

(12) STANDARD PATENT
(19) AUSTRALIAN PATENT OFFICE

(11) Application No. **AU 2018263923 B9**

(54) Title
LAMP (lysosomal associated membrane protein) constructs comprising cancer anti-gens

(51) International Patent Classification(s)
A61K 39/00 (2006.01)

(21) Application No: **2018263923**

(22) Date of Filing: **2018.05.02**

(87) WIPO No: **WO18/204534**

(30) Priority Data

(31) Number
62/561,760
62/500,053

(32) Date
2017.09.22
2017.05.02

(33) Country
US
US

(43) Publication Date: **2018.11.08**

(44) Accepted Journal Date: **2024.08.22**

(48) Corrigenda Journal Date: **2024.09.19**

(71) Applicant(s)
Immunomic Therapeutics, Inc.

(72) Inventor(s)
Heiland, Teri

(74) Agent / Attorney
Madderns Pty Ltd, GPO Box 2752, Adelaide, SA, 5001, AU

(56) Related Art
WO 2013/187906 A1



(51) International Patent Classification:

A61K 39/00 (2006.01)

(21) International Application Number:

PCT/US2018/030725

(22) International Filing Date:

02 May 2018 (02.05.2018)

(25) Filing Language:

English

(26) Publication Language:

English

(30) Priority Data:

62/500,053 02 May 2017 (02.05.2017) US

62/561,760 22 September 2017 (22.09.2017) US

(71) Applicant: IMMUNOMIC THERAPEUTICS, INC.

[US/US]; 15010 Broschart Road, Suite 250, Rockville,
Maryland 20850 (US).

(72) Inventor: HEILAND, Teri;

6241 Sawyer Road, New Mar-

ket, Maryland 21774 (US).

(74) Agent: WALES, Michele M.;

11816 Centurion Way, Po-

tomac, Maryland 20854 (US).

(81) Designated States (unless otherwise indicated, for every

kind of national protection available): AE, AG, AL, AM,
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, JO, 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).

Published:

- with international search report (Art. 21(3))
- with sequence listing part of description (Rule 5.2(a))

(54) Title: LAMP (LYSOSOMAL ASSOCIATED MEMBRANE PROTEIN) CONSTRUCTS COMPRISING CANCER ANTIGENS

(57) Abstract: The present invention provides LAMP Constructs comprising specific fragments of the LAMP luminal domain to deliver cancer antigens to immune cells for enhanced processing. These LAMP Constructs can be used for the treatment of disease and in particular hyperproliferative disorders and/or cancer. The LAMP Constructs allow for presentation of properly configured three dimensional epitopes for production of an immune response when administered to a subject. The LAMP Constructs can be multivalent molecules, and/or can be provided as part of a multivalent vaccine containing two or more LAMP Constructs. The LAMP Constructs as described herein can also be used to generate antibodies when administered to a non-human vertebrate.



WO 2018/204534 A1

Field of the Invention

[0001] The invention relates to improved LAMP Constructs comprising cancer antigens and their use in treating subjects suffering from hyperproliferative disorders and/or cancer. Prime boost protocols utilizing the improved LAMP Constructs described herein are also described.

Discussion of the Related Art

[0002] In the following discussion, certain articles and methods will be described for background and introductory purposes. Nothing contained herein is to be construed as an "admission" of prior art. Applicant expressly reserves the right to demonstrate, where appropriate, that the articles and methods referenced herein do not constitute prior art under the applicable statutory provisions.

[0003] DNA vaccines are new and promising candidates for the development of both prophylactic and therapeutic vaccines. They are proven to be safe and the lack of immune responses to a vector backbone may be a definitive advantage if repetitive cycles of vaccination are required to achieve clinical benefits. However, one perceived disadvantage of conventional DNA vaccines is their low immunogenicity in humans. A key limiting step in the immunogenicity of epitope-based DNA vaccines may be the access of epitopes to the MHCII presentation pathway to T cells, which is likely a stochastic process in the case of a vaccine without targeting technology.

[0004] U.S. Pat. No. 5,633,234 describes chimeric proteins comprising an antigenic domain of modified influenza hemagglutinin (HA) and a cytoplasmic endosomal/lysosomal targeting signal which effectively target antigens to that compartment. The antigenic domain was processed and peptides from it presented on the cell surface in association with major histocompatibility (MHC) class II molecules. The cytoplasmic tail of LAMP-1 was used to form the endosomal/lysosomal targeting domain of the chimeric protein.

[0005] U.S. Pat. No. 8,318,173 extended these initial observations to describe chimeric proteins (and the corresponding DNAs that encode these proteins) comprising the HIV-1 Gag protein inserted between the full luminal domain and a transmembrane domain of LAMP-1. This construct was introduced into dendritic cells which were then reported to target the MHC II pathway.

[0006] This approach has proved useful in increasing cellular and humoral responses to several virus antigens, human papillomavirus E7, dengue virus membrane protein, HIV-1 gp160 membrane protein, HIV-1 p55 Gag, West Nile membrane protein, hepatitis C virus NS3 protein and cytomegalovirus pp65 (see, e.g., Bonini, et al., J. Immunol. 166: 5250-5257, 2001). The enhanced immune response can be attributed to co-localization of LAMP with MHC II and the more efficient processing and delivery of antigenic peptides. In addition, LAMP-targeting is reported to result in the presentation of an increased number of immunogenic

epitopes, thus inducing a qualitatively broadened immune response compared to untargeted antigen. For example, Fernandes et al., 2000, Eur. J. Immunol. 30(8): 2333-43, demonstrated an increase in the number of presented peptides of a LAMP-trafficked OVA antigen encoded in a vaccinia vector. Of 12 peptides generated from exogenously supplied OVA, 9 were presented by an OVA/LAMP chimera, as compared to only 2 by the construct without LAMP.

[0007] While it has been determined that the cytoplasmic domain of LAMP is necessary (in conjunction with a signal sequence and transmembrane domain), it is not always sufficient for endosomal/lysosomal trafficking of all antigens. Instead, the full luminal domain of LAMP has been shown to be also required for the trafficking of proteins to the lysosomal vesicular pathway.

[0008] However, even with the presence of the complete luminal domain and the complete transmembrane/cytoplasmic tail of LAMP ("complete LAMP Constructs"), it has increasingly been found that the efficacy of a particular antigen to raise an immune response is highly dependent on the particular sequence used in these constructs. In fact, different antigenic fragments of the same protein when inserted into the complete LAMP constructs have been found to not elicit the same immune response. Sometimes the antigen fragment generates an immune response and other times it does not. These observations make the ability to predict ahead of time which particular antigenic sequence from a protein of interest will raise an immune response difficult with the complete LAMP Constructs.

[0009] Moreover, in generating the complete LAMP Constructs, it has been repeatedly observed that the full luminal domain is required to properly express and process an antigen. For example, in Godinho et al., PLoS ONE 9(6): 9(6): e99887. doi:10.1371/journal.pone.0099887, the authors reported that the complete and intact luminal domain was the necessary minimal region needed to target an antigen to the lysosomes and that fragments of the luminal domain did not work. *See, id.* at page 6.

[0010] Specifically, the Godinho authors showed that by completely removing the first luminal domain and some of the second luminal domain (i.e., T1-Lum/gag construct), both protein expression and antibody response is decreased. Similarly, removing 25% of first luminal domain but having an intact second luminal domain (i.e., T2-lum/gag), both protein expression and antibody response comparatively increased but still less than the results obtained with the complete LAMP construct.

[0011] Moreover, the authors acknowledged that the ability to raise an immune response is dependent upon the particular antigen and the epitopes used in these complete LAMP Constructs. For example, on page 9, column 2, the authors state "accordingly, previous studies demonstrated that DNA vaccines that generate Gag secreted as VLP, or in a soluble form, induce different levels of T and B cell activation, which were also different from the response induced by cytoplasmic Gag." Moreover, insertion of an antigenic sequence between the full luminal domain of LAMP and the full transmembrane/cytoplasmic domain of LAMP as has been described in the literature can result in such large polynucleotide sequences that it can become either too costly to produce at commercial levels or impractical from a scientific perspective.

[0012] Thus, there is a need to design new and improved LAMP Constructs that can be used as vaccines to effectively treat, for example, hyperproliferative disorders and/or cancer. Moreover, once improved, these new LAMP Constructs can be used to generate antibodies.

SUMMARY OF THE INVENTION

[0013] This Summary is provided to introduce a selection of concepts in a simplified form that are further described below in the Detailed Description. This Summary is not intended to identify key or essential features of the claimed subject matter, nor is it intended to be used to limit the scope of the claimed subject matter. Other features, details, utilities, and advantages of the claimed subject matter will be apparent from the following written Detailed Description including those aspects illustrated in the accompanying drawings and defined in the appended claims.

[0013a] In an aspect, the invention provides a LAMP Construct comprising two homology domains of a luminal domain of a LAMP protein, and an antigenic domain, wherein the antigen domain is placed between the first homology domain of the LAMP protein and the second homology domain of the LAMP protein, and wherein the antigenic domain comprises one or more of: at least one epitope of pp65, at least one epitope of gB, and at least one epitope of IE1. In certain embodiments, the antigenic domain comprises at least one epitope of pp65 and at least one epitope of IE1. In certain embodiments, the antigenic domain comprises at least one epitope of gB.

[0013b] In certain embodiments, the LAMP protein is selected from LAMP-1, LAMP2, LAMP-3, LIMP 2, Macrosailin, Endolyn, LAMP5 or LIMBIC. In certain embodiments, the LAMP Protein comprises an amino acid sequence selected from any one of SEQ ID NO:1-113. In certain embodiments, the LAMP Protein comprises an amino acid sequence at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, 96%, 97%, 98% or 99% identical to SEQ ID NO:1-113. In certain embodiments, the LAMP Protein is LAMP-1. In certain embodiments, the LAMP Construct comprises LAMP-1 Homology Domain 1 and LAMP-1 Homology Domain 2. In certain embodiments, the LAMP-1 Homology Domain 1 comprises (a) the amino acid sequence of residues 29-194 of SEQ ID NO: 1, or (b) a variant of (a) wherein said variant comprises an amino acid sequence at least 95% or at least 97% identical to the amino acid sequence of (a); and/or the LAMP-1 Homology Domain 2 comprises residues 228-381 of SEQ ID NO: 1. In certain embodiments, the LAMP Construct further comprises a Transmembrane Domain and a cytosolic tail of a LAMP Protein. In certain embodiments, the Transmembrane Domain comprises residues 383-405 of SEQ ID NO: 1 and/or wherein the cytosolic tail comprises residues 406-417 of SEQ ID NO: 1.

[0013c] In certain embodiments, the LAMP Construct further comprises a signal sequence. In certain embodiments, the signal sequence is derived from a LAMP Protein.

[0013d] In certain embodiments, the antigenic domain comprises more than one epitope and wherein the epitopes of the antigenic domain are separated by linkers. In certain embodiments, the linkers are selected from the amino acid sequence GP GPG or PMGLP. In certain embodiments, the at least one pp65 epitope comprises the amino acid sequence of SEQ ID NO: 114, or comprises an amino acid sequence at least about 95%, 96%, 97%, 98% or 99% identical to SEQ ID NO: 114. In certain embodiments, the at least one gB epitope comprises the amino acid sequence of SEQ ID NO: 117, or comprises an amino acid sequence at least about 95%, 96%, 97%, 98% or 99% identical to SEQ ID NO: 117. In certain embodiments, the at least one 1E1 epitope comprises the amino acid sequence of SEQ ID NO: 121, or comprises an amino acid sequence at least about 95%, 96%, 97%, 98% or 99% identical to SEQ ID NO: 121. In certain embodiments, the at least one pp65 epitope comprises one or more of: LLQTGIHVRVSQPSL, ALPLKMLNIPSINVH, DQYVKVYLESFCEDV, IIKPGKISHIMLDVAFTSH, PQYSEHPTFTSQYRIQGKL, PPWQAGILARNLVPMV, or KYQEFFWDANDIYRIFA ; and/or

wherein the at least one gB epitope comprises one or more of: TTSAQTRSVYSQHVT, QLIPDDYSNTHSTRYV, VSVFETSGGLVFWQ, or NSAYEYVDYLFKRMIDLS; and/or

wherein the at least one 1E1 epitope comprises one or more of: VLAELVKQIKVRVDMVRHRIKEHMLKKYTQ, IVPEDKREMWMACIKELH, KDELRRKMMYMCYRNIEFFTKNSAFPKTT, SVMKRRIEEICMKVFAQYI, AIAEESDEEEAIVAY, or VKSEPVSEIEEVAPEEEEDG.

[0013e] In certain embodiments, the Construct comprises one or more of SEQ ID NO: 115, 116, 119, 120, 122, or 123. In certain embodiments, the antigenic domain comprises each of SEQ ID NO: 114, SEQ ID NO: 117, and SEQ ID NO: 121. In certain embodiments, the antigenic domain comprises SEQ ID NO: 114 and SEQ ID NO: 121. In certain embodiments, the antigenic domain comprises SEQ ID NO: 117.

[0013f] In an aspect, the invention provides a LAMP Construct comprising two homology domains of a luminal domain of a LAMP protein, and an antigenic domain, wherein the antigen domain is placed between the two homology domains, wherein the antigenic domain is at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, 96%, 97%, 98% or 99% identical to SEQ ID NO:124-197.

[0013g] In an aspect, the invention provides a polynucleotide encoding the LAMP Construct of the invention. In certain embodiments, the polynucleotide is DNA. In certain embodiments, the polynucleotide is RNA. In certain embodiments, the polynucleotide is a viral vector. In certain embodiments, the polynucleotide is a self-replicating RNA viral vector.

[0013h] In an aspect, the invention provides a host cell comprising the polynucleotide of the invention. In an aspect, the invention provides an antigen presenting cell comprising the polynucleotide of the invention. In certain embodiments, the cell is a dendritic cell.

[0013i] In an aspect, the invention provides a pharmaceutical composition comprising

polynucleotides encoding a mixture of LAMP Constructs, wherein the mixture of LAMP constructs collectively comprises pp65, IE1, and gB antigens,

wherein each LAMP Construct of the mixture comprises two homology domains of a luminal domain of a LAMP protein, and an antigenic domain, wherein the antigenic domain is placed between the first homology domain of the LAMP protein and the second homology domain of the LAMP protein, wherein the antigenic domain comprises one or more of: at least one epitope of pp65, at least one epitope of gB, and at least one epitope of IE1. In certain embodiments, the at least one pp65 epitope comprises the amino acid sequence of SEQ ID NO: 114, or comprises an amino acid sequence at least 95%, at least 96%, at least 97%, at least 98% or at least 99% identical to SEQ ID NO: 114; and/or wherein the at least one gB epitope comprises the amino acid sequence of SEQ ID NO: 117, or comprises an amino acid sequence at least 95%, at least 96%, at least 97%, at least 98% or at least 99% identical to SEQ ID NO: 117; and/or wherein the at least one IE1 epitope comprises the amino acid sequence of SEQ ID NO: 121, or comprises an amino acid sequence at least 95%, 96%, 97%, 98% or 99% identical to SEQ ID NO: 121. In certain embodiments, the at least one pp65 epitope comprises one or more of: LLQTGIHVRVSQPSL, ALPLKMLNIPSINVH, DQYVKVYLESFCEDV, IIKPGKISHIMLDVAFTSH, PQYSEHPTFTSQYRIQGKL, PPWQAGILARNLVPMV, or KYQEFFWDANDIYRIFA; and/or wherein the at least one gB epitope comprises one or more of: TTSAQTRSVYSQHVT, QLIPDDYSNTHSTRYV, VSVFETSGGLVVFQW, or NSAYEYVDYLFKRMIDLS; and/or wherein the at least one IE1 epitope comprises one or more of: VLAELVKQIKVRVDMVRHRIKEHMLKKYTQ, IVPEDKREMWMACIKELH, KDELRRKMMYMCYRNIEFFTKNSAFPKTT, SVMKRRIEEICMKVFAQYI, AIAEESDEEEAIVAY, or VKSEPVSIEEEVAPEEEEDG. In certain embodiments, the antigenic domain of each LAMP Construct comprises one or more of SEQ ID NO: 115, 116, 119, 120, 122, or 123. In certain embodiments, the antigenic domain of one LAMP Construct comprises at least one epitope of pp65 and at least one epitope of IE1 and the antigenic domain of a second LAMP Construct comprises at least one epitope of gB. In certain embodiments, the antigenic domain of one LAMP Construct comprises SEQ ID NO: 114 and 121 and the antigenic domain of a second LAMP Construct comprises SEQ ID NO: 117.

[0013j] In an aspect, the invention provides a method of treating a subject having a disease or a disorder characterized by the expression of one or more epitope of pp65, gB, or IE1, wherein the method comprises administering to the subject the LAMP Construct of the invention, the polynucleotide of the invention, or the host cell of the invention, the antigen presenting cell of the invention, or the pharmaceutical composition of the invention in an amount sufficient to reduce or treat the disease or disorder.

