtgcaagaac	gtcgtgcctc	tgtccgatct	gctcctggaa		780
atgctggacg	cgcacagact	cggaaccggc	gcggaagacc	cccggccctc	caggaagcga		840
aggtcctctg	gagacgtggg	tcaagtgcaa	ctcgtccaaa	gcggagcgga	agtcaagaaa		900
cccggagcga	gcgtgaaagt	gtcctgcaaa	gcctccggct	acacctttac	gggctactac		960
atgcactggg	tgcgccaggc	accaggacag	ggtcttgaat	ggatgggatg	gatcaaccct		1020
aattcgggcg	gaactaacta	cgcacagaag	ttccagggga	gagtgactct	gactcgggat		1080
acctccatct	caactgtcta	catggaactc	tcccgcttgc	ggtcagatga	tacggcagtg		1140
tactactgcg	cccgcgacat	gaatatcctg	gctaccgtgc	cgttcgacat	ctggggacag		1200
gggactatgg	ttactgtctc	atcgggcggg	ggaggttcag	gaggaggcgg	ctcgggaggc		1260
ggaggttcgg	acattcagat	gaccagtc	ccatcctctc	tgtcggccag	cgtcggagat		1320
agggtgacca	ttacctgtcg	ggcctcgcaa	agcatctcct	cgtacctcaa	ctggtatcag		1380
caaaagccgg	gaaaggcgcc	taagctgctg	atctacgccg	cttcgagctt	gcaaagcggg		1440
gtgccatcca	gattctcggg	atcaggctca	ggaaccgact	tcacctgac	cgtgaacagc		1500
ctccagccgg	aggactttgc	cacttactac	tgccagcagg	gagactccgt	gccgcttact		1560
ttcggggggg	gtacccgcct	ggagatcaag	accactaccc	cagcaccgag	gccacccacc		1620
ccggctccta	ccatcgcctc	ccagcctctg	tccctgcgtc	cggaggcatg	tagaccgcga		1680
gctggtgggg	ccgtgcatac	ccgggggtctt	gacttcgcct	gcgatatcta	catttgggcc		1740
cctctggctg	gtacttgcg	ggtcctgctg	ctttcactcg	tgatcactct	ttactgtaag		1800
cgcggtcgga	agaagctgct	gtacatcttt	aagcaaccct	tcatgaggcc	tgtgcagact		1860
actcaagagg	aggacggctg	ttcatgccgg	ttcccagagg	aggaggaagg	cggctgcgaa		1920
ctgcgcgtga	aattcagccg	cagcgcagat	gctccagcct	accagcaggg	gcagaaccag		1980
ctctacaacg	aactcaatct	tggtcggaga	gaggagtacg	acgtgctgga	caagcggaga		2040
ggacgggacc	cagaaatggg	cgggaagccg	cgcagaaaga	atccccaaga	gggcctgtac		2100
aacgagctcc	aaaaggataa	gatggcagaa	gcctatagcg	agattggtat	gaaaggggaa		2160
cgcagaagag	gcaaaggcca	cgacggactg	taccagggac	tcagcaccgc	caccaaggac		2220

acctatgacg ctcttcacat gcaggccctg cgcctcgg ^{_SL} 2259

<210> 1104
 <211> 2241
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1104
 atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60
 cccagtcgt tggcactttc cctgactgcc gaccagatgg tgtccgccct tctggacgcc 120
 gagcctccaa ttctgtactc ggagtacgat ccgactcgcc cgttctccga agccagcatg 180
 atgggcctgt tgactaacct ggcggaccgc gagttggtgc acatgattaa ctgggctaag 240
 cgggtgccgg gcttcgtgga cctggccctg caccaccaag tgcacctcct ggaatgcgcc 300
 tggatggaaa tcctcatgat cggcctcgtg tggagatcca tggagcatcc cggaaagctc 360
 ctgtttgcac ccaacctcct gcttgatcgc aaccagggaa aatgcgtgga agggggtgtc 420
 gagattttcg acatgctgct cgccacctct tcccggttcc ggatgatgaa tctgcaggga 480
 gaagagtctg tgtgtctgaa gtcaatcatc ctgctgaact ccgggggtcta taccttcctg 540
 agctcgaccc tcaagtcact ggaggaaaaa gaccacatcc atcgcgtgct cgataagatc 600
 accgacaccc ttatccatct catggcgaag gctggactga ccctgcaaca gcagcaccag 660
 aggctggccc agttgctgct gattctgagc cacatccggc acatgtcgtc caagaggatg 720
 gaacacctgt acagcatgaa gtgcaagaac gtcgtgcctc tgtccgatct gtcctggaa 780
 atgctggacg cgcacagact cggaaccggc gcggaagacc cccggccctc caggaagcga 840
 aggcaagtgc aactcgtcca aagcggagcg gaagtcaaga aaccgggagc gagcgtgaaa 900
 gtgtcctgca aagcctccgg ctacaccttt acgggctact acatgcactg ggtgcgccag 960
 gcaccaggac agggctcttg atggatggga tggatcaacc ctaattcggg cggaactaac 1020
 tacgcacaga agttccaggg gagagtgact ctgactcggg atacctccat ctcaactgtc 1080
 tacatggaac tctcccgctt gcggtcagat gatacggcag tgtactactg cgcccgcgac 1140
 atgaatatcc tggctaccgt gccgttcgac atctggggac aggggactat ggttactgtc 1200
 tcatcgggcg gtggagggtc aggaggaggc ggctcgggag gcggagggtc ggacattcag 1260
 atgaccaggt ccccatcctc tctgtcggcc agcgtcggag atagggtgac cattacctgt 1320
 cgggcctcgc aaagcatctc ctcgtacctc aactggtatc agcaaaagcc gggaaaggcg 1380
 cctaagctgc tgatctacgc cgcttcgagc ttgcaaagcg gggtgccatc cagattctcg 1440
 ggatcaggct caggaaccga cttcacctg accgtgaaca gcctccagcc ggaggacttt 1500
 gccacttact actgccagca gggagactcc gtgccgctta ctttcggggg gggtagccgc 1560
 ctggagatca agaccactac ccagcaccg aggccacca cccgggtcc taccatcgcc 1620

tcccagcctc	tgtccctgcg	tccggaggca	tgtagacccg	cagctggtgg	ggccgtgcat	1680
acccgggggtc	ttgacttcgc	ctgcgatatc	tacatttggg	cccctctggc	tggtacttgc	1740
ggggtcctgc	tgctttcact	cgtgatcact	ctttactgta	agcgcggtcg	gaagaagctg	1800
ctgtacatct	ttaagcaacc	cttcatgagg	cctgtgcaga	ctactcaaga	ggaggacggc	1860
tgttcatgcc	ggttcccaga	ggaggaggaa	ggcggctgcg	aactgcgcgt	gaaattcagc	1920
cgcagcgag	atgctccagc	ctaccagcag	gggcagaacc	agctctacaa	cgaactcaat	1980
cttggtcggg	gagaggagta	cgacgtgctg	gacaagcgga	gaggacggga	cccagaaatg	2040
ggcgggaagc	cgcgcagaaa	gaatcccca	gagggcctgt	acaacgagct	ccaaaaggat	2100
aagatggcag	aagcctatag	cgagattggt	atgaaagggg	aacgcagaag	aggcaaaggc	2160
cacgacggac	tgtaccaggg	actcagcacc	gccaccaagg	acacctatga	cgctcttcac	2220
atgcaggccc	tgccgcctcg	g				2241

<210> 1105

<211> 2241

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1105

atggccctcc	ctgtcaccgc	cctgctgctt	ccgctggctc	ttctgctcca	cgccgctcgg	60
ccccagtcgt	tggcactttc	cctgactgcc	gaccagatgg	tgtccgccct	tctggacgcc	120
gagcctccaa	ttctgtactc	ggagtacgat	ccgactcgcc	cgttctccga	agccagcatg	180
atgggcctgt	tgactaacct	ggcggaccgc	gagttggtgc	acatgattaa	ctgggctaag	240
cgggtgccgg	gcttcgtgga	cctgaccctg	cacgaccaag	tgcacctcct	ggaatgcgcc	300
tggatggaaa	tcctcatgat	cggcctcgtg	tggagatcca	tggagcatcc	cggaaagctc	360
ctgtttgcac	ccaacctcct	gcttgatcgc	aaccagggaa	aatgcgtgga	agggggtgtc	420
gagattttcg	acatgctgct	cgccacctct	tcccggttcc	ggatgatgaa	tctgcaggga	480
gaagagttcg	tgtgtctgaa	gtcaatcatc	ctgctgaact	ccgggggtcta	taccttcctg	540
agctcgaccc	tcaagtcact	ggaggaaaaa	gaccacatcc	atcgctgctg	cgataagatc	600
accgacaccc	ttatccatct	catggcgaag	gctggactga	ccctgcaaca	gcagcaccag	660
aggctggccc	agttgctgct	gattctgagc	cacatccggc	acatgtcgaa	caagaggatg	720
gaacacctgt	acagcatgaa	gtgcaagaac	gtcgtgcctc	tgtccgatct	gctcctggaa	780
atgctggacg	cgcacagact	cgggacggga	gctgaagatc	cacgaccag	cagaaagcga	840
cggcaagtgc	aactcgtcca	aagcggagcg	gaagtcaaga	aaccgggagc	gagcgtgaaa	900
gtgtcctgca	aagcctccgg	ctacaccttt	acgggctact	acatgcactg	ggtgcgccag	960
gcaccaggac	agggtcttga	atggatggga	tggatcaacc	ctaattcggg	cggaactaac	1020

tacgcacaga	agttccaggg	gagagtgact	ctgactcggg	atacctccat	ctcaactgtc	1080
tacatggaac	tctcccgtt	gcggtcagat	gatacggcag	tgtactactg	cgcccgcgac	1140
atgaatatcc	tggctaccgt	gccgttcgac	atctggggac	aggggactat	ggttactgtc	1200
tcatcgggcg	gtggagggtt	aggaggaggc	ggctcgggag	gcggagggtt	ggacattcag	1260
atgacccagt	ccccatcctc	tctgtcggcc	agcgtcggag	atagggtgac	cattacctgt	1320
cgggcctcgc	aaagcatctc	ctcgtacctc	aactgggtatc	agcaaaagcc	gggaaaggcg	1380
cctaagctgc	tgatctacgc	cgcttcgagc	ttgcaaagcg	gggtgccatc	cagatttctcg	1440
ggatcaggct	caggaaccga	cttcaccctg	accgtgaaca	gcctccagcc	ggaggacttt	1500
gccacttact	actgccagca	gggagactcc	gtgccgctta	ctttcggggg	gggtaccgcg	1560
ctggagatca	agaccactac	cccagcaccg	aggccacca	ccccggctcc	taccatcgcc	1620
tcccagcctc	tgtccctgcg	tccggaggca	tgtagaccgc	cagctgggtg	ggccgtgcat	1680
acccggggtc	ttgacttcgc	ctgcgatatc	tacatttggg	cccctctggc	tggtacttgc	1740
ggggtcctgc	tgctttcact	cgtgatcact	ctttactgta	agcgcggctc	gaagaagctg	1800
ctgtacatct	ttaagcaacc	cttcattgag	cctgtgcaga	ctactcaaga	ggaggacggc	1860
tgttcatgcc	ggttcccaga	ggaggaggaa	ggcggctgcg	aactgcgcgt	gaaattcagc	1920
cgcagcgag	atgctccagc	ctaccagcag	gggcagaacc	agctctacaa	cgaactcaat	1980
cttggtcggg	gagaggagta	cgacgtgctg	gacaagcgga	gaggacggga	cccagaaatg	2040
ggcgggaagc	cgcgagaaa	gaatccccaa	gagggcctgt	acaacgagct	ccaaaaggat	2100
aagatggcag	aagcctatag	cgagattggt	atgaaagggg	aacgcagaag	aggcaaaggc	2160
cacgacggac	tgtaccaggg	actcagcacc	gccaccaagg	acacctatga	cgctcttcac	2220
atgcaggccc	tgccgcctcg	g				2241

<210> 1106

<211> 2247

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1106

atggccctcc	ctgtcaccgc	cctgctgctt	ccgctggctc	ttctgctcca	cgccgctcgg	60
ccccagtcgt	tggcactttc	cctgactgcc	gaccagatgg	tgtccgccct	tctggacgcc	120
gagcctccaa	ttctgtactc	ggagtacgat	ccgactcgcc	cgttctccga	agccagcatg	180
atgggcctgt	tgactaacct	ggcggaccgc	gagttggtgc	acatgattaa	ctgggctaag	240
cgggtgccgg	gcttcgtgga	cctggccctg	cacgaccaag	tgcacctcct	ggaatgcgcc	300
tggatggaaa	tcctcatgat	cggcctcgtg	tggagatcca	tggagcatcc	cggaaagctc	360
ctgtttgcac	ccaacctcct	gcttgatcgc	aaccagggaa	aatgcgtgga	aggggggtgc	420

	_SL	
gagatttttcg	acatgctgct	cgccacctct
gaagagttcg	tgtgtctgaa	gtcaatcatc
agctcgaccc	tcaagtcact	ggaggaaaaa
accgacaccc	ttatccatct	catggcgaag
aggctggccc	agttgctgct	gattctgagc
gaacacctgt	acagcatgaa	gtgcaagaac
atgctggacg	cgcacagact	cgaacccggc
aggtccctcg	gagacgtggg	tgaagtgcaa
cctggaggat	cgctgagact	gtcatgtgcc
atgtcctggg	tccgccgcgc	gcctggaaaag
agcggtagca	cctactatgc	cgcacccgtg
tccaggaaca	ctctgtacct	ccaaatgaat
tactgtccg	cgcacagcgc	agagtcggac
tctagcgcgt	ccggcggagg	cggcagcggg
atccagctca	cccagtcctc	gagctcgctg
acgtgccgcg	ccagccagtc	gatttcctcc
aaagccccga	agctttctcat	ctacgccgcc
ttctccggct	ccgggttcgg	tactgatttc
gacttcgcta	cttactactg	ccagcagtcg
accaaggtcg	aaatcaagac	cactacccca
atgcctccc	agcctctgtc	cctgcgtccg
gtgcataccc	ggggctctga	cttcgcctgc
acttgccggg	tcctgctgct	ttcactcgtg
aagctgctgt	acatctttta	gcaacccttc
gacggctgtt	catgccgggt	cccagaggag
ttcagccgca	gcgcagatgc	tccagcctac
ctcaatcttg	gtcggagaga	ggagtacgac
gaaatgggcg	ggaagccgcg	cagaaagaat
aaggataaga	tggcagaagc	ctatagcgag
aaaggccacg	acggactgta	ccagggactc
cttcacatgc	aggccctgcc	gcctcgg

480
540
600
660
720
780
840
900
960
1020
1080
1140
1200
1260
1320
1380
1440
1500
1560
1620
1680
1740
1800
1860
1920
1980
2040
2100
2160
2220
2247

<210> 1107
 <211> 2247
 <212> DNA
 <213> Artificial Sequence

_SL

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1107

atggccctcc	ctgtcaccgc	cctgctgctt	ccgctggctc	ttctgctcca	cgccgctcgg	60
ccccagtcgt	tggcactttc	cctgactgcc	gaccagatgg	tgtccgccct	tctggacgcc	120
gagcctccaa	ttctgtactc	ggagtacgat	ccgactcgcc	cgttctccga	agccagcatg	180
atgggcctgt	tgactaacct	ggcggaccgc	gagttggtgc	acatgattaa	ctgggctaag	240
cgggtgccgg	gcttcgtgga	cctgaccctg	cacgaccaag	tgcacctcct	ggaatgcgcc	300
tggatggaaa	tcctcatgat	cggcctcgtg	tggagatcca	tggagcatcc	cggaaagctc	360
ctgtttgcac	ccaacctcct	gcttgatcgc	aaccagggaa	aatgcgtgga	agggggtgtc	420
gagattttcg	acatgctgct	cgccacctct	tcccggttcc	ggatgatgaa	tctgcaggga	480
gaagagttcg	tgtgtctgaa	gtcaatcatc	ctgctgaact	ccgggggtcta	taccttcctg	540
agctcgaccc	tcaagtcact	ggaggaaaaa	gaccacatcc	atcgctgct	cgataagatc	600
accgacaccc	ttatccatct	catggcgaag	gctggactga	ccctgcaaca	gcagcaccag	660
aggctggccc	agttgctgct	gattctgagc	cacatccggc	acatgtcgaa	caagaggatg	720
gaacacctgt	acagcatgaa	gtgcaagaac	gtcgtgcctc	tgtccgatct	gctcctggaa	780
atgctggacg	cgcacagact	cgggaaccggc	gcggaagacc	cccggccctc	caggaagcga	840
aggtcctctg	gagacgtggg	tgaagtgcaa	ttggtggaat	cagggggagg	acttgtgcag	900
cctggaggat	cgctgagact	gtcatgtgcc	gtgtccggct	ttgccctgtc	caaccacggg	960
atgtcctggg	tccgccgcgc	gcctggaaaag	ggcctcgaat	gggtgtcggg	tattgtgtac	1020
agcggtagca	cctactatgc	cgcacccgtg	aaggggagat	tcaccatcag	ccgggacaac	1080
tccaggaaca	ctctgtacct	ccaaatgaat	tcgctgaggc	cagaggacac	tgccatctac	1140
tactgtcccg	cgcattggcg	agagtccgac	gtctggggac	aggggaccac	cgtgaccgtg	1200
tctagcgcgt	ccggcggagg	cggcagcggg	ggtcgggcat	cagggggcgg	cggatcggac	1260
atccagctca	cccagtcccc	gagctcgctg	tccgcctccg	tgggagatcg	ggtcaccatc	1320
acgtgcccg	ccagccagtc	gatttcctcc	tacctgaact	ggtaccaaca	gaagcccgga	1380
aaagccccga	agctttctcat	ctacgccgcc	tcgagcctgc	agtcaggagt	gccctcacgg	1440
ttctccggct	ccggttccgg	tactgatttc	accctgacca	tttcctccct	gcaaccggag	1500
gacttcgcta	cttactactg	ccagcagtcg	tactccaccc	cctacacttt	cggacaaggc	1560
accaaggctg	aaatcaagac	cactacccca	gcaccgaggc	caccaccccc	ggctcctacc	1620
atgcctccc	agcctctgtc	cctgcgtccg	gaggcatgta	gaccgcagc	tggtggggcc	1680
gtgcataccc	ggggtcttga	cttcgcctgc	gatattctaca	tttgggcccc	tctggctggt	1740
acttgccggg	tcctgctgct	ttcactcgtg	atcactcttt	actgtaagcg	cggtcggaag	1800
aagctgctgt	acatctttaa	gcaacccttc	atgaggcctg	tgcagactac	tcaagaggag	1860

	_SL	
gacggctgtt catgccgggtt cccagaggag gaggaaggcg gctgcgaact ggcgctgaaa		1920
ttcagccgca gcgcagatgc tccagcctac cagcaggggc agaaccagct ctacaacgaa		1980
ctcaatcttg gtcggagaga ggagtacgac gtgctggaca agcggagagg acgggaccca		2040
gaaatgggcg ggaagccgcg cagaaagaat cccaagagg gcctgtacaa cgagctccaa		2100
aaggataaga tggcagaagc ctatagcgag attggtatga aaggggaacg cagaagaggc		2160
aaaggccacg acggactgta ccagggactc agcaccgcc acaaggacac ctatgacgct		2220
cttcacatgc aggccctgcc gcctcgg		2247

<210> 1108
 <211> 2229
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1108	
atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg	60
ccccagtcgt tggcactttc cctgactgcc gaccagatgg tgtccgccct tctggacgcc	120
gagcctccaa ttctgtactc ggagtacgat ccgactcgcc cgttctccga agccagcatg	180
atgggcctgt tgactaacct ggcggaccgc gagttggtgc acatgattaa ctgggctaag	240
cgggtgccgg gcttcgtgga cctggccctg caccaccaag tgcacctcct ggaatgcgcc	300
tggatgga aa tcctcatgat cggcctcgtg tggagatcca tggagcatcc cggaaagctc	360
ctgtttgcac ccaacctcct gcttgatcgc aaccaggga aatgcgtgga agggggtgtc	420
gagattttcg acatgctgct cgccacctct tcccggttcc ggatgatgaa tctgcaggga	480
gaagagtctg tgtgtctgaa gtcaatcatc ctgctgaact ccgggggtcta taccttcctg	540
agctcgaccc tcaagtcact ggaggaaaaa gaccacatcc atcgcgtgct cgataagatc	600
accgacaccc ttatccatct catggcgaag gctggactga ccctgcaaca gcagcaccag	660
aggctggccc agttgctgct gattctgagc cacatccggc acatgtcgtc caagaggatg	720
gaacacctgt acagcatgaa gtgcaagaac gtcgtgcctc tgtccgatct gtcctggaa	780
atgctggacg cgcacagact cgggacggga gctgaagatc caccgaccag cagaaagcga	840
cgggaagtgc aattggtgga atcaggggga ggacttgtgc agcctggagg atcgtgaga	900
ctgtcatgtg ccgtgtccgg ctttgccctg tccaaccacg ggatgtcctg ggtccgccgc	960
gcgcctggaa agggcctcga atgggtgtcg ggtatttgtt acagcggtag cacctactat	1020
gccgcatccg tgaaggggag attcaccatc agccgggaca actccaggaa cactctgtac	1080
ctccaaatga attcgtgag gccagaggac actgccatct actactgtc cgcgcatggc	1140
ggagagtccg acgtctgggg acaggggacc accgtgaccg tgtctagcgc gtccggcgga	1200
ggcggcagcg ggggtcgggc atcagggggc ggcggatcgg acatccagct caccagctcc	1260

	_SL	
ccgagctcgc tgtccgcctc cgtgggagat cgggtcacca tcacgtgccg cgccagccag		1320
tcgatttcct cctacctgaa ctggtaccaa cagaagcccc gaaaagcccc gaagcttctc		1380
atctacgccg cctcgagcct gcagtcagga gtgccctcac ggttctccgg ctccggttcc		1440
ggtactgatt tcacctgac catttcctcc ctgcaaccgg aggacttcgc tacttactac		1500
tgccagcagt cgtactccac cccctacact ttccggacaag gcaccaaggt cgaaatcaag		1560
accactaccc cagcaccgag gccaccacc ccggctccta ccatcgctc ccagcctctg		1620
tccctgcgtc cggaggcatg tagaccgca gctggtgggg ccgtgcatac ccggggctct		1680
gacttcgcct gcgatatcta catttgggcc cctctggctg gtacttgccg ggtcctgctg		1740
ctttcactcg tgatcactct ttactgtaag cgcggtcgga agaagctgct gtacatcttt		1800
aagcaaccct tcatgaggcc tgtgcagact actcaagagg aggacggctg ttcatgccgg		1860
ttcccagagg aggaggaagg cggctgcgaa ctgcgcgtga aattcagccg cagcgcagat		1920
gctccagcct accagcaggg gcagaaccag ctctacaacg aactcaatct tggtcggaga		1980
gaggagtacg acgtgctgga caagcggaga ggacgggacc cagaaatggg cgggaagccg		2040
cgcagaaaaga atccccaaga gggcctgtac aacgagctcc aaaaggataa gatggcagaa		2100
gcctatagcg agattggtat gaaaggggaa cgcagaagag gcaaaggcca cgacggactg		2160
taccagggac tcagcaccgc caccaaggac acctatgacg ctcttcacat gcaggccctg		2220
ccgcctcgg		2229

<210> 1109

<211> 2229

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1109

atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg		60
ccccagtcgt tggcactttc cctgactgcc gaccagatgg tgtccgccct tctggacgcc		120
gagcctccaa ttctgtactc ggagtacgat ccgactcgcc cgttctccga agccagcatg		180
atgggcctgt tgactaacct ggcggaccgc gagttggtgc acatgattaa ctgggctaag		240
cgggtgccgg gcttcgtgga cctgaccctg caccaccaag tgcacctcct ggaatgcgcc		300
tggatggaaa tcctcatgat cggcctcgtg tggagatcca tggagcatcc cggaaagctc		360
ctgtttgcac ccaacctcct gcttgatcgc aaccagggaa aatgcgtgga agggggtgtc		420
gagattttcg acatgctgct cgccacctct tcccggttcc ggatgatgaa tctgcaggga		480
gaagagttcg tgtgtctgaa gtcaatcatc ctgctgaact ccgggggtcta taccttcctg		540
agctcgaccc tcaagtcact ggaggaaaaa gaccacatcc atcgcgtgct cgataagatc		600
accgacaccc ttatccatct catggcgaag gctggactga ccctgcaaca gcagcaccag		660

	_SL	
aggctggccc agttgctgct gattctgagc cacatccggc acatgtcgaa caagaggatg		720
gaacacctgt acagcatgaa gtgcaagaac gtcgtgcctc tgtccgatct gtccttgaa		780
atgctggacg cgcacagact cgggacggga gctgaagatc cacgaccag cagaaagcga		840
cgggaagtgc aattggtgga atcaggggga ggacttgctc agcctggagg atcgtgaga		900
ctgtcatgtg ccgtgtccgg ctttgccctg tccaaccacg ggatgtcctg ggtccgccgc		960
gcgcctggaa agggcctcga atgggtgtcg ggtatttgtt acagcggtag cacctactat		1020
gccgcatccg tgaaggggag attcaccatc agccgggaca actccaggaa cactctgtac		1080
ctccaaatga attcgctgag gccagaggac actgccatct actactgctc cgcgcatggc		1140
ggagagtccg acgtctgggg acaggggacc accgtgaccg tgtctagcgc gtccggcgga		1200
ggcggcagcg ggggtcgggc atcagggggc ggcggtatcg acatccagct caccagttcc		1260
ccgagctcgc tgtccgcctc cgtgggagat cgggtcacca tcacgtgccg cgccagccag		1320
tcgatttcct cctacctgaa ctggtaccaa cagaagcccc gaaaagcccc gaagcttctc		1380
atctacgccg cctcgagcct gcagtcagga gtgccctcac ggttctccgg ctccggttcc		1440
ggtactgatt tcaccctgac catttcctcc ctgcaaccgg aggacttcgc tacttactac		1500
tgccagcagt cgtactccac cccctacact ttcggacaag gcaccaaggt cgaaatcaag		1560
accactacc cagcaccgag gccaccacc ccggctccta ccatcgctc ccagcctctg		1620
tccctgcgtc cggaggcatg tagaccgca gctggtgggg ccgtgcatac ccgggggtctt		1680
gacttcgcct gcgatatcta catttgggcc cctctggctg gtacttgctg ggtcctgctg		1740
ctttcactcg tgatcactct ttactgtaag cgcggtcgga agaagctgct gtacatcttt		1800
aagcaaccct tcatgaggcc tgtgcagact actcaagagg aggacggctg ttcatgccgg		1860
ttcccagagg aggaggaagg cggctgcgaa ctgcgcgtga aattcagccg cagcgcagat		1920
gctccagcct accagcaggg gcagaaccag ctctacaacg aactcaatct tggtcggaga		1980
gaggagtacg acgtgctgga caagcggaga ggacgggacc cagaaatggg cgggaagccg		2040
cgcagaaaga atccccaaga gggcctgtac aacgagctcc aaaaggataa gatggcagaa		2100
gcctatagcg agattggtat gaaaggggaa cgcagaagag gcaaaggcca cgacggactg		2160
taccagggac tcagcaccgc caccaaggac acctatgacg ctcttcacat gcaggccctg		2220
ccgcctcgg		2229