[0013k] In an aspect, the invention provides a method of treating a subject having glioblastoma multiforme characterized by the expression of one or more epitope of pp65, gB, or IE1, wherein the method comprises administering to the subject the LAMP Construct of the invention, the polynucleotide of the

invention, or the host cell of the invention, the antigen presenting cell of the invention, or the pharmaceutical composition of the invention in an amount sufficient to treat the glioblastoma.

[0013l] In certain embodiments, the method comprises a priming step and at least one boosting step, optionally wherein more than one antigenic domain is used to prime and/or boost. In certain embodiments, the LAMP Construct of the invention, the polynucleotide of the invention, the host cell of the invention, the antigen presenting cell of the invention or the pharmaceutical composition of the invention is administered in the priming step. In certain embodiments, the LAMP Construct of the invention, the polynucleotide of the invention, or the host cell of the invention, or the pharmaceutical composition of the invention is administered in the boosting step.

[0013m] In an aspect, the invention provides a use of the LAMP Construct of the invention, the polynucleotide of the invention, the host cell of the invention, the antigen presenting cell of the invention or the pharmaceutical composition of the invention in the preparation of a medicament for reducing or treating a disease or disorder, characterized by the expression of one or more epitope of pp65, gB, or IE1, in a subject.

[0013n] In an aspect, the invention provides a use of the LAMP Construct of the invention, the polynucleotide of the invention, the host cell of the invention, the antigen presenting cell of the invention or the pharmaceutical composition of the invention in the preparation of a medicament for treating glioblastoma multiforme, characterized by the expression of one or more epitope of pp65, gB, or IE1, in a subject.

[0013o] In certain embodiments, the use comprises a priming step and at least one boosting step, optionally wherein more than one antigenic domain is used to prime and/or boost. In certain embodiments, the use comprises administration of the LAMP Construct of the invention, the polynucleotide of the invention, the host cell of the invention, the antigen presenting cell of the invention or the pharmaceutical composition of the invention in the priming step. In certain embodiments, the use comprises administration of the LAMP Construct of the invention, the polynucleotide of the invention, the host cell of the invention, the antigen presenting cell of the invention or the pharmaceutical composition of the invention in the boosting step.

[0014] This invention desirably provides novel constructs ("improved LAMP Constructs") comprising specific fragments and/or variants of LAMP domains that effectively present the cancer antigens specified herein to the immune system to generate an enhanced immune response. These improved LAMP Constructs desirably effectively direct the antigens to the lysosomal/endosomal compartment where they are processed and presented to major histocompatibility complex (MHC) class II molecules so that helper T cells are preferentially stimulated and/or antibodies are generated.

[0015] The improved LAMP Constructs and methods described herein may elicit an immune response in a subject. The immune response may be an immune response to the epitopes of the antigens in the improved LAMP Construct (e.g., vaccine). Vaccines arm the immune system of the subject such that the immune system may detect and destroy that which contains the antigens of the vaccines in the subject. The improved LAMP Constructs and methods described herein may elicit a Th1 immune response in the subject. Th1 immune

responses may include secretion of inflammatory cytokines (e.g., $\text{IFN}\gamma$, $\text{TNF}\alpha$) by a subset of immune cells (e.g., antigen specific T-cells). In some cases, the inflammatory cytokines activate another subtype of immune cells (e.g., cytotoxic T-cells) which may destroy that which contains the antigen in the subject.

[0016] In some cases, the epitopes and/or antigens used in the improved LAMP Constructs and methods described herein may be recognized by the immune system of a subject to elicit a Th1 immune response and release Type I cytokines. The Th1 response may be initiated by the interaction between the epitope and the T-cell, more specifically, the major histocompatibility complex (MHC) expressed by the T-cell. For example, high affinity binding of an epitope to an MHC receptor may stimulate a Th1 response. MHC receptors may be at least one of a plurality of types of MHC receptors. The MHC receptors engaged on a T-cell may vary across individuals in a population.

[0017] In some cases, the immune response is a Type 1 immune response. In some cases, the immune response is characterized by a ratio of Type I cytokine production to Type II cytokine production that is greater than 1. In some cases, the immune response is characterized by a ratio of Type I cytokine production to Type II cytokine production that is less than 1. In some cases, the immune response is characterized by a ratio of $\text{IFN}\gamma$ production to IL-10 production that is greater than 1. In some cases, the immune response is characterized by a ratio of $\text{IFN}\gamma$ production to IL-10 production that is less than 1.

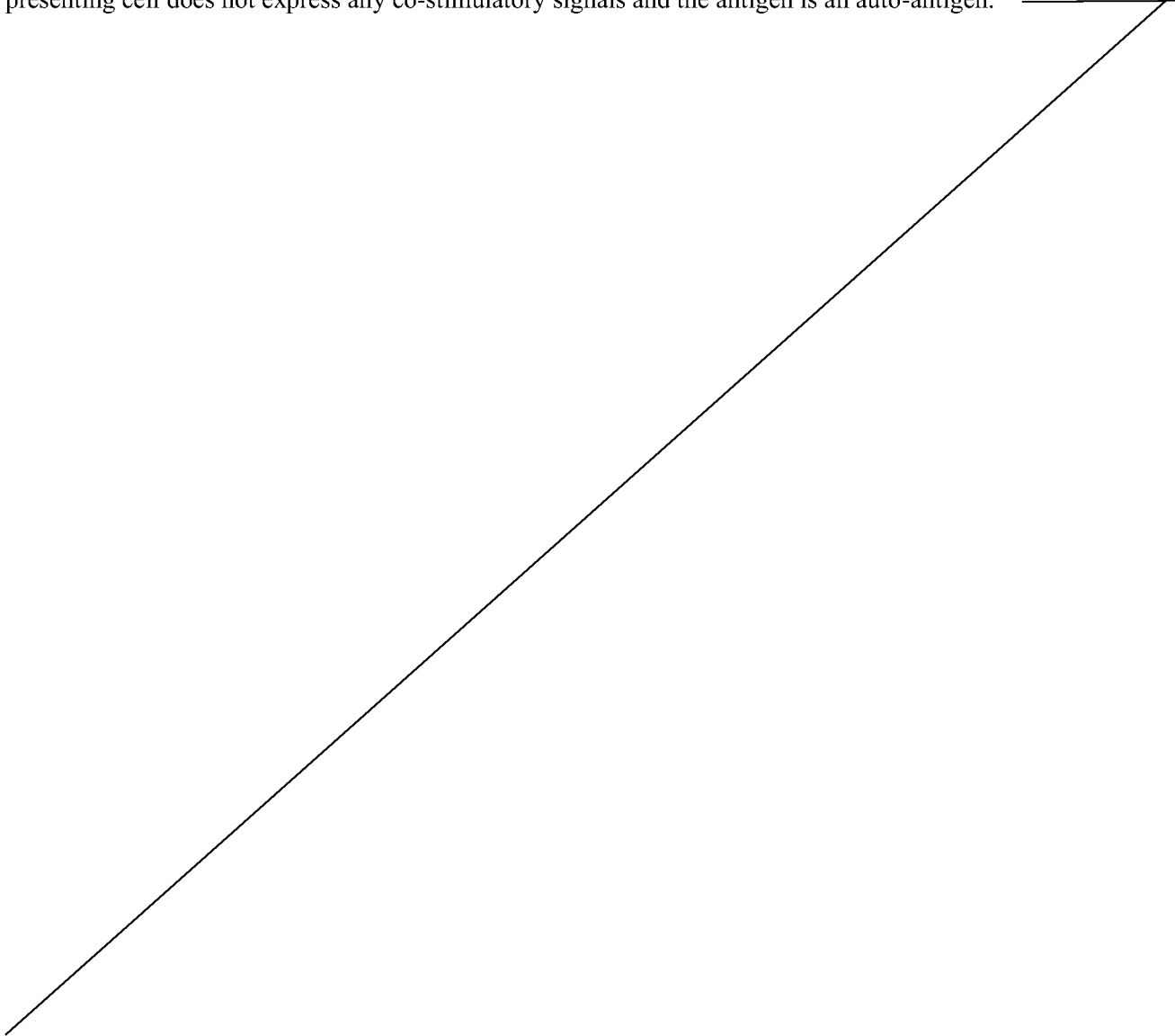
[0018] Prime boost protocols are also contemplated. For example, the invention further provides a method for generating an immune response in a subject to a cancer antigen, comprising priming the subject with an improved LAMP Construct comprising a cancer antigen as described herein followed by at least one boosting of the subject with the antigen or a related antigen (e.g., a second antigen derived from the same or highly similar protein sequence). Mixtures of antigens can be used in either or both the priming and the boosting step. Use of an improved LAMP Construct for the prime step followed by an antigen boost step has been shown to significantly produce higher titers, indicating the power of LAMP in enhancing antibody response.

[0019] This invention also desirably provides improved methods of treatment for cancer and/or hyperproliferative disorders by eliciting an anti-tumor immune response through stimulation of helper T cells.

[0020] The invention further provides a nucleic acid molecule encoding any of the improved LAMP Constructs comprising the cancer antigens described herein. The invention also provides an improved LAMP Construct comprising an antigen to generate antibodies. The improved LAMP Construct can comprise a nucleic acid wherein the nucleic acid molecule is operably linked to an expression control sequence. In one preferred aspect, the improved LAMP Construct is a vaccine vector, suitable for vaccinating a patient. In another aspect, the invention provides a delivery vehicle comprising the improved LAMP Construct for facilitating the introduction of the nucleic acid molecule encoding the antigen into a cell. The delivery vehicle may be lipid-based (e.g., a liposome formulation), viral-based (e.g., comprising viral proteins encapsulating the nucleic acid molecule), or cell-based.

[0021] In preferred embodiments, the invention provides an injectable composition comprising an improved LAMP Construct comprising a cancer antigen of interest for eliciting an immune response (e.g., generation of antibodies) in a mammal to the cancer antigen. In preferred embodiments, this vaccine generates a preferential Th1 response to a Th2 response. The improved LAMP Constructs comprise at least one epitope of a cancer antigen as described herein.

[0022] The invention also provides a cell comprising any of the improved LAMP Constructs described herein. In one aspect, the cell is an antigen presenting cell. The antigen presenting cell may be a professional antigen presenting cell (e.g., a dendritic cell, macrophage, B cell, and the like) or an engineered antigen presenting cell (e.g., a non-professional antigen presenting cell engineered to express molecules required for antigen presentation, such as MHC class II molecules). The molecules required for antigen presentation may be derived from other cells, e.g., naturally occurring, or may themselves be engineered (e.g. mutated or modified to express desired properties, such as higher or lower affinity for an antigenic epitope). In one aspect, the antigen presenting cell does not express any co-stimulatory signals and the antigen is an auto-antigen.



[0023] The invention additionally provides a kit comprising a plurality of cells comprising any of the improved LAMP Constructs described herein. At least two of the cells express different MHC class II molecules, and each cell comprises the same LAMP Construct. In one aspect, a kit is provided comprising an improved LAMP Construct and a cell for receiving the vector.

[0024] The invention also provides a transgenic animal comprising at least one of the cells and/or at least one of the improved LAMP Constructs described herein. The invention also provides a transgenic animal comprising at least one of the cells described herein.

[0025] The invention further provides a method for generating an immune response in an animal (e.g., a human or a non-human vertebrate) to an antigen, comprising: administering to the animal a cell as described above, wherein the cell expresses, or can be induced to express, the improved LAMP Construct in the animal. In one aspect, the cell comprises an MHC class II molecule compatible with MHC proteins of the animal, such that the animal does not generate an immune response against the MHC class II molecule. In one preferred aspect, the animal is a human.

[0026] In one further aspect, the invention provides a method for eliciting an immune response to a cancer antigen, comprising administering to an animal, such as a human or a non-human vertebrate, any of the improved LAMP Constructs described herein. Preferably, the improved LAMP Construct is infectious for a cell of the animal. For example, the improved LAMP Construct may be a viral vector, such as a vaccinia improved LAMP Construct.

[0027] For example, the invention further provides a method for generating an immune response in an animal to a cancer antigen, comprising priming the animal with an improved LAMP Construct comprising an antigen as described herein followed by at least one boosting of the animal. Use of an improved LAMP Construct for the prime step followed by an antigen boost step has been shown to significantly produce higher titers, indicating the power of LAMP in enhancing antibody response.

[0028] In a further aspect, a cell is obtained from a patient, the improved LAMP Construct described herein is introduced into the cell and the cell or progeny of the cell is reintroduced into the patient. In one aspect, the cell is a stem cell-capable of differentiating into an antigen presenting cell. Treatments of human patients as well as veterinary use are specifically contemplated.

[0029] The present invention also comprises methods of generating antibodies in a non-human vertebrate wherein the non-human vertebrate is injected with an improved LAMP Construct comprising an antigen of interest as described herein. The cancer antigen of interest is then efficiently presented to the immune system with the help of LAMP in the non-human vertebrate to raise antibodies against the antigen.

[0030] Specifically, by combining presentation of the antigen of interest with LAMP, the antigen is then effectively transported to the cytoplasmic endosomal/lysosomal compartments, where the antigen can be processed and peptides from it presented on the cell surface in association with major histocompatibility (MHC) class II molecules.

[0031] These generated antibodies can be isolated from the blood of the vertebrate (as polyclonals) and then further isolated to generate monoclonal antibodies using standard techniques.

[0032] In preferred embodiments, the genome of the non-human vertebrate comprises an introduced partially human immunoglobulin region, said introduced region comprising human immunoglobulin variable region locus coding sequences and non-coding sequences based on the endogenous immunoglobulin variable region locus of the non-human vertebrate. Preferably, non-human vertebrate's genome has at least part or all of the endogenous immunoglobulin region removed.

[0033] In further preferred embodiments, the production of human monoclonal antibodies in the non-human vertebrate requires that the host have at least one locus that will express human heavy chain immunoglobulin proteins and one locus that will express human light chain immunoglobulin proteins.

[0034] In some aspects, the partially human immunoglobulin variable region locus comprises human V_H coding sequences and non-coding V_H sequences based on the endogenous V_H region of the non-human vertebrate. In these aspects, the partially human immunoglobulin variable region locus further comprises human D and J gene coding sequences and non-coding D and J gene sequences based on the endogenous genome of the non-human vertebrate host.

[0035] In other aspects, the immunoglobulin region comprises an introduced region comprising human V_L coding sequences and non-coding V_L sequences based on the endogenous V_L region of the non-human vertebrate. More preferably, the introduced partially human immunoglobulin region comprising human V_L coding sequences further comprises human J gene coding sequences and non-coding J gene sequences based on the endogenous genome of the non-human vertebrate host.

[0036] In certain aspects, the vertebrate is a mammal, and preferably the mammal is a rodent, e.g., a mouse or rat. In other aspects, the vertebrate is avian, e.g., a chicken. Other non-human vertebrates include rabbits, llamas, camels, a cow, a guinea pig, a hamster, a dog, a cat, a horse, a non-human primate, a simian (e.g. a monkey or ape), a monkey (e.g. marmoset, baboon, rhesus macaque), or an ape (e.g. gorilla, chimpanzee, orangutan, gibbon).

[0037] In further embodiments, the partially human immunoglobulin region comprises human V_H gene coding regions, and further comprises i) human D and J gene coding sequences and ii) non-coding D and J gene and pre-DJ sequences based on the endogenous genome of the non-human vertebrate host. In other aspects, the V_H gene coding regions derive (at least partially) from other sources--e.g., they could be rationally or otherwise designed sequences, sequences that are a combination of human and other designed sequences, or sequences from other species, such as nonhuman primates.

[0038] In yet another specific aspect, the partially human immunoglobulin region comprises human V_L gene coding regions, and further comprises i) human J gene coding sequences and ii) non-coding J gene sequences based on the endogenous genome of the non-human vertebrate host. In a specific aspect, the partially human immunoglobulin region comprises human V_H coding regions, human D and J gene coding sequences,

and non-coding D and J gene and pre-DJ sequences based on the endogenous genome of the non-human vertebrate host.

[0039] The methods described herein can be used in the production and/or optimization of antibodies, including fully human antibodies, humanized antibodies, chimeric antibodies, for diagnostic and therapeutic uses. Hybridomas producing such antibodies are also a further object of the invention.

[0040] These and other aspects, objects and features are described in more detail below.

BRIEF DESCRIPTION OF THE FIGURES

[0041] The objects and features of the invention can be better understood with reference to the following detailed description and accompanying drawings.

[0042] **Figure 1** illustrates the general scheme of different types of improved LAMP Constructs (identified as ILC-1, ILC-2, ILC-3, ILC-4, ILC-5 and ILC-6) that can be used as described herein.

[0043] **Figure 2B** illustrates the domains of the LAMP proteins defined herein while **Figure 2A** defines the specific amino acid boundaries of these domains for human LAMP-1 (SEQ ID NO:1), human LAMP-2 (SEQ ID NO:2), human LAMP-3 (SEQ ID NO:3), human LIMP-2 (SEQ ID NO:4), human Endolyn (SEQ ID NO:5), human Macrosailin (SEQ ID NO:80), human LAMP-5 (SEQ ID NO:93) and human LIMBIC (SEQ ID NO:67). As described herein the LAMP luminal domains, homology domains, transmembrane domains, the cytoplasmic tail and the signal sequences can be used to generate the improved LAMP Constructs ILC-1, ILC-2, ILC-3, ILC-4, ILC-5 and ILC-6 as described herein.