<210> 1110

<211> 735

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1110

tcgttggcac tttccctgac tgccgaccag atggtgtccg cccttctgga cgccgagcct	60
---	----

ccaattctgt actcggagta cgatccgact cgcccgttct ccgaagccag catgatgggc 120
ctgttgacta acctggcgga ccgcgagttg gtgcacatga ttaactgggc taagcgggtg 180
ccgggcttcg tggacctggc cctgcacgac caagtgcacc tcctggaatg cgcctggatg 240
gaaatcctca tgatcggcct cgtgtggaga tccatggagc atcccgaaa gctcctgttt 300
gcaccaacc tcctgcttga tcgcaaccag ggaaaatgcg tggaaggggg tgctgagatt 360
ttcgacatgc tgctcgccac ctcttcccgg ttccggatga tgaatctgca gggagaagag 420
ttcgtgtgtc tgaagtcaat catcctgctg aactccgggg tctatacctt cctgagctcg 480
accctcaagt cactggagga aaaagaccac atccatcgcg tgctcgataa gatcaccgac 540
acccttatcc atctcatggc gaaggctgga ctgaccctgc aacagcagca ccagaggctg 600
gccagttgc tgctgattct gagccacatc cggcacatgt cgtccaagag gatggaacac 660
ctgtacagca tgaagtgcaa gaacgtcgtg cctctgtccg atctgctcct ggaaatgctg 720
gacgcgcaca gactc 735

<210> 1111
<211> 105
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1111
acaaaaaaga agtattcatc cagtgtgcac gaccctaacg gtgaatacat gttcatgaga 60
gcagtgaaca cagccaaaaa atccagactc acagatgtga cccta 105

<210> 1112
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic oligonucleotide"

<400> 1112
cgtactaaaa ga 12

<210> 1113
<211> 123
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1113
aggagtaaga ggagcaggct cctgcacagt gactacatga acatgactcc ccgccgcccc 60

_SL
 gggcccaccc gcaagcatta ccagccctat gccccaccac gcgacttcgc agcctatcgc 120
 tcc 123

<210> 1114
 <211> 21
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1114
 Met Gly Leu Leu Gln Leu Leu Ala Phe Ser Phe Leu Ala Leu Cys Arg
 1 5 10 15

Ala Arg Val Arg Ala
 20

<210> 1115
 <211> 21
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1115
 Met Leu Leu Ala Trp Val Gln Ala Phe Leu Val Ser Asn Met Leu Leu
 1 5 10 15

Ala Glu Ala Tyr Gly
 20

<210> 1116
 <211> 21
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1116
 Met Lys Phe Gln Gly Pro Leu Ala Cys Leu Leu Leu Ala Leu Cys Leu
 1 5 10 15

Gly Ser Gly Glu Ala
 20

<210> 1117
 <211> 22
 <212> PRT
 <213> Artificial Sequence

<220>

_SL

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1117

Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
1 5 10 15

Ala Val Phe Val Ser Pro
20

<210> 1118

<211> 35

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1118

Met Gly Thr Val Ser Ser Arg Arg Ser Trp Trp Pro Leu Pro Leu Leu
1 5 10 15

Leu Leu Leu Leu Leu Leu Leu Gly Pro Ala Gly Ala Arg Ala Gln Glu
20 25 30

Asp Glu Asp
35

<210> 1119

<211> 247

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1119

Arg Ser Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln Met Val Ser Ala
1 5 10 15

Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu Tyr Asp Pro Thr
20 25 30

Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu Thr Asn Leu Ala
35 40 45

Asp Arg Glu Leu Val His Met Ile Asn Trp Ala Lys Arg Val Pro Gly
50 55 60

Phe Val Asp Leu Ala Leu His Asp Gln Val His Leu Leu Glu Cys Ala
65 70 75 80

Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp Arg Ser Met Glu His
Page 1019

_SL

<400> 1124
000

<210> 1125

<400> 1125
000

<210> 1126

<400> 1126
000

<210> 1127

<400> 1127
000

<210> 1128

<400> 1128
000

<210> 1129

<400> 1129
000

<210> 1130

<400> 1130
000

<210> 1131

<400> 1131
000

<210> 1132

<400> 1132
000

<210> 1133

<400> 1133
000

<210> 1134

<400> 1134
000

<210> 1135

<400> 1135

000

<210> 1136

<400> 1136
000

<210> 1137

<400> 1137
000

<210> 1138

<400> 1138
000

<210> 1139

<400> 1139
000

<210> 1140

<400> 1140
000

<210> 1141

<400> 1141
000

<210> 1142

<400> 1142
000

<210> 1143

<400> 1143
000

<210> 1144

<400> 1144
000

<210> 1145

<400> 1145
000

<210> 1146

<400> 1146
000

<210> 1147

<400> 1147
000

<210> 1148

<400> 1148
000

<210> 1149

<400> 1149
000

<210> 1150

<400> 1150
000

<210> 1151

<400> 1151
000

<210> 1152

<400> 1152
000

<210> 1153

<400> 1153
000

<210> 1154

<400> 1154
000

<210> 1155

<400> 1155
000

<210> 1156

<400> 1156
000

<210> 1157

<400> 1157
000

<210> 1158

_SL

<400> 1158
000

<210> 1159

<400> 1159
000

<210> 1160

<400> 1160
000

<210> 1161

<400> 1161
000

<210> 1162

<400> 1162
000

<210> 1163

<400> 1163
000

<210> 1164

<400> 1164
000

<210> 1165

<400> 1165
000

<210> 1166

<400> 1166
000

<210> 1167

<400> 1167
000

<210> 1168

<400> 1168
000

<210> 1169

<400> 1169

000

<210> 1170

<400> 1170
000

<210> 1171

<400> 1171
000

<210> 1172

<400> 1172
000

<210> 1173

<400> 1173
000

<210> 1174

<400> 1174
000

<210> 1175

<400> 1175
000

<210> 1176

<400> 1176
000

<210> 1177

<400> 1177
000

<210> 1178

<400> 1178
000

<210> 1179

<400> 1179
000

<210> 1180

<400> 1180

000

<210> 1181

<400> 1181
000

<210> 1182

<400> 1182
000

<210> 1183

<400> 1183
000

<210> 1184

<400> 1184
000

<210> 1185

<400> 1185
000

<210> 1186

<400> 1186
000

<210> 1187

<400> 1187
000

<210> 1188

<400> 1188
000

<210> 1189

<400> 1189
000

<210> 1190

<400> 1190
000

<210> 1191

<400> 1191
000

_SL

<210> 1192

<400> 1192
000

<210> 1193

<400> 1193
000

<210> 1194

<400> 1194
000

<210> 1195

<400> 1195
000

<210> 1196

<400> 1196
000

<210> 1197

<400> 1197
000

<210> 1198

<400> 1198
000

<210> 1199

<400> 1199
000

<210> 1200

<400> 1200
000

<210> 1201

<400> 1201
000

<210> 1202

<400> 1202
000

<210> 1203

<400> 1203
000

<210> 1204

<400> 1204
000

<210> 1205

<400> 1205
000

<210> 1206

<400> 1206
000

<210> 1207

<400> 1207
000

<210> 1208

<400> 1208
000

<210> 1209

<400> 1209
000

<210> 1210

<400> 1210
000

<210> 1211

<400> 1211
000

<210> 1212

<400> 1212
000

<210> 1213

<400> 1213
000

<210> 1214

_SL

<400> 1214
000

<210> 1215

<400> 1215
000

<210> 1216

<400> 1216
000

<210> 1217

<400> 1217
000

<210> 1218

<400> 1218
000

<210> 1219

<400> 1219
000

<210> 1220

<400> 1220
000

<210> 1221

<400> 1221
000

<210> 1222

<400> 1222
000

<210> 1223

<400> 1223
000

<210> 1224

<400> 1224
000

<210> 1225

<400> 1225

000

<210> 1226

<400> 1226
000

<210> 1227

<400> 1227
000

<210> 1228

<400> 1228
000

<210> 1229

<400> 1229
000

<210> 1230

<400> 1230
000

<210> 1231

<400> 1231
000

<210> 1232

<400> 1232
000

<210> 1233

<400> 1233
000

<210> 1234

<400> 1234
000

<210> 1235

<400> 1235
000

<210> 1236

<400> 1236

000

<210> 1237

<400> 1237
000

<210> 1238

<400> 1238
000

<210> 1239

<400> 1239
000

<210> 1240

<400> 1240
000

<210> 1241

<400> 1241
000

<210> 1242

<400> 1242
000

<210> 1243

<400> 1243
000

<210> 1244

<400> 1244
000

<210> 1245

<400> 1245
000

<210> 1246

<400> 1246
000

<210> 1247

<400> 1247
000

<210> 1248

<400> 1248
000

<210> 1249

<400> 1249
000

<210> 1250

<400> 1250
000

<210> 1251

<400> 1251
000

<210> 1252

<400> 1252
000

<210> 1253

<400> 1253
000

<210> 1254

<400> 1254
000

<210> 1255

<400> 1255
000

<210> 1256

<400> 1256
000

<210> 1257

<400> 1257
000

<210> 1258

<400> 1258
000

<210> 1259

_SL

<400> 1259
000

<210> 1260

<400> 1260
000

<210> 1261

<400> 1261
000

<210> 1262

<400> 1262
000

<210> 1263

<400> 1263
000

<210> 1264

<400> 1264
000

<210> 1265

<400> 1265
000

<210> 1266

<400> 1266
000

<210> 1267

<400> 1267
000

<210> 1268

<400> 1268
000

<210> 1269

<400> 1269
000

<210> 1270

<400> 1270

000

<210> 1271

<400> 1271
000

<210> 1272

<400> 1272
000

<210> 1273

<400> 1273
000

<210> 1274

<400> 1274
000

<210> 1275

<400> 1275
000

<210> 1276

<400> 1276
000

<210> 1277

<400> 1277
000

<210> 1278

<400> 1278
000

<210> 1279

<400> 1279
000

<210> 1280

<400> 1280
000

<210> 1281

<400> 1281

000

<210> 1282

<400> 1282
000

<210> 1283

<400> 1283
000

<210> 1284

<400> 1284
000

<210> 1285

<400> 1285
000

<210> 1286

<400> 1286
000

<210> 1287

<400> 1287
000

<210> 1288

<400> 1288
000

<210> 1289

<400> 1289
000

<210> 1290

<400> 1290
000

<210> 1291

<400> 1291
000

<210> 1292

<400> 1292

000

<210> 1293

<400> 1293
000

<210> 1294

<400> 1294
000

<210> 1295

<400> 1295
000

<210> 1296

<400> 1296
000

<210> 1297

<400> 1297
000

<210> 1298

<400> 1298
000

<210> 1299

<400> 1299
000

<210> 1300

<400> 1300
000

<210> 1301

<400> 1301
000

<210> 1302

<400> 1302
000

<210> 1303

<400> 1303
000

<210> 1304

<400> 1304
000

<210> 1305

<400> 1305
000

<210> 1306

<400> 1306
000

<210> 1307

<400> 1307
000

<210> 1308

<400> 1308
000

<210> 1309

<400> 1309
000

<210> 1310

<400> 1310
000

<210> 1311

<400> 1311
000

<210> 1312

<400> 1312
000

<210> 1313

<400> 1313
000

<210> 1314

<400> 1314
000

<210> 1315

_SL

<400> 1315
000

<210> 1316

<400> 1316
000

<210> 1317

<400> 1317
000

<210> 1318

<400> 1318
000

<210> 1319

<400> 1319
000

<210> 1320

<400> 1320
000

<210> 1321

<400> 1321
000

<210> 1322

<400> 1322
000

<210> 1323

<400> 1323
000

<210> 1324

<400> 1324
000

<210> 1325

<400> 1325
000

<210> 1326

<400> 1326

000

<210> 1327

<400> 1327
000

<210> 1328

<400> 1328
000

<210> 1329

<400> 1329
000

<210> 1330

<400> 1330
000

<210> 1331

<400> 1331
000

<210> 1332

<400> 1332
000

<210> 1333

<400> 1333
000

<210> 1334

<400> 1334
000

<210> 1335

<400> 1335
000

<210> 1336

<400> 1336
000

<210> 1337

<400> 1337

000

<210> 1338

<400> 1338
000

<210> 1339

<400> 1339
000

<210> 1340

<400> 1340
000

<210> 1341

<400> 1341
000

<210> 1342

<400> 1342
000

<210> 1343

<400> 1343
000

<210> 1344

<400> 1344
000

<210> 1345

<400> 1345
000

<210> 1346

<400> 1346
000

<210> 1347

<400> 1347
000

<210> 1348

<400> 1348
000

_SL

<210> 1349

<400> 1349
000

<210> 1350

<400> 1350
000

<210> 1351

<400> 1351
000

<210> 1352

<400> 1352
000

<210> 1353

<400> 1353
000

<210> 1354

<400> 1354
000

<210> 1355

<400> 1355
000

<210> 1356

<400> 1356
000

<210> 1357

<400> 1357
000

<210> 1358

<400> 1358
000

<210> 1359

<400> 1359
000

<210> 1360

<400> 1360
000

<210> 1361

<400> 1361
000

<210> 1362

<400> 1362
000

<210> 1363

<400> 1363
000

<210> 1364

<400> 1364
000

<210> 1365

<400> 1365
000

<210> 1366

<400> 1366
000

<210> 1367

<400> 1367
000

<210> 1368

<400> 1368
000

<210> 1369

<400> 1369
000

<210> 1370

<400> 1370
000

<210> 1371

_SL

<400> 1371
000

<210> 1372

<400> 1372
000

<210> 1373

<400> 1373
000

<210> 1374

<400> 1374
000

<210> 1375

<400> 1375
000

<210> 1376

<400> 1376
000

<210> 1377

<400> 1377
000

<210> 1378

<400> 1378
000

<210> 1379

<400> 1379
000

<210> 1380

<400> 1380
000

<210> 1381

<400> 1381
000

<210> 1382

<400> 1382

000

<210> 1383

<400> 1383
000

<210> 1384

<400> 1384
000

<210> 1385

<400> 1385
000

<210> 1386

<400> 1386
000

<210> 1387

<400> 1387
000

<210> 1388

<400> 1388
000

<210> 1389

<400> 1389
000

<210> 1390

<400> 1390
000

<210> 1391

<400> 1391
000

<210> 1392

<400> 1392
000

<210> 1393

<400> 1393
000

_SL

<210> 1394

<400> 1394
000

<210> 1395

<400> 1395
000

<210> 1396

<400> 1396
000

<210> 1397

<400> 1397
000

<210> 1398

<400> 1398
000

<210> 1399

<400> 1399
000

<210> 1400

<400> 1400
000

<210> 1401

<400> 1401
000

<210> 1402

<400> 1402
000

<210> 1403

<400> 1403
000

<210> 1404

<400> 1404
000

_SL

<210> 1405

<400> 1405
000

<210> 1406

<400> 1406
000

<210> 1407

<400> 1407
000

<210> 1408

<400> 1408
000

<210> 1409

<400> 1409
000

<210> 1410

<400> 1410
000

<210> 1411

<400> 1411
000

<210> 1412

<400> 1412
000

<210> 1413

<400> 1413
000

<210> 1414

<400> 1414
000

<210> 1415

<400> 1415
000

<210> 1416

<400> 1416
000

<210> 1417

<400> 1417
000

<210> 1418

<400> 1418
000

<210> 1419

<400> 1419
000

<210> 1420

<400> 1420
000

<210> 1421

<400> 1421
000

<210> 1422

<400> 1422
000

<210> 1423

<400> 1423
000

<210> 1424

<400> 1424
000

<210> 1425

<400> 1425
000

<210> 1426

<400> 1426
000

<210> 1427

_SL

<400> 1427
000

<210> 1428

<400> 1428
000

<210> 1429

<400> 1429
000

<210> 1430

<400> 1430
000

<210> 1431

<400> 1431
000

<210> 1432

<400> 1432
000

<210> 1433

<400> 1433
000

<210> 1434

<400> 1434
000

<210> 1435

<400> 1435
000

<210> 1436

<400> 1436
000

<210> 1437

<400> 1437
000

<210> 1438

<400> 1438

000

<210> 1439

<400> 1439
000

<210> 1440

<400> 1440
000

<210> 1441

<400> 1441
000

<210> 1442

<400> 1442
000

<210> 1443

<400> 1443
000

<210> 1444

<400> 1444
000

<210> 1445

<400> 1445
000

<210> 1446

<400> 1446
000

<210> 1447

<400> 1447
000

<210> 1448

<400> 1448
000

<210> 1449

<400> 1449
000

<210> 1450

<400> 1450
000

<210> 1451

<400> 1451
000

<210> 1452

<400> 1452
000

<210> 1453

<400> 1453
000

<210> 1454

<400> 1454
000

<210> 1455

<400> 1455
000

<210> 1456

<400> 1456
000

<210> 1457

<400> 1457
000

<210> 1458

<400> 1458
000

<210> 1459

<400> 1459
000

<210> 1460

<400> 1460
000

<210> 1461

_SL

<400> 1461
000

<210> 1462

<400> 1462
000

<210> 1463

<400> 1463
000

<210> 1464

<400> 1464
000

<210> 1465

<400> 1465
000

<210> 1466

<400> 1466
000

<210> 1467

<400> 1467
000

<210> 1468

<400> 1468
000

<210> 1469

<400> 1469
000

<210> 1470

<400> 1470
000

<210> 1471

<400> 1471
000

<210> 1472

_SL

<400> 1472
000

<210> 1473

<400> 1473
000

<210> 1474

<400> 1474
000

<210> 1475

<400> 1475
000

<210> 1476

<400> 1476
000

<210> 1477

<400> 1477
000

<210> 1478

<400> 1478
000

<210> 1479

<400> 1479
000

<210> 1480

<400> 1480
000

<210> 1481

<400> 1481
000

<210> 1482

<400> 1482
000

<210> 1483

_SL

<400> 1483
000

<210> 1484

<400> 1484
000

<210> 1485

<400> 1485
000

<210> 1486

<400> 1486
000

<210> 1487

<400> 1487
000

<210> 1488

<400> 1488
000

<210> 1489

<400> 1489
000

<210> 1490

<400> 1490
000

<210> 1491

<400> 1491
000

<210> 1492

<400> 1492
000

<210> 1493

<400> 1493
000

<210> 1494

<400> 1494

000

<210> 1495

<400> 1495
000

<210> 1496

<400> 1496
000

<210> 1497

<400> 1497
000

<210> 1498

<400> 1498
000

<210> 1499

<400> 1499
000

<210> 1500

<400> 1500
000

<210> 1501

<400> 1501
000

<210> 1502

<400> 1502
000

<210> 1503

<400> 1503
000

<210> 1504

<400> 1504
000

<210> 1505

<400> 1505
000

_SL

<210> 1506

<400> 1506
000

<210> 1507

<400> 1507
000

<210> 1508

<400> 1508
000

<210> 1509

<400> 1509
000

<210> 1510

<400> 1510
000

<210> 1511

<400> 1511
000

<210> 1512

<400> 1512
000

<210> 1513

<400> 1513
000

<210> 1514

<400> 1514
000

<210> 1515

<400> 1515
000

<210> 1516

<400> 1516
000

<210> 1517

_SL

<400> 1517
000

<210> 1518

<400> 1518
000

<210> 1519

<400> 1519
000

<210> 1520

<400> 1520
000

<210> 1521

<400> 1521
000

<210> 1522

<400> 1522
000

<210> 1523

<400> 1523
000

<210> 1524

<400> 1524
000

<210> 1525

<400> 1525
000

<210> 1526

<400> 1526
000

<210> 1527

<400> 1527
000

<210> 1528

_SL

<400> 1528
000

<210> 1529

<400> 1529
000

<210> 1530

<400> 1530
000

<210> 1531

<400> 1531
000

<210> 1532

<400> 1532
000

<210> 1533

<400> 1533
000

<210> 1534

<400> 1534
000

<210> 1535

<400> 1535
000

<210> 1536

<400> 1536
000

<210> 1537

<400> 1537
000

<210> 1538

<400> 1538
000

<210> 1539

<400> 1539

000

<210> 1540

<400> 1540
000

<210> 1541

<400> 1541
000

<210> 1542

<400> 1542
000

<210> 1543

<400> 1543
000

<210> 1544

<400> 1544
000

<210> 1545

<400> 1545
000

<210> 1546

<400> 1546
000

<210> 1547

<400> 1547
000

<210> 1548

<400> 1548
000

<210> 1549

<400> 1549
000

<210> 1550

<400> 1550

000

<210> 1551

<400> 1551
000

<210> 1552

<400> 1552
000

<210> 1553

<400> 1553
000

<210> 1554

<400> 1554
000

<210> 1555

<400> 1555
000

<210> 1556

<400> 1556
000

<210> 1557

<400> 1557
000

<210> 1558

<400> 1558
000

<210> 1559

<400> 1559
000

<210> 1560

<400> 1560
000

<210> 1561

<400> 1561
000

<210> 1562

<400> 1562
000

<210> 1563

<400> 1563
000

<210> 1564

<400> 1564
000

<210> 1565

<400> 1565
000

<210> 1566

<400> 1566
000

<210> 1567

<400> 1567
000

<210> 1568

<400> 1568
000

<210> 1569

<400> 1569
000

<210> 1570

<400> 1570
000

<210> 1571

<400> 1571
000

<210> 1572

<400> 1572
000

<210> 1573

_SL

<400> 1573
000

<210> 1574

<400> 1574
000

<210> 1575

<400> 1575
000

<210> 1576

<400> 1576
000

<210> 1577

<400> 1577
000

<210> 1578

<400> 1578
000

<210> 1579

<400> 1579
000

<210> 1580

<400> 1580
000

<210> 1581

<400> 1581
000

<210> 1582

<400> 1582
000

<210> 1583

<400> 1583
000

<210> 1584

<400> 1584

000

<210> 1585

<400> 1585
000

<210> 1586

<400> 1586
000

<210> 1587

<400> 1587
000

<210> 1588

<400> 1588
000

<210> 1589

<400> 1589
000

<210> 1590

<400> 1590
000

<210> 1591

<400> 1591
000

<210> 1592

<400> 1592
000

<210> 1593

<400> 1593
000

<210> 1594

<400> 1594
000

<210> 1595

<400> 1595

000

<210> 1596

<400> 1596
000

<210> 1597

<400> 1597
000

<210> 1598

<400> 1598
000

<210> 1599

<400> 1599
000

<210> 1600

<400> 1600
000

<210> 1601

<400> 1601
000

<210> 1602

<400> 1602
000

<210> 1603

<400> 1603
000

<210> 1604

<400> 1604
000

<210> 1605

<400> 1605
000

<210> 1606

<400> 1606
000

_SL

<210> 1607

<400> 1607
000

<210> 1608

<400> 1608
000

<210> 1609

<400> 1609
000

<210> 1610

<400> 1610
000

<210> 1611

<400> 1611
000

<210> 1612

<400> 1612
000

<210> 1613

<400> 1613
000

<210> 1614

<400> 1614
000

<210> 1615

<400> 1615
000

<210> 1616

<400> 1616
000

<210> 1617

<400> 1617
000

_SL

<210> 1618

<400> 1618
000

<210> 1619

<400> 1619
000

<210> 1620

<400> 1620
000

<210> 1621

<400> 1621
000

<210> 1622

<400> 1622
000

<210> 1623

<400> 1623
000

<210> 1624

<400> 1624
000

<210> 1625

<400> 1625
000

<210> 1626

<400> 1626
000

<210> 1627

<400> 1627
000

<210> 1628

<400> 1628
000

<210> 1629

_SL

<400> 1629
000

<210> 1630

<400> 1630
000

<210> 1631

<400> 1631
000

<210> 1632

<400> 1632
000

<210> 1633

<400> 1633
000

<210> 1634

<400> 1634
000

<210> 1635

<400> 1635
000

<210> 1636

<400> 1636
000

<210> 1637

<400> 1637
000

<210> 1638

<400> 1638
000

<210> 1639

<400> 1639
000

<210> 1640

<400> 1640

000

<210> 1641

<400> 1641
000

<210> 1642

<400> 1642
000

<210> 1643

<400> 1643
000

<210> 1644

<400> 1644
000

<210> 1645

<400> 1645
000

<210> 1646

<400> 1646
000

<210> 1647

<400> 1647
000

<210> 1648

<400> 1648
000

<210> 1649

<400> 1649
000

<210> 1650

<400> 1650
000

<210> 1651

<400> 1651
000

_SL

<210> 1652

<400> 1652
000

<210> 1653

<400> 1653
000

<210> 1654

<400> 1654
000

<210> 1655

<400> 1655
000

<210> 1656

<400> 1656
000

<210> 1657

<400> 1657
000

<210> 1658

<400> 1658
000

<210> 1659

<400> 1659
000

<210> 1660

<400> 1660
000

<210> 1661

<400> 1661
000

<210> 1662

<400> 1662
000

<210> 1663

<400> 1663
000

<210> 1664

<400> 1664
000

<210> 1665

<400> 1665
000

<210> 1666

<400> 1666
000

<210> 1667

<400> 1667
000

<210> 1668

<400> 1668
000

<210> 1669

<400> 1669
000

<210> 1670

<400> 1670
000

<210> 1671

<400> 1671
000

<210> 1672

<400> 1672
000

<210> 1673

<400> 1673
000

<210> 1674

<400> 1674
000

<210> 1675

<400> 1675
000

<210> 1676

<400> 1676
000

<210> 1677

<400> 1677
000

<210> 1678

<400> 1678
000

<210> 1679

<400> 1679
000

<210> 1680

<400> 1680
000

<210> 1681

<400> 1681
000

<210> 1682

<400> 1682
000

<210> 1683

<400> 1683
000

<210> 1684

<400> 1684
000

<210> 1685

_SL

<400> 1685
000

<210> 1686

<400> 1686
000

<210> 1687

<400> 1687
000

<210> 1688

<400> 1688
000

<210> 1689

<400> 1689
000

<210> 1690

<400> 1690
000

<210> 1691

<400> 1691
000

<210> 1692

<400> 1692
000

<210> 1693

<400> 1693
000

<210> 1694

<400> 1694
000

<210> 1695

<400> 1695
000

<210> 1696

<400> 1696

000

<210> 1697

<400> 1697
000

<210> 1698

<400> 1698
000

<210> 1699

<400> 1699
000

<210> 1700

<400> 1700
000

<210> 1701

<400> 1701
000

<210> 1702

<400> 1702
000

<210> 1703

<400> 1703
000

<210> 1704

<400> 1704
000

<210> 1705

<400> 1705
000

<210> 1706

<400> 1706
000

<210> 1707

<400> 1707
000

_SL

<210> 1708

<400> 1708
000

<210> 1709

<400> 1709
000

<210> 1710

<400> 1710
000

<210> 1711

<400> 1711
000

<210> 1712

<400> 1712
000

<210> 1713

<400> 1713
000

<210> 1714

<400> 1714
000

<210> 1715

<400> 1715
000

<210> 1716

<400> 1716
000

<210> 1717

<400> 1717
000

<210> 1718

<400> 1718
000

<210> 1719

_SL

<400> 1719
000

<210> 1720

<400> 1720
000

<210> 1721

<400> 1721
000

<210> 1722

<400> 1722
000

<210> 1723

<400> 1723
000

<210> 1724

<400> 1724
000

<210> 1725

<400> 1725
000

<210> 1726

<400> 1726
000

<210> 1727

<400> 1727
000

<210> 1728

<400> 1728
000

<210> 1729

<400> 1729
000

<210> 1730

_SL

<400> 1730
000

<210> 1731

<400> 1731
000

<210> 1732

<400> 1732
000

<210> 1733

<400> 1733
000

<210> 1734

<400> 1734
000

<210> 1735

<400> 1735
000

<210> 1736

<400> 1736
000

<210> 1737

<400> 1737
000

<210> 1738

<400> 1738
000

<210> 1739

<400> 1739
000

<210> 1740

<400> 1740
000

<210> 1741

_SL

<400> 1741
000

<210> 1742

<400> 1742
000

<210> 1743

<400> 1743
000

<210> 1744

<400> 1744
000

<210> 1745

<400> 1745
000

<210> 1746

<400> 1746
000

<210> 1747

<400> 1747
000

<210> 1748

<400> 1748
000

<210> 1749

<400> 1749
000

<210> 1750

<400> 1750
000

<210> 1751

<400> 1751
000

<210> 1752

<400> 1752

000

<210> 1753

<400> 1753
000

<210> 1754

<400> 1754
000

<210> 1755

<400> 1755
000

<210> 1756

<400> 1756
000

<210> 1757

<400> 1757
000

<210> 1758

<400> 1758
000

<210> 1759

<400> 1759
000

<210> 1760

<400> 1760
000

<210> 1761

<400> 1761
000

<210> 1762

<400> 1762
000

<210> 1763

<400> 1763
000

_SL

<210> 1764

<400> 1764
000

<210> 1765

<400> 1765
000

<210> 1766

<400> 1766
000

<210> 1767

<400> 1767
000

<210> 1768

<400> 1768
000

<210> 1769

<400> 1769
000

<210> 1770

<400> 1770
000

<210> 1771

<400> 1771
000

<210> 1772

<400> 1772
000

<210> 1773

<400> 1773
000

<210> 1774

<400> 1774
000

<210> 1775

_SL

<400> 1775
000

<210> 1776

<400> 1776
000

<210> 1777

<400> 1777
000

<210> 1778

<400> 1778
000

<210> 1779

<400> 1779
000

<210> 1780

<400> 1780
000

<210> 1781

<400> 1781
000

<210> 1782

<400> 1782
000

<210> 1783

<400> 1783
000

<210> 1784

<400> 1784
000

<210> 1785

<400> 1785
000

<210> 1786

_SL

<400> 1786
000

<210> 1787

<400> 1787
000

<210> 1788

<400> 1788
000

<210> 1789

<400> 1789
000

<210> 1790

<400> 1790
000

<210> 1791

<400> 1791
000

<210> 1792

<400> 1792
000

<210> 1793

<400> 1793
000

<210> 1794

<400> 1794
000

<210> 1795

<400> 1795
000

<210> 1796

<400> 1796
000

<210> 1797

<400> 1797

000

<210> 1798

<400> 1798
000

<210> 1799

<400> 1799
000

<210> 1800

<400> 1800
000

<210> 1801

<400> 1801
000

<210> 1802

<400> 1802
000

<210> 1803

<400> 1803
000

<210> 1804

<400> 1804
000

<210> 1805

<400> 1805
000

<210> 1806

<400> 1806
000

<210> 1807

<400> 1807
000

<210> 1808

<400> 1808

000

<210> 1809

<400> 1809
000

<210> 1810

<400> 1810
000

<210> 1811

<400> 1811
000

<210> 1812

<400> 1812
000

<210> 1813

<400> 1813
000

<210> 1814

<400> 1814
000

<210> 1815

<400> 1815
000

<210> 1816

<400> 1816
000

<210> 1817

<400> 1817
000

<210> 1818

<400> 1818
000

<210> 1819

<400> 1819
000

<210> 1820

<400> 1820
000

<210> 1821

<400> 1821
000

<210> 1822

<400> 1822
000

<210> 1823

<400> 1823
000

<210> 1824

<400> 1824
000

<210> 1825

<400> 1825
000

<210> 1826

<400> 1826
000

<210> 1827

<400> 1827
000

<210> 1828

<400> 1828
000

<210> 1829

<400> 1829
000

<210> 1830

<400> 1830
000

<210> 1831

_SL

<400> 1831
000

<210> 1832

<400> 1832
000

<210> 1833

<400> 1833
000

<210> 1834

<400> 1834
000

<210> 1835

<400> 1835
000

<210> 1836

<400> 1836
000

<210> 1837

<400> 1837
000

<210> 1838

<400> 1838
000

<210> 1839

<400> 1839
000

<210> 1840

<400> 1840
000

<210> 1841

<400> 1841
000

<210> 1842

<400> 1842

000

<210> 1843

<400> 1843
000

<210> 1844

<400> 1844
000

<210> 1845

<400> 1845
000

<210> 1846

<400> 1846
000

<210> 1847

<400> 1847
000

<210> 1848

<400> 1848
000

<210> 1849

<400> 1849
000

<210> 1850

<400> 1850
000

<210> 1851

<400> 1851
000

<210> 1852

<400> 1852
000

<210> 1853

<400> 1853

000

<210> 1854

<400> 1854
000

<210> 1855

<400> 1855
000

<210> 1856

<400> 1856
000

<210> 1857

<400> 1857
000

<210> 1858

<400> 1858
000

<210> 1859

<400> 1859
000

<210> 1860

<400> 1860
000

<210> 1861

<400> 1861
000

<210> 1862

<400> 1862
000

<210> 1863

<400> 1863
000

<210> 1864

<400> 1864
000

_SL

<210> 1865

<400> 1865
000

<210> 1866

<400> 1866
000

<210> 1867

<400> 1867
000

<210> 1868

<400> 1868
000

<210> 1869

<400> 1869
000

<210> 1870

<400> 1870
000

<210> 1871

<400> 1871
000

<210> 1872

<400> 1872
000

<210> 1873

<400> 1873
000

<210> 1874

<400> 1874
000

<210> 1875

<400> 1875
000

<210> 1876

<400> 1876
000

<210> 1877

<400> 1877
000

<210> 1878

<400> 1878
000

<210> 1879

<400> 1879
000

<210> 1880

<400> 1880
000

<210> 1881

<400> 1881
000

<210> 1882

<400> 1882
000

<210> 1883

<400> 1883
000

<210> 1884

<400> 1884
000

<210> 1885

<400> 1885
000

<210> 1886

<400> 1886
000

<210> 1887

_SL

<400> 1887
000

<210> 1888

<400> 1888
000

<210> 1889

<400> 1889
000

<210> 1890

<400> 1890
000

<210> 1891

<400> 1891
000

<210> 1892

<400> 1892
000

<210> 1893

<400> 1893
000

<210> 1894

<400> 1894
000

<210> 1895

<400> 1895
000

<210> 1896

<400> 1896
000

<210> 1897

<400> 1897
000

<210> 1898

<400> 1898

000

<210> 1899

<400> 1899
000

<210> 1900

<400> 1900
000

<210> 1901

<400> 1901
000

<210> 1902

<400> 1902
000

<210> 1903

<400> 1903
000

<210> 1904

<400> 1904
000

<210> 1905

<400> 1905
000

<210> 1906

<400> 1906
000

<210> 1907

<400> 1907
000

<210> 1908

<400> 1908
000

<210> 1909

<400> 1909
000

_SL

<210> 1910

<400> 1910
000

<210> 1911

<400> 1911
000

<210> 1912

<400> 1912
000

<210> 1913

<400> 1913
000

<210> 1914

<400> 1914
000

<210> 1915

<400> 1915
000

<210> 1916

<400> 1916
000

<210> 1917

<400> 1917
000

<210> 1918

<400> 1918
000

<210> 1919

<400> 1919
000

<210> 1920

<400> 1920
000

_SL

<210> 1921

<400> 1921
000

<210> 1922

<400> 1922
000

<210> 1923

<400> 1923
000

<210> 1924

<400> 1924
000

<210> 1925

<400> 1925
000

<210> 1926

<400> 1926
000

<210> 1927

<400> 1927
000

<210> 1928

<400> 1928
000

<210> 1929

<400> 1929
000

<210> 1930

<400> 1930
000

<210> 1931

<400> 1931
000

<210> 1932

<400> 1932
000

<210> 1933

<400> 1933
000

<210> 1934

<400> 1934
000

<210> 1935

<400> 1935
000

<210> 1936

<400> 1936
000

<210> 1937

<400> 1937
000

<210> 1938

<400> 1938
000

<210> 1939

<400> 1939
000

<210> 1940

<400> 1940
000

<210> 1941

<400> 1941
000

<210> 1942

<400> 1942
000

<210> 1943

_SL

<400> 1943
000

<210> 1944

<400> 1944
000

<210> 1945

<400> 1945
000

<210> 1946

<400> 1946
000

<210> 1947

<400> 1947
000

<210> 1948

<400> 1948
000

<210> 1949

<400> 1949
000

<210> 1950

<400> 1950
000

<210> 1951

<400> 1951
000

<210> 1952

<400> 1952
000

<210> 1953

<400> 1953
000

<210> 1954

<400> 1954

000

<210> 1955

<400> 1955
000

<210> 1956

<400> 1956
000

<210> 1957

<400> 1957
000

<210> 1958

<400> 1958
000

<210> 1959

<400> 1959
000

<210> 1960

<400> 1960
000

<210> 1961

<400> 1961
000

<210> 1962

<400> 1962
000

<210> 1963

<400> 1963
000

<210> 1964

<400> 1964
000

<210> 1965

<400> 1965
000

_SL

<210> 1966

<400> 1966
000

<210> 1967

<400> 1967
000

<210> 1968

<400> 1968
000

<210> 1969

<400> 1969
000

<210> 1970

<400> 1970
000

<210> 1971

<400> 1971
000

<210> 1972

<400> 1972
000

<210> 1973

<400> 1973
000

<210> 1974

<400> 1974
000

<210> 1975

<400> 1975
000

<210> 1976

<400> 1976
000

<210> 1977

<400> 1977
000

<210> 1978

<400> 1978
000

<210> 1979

<400> 1979
000

<210> 1980

<400> 1980
000

<210> 1981

<400> 1981
000

<210> 1982

<400> 1982
000

<210> 1983

<400> 1983
000

<210> 1984

<400> 1984
000

<210> 1985

<400> 1985
000

<210> 1986

<400> 1986
000

<210> 1987

<400> 1987
000

<210> 1988

<400> 1988
000

<210> 1989

<400> 1989
000

<210> 1990

<400> 1990
000

<210> 1991

<400> 1991
000

<210> 1992

<400> 1992
000

<210> 1993

<400> 1993
000

<210> 1994

<400> 1994
000

<210> 1995

<400> 1995
000

<210> 1996

<400> 1996
000

<210> 1997

<400> 1997
000

<210> 1998

<400> 1998
000

<210> 1999

_SL

<400> 1999
000

<210> 2000

<400> 2000
000

<210> 2001

<400> 2001
000

<210> 2002

<400> 2002
000

<210> 2003

<400> 2003
000

<210> 2004

<400> 2004
000

<210> 2005

<400> 2005
000

<210> 2006

<400> 2006
000

<210> 2007

<400> 2007
000

<210> 2008

<400> 2008
000

<210> 2009

<400> 2009
000

<210> 2010

<400> 2010

000

<210> 2011

<400> 2011
000

<210> 2012

<400> 2012
000

<210> 2013

<400> 2013
000

<210> 2014

<400> 2014
000

<210> 2015

<400> 2015
000

<210> 2016

<400> 2016
000

<210> 2017

<400> 2017
000

<210> 2018

<400> 2018
000

<210> 2019

<400> 2019
000

<210> 2020

<400> 2020
000

<210> 2021

<400> 2021
000

<210> 2022

<400> 2022
000

<210> 2023

<400> 2023
000

<210> 2024

<400> 2024
000

<210> 2025

<400> 2025
000

<210> 2026

<400> 2026
000

<210> 2027

<400> 2027
000

<210> 2028

<400> 2028
000

<210> 2029

<400> 2029
000

<210> 2030

<400> 2030
000

<210> 2031

<400> 2031
000

<210> 2032

<400> 2032
000

<210> 2033

_SL

<400> 2033
000

<210> 2034

<400> 2034
000

<210> 2035

<400> 2035
000

<210> 2036

<400> 2036
000

<210> 2037

<400> 2037
000

<210> 2038

<400> 2038
000

<210> 2039

<400> 2039
000

<210> 2040

<400> 2040
000

<210> 2041

<400> 2041
000

<210> 2042

<400> 2042
000

<210> 2043

<400> 2043
000

<210> 2044

_SL

<400> 2044
000

<210> 2045

<400> 2045
000

<210> 2046

<400> 2046
000

<210> 2047

<400> 2047
000

<210> 2048

<400> 2048
000

<210> 2049

<400> 2049
000

<210> 2050

<400> 2050
000

<210> 2051

<400> 2051
000

<210> 2052

<400> 2052
000

<210> 2053

<400> 2053
000

<210> 2054

<400> 2054
000

<210> 2055

<400> 2055

000

<210> 2056

<400> 2056
000

<210> 2057

<400> 2057
000

<210> 2058

<400> 2058
000

<210> 2059

<400> 2059
000

<210> 2060

<400> 2060
000

<210> 2061

<400> 2061
000

<210> 2062

<400> 2062
000

<210> 2063

<400> 2063
000

<210> 2064

<400> 2064
000

<210> 2065

<400> 2065
000

<210> 2066

<400> 2066

_SL

000

<210> 2067

<400> 2067
000

<210> 2068

<400> 2068
000

<210> 2069

<400> 2069
000

<210> 2070

<400> 2070
000

<210> 2071

<400> 2071
000

<210> 2072

<400> 2072
000

<210> 2073

<400> 2073
000

<210> 2074

<400> 2074
000

<210> 2075

<400> 2075
000

<210> 2076

<400> 2076
000

<210> 2077

<400> 2077
000

_SL

<210> 2078

<400> 2078
000

<210> 2079

<400> 2079
000

<210> 2080

<400> 2080
000

<210> 2081

<400> 2081
000

<210> 2082

<400> 2082
000

<210> 2083

<400> 2083
000

<210> 2084

<400> 2084
000

<210> 2085

<400> 2085
000

<210> 2086

<400> 2086
000

<210> 2087

<400> 2087
000

<210> 2088

<400> 2088
000

<210> 2089

_SL

<400> 2089
000

<210> 2090

<400> 2090
000

<210> 2091

<400> 2091
000

<210> 2092

<400> 2092
000

<210> 2093

<400> 2093
000

<210> 2094

<400> 2094
000

<210> 2095

<400> 2095
000

<210> 2096

<400> 2096
000

<210> 2097

<400> 2097
000

<210> 2098

<400> 2098
000

<210> 2099

<400> 2099
000

<210> 2100

<400> 2100

000

<210> 2101

<400> 2101
000

<210> 2102

<400> 2102
000

<210> 2103

<400> 2103
000

<210> 2104

<400> 2104
000

<210> 2105

<400> 2105
000

<210> 2106

<400> 2106
000

<210> 2107

<400> 2107
000

<210> 2108

<400> 2108
000

<210> 2109

<400> 2109
000

<210> 2110

<400> 2110
000

<210> 2111

<400> 2111

000

<210> 2112

<400> 2112
000

<210> 2113

<400> 2113
000

<210> 2114

<400> 2114
000

<210> 2115