[0044] **Figure 3** provides alignment of LAMP-1 proteins found in other species as compared to human LAMP-1 (SEQ ID NO:1). The equivalent domains of these other species can be used to generate the improved LAMP Constructs described herein and are readily identifiable by comparing the domains identified for human LAMP-1 in Figures 2 and Figure 3 to the alignments shown in Figure 3.

[0045] **Figure 4** provides alignment of LAMP-2 proteins found in other species as compared to human LAMP-2 (SEQ ID NO:2). The equivalent domains of these other species can be used to generate the improved LAMP Constructs described herein and are readily identifiable by comparing the domains identified for human LAMP-2 in Figures 2 and Figure 4 to the alignments shown in Figure 4.

[0046] **Figure 5** provides alignment of LAMP-3 proteins found in other species as compared to human LAMP-3 (SEQ ID NO:3). The equivalent domains of these other species can be used to generate the improved LAMP Constructs described herein and are readily identifiable by comparing the domains identified for human LAMP-3 in Figures 2 and Figure 5 to the alignments shown in Figure 5.

[0047] **Figure 6** provides alignment of LIMP-2 proteins found in other species as compared to human LIMP-2 (SEQ ID NO:4). The equivalent domains of these other species can be used to generate the improved LAMP Constructs described herein and are readily identifiable by comparing the domains identified for human LIMP-2 in Figures 2 and Figure 6 to the alignments shown in Figure 6.

[0048] **Figure 7** provides alignment of LIMBIC proteins found in other species as compared to human LIMBIC (SEQ ID NO:67). The equivalent domains of these other species can be used to generate the improved LAMP Constructs described herein and are readily identifiable by comparing the domains identified for human LIMBIC in Figures 2 and Figure 7 to the alignments shown in Figure 7.

[0049] **Figure 8** provides alignment of Endolyn proteins found in other species as compared to human Endolyn (SEQ ID NO:5). The equivalent domains of these other species can be used to generate the improved LAMP Constructs described herein and are readily identifiable by comparing the domains identified for human Endolyn in Figures 2 and Figure 8 to the alignments shown in Figure 8.

[0050] **Figure 9** provides alignment of Macrosailin proteins found in other species as compared to human Macrosailin (SEQ ID NO:80). The equivalent domains of these other species can be used to generate the improved LAMP Constructs described herein and are readily identifiable by comparing the domains identified for human Macrosailin in Figures 2 and Figure 9 to the alignments shown in Figure 9.

[0051] **Figure 10** provides alignment of LAMP-5 proteins found in other species as compared to human LAMP-5 (SEQ ID NO:93). The equivalent domains of these other species can be used to generate the improved LAMP Constructs described herein and are readily identifiable by comparing the domains identified for human LAMP-5 in Figures 2 and Figure 10 to the alignments shown in Figure 10.

[0052] **Figure 11** shows results obtained when mice were immunized with HVEM-LAMP, HVEM, or LAMP on day 0, 7, and 14. On day 28, mice were bled and serum samples were isolated. HVEM specific IgG was examined by ELISA. Data represent geometric mean of antibody titers $\pm$ geometric SD, n=6. ** p value <0.01

[0053] **Figure 12** shows results obtained when mice were immunized with HVEM-LAMP, HVEM, or LAMP on day 0, 7, and 14. On day 35, mice were boosted with 5 μ g HVEM protein in the presence of alum adjuvant. Mice were bled on day 49 and serum samples were isolated. HVEM specific IgG was examined by ELISA. Data represent geometric mean of antibody titers $\pm$ geometric SD, n=6. *** p value <0.001; **** p value <0.0001.

[0054] **Figure 13** shows that LAMP alters the binding affinity of epitopes in CRD3/4 of HVEM.

[0055] **Figure 14** confirms protein expression of tested improved LAMP Constructs. In each of Figures 14-28, the labels “complete LAMP Construct”, ILC-1, ILC-2, ILC-3 and ILC-4 correspond to the constructs as depicted in Figure 1.

[0056] **Figure 15** shows that the improved LAMP Constructs induce Th1 effector T cells producing INF γ .

[0057] **Figure 16** shows a particular improved LAMP construct (e.g., ILC-4 as shown in Figure 1) elicited a significantly higher T cell response against all Survivin peptide pools.

[0058] **Figure 17** shows that CD4 T cells are the major source of IFN γ producing cells and that the improved LAMP Constructs demonstrate an increase in the CD4 effector memory cell population over the Complete LAMP construct.

[0059] **Figure 18** shows that the improved LAMP Constructs produced stronger Survivin-specific total IgG response in BALB/c mice.

[0060] **Figures 19 and 20** provides the amino acid sequence of the cancer antigens that can be cloned, either singularly or in combination as described in Table 1 and paragraph [150], into the LAMP Constructs described herein and in Figures 1-10. Furthermore, Figure 19 provides the amino acid sequence of Survivin-LAMP construct tested in the Examples. The signal sequence of each construct is depicted as lower case and underlined letters; the Survivin sequence is depicted in capitalized, white letters, shaded in black; the luminal domain is depicted in italics and capitalized letters and the transmembrane/cytoplasmic domain is depicted in capitalized letter and shaded in grey, and in ILC-4, the second homology domain is bolded. Additional amino acids (LE and EF) may be included as part of the cloning linkers.

[0061] **Figure 21** shows that IGFBP2 (39-328)-ILC-1 Construct induced significantly higher IFN γ producing effector T cells at the dose of 10ug IM/EP immunization.

[0062] **Figure 22** shows that IGFBP2 (39-328)-ILC-1 Construct induced IFN γ and/or TNF α producing CD4⁺ and CD8⁺ effector memory T cells at the dose of 10ug IM/EP immunization.

[0063] **Figure 23** shows that IGFBP-2-specific IgG production in C57BL/6 albino mice immunized with IGFBP2 (39-328)-ILC-1 Construct by IM/EP immunization.

[0064] **Figure 24** shows that IFN γ induction with both pp65 and gB peptides.

[0065] **Figure 25** shows that total IgG (left) and IgG2a (right) antibodies titers in serum of immunized mice against CMV-transfected cell lysate.

[0066] **Figure 26** shows PSMA-ILC-1 LAMP Construct induced significantly higher IFN γ producing effector T cells at the dose of 20ug ID/EP immunization.

[0067] **Figure 27** shows PSMA-ILC-1 LAMP Construct induced IFN γ producing CD4⁺ and CD8⁺ effector memory T cells at the dose of 20ug ID/EP immunization.

[0068] **Figure 28** shows total IgG and IgG2A production in C57BL/6 mice immunized with PSMA-ILC-1 LAMP Construct by immunization via ID/EP.

DETAILED DESCRIPTION

[0069] The invention provides improved LAMP Constructs which can be used to generate vaccines and/or used to raise antibodies. The improved LAMP Constructs can be used to modulate or enhance an immune response. In one preferred aspect, the invention provides a method for treating a patient with cancer or a hyperproliferative disorder by providing an improved LAMP Construct comprising one or more of the cancer

antigens as described herein. The improved LAMP Constructs can also be used to raise antibodies in non-human vertebrates, and in preferably, non-human mammals.

DEFINITIONS

[0070] The following definitions are provided for specific terms which are used in the following written description.

[0071] As used in the specification and claims, the singular form "a", "an" and "the" include plural references unless the context clearly dictates otherwise. For example, the term "a cell" includes a plurality of cells, including mixtures thereof. The term "a nucleic acid molecule" includes a plurality of nucleic acid molecules.

[0072] As used herein, the term "comprising" is intended to mean that the improved LAMP Constructs and methods include the recited elements, but do not exclude other elements. "Consisting essentially of", when used to define improved LAMP Constructs and methods, shall mean excluding other elements of any essential significance to the combination. Thus, an improved LAMP Construct consisting essentially of the elements as defined herein would not exclude trace contaminants from the isolation and purification method and pharmaceutically acceptable carriers, such as phosphate buffered saline, preservatives, and the like. "Consisting of" shall mean excluding more than trace elements of other ingredients and substantial method steps for administering the improved LAMP Constructs of this invention. Embodiments defined by each of these transition terms are within the scope of this invention.

[0073] The term "about" or "approximately" means within an acceptable range for the particular value as determined by one of ordinary skill in the art, which will depend in part on how the value is measured or determined, e.g., the limitations of the measurement system. For example, "about" can mean a range of up to 20%, preferably up to 10%, more preferably up to 5%, and more preferably still up to 1% of a given value. Alternatively, particularly with respect to biological systems or processes, the term can mean within an order of magnitude, preferably within 5 fold, and more preferably within 2 fold, of a value. Unless otherwise stated, the term 'about' means within an acceptable error range for the particular value, such as $\pm 1-20\%$, preferably $\pm 1-10\%$ and more preferably $\pm 1-5\%$.

[0074] Where a range of values is provided, it is understood that each intervening value, between the upper and lower limit of that range and any other stated or intervening value in that stated range is encompassed within the invention. The upper and lower limits of these smaller ranges may independently be included in the smaller ranges, and are also encompassed within the invention, subject to any specifically excluded limit in the stated range. Where the stated range includes one or both of the limits, ranges excluding either both of those included limits are also included in the invention.

[0075] As used herein, "the lysosomal/endosomal compartment" refers to membrane-bound acidic vacuoles containing LAMP molecules in the membrane, hydrolytic enzymes that function in antigen processing,

and MHC class II molecules for antigen recognition and presentation. This compartment functions as a site for degradation of foreign materials internalized from the cell surface by any of a variety of mechanisms including endocytosis, phagocytosis and pinocytosis, and of intracellular material delivered to this compartment by specialized autolytic phenomena (de Duve, *Eur. J. Biochem.* 137: 391, 1983). The term "endosome" as used herein and in the claims encompasses a lysosome.

[0076] As used herein, a "lysosome-related organelle" refers to any organelle which comprises lysosomes and includes, but is not limited to, MIIC, CIIV, melanosomes, secretory granules, lytic granules, platelet-dense granules, basophil granules, Birbeck granules, phagolysosomes, secretory lysosomes, and the like. Preferably, such an organelle lacks mannose 6-phosphate receptors and comprises LAMP, but may or may not comprise an MHC class II molecule. For reviews, see, e.g., Blott and Griffiths, *Nature Reviews, Molecular Cell Biology*, 2002; Dell'Angelica, et al., *The FASEB Journal* 14: 1265-1278, 2000.

[0077] As used herein, the terms "polynucleotide" and "nucleic acid molecule" are used interchangeably to refer to polymeric forms of nucleotides of any length. The polynucleotides may contain deoxyribonucleotides, ribonucleotides, and/or their analogs. Nucleotides may have any three-dimensional structure, and may perform any function, known or unknown. The term "polynucleotide" includes, for example, single-, double-stranded and triple helical molecules, a gene or gene fragment, exons, introns, mRNA, tRNA, rRNA, ribozymes, antisense molecules, cDNA, recombinant polynucleotides, branched polynucleotides, aptamers, plasmids, vectors, isolated DNA of any sequence, isolated RNA of any sequence, nucleic acid probes, and primers. A nucleic acid molecule may also comprise modified nucleic acid molecules (e.g., comprising modified bases, sugars, and/or internucleotide linkers).

[0078] As used herein, the term "peptide" refers to a compound of two or more subunit amino acids, amino acid analogs, or peptidomimetics. The subunits may be linked by peptide bonds or by other bonds (e.g., as esters, ethers, and the like).

[0079] As used herein, the term "amino acid" refers to either natural and/or unnatural or synthetic amino acids, including glycine and both D or L optical isomers, and amino acid analogs and peptidomimetics. A peptide of three or more amino acids is commonly called an oligopeptide if the peptide chain is short. If the peptide chain is long (e.g., greater than about 10 amino acids), the peptide is commonly called a polypeptide or a protein. While the term "protein" encompasses the term "polypeptide", a "polypeptide" may be a less than full-length protein.

[0080] As used herein a "LAMP polypeptide" refers to the mammalian lysosomal associated membrane proteins human LAMP-1, human LAMP-2, human LAMP-3, human LIMP-2, human Endolyn, human LIMBIC, human LAMP-5, or human Macrosailin as described herein, as well as orthologs (such as, for example, the LAMP proteins shown in Figures 3-10), and allelic variants.

[0081] As used herein, "expression" refers to the process by which polynucleotides are transcribed into mRNA and/or translated into peptides, polypeptides, or proteins. If the polynucleotide is derived from genomic DNA, expression may include splicing of the mRNA transcribed from the genomic DNA.

[0082] As used herein, "under transcriptional control" or "operably linked" refers to expression (e.g., transcription or translation) of a polynucleotide sequence which is controlled by an appropriate juxtaposition of an expression control element and a coding sequence. In one aspect, a DNA sequence is "operatively linked" to an expression control sequence when the expression control sequence controls and regulates the transcription of that DNA sequence.

[0083] As used herein, "coding sequence" is a sequence which is transcribed and translated into a polypeptide when placed under the control of appropriate expression control sequences. The boundaries of a coding sequence are determined by a start codon at the 5' (amino) terminus and a translation stop codon at the 3' (carboxyl) terminus. A coding sequence can include, but is not limited to, a prokaryotic sequence, cDNA from eukaryotic mRNA, a genomic DNA sequence from eukaryotic (e.g., mammalian) DNA, and even synthetic DNA sequences. A polyadenylation signal and transcription termination sequence will usually be located 3' to the coding sequence.

[0084] As used herein, two coding sequences "correspond" to each other if the sequences or their complementary sequences encode the same amino acid sequences.

[0085] As used herein, "signal sequence" denotes the endoplasmic reticulum translocation sequence. This sequence encodes a signal peptide that communicates to a cell to direct a polypeptide to which it is linked (e.g., via a chemical bond) to an endoplasmic reticulum vesicular compartment, to enter an exocytic/endocytic organelle, to be delivered either to a cellular vesicular compartment, the cell surface or to secrete the polypeptide. This signal sequence is sometimes clipped off by the cell in the maturation of a protein. Signal sequences can be found associated with a variety of proteins native to prokaryotes and eukaryotes.

[0086] As used herein, "trafficking" denotes movement or progression of the polypeptide encoded by the improved LAMP Construct through cellular organelles or compartments in the pathway from the rough endoplasmic reticulum to the endosomal/lysosomal compartment or related organelles where antigen processing and binding to MHC II occurs.

[0087] As used herein, an "improved LAMP Construct" and an "improved LAMP Construct comprising an antigen" and an "improved LAMP Construct comprising an antigen of interest" are used interchangeably. The different arrangements of the improved LAMP Constructs are illustrated in Figure 1 as ILC1-ILC6. Moreover, the use of an "improved LAMP Construct" encompasses both the polynucleotide sequence of the improved LAMP Construct as well as the protein encoded by the polynucleotide sequence of the improved LAMP Construct.

[0088] As used herein, an "improved LAMP Construct delivery vehicle" is defined as any molecule or group of molecules or macromolecules that can carry an improved LAMP Construct into a host cell (e.g., such

as genes or gene fragments, antisense molecules, ribozymes, aptamers, and the like) and which occurs in association with an improved LAMP Construct as described herein.

[0089] As used herein, "improved LAMP Construct delivery," or "improved LAMP Construct transfer," refers to the introduction of the improved LAMP Construct into a host cell, irrespective of the method used for the introduction. The introduced improved LAMP Constructs may be stably or transiently maintained in the host cell. Stable maintenance typically requires that the introduced improved LAMP Construct either contains an origin of replication compatible with the host cell or integrates into a replicon of the host cell such as an extrachromosomal replicon (e.g., a plasmid) or a nuclear or mitochondrial chromosome.

[0090] As used herein, a "viral improved LAMP Construct" refers to a virus or viral particle that comprises the improved LAMP Construct to be delivered into a host cell, either *in vivo*, *ex vivo* or *in vitro*. Examples of viral improved LAMP Constructs include, but are not limited to, adenovirus vectors, adeno-associated virus vectors, retroviral vectors, and the like. In aspects where gene transfer is mediated by an adenoviral vector, an improved LAMP Construct includes the adenovirus genome or part thereof, and a selected, non-adenoviral gene, in association with adenoviral capsid proteins.

[0091] As used herein, "adenoviral-mediated gene transfer" or "adenoviral transduction" refers to the process by which an improved LAMP Construct is transferred into a host cell by virtue of the adenovirus entering the cell. Preferably, the improved LAMP Construct is able to replicate and/or integrate and be transcribed within the cell.

[0092] As used herein, "adenovirus particles" are individual adenovirus virions comprised of an external capsid and an improved LAMP Construct, where the capsid is further comprised of adenovirus envelope proteins. The adenovirus envelope proteins may be modified to comprise a fusion polypeptide which contains a polypeptide ligand covalently attached to the viral protein, e.g., for targeting the adenoviral particle to a particular cell and/or tissue type.