<400> 2115
000

<210> 2116

<400> 2116
000

<210> 2117

<400> 2117
000

<210> 2118

<400> 2118
000

<210> 2119

<400> 2119
000

<210> 2120

<400> 2120
000

<210> 2121

<400> 2121
000

<210> 2122

<400> 2122
000

<210> 2123

<400> 2123
000

<210> 2124

<400> 2124
000

<210> 2125

<400> 2125
000

<210> 2126

<400> 2126
000

<210> 2127

<400> 2127
000

<210> 2128

<400> 2128
000

<210> 2129

<400> 2129
000

<210> 2130

<400> 2130
000

<210> 2131

<400> 2131
000

<210> 2132

<400> 2132
000

<210> 2133

<400> 2133
000

<210> 2134

_SL

<400> 2134
000

<210> 2135

<400> 2135
000

<210> 2136

<400> 2136
000

<210> 2137

<400> 2137
000

<210> 2138

<400> 2138
000

<210> 2139

<400> 2139
000

<210> 2140

<400> 2140
000

<210> 2141

<400> 2141
000

<210> 2142

<400> 2142
000

<210> 2143

<400> 2143
000

<210> 2144

<400> 2144
000

<210> 2145

<400> 2145

000

<210> 2146

<400> 2146
000

<210> 2147

<400> 2147
000

<210> 2148

<400> 2148
000

<210> 2149

<400> 2149
000

<210> 2150

<400> 2150
000

<210> 2151

<400> 2151
000

<210> 2152

<400> 2152
000

<210> 2153

<400> 2153
000

<210> 2154

<400> 2154
000

<210> 2155

<400> 2155
000

<210> 2156

<400> 2156
000

<210> 2157

<400> 2157
000

<210> 2158

<400> 2158
000

<210> 2159

<400> 2159
000

<210> 2160

<400> 2160
000

<210> 2161

<400> 2161
000

<210> 2162

<400> 2162
000

<210> 2163

<400> 2163
000

<210> 2164

<400> 2164
000

<210> 2165

<400> 2165
000

<210> 2166

<400> 2166
000

<210> 2167

<400> 2167
000

<210> 2168

_SL

<400> 2168
000

<210> 2169

<400> 2169
000

<210> 2170

<400> 2170
000

<210> 2171

<400> 2171
000

<210> 2172

<400> 2172
000

<210> 2173

<400> 2173
000

<210> 2174

<400> 2174
000

<210> 2175

<400> 2175
000

<210> 2176

<400> 2176
000

<210> 2177

<400> 2177
000

<210> 2178

<400> 2178
000

<210> 2179

<400> 2179

000

<210> 2180

<400> 2180
000

<210> 2181

<400> 2181
000

<210> 2182

<400> 2182
000

<210> 2183

<400> 2183
000

<210> 2184

<400> 2184
000

<210> 2185

<400> 2185
000

<210> 2186

<400> 2186
000

<210> 2187

<400> 2187
000

<210> 2188

<400> 2188
000

<210> 2189

<400> 2189
000

<210> 2190

<400> 2190
000

_SL

<210> 2191

<400> 2191
000

<210> 2192

<400> 2192
000

<210> 2193

<400> 2193
000

<210> 2194

<400> 2194
000

<210> 2195

<400> 2195
000

<210> 2196

<400> 2196
000

<210> 2197

<400> 2197
000

<210> 2198

<400> 2198
000

<210> 2199

<400> 2199
000

<210> 2200

<400> 2200
000

<210> 2201

<400> 2201
000

_SL

<210> 2202

<400> 2202
000

<210> 2203

<400> 2203
000

<210> 2204

<400> 2204
000

<210> 2205

<400> 2205
000

<210> 2206

<400> 2206
000

<210> 2207

<400> 2207
000

<210> 2208

<400> 2208
000

<210> 2209

<400> 2209
000

<210> 2210

<400> 2210
000

<210> 2211

<400> 2211
000

<210> 2212

<400> 2212
000

_SL

<210> 2213

<400> 2213
000

<210> 2214

<400> 2214
000

<210> 2215

<400> 2215
000

<210> 2216

<400> 2216
000

<210> 2217

<400> 2217
000

<210> 2218

<400> 2218
000

<210> 2219

<400> 2219
000

<210> 2220

<400> 2220
000

<210> 2221

<400> 2221
000

<210> 2222

<400> 2222
000

<210> 2223

<400> 2223
000

<210> 2224

<400> 2224
000

<210> 2225

<400> 2225
000

<210> 2226

<400> 2226
000

<210> 2227

<400> 2227
000

<210> 2228

<400> 2228
000

<210> 2229

<400> 2229
000

<210> 2230

<400> 2230
000

<210> 2231

<400> 2231
000

<210> 2232

<400> 2232
000

<210> 2233

<400> 2233
000

<210> 2234

<400> 2234
000

<210> 2235

_SL

<400> 2235
000

<210> 2236

<400> 2236
000

<210> 2237

<400> 2237
000

<210> 2238

<400> 2238
000

<210> 2239

<400> 2239
000

<210> 2240

<400> 2240
000

<210> 2241

<400> 2241
000

<210> 2242

<400> 2242
000

<210> 2243

<400> 2243
000

<210> 2244

<400> 2244
000

<210> 2245

<400> 2245
000

<210> 2246

<400> 2246

000

<210> 2247

<400> 2247
000

<210> 2248

<400> 2248
000

<210> 2249

<400> 2249
000

<210> 2250

<400> 2250
000

<210> 2251

<400> 2251
000

<210> 2252

<400> 2252
000

<210> 2253

<400> 2253
000

<210> 2254

<400> 2254
000

<210> 2255

<400> 2255
000

<210> 2256

<400> 2256
000

<210> 2257

<400> 2257
000

_SL

<210> 2258

<400> 2258
000

<210> 2259

<400> 2259
000

<210> 2260

<400> 2260
000

<210> 2261

<400> 2261
000

<210> 2262

<400> 2262
000

<210> 2263

<400> 2263
000

<210> 2264

<400> 2264
000

<210> 2265

<400> 2265
000

<210> 2266

<400> 2266
000

<210> 2267

<400> 2267
000

<210> 2268

<400> 2268
000

<210> 2269

_SL

<400> 2269
000

<210> 2270

<400> 2270
000

<210> 2271

<400> 2271
000

<210> 2272

<400> 2272
000

<210> 2273

<400> 2273
000

<210> 2274

<400> 2274
000

<210> 2275

<400> 2275
000

<210> 2276

<400> 2276
000

<210> 2277

<400> 2277
000

<210> 2278

<400> 2278
000

<210> 2279

<400> 2279
000

<210> 2280

<400> 2280

000

<210> 2281

<400> 2281
000

<210> 2282

<400> 2282
000

<210> 2283

<400> 2283
000

<210> 2284

<400> 2284
000

<210> 2285

<400> 2285
000

<210> 2286

<400> 2286
000

<210> 2287

<400> 2287
000

<210> 2288

<400> 2288
000

<210> 2289

<400> 2289
000

<210> 2290

<400> 2290
000

<210> 2291

<400> 2291
000

_SL

<210> 2292

<400> 2292
000

<210> 2293

<400> 2293
000

<210> 2294

<400> 2294
000

<210> 2295

<400> 2295
000

<210> 2296

<400> 2296
000

<210> 2297

<400> 2297
000

<210> 2298

<400> 2298
000

<210> 2299

<400> 2299
000

<210> 2300

<400> 2300
000

<210> 2301

<400> 2301
000

<210> 2302

<400> 2302
000

<210> 2303

_SL

<400> 2303
000

<210> 2304

<400> 2304
000

<210> 2305

<400> 2305
000

<210> 2306

<400> 2306
000

<210> 2307

<400> 2307
000

<210> 2308

<400> 2308
000

<210> 2309

<400> 2309
000

<210> 2310

<400> 2310
000

<210> 2311

<400> 2311
000

<210> 2312

<400> 2312
000

<210> 2313

<400> 2313
000

<210> 2314

<400> 2314

000

<210> 2315

<400> 2315
000

<210> 2316

<400> 2316
000

<210> 2317

<400> 2317
000

<210> 2318

<400> 2318
000

<210> 2319

<400> 2319
000

<210> 2320

<400> 2320
000

<210> 2321

<400> 2321
000

<210> 2322

<400> 2322
000

<210> 2323

<400> 2323
000

<210> 2324

<400> 2324
000

<210> 2325

<400> 2325
000

_SL

<210> 2326

<400> 2326
000

<210> 2327

<400> 2327
000

<210> 2328

<400> 2328
000

<210> 2329

<400> 2329
000

<210> 2330

<400> 2330
000

<210> 2331

<400> 2331
000

<210> 2332

<400> 2332
000

<210> 2333

<400> 2333
000

<210> 2334

<400> 2334
000

<210> 2335

<400> 2335
000

<210> 2336

<400> 2336
000

<210> 2337

<400> 2337
000

<210> 2338

<400> 2338
000

<210> 2339

<400> 2339
000

<210> 2340

<400> 2340
000

<210> 2341

<400> 2341
000

<210> 2342

<400> 2342
000

<210> 2343

<400> 2343
000

<210> 2344

<400> 2344
000

<210> 2345

<400> 2345
000

<210> 2346

<400> 2346
000

<210> 2347

<400> 2347

000

<210> 2348

<400> 2348
000

<210> 2349

<400> 2349
000

<210> 2350

<400> 2350
000

<210> 2351

<400> 2351
000

<210> 2352

<400> 2352
000

<210> 2353

<400> 2353
000

<210> 2354

<400> 2354
000

<210> 2355

<400> 2355
000

<210> 2356

<400> 2356
000

<210> 2357

<400> 2357
000

<210> 2358

<400> 2358
000

_SL

<210> 2359

<400> 2359
000

<210> 2360

<400> 2360
000

<210> 2361

<400> 2361
000

<210> 2362

<400> 2362
000

<210> 2363

<400> 2363
000

<210> 2364

<400> 2364
000

<210> 2365

<400> 2365
000

<210> 2366

<400> 2366
000

<210> 2367

<400> 2367
000

<210> 2368

<400> 2368
000

<210> 2369

<400> 2369
000

<210> 2370

_SL

<400> 2370
000

<210> 2371

<400> 2371
000

<210> 2372

<400> 2372
000

<210> 2373

<400> 2373
000

<210> 2374

<400> 2374
000

<210> 2375

<400> 2375
000

<210> 2376

<400> 2376
000

<210> 2377

<400> 2377
000

<210> 2378

<400> 2378
000

<210> 2379

<400> 2379
000

<210> 2380

<400> 2380
000

<210> 2381

<400> 2381

000

<210> 2382

<400> 2382
000

<210> 2383

<400> 2383
000

<210> 2384

<400> 2384
000

<210> 2385

<400> 2385
000

<210> 2386

<400> 2386
000

<210> 2387

<400> 2387
000

<210> 2388

<400> 2388
000

<210> 2389

<400> 2389
000

<210> 2390

<400> 2390
000

<210> 2391

<400> 2391
000

<210> 2392

<400> 2392
000

<210> 2393

<400> 2393
000

<210> 2394

<400> 2394
000

<210> 2395

<400> 2395
000

<210> 2396

<400> 2396
000

<210> 2397

<400> 2397
000

<210> 2398

<400> 2398
000

<210> 2399

<400> 2399
000

<210> 2400

<400> 2400
000

<210> 2401

<400> 2401
000

<210> 2402

<400> 2402
000

<210> 2403

<400> 2403
000

<210> 2404

_SL

<400> 2404
000

<210> 2405

<400> 2405
000

<210> 2406

<400> 2406
000

<210> 2407

<400> 2407
000

<210> 2408

<400> 2408
000

<210> 2409

<400> 2409
000

<210> 2410

<400> 2410
000

<210> 2411

<400> 2411
000

<210> 2412

<400> 2412
000

<210> 2413

<400> 2413
000

<210> 2414

<400> 2414
000

<210> 2415

<400> 2415

000

<210> 2416

<400> 2416
000

<210> 2417

<400> 2417
000

<210> 2418

<400> 2418
000

<210> 2419

<400> 2419
000

<210> 2420

<400> 2420
000

<210> 2421

<400> 2421
000

<210> 2422

<400> 2422
000

<210> 2423

<400> 2423
000

<210> 2424

<400> 2424
000

<210> 2425

<400> 2425
000

<210> 2426

<400> 2426
000

_SL

<210> 2427

<400> 2427
000

<210> 2428

<400> 2428
000

<210> 2429

<400> 2429
000

<210> 2430

<400> 2430
000

<210> 2431

<400> 2431
000

<210> 2432

<400> 2432
000

<210> 2433

<400> 2433
000

<210> 2434

<400> 2434
000

<210> 2435

<400> 2435
000

<210> 2436

<400> 2436
000

<210> 2437

<400> 2437
000

<210> 2438

_SL

<400> 2438
000

<210> 2439

<400> 2439
000

<210> 2440

<400> 2440
000

<210> 2441

<400> 2441
000

<210> 2442

<400> 2442
000

<210> 2443

<400> 2443
000

<210> 2444

<400> 2444
000

<210> 2445

<400> 2445
000

<210> 2446

<400> 2446
000

<210> 2447

<400> 2447
000

<210> 2448

<400> 2448
000

<210> 2449

<400> 2449

000

<210> 2450

<400> 2450
000

<210> 2451

<400> 2451
000

<210> 2452

<400> 2452
000

<210> 2453

<400> 2453
000

<210> 2454

<400> 2454
000

<210> 2455

<400> 2455
000

<210> 2456

<400> 2456
000

<210> 2457

<400> 2457
000

<210> 2458

<400> 2458
000

<210> 2459

<400> 2459
000

<210> 2460

<400> 2460

000

<210> 2461

<400> 2461
000

<210> 2462

<400> 2462
000

<210> 2463

<400> 2463
000

<210> 2464

<400> 2464
000

<210> 2465

<400> 2465
000

<210> 2466

<400> 2466
000

<210> 2467

<400> 2467
000

<210> 2468

<400> 2468
000

<210> 2469

<400> 2469
000

<210> 2470

<400> 2470
000

<210> 2471

<400> 2471

000

<210> 2472

<400> 2472
000

<210> 2473

<400> 2473
000

<210> 2474

<400> 2474
000

<210> 2475

<400> 2475
000

<210> 2476

<400> 2476
000

<210> 2477

<400> 2477
000

<210> 2478

<400> 2478
000

<210> 2479

<400> 2479
000

<210> 2480

<400> 2480
000

<210> 2481

<400> 2481
000

<210> 2482

<400> 2482

000

<210> 2483

<400> 2483
000

<210> 2484

<400> 2484
000

<210> 2485

<400> 2485
000

<210> 2486

<400> 2486
000

<210> 2487

<400> 2487
000

<210> 2488

<400> 2488
000

<210> 2489

<400> 2489
000

<210> 2490

<400> 2490
000

<210> 2491

<400> 2491
000

<210> 2492

<400> 2492
000

<210> 2493

<400> 2493
000

<210> 2494

<400> 2494
000

<210> 2495

<400> 2495
000

<210> 2496

<400> 2496
000

<210> 2497

<400> 2497
000

<210> 2498

<400> 2498
000

<210> 2499

<400> 2499
000

<210> 2500

<400> 2500
000

<210> 2501

<400> 2501
000

<210> 2502

<400> 2502
000

<210> 2503

<400> 2503
000

<210> 2504

<400> 2504
000

<210> 2505

_SL

<400> 2505
000

<210> 2506

<400> 2506
000

<210> 2507

<400> 2507
000

<210> 2508

<400> 2508
000

<210> 2509

<400> 2509
000

<210> 2510

<400> 2510
000

<210> 2511

<400> 2511
000

<210> 2512

<400> 2512
000

<210> 2513

<400> 2513
000

<210> 2514

<400> 2514
000

<210> 2515

<400> 2515
000

<210> 2516

<400> 2516

000

<210> 2517

<400> 2517
000

<210> 2518

<400> 2518
000

<210> 2519

<400> 2519
000

<210> 2520

<400> 2520
000

<210> 2521

<400> 2521
000

<210> 2522

<400> 2522
000

<210> 2523

<400> 2523
000

<210> 2524

<400> 2524
000

<210> 2525

<400> 2525
000

<210> 2526

<400> 2526
000

<210> 2527

<400> 2527
000

_SL

<210> 2528

<400> 2528
000

<210> 2529

<400> 2529
000

<210> 2530

<400> 2530
000

<210> 2531

<400> 2531
000

<210> 2532

<400> 2532
000

<210> 2533

<400> 2533
000

<210> 2534

<400> 2534
000

<210> 2535

<400> 2535
000

<210> 2536

<400> 2536
000

<210> 2537

<400> 2537
000

<210> 2538

<400> 2538
000

<210> 2539

_SL

<400> 2539
000

<210> 2540

<400> 2540
000

<210> 2541

<400> 2541
000

<210> 2542

<400> 2542
000

<210> 2543

<400> 2543
000

<210> 2544

<400> 2544
000

<210> 2545

<400> 2545
000

<210> 2546

<400> 2546
000

<210> 2547

<400> 2547
000

<210> 2548

<400> 2548
000

<210> 2549

<400> 2549
000

<210> 2550

<400> 2550

000

<210> 2551

<400> 2551
000

<210> 2552

<400> 2552
000

<210> 2553

<400> 2553
000

<210> 2554

<400> 2554
000

<210> 2555

<400> 2555
000

<210> 2556

<400> 2556
000

<210> 2557

<400> 2557
000

<210> 2558

<400> 2558
000

<210> 2559

<400> 2559
000

<210> 2560

<400> 2560
000

<210> 2561

<400> 2561
000

<210> 2562

<400> 2562
000

<210> 2563

<400> 2563
000

<210> 2564

<400> 2564
000

<210> 2565

<400> 2565
000

<210> 2566

<400> 2566
000

<210> 2567

<400> 2567
000

<210> 2568

<400> 2568
000

<210> 2569

<400> 2569
000

<210> 2570

<400> 2570
000

<210> 2571

<400> 2571
000

<210> 2572

<400> 2572
000

<210> 2573

_SL

<400> 2573
000

<210> 2574

<400> 2574
000

<210> 2575

<400> 2575
000

<210> 2576

<400> 2576
000

<210> 2577

<400> 2577
000

<210> 2578

<400> 2578
000

<210> 2579

<400> 2579
000

<210> 2580

<400> 2580
000

<210> 2581

<400> 2581
000

<210> 2582

<400> 2582
000

<210> 2583

<400> 2583
000

<210> 2584

<400> 2584

000

<210> 2585

<400> 2585
000

<210> 2586

<400> 2586
000

<210> 2587

<400> 2587
000

<210> 2588

<400> 2588
000

<210> 2589

<400> 2589
000

<210> 2590

<400> 2590
000

<210> 2591

<400> 2591
000

<210> 2592

<400> 2592
000

<210> 2593

<400> 2593
000

<210> 2594

<400> 2594
000

<210> 2595

_SL

<400> 2595
000

<210> 2596

<400> 2596
000

<210> 2597

<400> 2597
000

<210> 2598

<400> 2598
000

<210> 2599

<400> 2599
000

<210> 2600

<400> 2600
000

<210> 2601

<400> 2601
000

<210> 2602

<400> 2602
000

<210> 2603

<400> 2603
000

<210> 2604

<400> 2604
000

<210> 2605

<400> 2605
000

<210> 2606

_SL

<400> 2606
000

<210> 2607

<400> 2607
000

<210> 2608

<400> 2608
000

<210> 2609

<400> 2609
000

<210> 2610

<400> 2610
000

<210> 2611

<400> 2611
000

<210> 2612

<400> 2612
000

<210> 2613

<400> 2613
000

<210> 2614

<400> 2614
000

<210> 2615

<400> 2615
000

<210> 2616

<400> 2616
000

<210> 2617

<400> 2617

_SL

000

<210> 2618

<400> 2618
000

<210> 2619

<400> 2619
000

<210> 2620

<400> 2620
000

<210> 2621

<400> 2621
000

<210> 2622

<400> 2622
000

<210> 2623

<400> 2623
000

<210> 2624

<400> 2624
000

<210> 2625

<400> 2625
000

<210> 2626

<400> 2626
000

<210> 2627

<400> 2627
000

<210> 2628

<400> 2628
000

<210> 2629

<400> 2629
000

<210> 2630

<400> 2630
000

<210> 2631

<400> 2631
000

<210> 2632

<400> 2632
000

<210> 2633

<400> 2633
000

<210> 2634

<400> 2634
000

<210> 2635

<400> 2635
000

<210> 2636

<400> 2636
000

<210> 2637

<400> 2637
000

<210> 2638

<400> 2638
000

<210> 2639

<400> 2639
000

<210> 2640

_SL

<400> 2640
000

<210> 2641

<400> 2641
000

<210> 2642

<400> 2642
000

<210> 2643

<400> 2643
000

<210> 2644

<400> 2644
000

<210> 2645

<400> 2645
000

<210> 2646

<400> 2646
000

<210> 2647

<400> 2647
000

<210> 2648

<400> 2648
000

<210> 2649

<400> 2649
000

<210> 2650

<400> 2650
000

<210> 2651

<400> 2651

000

<210> 2652

<400> 2652
000

<210> 2653

<400> 2653
000

<210> 2654

<400> 2654
000

<210> 2655

<400> 2655
000

<210> 2656

<400> 2656
000

<210> 2657

<400> 2657
000

<210> 2658

<400> 2658
000

<210> 2659

<400> 2659
000

<210> 2660

<400> 2660
000

<210> 2661

<400> 2661
000

<210> 2662

<400> 2662
000

_SL

<210> 2663

<400> 2663
000

<210> 2664

<400> 2664
000

<210> 2665

<400> 2665
000

<210> 2666

<400> 2666
000

<210> 2667

<400> 2667
000

<210> 2668

<400> 2668
000

<210> 2669

<400> 2669
000

<210> 2670

<400> 2670
000

<210> 2671

<400> 2671
000

<210> 2672

<400> 2672
000

<210> 2673

<400> 2673
000

<210> 2674

_SL

<400> 2674
000

<210> 2675

<400> 2675
000

<210> 2676

<400> 2676
000

<210> 2677

<400> 2677
000

<210> 2678

<400> 2678
000

<210> 2679

<400> 2679
000

<210> 2680

<400> 2680
000

<210> 2681

<400> 2681
000

<210> 2682

<400> 2682
000

<210> 2683

<400> 2683
000

<210> 2684

<400> 2684
000

<210> 2685

<400> 2685

000

<210> 2686

<400> 2686
000

<210> 2687

<400> 2687
000

<210> 2688

<400> 2688
000

<210> 2689

<400> 2689
000

<210> 2690

<400> 2690
000

<210> 2691

<400> 2691
000

<210> 2692

<400> 2692
000

<210> 2693

<400> 2693
000

<210> 2694

<400> 2694
000

<210> 2695

<400> 2695
000

<210> 2696

<400> 2696
000

_SL

<210> 2697

<400> 2697
000

<210> 2698

<400> 2698
000

<210> 2699

<400> 2699
000

<210> 2700

<400> 2700
000

<210> 2701

<400> 2701
000

<210> 2702

<400> 2702
000

<210> 2703

<400> 2703
000

<210> 2704

<400> 2704
000

<210> 2705

<400> 2705
000

<210> 2706

<400> 2706
000

<210> 2707

<400> 2707
000

<210> 2708

_SL

<400> 2708
000

<210> 2709

<400> 2709
000

<210> 2710

<400> 2710
000

<210> 2711

<400> 2711
000

<210> 2712

<400> 2712
000

<210> 2713

<400> 2713
000

<210> 2714

<400> 2714
000

<210> 2715

<400> 2715
000

<210> 2716

<400> 2716
000

<210> 2717

<400> 2717
000

<210> 2718

<400> 2718
000

<210> 2719

_SL

<400> 2719
000

<210> 2720

<400> 2720
000

<210> 2721

<400> 2721
000

<210> 2722

<400> 2722
000

<210> 2723

<400> 2723
000

<210> 2724

<400> 2724
000

<210> 2725

<400> 2725
000

<210> 2726

<400> 2726
000

<210> 2727

<400> 2727
000

<210> 2728

<400> 2728
000

<210> 2729

<400> 2729
000

_SL

<210> 2730

<400> 2730
000

<210> 2731

<400> 2731
000

<210> 2732

<400> 2732
000

<210> 2733

<400> 2733
000

<210> 2734

<400> 2734
000

<210> 2735

<400> 2735
000

<210> 2736

<400> 2736
000

<210> 2737

<400> 2737
000

<210> 2738

<400> 2738
000

<210> 2739

<400> 2739
000

<210> 2740

<400> 2740
000

<210> 2741

_SL

<400> 2741
000

<210> 2742

<400> 2742
000

<210> 2743

<400> 2743
000

<210> 2744

<400> 2744
000

<210> 2745

<400> 2745
000

<210> 2746

<400> 2746
000

<210> 2747

<400> 2747
000

<210> 2748

<400> 2748
000

<210> 2749

<400> 2749
000

<210> 2750

<400> 2750
000

<210> 2751

<400> 2751
000

<210> 2752

<400> 2752

000

<210> 2753

<400> 2753
000

<210> 2754

<400> 2754
000

<210> 2755

<400> 2755
000

<210> 2756

<400> 2756
000

<210> 2757

<400> 2757
000

<210> 2758

<400> 2758
000

<210> 2759

<400> 2759
000

<210> 2760

<400> 2760
000

<210> 2761

<400> 2761
000

<210> 2762

<400> 2762
000

<210> 2763

<400> 2763
000

_SL

<210> 2764

<400> 2764
000

<210> 2765

<400> 2765
000

<210> 2766

<400> 2766
000

<210> 2767

<400> 2767
000

<210> 2768

<400> 2768
000

<210> 2769

<400> 2769
000

<210> 2770

<400> 2770
000

<210> 2771

<400> 2771
000

<210> 2772

<400> 2772
000

<210> 2773

<400> 2773
000

<210> 2774

<400> 2774
000

<210> 2775

_SL

<400> 2775
000

<210> 2776

<400> 2776
000

<210> 2777

<400> 2777
000

<210> 2778

<400> 2778
000

<210> 2779

<400> 2779
000

<210> 2780

<400> 2780
000

<210> 2781

<400> 2781
000

<210> 2782

<400> 2782
000

<210> 2783

<400> 2783
000

<210> 2784

<400> 2784
000

<210> 2785

<400> 2785
000

<210> 2786

<400> 2786

000

<210> 2787

<400> 2787
000

<210> 2788

<400> 2788
000

<210> 2789

<400> 2789
000

<210> 2790

<400> 2790
000

<210> 2791

<400> 2791
000

<210> 2792

<400> 2792
000

<210> 2793

<400> 2793
000

<210> 2794

<400> 2794
000

<210> 2795

<400> 2795
000

<210> 2796

<400> 2796
000

<210> 2797

<400> 2797
000

_SL

<210> 2798

<400> 2798
000

<210> 2799

<400> 2799
000

<210> 2800

<400> 2800
000

<210> 2801

<400> 2801
000

<210> 2802

<400> 2802
000

<210> 2803

<400> 2803
000

<210> 2804

<400> 2804
000

<210> 2805

<400> 2805
000

<210> 2806

<400> 2806
000

<210> 2807

<400> 2807
000

<210> 2808

<400> 2808
000

<210> 2809

_SL

<400> 2809
000

<210> 2810

<400> 2810
000

<210> 2811

<400> 2811
000

<210> 2812

<400> 2812
000

<210> 2813

<400> 2813
000

<210> 2814

<400> 2814
000

<210> 2815

<400> 2815
000

<210> 2816

<400> 2816
000

<210> 2817

<400> 2817
000

<210> 2818

<400> 2818
000

<210> 2819

<400> 2819
000

<210> 2820

<400> 2820

000

<210> 2821

<400> 2821
000

<210> 2822

<400> 2822
000

<210> 2823

<400> 2823
000

<210> 2824

<400> 2824
000

<210> 2825

<400> 2825
000

<210> 2826

<400> 2826
000

<210> 2827

<400> 2827
000

<210> 2828

<400> 2828
000

<210> 2829

<400> 2829
000

<210> 2830

<400> 2830
000

<210> 2831

<400> 2831
000

_SL

<210> 2832

<400> 2832
000

<210> 2833

<400> 2833
000

<210> 2834

<400> 2834
000

<210> 2835

<400> 2835
000

<210> 2836

<400> 2836
000

<210> 2837

<400> 2837
000

<210> 2838

<400> 2838
000

<210> 2839

<400> 2839
000

<210> 2840

<400> 2840
000

<210> 2841

<400> 2841
000

<210> 2842

<400> 2842
000

_SL

<210> 2843

<400> 2843
000

<210> 2844

<400> 2844
000

<210> 2845

<400> 2845
000

<210> 2846

<400> 2846
000

<210> 2847

<400> 2847
000

<210> 2848

<400> 2848
000

<210> 2849

<400> 2849
000

<210> 2850

<400> 2850
000

<210> 2851

<400> 2851
000

<210> 2852

<400> 2852
000

<210> 2853

<400> 2853
000

_SL

<210> 2854

<400> 2854
000

<210> 2855

<400> 2855
000

<210> 2856

<400> 2856
000

<210> 2857

<400> 2857
000

<210> 2858

<400> 2858
000

<210> 2859

<400> 2859
000

<210> 2860

<400> 2860
000

<210> 2861

<400> 2861
000

<210> 2862

<400> 2862
000

<210> 2863

<400> 2863
000

<210> 2864

<400> 2864
000

_SL

<210> 2865

<400> 2865
000

<210> 2866

<400> 2866
000

<210> 2867

<400> 2867
000

<210> 2868

<400> 2868
000

<210> 2869

<400> 2869
000

<210> 2870

<400> 2870
000

<210> 2871

<400> 2871
000

<210> 2872

<400> 2872
000

<210> 2873

<400> 2873
000

<210> 2874

<400> 2874
000

<210> 2875

<400> 2875
000

<210> 2876

_SL

<400> 2876
000

<210> 2877

<400> 2877
000

<210> 2878

<400> 2878
000

<210> 2879

<400> 2879
000

<210> 2880

<400> 2880
000

<210> 2881

<400> 2881
000

<210> 2882

<400> 2882
000

<210> 2883

<400> 2883
000

<210> 2884

<400> 2884
000

<210> 2885

<400> 2885
000

<210> 2886

<400> 2886
000

<210> 2887

<400> 2887

000

<210> 2888

<400> 2888
000

<210> 2889

<400> 2889
000

<210> 2890

<400> 2890
000

<210> 2891

<400> 2891
000

<210> 2892

<400> 2892
000

<210> 2893

<400> 2893
000

<210> 2894

<400> 2894
000

<210> 2895

<400> 2895
000

<210> 2896

<400> 2896
000

<210> 2897

<400> 2897
000

<210> 2898

<400> 2898
000

_SL

<210> 2899

<400> 2899
000

<210> 2900

<400> 2900
000

<210> 2901

<400> 2901
000

<210> 2902

<400> 2902
000

<210> 2903

<400> 2903
000

<210> 2904

<400> 2904
000

<210> 2905

<400> 2905
000

<210> 2906

<400> 2906
000

<210> 2907

<400> 2907
000

<210> 2908

<400> 2908
000

<210> 2909

<400> 2909
000

<210> 2910

_SL

<400> 2910
000

<210> 2911

<400> 2911
000

<210> 2912

<400> 2912
000

<210> 2913

<400> 2913
000

<210> 2914

<400> 2914
000

<210> 2915

<400> 2915
000

<210> 2916

<400> 2916
000

<210> 2917

<400> 2917
000

<210> 2918

<400> 2918
000

<210> 2919

<400> 2919
000

<210> 2920

<400> 2920
000

<210> 2921

<400> 2921

000

<210> 2922

<400> 2922
000

<210> 2923

<400> 2923
000

<210> 2924

<400> 2924
000

<210> 2925

<400> 2925
000

<210> 2926

<400> 2926
000

<210> 2927

<400> 2927
000

<210> 2928

<400> 2928
000

<210> 2929

<400> 2929
000

<210> 2930

<400> 2930
000

<210> 2931

<400> 2931
000

<210> 2932

<400> 2932
000

<210> 2933

<400> 2933
000

<210> 2934

<400> 2934
000

<210> 2935

<400> 2935
000

<210> 2936

<400> 2936
000

<210> 2937

<400> 2937
000

<210> 2938

<400> 2938
000

<210> 2939

<400> 2939
000

<210> 2940

<400> 2940
000

<210> 2941

<400> 2941
000

<210> 2942

<400> 2942
000

<210> 2943

<400> 2943
000

<210> 2944

_SL

<400> 2944
000

<210> 2945

<400> 2945
000

<210> 2946

<400> 2946
000

<210> 2947

<400> 2947
000

<210> 2948

<400> 2948
000

<210> 2949

<400> 2949
000

<210> 2950

<400> 2950
000

<210> 2951

<400> 2951
000

<210> 2952

<400> 2952
000

<210> 2953

<400> 2953
000

<210> 2954

<400> 2954
000

<210> 2955

<400> 2955

000

<210> 2956

<400> 2956
000

<210> 2957

<400> 2957
000

<210> 2958

<400> 2958
000

<210> 2959

<400> 2959
000

<210> 2960

<400> 2960
000

<210> 2961

<400> 2961
000

<210> 2962

<400> 2962
000

<210> 2963

<400> 2963
000

<210> 2964

<400> 2964
000

<210> 2965

<400> 2965
000

<210> 2966

<400> 2966
000

_SL

<210> 2967

<400> 2967
000

<210> 2968

<400> 2968
000

<210> 2969

<400> 2969
000

<210> 2970

<400> 2970
000

<210> 2971

<400> 2971
000

<210> 2972

<400> 2972
000

<210> 2973

<400> 2973
000

<210> 2974

<400> 2974
000

<210> 2975

<400> 2975
000

<210> 2976

<400> 2976
000

<210> 2977

<400> 2977

000

<210> 2978

<400> 2978
000

<210> 2979

<400> 2979
000

<210> 2980

<400> 2980
000

<210> 2981

<400> 2981
000

<210> 2982

<400> 2982
000

<210> 2983

<400> 2983
000

<210> 2984

<400> 2984
000

<210> 2985

<400> 2985
000

<210> 2986

<400> 2986
000

<210> 2987

<400> 2987
000

<210> 2988

<400> 2988

000

<210> 2989

<400> 2989
000

<210> 2990

<400> 2990
000

<210> 2991

<400> 2991
000

<210> 2992

<400> 2992
000

<210> 2993

<400> 2993
000

<210> 2994

<400> 2994
000

<210> 2995

<400> 2995
000

<210> 2996

<400> 2996
000

<210> 2997

<400> 2997
000

<210> 2998

<400> 2998
000

<210> 2999

<400> 2999
000

<210> 3000

<400> 3000
000

<210> 3001

<211> 1200

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 3001

atgctcgagg gggttcaggt ggagactatc agcccgggcg acggacggac attcccaaag	60
cgcggggcaga cgtgtgtggt gcattacacc gggatgcttg aggacggaaa gaaagtggac	120
tcttcccagag accgaaataa accattcaag ttcattgttg gcaagcagga ggttatcaga	180
gggtgggagg agggcgctgc tcagatgagt gtcggacaga gggccaagct cacgatctcc	240
cctgattacg cctacggggc aactggtcac cccggaatca tccccctca cgcaaccctc	300
gtgttcgacg tcgagctgct caaactggaa tcaggcggag gcagtggcgc tagcgggttt	360
ggcgatgtcg gtgcccttga aagcttgaga ggaaatgccg atctcgctta catcttgagc	420
atggagccct gtgggactg tctgatcatc aacaatgtta acttttgccg ggagtccggc	480
ctgcgcacac gcacaggctc caacattgac tgcgaaaaac ttcgaaggag gtttagctct	540
ctgcatttca tggtagaggt gaagggggat ctgaccgcca agaaaatggt tctcgccctt	600
ctcgagcttg cgcagcagga ccatggagcg cttgactgtt gtgtcgttgt gatactgagc	660
catggctgtc aggcttccca tctccagttt ccagggggccg tgtacggaac cgatggatgc	720
cctgtgtcag ttgaaaagat cgtaaacatc tttaacggaa catcttgccc gagcctcggc	780
ggtaaaccga agcttttttt tatccaggcc tgcggcgggtg aacagaaaga tcatggcttc	840
gaggttgcca gtaccagccc tgaagacgaa tccccgggt caaatcctga accagatgcg	900
acccttttcc aggaaggact ccgcactttt gaccagcttg acgccatttc ctccctgcca	960
acaccttccg acatatttgt aagctactcc acctttccag gattcgtgag ctggcgcgac	1020
ccaaaatccg gcagttggta tgttgaaacc ctggacgata ttttcgaaca atggggccac	1080
agtgaggacc tgagtcctt tcttctgctg gtagccaatg ccgtgtcagt caaagggatt	1140
tacaagcaga tgccaggctg ctttaatttc ctgcgcaaga aactgttttt taagaccagt	1200

<210> 3002

<211> 1172

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

_SL

<400> 3002
cggacggaca ttcccaaagc gcgggcagac gtgtgtggtg cattacaccg ggatgcttga 60
ggacggaaaag aaagtggact cttcccgaga ccgaaataaa ccattcaagt tcatgttggg 120
caagcaggag gttatcagag ggtgggagga gggcgtcgct cagatgagtg tcggacagag 180
ggccaagctc acgatctccc ctgattacgc ctacggggca actggtcacc ccggaatcat 240
ccccctcac gcaaccctcg tgttcgacgt cgagctgctc aaactggaat caggcggagg 300
cagtggcggg tttggcgatg tcggtgccct tgaaagcttg agaggaaatg ccgatctcgc 360
ttacatcttg agcatggagc cctgtgggca ctgtctgata atcaacaatg ttaacttttg 420
ccgggagtcg ggcttgcgca cacgcacagg ctccaacatt gactgcgaaa aacttcgaag 480
gaggttttagc tctctgcatt tcatggtaga ggtgaagggg gatctgaccg ccaagaaaat 540
ggttctcgcc cttctcgagc ttgctgcagca ggaccatgga gcgcttgact gttgtgtcgt 600
tgtgatactg agccatggct gtcaggcttc ccatctccag tttccagggg ccgtgtacgg 660
aaccgatgga tgccctgtgt cagttgaaaa gatcgtaaac atctttaacg gaacatcttg 720
cccgagcctc ggcggtaaac cgaagctttt ttttatccag gcctgcggcg gtgaacagaa 780
agatcatggc ttcgaggttg ccagtaccag ccctgaagac gaatcccccg ggtcaaatcc 840
tgaaccagat gcgaccctt tccaggaagg actccgcact tttgaccagc ttgacgccat 900
ttcctccctg ccaacacctt ccgacatatt tgtaagctac tccacctttc caggattcgt 960
gagctggcgc gacccaaaat ccggcagttg gtatgttgaa accctggacg atatcttcga 1020
acaatgggcc cacagtgagg acctgcagtc cttctttctg cgcgtagcca atgccgtgtc 1080
agtcaaaggg atttacaagc agatgccagg ctgctttaat ttcttgcgca agaaactgtt 1140
ttttaagacc agttgagtcg acggaggagg ag 1172

<210> 3003
<211> 1188
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 3003
ggggttcagg tggagactat cagcccgggc gacggacgga cattcccaa ggcggggcag 60
acgtgtgtgg tgcattacac cgggatgctt gaggacggaa agaaagtgga ctcttcccg 120
gaccgaaata aaccattcaa gttcatgttg ggcaagcagg aggttatcag aggggtgggag 180
gagggcgctc ctcatgagc tctcggacag agggccaagc tcacgatctc ccctgattac 240
gcctacgggg caactgtgta ccccggaatc atccccctc acgcaaccct cgtgttcgac 300
gtcgagctgc tcaaactgga atcaggcgga ggcagtggcg ggtttggcga tgtcgggtgc 360
cttgaaagct tgagaggaaa tgccgatctc gcttacatct tgagcatgga gccctgtggg 420

	_SL	
cactgtctga tcatcaacaa tgttaacttt tgccgggagt ccggcctgcg cacacgcaca	480	
ggctccaaca ttgactgcga aaaacttcga aggaggttta gctctctgca tttcatggta	540	
gaggtgaagg gggatctgac cgccaagaaa atggttctcg cccttctcga gcttgcgag	600	
caggaccatg gagcgcttga ctgttggtgc gttgtgatac tgagccatgg ctgtcaggct	660	
tcccatctcc agtttccagg ggccgtgtac ggaaccgatg gatgccctgt gtcagttgaa	720	
aagatcgtaa acatctttta cggaacatct tgcccagacc tcggcggtaa accgaagctt	780	
ttttttatcc aggctgcgg cggatgaacag aaagatcatg gcttcgaggt tgccagtacc	840	
agccctgaag acgaatcccc cgggtcaaatt cctgaaccag atgcgacccc tttccaggaa	900	
ggactccgca cttttgacca gcttgacgcc atttcctccc tgccaacacc ttccgacata	960	
tttgtaagct actccacctt tccaggattc gtgagctggc gcgacccaaa atccggcagt	1020	
tggtatgttg aaaccctgga cgatatcttc gaacaatggg cccacagtga ggacctgcag	1080	
tcccttcttc tgcgcgtagc caatgccgtg tcagtcaaag ggatttaca gcagatgcc	1140	
ggctgcttta atttcctgcg caagaaactg tttttaaga ccagttga	1188	

<210> 3004

<211> 1518

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 3004

agaggcgtgc aggtggaaac catctctccc ggcgacggca gaaccttccc taagaggggc	60
cagacctgcg tggtgacta caccggcatg ctggaagatg gcaagaagat ggacagctcc	120
cgggaccgga acaagccctt caagttcatg ctgggcaagc aggaagtgat ccggggctgg	180
gaagagggcg tggcacagat gtctgtgggc cagagagcca agctgaccat cagccccgat	240
tacgcctacg gcgccacagg ccaccctggc atcattcctc cacacgccac actggtgttc	300
gatgtggaac tgctgaagct ggaaacccgg ggagtgcagg tggaacaat cagccctggc	360
gacggccgga cttttcaaaa acggggacag acatgtgtgg tgcattatac agggatgctg	420
gaagatggga aaaaaatgga tagcagccgc gaccgcaaca aaccttttaa gtttatgctg	480
gggaaacagg aagtgattag aggctgggaa gagggggtgg cacagatgag cgtgggacag	540
cgggccaaac tgacaatctc ccccactat gcctatgggg ccaccggaca ccccggaatc	600
atcccacctc atgctaccct ggtgtttgac gtggaactgc tgaaactgga aacaagcggc	660
ggaggcagcg gcggctttgg agatgtggga gccctggaaa gcctgcgggg caatgccgat	720
ctggcctaca tcctgagcat ggaaccctgc ggccactgcc tgattatcaa caacgtgaac	780
ttctgcagag agagcggcct gcggaccaga accggcagca acatcgactg cgagaagctg	840
cggcggagat tcagcagcct gcacttcatg gtggaagtga agggggacct gaccgccaag	900

_SL

aaaatggtgc tggctctgct ggaactggcc cagcaggatc atggcgccct ggactgttgc	960
gtggtcgtga tcctgagcca cggctgccag gccagccatc tgcagtttcc cggcgctgtg	1020
tatggcaccg atggctgccc tgtgtccgtg gaaaagatcg tgaatatctt caacggcacc	1080
agctgccccca gcctgggcg gaaagcctaag ctgttcttta ttcaagcctg tgggggagag	1140
cagaaggacc acggatttga ggtggccagc acctcccccg aggatgagag ccctggcagc	1200
aacctgagc ctgacgccac ccattccag gaaggactgc ggaccttcga ccagctggac	1260
gccatctcta gcctgcccac cccagcgac atcttcgtgt cctacagcac cttccctggc	1320
tttgtgtcct ggcgggaccc caagtccggc tcttggtacg tggaaaccct ggacgacatc	1380
tttgagcagt gggcccatag cgaggacctg cagagcctgc tgctgagggt ggccaatgcc	1440
gtgtccgtga agggcatcta caagcagatg cccggctgct tcaacttcct gcggaagaag	1500
ctgtttttca agaccagc	1518

<210> 3005
 <211> 400
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 3005
 Met Leu Glu Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg
 1 5 10 15

Thr Phe Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met
 20 25 30

Leu Glu Asp Gly Lys Lys Val Asp Ser Ser Arg Asp Arg Asn Lys Pro
 35 40 45

Phe Lys Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu
 50 55 60

Gly Val Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser
 65 70 75 80

Pro Asp Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro
 85 90 95

His Ala Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu Ser Gly
 100 105 110

Gly Gly Ser Gly Ala Ser Gly Phe Gly Asp Val Gly Ala Leu Glu Ser
 115 120 125

Leu Arg Gly Asn Ala Asp Leu Ala Tyr Ile Leu Ser Met Glu Pro Cys
 130 135 140

_SL

Gly His Cys Leu Ile Ile Asn Asn Val Asn Phe Cys Arg Glu Ser Gly
145 150 155 160

Leu Arg Thr Arg Thr Gly Ser Asn Ile Asp Cys Glu Lys Leu Arg Arg
165 170 175

Arg Phe Ser Ser Leu His Phe Met Val Glu Val Lys Gly Asp Leu Thr
180 185 190

Ala Lys Lys Met Val Leu Ala Leu Leu Glu Leu Ala Gln Gln Asp His
195 200 205

Gly Ala Leu Asp Cys Cys Val Val Val Ile Leu Ser His Gly Cys Gln
210 215 220

Ala Ser His Leu Gln Phe Pro Gly Ala Val Tyr Gly Thr Asp Gly Cys
225 230 235 240

Pro Val Ser Val Glu Lys Ile Val Asn Ile Phe Asn Gly Thr Ser Cys
245 250 255

Pro Ser Leu Gly Gly Lys Pro Lys Leu Phe Phe Ile Gln Ala Cys Gly
260 265 270

Gly Glu Gln Lys Asp His Gly Phe Glu Val Ala Ser Thr Ser Pro Glu
275 280 285

Asp Glu Ser Pro Gly Ser Asn Pro Glu Pro Asp Ala Thr Pro Phe Gln
290 295 300

Glu Gly Leu Arg Thr Phe Asp Gln Leu Asp Ala Ile Ser Ser Leu Pro
305 310 315 320

Thr Pro Ser Asp Ile Phe Val Ser Tyr Ser Thr Phe Pro Gly Phe Val
325 330 335

Ser Trp Arg Asp Pro Lys Ser Gly Ser Trp Tyr Val Glu Thr Leu Asp
340 345 350

Asp Ile Phe Glu Gln Trp Ala His Ser Glu Asp Leu Gln Ser Leu Leu
355 360 365

Leu Arg Val Ala Asn Ala Val Ser Val Lys Gly Ile Tyr Lys Gln Met
370 375 380

Pro Gly Cys Phe Asn Phe Leu Arg Lys Lys Leu Phe Phe Lys Thr Ser
385 390 395 400

<210> 3006

<211> 395

_SL

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 3006

Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe Pro
1 5 10 15

Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu Asp
20 25 30

Gly Lys Lys Val Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys Phe
35 40 45

Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val Ala
50 55 60

Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp Tyr
65 70 75 80

Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala Thr
85 90 95

Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu Ser Gly Gly Gly Ser
100 105 110

Gly Gly Phe Gly Asp Val Gly Ala Leu Glu Ser Leu Arg Gly Asn Ala
115 120 125

Asp Leu Ala Tyr Ile Leu Ser Met Glu Pro Cys Gly His Cys Leu Ile
130 135 140

Ile Asn Asn Val Asn Phe Cys Arg Glu Ser Gly Leu Arg Thr Arg Thr
145 150 155 160

Gly Ser Asn Ile Asp Cys Glu Lys Leu Arg Arg Arg Phe Ser Ser Leu
165 170 175

His Phe Met Val Glu Val Lys Gly Asp Leu Thr Ala Lys Lys Met Val
180 185 190

Leu Ala Leu Leu Glu Leu Ala Gln Gln Asp His Gly Ala Leu Asp Cys
195 200 205

Cys Val Val Val Ile Leu Ser His Gly Cys Gln Ala Ser His Leu Gln
210 215 220

Phe Pro Gly Ala Val Tyr Gly Thr Asp Gly Cys Pro Val Ser Val Glu
225 230 235 240

_SL

Lys Ile Val Asn Ile Phe Asn Gly Thr Ser Cys Pro Ser Leu Gly Gly
245 250 255

Lys Pro Lys Leu Phe Phe Ile Gln Ala Cys Gly Gly Glu Gln Lys Asp
260 265 270

His Gly Phe Glu Val Ala Ser Thr Ser Pro Glu Asp Glu Ser Pro Gly
275 280 285

Ser Asn Pro Glu Pro Asp Ala Thr Pro Phe Gln Glu Gly Leu Arg Thr
290 295 300

Phe Asp Gln Leu Asp Ala Ile Ser Ser Leu Pro Thr Pro Ser Asp Ile
305 310 315 320

Phe Val Ser Tyr Ser Thr Phe Pro Gly Phe Val Ser Trp Arg Asp Pro
325 330 335

Lys Ser Gly Ser Trp Tyr Val Glu Thr Leu Asp Asp Ile Phe Glu Gln
340 345 350

Trp Ala His Ser Glu Asp Leu Gln Ser Leu Leu Leu Arg Val Ala Asn
355 360 365

Ala Val Ser Val Lys Gly Ile Tyr Lys Gln Met Pro Gly Cys Phe Asn
370 375 380

Phe Leu Arg Lys Lys Leu Phe Phe Lys Thr Ser
385 390 395

<210> 3007

<211> 506

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 3007

Arg Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe
1 5 10 15

Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu
20 25 30

Asp Gly Lys Lys Met Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys
35 40 45

Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val
50 55 60

Ala Gln Met Ser Val Gly Gln Arg Ala Lys^{-SL} Leu Thr Ile Ser Pro Asp
 65 70 75 80
 Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala
 85 90 95
 Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu Thr Arg Gly Val
 100 105 110
 Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe Pro Lys Arg
 115 120 125
 Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu Asp Gly Lys
 130 135 140
 Lys Met Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys Phe Met Leu
 145 150 155 160
 Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val Ala Gln Met
 165 170 175
 Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp Tyr Ala Tyr
 180 185 190
 Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala Thr Leu Val
 195 200 205
 Phe Asp Val Glu Leu Leu Lys Leu Glu Thr Ser Gly Gly Gly Ser Gly
 210 215 220
 Gly Phe Gly Asp Val Gly Ala Leu Glu Ser Leu Arg Gly Asn Ala Asp
 225 230 235 240
 Leu Ala Tyr Ile Leu Ser Met Glu Pro Cys Gly His Cys Leu Ile Ile
 245 250 255
 Asn Asn Val Asn Phe Cys Arg Glu Ser Gly Leu Arg Thr Arg Thr Gly
 260 265 270
 Ser Asn Ile Asp Cys Glu Lys Leu Arg Arg Arg Phe Ser Ser Leu His
 275 280 285
 Phe Met Val Glu Val Lys Gly Asp Leu Thr Ala Lys Lys Met Val Leu
 290 295 300
 Ala Leu Leu Glu Leu Ala Gln Gln Asp His Gly Ala Leu Asp Cys Cys
 305 310 315 320
 Val Val Val Ile Leu Ser His Gly Cys Gln Ala Ser His Leu Gln Phe
 325 330 335

Pro Gly Ala Val Tyr Gly Thr Asp Gly Cys^{-SL} Pro Val Ser Val Glu Lys
340 345 350

Ile Val Asn Ile Phe Asn Gly Thr Ser Cys Pro Ser Leu Gly Gly Lys
355 360 365

Pro Lys Leu Phe Phe Ile Gln Ala Cys Gly Gly Glu Gln Lys Asp His
370 375 380

Gly Phe Glu Val Ala Ser Thr Ser Pro Glu Asp Glu Ser Pro Gly Ser
385 390 395 400

Asn Pro Glu Pro Asp Ala Thr Pro Phe Gln Glu Gly Leu Arg Thr Phe
405 410 415

Asp Gln Leu Asp Ala Ile Ser Ser Leu Pro Thr Pro Ser Asp Ile Phe
420 425 430

Val Ser Tyr Ser Thr Phe Pro Gly Phe Val Ser Trp Arg Asp Pro Lys
435 440 445

Ser Gly Ser Trp Tyr Val Glu Thr Leu Asp Asp Ile Phe Glu Gln Trp
450 455 460

Ala His Ser Glu Asp Leu Gln Ser Leu Leu Leu Arg Val Ala Asn Ala
465 470 475 480

Val Ser Val Lys Gly Ile Tyr Lys Gln Met Pro Gly Cys Phe Asn Phe
485 490 495

Leu Arg Lys Lys Leu Phe Phe Lys Thr Ser
500 505

<210> 3008
<211> 66
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 3008
ggaagcggcg ccaccaattt cagcctgctg aaacaggccg gcgacgtgga agagaaccct 60
ggccct 66

<210> 3009
<211> 69
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
Page 1196

_SL

oligonucleotide"

<400> 3009
agtggctccg gcgcaacaaa tttctccttg ctgaaacagg caggcgacgt tgaggaaaat 60
cccggccca 69

<210> 3010
<211> 66
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 3010
ggctccggcg caacaaattt ctccttgctg aaacaggcag gcgacgttga ggaaaatccc 60
ggccca 66

<210> 3011
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 3011
ggggttcagg tggagactat cagcccgggc ga 32

<210> 3012
<211> 66
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 3012
ggctccggcg caacaaattt ctccttgctg aaacaggcag gcgacgttga ggaaaatccc 60
ggccca 66

<210> 3013
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 3013
Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val
1 5 10 15

_SL

Glu Glu Asn Pro Gly Pro
20

<210> 3014
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 3014
Arg Lys Arg Arg Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln
1 5 10 15

Ala Gly Asp Val Glu Glu Asn Pro Gly Pro
20 25

<210> 3015
<211> 1308
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 3015
cggggctgc aggttgagac aatttcccca ggagatgggc gaacgttccc caagcgcgga 60
cagacatgcg ttgtgcacta cacaggaatg ttggaggacg gaaagaaaat ggacagttca 120
agagatcgga acaaaccatt caaattcatg ttgggaaaac aggaagtgat acggggctgg 180
gaagaggggtg tagcgcaaat gtccgttggc caacgagcaa aactcacgat aagtcccgat 240
tatgcttacg gcgcaaccgg tcacccgggc atcataccgc ctcatgcgac tttggtcttt 300
gatgtggagc tggtgaaact tgaaactcgc ggagtacagg ttgaaacaat atcaccggg 360
gacgggcgga cttttccgaa gagaggtcag acctgcgtcg tccattatac cggtagctg 420
gaggacggaa agaaaatgga cagctcacgg gaccgaaata aaccattcaa atttatgttg 480
gggaaacaag aggttatcag gggctgggag gaggggtgtg cccagatgtc tgtcggtcag 540
cgcgcgaaac tcacaatctc tccggattat gcgtatgggg cgacagggca tccgggaatt 600
atccctcccc acgctacctt ggttttcgat gttgagcttc tgaagttgga gaccagagga 660
gttcaagtgg agacaatatc tcctggggat ggacggacgt tccccaagcg cggccagacc 720
tgtgtagtcc actacacagg gatgcttgaa gacggaaaaa agatggatag cagtagagat 780
cgcaacaaac catttaagtt catgctgggg aagcaggaag taatacgcg ctgggaggaa 840
ggcgtggcac agatgagtgt tggcaacgg gccaaactta ctatttctcc cgattatgcg 900
tatggagcca ccgggcaccc tggcattatc ccaccccatg ccacattggt ttttgacgtt 960
gaattgctta aattggagac caggggagtc caagtggaaa caatatcacc gggggatggt 1020

_SL

cggacttttc ctaaaagggg ccaaacctgt gtagtccatt ataccggaat gctcgaagac 1080
ggaaagaaaa tggactcttc tagagaccgc aataagccct tcaagttcat gttgggtaag 1140
caagagggtga tccggggctg ggaagagggg gtcgctcaaa tgtccgtcgg tcagcgagct 1200
aaactgacta tttcccaga ctacgcatat ggagcgactg gccaccccg tttatttctt 1260
cccatgcca ctctcgtgtt cgacgtagaa ctcttgaaat tggaaacg 1308

<210> 3016
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 3016
tcagcccga acaggcggaa gaga 24

<210> 3017
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 3017
Ser Ala Arg Asn Arg Arg Lys Arg
1 5

<210> 3018
<211> 2727
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 3018
atgctcgagg gggttcaggt ggagactatc agcccgggag acggacggac attcccaaag 60
cgcgggcaga cgtgtgtggt gcattacacc gggatgcttg aggacggaaa gaaagtggac 120
tcttcccag accgaaataa accattcaag ttcatgttg gcaagcagga ggttatcaga 180
gggtgggagg agggcgctgc tcagatgagt gtcggacaga gggccaagct cacgatctcc 240
cctgattacg cctacggggc aactggtcac cccggaatca tccccctca cgcaaccctc 300
gtgttcgacg tcgagctgct caaactggaa tcaggcggag gcagtggcgc tagcgggttt 360
ggcgatgtcg gtgcccttga aagcttgaga ggaaatgccg atctcgctta catcttgagc 420
atggagccct gtgggcactg tctgatcatc aacaatgtta acttttgccg ggagtccggc 480

						_SL	
ctgcgcacac	gcacaggctc	caacattgac	tgcgaaaaac	ttcgaaggag	gtttagctct		540
ctgcatttca	tggtagaggt	gaagggggat	ctgaccgccca	agaaaatggt	tctcgccctt		600
ctcgagcttg	cgcagcagga	ccatggagcg	cttgactgtt	gtgtcgttgt	gatactgagc		660
catggctgtc	aggcttccca	tctccagttt	ccagggggccg	tgtacggaac	cgatggatgc		720
cctgtgtcag	ttgaaaagat	cgtaaacatc	tttaacggaa	catcttgccc	gagcctcggc		780
ggtaaaccga	agcttttttt	tatccaggcc	tgcgggcgggtg	aacagaaaga	tcatggcttc		840
gaggttgcca	gtaccagccc	tgaagacgaa	tcccccggtt	caaatcctga	accagatgcg		900
acccctttcc	aggaaggact	ccgcactttt	gaccagcttg	acgccatttc	ctccctgccca		960
acaccttccg	acatatttgt	aagctactcc	acctttccag	gattcgtgag	ctggcgcgac		1020
ccaaaatccg	gcagttggta	tgttgaaacc	ctggacgata	ttttcgaaca	atgggcccac		1080
agtgaggacc	tgcagtccct	tcttctgctc	gtagccaatg	ccgtgtcagt	caaagggatt		1140
tacaagcaga	tgccaggctg	ctttaatttc	ctgcgcaaga	aactgttttt	taagaccagt		1200
ggctccggcg	caacaaatth	ctccttgctg	aaacaggcag	gcgacgttga	ggaaaatccc		1260
ggcccaatgg	ccttaccagt	gaccgccttg	ctcctgccgc	tggccttgct	gctccacgcc		1320
gccaggccgg	acatccagat	gacacagact	acatcctccc	tgtctgcctc	tctgggagac		1380
agagtcacca	tcagttgcag	ggcaagtcag	gacattagta	aatattttaa	ttggtatcag		1440
cagaaaccag	atggaactgt	taaactcctg	atctaccata	catcaagatt	acactcagga		1500
gtcccatcaa	ggttcagtgg	cagtgggtct	ggaacagatt	attctctcac	cattagcaac		1560
ctggagcaag	aagatattgc	cacttacttt	tgccaacagg	gtaatacgct	tccgtacacg		1620
ttcggagggg	ggactaagtt	ggaaataaca	ggtggcggtg	gctcgggcgg	tgggtgggtcg		1680
ggtggcgggc	gatctgaggt	gaaactgcag	gagtcaggac	ctggcctggt	ggcgccctca		1740
cagagcctgt	ccgtcacatg	cactgtctca	gggtctctcat	tacccgacta	tgggtgtaagc		1800
tggattcgcc	agcctccacg	aaaggtctctg	gagtggctgg	gagtaatatg	gggtagtgaa		1860
accacatact	ataattcagc	tctcaaattcc	agactgacca	tcatcaagga	caactccaag		1920
agccaagttt	tcttaaaaat	gaacagtctg	caaactgatg	acacagccat	ttactactgt		1980
gccaaacatt	attactacgg	tggtagctat	gctatggact	actgggggtca	aggaacctca		2040
gtcaccgtct	cctcaaccac	gacgccagcg	ccgcgaccac	caacaccggc	gcccaccatc		2100
gcgtcgcagc	ccctgtccct	gcgcccagag	gcgtgccggc	cagcggcggg	gggcgcagtg		2160
cacacgaggg	ggctggactt	cgcctgtgat	atctacatct	gggcgccctt	ggccgggact		2220
tgtgggggtcc	ttctcctgtc	actggttatc	accctttact	gcaaacgggg	cagaaagaaa		2280
ctcctgtata	tattcaaaca	accatttatg	agaccagtac	aaactactca	agaggaagat		2340
ggctgtagct	gccgatttcc	agaagaagaa	gaaggaggat	gtgaactgag	agtgaagttc		2400
agcaggagcg	cagacgcccc	cgcgtaccag	cagggccaga	accagctcta	taacgagctc		2460
aatctaggac	gaagagagga	gtacgatgtt	ttggacaaga	gacgtggccg	ggaccctgag		2520

atgggggggaa agccgagaag gaagaaccct caggaaggcc tgtacaatga actgcagaaa 2580
 gataagatgg cggaggccta cagtgaatt gggatgaaag gcgagcgccg gaggggcaag 2640
 gggcacgatg gcctttacca ggggtctcagt acagccacca aggacaccta cgacgccctt 2700
 cacatgcagg ccctgcccc tcgctaa 2727

<210> 3019
 <211> 908
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 3019
 Met Leu Glu Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg
 1 5 10 15

Thr Phe Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met
 20 25 30

Leu Glu Asp Gly Lys Lys Val Asp Ser Ser Arg Asp Arg Asn Lys Pro
 35 40 45

Phe Lys Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu
 50 55 60

Gly Val Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser
 65 70 75 80

Pro Asp Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro
 85 90 95

His Ala Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu Ser Gly
 100 105 110

Gly Gly Ser Gly Ala Ser Gly Phe Gly Asp Val Gly Ala Leu Glu Ser
 115 120 125

Leu Arg Gly Asn Ala Asp Leu Ala Tyr Ile Leu Ser Met Glu Pro Cys
 130 135 140

Gly His Cys Leu Ile Ile Asn Asn Val Asn Phe Cys Arg Glu Ser Gly
 145 150 155 160

Leu Arg Thr Arg Thr Gly Ser Asn Ile Asp Cys Glu Lys Leu Arg Arg
 165 170 175

Arg Phe Ser Ser Leu His Phe Met Val Glu Val Lys Gly Asp Leu Thr
 180 185 190

Ala Lys Lys₁₉₅ Met Val Leu Ala Leu₂₀₀ Leu Glu^{-SL} Leu Ala Gln₂₀₅ Gln Asp His
 Gly Ala₂₁₀ Leu Asp Cys Cys Val₂₁₅ Val Val Ile Leu Ser₂₂₀ His Gly Cys Gln
 Ala₂₂₅ Ser His Leu Gln Phe₂₃₀ Pro Gly Ala Val Tyr₂₃₅ Gly Thr Asp Gly Cys₂₄₀
 Pro Val Ser Val₂₄₅ Glu Lys Ile Val Asn₂₅₀ Ile Phe Asn Gly Thr Ser₂₅₅ Cys
 Pro Ser Leu Gly₂₆₀ Gly Lys Pro Lys Leu₂₆₅ Phe Phe Ile Gln Ala₂₇₀ Cys Gly
 Gly Glu Gln₂₇₅ Lys Asp His Gly Phe₂₈₀ Glu Val Ala Ser Thr₂₈₅ Ser Pro Glu
 Asp Glu₂₉₀ Ser Pro Gly Ser Asn₂₉₅ Pro Glu Pro Asp Ala₃₀₀ Thr Pro Phe Gln
 Glu₃₀₅ Gly Leu Arg Thr Phe₃₁₀ Asp Gln Leu Asp Ala₃₁₅ Ile Ser Ser Leu Pro₃₂₀
 Thr Pro Ser Asp₃₂₅ Ile Phe Val Ser Tyr Ser₃₃₀ Thr Phe Pro Gly Phe₃₃₅ Val
 Ser Trp Arg Asp₃₄₀ Pro Lys Ser Gly Ser₃₄₅ Trp Tyr Val Glu Thr₃₅₀ Leu Asp
 Asp Ile Phe₃₅₅ Glu Gln Trp Ala His₃₆₀ Ser Glu Asp Leu Gln₃₆₅ Ser Leu Leu
 Leu Arg₃₇₀ Val Ala Asn Ala Val₃₇₅ Ser Val Lys Gly Ile₃₈₀ Tyr Lys Gln Met
 Pro Gly Cys Phe Asn Phe₃₉₀ Leu Arg Lys Lys Leu₃₉₅ Phe Phe Lys Thr Ser₄₀₀
 Gly Ser Gly Ala Thr₄₀₅ Asn Phe Ser Leu Leu₄₁₀ Lys Gln Ala Gly Asp₄₁₅ Val
 Glu Glu Asn₄₂₀ Pro Gly Pro Met Ala Leu₄₂₅ Pro Val Thr Ala Leu₄₃₀ Leu Leu
 Pro Leu Ala₄₃₅ Leu Leu Leu His Ala₄₄₀ Ala Arg Pro Asp Ile₄₄₅ Gln Met Thr
 Gln Thr₄₅₀ Thr Ser Ser Leu Ser₄₅₅ Ala Ser Leu Gly Asp₄₆₀ Arg Val Thr Ile

Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys^{-SL} Tyr Leu Asn Trp Tyr Gln
 465 470 475 480
 Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile Tyr His Thr Ser Arg
 485 490 495
 Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
 500 505 510
 Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln Glu Asp Ile Ala Thr
 515 520 525
 Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gly Gly
 530 535 540
 Thr Lys Leu Glu Ile Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 545 550 555 560
 Gly Gly Gly Gly Ser Glu Val Lys Leu Gln Glu Ser Gly Pro Gly Leu
 565 570 575
 Val Ala Pro Ser Gln Ser Leu Ser Val Thr Cys Thr Val Ser Gly Val
 580 585 590
 Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln Pro Pro Arg Lys
 595 600 605
 Gly Leu Glu Trp Leu Gly Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr
 610 615 620
 Asn Ser Ala Leu Lys Ser Arg Leu Thr Ile Ile Lys Asp Asn Ser Lys
 625 630 635 640
 Ser Gln Val Phe Leu Lys Met Asn Ser Leu Gln Thr Asp Asp Thr Ala
 645 650 655
 Ile Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met
 660 665 670
 Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Thr Thr Thr
 675 680 685
 Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro
 690 695 700
 Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val
 705 710 715 720
 His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro
 725 730 735