[0093] As used herein, the term "administering" or "immunizing" or "injecting" an improved LAMP Construct refers to transducing, transfecting, microinjecting, electroporating, or shooting the cell with the improved LAMP Construct. In some aspects, improved LAMP Constructs are introduced into a target cell by contacting the target cell with a delivery cell (e.g., by cell fusion or by lysing the delivery cell when it is in proximity to the target cell).

[0094] As used herein, the phrase "prime boost" describes the use of an improved LAMP Construct described herein used to prime a T-cell response followed by the use of a second improved LAMP Construct comprising an antigen, a DNA vaccine comprising an antigen or a recombinant antigen to boost the response (or *visa versa*). These heterologous prime-boost immunizations elicit immune responses of greater height and breadth than can be achieved by priming and boosting with the same vector. The priming with an improved LAMP Construct comprising an antigen initiates memory cells; the boost step expands the memory response. Preferably, two different agents that do not raise responses against each other are used and thus do not interfere

with each other's activity. Mixtures of antigens are specifically contemplated in the prime and/or boost step. Boosting can occur once or multiple times.

[0095] As used herein, "hybridization" refers to a reaction in which one or more polynucleotides react to form a complex that is stabilized via hydrogen bonding between the bases of the nucleotide residues. The hydrogen bonding may occur by Watson-Crick base pairing, Hoogsteen binding, or in any other sequence-specific manner. The complex may comprise two strands forming a duplex structure, three or more strands forming a multi-stranded complex, a single self-hybridizing strand, or any combination of these. A hybridization reaction may constitute a step in a more extensive process, such as the initiation of a PCR reaction, or the enzymatic cleavage of a polynucleotide by a ribozyme.

[0096] As used herein, a polynucleotide or polynucleotide region (or a polypeptide or polypeptide region) which has a certain percentage (for example, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 99%) of "sequence identity" to another sequence means that, when maximally aligned, using software programs routine in the art, that percentage of bases (or amino acids) are the same in comparing the two sequences.

[0097] Two sequences are "substantially homologous" or "substantially similar" when at least about 50%, at least about 60%, at least about 70%, at least about 75%, and preferably at least about 80%, and most preferably at least about 90 or 95% of the nucleotides match over the defined length of the DNA sequences. Similarly, two polypeptide sequences are "substantially homologous" or "substantially similar" when at least about 50%, at least about 60%, at least about 66%, at least about 70%, at least about 75%, and preferably at least about 80%, and most preferably at least about 90 or 95% of the amino acid residues of the polypeptide match over a defined length of the polypeptide sequence. Sequences that are substantially homologous can be identified by comparing the sequences using standard software available in sequence data banks. Substantially homologous nucleic acid sequences also can be identified in a Southern hybridization experiment under, for example, stringent conditions as defined for that particular system. Defining appropriate hybridization conditions is within the skill of the art. For example, stringent conditions can be: hybridization at 5xSSC and 50% formamide at 42°C, and washing at 0.1xSSC and 0.1% sodium dodecyl sulfate at 60°C. Further examples of stringent hybridization conditions include: incubation temperatures of about 25 degrees C to about 37 degrees C; hybridization buffer concentrations of about 6xSSC to about 10xSSC; formamide concentrations of about 0% to about 25%; and wash solutions of about 6xSSC. Examples of moderate hybridization conditions include: incubation temperatures of about 40 degrees C to about 50 degrees C.; buffer concentrations of about 9xSSC to about 2xSSC; formamide concentrations of about 30% to about 50%; and wash solutions of about 5xSSC to about 2xSSC. Examples of high stringency conditions include: incubation temperatures of about 55 degrees C to about 68 degrees C.; buffer concentrations of about 1xSSC to about 0.1xSSC; formamide concentrations of about 55% to about 75%; and wash solutions of about 1xSSC, 0.1xSSC, or deionized water. In general, hybridization incubation times are from 5 minutes to 24 hours, with 1, 2, or more washing steps, and wash

incubation times are about 1, 2, or 15 minutes. SSC is 0.15 M NaCl and 15 mM citrate buffer. It is understood that equivalents of SSC using other buffer systems can be employed. Similarity can be verified by sequencing, but preferably, is also or alternatively, verified by function (e.g., ability to traffic to an endosomal compartment, and the like), using assays suitable for the particular domain in question.

[0098] The terms "percent (%) sequence similarity", "percent (%) sequence identity", and the like, generally refer to the degree of identity or correspondence between different nucleotide sequences of nucleic acid molecules or amino acid sequences of polypeptides that may or may not share a common evolutionary origin (see Reeck et al., *supra*). Sequence identity can be determined using any of a number of publicly available sequence comparison algorithms, such as BLAST, FASTA, DNA Strider, GCG (Genetics Computer Group, Program Manual for the GCG Package, Version 7, Madison, Wisconsin), etc.

[0099] To determine the percent identity between two amino acid sequences or two nucleic acid molecules, the sequences are aligned for optimal comparison purposes. The percent identity between the two sequences is a function of the number of identical positions shared by the sequences (i.e., percent identity = number of identical positions/total number of positions (e.g., overlapping positions) x 100). In one embodiment, the two sequences are, or are about, of the same length. The percent identity between two sequences can be determined using techniques similar to those described below, with or without allowing gaps. In calculating percent sequence identity, typically exact matches are counted.

[0100] The determination of percent identity between two sequences can be accomplished using a mathematical algorithm. A non-limiting example of a mathematical algorithm utilized for the comparison of two sequences is the algorithm of Karlin and Altschul, *Proc. Natl. Acad. Sci. USA* 1990, 87:2264, modified as in Karlin and Altschul, *Proc. Natl. Acad. Sci. USA* 1993, 90:5873-5877. Such an algorithm is incorporated into the NBLAST and XBLAST programs of Altschul et al, *J. Mol. Biol.* 1990; 215: 403. BLAST nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12, to obtain nucleotide sequences homologous to sequences of the invention. BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength = 3, to obtain amino acid sequences homologous to protein sequences of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul et al, *Nucleic Acids Res.* 1997, 25:3389. Alternatively, PSI-Blast can be used to perform an iterated search that detects distant relationship between molecules. See Altschul et al. (1997) *supra*. When utilizing BLAST, Gapped BLAST, and PSI-Blast programs, the default parameters of the respective programs (e.g., XBLAST and NBLAST) can be used. See ncbi.nlm.nih.gov/BLAST/ on the WorldWideWeb.

[0101] Another non-limiting example of a mathematical algorithm utilized for the comparison of sequences is the algorithm of Myers and Miller, *CABIOS* 1988; 4: 1 1-17. Such an algorithm is incorporated into the ALIGN program (version 2.0), which is part of the GCG sequence alignment software package. When utilizing the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used.

[0102] In a preferred embodiment, the percent identity between two amino acid sequences is determined using the algorithm of Needleman and Wunsch (J. Mol. Biol. 1970, 48:444-453), which has been incorporated into the GAP program in the GCG software package (Accelrys, Burlington, MA; available at accelrys.com on the WorldWideWeb), using either a Blossum 62 matrix or a PAM250 matrix, 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 yet another preferred embodiment, the percent identity between two nucleotide sequences is determined using the GAP program in the GCG software package using a NWSgapdna.CMP matrix, a gap weight of 40, 50, 60, 70, or 80, and a length weight of 1, 2, 3, 4, 5, or 6. A particularly preferred set of parameters (and the one that can be used if the practitioner is uncertain about what parameters should be applied to determine if a molecule is a sequence identity or homology limitation of the invention) is using a Blossum 62 scoring matrix with a gap open penalty of 12, a gap extend penalty of 4, and a frameshift gap penalty of 5.

[0103] Another non-limiting example of how percent identity can be determined is by using software programs such as those described in Current Protocols In Molecular Biology (F. M. Ausubel et al., eds., 1987) Supplement 30, section 7.7.18, Table 7.7.1. Preferably, default parameters are used for alignment. A preferred alignment program is BLAST, using default parameters. In particular, preferred programs are BLASTN and BLASTP, using the following default parameters: Genetic code=standard; filter=none; strand=both; cutoff=60; expect=10; Matrix=BLOSUM62; Descriptions=50 sequences; sort by=HIGH SCORE; Databases=non-redundant, GenBank+EMBL+DDBJ+PDB+GenBank CDS translations+SwissProtein+SPupdate+PIR. Details of these programs can be found at the following Internet address: <http://www.ncbi.nlm.nih.gov/cgi-bin/BLAST>.

[0104] Statistical analysis of the properties described herein may be carried out by standard tests, for example, t-tests, ANOVA, or Chi squared tests. Typically, statistical significance will be measured to a level of $p=0.05$ (5%), more preferably $p=0.01$, $p=0.001$, $p=0.0001$, $p=0.000001$

[0105] "Conservatively modified variants" of domain sequences also can be provided. With respect to particular nucleic acid sequences, conservatively modified variants refer to those nucleic acids which encode identical or essentially identical amino acid sequences, or where the nucleic acid does not encode an amino acid sequence, to essentially identical sequences. Specifically, degenerate codon substitutions can 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., 1991, Nucleic Acid Res. 19: 5081; Ohtsuka, et al., 1985, J. Biol. Chem. 260: 2605-2608; Rossolini et al., 1994, Mol. Cell. Probes 8: 91-98).

[0106] The term "biologically active fragment", "biologically active form", "biologically active equivalent" of and "functional derivative" of a wild-type protein, possesses a biological activity that is at least substantially equal (e.g., not significantly different from) the biological activity of the wild type protein as measured using an assay suitable for detecting the activity.

[0107] As used herein, "*in vivo*" nucleic acid delivery, nucleic acid transfer, nucleic acid therapy" and the like, refer to the introduction of an improved LAMP Construct directly into the body of an organism, such

as a human or non-human mammal, whereby the improved LAMP Construct is introduced to a cell of such organism *in vivo*.

[0108] As used herein, the term "*in situ*" refers to a type of *in vivo* nucleic acid delivery in which the improved LAMP Construct is brought into proximity with a target cell (e.g., the nucleic acid is not administered systemically). For example, *in situ* delivery methods include, but are not limited to, injecting an improved LAMP Construct directly at a site (e.g., into a tissue, such as a tumor or heart muscle), contacting the improved LAMP Construct with cell(s) or tissue through an open surgical field, or delivering the improved LAMP Constructs to a site using a medical access device such as a catheter.

[0109] As used herein, the term "isolated" or "purified" means separated (or substantially free) from constituents, cellular and otherwise, in which the polynucleotide, peptide, polypeptide, protein, antibody, or fragments thereof, are normally associated with in nature. For example, with respect to an improved LAMP Construct, an isolated polynucleotide is one that is separated from the 5' and 3' sequences with which it is normally associated in the chromosome. As is apparent to those of skill in the art, a non-naturally occurring polynucleotide, peptide, polypeptide, protein, antibody, or fragments thereof, does not require "isolation" to distinguish it from its naturally occurring counterpart. By substantially free or substantially purified, it is meant at least 50% of the population, preferably at least 70%, more preferably at least 80%, and even more preferably at least 90%, are free of the components with which they are associated in nature.

[0110] As used herein, a "target cell" or "recipient cell" refers to an individual cell or cell which is desired to be, or has been, a recipient of the improved LAMP Constructs described herein. The term is also intended to include progeny of a single cell, and the progeny may not necessarily be completely identical (in morphology or in genomic or total DNA complement) to the original parent cell due to natural, accidental, or deliberate mutation. A target cell may be in contact with other cells (e.g., as in a tissue) or may be found circulating within the body of an organism.

[0111] As used herein, a "subject" is a vertebrate, preferably a mammal, more preferably a human. Mammals include, but are not limited to, murines, simians, humans, farm animals, sport animals, and pets. In other preferred embodiments, the "subject" is a rodent (e.g. a rat, a mouse, a rabbit, a llama, camels, a cow, a guinea pig, a hamster, a dog, a cat, a horse, a non-human primate, a simian (e.g. a monkey or ape), a monkey (e.g. marmoset, baboon, rhesus macaque), or an ape (e.g. gorilla, chimpanzee, orangutan, gibbon). In other embodiments, non-human mammals, especially mammals that are conventionally used as models for demonstrating therapeutic efficacy in humans (e.g. murine, primate, porcine, canine, or rabbit animals) may be employed.

[0112] The terms "cancer," "neoplasm," and "tumor," are used interchangeably and in either the singular or plural form, refer to cells that have undergone a malignant transformation that makes them pathological to the host organism. Primary cancer cells transformation that makes them pathological to the host organism. Primary cancer cells (that is, cells obtained from near the site of malignant transformation) can be

readily distinguished from non-cancerous cells by well-established techniques, particularly histological examination. The definition of a cancer cell, as used herein, includes not only a primary cancer cell, but any cell derived from a cancer cell ancestor. This includes metastasized cancer cells, and in vitro cultures and cell lines derived from cancer cells. When referring to a type of cancer that normally manifests as a solid tumor, a "clinically detectable" tumor is one that is detectable on the basis of tumor mass, e.g., by procedures such as CAT scan, MR imaging, X-ray, ultrasound or palpation, and/or which is detectable because of the expression of one or more cancer-specific antigens in a sample obtainable from a patient.

[0113] In preferred embodiments, the cancer (including all stages of progression, including hyperplasia) is an adenocarcinoma, sarcoma, skin cancer, melanoma, bladder cancer, brain cancer (including glioblastoma multiforme), breast cancer, uterine cancer, ovarian cancer, prostate cancer, lung cancer (including, but not limited to NSCLC, SCLC, squamous cell cancer), colorectal cancer, anal cancer, rectal cancer, cervical cancer, liver cancer, head and neck cancer, oral cancer, salivary gland cancer, esophageal cancer, pancreas cancer, pancreatic ductal adenocarcinoma (PDA), renal cancer, stomach cancer, kidney cancer, multiple myeloma or cerebral cancer. Also, preferred diseases to be treated with the LAMP Constructs described herein include those hyperproliferative disorders or cancer caused by cytomegalovirus (CMV).

[0114] As used herein, the term "pharmaceutically acceptable carrier" encompasses any of the standard pharmaceutical carriers, such as a phosphate buffered saline solution, water, and emulsions, such as an oil/water or water/oil emulsion, and various types of wetting agents. Compositions comprising the improved LAMP Constructs also can include stabilizers and preservatives. For examples of carriers, stabilizers and adjuvants, see Martin Remington's Pharm. Sci., 15th Ed. (Mack Publ. Co., Easton (1975)).

[0115] A cell has been "transformed", "transduced", or "transfected" by the improved LAMP Constructs when such nucleic acids have been introduced inside the cell. Transforming DNA may or may not be integrated (covalently linked) with chromosomal DNA making up the genome of the cell. In prokaryotes, yeast, and mammalian cells for example, the improved LAMP Constructs may be maintained on an episomal element, such as a plasmid. In a eukaryotic cell, a stably transformed cell is one in which the improved LAMP Constructs have become integrated into a chromosome so that it is inherited by daughter cells through chromosome replication. This stability is demonstrated by the ability of the eukaryotic cell to establish cell lines or clones comprised of a population of daughter cells containing the improved LAMP Constructs. A "clone" is a population of cells derived from a single cell or common ancestor by mitosis. A "cell line" is a clone of a primary cell that is capable of stable growth in vitro for many generations (e.g., at least about 10).

[0116] As used herein, an "effective amount" is an amount sufficient to affect beneficial or desired results, e.g., such as an effective amount of the improved LAMP Construct transfer and/or expression, and/or the attainment of a desired therapeutic endpoint. An effective amount can be administered in one or more administrations, applications or dosages. In one aspect, an effective amount of an improved LAMP Construct is

an amount sufficient to transform/transduce/transfect at least one cell in a population of cells comprising at least two cells.

[0117] As used herein, a "therapeutically effective amount" is used herein to mean an amount sufficient to prevent, correct and/or normalize an abnormal physiological response. In one aspect, a "therapeutically effective amount" is an amount sufficient to reduce by at least about 30 percent, more preferably by at least 50 percent, most preferably by at least 90 percent, a clinically significant feature of pathology, such as for example, size of a tumor mass, antibody production, cytokine production, fever or white cell count, etc.

[0118] An "antibody" is any immunoglobulin, including antibodies and fragments thereof, that binds a specific antigen. The term encompasses polyclonal, monoclonal, and chimeric antibodies (e.g., bispecific antibodies). An "antibody combining site" is that structural portion of an antibody molecule comprised of heavy and light chain variable and hypervariable regions that specifically binds antigen. Exemplary antibody molecules are intact immunoglobulin molecules, substantially intact immunoglobulin molecules, and those portions of an immunoglobulin molecule that contains the paratope, including Fab, Fab', F(ab')₂ and F(v) portions, which portions are preferred for use in the therapeutic methods described herein. Thus, the term antibody encompasses not only whole antibody molecules, but also antibody fragments as well as variants (including derivatives such as fusion proteins) of antibodies and antibody fragments. Examples of molecules which are described by the term "antibody" in this application include, but are not limited to: single chain Fvs (scFvs), Fab fragments, Fab' fragments, F(ab')₂, disulfide linked Fvs (sdFvs), Fvs, and fragments comprising or alternatively consisting of, either a VL or a VH domain. The term "single chain Fv" or "scFv" as used herein refers to a polypeptide comprising a VL domain of an antibody linked to a VH domain of an antibody. See Carter (2006) Nature Rev. Immunol. 6:243.