Leu Ala Gly Thr Cys Gly Val Leu Leu ^{-SL} Ser Leu Val Ile Thr Leu
 740 745 750
 Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro
 755 760 765
 Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys
 770 775 780
 Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe
 785 790 795 800
 Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu
 805 810 815
 Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp
 820 825 830
 Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys
 835 840 845
 Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala
 850 855 860
 Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
 865 870 875 880
 Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
 885 890 895
 Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
 900 905

<210> 3020
 <211> 2741
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 3020
 atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60
 ccggacatcc agatgacaca gactacatcc tccctgtctg cctctctggg agacagagtc 120
 accatcagtt gcagggcaag tcaggacatt agtaaattatt taaattggta tcagcagaaa 180
 ccagatggaa ctgttaaact cctgatctac catacatcaa gattacactc aggagtccca 240
 tcaaggttca gtggcagtgg gtctggaaca gattattctc tcaccattag caacctggag 300
 caagaagata ttgccactta cttttgccaa cagggttaata cgcttcgta cacgttcgga 360
 ggggggacta agttggaaat aacaggtggc ggtggctcgg gcggtggtgg gtcgggtggc 420

_SL

ggcggatctg	aggtgaaact	gcaggagtca	ggacctggcc	tggtggcgcc	ctcacagagc	480
ctgtccgtca	catgcactgt	ctcaggggtc	tcattaccgc	actatggtgt	aagctggatt	540
cgccagcctc	cacgaaaggg	tctggagtgg	ctgggagtaa	tatggggtag	tgaaccaca	600
tactataatt	cagctctcaa	atccagactg	accatcatca	aggacaactc	caagagccaa	660
gttttcttaa	aatgaacag	tctgcaaact	gatgacacag	ccatttacta	ctgtgccaaa	720
cattattact	acggtggtag	ctatgctatg	gactactggg	gtcaaggaac	ctcagtcacc	780
gtctcctcaa	ccacgacgcc	agcgccgcga	ccaccaacac	cggcgcccac	catcgcgctc	840
cagcccctgt	ccctgcgccc	agaggcgtgc	cggccagcgg	cggggggcgc	agtgcacacg	900
agggggctgg	acttcgcctg	tgatatctac	atctgggcgc	ccttggccgg	gacttgtggg	960
gtccttctcc	tgtactggt	tatcacctt	tactgcaaac	ggggcagaaa	gaaactcctg	1020
tatatattca	aacaaccatt	tatgagacca	gtacaaacta	ctcaagagga	agatggctgt	1080
agctgccgat	ttccagaaga	agaagaagga	ggatgtgaac	tgagagtga	gttcagcagg	1140
agcgagacg	ccccgcgta	ccagcagggc	cagaaccagc	tctataacga	gctcaatcta	1200
ggacgaagag	aggagtacga	tgttttggac	aagagacgtg	gccgggaccc	tgagatgggg	1260
ggaaagccga	gaaggaagaa	ccctcaggaa	ggcctgtaca	atgaactgca	gaaagataag	1320
atggcggagg	cctacagtga	gattgggatg	aaaggcgagc	gccggagggg	caaggggcac	1380
gatggccttt	accaggtct	cagtacagcc	accaaggaca	cctacgacgc	ccttcacatg	1440
caggccctgc	cccctcgctc	ggaagcgacg	gggctccggc	gcaacaaatt	tctccttgct	1500
gaaacaggca	ggcgacgttg	aggaaaatcc	cggcccaggg	gttcaggtgg	agactatcag	1560
cccgggcgac	ggacggacat	tcccaaagcg	cgggcagacg	tgtgtggtgc	attacaccgg	1620
gatgcttgag	gacggaaaga	aagtggactc	ttcccagac	cgaaataaac	cattcaagtt	1680
catgttgggc	aagcaggagg	ttatcagagg	gtgggaggag	ggcgctcgctc	agatgagtgt	1740
cggacagagg	gccaaagtca	cgatctcccc	tgattacgcc	tacggggcaa	ctggtcaccc	1800
cggaatcatc	ccccctcacg	caaccctcgt	gttcgacgtc	gagctgctca	aactggaatc	1860
aggcggaggc	agtggcgggt	ttggcgatgt	cggtgccctt	gaaagcttga	gaggaaatgc	1920
cgatctcgct	tacatcttga	gcatggagcc	ctgtgggcac	tgtctgatca	tcaacaatgt	1980
taacttttgc	cgggagtcgg	gcctgcgcac	acgcacaggc	tccaacattg	actgcgaaaa	2040
acttcgaagg	aggttttagct	ctctgcattt	catggttagag	gtgaaggggg	atctgaccgc	2100
caagaaaatg	gttctcgccc	ttctcgagct	tgcgacagcag	gaccatggag	cgcttgactg	2160
ttgtgtcggt	gtgatactga	gccatggctg	tcaggcttcc	catctccagt	ttccaggggc	2220
cgtgtacgga	accgatggat	gccctgtgtc	agttgaaaag	atcgtaaaca	tctttaacgg	2280
aacatcttgc	ccgagcctcg	gcggtaaacc	gaagcttttt	tttatccagg	cctgcggcgg	2340
tgaacagaaa	gatcatggct	tcgaggttgc	cagtaccagc	cctgaagacg	aatcccccg	2400
gtcaaatacct	gaaccagatg	cgaccctttt	ccaggaagga	ctccgcactt	ttgaccagct	2460

_SL

tgacgccatt tcctccctgc caacaccttc cgacatattt gtaagctact ccacctttcc 2520
aggattcgtg agctggcgcg acccaaatc cggcagttgg tatgttgaaa cctgggacga 2580
tatcttcgaa caatggggccc acagtgagga cctgcagtcc cttcttctgc gcgtagccaa 2640
tgccgtgtca gtcaaaggga ttacaagca gatgccaggc tgctttaatt tcctgcgcaa 2700
gaaactgttt tttaagacca gttgagtcga cggaggagga g 2741

<210> 3021

<211> 907

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 3021

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu
20 25 30

Ser Ala Ser Leu Gly Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln
35 40 45

Asp Ile Ser Lys Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr
50 55 60

Val Lys Leu Leu Ile Tyr His Thr Ser Arg Leu His Ser Gly Val Pro
65 70 75 80

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile
85 90 95

Ser Asn Leu Glu Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly
100 105 110

Asn Thr Leu Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu
130 135 140

Val Lys Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser
145 150 155 160

Leu Ser Val Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly
165 170 175

Val Ser Trp Ile Arg Gln Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly

_SL

180		185		190											
Val	Ile	Trp 195	Gly	Ser	Glu	Thr	Thr 200	Tyr	Tyr	Asn	Ser	Ala 205	Leu	Lys	Ser
Arg	Leu 210	Thr	Ile	Ile	Lys	Asp 215	Asn	Ser	Lys	Ser	Gln 220	Val	Phe	Leu	Lys
Met 225	Asn	Ser	Leu	Gln	Thr 230	Asp	Asp	Thr	Ala	Ile 235	Tyr	Tyr	Cys	Ala	Lys 240
His	Tyr	Tyr	Tyr	Gly 245	Gly	Ser	Tyr	Ala	Met 250	Asp	Tyr	Trp	Gly	Gln 255	Gly
Thr	Ser	Val	Thr 260	Val	Ser	Ser	Thr	Thr 265	Thr	Pro	Ala	Pro	Arg 270	Pro	Pro
Thr	Pro	Ala 275	Pro	Thr	Ile	Ala	Ser 280	Gln	Pro	Leu	Ser	Leu 285	Arg	Pro	Glu
Ala	Cys 290	Arg	Pro	Ala	Ala	Gly 295	Gly	Ala	Val	His	Thr 300	Arg	Gly	Leu	Asp
Phe 305	Ala	Cys	Asp	Ile	Tyr 310	Ile	Trp	Ala	Pro	Leu 315	Ala	Gly	Thr	Cys	Gly 320
Val	Leu	Leu	Leu	Ser 325	Leu	Val	Ile	Thr	Leu 330	Tyr	Cys	Lys	Arg	Gly 335	Arg
Lys	Lys	Leu	Leu 340	Tyr	Ile	Phe	Lys	Gln 345	Pro	Phe	Met	Arg	Pro 350	Val	Gln
Thr	Thr	Gln 355	Glu	Glu	Asp	Gly	Cys 360	Ser	Cys	Arg	Phe	Pro 365	Glu	Glu	Glu
Glu	Gly 370	Gly	Cys	Glu	Leu	Arg 375	Val	Lys	Phe	Ser	Arg 380	Ser	Ala	Asp	Ala
Pro 385	Ala	Tyr	Gln	Gln	Gly 390	Gln	Asn	Gln	Leu	Tyr 395	Asn	Glu	Leu	Asn	Leu 400
Gly	Arg	Arg	Glu	Glu 405	Tyr	Asp	Val	Leu	Asp 410	Lys	Arg	Arg	Gly	Arg 415	Asp
Pro	Glu	Met	Gly 420	Gly	Lys	Pro	Arg	Arg 425	Lys	Asn	Pro	Gln	Glu 430	Gly	Leu
Tyr	Asn	Glu 435	Leu	Gln	Lys	Asp	Lys 440	Met	Ala	Glu	Ala	Tyr 445	Ser	Glu	Ile
Gly	Met	Lys	Gly	Glu	Arg	Arg	Arg	Gly	Lys	Gly	His	Asp	Gly	Leu	Tyr

					_SL										
450					455					460					
Gln	Gly	Leu	Ser	Thr	Ala	Thr	Lys	Asp	Thr	Tyr	Asp	Ala	Leu	His	Met
465					470					475					480
Gln	Ala	Leu	Pro	Pro	Arg	Arg	Lys	Arg	Arg	Gly	Ser	Gly	Ala	Thr	Asn
				485					490					495	
Phe	Ser	Leu	Leu	Lys	Gln	Ala	Gly	Asp	Val	Glu	Glu	Asn	Pro	Gly	Pro
			500					505					510		
Gly	Val	Gln	Val	Glu	Thr	Ile	Ser	Pro	Gly	Asp	Gly	Arg	Thr	Phe	Pro
		515					520					525			
Lys	Arg	Gly	Gln	Thr	Cys	Val	Val	His	Tyr	Thr	Gly	Met	Leu	Glu	Asp
	530					535					540				
Gly	Lys	Lys	Val	Asp	Ser	Ser	Arg	Asp	Arg	Asn	Lys	Pro	Phe	Lys	Phe
545					550					555					560
Met	Leu	Gly	Lys	Gln	Glu	Val	Ile	Arg	Gly	Trp	Glu	Glu	Gly	Val	Ala
				565					570					575	
Gln	Met	Ser	Val	Gly	Gln	Arg	Ala	Lys	Leu	Thr	Ile	Ser	Pro	Asp	Tyr
			580					585					590		
Ala	Tyr	Gly	Ala	Thr	Gly	His	Pro	Gly	Ile	Ile	Pro	Pro	His	Ala	Thr
		595					600					605			
Leu	Val	Phe	Asp	Val	Glu	Leu	Leu	Lys	Leu	Glu	Ser	Gly	Gly	Gly	Ser
	610					615					620				
Gly	Gly	Phe	Gly	Asp	Val	Gly	Ala	Leu	Glu	Ser	Leu	Arg	Gly	Asn	Ala
625					630					635					640
Asp	Leu	Ala	Tyr	Ile	Leu	Ser	Met	Glu	Pro	Cys	Gly	His	Cys	Leu	Ile
				645					650					655	
Ile	Asn	Asn	Val	Asn	Phe	Cys	Arg	Glu	Ser	Gly	Leu	Arg	Thr	Arg	Thr
			660					665					670		
Gly	Ser	Asn	Ile	Asp	Cys	Glu	Lys	Leu	Arg	Arg	Arg	Phe	Ser	Ser	Leu
		675					680					685			
His	Phe	Met	Val	Glu	Val	Lys	Gly	Asp	Leu	Thr	Ala	Lys	Lys	Met	Val
	690					695					700				
Leu	Ala	Leu	Leu	Glu	Leu	Ala	Gln	Gln	Asp	His	Gly	Ala	Leu	Asp	Cys
705					710					715					720
Cys	Val	Val	Val	Ile	Leu	Ser	His	Gly	Cys	Gln	Ala	Ser	His	Leu	Gln

725 730^{-SL} 735

Phe Pro Gly Ala Val Tyr Gly Thr Asp Gly Cys Pro Val Ser Val Glu
740 745 750

Lys Ile Val Asn Ile Phe Asn Gly Thr Ser Cys Pro Ser Leu Gly Gly
755 760 765

Lys Pro Lys Leu Phe Phe Ile Gln Ala Cys Gly Gly Glu Gln Lys Asp
770 775 780

His Gly Phe Glu Val Ala Ser Thr Ser Pro Glu Asp Glu Ser Pro Gly
785 790 795 800

Ser Asn Pro Glu Pro Asp Ala Thr Pro Phe Gln Glu Gly Leu Arg Thr
805 810 815

Phe Asp Gln Leu Asp Ala Ile Ser Ser Leu Pro Thr Pro Ser Asp Ile
820 825 830

Phe Val Ser Tyr Ser Thr Phe Pro Gly Phe Val Ser Trp Arg Asp Pro
835 840 845

Lys Ser Gly Ser Trp Tyr Val Glu Thr Leu Asp Asp Ile Phe Glu Gln
850 855 860

Trp Ala His Ser Glu Asp Leu Gln Ser Leu Leu Leu Arg Val Ala Asn
865 870 875 880

Ala Val Ser Val Lys Gly Ile Tyr Lys Gln Met Pro Gly Cys Phe Asn
885 890 895

Phe Leu Arg Lys Lys Leu Phe Phe Lys Thr Ser
900 905

<210> 3022

<211> 1479

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 3022

atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg	60
ccgggatccg atattcaact tacacagtcc cctagttcct tgtccgcctc cgtcggcgac	120
agagttacca tgacttgctg agcgtcttct agcgtttcct acattcattg gttccaacag	180
aagcccggaa aggcaccaa accttgatc tacgccacgt ccaatttggc tagtggtgtt	240
ccggtgcatg tttccgggtc aggtagcggg acggactata cttttaccat ttcaagcctt	300

_SL

cagcctgaag acatcgcgac gtactattgt cagcagtggg cctctaacc	tcctacctt	360
ggcgggtggaa caaagctgga gatcaaacga ggcgggggtg gctctgggg	aggaggttcc	420
ggtgggggag gctctcaagt acaactgcaa caaagtgggg ctgaagtga	gaagcccgt	480
tcttcagtca aagtatcatg taaggcaagt ggttatactt ttacgtctta	taacatgcat	540
tgggtaaagc aagcccctgg tcagggcctc gagtggattg gtgcgatcta	ccctggaatg	600
ggtgatacga gctataatca gaaattcaag gggaaagcca ccttgactgc	agacgaatct	660
acgaacacgg cttacatgga gcttagctca ctcagatcag aggatacagc	cttttactac	720
tgcgctagat caacttatta cggaggagac tggtatTTTg atgtatgggg	tcaggggacc	780
acagtactg ttagctctgc tagcaccacg acgccagcgc cgcgaccacc	aacaccggcg	840
cccaccatcg cgtcgcagcc cctgtccctg cgcccagagg cgtgccggcc	agcggcgggg	900
ggcgcagtgc acacgagggg gctggacttc gcctgtgatt ccggaatcta	catctgggcg	960
cccttggccg ggacttgtgg ggtccttctc ctgtcactgg ttatcacct	ttactgcaa	1020
cggggcagaa agaaactcct gtatatattc aaacaaccat ttatgagacc	agtacaaact	1080
actcaagagg aagatggctg tagctgccga tttccagaag aagaagaagg	aggatgtgaa	1140
ctgagagtga agttcagcag gagcgcagac gccccgcgt accagcaggg	ccagaaccag	1200
ctctataacg agtcaatct aggacgaaga gaggagtacg atgttttgga	caagagacgt	1260
ggccgggacc ctgagatggg gggaaagccg agaaggaaga accctcagga	aggcctgtac	1320
aatgaactgc agaaagataa gatggcggag gcctacagt agattgggat	gaaaggcgag	1380
cgccggaggg gcaaggggca cgatggcctt taccagggtc tcagtacagc	caccaaggac	1440
acctacgacg cccttcacat gcaggccctg cccctcgc		1479

<210> 3023

<211> 494

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 3023

Met	Ala	Leu	Pro	Val	Thr	Ala	Leu	Leu	Pro	Leu	Ala	Leu	Leu	Leu
1				5				10				15		

His	Ala	Ala	Arg	Pro	Gly	Ser	Asp	Ile	Gln	Leu	Thr	Gln	Ser	Pro	Ser
			20					25				30			

Ser	Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg	Val	Thr	Met	Thr	Cys	Arg	Ala
		35					40				45				

Ser	Ser	Ser	Val	Ser	Tyr	Ile	His	Trp	Phe	Gln	Gln	Lys	Pro	Gly	Lys
		50				55				60					

Ala Pro Lys Pro Trp Ile Tyr Ala Thr Ser^{-SL} Asn Leu Ala Ser Gly Val
 65 70 75 80
 Pro Val Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Phe Thr
 85 90 95
 Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln
 100 105 110
 Trp Thr Ser Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
 115 120 125
 Lys Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 130 135 140
 Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Val Lys Lys Pro Gly
 145 150 155 160
 Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser
 165 170 175
 Tyr Asn Met His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp
 180 185 190
 Ile Gly Ala Ile Tyr Pro Gly Met Gly Asp Thr Ser Tyr Asn Gln Lys
 195 200 205
 Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Glu Ser Thr Asn Thr Ala
 210 215 220
 Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Phe Tyr Tyr
 225 230 235 240
 Cys Ala Arg Ser Thr Tyr Tyr Gly Gly Asp Trp Tyr Phe Asp Val Trp
 245 250 255
 Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Thr Thr Pro
 260 265 270
 Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu
 275 280 285
 Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His
 290 295 300
 Thr Arg Gly Leu Asp Phe Ala Cys Asp Ser Gly Ile Tyr Ile Trp Ala
 305 310 315 320
 Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr
 325 330 335

Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu^{-SL} Leu Tyr Ile Phe Lys Gln
 340 345 350
 Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser
 355 360 365
 Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys
 370 375 380
 Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln
 385 390 395 400
 Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
 405 410 415
 Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg
 420 425 430
 Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met
 435 440 445
 Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly
 450 455 460
 Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp
 465 470 475 480
 Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg Glx
 485 490

<210> 3024
 <211> 2733
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 3024
 atggctctgc ctgtgacagc tctgctgctg cctctggccc tgctgctgca tgctgccaga 60
 cctggctccg atattcaact tacacagtcc cctagttcct tgtccgcctc cgtcggcgac 120
 agagttacca tgacttgtcg agcgtcttct agcgtttcct acattcattg gttccaacag 180
 aagcccggaa aggcaccaa accttgatc tacgccacgt ccaatttggc tagtggtgtt 240
 ccggtgcatg tttccgggtc aggtagcggg acggactata cttttaccat ttcaagcctt 300
 cagcctgaag acatcgcgac gtactattgt cagcagtggg cctctaacc tcctaccttt 360
 ggcggtggaa caaagctgga gatcaaacga ggcgggggtg gctctggggg aggaggttcc 420
 ggtgggggag gctctcaagt acaactgcaa caaagtgggg ctgaagtga gaagcccgtt 480
 tcttcagtca aagtatcatg taaggcaagt gggtatactt ttacgtctta taacatgcat 540

_SL

tgggtaaagc	aagcccctgg	tcagggcctc	gagtggattg	gtgcgatcta	ccctggaatg	600
ggtgatacga	gctataatca	gaaattcaag	gggaaagcca	ccttgactgc	agacgaatct	660
acgaacacgg	cttacaatga	gcttagctca	ctcagatcag	aggatacagc	cttttactac	720
tgcgctagat	caacttatta	cggaggagac	tggtattttg	atgtatgggg	tcaggggacc	780
acagtacttg	ttagctctgc	tagcaccacg	acgccagcgc	cgcgaccacc	aacaccggcg	840
cccaccatcg	cgtcgcagcc	cctgtccctg	cgcccagagg	cgtgccggcc	agcggcgggg	900
ggcgcagtgc	acacgagggg	gctggacttc	gcctgtgatt	ccggaatcta	catctgggag	960
cccttggccg	ggacttgtgg	ggtccttctc	ctgtcactgg	ttatcacctt	ttactgcaaa	1020
cggggcagaa	agaaactcct	gtatatattc	aaacaacat	ttatgagacc	agtacaaact	1080
actcaagagg	aagatggctg	tagctgccga	tttccagaag	aagaagaagg	aggatgtgaa	1140
ctgagagtga	agttcagcag	gagcgcagac	gccccgcgt	accagcaggg	ccagaaccag	1200
ctctataacg	agctcaatct	aggacgaaga	gaggagtacg	atgttttgga	caagagacgt	1260
ggccgggacc	ctgagatggg	gggaaagccg	agaaggaaga	accctcagga	aggcctgtac	1320
aatgaactgc	agaaagataa	gatggcggag	gcctacagtg	agattgggat	gaaaggcgag	1380
cgccggaggg	gcaaggggca	cgatggcctt	taccagggtc	tcagtacagc	caccaaggac	1440
acctacgacg	cccttcacat	gcaggccctg	ccccctcgcg	gctccggcgc	aacaaatttc	1500
tccttgctga	aacaggcagg	cgacgttgag	gaaaatcccg	gccaggggt	tcagggtggag	1560
actatcagcc	cgggcgacgg	acggacattc	ccaaagcgcg	ggcagacgtg	tgtggtgcat	1620
tacaccggga	tgcttgagga	cggaaagaaa	gtggactctt	cccgagaccg	aaataaacca	1680
ttcaagttca	tggtgggcaa	gcaggagggt	atcagagggt	gggaggaggg	cgtcgcctcag	1740
atgagtgtcg	gacagagggc	caagctcacg	atctcccctg	attacgccta	cggggcaact	1800
ggtcaccccg	gaatcatccc	ccctcacgca	accctcgtgt	tcgacgtcga	gctgctcaaa	1860
ctggaatcag	gcggaggcag	tggcgggttt	ggcgtgtcgc	gtgcccttga	aagcttgaga	1920
ggaaatgccg	atctcgttta	catcttgagc	atggagccct	gtgggcactg	tctgatcatc	1980
aacaatgtta	acttttgccg	ggagtccggc	ctgcgcacac	gcacaggctc	caacattgac	2040
tgcgaaaaac	ttcgaaggag	gtttagctct	ctgcatttca	tggtagaggt	gaagggggat	2100
ctgaccgcca	agaaaatggg	tctcgccctt	ctcgagcttg	cgcagcagga	ccatggagcg	2160
cttgactgtt	gtgtcgttgt	gatactgagc	catggctgtc	aggcttccca	tctccagttt	2220
ccagggggccg	tgtacggaac	cgatggatgc	cctgtgtcag	ttgaaaagat	cgtaaacatc	2280
tttaacggaa	catcttgccc	gagcctcggc	ggtaaaccga	agcttttttt	tatccaggcc	2340
tgcgggcgtg	aacagaaaga	tcattggcttc	gaggttgcca	gtaccagccc	tgaagacgaa	2400
tccccgggt	caaactctga	accagatgcg	acccttttcc	aggaaggact	ccgcactttt	2460
gaccagcttg	acgccatttc	ctccctgcca	acaccttccg	acatatttgt	aagctactcc	2520
acctttccag	gattcgtgag	ctggcgcgac	ccaaaatccg	gcagttggta	tgttgaaacc	2580

_SL

ctggacgata tcttcgaaca atgggcccac agtgaggacc tgcagtcctt tcttctgcgc 2640
gtagccaatg ccgtgtcagt caaagggatt tacaagcaga tgccaggctg ctttaatttc 2700
ctgcgcaaga aactgttttt taagaccagt tga 2733

<210> 3025
<211> 911
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 3025
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gly Ser Asp Ile Gln Leu Thr Gln Ser Pro Ser
20 25 30

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys Arg Ala
35 40 45

Ser Ser Ser Val Ser Tyr Ile His Trp Phe Gln Gln Lys Pro Gly Lys
50 55 60

Ala Pro Lys Pro Trp Ile Tyr Ala Thr Ser Asn Leu Ala Ser Gly Val
65 70 75 80

Pro Val Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Phe Thr
85 90 95

Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln
100 105 110

Trp Thr Ser Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
115 120 125

Lys Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
130 135 140

Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Val Lys Lys Pro Gly
145 150 155 160

Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser
165 170 175

Tyr Asn Met His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp
180 185 190

Ile Gly Ala Ile Tyr Pro Gly Met Gly Asp Thr Ser Tyr Asn Gln Lys
Page 1214

_SL

195		200		205											
Phe	Lys ₂₁₀	Gly	Lys	Ala	Thr	Leu ₂₁₅	Thr	Ala	Asp	Glu	Ser ₂₂₀	Thr	Asn	Thr	Ala
Tyr ₂₂₅	Met	Glu	Leu	Ser	Ser ₂₃₀	Leu	Arg	Ser	Glu	Asp ₂₃₅	Thr	Ala	Phe	Tyr	Tyr ₂₄₀
Cys	Ala	Arg	Ser	Thr ₂₄₅	Tyr	Tyr	Gly	Gly	Asp ₂₅₀	Trp	Tyr	Phe	Asp	Val ₂₅₅	Trp
Gly	Gln	Gly	Thr ₂₆₀	Thr	Val	Thr	Val	Ser ₂₆₅	Ser	Ala	Ser	Thr	Thr ₂₇₀	Thr	Pro
Ala	Pro	Arg ₂₇₅	Pro	Pro	Thr	Pro	Ala ₂₈₀	Pro	Thr	Ile	Ala	Ser ₂₈₅	Gln	Pro	Leu
Ser	Leu ₂₉₀	Arg	Pro	Glu	Ala	Cys ₂₉₅	Arg	Pro	Ala	Ala	Gly ₃₀₀	Gly	Ala	Val	His
Thr ₃₀₅	Arg	Gly	Leu	Asp	Phe ₃₁₀	Ala	Cys	Asp	Ser	Gly ₃₁₅	Ile	Tyr	Ile	Trp	Ala ₃₂₀
Pro	Leu	Ala	Gly	Thr ₃₂₅	Cys	Gly	Val	Leu	Leu ₃₃₀	Leu	Ser	Leu	Val	Ile ₃₃₅	Thr
Leu	Tyr	Cys	Lys ₃₄₀	Arg	Gly	Arg	Lys	Lys ₃₄₅	Leu	Leu	Tyr	Ile	Phe ₃₅₀	Lys	Gln
Pro	Phe	Met ₃₅₅	Arg	Pro	Val	Gln	Thr ₃₆₀	Thr	Gln	Glu	Glu	Asp ₃₆₅	Gly	Cys	Ser
Cys	Arg ₃₇₀	Phe	Pro	Glu	Glu	Glu ₃₇₅	Glu	Gly	Gly	Cys	Glu ₃₈₀	Leu	Arg	Val	Lys
Phe ₃₈₅	Ser	Arg	Ser	Ala	Asp ₃₉₀	Ala	Pro	Ala	Tyr	Gln ₃₉₅	Gln	Gly	Gln	Asn	Gln ₄₀₀
Leu	Tyr	Asn	Glu	Leu ₄₀₅	Asn	Leu	Gly	Arg	Arg ₄₁₀	Glu	Glu	Tyr	Asp	Val ₄₁₅	Leu
Asp	Lys	Arg	Arg ₄₂₀	Gly	Arg	Asp	Pro	Glu ₄₂₅	Met	Gly	Gly	Lys	Pro ₄₃₀	Arg	Arg
Lys	Asn	Pro ₄₃₅	Gln	Glu	Gly	Leu	Tyr ₄₄₀	Asn	Glu	Leu	Gln	Lys ₄₄₅	Asp	Lys	Met
Ala	Glu ₄₅₀	Ala	Tyr	Ser	Glu	Ile ₄₅₅	Gly	Met	Lys	Gly	Glu ₄₆₀	Arg	Arg	Arg	Gly
Lys	Gly	His	Asp	Gly	Leu	Tyr	Gln	Gly	Leu	Ser	Thr	Ala	Thr	Lys	Asp

465					470					-SL 475					480
Thr	Tyr	Asp	Ala	Leu 485	His	Met	Gln	Ala	Leu 490	Pro	Pro	Arg	Gly	Ser 495	Gly
Ala	Thr	Asn	Phe 500	Ser	Leu	Leu	Lys	Gln 505	Ala	Gly	Asp	Val	Glu 510	Glu	Asn
Pro	Gly	Pro 515	Gly	Val	Gln	Val	Glu 520	Thr	Ile	Ser	Pro	Gly 525	Asp	Gly	Arg
Thr	Phe 530	Pro	Lys	Arg	Gly	Gln 535	Thr	Cys	Val	Val	His 540	Tyr	Thr	Gly	Met
Leu 545	Glu	Asp	Gly	Lys	Lys 550	Val	Asp	Ser	Ser	Arg 555	Asp	Arg	Asn	Lys	Pro 560
Phe	Lys	Phe	Met	Leu 565	Gly	Lys	Gln	Glu	Val 570	Ile	Arg	Gly	Trp	Glu 575	Glu
Gly	Val	Ala	Gln 580	Met	Ser	Val	Gly	Gln 585	Arg	Ala	Lys	Leu	Thr 590	Ile	Ser
Pro	Asp	Tyr 595	Ala	Tyr	Gly	Ala	Thr 600	Gly	His	Pro	Gly	Ile 605	Ile	Pro	Pro
His	Ala 610	Thr	Leu	Val	Phe	Asp 615	Val	Glu	Leu	Leu	Lys 620	Leu	Glu	Ser	Gly
Gly 625	Gly	Ser	Gly	Gly	Phe 630	Gly	Asp	Val	Gly	Ala 635	Leu	Glu	Ser	Leu	Arg 640
Gly	Asn	Ala	Asp	Leu 645	Ala	Tyr	Ile	Leu	Ser 650	Met	Glu	Pro	Cys	Gly 655	His
Cys	Leu	Ile	Ile 660	Asn	Asn	Val	Asn	Phe 665	Cys	Arg	Glu	Ser	Gly 670	Leu	Arg
Thr	Arg	Thr 675	Gly	Ser	Asn	Ile	Asp 680	Cys	Glu	Lys	Leu	Arg 685	Arg	Arg	Phe
Ser	Ser 690	Leu	His	Phe	Met	Val 695	Glu	Val	Lys	Gly	Asp 700	Leu	Thr	Ala	Lys
Lys 705	Met	Val	Leu	Ala	Leu 710	Leu	Glu	Leu	Ala	Gln 715	Gln	Asp	His	Gly	Ala 720
Leu	Asp	Cys	Cys	Val 725	Val	Val	Ile	Leu	Ser 730	His	Gly	Cys	Gln	Ala 735	Ser
His	Leu	Gln	Phe	Pro	Gly	Ala	Val	Tyr	Gly	Thr	Asp	Gly	Cys	Pro	Val

Page 1216

_SL

740 745 750

Ser Val Glu Lys Ile Val Asn Ile Phe Asn Gly Thr Ser Cys Pro Ser
755 760 765

Leu Gly Gly Lys Pro Lys Leu Phe Phe Ile Gln Ala Cys Gly Gly Glu
770 775 780

Gln Lys Asp His Gly Phe Glu Val Ala Ser Thr Ser Pro Glu Asp Glu
785 790 795 800

Ser Pro Gly Ser Asn Pro Glu Pro Asp Ala Thr Pro Phe Gln Glu Gly
805 810 815

Leu Arg Thr Phe Asp Gln Leu Asp Ala Ile Ser Ser Leu Pro Thr Pro
820 825 830

Ser Asp Ile Phe Val Ser Tyr Ser Thr Phe Pro Gly Phe Val Ser Trp
835 840 845

Arg Asp Pro Lys Ser Gly Ser Trp Tyr Val Glu Thr Leu Asp Asp Ile
850 855 860

Phe Glu Gln Trp Ala His Ser Glu Asp Leu Gln Ser Leu Leu Leu Arg
865 870 875 880

Val Ala Asn Ala Val Ser Val Lys Gly Ile Tyr Lys Gln Met Pro Gly
885 890 895

Cys Phe Asn Phe Leu Arg Lys Lys Leu Phe Phe Lys Thr Ser Glx
900 905 910

<210> 3026
<211> 2745
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 3026
atgctcgagg ggggttcaggt ggagactatc agcccgggacg acggacggac attcccaaag 60
cgcggggcaga cgtgtgtggt gcattacacc gggatgcttg aggacggaaa gaaagtggac 120
tcttcccagag accgaaataa accattcaag ttcattgttg gcaagcagga gggttatcaga 180
gggtgggagg agggcgctgc tcagatgagt gtcggacaga gggccaagct cacgatctcc 240
cctgattacg cctacggggc aactggtcac cccggaatca tccccctca cgcaaccctc 300
gtgttcgacg tcgagctgct caaactggaa tcaggcggag gcagtggcgc tagcggggtt 360
ggcgatgtcg gtgcccttga aagcttgaga ggaaatgccg atctcgctta catcttgagc 420

						_SL	
atggagccct	gtgggcactg	tctgatcatc	aacaatgtta	acttttgccg	ggagtccggc		480
ctgcgcacac	gcacaggctc	caacattgac	tgcgaaaaac	ttcgaaggag	gtttagctct		540
ctgcatttca	tggtagaggt	gaaggggat	ctgaccgcc	agaaaatggt	tctcgccctt		600
ctcgagcttg	cgcagcagga	ccatggagcg	cttgactgtt	gtgtcgttgt	gatactgagc		660
catggctgtc	aggcttccca	tctccagttt	ccaggggccg	tgtacggaac	cgatggatgc		720
cctgtgtcag	ttgaaaagat	cgtaaacatc	tttaacggaa	catcttgccc	gagcctcggc		780
ggtaaaccga	agcttttttt	tatccaggcc	tgcggcgggtg	aacagaaaga	tcatggcttc		840
gaggttgcca	gtaccagccc	tgaagacgaa	tccccgggt	caaatcctga	accagatgcg		900
acccctttcc	aggaaggact	ccgcactttt	gaccagcttg	acgccatttc	ctccctgcc		960
acaccttccg	acatatttgt	aagctactcc	acctttccag	gattcgtgag	ctggcgcgac		1020
ccaaaatccg	gcagttggta	tgttgaaacc	ctggacgata	ttttcgaaca	atggggccac		1080
agtgaggacc	tgcagtcctt	tcttctgctc	gtagccaatg	ccgtgtcagt	caaagggatt		1140
tacaagcaga	tgccaggctg	ctttaatttc	ctgcgcaaga	aactgttttt	taagaccagt		1200
ggctccggcg	caacaaattt	ctccttgctg	aaacaggcag	gcgacgttga	ggaaaatccc		1260
ggcccaatgg	ccttaccagt	gaccgccttg	ctcctgccgc	tggccttgct	gctccacgcc		1320
gccaggccgg	gatccgatat	tcaacttaca	cagtccccta	gttccttgtc	cgcctccgtc		1380
ggcgacagag	ttaccatgac	ttgtcgagcg	tcttctagcg	tttcctacat	tcattggttc		1440
caacagaagc	ccggaaggc	acaaaaacct	tggatctacg	ccacgtccaa	tttggctagt		1500
ggtgttccgg	tgcgattttc	cgggtcaggt	agcgggacgg	actatacttt	taccatttca		1560
agccttcagc	ctgaagacat	cgcgacgtac	tattgtcagc	agtggacctc	taaccctcct		1620
acctttggcg	gtggaacaaa	gctggagatc	aaacgaggcg	ggggtggctc	tgggggagga		1680
ggttccggtg	ggggaggctc	tcaagtacaa	ctgcaacaaa	gtggggctga	agtgaagaag		1740
cccggttctt	cagtcaaagt	atcatgtaag	gcaagtgggt	atacttttac	gtcttataac		1800
atgcattggg	taaagcaagc	ccctggtcag	ggcctcgagt	ggattgggtg	gatctaccct		1860
ggaatgggtg	atacgagcta	taatcagaaa	ttcaagggga	aagccacctt	gactgcagac		1920
gaatctacga	acacggctta	catggagctt	agctcactca	gatcagagga	tacagccttt		1980
tactactgcg	ctagatcaac	ttattacgga	ggagactggg	attttgatgt	atggggtcag		2040
gggaccacag	tactgttag	ctctgctagc	accacgacgc	cagcgccgcg	accaccaaca		2100
ccggcgccca	ccatcgctc	gcagcccctg	tccctgcgcc	cagaggcggtg	ccggccagcg		2160
gcggggggcg	cagtgcacac	gagggggctg	gacttcgcct	gtgattccgg	aatctacatc		2220
tgggcgccct	tggccgggac	ttgtggggtc	cttctcctgt	cactggttat	caccctttac		2280
tgcaaacggg	gcagaaagaa	actcctgtat	atattcaaac	aaccatttat	gagaccagta		2340
caaactactc	aagaggaaga	tggctgtagc	tgccgatttc	cagaagaaga	agaaggagga		2400
tgtgaactga	gagtgaagtt	cagcaggagc	gcagacgccc	ccgcgtacca	gcagggccag		2460

aaccagctct ataacgagct caatctagga cgaagagagg agtacgatgt tttggacaag 2520
 agacgtggcc gggaccctga gatgggggga aagccgagaa ggaagaacc tcaggaaggc 2580
 ctgtacaatg aactgcagaa agataagatg gcggaggcct acagtgagat tgggatgaaa 2640
 ggcgagcgcc ggaggggcaa ggggcacgat ggcctttacc aggttctcag tacagccacc 2700
 aaggacacct acgacgccct tcacatgcag gccctgcccc ctcgc 2745

<210> 3027
 <211> 916
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 3027
 Met Leu Glu Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg
 1 5 10 15

Thr Phe Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met
 20 25 30

Leu Glu Asp Gly Lys Lys Val Asp Ser Ser Arg Asp Arg Asn Lys Pro
 35 40 45

Phe Lys Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu
 50 55 60

Gly Val Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser
 65 70 75 80

Pro Asp Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro
 85 90 95

His Ala Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu Ser Gly
 100 105 110

Gly Gly Ser Gly Ala Ser Gly Phe Gly Asp Val Gly Ala Leu Glu Ser
 115 120 125

Leu Arg Gly Asn Ala Asp Leu Ala Tyr Ile Leu Ser Met Glu Pro Cys
 130 135 140

Gly His Cys Leu Ile Ile Asn Asn Val Asn Phe Cys Arg Glu Ser Gly
 145 150 155 160

Leu Arg Thr Arg Thr Gly Ser Asn Ile Asp Cys Glu Lys Leu Arg Arg
 165 170 175

Arg Phe Ser Ser Leu His Phe Met Val Glu Val Lys Gly Asp Leu Thr
 180 185 190

_SL

Ala Lys Lys Met Val Leu Ala Leu Leu Glu Leu Ala Gln Gln Asp His
195 200 205

Gly Ala Leu Asp Cys Cys Val Val Val Ile Leu Ser His Gly Cys Gln
210 215 220

Ala Ser His Leu Gln Phe Pro Gly Ala Val Tyr Gly Thr Asp Gly Cys
225 230 235 240

Pro Val Ser Val Glu Lys Ile Val Asn Ile Phe Asn Gly Thr Ser Cys
245 250 255

Pro Ser Leu Gly Gly Lys Pro Lys Leu Phe Phe Ile Gln Ala Cys Gly
260 265 270

Gly Glu Gln Lys Asp His Gly Phe Glu Val Ala Ser Thr Ser Pro Glu
275 280 285

Asp Glu Ser Pro Gly Ser Asn Pro Glu Pro Asp Ala Thr Pro Phe Gln
290 295 300

Glu Gly Leu Arg Thr Phe Asp Gln Leu Asp Ala Ile Ser Ser Leu Pro
305 310 315 320

Thr Pro Ser Asp Ile Phe Val Ser Tyr Ser Thr Phe Pro Gly Phe Val
325 330 335

Ser Trp Arg Asp Pro Lys Ser Gly Ser Trp Tyr Val Glu Thr Leu Asp
340 345 350

Asp Ile Phe Glu Gln Trp Ala His Ser Glu Asp Leu Gln Ser Leu Leu
355 360 365

Leu Arg Val Ala Asn Ala Val Ser Val Lys Gly Ile Tyr Lys Gln Met
370 375 380

Pro Gly Cys Phe Asn Phe Leu Arg Lys Lys Leu Phe Phe Lys Thr Ser
385 390 395 400

Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val
405 410 415

Glu Glu Asn Pro Gly Pro Met Ala Leu Pro Val Thr Ala Leu Leu Leu
420 425 430

Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Gly Ser Asp Ile Gln
435 440 445

Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val
450 455 460

_SL

Thr Met Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Ile His Trp Phe
465 470 475 480

Gln Gln Lys Pro Gly Lys Ala Pro Lys Pro Trp Ile Tyr Ala Thr Ser
485 490 495

Asn Leu Ala Ser Gly Val Pro Val Arg Phe Ser Gly Ser Gly Ser Gly
500 505 510

Thr Asp Tyr Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala
515 520 525

Thr Tyr Tyr Cys Gln Gln Trp Thr Ser Asn Pro Pro Thr Phe Gly Gly
530 535 540

Gly Thr Lys Leu Glu Ile Lys Arg Gly Gly Gly Ser Gly Gly Gly
545 550 555 560

Gly Ser Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser Gly Ala
565 570 575

Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser
580 585 590

Gly Tyr Thr Phe Thr Ser Tyr Asn Met His Trp Val Lys Gln Ala Pro
595 600 605

Gly Gln Gly Leu Glu Trp Ile Gly Ala Ile Tyr Pro Gly Met Gly Asp
610 615 620

Thr Ser Tyr Asn Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp
625 630 635 640

Glu Ser Thr Asn Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
645 650 655

Asp Thr Ala Phe Tyr Tyr Cys Ala Arg Ser Thr Tyr Tyr Gly Gly Asp
660 665 670

Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
675 680 685

Ala Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr
690 695 700

Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala
705 710 715 720

Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ser
725 730 735

_SL

Gly Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu
740 745 750

Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu
755 760 765

Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln
770 775 780

Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly
785 790 795 800

Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr
805 810 815

Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg
820 825 830

Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met
835 840 845

Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu
850 855 860

Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys
865 870 875 880

Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu
885 890 895

Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu
900 905 910

Pro Pro Arg Glx
915

<210> 3028
<211> 3060
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 3028
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60
ccgggatccg acatccagat gacacagact acatcctccc tgtctgcctc tctgggagac 120
agagtcacca tcagttgcag ggcaagtcag gacattagta aatattttaa ttggtatcag 180
cagaaaccag atggaactgt taaactcctg atctaccata catcaagatt acactcagga 240

_SL

gtcccatcaa	ggttcagtgg	cagtgggtct	ggaacagatt	attctctcac	cattagcaac	300
ctggagcaag	aagatattgc	cacttacttt	tgccaacagg	gtaatacgct	tccgtacacg	360
ttcggagggg	ggactaagtt	ggaaataaca	ggtggcggtg	gctcgggcgg	tggtgggtcg	420
ggtggcgggc	gatctgaggt	gaaactgcag	gagtcaggac	ctggcctggt	ggcgccctca	480
cagagcctgt	ccgtcacatg	cactgtctca	ggggtctcat	tacccgacta	tggtgtaagc	540
tggattcgcc	agcctccacg	aaagggctctg	gagtggctgg	gagtaatatg	gggtagtgaa	600
accacatact	ataattcagc	tctcaaatcc	agactgacca	tcatcaagga	caactccaag	660
agccaagttt	tcttaaaaat	gaacagtctg	caaactgatg	acacagccat	ttactactgt	720
gccaacatt	attactacgg	tggtagctat	gctatggact	actgggggtca	aggaacctca	780
gtcaccgtct	cctcagctag	caccacgacg	ccagcgccgc	gaccaccaac	accggcgccc	840
accatcgctg	cgcagcccct	gtccctgctg	ccagaggcgt	gccggccagc	ggcggggggc	900
gcagtgcaca	cgagggggct	ggacttcgcc	tgtgattccg	gaatctacat	ctggggcccct	960
ctggccggca	cctgtggcgt	gctgctgctg	tctctcgtga	tcaccctgta	ctgcaagcgg	1020
ggcagaaaga	agctgctgta	catcttcaag	cagcccttca	tgcgggccgt	gcagaccacc	1080
caggaagagg	acggctgctc	ctgcagattc	cccaggaag	aagaaggcgg	ctgcgagctg	1140
agagtgaagt	tcagcagaag	cgccgacgcc	cctgcctatc	agcagggcca	gaaccagctg	1200
tacaacgagc	tgaacctggg	cagacgggaa	gagtacgacg	tgctggacaa	gcgagagggc	1260
agggaccctg	agatgggcgg	caagcccaga	agaaagaacc	cccaggaagg	cctgtataac	1320
gaactgcaga	aagacaagat	ggccgaggcc	tacagcgaga	tcggaatgaa	gggcgagcgg	1380
agaagaggca	agggccacga	tggcctgtac	cagggcctga	gcaccgccac	caaggacacc	1440
tatgacgccc	tgcacatgca	ggccctgcct	ccaagaggaa	gcggcgccac	caatttcagc	1500
ctgctgaaac	aggccggcga	cgtggaagag	aaccctggcc	ctagaggcgt	gcaggtggaa	1560
accatctctc	ccggcgacgg	cagaaccttc	cctaagaggg	gccagacctg	cgtggtgcac	1620
tacaccggca	tgctggaaga	tggcaagaag	atggacagct	cccgggaccg	gaacaagccc	1680
ttcaagttca	tgctgggcaa	gcaggaagtg	atccggggct	gggaagaggg	cgtggcacag	1740
atgtctgtgg	gccagagagc	caagctgacc	atcagccccg	attacgccta	cggcgccaca	1800
ggccaccctg	gcatcattcc	tccacacgcc	acactggtgt	tcgatgtgga	actgctgaag	1860
ctggaaaccc	ggggagtgca	ggtggaaaca	atcagccctg	gcgacggccg	gacctttcca	1920
aaacggggac	agacatgtgt	ggtgcattat	acagggatgc	tggaagatgg	gaaaaaaatg	1980
gatagcagcc	gcgaccgcaa	caaacctttt	aagtttatgc	tggggaaaca	ggaagtgatt	2040
agaggctggg	aagagggggg	ggcacagatg	agcgtgggac	agcggggcaa	actgacaatc	2100
tccccgact	atgcctatgg	ggccaccgga	caccccgga	tcatcccacc	tcatgctacc	2160
ctggtgtttg	acgtggaact	gctgaaactg	gaaacaagcg	gcggaggcag	cggcggcttt	2220
ggagatgtgg	gagccctgga	aagcctgcgg	ggcaatgccg	atctggccta	catcctgagc	2280

_SL

atggaaccct gcggccactg cctgattatc aacaacgtga acttctgcag agagagcggc 2340
ctgcggacca gaaccggcag caacatcgac tgcgagaagc tgcggcggag attcagcagc 2400
ctgcacttca tgggtggaagt gaagggggac ctgaccgcca agaaaatggt gctggctctg 2460
ctggaactgg cccagcagga tcatggcgcc ctggactgtt gcgtggtcgt gatcctgagc 2520
cacggctgcc aggccagcca tctgcagttt cccggcgctg tgtatggcac cgatggctgc 2580
cctgtgtccg tggaaaagat cgtgaatatc ttcaacggca ccagctgccc cagcctgggc 2640
ggaaagccta agctgttctt tattcaagcc tgtgggggag agcagaagga ccacggattt 2700
gaggtggcca gcacctccc cgaggatgag agccctggca gcaaccctga gcctgacgcc 2760
acccatttcc aggaaggact gcggaccttc gaccagctgg acgcatctc tagcctgccc 2820
acccccagcg acatcttcgt gtcctacagc accttcctg gctttgtgtc ctggcgggac 2880
cccaagtccg gctcttggtg cgtggaaacc ctggacgaca tctttgagca gtggggccat 2940
agcgaggacc tgcagagcct gctgctgagg gtggccaatg ccgtgtccgt gaagggcatc 3000
tacaagcaga tgcccggctg cttcaacttc ctgcggaaga agctgttttt caagaccagc 3060

<210> 3029

<211> 1020

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 3029

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gly Ser Asp Ile Gln Met Thr Gln Thr Thr Ser
20 25 30

Ser Leu Ser Ala Ser Leu Gly Asp Arg Val Thr Ile Ser Cys Arg Ala
35 40 45

Ser Gln Asp Ile Ser Lys Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp
50 55 60

Gly Thr Val Lys Leu Leu Ile Tyr His Thr Ser Arg Leu His Ser Gly
65 70 75 80

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu
85 90 95

Thr Ile Ser Asn Leu Glu Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln
100 105 110

Gln Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu

_SL

115		120		125											
Ile	Thr	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly
	130					135					140				
Ser	Glu	Val	Lys	Leu	Gln	Glu	Ser	Gly	Pro	Gly	Leu	Val	Ala	Pro	Ser
145					150					155					160
Gln	Ser	Leu	Ser	Val	Thr	Cys	Thr	Val	Ser	Gly	Val	Ser	Leu	Pro	Asp
				165					170					175	
Tyr	Gly	Val	Ser	Trp	Ile	Arg	Gln	Pro	Pro	Arg	Lys	Gly	Leu	Glu	Trp
			180					185					190		
Leu	Gly	Val	Ile	Trp	Gly	Ser	Glu	Thr	Thr	Tyr	Tyr	Asn	Ser	Ala	Leu
		195					200					205			
Lys	Ser	Arg	Leu	Thr	Ile	Ile	Lys	Asp	Asn	Ser	Lys	Ser	Gln	Val	Phe
	210					215					220				
Leu	Lys	Met	Asn	Ser	Leu	Gln	Thr	Asp	Asp	Thr	Ala	Ile	Tyr	Tyr	Cys
225					230					235					240
Ala	Lys	His	Tyr	Tyr	Tyr	Gly	Gly	Ser	Tyr	Ala	Met	Asp	Tyr	Trp	Gly
				245					250					255	
Gln	Gly	Thr	Ser	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Thr	Thr	Pro	Ala
			260					265					270		
Pro	Arg	Pro	Pro	Thr	Pro	Ala	Pro	Thr	Ile	Ala	Ser	Gln	Pro	Leu	Ser
		275					280					285			
Leu	Arg	Pro	Glu	Ala	Cys	Arg	Pro	Ala	Ala	Gly	Gly	Ala	Val	His	Thr
	290					295					300				
Arg	Gly	Leu	Asp	Phe	Ala	Cys	Asp	Ser	Gly	Ile	Tyr	Ile	Trp	Ala	Pro
305					310					315					320
Leu	Ala	Gly	Thr	Cys	Gly	Val	Leu	Leu	Leu	Ser	Leu	Val	Ile	Thr	Leu
				325					330					335	
Tyr	Cys	Lys	Arg	Gly	Arg	Lys	Lys	Leu	Leu	Tyr	Ile	Phe	Lys	Gln	Pro
			340					345					350		
Phe	Met	Arg	Pro	Val	Gln	Thr	Thr	Gln	Glu	Glu	Asp	Gly	Cys	Ser	Cys
		355					360					365			
Arg	Phe	Pro	Glu	Glu	Glu	Glu	Gly	Gly	Cys	Glu	Leu	Arg	Val	Lys	Phe
	370					375					380				
Ser	Arg	Ser	Ala	Asp	Ala	Pro	Ala	Tyr	Gln	Gln	Gly	Gln	Asn	Gln	Leu

385		390		-SL 395		400									
Tyr	Asn	Glu	Leu	Asn 405	Leu	Gly	Arg	Arg	Glu	Glu	Tyr	Asp	Val	Leu	Asp 415
Lys	Arg	Arg	Gly 420	Arg	Asp	Pro	Glu	Met 425	Gly	Gly	Lys	Pro	Arg 430	Arg	Lys
Asn	Pro	Gln 435	Glu	Gly	Leu	Tyr	Asn 440	Glu	Leu	Gln	Lys	Asp 445	Lys	Met	Ala
Glu	Ala 450	Tyr	Ser	Glu	Ile	Gly 455	Met	Lys	Gly	Glu	Arg 460	Arg	Arg	Gly	Lys
Gly 465	His	Asp	Gly	Leu	Tyr 470	Gln	Gly	Leu	Ser	Thr 475	Ala	Thr	Lys	Asp	Thr 480
Tyr	Asp	Ala	Leu	His 485	Met	Gln	Ala	Leu	Pro 490	Pro	Arg	Gly	Ser	Gly 495	Ala
Thr	Asn	Phe	Ser 500	Leu	Leu	Lys	Gln	Ala 505	Gly	Asp	Val	Glu	Glu 510	Asn	Pro
Gly	Pro	Arg 515	Gly	Val	Gln	Val	Glu 520	Thr	Ile	Ser	Pro	Gly 525	Asp	Gly	Arg
Thr	Phe 530	Pro	Lys	Arg	Gly	Gln 535	Thr	Cys	Val	Val	His 540	Tyr	Thr	Gly	Met
Leu 545	Glu	Asp	Gly	Lys	Lys 550	Met	Asp	Ser	Ser	Arg 555	Asp	Arg	Asn	Lys	Pro 560
Phe	Lys	Phe	Met	Leu 565	Gly	Lys	Gln	Glu	Val 570	Ile	Arg	Gly	Trp	Glu 575	Glu
Gly	Val	Ala	Gln 580	Met	Ser	Val	Gly	Gln 585	Arg	Ala	Lys	Leu	Thr 590	Ile	Ser
Pro	Asp	Tyr 595	Ala	Tyr	Gly	Ala	Thr 600	Gly	His	Pro	Gly	Ile 605	Ile	Pro	Pro
His	Ala 610	Thr	Leu	Val	Phe	Asp 615	Val	Glu	Leu	Leu	Lys 620	Leu	Glu	Thr	Arg
Gly 625	Val	Gln	Val	Glu	Thr 630	Ile	Ser	Pro	Gly	Asp 635	Gly	Arg	Thr	Phe	Pro 640
Lys	Arg	Gly	Gln	Thr 645	Cys	Val	Val	His	Tyr 650	Thr	Gly	Met	Leu	Glu 655	Asp
Gly	Lys	Lys	Met	Asp	Ser	Ser	Arg	Asp	Arg	Asn	Lys	Pro	Phe	Lys	Phe