[0119] Additionally, antibodies of the invention include, but are not limited to, monoclonal, multi-specific, bi-specific, human, humanized, mouse, or chimeric antibodies, single chain antibodies, camelid antibodies, Fab fragments, F(ab') fragments, anti-idiotypic (anti-Id) antibodies (including, e.g., anti-Id antibodies to antibodies of the invention), domain antibodies and epitope-binding fragments of any of the above. The immunoglobulin molecules of the invention can be of any type (e.g., IgG, IgE, IgM, IgD, IgA and IgY), class (e.g., IgG1, IgG2, IgG3, IgG4, IgA1 and IgA2) or subclass of immunoglobulin molecule.

[0120] Most preferably, the antibodies are human antibodies. As used herein, "human" antibodies include antibodies having the amino acid sequence of a human immunoglobulin and include antibodies isolated from human immunoglobulin libraries and xenomice or other organisms that have been genetically engineered to produce human antibodies. The improved LAMP Constructs described herein can be used in combination with known techniques for generating human antibodies and human monoclonal antibodies as described in the exemplified protocols, see, e.g., PCT publications WO 98/24893; WO 92/01047; WO 96/34096; WO 96/33735; European Patent No. 0598877; U.S. Patent Nos. 5,413,923; 5,625,126; 5,633,425; 5,569,825; 5,661,016;

5,545,806; 5,814,318; 5,885,793; 5,916,771; and 5,939,598; and Lonberg and Huszar, *Int. Rev. Immunol.* 13:65-93 (1995).

[0121] Human antibodies or "humanized" chimeric monoclonal antibodies can be produced using the improved LAMP Constructs in combination with techniques described herein or otherwise known in the art. For example, standard methods for producing chimeric antibodies are known in the art. See, for review the following references: Morrison, *Science* 229:1202 (1985); Oi et al., *BioTechniques* 4:214 (1986); Cabilly et al., U.S. Patent No. 4,816,567; Taniguchi et al., EP 171496; Morrison et al., EP 173494; Neuberger et al., WO 8601533; Robinson et al., WO 8702671; Boulianne et al., *Nature* 312:643 (1984); Neuberger et al., *Nature* 314:268 (1985).

[0122] The antibodies of the present invention may be monovalent, bivalent, trivalent or multivalent. For example, monovalent scFvs can be multimerized either chemically or by association with another protein or substance. A scFv that is fused to a hexahistidine tag or a Flag tag can be multimerized using Ni-NTA agarose (Qiagen) or using anti-Flag antibodies (Stratagene, Inc.). Additionally, the improved LAMP Constructs can be used to generate monospecific, bispecific, trispecific or of greater multispecificity for the encoded antigen(s) contained in the improved LAMP Construct. See, e.g., PCT publications WO 93/17715; WO 92/08802; WO 91/00360; WO 92/05793; Tutt, et al., *J. Immunol.* 147:60-69 (1991); U.S. Patent Nos. 4,474,893; 4,714,681; 4,925,648; 5,573,920; 5,601,819; Kostelny et al., *J. Immunol.* 148:1547-1553 (1992).

[0123] An "epitope" is a structure, usually made up of a short peptide sequence or oligosaccharide, that is specifically recognized or specifically bound by a component of the immune system. T-cell epitopes have generally been shown to be linear oligopeptides. Two epitopes correspond to each other if they can be specifically bound by the same antibody. Two epitopes correspond to each other if both are capable of binding to the same B cell receptor or to the same T cell receptor, and binding of one antibody to its epitope substantially prevents binding by the other epitope (e.g., less than about 30%, preferably, less than about 20%, and more preferably, less than about 10%, 5%, 1%, or about 0.1% of the other epitope binds). In the present invention, multiple epitopes can make up an antigen.

[0124] The term "antigen" or "antigen of interest" as used herein covers any polypeptide sequence encoded by a polynucleotide sequence cloned into the improved LAMP Construct which is used to elicit an innate or adaptive immune response as shown in Table 1. An "antigen" encompasses both a single antigen as well as multiple antigenic sequences (derived from the same or different proteins) cloned into the improved LAMP Construct.

[0125] The term "antigen presenting cell" as used herein includes any cell which presents on its surface an antigen in association with a major histocompatibility complex molecule, or portion thereof, or, alternatively, one or more non-classical MHC molecules, or a portion thereof. Examples of suitable APCs are discussed in detail below and include, but are not limited to, whole cells such as macrophages, dendritic cells, B cells, hybrid APCs, and foster antigen presenting cells.

[0126] As used herein an "engineered antigen-presenting cell" refers to an antigen-presenting cell that has a non-natural molecular moiety on its surface. For example, such a cell may not naturally have a costimulator on its surface or may have an additional artificial costimulator in addition to a natural costimulator on its surface, or may express a non-natural class II molecule on its surface. In preferred embodiments, the engineered antigen-presenting cell has the antigen expressed from the improved LAMP Construct on its surface.

[0127] As used herein, "immune effector cells" refers to cells capable of binding an antigen and which mediate an immune response. These cells include, but are not limited to, T cells, B cells, monocytes, macrophages, NK cells and cytotoxic T lymphocytes (CTLs), for example CTL lines, CTL clones, and CTLs from tumor, inflammatory, or other infiltrates.

[0128] As used herein, "partially human" refers to a nucleic acid having sequences from both a human and a non-human vertebrate. In the context of partially human sequences, the partially human nucleic acids have sequences of human immunoglobulin coding regions and sequences based on the non-coding sequences of the endogenous immunoglobulin region of the non-human vertebrate. The term "based on" when used with reference to endogenous non-coding sequences from a non-human vertebrate refers to sequences that correspond to the non-coding sequence and share a relatively high degree of homology with the non-coding sequences of the endogenous loci of the host vertebrate, e.g., the non-human vertebrate from which the ES cell is derived. Preferably, the non-coding sequences share at least an 80%, more preferably 90% homology with the corresponding non-coding sequences found in the endogenous loci of the non-human vertebrate host cell into which a partially human molecule comprising the non-coding sequences has been introduced.

[0129] The term "immunoglobulin variable region" as used herein refers to a nucleotide sequence that encodes all or a portion of a variable region of an antibody molecule or all or a portion of a regulatory nucleotide sequence that controls expression of an antibody molecule. Immunoglobulin regions for heavy chains may include but are not limited to all or a portion of the V, D, J, and switch regions, including introns. Immunoglobulin region for light chains may include but are not limited to the V and J regions, their upstream flanking sequences, introns, associated with or adjacent to the light chain constant region gene.

[0130] By "transgenic animal" is meant a non-human animal, usually a mammal, having an exogenous nucleic acid sequence present as an extrachromosomal element in a portion of its cells or stably integrated into its germ line DNA (i.e., in the genomic sequence of most or all of its cells). In generating a transgenic animal comprising human sequences, a partially human nucleic acid is introduced into the germ line of such transgenic animals by genetic manipulation of, for example, embryos or embryonic stem cells of the host animal according to methods well known in the art.

[0131] A "vector" includes plasmids and viruses and any DNA or RNA molecule, whether self-replicating or not, which can be used to transform or transfect a cell.

[0132] An "isolated" or "purified" population of cells is substantially free of cells and materials with which it is associated in nature. By substantially free or substantially purified APCs it is meant at least 50% of

the population are APCs, preferably at least 70%, more preferably at least 80%, and even more preferably at least 90%, are free of non-APCs cells with which they are associated in nature.

[0133] As used herein, a "genetic modification" refers to any addition, deletion or disruption to a cell's normal nucleotides. Any method which can achieve the genetic modification of APCs are within the spirit and scope of this invention. Art recognized methods include viral mediated gene transfer, liposome mediated transfer, transformation, transfection and transduction, e.g., viral-mediated gene transfer such as the use of the improved LAMP Constructs based on DNA viruses such as adenovirus, adeno-associated virus and herpes virus, as well as retroviral based vectors.

[0134] The practice of the present invention employs, unless otherwise indicated, conventional molecular biology, microbiology, and recombinant DNA techniques within the skill of the art. Such techniques are explained fully in the literature. See, e.g., Maniatis, Fritsch & Sambrook, In *Molecular Cloning: A Laboratory Manual* (1982); *DNA Cloning: A Practical Approach*, Volumes I and II (D. N. Glover, ed., 1985); *Oligonucleotide Synthesis* (M. J. Gait, ed., 1984); *Nucleic Acid Hybridization* (B. D. Hames & S. J. Higgins, eds., 1985); *Transcription and Translation* (B. D. Hames & S. I. Higgins, eds., 1984); *Animal Cell Culture* (R. I. Freshney, ed., 1986); *Immobilized Cells and Enzymes* (IRL Press, 1986); B. Perbal, *A Practical Guide to Molecular Cloning* (1984).

[0135] Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. All publications mentioned herein are incorporated by reference for the purpose of describing and disclosing devices, formulations and methodologies that may be used in connection with the presently described invention

LAMP Constructs

[0136] LAMP-1, as deduced from a cDNA clone (Chen, et al., *J. Biol. Chem.* 263: 8754, 1988) consists of a polypeptide core of about 382 amino acids with a large (346-residue) luminal amino-terminal domain followed by a 24-residue hydrophobic transmembrane region and short (12-residue) carboxyl-terminal cytoplasmic tail. See, Figure 2A and 2B. The luminal domain is highly glycosylated, being substituted with about 20 asparagine linked complex-type oligosaccharides and consists of two approximately 160-residue "homology domains" that are separated by a proline/serine-rich hinge region. Each of these "homology domains" contains 4 uniformly spaced cysteine residues, disulfide bonded to form four 36-38-residue loops symmetrically placed within the two halves of the luminal domain (Arterburn, et al., *J. Biol. Chem.* 265: 7419, 1990; see, also Chen, et al., *J. Biol. Chem.* 263(18): 8754-8, 1988). Figure 2A schematically shows the conserved domains between LAMP-1, LAMP-2, LAMP-3, Endolyn, LIMBIC, LAMP5, or Macrosailin.

[0137] Previously reported LAMP constructs comprise the following elements in this specific arrangement: (a) a full luminal domain of LAMP-1 protein, the antigen and then the full transmembrane/cytoplasmic tail of LAMP-1 protein; or (b) the antigen and the full transmembrane/cytoplasmic

tail of a LAMP-1 protein. In example (a), the antigenic sequence is inserted in between the full luminal domain of a LAMP-1 protein and the LAMP-1 full transmembrane domain/cytoplasmic tail. Both constructs have been shown to successfully target an antigenic sequence to the lysosome/endosome and will be referred to as “complete LAMP Constructs” as shown in Figure 1 as compared to the improved LAMP Constructs ILC1-ILC6 described herein. The improved LAMP Constructs described herein do not include the complete LAMP Constructs described in the prior art.

[0138] Although it has been widely reported in the literature that fragments smaller than the full luminal domain of LAMP-1 were not effective in generating a robust immune response (*see, e.g.* Godinho et al.). In contrast, the inventors unexpectedly discovered that specific fragments, in certain arrangements, did in fact effectively present antigens to the immune system, generating in many cases a more robust immune response, including the generation of a different repertoire of antibodies. For example, the inventors have identified that the minimal LAMP luminal domain fragment that is effective for generating a robust immune response is not the full luminal domain (as widely reported in the literature) but rather a single Homology Domain of the Luminal Domain of a LAMP Protein.

[0139] For example, constructs can comprise, not the full luminal domain, but instead a single Homology Domain of the Luminal Domain of a LAMP Protein. As used herein, the “Homology Domain” comprises at least the 4 uniformly spaced cysteine residues shown in Figures 3-10. These cysteine residues are labeled 1, 2, 3, and 4 (and in LIMP-2 and Macrosailin – five cysteines are identified, LIMBIC – six cysteines are identified and Endolyn – eight cysteines are identified) in each Homology Domain as shown in Figures 3-10 and are defined herein as the “Cysteine Conserved Fragment.” Additional amino acids can be included to either the N-terminus end and/or the C-terminus end of the Cysteine Conserved Fragment to generate, up to and including a full Homology Domain of a LAMP protein. These additional added amino acids can be derived from the Homology Domain from which the Cysteine Conserved Fragment is derived or from other LAMP Protein Homology Domains. Thus, as used herein, a LAMP Homology Domain comprises and/or consists of one Cysteine Conserved Fragment. At least two LAMP Homology Domains make up the Luminal Domain of LAMP-1, LAMP-2, LAMP-3, or Endolyn.

[0140] Specifically, in one preferred embodiment, the improved LAMP Construct comprises at least one cancer antigen described in Table 1 (preferably the sequences/fragments/epitopes described in column 4 of Table 1) and/or the combinations described in paragraph [150] fused to the N-terminus of the luminal domain of a LAMP protein, at least one homology domain of a LAMP protein, or at least one Cysteine Conserved Fragment of a LAMP protein. See, for example ILC-2 and ILC-6 of Figure 1. In preferred embodiments, these constructs also comprise a transmembrane domain of a LAMP protein, and/or the cytosolic tail of a LAMP protein. In other preferred embodiments, when an antigen contains a transmembrane domain, the transmembrane domain of a LAMP protein and/or the cytosolic tail of a LAMP protein is unnecessary. In preferred embodiments, two homology domains are included in the improved LAMP Construct (e.g., ILC-1 of

Figure 1). In further preferred embodiments, the two homology domains are derived from a LAMP-1, LAMP-2, LAMP-3, or an Endolyn protein. Alternatively, the two homology domains are derived from different LAMP proteins. In these constructs comprising two homology domains, a LAMP hinge domain may also be included. The improved LAMP Constructs described in this paragraph are unexpected in view of the prior art as the antigen has always been placed in between the full luminal LAMP-1 domain and the full LAMP-1 transmembrane/cytoplasmic tail, as fragments of the luminal domain have not been reported to be effective in generating a robust immune response.

[0141] In another preferred embodiment, the improved LAMP Construct comprises at least one cancer antigen described in Table 1 (preferably the sequences/fragments/epitopes described in column 4 of Table 1) and/or the combinations described in paragraph [150] fused to the C-terminus of a single homology domain of a LAMP protein or a single Cysteine Conserved Fragment of a LAMP protein (e.g., ILC-5 of Figure 1). In preferred embodiments, these constructs also comprise a transmembrane domain of a LAMP protein, and/or the cytosolic tail of a LAMP protein (e.g., ILC-3 of Figure 1). In other preferred embodiments, when an antigen contains a transmembrane domain, the transmembrane domain of a LAMP protein and/or the cytosolic tail of a LAMP protein is unnecessary. Cancer antigens described in Table 1 can also be inserted into the complete LAMP constructs as depicted in Figure 1. Alternatively, two homology domains from two different LAMP proteins may be used. The improved LAMP Constructs described in this paragraph are unexpected in view of the prior art as the antigen has always been placed in between the full luminal LAMP-1 domain and the full LAMP-1 transmembrane/cytoplasmic tail, as fragments of the luminal domain have not been reported to be effective in generating a robust immune response.

[0142] Thus, the improved LAMP Construct comprises at least one cancer antigen described in Table 1 (preferably the sequences/fragments/epitopes described in column 4 of Table 1) and/or the combinations described in paragraph [150] fused to the C-terminus of a single homology domain of a LAMP protein or a single Cysteine Conserved Fragment of a LAMP protein. See, for example, ILC-3 and ILC-5 of Figure 1. In preferred embodiments, these constructs also comprise a transmembrane domain of a LAMP protein, and/or the cytosolic tail of a LAMP protein. In other preferred embodiments, when an antigen contains a transmembrane domain, the transmembrane domain of a LAMP protein and/or the cytosolic tail of a LAMP protein is unnecessary. The improved LAMP Constructs described in this paragraph are unexpected in view of the prior art as described above.

[0143] In another preferred embodiment, the improved LAMP Construct comprises at least one antigen of interest fused in between a first homology domain of a LAMP protein and a second homology domain of a LAMP protein (or at least between two Cysteine Conserved Fragments). See, for example, ILC-4 of Figure 1. In preferred embodiments, the two homology domains are derived from LAMP-1, LAMP-2, LAMP-3, or an Endolyn protein. In these constructs, the antigen may be placed in the LAMP hinge region. Alternatively, two homology domains from two different LAMP proteins may be used. This arrangement of at least one cancer

antigen described in Table 1 (preferably the sequences/fragments/epitopes described in column 4 of Table 1) and/or the combinations described in paragraph [150] fused in between two LAMP homology domains (including Cysteine Conserved Fragments) is unexpected in view of the prior art as described above.

[0144] Each of the improved LAMP Constructs defined above can be generated using the domains defined in the Figures. For example, it is specifically contemplated that the domains included in the improved LAMP Construct illustrated in Figure 1, for example, can originate from sequences derived from orthologous sequences. See, Figures 3-10 for example. It is expressly contemplated that the equivalent domains defined in Figures 2A and 2B be used to generate the improved LAMP Constructs illustrated in Figure 1 for orthologous sequences. Moreover, the orthologous sequences shown in Figures 3-10 are representative of the sequences that can be used to generate the domains. It is well within the skill in the art to identify other orthologous sequences and/or isotypes and comparing them to the alignments shown in Figures 3-10. Thus, by identifying the equivalent boundaries defined in Figure 2A and 2B for a human LAMP protein with the alignments shown in Figures 3-10, one can generate the improved LAMP Constructs illustrated in Figure 1.

[0145] As would be well understood by the skilled artisan, the boundaries of each domain are an approximation and may be adjusted at least 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 amino acids based on cloning considerations and restriction enzyme placement. Therefore, when a particular domain (e.g., a LAMP Homology Domain) is included in the improved LAMP Construct, the amino acids beginning and ending of the domain may be adjust by at least 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 amino acids as those boundaries defined in Figure 2A.

[0146] Each of the improved LAMP Constructs described above can additionally comprise a signal sequence and/or additional amino acids in between each domain for cloning purposes as is well known in the art. Additionally, the LAMP homologous domains, the LAMP luminal domain, the LAMP transmembrane domain, and/or the LAMP cytosolic tail domain can originate from the same LAMP protein (e.g., human LAMP-1) or different LAMP proteins (e.g., luminal domain from human LAMP-1 and transmembrane domain from human LAMP-2, and/or mixing of orthologous domains in the same gene family (e.g., LAMP-1) or different gene family (LAMP-1 and LAMP-2).

[0147] Polypeptide variants of the described LAMP Constructs are contemplated. For example, polypeptides at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, 96%, 97%, 98% or 99% identity to any of the improved LAMP Constructs described herein as well as polynucleotides encoding these variants. Variants of the improved LAMP Constructs retain the ability to function by targeting the antigenic sequence to the lysosome. For example, a modified luminal sequence must retain the ability to traffic both membrane and non-membrane antigenic materials to an endosomal compartment with at least about 50%, at least about 60%, at least 70%, at least about 80%, at least about 90%, or at least about 100% efficacy compared to the original domain sequence, i.e., an efficacy that results in sufficient antigen presentation by a cell comprising the chimeric sequence for it to mount an immune

response. In one aspect, sequences containing a suitable trafficking signal may be identified by constructing an improved LAMP Construct containing the well-characterized antigenic domain of ovalbumin, a transmembrane domain, and the cytoplasmic domain of a protein containing a putative lysosomal/endosomal targeting signal. Efficiency of targeting can be measured by determining the ability of antigen presenting cells, expressing the improved LAMP Construct, to stimulate HA epitope-specific, MHC class II restricted T-cells (see, e.g., Example 5 of U.S. Pat. No. 5,633,234).

[0148] Polynucleotides encoding any of the described improved LAMP Constructs are preferred embodiments of the invention, along with polynucleotides at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, 96%, 97%, 98% or 99% identity to any of the improved LAMP Construct polynucleotides described herein. Variants of the improved LAMP Constructs retain the ability to function by targeting the antigenic sequence to the lysosome. For example, a modified luminal sequence must retain the ability to traffic both membrane and non-membrane antigenic materials to an endosomal compartment with at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, or at least about 100% efficacy compared to the original domain sequence, i.e., an efficacy that results in sufficient antigen presentation by a cell comprising the chimeric sequence for it to mount an immune response. In one aspect, sequences containing a suitable trafficking signal may be identified by constructing an improved LAMP Construct containing the well-characterized antigenic domain of ovalbumin, a transmembrane domain, and the cytoplasmic domain of a protein containing a putative lysosomal/endosomal targeting signal. Efficiency of targeting can be measured by determining the ability of antigen presenting cells, expressing the improved LAMP Construct, to stimulate HA epitope-specific, MHC class II restricted T-cells (see, e.g., Example 5 of U.S. Pat. No. 5,633,234).

Cancer Antigens

[0149] The following antigens shown in Table 1 can be cloned into each of the LAMP Constructs described herein using techniques well known to the skilled artisan. The sequences/fragments/epitopes described in the fourth column can be also cloned into the improved LAMP Constructs as described herein. Moreover, it is specifically contemplated that any one of the cancer antigen listed in Table 1 can be combined with any other antigen listed in Table 1 (including the sequences/fragments/epitopes described in the fourth column) and inserted into the improved LAMP Constructs as described herein.

SEQ ID NO:	Protein Name of each Antigen	Accession/ Derived From	Preferred Epitopes/Fragments that can be cloned into the LAMP Constructs described herein, comprise at least
114	pp65	ABQ23593	The highlighted epitopes shown in Figure 20, which include LLQTGIHVRVSQPSL and/or ALPLKMLNIPSINVH and/or DQYVKVLESFCEVDV and/or IIKPGKISHIMLDV/AFTSH and/or PQYSEHPFTTSQYRIQGKL and/or PPWQAGILARNLVP MV and/or KYQEFFWDANDIYRIFA wherein each epitope can be combined in any order and/or in any combination and cloned into a LAMP Construct described herein, wherein each epitope is preferably separated by a linker, such as, for example GPGPG or PMGLP. Representative construct inserts are shown as SEQ ID NO:115 and SEQ ID NO:116.
117 and 118	gB	P06473	The highlighted epitopes shown in Figure 20, which include TTSAQTRSVYSQHVT and/or QLIPDDYSNTHSTRYV and/or VSVFETSGGLVFWQ and/or NSAYEYVDYLFKRMIDLS wherein each epitope can be combined in any order and/or in any combination and cloned into a LAMP Construct described herein, wherein each epitope is preferably separated by a linker, such as, for example GPGPG or PMGLP. Representative construct inserts are shown as SEQ ID NO:119 and SEQ ID NO:120.
121	IE1	P13202	The highlighted epitopes shown in Figure 20, which include VLAELVKQIKVRVDMVRHRIKEHMLKKYTQ and/or IVPEDKREMWMACIKELH and/or KDELRKMMYMCYRNIIEFTKNSAFP KTT and/or SVMKRRIEEICMKVFAQYI and/or AIAEESDEEEAIVAY and/or VKSEPVSIEIEVAPEEEEEDG wherein each epitope can be combined in any order and/or in any combination and cloned into a LAMP Construct described herein, wherein each epitope is preferably separated by a linker, such as, for example GPGPG or PMGLP. Representative construct inserts are shown as SEQ ID NO:122 and SEQ ID NO:123.
124	Morphological transforming region II ("MTRII")	AAA66543	SEQ ID NO:125
126	US28	AMJ53524	SEQ ID NO:127
128	IGFBP2	NP_000588	(a) about amino acids 39-328 of SEQ ID NO:128; (b) about amino acids 40-328 of SEQ ID NO:128; (c) about amino acids 43-135 of SEQ ID NO:128; (d) about amino acids 1-163 of SEQ ID NO:128; (e) about amino acids 2-163 of SEQ ID NO:128; (f) about amino acids 39-163 of SEQ ID NO:128; (g) about amino acids 40-163 of SEQ ID NO:128; (h) about amino acids 229-309 of SEQ ID NO:128; (i) amino acids 2-328 of SEQ ID NO:128; and/or (j) about amino acids 1-328 of SEQ ID NO:128
129	HCMVA Viral interleukin-10 ("IL10")	P17150	SEQ ID NO:130

131	HCMVM Membrane glycoprotein UL144 ("UL144")	F5HAM0	SEQ ID NO:132	
133	HCMVM Protein UL141 ("UL141")	Q6RJJQ3	SEQ ID NO:134	
135	HCMVA Unique short US11 glycoprotein ("US11")	P09727	SEQ ID NO:136	
137 and 138	HCMV Envelope glycoprotein H OS ("HOS")	A0A0G2TM81	The highlighted epitopes shown in Figure 20, which include and/or TYNSSLRNSTVRENAISFNFFQSYNQYVFFHMPR DLTEFLERYQQRNLNTYALVSKDLASYRSFS SHTTSGLHRPHFNQTCILFD and/or QLNRRHSYKDPDFLDAALDF wherein each epitope can be combined in any order and/or in any combination and cloned into a LAMP Construct described herein, wherein each epitope is preferably separated by a linker, such as, for example GPGPG or PMGLP. Representative construct inserts are shown as SEQ ID NO:139 and SEQ ID NO:140.	
141	HCMVT Viral transcription factor IE2 ("IE2")	Q6SWP7	The highlighted epitopes shown in Figure 20, which include RRGVRKIDEVSRMFR and/or GIQIITYTRNHEVKSE and/or LSTPFLMEHTMPVTHPPEVA wherein each epitope can be combined in any order and/or in any combination and cloned into a LAMP Construct described herein, wherein each epitope is preferably separated by a linker, such as, for example GPGPG or PMGLP. Representative construct inserts are shown as SEQ ID NO:142 and SEQ ID NO:143.	
144	TERT Isoform 1 ("TERT")	NP_937983.2	SEQ ID NO:145 SEQ ID NO:146	
147	Survivin	NP_001125727	SEQ ID NO:147; representative constructs include SEQ ID NO:193-197.	
148	Tetanus	1AF9_A	The highlighted epitopes shown in Figure 20, which include PGINGKAIHLVNNESE and/or FNNFTVSFWLRVPKVSASHLEQYGT and/or YVSIDKFRIFCKALNPKEIEKLYTSYLS ILRVGYNAPGIPLYKKMEAVKLRLDK wherein each epitope can be combined in any order and/or in any combination and cloned into a LAMP Construct described herein, wherein each epitope is preferably separated by a linker, such as, for example GPGPG or PMGLP. Representative construct inserts are shown as SEQ ID NO:149 and SEQ ID NO:150.	
151	Cancer Testis Antigen NY-ESO-1 ("NY-ESO-1")	NP-001318.1 (SEQ ID NO:151)	Amino acids 1-155 of SEQ ID NO:151 Amino acids 80-155 of SEQ ID NO:151	

152	HER2	AAA75493.1 (SEQ ID NO:152)	Construct comprising at least one of: amino acids 23-652 and/or 690-1255 of SEQ ID NO:152 wherein each epitope can be combined in any order and/or in any combination and cloned into a LAMP Construct described herein, wherein each epitope is preferably separated by a linker, such as, for example GPGPG or PMGLP. Representative construct inserts are shown as SEQ ID NO:153 and SEQ ID NO:154.
155	HER3	NP_001973.2 (SEQ ID NO:155)	Construct comprising at least one of: amino acids 20-643, 665-1201, and/or 1209-1342 of SEQ ID NO:155, wherein each epitope can be combined in any order and/or in any combination and cloned into a LAMP Construct described herein, wherein each epitope is preferably separated by a linker, such as, for example GPGPG or PMGLP. Representative construct inserts are shown as SEQ ID NO:156 and SEQ ID NO:157
158	HVEM	NP_003811.2 (SEQ ID NO:158)	Amino acids 39-202 (SEQ ID NO:159)
160-163	HPV Constructs		Sequences used to create the constructs: (a) HPV 16 E6 (SEQ ID NO:160); (b) HPV 18 E6 (SEQ ID NO:161); (c) HPV 16 E7 (SEQ ID NO:162); (d) HPV 18 E7 (SEQ ID NO:163) Representative Constructs: SEQ ID NO:164 (Representative HPV 16 E6-E7 Construct) SEQ ID NO:165 (Representative HPV 18 E6-E7 Construct) SEQ ID NO:166 (HPV 16 E6 – linker-HPV 18 E6–linker-HPV 16 E7–linker-HPV 18 E7)
169-172	EBV Constructs		Any of the following sequences, in any combination, could be used to create the constructs (a) EBV EBNA1 (SEQ ID NO:169); (b) EBV Truncated EBNA-1 (SEQ ID NO:170); (c) EBV gp350 (SEQ ID NO:171); (d) EBV LMP2 (SEQ ID NO:172). For example, a representative construct could comprise truncated EBNA-1 and LMP2.
174-175	HBV Constructs		Any of the following sequences could be used (in either orientation) to create the constructs: HBV Middle S Protein (SEQ ID NO: 174) and HBV X Protein (SEQ ID NO: 175). For example, a representative construct could comprise Middle S Protein - X protein.
176	TIGIT		SEQ ID NO:176
177	TEM8		SEQ ID NO:177
178	TEM1		SEQ ID NO:178
179	HER2 ECD+TM		SEQ ID NO:179
180	CEA		SEQ ID NO:180
181	TARP		SEQ ID NO:181
182	PROSTEIN		SEQ ID NO:182

183	PSMA		SEQ ID NO:183
184	BIRC4		SEQ ID NO:184
185	Mucin-1		SEQ ID NO:185
186	Mucin-1 Isoform		SEQ ID NO:186
187	CD40 Ligand		SEQ ID NO:187
188	WT-1		SEQ ID NO:188
189	WT-1 Truncated		SEQ ID NO:189
190	PRAME		SEQ ID NO:190
191	LAGE-1		SEQ ID NO:191
192	MAGE A3		SEQ ID NO:192
198	1A01_HLA-A/m	UniProtKB: P30443	SEQ ID NO:198
199	1A02	UniProtKB: P01892	SEQ ID NO:199
200	5T4	UniProtKB: Q13641	SEQ ID NO:200
201	ACRBP	UniProtKB: Q8NEB7	SEQ ID NO:201
202	AFP	UniProtKB: P02771	SEQ ID NO:202
203	AKAP4	UniProtKB: Q5JQC9	SEQ ID NO:203
204	alpha-actinin- 4/m	UniProtKB: B4DSX0	SEQ ID NO:204
205	alpha-actinin- 4/m	UniProtKB: B4E337	SEQ ID NO:205
206	alpha-actinin- 4/m	UniProtKB: O43707	SEQ ID NO:206
207	alpha-methylacyl-coenzyme A_racemase	UniProtKB: A0A024RE16	SEQ ID NO:207
208	alpha-methylacyl-coenzyme A_racemase	UniProtKB: A8KAC3	SEQ ID NO:208
209	ANDR	UniProtKB: P10275	SEQ ID NO:209
210	ART-4	UniProtKB: Q9ULX3	SEQ ID NO:210
211	ARTC1/m	UniProtKB: P52961	SEQ ID NO:211
212	AURKB	UniProtKB: Q96GD4	SEQ ID NO:212
213	B2MG	UniProtKB: P61769	SEQ ID NO:213
214	B3GN5	UniProtKB: Q9BYG0	SEQ ID NO:214
215	B4GN1	UniProtKB: Q00973	SEQ ID NO:215
216	B7H4	UniProtKB: Q7Z7D3	SEQ ID NO:216
217	BAGE-1	UniProtKB: Q13072	SEQ ID NO:217
218	BASI	UniProtKB: P35613	SEQ ID NO:218
219	BCL-2	UniProtKB: A9QXG9	SEQ ID NO:219
220	ber/abl	UniProtKB: A9UEZ4	SEQ ID NO:220
221	ber/abl	UniProtKB: A9UEZ7	SEQ ID NO:221
222	ber/abl	UniProtKB: A9UEZ8	SEQ ID NO:222
223	ber/abl	UniProtKB: A9UEZ9	SEQ ID NO:223
224	ber/abl	UniProtKB: A9UF00	SEQ ID NO:224

225	bcr/abl	UniProtKB: A9UF01	SEQ ID NO:225
226	bcr/abl	UniProtKB: A9UF03	SEQ ID NO:226
227	bcr/abl	UniProtKB: A9UF04	SEQ ID NO:227
228	bcr/abl	UniProtKB: A9UF05	SEQ ID NO:228
229	bcr/abl	UniProtKB: A9UF06	SEQ ID NO:229
230	bcr/abl	UniProtKB: A9UF08	SEQ ID NO:230
231	beta-catenin/m	UniProtKB: P35222	SEQ ID NO:231
232	beta-catenin/m	UniProtKB: Q8WYA6	SEQ ID NO:232
233	BING-4	UniProtKB: O15213	SEQ ID NO:233
234	BIRC7	UniProtKB: Q96CA5	SEQ ID NO:234
235	BRCA1/m	UniProtKB: A0A024R1V0	SEQ ID NO:235
236	BRCA1/m	UniProtKB: A0A024R1V7	SEQ ID NO:236
237	BRCA1/m	UniProtKB: A0A024R1Z8	SEQ ID NO:237
238	BRCA1/m	UniProtKB: A0A068BFX7	SEQ ID NO:238
239	BRCA1/m	UniProtKB: C6YB45	SEQ ID NO:239
240	BRCA1/m	UniProtKB: C6YB47	SEQ ID NO:240
241	BRCA1/m	UniProtKB: G3XAC3	SEQ ID NO:241
242	BY55	UniProtKB: Q95971	SEQ ID NO:242
243	CAMEL	UniProtKB: Q95987	SEQ ID NO:243
244	CASPA	UniProtKB: Q92851-4	SEQ ID NO:244
245	cathepsin_B	UniProtKB: A0A024R374	SEQ ID NO:245
246	cathepsin_B	UniProtKB: P07858	SEQ ID NO:246
247	cathepsin_L	UniProtKB: A0A024R276	SEQ ID NO:247
248	cathepsin_L	UniProtKB: P07711	SEQ ID NO:248
249	cathepsin_L	UniProtKB: Q9HBQ7	SEQ ID NO:249
250	CD1A	UniProtKB: P06126	SEQ ID NO:250
251	CD1B	UniProtKB: P29016	SEQ ID NO:251
252	CD1C	UniProtKB: P29017	SEQ ID NO:252
253	CD1D	UniProtKB: P15813	SEQ ID NO:253
254	CD1E	UniProtKB: P15812	SEQ ID NO:254
255	CD20	UniProtKB: P11836	SEQ ID NO:255
256	CD22	UniProtKB: O60926	SEQ ID NO:256
257	CD22	UniProtKB: P20273	SEQ ID NO:257
258	CD22	UniProtKB: Q0EAF5	SEQ ID NO:258
259	CD276	UniProtKB: Q5ZPR3	SEQ ID NO:259
260	CD33	UniProtKB: B4DF51	SEQ ID NO:260
261	CD33	UniProtKB: P20138	SEQ ID NO:261
262	CD33	UniProtKB: Q546G0	SEQ ID NO:262