_SL

660	665	670													
Met	Leu	Gly	Lys	Gln	Glu	Val	Ile	Arg	Gly	Trp	Glu	Glu	Gly	Val	Ala
		675					680					685			
Gln	Met	Ser	Val	Gly	Gln	Arg	Ala	Lys	Leu	Thr	Ile	Ser	Pro	Asp	Tyr
	690					695					700				
Ala	Tyr	Gly	Ala	Thr	Gly	His	Pro	Gly	Ile	Ile	Pro	Pro	His	Ala	Thr
705					710					715					720
Leu	Val	Phe	Asp	Val	Glu	Leu	Leu	Lys	Leu	Glu	Thr	Ser	Gly	Gly	Gly
				725					730					735	
Ser	Gly	Gly	Phe	Gly	Asp	Val	Gly	Ala	Leu	Glu	Ser	Leu	Arg	Gly	Asn
			740					745					750		
Ala	Asp	Leu	Ala	Tyr	Ile	Leu	Ser	Met	Glu	Pro	Cys	Gly	His	Cys	Leu
		755					760					765			
Ile	Ile	Asn	Asn	Val	Asn	Phe	Cys	Arg	Glu	Ser	Gly	Leu	Arg	Thr	Arg
	770					775					780				
Thr	Gly	Ser	Asn	Ile	Asp	Cys	Glu	Lys	Leu	Arg	Arg	Arg	Phe	Ser	Ser
785					790					795					800
Leu	His	Phe	Met	Val	Glu	Val	Lys	Gly	Asp	Leu	Thr	Ala	Lys	Lys	Met
				805					810					815	
Val	Leu	Ala	Leu	Leu	Glu	Leu	Ala	Gln	Gln	Asp	His	Gly	Ala	Leu	Asp
			820					825					830		
Cys	Cys	Val	Val	Val	Ile	Leu	Ser	His	Gly	Cys	Gln	Ala	Ser	His	Leu
		835					840					845			
Gln	Phe	Pro	Gly	Ala	Val	Tyr	Gly	Thr	Asp	Gly	Cys	Pro	Val	Ser	Val
	850					855					860				
Glu	Lys	Ile	Val	Asn	Ile	Phe	Asn	Gly	Thr	Ser	Cys	Pro	Ser	Leu	Gly
865					870					875					880
Gly	Lys	Pro	Lys	Leu	Phe	Phe	Ile	Gln	Ala	Cys	Gly	Gly	Glu	Gln	Lys
				885					890					895	
Asp	His	Gly	Phe	Glu	Val	Ala	Ser	Thr	Ser	Pro	Glu	Asp	Glu	Ser	Pro
			900					905					910		
Gly	Ser	Asn	Pro	Glu	Pro	Asp	Ala	Thr	Pro	Phe	Gln	Glu	Gly	Leu	Arg
		915					920					925			
Thr	Phe	Asp	Gln	Leu	Asp	Ala	Ile	Ser	Ser	Leu	Pro	Thr	Pro	Ser	Asp

_SL															
930					935					940					
Ile	Phe	Val	Ser	Tyr	Ser	Thr	Phe	Pro	Gly	Phe	Val	Ser	Trp	Arg	Asp
945					950					955					960
Pro	Lys	Ser	Gly	Ser	Trp	Tyr	Val	Glu	Thr	Leu	Asp	Asp	Ile	Phe	Glu
				965					970					975	
Gln	Trp	Ala	His	Ser	Glu	Asp	Leu	Gln	Ser	Leu	Leu	Leu	Arg	Val	Ala
			980					985					990		
Asn	Ala	Val	Ser	Val	Lys	Gly	Ile	Tyr	Lys	Gln	Met	Pro	Gly	Cys	Phe
		995					1000					1005			
Asn	Phe	Leu	Arg	Lys	Lys	Leu	Phe	Phe	Lys	Thr	Ser				
	1010					1015					1020				

						_SL	
cggggcagaa	agaaactcct	gtatatattc	aaacaacccat	ttatgagacc	agtacaaact		1080
actcaagagg	aagatggctg	tagctgccga	tttccagaag	aagaagaagg	aggatgtgaa		1140
ctgagagtga	agttcagcag	gagcgcagac	gccccgcgt	accagcaggg	ccagaaccag		1200
ctctataacg	agctcaatct	aggacgaaga	gaggagtacg	atgttttgga	caagagacgt		1260
ggccgggacc	ctgagatggg	gggaaagccg	agaaggaaga	accctcagga	aggcctgtac		1320
aatgaactgc	agaaagataa	gatggcggag	gcctacagtg	agattgggat	gaaaggcgag		1380
cgccggaggg	gcaaggggca	cgatggcctt	taccagggtc	tcagtacagc	caccaaggac		1440
acctacgacg	cccttcacat	gcaggccctg	ccccctcgcg	gaagcggcgc	caccaatttc		1500
agcctgctga	aacaggccgg	cgacgtggaa	gagaaccctg	gccctagagg	cgtgcagggtg		1560
gaaaccatct	ctcccggcga	cggcagaacc	ttccctaaga	ggggccagac	ctgcgtggtg		1620
cactacaccg	gcatgctgga	agatggcaag	aagatggaca	gctcccggga	ccggaacaag		1680
cccttcaagt	tcatgctggg	caagcaggaa	gtgatccggg	gctgggaaga	gggcgtggca		1740
cagatgtctg	tgggccagag	agccaagctg	accatcagcc	ccgattacgc	ctacggcgcc		1800
acaggccacc	ctggcatcat	tcctccacac	gccacactgg	tgttcgatgt	ggaactgctg		1860
aagctggaaa	cccggggagt	gcagggtgaa	acaatcagcc	ctggcgacgg	ccggaccttt		1920
ccaaaacggg	gacagacatg	tgtggtgcat	tatacagggg	tgctggaaga	tgggaaaaaa		1980
atggatagca	gccgcgaccg	caacaaacct	tttaagttta	tgctggggaa	acaggaagtg		2040
attagaggct	gggaagaggg	ggtggcacag	atgagcgtgg	gacagcgggc	caaactgaca		2100
atctcccccg	actatgccta	tggggccacc	ggacaccccg	gaatcatccc	acctcatgct		2160
accctggtgt	ttgacgtgga	actgctgaaa	ctggaaacaa	gcggcggagg	cagcggcggc		2220
tttgagatg	tgggagccct	ggaaagcctg	cggggcaatg	ccgatctggc	ctacatcctg		2280
agcatggaac	cctgcggcca	ctgcctgatt	atcaacaacg	tgaacttctg	cagagagagc		2340
ggcctgcgga	ccagaaccgg	cagcaacatc	gactgcgaga	agctgcggcg	gagattcagc		2400
agcctgcact	tcatggtgga	agtgaagggg	gacctgaccg	ccaagaaaat	ggtgctggct		2460
ctgctggaac	tggcccagca	ggatcatggc	gccctggact	gttgcggtgt	cgtgatcctg		2520
agccacggct	gccaggccag	ccatctgcag	tttcccggcg	ctgtgtatgg	caccgatggc		2580
tgccctgtgt	ccgtggaaaa	gatcgtgaat	atcttcaacg	gcaccagctg	ccccagcctg		2640
ggcggaaagc	ctaagctgtt	ctttattcaa	gcctgtgggg	gcgagcagaa	ggaccacgga		2700
tttgaggtgg	ccagcacctc	ccccagggat	gagagccctg	gcagcaaccc	tgagcctgac		2760
gccaccccat	tccaggaagg	actgcggacc	ttcgaccagc	tggacgccat	ctctagcctg		2820
cccaccccca	gcgacatctt	cgtgtcctac	agcaccttcc	ctggctttgt	gtcctggcgg		2880
gaccccaagt	ccggctcttg	gtacgtggaa	accctggacg	acatctttga	gcagtgggcc		2940
catagcgagg	acctgcagag	cctgctgctg	aggggtggcca	atgccgtgtc	cgtgaagggc		3000
atctacaagc	agatgcccgg	ctgcttcaac	ttcctgcgga	agaagctgtt	tttcaagacc		3060

<210> 3031
 <211> 1021
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 3031
 Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
 1 5 10 15

His Ala Ala Arg Pro Gly Ser Asp Ile Gln Leu Thr Gln Ser Pro Ser
 20 25 30

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys Arg Ala
 35 40 45

Ser Ser Ser Val Ser Tyr Ile His Trp Phe Gln Gln Lys Pro Gly Lys
 50 55 60

Ala Pro Lys Pro Trp Ile Tyr Ala Thr Ser Asn Leu Ala Ser Gly Val
 65 70 75 80

Pro Val Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Phe Thr
 85 90 95

Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln
 100 105 110

Trp Thr Ser Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
 115 120 125

Lys Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 130 135 140

Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Val Lys Lys Pro Gly
 145 150 155 160

Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser
 165 170 175

Tyr Asn Met His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp
 180 185 190

Ile Gly Ala Ile Tyr Pro Gly Met Gly Asp Thr Ser Tyr Asn Gln Lys
 195 200 205

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Glu Ser Thr Asn Thr Ala
 210 215 220

_SL

Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Phe Tyr Tyr
225 230 235 240

Cys Ala Arg Ser Thr Tyr Tyr Gly Gly Asp Trp Tyr Phe Asp Val Trp
245 250 255

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Thr Thr Pro
260 265 270

Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu
275 280 285

Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His
290 295 300

Thr Arg Gly Leu Asp Phe Ala Cys Asp Ser Gly Ile Tyr Ile Trp Ala
305 310 315 320

Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr
325 330 335

Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln
340 345 350

Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser
355 360 365

Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys
370 375 380

Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln
385 390 395 400

Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
405 410 415

Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg
420 425 430

Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met
435 440 445

Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly
450 455 460

Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp
465 470 475 480

Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg Gly Ser Gly
485 490 495

_SL

Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn
500 505 510

Pro Gly Pro Arg Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly
515 520 525

Arg Thr Phe Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly
530 535 540

Met Leu Glu Asp Gly Lys Lys Met Asp Ser Ser Arg Asp Arg Asn Lys
545 550 555 560

Pro Phe Lys Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu
565 570 575

Glu Gly Val Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile
580 585 590

Ser Pro Asp Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro
595 600 605

Pro His Ala Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu Thr
610 615 620

Arg Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe
625 630 635 640

Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu
645 650 655

Asp Gly Lys Lys Met Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys
660 665 670

Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val
675 680 685

Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp
690 695 700

Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala
705 710 715 720

Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu Thr Ser Gly Gly
725 730 735

Gly Ser Gly Gly Phe Gly Asp Val Gly Ala Leu Glu Ser Leu Arg Gly
740 745 750

Asn Ala Asp Leu Ala Tyr Ile Leu Ser Met Glu Pro Cys Gly His Cys
755 760 765

_SL

Leu Ile Ile Asn Asn Val Asn Phe Cys Arg Glu Ser Gly Leu Arg Thr
770 775 780

Arg Thr Gly Ser Asn Ile Asp Cys Glu Lys Leu Arg Arg Arg Phe Ser
785 790 795 800

Ser Leu His Phe Met Val Glu Val Lys Gly Asp Leu Thr Ala Lys Lys
805 810 815

Met Val Leu Ala Leu Leu Glu Leu Ala Gln Gln Asp His Gly Ala Leu
820 825 830

Asp Cys Cys Val Val Val Ile Leu Ser His Gly Cys Gln Ala Ser His
835 840 845

Leu Gln Phe Pro Gly Ala Val Tyr Gly Thr Asp Gly Cys Pro Val Ser
850 855 860

Val Glu Lys Ile Val Asn Ile Phe Asn Gly Thr Ser Cys Pro Ser Leu
865 870 875 880

Gly Gly Lys Pro Lys Leu Phe Phe Ile Gln Ala Cys Gly Gly Glu Gln
885 890 895

Lys Asp His Gly Phe Glu Val Ala Ser Thr Ser Pro Glu Asp Glu Ser
900 905 910

Pro Gly Ser Asn Pro Glu Pro Asp Ala Thr Pro Phe Gln Glu Gly Leu
915 920 925

Arg Thr Phe Asp Gln Leu Asp Ala Ile Ser Ser Leu Pro Thr Pro Ser
930 935 940

Asp Ile Phe Val Ser Tyr Ser Thr Phe Pro Gly Phe Val Ser Trp Arg
945 950 955 960

Asp Pro Lys Ser Gly Ser Trp Tyr Val Glu Thr Leu Asp Asp Ile Phe
965 970 975

Glu Gln Trp Ala His Ser Glu Asp Leu Gln Ser Leu Leu Leu Arg Val
980 985 990

Ala Asn Ala Val Ser Val Lys Gly Ile Tyr Lys Gln Met Pro Gly Cys
995 1000 1005

Phe Asn Phe Leu Arg Lys Lys Leu Phe Phe Lys Thr Ser
1010 1015 1020

<210> 3032

<211> 2811

<212> DNA
<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 3032

```
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg      60
ccgggatccc ggggctgtga ggttgagaca atttccccag gagatgggcg aacgttcccc      120
aagcgcggac agacatgcgt tgtgcactac acaggaatgt tggaggacgg aaagaaaatg      180
gacagttcaa gagatcggaa caaaccattc aaattcatgt tgggaaaaca ggaagtgata      240
cggggctggg aagaggggtgt agcgcaaatg tccgttggtc aacgagcaaa actcacgata      300
agtcccgatt atgcttacgg cgcaaccggg caccggggca tcataccgcc tcatgcgact      360
ttggctctttg atgtggagct gttgaaactt gaaactcgcg gagtacaggt tgaaacaata      420
tcacccgggg acgggcggac ttttccgaag agaggtcaga cctgcgtcgt ccattatacc      480
ggtatgctgg aggacggaaa gaaaatggac agctcacggg accgaaataa accattcaaa      540
tttatgttgg ggaaacaaga gggtatcagg ggctgggagg aggggtgtggc ccagatgtct      600
gtcggtcagc gcgcgaaact cacaatctct ccggattatg cgtatggggc gacagggcat      660
ccgggaatta tccctcccca cgctaccttg gttttcgatg ttgagcttct gaagttggag      720
accagaggag ttcaagtgga gacaatatct cctggggatg gacggacgtt cccaagcgc      780
ggccagacct gtgtagtcca ctacacaggg atgcttgaag acggaaaaaa gatggatagc      840
agtagagatc gcaacaaacc atttaagttc atgctgggga agcaggaagt aatacgcggc      900
tgggaggaag gcgtggcaca gatgagtgtt ggtcaacggg ccaaacttac tatttctccc      960
gattatgcgt atggagccac cgggcaccct ggcattatcc caccatgc cacattgggt      1020
tttgacgttg aattgcttaa attggagacc aggggagtc cagtggaaac aatatcaccg      1080
ggggatggtc ggacttttcc taaaaggggc caaacctgtg tagtccatta taccggaatg      1140
ctcgaagacg gaaagaaaat ggactcttct agagaccgca ataagccctt caagttcatg      1200
ttgggtaagc aagaggtgat ccggggctgg gaagaggggg tcgctcaaat gtccgtcggg      1260
cagcgagcta aactgactat ttccccagac tacgcatatg gagcgactgg ccaccccggt      1320
attattcctc cccatgcgac tctcgtgttc gacgtagaac tcttgaaatt ggaaacgtca      1380
gcccggaaca ggcggaagag agatattcaa cttacacagt cccctagtgc cttgtccgcc      1440
tccgtcggcg acagagttac catgacttgt cgagcgtctt ctacgctttc ctacattcat      1500
tggttccaac agaagcccgg aaaggcacca aaaccttga tctacgccac gtccaatttg      1560
gctagtggtg ttccgggtgcg attttccggg tcaggtagcg ggacggacta tacttttacc      1620
atttcaagcc ttcagcctga agacatcgcg acgtactatt gtcagcagtg gacctctaac      1680
cctcctacct ttggcgggtg aacaaagctg gagatcaaac gaggcggggg tggctctggg      1740
ggaggagggt ccggtggggg aggcctctca gtacaactgc aacaaagtgg ggctgaagtg      1800
```

_SL

aagaagcccg gttcttcagt caaagtatca tgtaaggcaa gtggttatac ttttacgtct 1860
tataacatgc attgggtaaa gcaagcccct ggtcagggcc tcgagtggat tgggtgcgac 1920
taccctggaa tgggtgatac gagctataat cagaaattca aggggaaagc caccttgact 1980
gcagacgaat ctacgaacac ggcttacatg gagcttagct cactcagatc agaggataca 2040
gccttttact actgcgctag atcaacttat tacggaggag actggtatit t gatgtatgg 2100
ggtcagggga ccacagtcac tgtagctct gctagcacca cgacgccagc gccgcgacca 2160
ccaacaccgg cgcccacat cgcgtcgag cccctgtccc tgcgcccaga ggcgtgccgg 2220
ccagcggcgg ggggcgagc gcacacgagg gggctggact tcgcctgtga ttccggaatc 2280
tacatctggg cgcccttggc cgggacttgt ggggtccttc tcctgtcact ggttatcacc 2340
ctttactgca aacggggcag aaagaaactc ctgtatatat tcaaacaacc atttatgaga 2400
ccagtacaaa ctactcaaga ggaagatggc tgtagctgcc gatttccaga agaagaagaa 2460
ggaggatgtg aactgagagt gaagttcagc aggagcgcag acgccccgc gtaccagcag 2520
ggccagaacc agctctataa cgagctcaat ctaggacgaa gagaggagta cgatgttttg 2580
gacaagagac gtggccggga ccctgagatg gggggaaagc cgagaaggaa gaaccctcag 2640
gaaggcctgt acaatgaact gcagaaagat aagatggcgg aggcctacag tgagattggg 2700
atgaaaggcg agcgccggag gggcaagggg cacgatggcc ttaccaggg tctcagtaca 2760
gccaccaagg acacctacga cgcccttcac atgcaggccc tgccccctcg c 2811

<210> 3033

<211> 939

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 3033

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gly Ser Arg Gly Val Gln Val Glu Thr Ile Ser
20 25 30

Pro Gly Asp Gly Arg Thr Phe Pro Lys Arg Gly Gln Thr Cys Val Val
35 40 45

His Tyr Thr Gly Met Leu Glu Asp Gly Lys Lys Met Asp Ser Ser Arg
50 55 60

Asp Arg Asn Lys Pro Phe Lys Phe Met Leu Gly Lys Gln Glu Val Ile
65 70 75 80

Arg Gly Trp Glu Glu Gly Val Ala Gln Met Ser Val Gly Gln Arg Ala

										_SL											
85										90		95									
Lys	Leu	Thr	Ile	Ser	Pro	Asp	Tyr	Ala	Tyr	Gly	Ala	Thr	Gly	His	Pro						
			100					105					110								
Gly	Ile	Ile	Pro	Pro	His	Ala	Thr	Leu	Val	Phe	Asp	Val	Glu	Leu	Leu						
		115					120					125									
Lys	Leu	Glu	Thr	Arg	Gly	Val	Gln	Val	Glu	Thr	Ile	Ser	Pro	Gly	Asp						
	130					135					140										
Gly	Arg	Thr	Phe	Pro	Lys	Arg	Gly	Gln	Thr	Cys	Val	Val	His	Tyr	Thr						
145					150					155					160						
Gly	Met	Leu	Glu	Asp	Gly	Lys	Lys	Met	Asp	Ser	Ser	Arg	Asp	Arg	Asn						
				165					170					175							
Lys	Pro	Phe	Lys	Phe	Met	Leu	Gly	Lys	Gln	Glu	Val	Ile	Arg	Gly	Trp						
			180					185					190								
Glu	Glu	Gly	Val	Ala	Gln	Met	Ser	Val	Gly	Gln	Arg	Ala	Lys	Leu	Thr						
		195					200					205									
Ile	Ser	Pro	Asp	Tyr	Ala	Tyr	Gly	Ala	Thr	Gly	His	Pro	Gly	Ile	Ile						
	210					215					220										
Pro	Pro	His	Ala	Thr	Leu	Val	Phe	Asp	Val	Glu	Leu	Leu	Lys	Leu	Glu						
225					230					235				240							
Thr	Arg	Gly	Val	Gln	Val	Glu	Thr	Ile	Ser	Pro	Gly	Asp	Gly	Arg	Thr						
				245					250					255							
Phe	Pro	Lys	Arg	Gly	Gln	Thr	Cys	Val	Val	His	Tyr	Thr	Gly	Met	Leu						
			260					265					270								
Glu	Asp	Gly	Lys	Lys	Met	Asp	Ser	Ser	Arg	Asp	Arg	Asn	Lys	Pro	Phe						
		275					280					285									
Lys	Phe	Met	Leu	Gly	Lys	Gln	Glu	Val	Ile	Arg	Gly	Trp	Glu	Glu	Gly						
	290					295					300										
Val	Ala	Gln	Met	Ser	Val	Gly	Gln	Arg	Ala	Lys	Leu	Thr	Ile	Ser	Pro						
305					310					315					320						
Asp	Tyr	Ala	Tyr	Gly	Ala	Thr	Gly	His	Pro	Gly	Ile	Ile	Pro	Pro	His						
				325					330					335							
Ala	Thr	Leu	Val	Phe	Asp	Val	Glu	Leu	Leu	Lys	Leu	Glu	Thr	Arg	Gly						
			340					345					350								
Val	Gln	Val	Glu	Thr	Ile	Ser	Pro	Gly	Asp	Gly	Arg	Thr	Phe	Pro	Lys						

_SL

355		360		365											
Arg	Gly	Gln	Thr	Cys	Val	Val	His	Tyr	Thr	Gly	Met	Leu	Glu	Asp	Gly
	370					375					380				
Lys	Lys	Met	Asp	Ser	Ser	Arg	Asp	Arg	Asn	Lys	Pro	Phe	Lys	Phe	Met
385					390					395					400
Leu	Gly	Lys	Gln	Glu	Val	Ile	Arg	Gly	Trp	Glu	Glu	Gly	Val	Ala	Gln
				405					410					415	
Met	Ser	Val	Gly	Gln	Arg	Ala	Lys	Leu	Thr	Ile	Ser	Pro	Asp	Tyr	Ala
			420					425					430		
Tyr	Gly	Ala	Thr	Gly	His	Pro	Gly	Ile	Ile	Pro	Pro	His	Ala	Thr	Leu
		435					440					445			
Val	Phe	Asp	Val	Glu	Leu	Leu	Lys	Leu	Glu	Thr	Ser	Ala	Arg	Asn	Arg
	450					455					460				
Arg	Lys	Arg	Gly	Ser	Asp	Ile	Gln	Leu	Thr	Gln	Ser	Pro	Ser	Ser	Leu
465					470					475					480
Ser	Ala	Ser	Val	Gly	Asp	Arg	Val	Thr	Met	Thr	Cys	Arg	Ala	Ser	Ser
				485					490					495	
Ser	Val	Ser	Tyr	Ile	His	Trp	Phe	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro
			500					505					510		
Lys	Pro	Trp	Ile	Tyr	Ala	Thr	Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro	Val
		515					520					525			
Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Tyr	Thr	Phe	Thr	Ile	Ser
	530					535					540				
Ser	Leu	Gln	Pro	Glu	Asp	Ile	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Trp	Thr
545					550					555					560
Ser	Asn	Pro	Pro	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Arg
				565					570					575	
Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gln
			580					585					590		
Val	Gln	Leu	Gln	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ser	Ser
		595					600					605			
Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Ser	Tyr	Asn
	610					615					620				
Met	His	Trp	Val	Lys	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Ile	Gly

625				630				-SL 635				640			
Ala	Ile	Tyr	Pro	Gly 645	Met	Gly	Asp	Thr	Ser 650	Tyr	Asn	Gln	Lys	Phe 655	Lys
Gly	Lys	Ala	Thr 660	Leu	Thr	Ala	Asp	Glu 665	Ser	Thr	Asn	Thr	Ala 670	Tyr	Met
Glu	Leu	Ser 675	Ser	Leu	Arg	Ser	Glu 680	Asp	Thr	Ala	Phe	Tyr 685	Tyr	Cys	Ala
Arg	Ser 690	Thr	Tyr	Tyr	Gly	Gly 695	Asp	Trp	Tyr	Phe	Asp 700	Val	Trp	Gly	Gln
Gly 705	Thr	Thr	Val	Thr	Val 710	Ser	Ser	Ala	Ser	Thr 715	Thr	Thr	Pro	Ala	Pro 720
Arg	Pro	Pro	Thr	Pro 725	Ala	Pro	Thr	Ile	Ala 730	Ser	Gln	Pro	Leu	Ser 735	Leu
Arg	Pro	Glu	Ala 740	Cys	Arg	Pro	Ala	Ala 745	Gly	Gly	Ala	Val	His 750	Thr	Arg
Gly	Leu	Asp 755	Phe	Ala	Cys	Asp	Ser 760	Gly	Ile	Tyr	Ile	Trp 765	Ala	Pro	Leu
Ala	Gly 770	Thr	Cys	Gly	Val	Leu 775	Leu	Leu	Ser	Leu	Val 780	Ile	Thr	Leu	Tyr
Cys 785	Lys	Arg	Gly	Arg	Lys 790	Lys	Leu	Leu	Tyr	Ile 795	Phe	Lys	Gln	Pro	Phe 800
Met	Arg	Pro	Val	Gln 805	Thr	Thr	Gln	Glu	Glu 810	Asp	Gly	Cys	Ser	Cys 815	Arg
Phe	Pro	Glu	Glu 820	Glu	Glu	Gly	Gly	Cys 825	Glu	Leu	Arg	Val	Lys 830	Phe	Ser
Arg	Ser	Ala 835	Asp	Ala	Pro	Ala	Tyr 840	Gln	Gln	Gly	Gln	Asn 845	Gln	Leu	Tyr
Asn	Glu 850	Leu	Asn	Leu	Gly	Arg 855	Arg	Glu	Glu	Tyr	Asp 860	Val	Leu	Asp	Lys
Arg 865	Arg	Gly	Arg	Asp	Pro 870	Glu	Met	Gly	Gly	Lys 875	Pro	Arg	Arg	Lys	Asn 880
Pro	Gln	Glu	Gly	Leu 885	Tyr	Asn	Glu	Leu	Gln 890	Lys	Asp	Lys	Met	Ala 895	Glu
Ala	Tyr	Ser	Glu	Ile	Gly	Met	Lys	Gly	Glu	Arg	Arg	Arg	Gly	Lys	Gly

His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr
915 920 925

Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
930 935

```
<210> 3034
<211> 63
<212> DNA
<213> Artificial Sequence
```

```
<220>  
<221> source  
<223> /note="Description of Artificial Sequence: Synthetic  
oligonucleotide"
```

[illegible]

```
<210> 3035
<211> 21
<212> PRT
<213> Artificial Sequence
```

```
<220>  
<221> source  
<223> /note="Description of Artificial Sequence: Synthetic  
peptide"
```

<400> 3035
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro
20

```
<210> 3036
<211> 5
<212> PRT
<213> Artificial Sequence
```

```
<220>  
<221> source  
<223> /note="Description of Artificial Sequence: Synthetic  
peptide"
```

<400> 3036
Ser Gly Gly Gly Ser
1 5