263	CD3E	UniProtKB: P07766	SEQ ID NO:263
264	CD3Z	UniProtKB: P20963	SEQ ID NO:264
265	CD44_Isoform_1	UniProtKB: P16070	SEQ ID NO:265
266	CD44_Isoform_6	UniProtKB: P16070-6	SEQ ID NO:266
267	CD4	UniProtKB: P01730	SEQ ID NO:267
268	CD52	UniProtKB: P31358	SEQ ID NO:268
269	CD52	UniProtKB: Q6IBD0	SEQ ID NO:269
270	CD52	UniProtKB: V9HWN9	SEQ ID NO:270
271	CD55	UniProtKB: B1AP15	SEQ ID NO:271
272	CD55	UniProtKB: D3DT85	SEQ ID NO:272
273	CD55	UniProtKB: D3DT86	SEQ ID NO:273
274	CD55	UniProtKB: P08174	SEQ ID NO:274
275	CD56	UniProtKB: P13591	SEQ ID NO:275
276	CD80	UniProtKB: A0N0P2	SEQ ID NO:276
277	CD80	UniProtKB: P33681	SEQ ID NO:277
278	CD86	UniProtKB: P42081	SEQ ID NO:278
279	CD8A	UniProtKB: P01732	SEQ ID NO:279
280	CDC27/m	UniProtKB: G5EA36	SEQ ID NO:280
281	CDC27/m	UniProtKB: P30260	SEQ ID NO:281
282	CDE30	UniProtKB: P28908	SEQ ID NO:282
283	CDK4/m	UniProtKB: A0A024RBB6	SEQ ID NO:283
284	CDK4/m	UniProtKB: P11802	SEQ ID NO:284
285	CDK4/m	UniProtKB: Q6LC83	SEQ ID NO:285
286	CDK4/m	UniProtKB: Q96BE9	SEQ ID NO:286
287	CDKN2A/m	UniProtKB: D1LYX3	SEQ ID NO:287
288	CDKN2A/m	UniProtKB: G3XAG3	SEQ ID NO:288
289	CDKN2A/m	UniProtKB: K7PML8	SEQ ID NO:289
290	CDKN2A/m	UniProtKB: L8E941	SEQ ID NO:290
291	CDKN2A/m	UniProtKB: Q8N726	SEQ ID NO:291
292	CEA	RefSeq: NP_004354	SEQ ID NO:292
293	CEAM6	UniProtKB: P40199	SEQ ID NO:293
294	CH3L2	UniProtKB: Q15782	SEQ ID NO:294
295	CLCA2	UniProtKB: Q9UQC9	SEQ ID NO:295
296	CML28	UniProtKB: Q9NQT4	SEQ ID NO:296
297	CML66	UniProtKB: Q96RS6	SEQ ID NO:297
298	COA-1/m	UniProtKB: Q5T124	SEQ ID NO:298
299	coactosin-like_protein	UniProtKB: Q14019	SEQ ID NO:299
300	collagen_XXIII	UniProtKB: L8EAS4	SEQ ID NO:300

301	collagen_XXIII	UniProtKB: Q86Y22	SEQ ID NO:301
302	COX-2	UniProtKB: Q6ZYK7	SEQ ID NO:302
303	CP1B1	UniProtKB: Q16678	SEQ ID NO:303
304	CSAG2	UniProtKB: Q9Y5P2-2	SEQ ID NO:304
305	CSAG2	UniProtKB: Q9Y5P2	SEQ ID NO:305
306	CT45A1	UniProtKB: Q5HYN5	SEQ ID NO:306
307	CT55	UniProtKB: Q8WUE5	SEQ ID NO:307
308	CT-9/BRD6	UniProtKB: Q58F21	SEQ ID NO:308
309	CTAG2_Isoform_LAGE-1A	UniProtKB: O75638-2	SEQ ID NO:309
310	CTAG2_Isoform_LAGE-1B	UniProtKB: O75638	SEQ ID NO:310
311	CTCFL	UniProtKB: Q8NI51	SEQ ID NO:311
312	Cten	UniProtKB: Q8IZW8	SEQ ID NO:312
313	cyclin_B1	UniProtKB: P14635	SEQ ID NO:313
314	cyclin_D1	UniProtKB: P24385	SEQ ID NO:314
315	cyp-B	UniProtKB: P23284	SEQ ID NO:315
316	DAM-10	UniProtKB: P43366	SEQ ID NO:316
317	DEP1A	UniProtKB: Q5TB30	SEQ ID NO:317
318	E7	UniProtKB: P03129	SEQ ID NO:318
319	E7	UniProtKB: P06788	SEQ ID NO:319
320	E7	UniProtKB: P17387	SEQ ID NO:320
321	E7	UniProtKB: P06429	SEQ ID NO:321
322	E7	UniProtKB: P27230	SEQ ID NO:322
323	E7	UniProtKB: P24837	SEQ ID NO:323
324	E7	UniProtKB: P21736	SEQ ID NO:324
325	E7	UniProtKB: P26558	SEQ ID NO:325
326	E7	UniProtKB: P36831	SEQ ID NO:326
327	E7	UniProtKB: P36833	SEQ ID NO:327
328	E7	UniProtKB: Q9QCZ1	SEQ ID NO:328
329	E7	UniProtKB: Q81965	SEQ ID NO:329
330	E7	UniProtKB: Q80956	SEQ ID NO:330
331	EF1A2	UniProtKB: Q05639	SEQ ID NO:331
332	EFTUD2/m	UniProtKB: Q15029	SEQ ID NO:332
333	EGFR	UniProtKB: A0A0B4J1Y5	SEQ ID NO:333
334	EGFR	UniProtKB: E7BSV0	SEQ ID NO:334
335	EGFR	UniProtKB: L0R6G1	SEQ ID NO:335
336	EGFR	UniProtKB: P00533-2	SEQ ID NO:336
337	EGFR	UniProtKB: P00533	SEQ ID NO:337
338	EGFR	UniProtKB: Q14717	SEQ ID NO:338

339	EGFR	UniProtKB: Q504U8	SEQ ID NO:339
340	EGFR	UniProtKB: Q8NDU8	SEQ ID NO:340
341	EGLN3	UniProtKB: Q9H6Z9	SEQ ID NO:341
342	ELF2/m	UniProtKB: B7Z720	SEQ ID NO:342
343	EMMPRIN	UniProtKB: Q54A51	SEQ ID NO:343
344	EpCam	UniProtKB: P16422	SEQ ID NO:344
345	EphA2	UniProtKB: P29317	SEQ ID NO:345
346	EphA3	UniProtKB: P29320	SEQ ID NO:346
347	EphA3	UniProtKB: Q6P4R6	SEQ ID NO:347
348	ErbB3	UniProtKB: B3KWW5	SEQ ID NO:348
349	ErbB3	UniProtKB: B4DGQ7	SEQ ID NO:349
350	ERBB4	UniProtKB: Q15303	SEQ ID NO:350
351	ERG	UniProtKB: P11308	SEQ ID NO:351
352	ETV6	UniProtKB: P41212	SEQ ID NO:352
353	EWS	UniProtKB: Q01844	SEQ ID NO:353
354	EZH2	UniProtKB: F2YMM1	SEQ ID NO:354
355	EZH2	UniProtKB: G3XAL2	SEQ ID NO:355
356	EZH2	UniProtKB: L0R855	SEQ ID NO:356
357	EZH2	UniProtKB: Q15910	SEQ ID NO:357
358	EZH2	UniProtKB: S4S3R8	SEQ ID NO:358
359	FABP7	UniProtKB: O15540	SEQ ID NO:359
360	FCGR3A_Version_1	UniProtKB: P08637	SEQ ID NO:360
361	FCGR3A_Version_2	CCDS: CCDS1232.1	SEQ ID NO:361
362	FGF5	UniProtKB: P12034	SEQ ID NO:362
363	FGF5	UniProtKB: Q60518	SEQ ID NO:363
364	FGFR2	UniProtKB: P21802	SEQ ID NO:364
365	fibronectin	UniProtKB: A0A024R5I6	SEQ ID NO:365
366	fibronectin	UniProtKB: A0A024RB01	SEQ ID NO:366
367	fibronectin	UniProtKB: A0A024RDT9	SEQ ID NO:367
368	fibronectin	UniProtKB: A0A024RDV5	SEQ ID NO:368
369	fibronectin	UniProtKB: A6NH44	SEQ ID NO:369
370	fibronectin	UniProtKB: A8K6A5	SEQ ID NO:370
371	fibronectin	UniProtKB: B2R627	SEQ ID NO:371
372	fibronectin	UniProtKB: B3KXM5	SEQ ID NO:372
373	fibronectin	UniProtKB: B4DIC5	SEQ ID NO:373
374	fibronectin	UniProtKB: B4DN21	SEQ ID NO:374
375	fibronectin	UniProtKB: B4DS98	SEQ ID NO:375
376	fibronectin	UniProtKB: B4DTH2	SEQ ID NO:376

377	fibronectin	UniProtKB: B4DTK1	SEQ ID NO:377
378	fibronectin	UniProtKB: B4DU16	SEQ ID NO:378
379	fibronectin	UniProtKB: B7Z3W5	SEQ ID NO:379
380	fibronectin	UniProtKB: B7Z939	SEQ ID NO:380
381	fibronectin	UniProtKB: G5E9X3	SEQ ID NO:381
382	fibronectin	UniProtKB: Q9H382	SEQ ID NO:382
383	FOS	UniProtKB: P01100	SEQ ID NO:383
384	FOXP3	UniProtKB: Q9BZS1	SEQ ID NO:384
385	FUT1	UniProtKB: P19526	SEQ ID NO:385
386	G250	UniProtKB: Q16790	SEQ ID NO:386
387	GAGE-1	Genbank: AAA82744	SEQ ID NO:387
388	GAGE-2	UniProtKB: Q6NT46	SEQ ID NO:388
389	GAGE-3	UniProtKB: Q13067	SEQ ID NO:389
390	GAGE-4	UniProtKB: Q13068	SEQ ID NO:390
391	GAGE-5	UniProtKB: Q13069	SEQ ID NO:391
392	GAGE-6	UniProtKB: Q13070	SEQ ID NO:392
393	GAGE7b	UniProtKB: O76087	SEQ ID NO:393
394	GAGE-8 (GAGE-2D)	UniProtKB: Q9UEU5	SEQ ID NO:394
395	GASR	UniProtKB: P32239	SEQ ID NO:395
396	GnT-V	UniProtKB: Q09328	SEQ ID NO:396
397	GPC3	UniProtKB: I6QJG3	SEQ ID NO:397
398	GPC3	UniProtKB: P51654	SEQ ID NO:398
399	GPC3	UniProtKB: Q8IYG2	SEQ ID NO:399
400	GPNMB/m	UniProtKB: A0A024RA55	SEQ ID NO:400
401	GPNMB/m	UniProtKB: Q14956	SEQ ID NO:401
402	GPNMB/m	UniProtKB: Q8IXJ5	SEQ ID NO:402
403	GPNMB/m	UniProtKB: Q96F58	SEQ ID NO:403
404	GRM3	UniProtKB: Q14832	SEQ ID NO:404
405	HAGE	UniProtKB: Q9NXZ2	SEQ ID NO:405
406	hepsin	UniProtKB: B2ZDQ2	SEQ ID NO:406
407	hepsin	UniProtKB: P05981	SEQ ID NO:407
408	Her2/neu	UniProtKB: B4DTR1	SEQ ID NO:408
409	Her2/neu	UniProtKB: L8E8G2	SEQ ID NO:409
410	Her2/neu	UniProtKB: P04626	SEQ ID NO:410
411	Her2/neu	UniProtKB: Q9UK79	SEQ ID NO:411
412	HLA-A2/m	UniProtKB: Q95387	SEQ ID NO:412
413	HLA-A2/m	UniProtKB: Q9MYF8	SEQ ID NO:413
414	homeobox_NKX3.1	UniProtKB: Q99801	SEQ ID NO:414

415	HOM-TES-85	UniProtKB: B2RBQ6	SEQ ID NO:415
416	HOM-TES-85	UniProtKB: Q9P127	SEQ ID NO:416
417	HPG1	Pubmed: 12543784	SEQ ID NO:417
418	HS71A	UniProtKB: P0DMV8	SEQ ID NO:418
419	HS71B	UniProtKB: P0DMV9	SEQ ID NO:419
420	HST-2	UniProtKB: P10767	SEQ ID NO:420
421	hTERT	UniProtKB: Q94807	SEQ ID NO:421
422	iCE	UniProtKB: O00748	SEQ ID NO:422
423	IF2B3	UniProtKB: O00425	SEQ ID NO:423
424	IL-13Ra2	UniProtKB: Q14627	SEQ ID NO:424
425	IL2-RA	UniProtKB: P01589	SEQ ID NO:425
426	IL2-RB	UniProtKB: P14784	SEQ ID NO:426
427	IL2-RG	UniProtKB: P31785	SEQ ID NO:427
428	IMP3	UniProtKB: Q9NV31	SEQ ID NO:428
429	ITA5	UniProtKB: P08648	SEQ ID NO:429
430	ITB1	UniProtKB: P05556	SEQ ID NO:430
431	ITB6	UniProtKB: P18564	SEQ ID NO:431
432	kallikrein-2	UniProtKB: A0A024R4J4	SEQ ID NO:432
433	kallikrein-2	UniProtKB: A0A024R4N3	SEQ ID NO:433
434	kallikrein-2	UniProtKB: B0AZU9	SEQ ID NO:434
435	kallikrein-2	UniProtKB: B4DU77	SEQ ID NO:435
436	kallikrein-2	UniProtKB: P20151	SEQ ID NO:436
437	kallikrein-2	UniProtKB: Q6T774	SEQ ID NO:437
438	kallikrein-2	UniProtKB: Q6T775	SEQ ID NO:438
439	kallikrein-4	UniProtKB: A0A0C4DFQ5	SEQ ID NO:439
440	kallikrein-4	UniProtKB: Q5BQA0	SEQ ID NO:440
441	kallikrein-4	UniProtKB: Q96PT0	SEQ ID NO:441
442	kallikrein-4	UniProtKB: Q96PT1	SEQ ID NO:442
443	kallikrein-4	UniProtKB: Q9Y5K2	SEQ ID NO:443
444	K120A	UniProtKB: Q95235	SEQ ID NO:444
445	K1AA0205	UniProtKB: Q92604	SEQ ID NO:445
446	KIF2C	UniProtKB: Q99661	SEQ ID NO:446
447	KK-LC-1	UniProtKB: Q5H943	SEQ ID NO:447
448	LDLR	UniProtKB: P01130	SEQ ID NO:448
449	LGMN	UniProtKB: Q99538	SEQ ID NO:449
450	LIRB2	UniProtKB: Q8N423	SEQ ID NO:450
451	LY6K	UniProtKB: Q17RY6	SEQ ID NO:451
452	MAGA5	UniProtKB: P43359	SEQ ID NO:452

453	MAGA8	UniProtKB: P43361	SEQ ID NO:453
454	MAGAB	UniProtKB: P43364	SEQ ID NO:454
455	MAGE-A10	UniProtKB: A0A024RC14	SEQ ID NO:455
456	MAGE-A12	UniProtKB: P43365	SEQ ID NO:456
457	MAGE-A1	UniProtKB: P43355	SEQ ID NO:457
458	MAGE-A2	UniProtKB: P43356	SEQ ID NO:458
459	MAGE-A3	UniProtKB: P43357	SEQ ID NO:459
460	MAGE-A4	UniProtKB: A0A024RC12	SEQ ID NO:460
461	MAGE-A4	UniProtKB: P43358	SEQ ID NO:461
462	MAGE-A4	UniProtKB: Q1RN33	SEQ ID NO:462
463	MAGE-A6	UniProtKB: A8K072	SEQ ID NO:463
464	MAGE-A6	UniProtKB: P43360	SEQ ID NO:464
465	MAGE-A6	UniProtKB: Q6FHI5	SEQ ID NO:465
466	MAGE-A9	UniProtKB: P43362	SEQ ID NO:466
467	MAGE-B10	UniProtKB: Q96LZ2	SEQ ID NO:467
468	MAGE-B16	UniProtKB: A2A368	SEQ ID NO:468
469	MAGE-B17	UniProtKB: A8MXT2	SEQ ID NO:469
470	MAGE-_B1	UniProtKB: Q96TG1	SEQ ID NO:470
471	MAGE-B2	UniProtKB: O15479	SEQ ID NO:471
472	MAGE-B3	UniProtKB: O15480	SEQ ID NO:472
473	MAGE-B4	UniProtKB: O15481	SEQ ID NO:473
474	MAGE-B5	UniProtKB: Q9BZ81	SEQ ID NO:474
475	MAGE-B6	UniProtKB: Q8N7X4	SEQ ID NO:475
476	MAGE-C1	UniProtKB: O60732	SEQ ID NO:476
477	MAGE-C2	UniProtKB: Q9UBF1	SEQ ID NO:477
478	MAGE-C3	UniProtKB: Q8TD91	SEQ ID NO:478
479	MAGE-D1	UniProtKB: Q9Y5V3	SEQ ID NO:479
480	MAGE-D2	UniProtKB: Q9UNF1	SEQ ID NO:480
481	MAGE-D4	UniProtKB: Q96JG8	SEQ ID NO:481
482	MAGE-_E1	UniProtKB: Q61AI7	SEQ ID NO:482
483	MAGE-E1 (MAGE1)	UniProtKB: Q9HC15	SEQ ID NO:483
484	MAGE-E2	UniProtKB: Q8TD90	SEQ ID NO:484
485	MAGE-F1	UniProtKB: Q9HAY2	SEQ ID NO:485
486	MAGE-H1	UniProtKB: Q9H213	SEQ ID NO:486
487	MAGEL2	UniProtKB: Q9UJ55	SEQ ID NO:487
488	mammaglobin_A	UniProtKB: Q13296	SEQ ID NO:488
489	mammaglobin_A	UniProtKB: Q6NX70	SEQ ID NO:489
490	MART-1/melan-A	UniProtKB: Q16655	SEQ ID NO:490

491	MART-2	UniProtKB: Q5VITY9	SEQ ID NO:491
492	MC1_R	UniProtKB: Q01726	SEQ ID NO:492
493	MC1_R	UniProtKB: Q1JUL4	SEQ ID NO:493
494	MC1_R	UniProtKB: Q1JUL6	SEQ ID NO:494
495	MC1_R	UniProtKB: Q1JUL8	SEQ ID NO:495
496	MC1_R	UniProtKB: Q1JUL9	SEQ ID NO:496
497	MC1_R	UniProtKB: Q1JUM0	SEQ ID NO:497
498	MC1_R	UniProtKB: Q1JUM2	SEQ ID NO:498
499	MC1_R	UniProtKB: Q1JUM3	SEQ ID NO:499
500	MC1_R	UniProtKB: Q1JUM4	SEQ ID NO:500
501	MC1_R	UniProtKB: Q1JUM5	SEQ ID NO:501
502	MC1_R	UniProtKB: Q6UR92	SEQ ID NO:502
503	MC1_R	UniProtKB: Q6UR94	SEQ ID NO:503
504	MC1_R	UniProtKB: Q6UR95	SEQ ID NO:504
505	MC1_R	UniProtKB: Q6UR96	SEQ ID NO:505
506	MC1_R	UniProtKB: Q6UR97	SEQ ID NO:506
507	MC1_R	UniProtKB: Q6UR98	SEQ ID NO:507
508	MC1_R	UniProtKB: Q6UR99	SEQ ID NO:508
509	MC1_R	UniProtKB: Q6URA0	SEQ ID NO:509
510	MC1_R	UniProtKB: Q86YW1	SEQ ID NO:510
511	MC1_R	UniProtKB: V9Q5S2	SEQ ID NO:511
512	MC1_R	UniProtKB: V9Q671	SEQ ID NO:512
513	MC1_R	UniProtKB: V9Q783	SEQ ID NO:513
514	MC1_R	UniProtKB: V9Q7F1	SEQ ID NO:514
515	MC1_R	UniProtKB: V9Q8N1	SEQ ID NO:515
516	MC1_R	UniProtKB: V9Q977	SEQ ID NO:516
517	MC1_R	UniProtKB: V9Q9P5	SEQ ID NO:517
518	MC1_R	UniProtKB: V9Q9R8	SEQ ID NO:518
519	MC1_R	UniProtKB: V9QAE0	SEQ ID NO:519
520	MC1_R	UniProtKB: V9QAR2	SEQ ID NO:520
521	MC1_R	UniProtKB: V9QAW3	SEQ ID NO:521
522	MC1_R	UniProtKB: V9QB02	SEQ ID NO:522
523	MC1_R	UniProtKB: V9QB58	SEQ ID NO:523
524	MC1_R	UniProtKB: V9QBY6	SEQ ID NO:524
525	MC1_R	UniProtKB: V9QC17	SEQ ID NO:525
526	MC1_R	UniProtKB: V9QC66	SEQ ID NO:526
527	MC1_R	UniProtKB: V9QCQ4	SEQ ID NO:527
528	MC1_R	UniProtKB: V9QDF4	SEQ ID NO:528

529	MC1_R	UniProtKB: V9QDN7	SEQ ID NO:529
530	MC1_R	UniProtKB: V9QDQ6	SEQ ID NO:530
531	mesothelin	UniProtKB: Q13421	SEQ ID NO:531
532	MTF	UniProtKB: O75030-8	SEQ ID NO:532
533	MTF	UniProtKB: O75030-9	SEQ ID NO:533
534	MTF	UniProtKB: O75030	SEQ ID NO:534
535	MMP1_1	UniProtKB: B3KQS8	SEQ ID NO:535
536	MMP7	UniProtKB: P09237	SEQ ID NO:536
537	MUC-1	Genbank: AAA60019	SEQ ID NO:537
538	MUM-1/m	RefSeq: NP_116242	SEQ ID NO:538
539	MUM-2/m	UniProtKB: Q9Y5R8	SEQ ID NO:539
540	MYO1A	UniProtKB: Q9UBC5	SEQ ID NO:540
541	MYO1B	UniProtKB: O43795	SEQ ID NO:541
542	MYO1C	UniProtKB: O00159	SEQ ID NO:542
543	MYO1D	UniProtKB: O94832	SEQ ID NO:543
544	MYO1E	UniProtKB: Q12965	SEQ ID NO:544
545	MYO1F	UniProtKB: O00160	SEQ ID NO:545
546	MYO1G	UniProtKB: B0I1T2	SEQ ID NO:546
547	MYO1H	RefSeq: NP_001094891	SEQ ID NO:547
548	NA17	UniProtKB: Q3V5L5	SEQ ID NO:548
549	NA88-A	Pubmed: 10790436	SEQ ID NO:549
550	Neo-PAP	UniProtKB: Q9BWT3	SEQ ID NO:550
551	NFYC/m	UniProtKB: Q13952	SEQ ID NO:551
552	NGEP	UniProtKB: Q6IWH7	SEQ ID NO:552
553	NPM	UniProtKB: P06748	SEQ ID NO:553
554	NRCAM	UniProtKB: Q92823	SEQ ID NO:554
555	NSE	UniProtKB: P09104	SEQ ID NO:555
556	NUF2	UniProtKB: Q9BZD4	SEQ ID NO:556
557	NY-ESO-1	UniProtKB: P78358	SEQ ID NO:557
558	OAI	UniProtKB: P51810	SEQ ID NO:558
559	OGT	UniProtKB: O15294	SEQ ID NO:559
560	OS-9	UniProtKB: B4DH11	SEQ ID NO:560
561	OS-9	UniProtKB: B4E321	SEQ ID NO:561
562	OS-9	UniProtKB: B7Z8E7	SEQ ID NO:562
563	OS-9	UniProtKB: Q13438	SEQ ID NO:563
564	osteocalcin	UniProtKB: P02818	SEQ ID NO:564
565	osteopontin	UniProtKB: A0A024RDE2	SEQ ID NO:565
566	osteopontin	UniProtKB: A0A024RDE6	SEQ ID NO:566

567	osteopontin	UniProtKB: A0A024RDJ0	SEQ ID NO:567
568	osteopontin	UniProtKB: B7Z351	SEQ ID NO:568
569	osteopontin	UniProtKB: F2YQ21	SEQ ID NO:569
570	osteopontin	UniProtKB: P10451	SEQ ID NO:570
571	p53	UniProtKB: P04637	SEQ ID NO:571
572	PAGE-4	UniProtKB: O60829	SEQ ID NO:572
573	PAI-1	UniProtKB: P05121	SEQ ID NO:573
574	PAI-2	UniProtKB: P05120	SEQ ID NO:574
575	PAP	UniProtKB: Q06141	SEQ ID NO:575
576	PAP	UniProtKB: Q53S56	SEQ ID NO:576
577	PATE	UniProtKB: Q8WXA2	SEQ ID NO:577
578	PAX3	UniProtKB: P23760	SEQ ID NO:578
579	PAX5	UniProtKB: Q02548	SEQ ID NO:579
580	PD1L1	UniProtKB: Q9NZQ7	SEQ ID NO:580
581	PDCD1	UniProtKB: Q15116	SEQ ID NO:581
582	PDEF	UniProtKB: O95238	SEQ ID NO:582
583	PECA1	UniProtKB: P16284	SEQ ID NO:583
584	PGCB	UniProtKB: Q96GW7	SEQ ID NO:584
585	PGFRB	UniProtKB: P09619	SEQ ID NO:585
586	Pim-1_Kinase	UniProtKB: A0A024RD25	SEQ ID NO:586
587	Pin-1	UniProtKB: O15428	SEQ ID NO:587
588	Pin-1	UniProtKB: Q13526	SEQ ID NO:588
589	Pin-1	UniProtKB: Q49AR7	SEQ ID NO:589
590	PLAC1	UniProtKB: Q9HBJ0	SEQ ID NO:590
591	PMEL	UniProtKB: P40967	SEQ ID NO:591
592	PML	UniProtKB: P29590	SEQ ID NO:592
593	POTEF	UniProtKB: A5A3E0	SEQ ID NO:593
594	POTE	UniProtKB: Q86YR6	SEQ ID NO:594
595	PRAME	UniProtKB: A0A024R1E6	SEQ ID NO:595
596	PRAME	UniProtKB: P78395	SEQ ID NO:596
597	PRDX5/m	UniProtKB: P30044	SEQ ID NO:597
598	PRM2	UniProtKB: P04554	SEQ ID NO:598
599	prostein	UniProtKB: Q96JT2	SEQ ID NO:599
600	proteinase-3	UniProtKB: D6CHE9	SEQ ID NO:600
601	proteinase-3	UniProtKB: P24158	SEQ ID NO:601
602	PSA	UniProtKB: P55786	SEQ ID NO:602
603	PSB9	UniProtKB: P28065	SEQ ID NO:603
604	PSCA	UniProtKB: D3DWI6	SEQ ID NO:604

605	PSCA	UniProtKB: O43653	SEQ ID NO:605
606	PSGR	UniProtKB: Q9H255	SEQ ID NO:606
607	PSM	UniProtKB: Q04609	SEQ ID NO:607
608	PTPRC	RefSeq: NP_002829	SEQ ID NO:608
609	RAB8A	UniProtKB: P61006	SEQ ID NO:609
610	RAGE-1	UniProtKB: Q9UQ07	SEQ ID NO:610
611	RARA	UniProtKB: P10276	SEQ ID NO:611
612	RASH	UniProtKB: P01112	SEQ ID NO:612
613	RASK	UniProtKB: P01116	SEQ ID NO:613
614	RASN	UniProtKB: P01111	SEQ ID NO:614
615	RGS5	UniProtKB: O15539	SEQ ID NO:615
616	RHAMM/CD168	UniProtKB: O75330	SEQ ID NO:616
617	RHOC	UniProtKB: P08134	SEQ ID NO:617
618	RSSA	UniProtKB: P08865	SEQ ID NO:618
619	RU1	UniProtKB: Q9UHI3	SEQ ID NO:619
620	RU2	UniProtKB: Q9UHG0	SEQ ID NO:620
621	RUNX1	UniProtKB: Q01196	SEQ ID NO:621
622	S-100	UniProtKB: V9HW39	SEQ ID NO:622
623	SAGE	UniProtKB: Q9NXX1	SEQ ID NO:623
624	SART-1	UniProtKB: O43290	SEQ ID NO:624
625	SART-2	UniProtKB: Q9UL01	SEQ ID NO:625
626	SART-3	UniProtKB: Q15020	SEQ ID NO:626
627	SEPR	UniProtKB: Q12884	SEQ ID NO:627
628	SIA7F	UniProtKB: Q969X2	SEQ ID NO:628
629	SIA8A	UniProtKB: Q92185	SEQ ID NO:629
630	SIAT9	UniProtKB: Q9UNP4	SEQ ID NO:630
631	SIRT2/m	UniProtKB: A0A024R0G8	SEQ ID NO:631
632	SIRT2/m	UniProtKB: Q8IXJ6	SEQ ID NO:632
633	SOX10	UniProtKB: P56693	SEQ ID NO:633
634	SPI7	UniProtKB: Q15506	SEQ ID NO:634
635	SPNXA	UniProtKB: Q9NS26	SEQ ID NO:635
636	SPXN3	UniProtKB: Q5MJ09	SEQ ID NO:636
637	SSX-1	UniProtKB: Q16384	SEQ ID NO:637
638	SSX-2	UniProtKB: Q16385	SEQ ID NO:638
639	SSX3	UniProtKB: Q99909	SEQ ID NO:639
640	SSX-4	UniProtKB: O60224	SEQ ID NO:640
641	ST1A1	UniProtKB: P50225	SEQ ID NO:641
642	STAG2	UniProtKB: Q8N3U4-2	SEQ ID NO:642

643	STAMP-1	UniProtKB: Q8NFT2	SEQ ID NO:643
644	STEAP-1	UniProtKB: A0A024RA63	SEQ ID NO:644
645	STEAP-1	UniProtKB: Q9UHE8	SEQ ID NO:645
646	Survivin-2B	UniProtKB: O15392-2	SEQ ID NO:646
647	survivin	UniProtKB: O15392	SEQ ID NO:647
648	SYCP1	UniProtKB: A0A024R0I2	SEQ ID NO:648
649	SYCP1	UniProtKB: B7ZLS9	SEQ ID NO:649
650	SYCP1	UniProtKB: Q15431	SEQ ID NO:650
651	SYCP1	UniProtKB: Q3MHC4	SEQ ID NO:651
652	SYT-SSX-1	UniProtKB: A4PIV7	SEQ ID NO:652
653	SYT-SSX-1	UniProtKB: A4PIV8	SEQ ID NO:653
654	SYT-SSX-2	UniProtKB: A4PIV9	SEQ ID NO:654
655	SYT-SSX-2	UniProtKB: A4PIW0	SEQ ID NO:655
656	TARP	UniProtKB: Q0VGM3	SEQ ID NO:656
657	TCRg	UniProtKB: A2JGV3	SEQ ID NO:657
658	TF2AA	UniProtKB: P52655	SEQ ID NO:658
659	TGFR2	UniProtKB: P37173	SEQ ID NO:659
660	TGM-4	UniProtKB: B2R7D1	SEQ ID NO:660
661	TIE2	UniProtKB: Q02763	SEQ ID NO:661
662	TKTL1	UniProtKB: P51854	SEQ ID NO:662
663	TPI/m	UniProtKB: P60174	SEQ ID NO:663
664	TRGV11	UniProtKB: Q99601	SEQ ID NO:664
665	TRGV9	UniProtKB: A4D1X2	SEQ ID NO:665
666	TRGV9	UniProtKB: Q99603	SEQ ID NO:666
667	TRGV9	UniProtKB: Q99604	SEQ ID NO:667
668	TRPC1	UniProtKB: P48995	SEQ ID NO:668
669	TRP-p8	UniProtKB: Q7Z2W7	SEQ ID NO:669
670	TSG10	UniProtKB: Q9BZW7	SEQ ID NO:670
671	TSPY1	UniProtKB: Q01534	SEQ ID NO:671
672	TVC (TRGV3)	Genbank: M13231.1	SEQ ID NO:672
673	TX101	UniProtKB: Q9BY14-2	SEQ ID NO:673
674	tyrosinase	UniProtKB: A0A024DBG7	SEQ ID NO:674
675	tyrosinase	UniProtKB: L8B082	SEQ ID NO:675
676	tyrosinase	UniProtKB: L8B086	SEQ ID NO:676
677	tyrosinase	UniProtKB: L8B0B9	SEQ ID NO:677
678	tyrosinase	UniProtKB: O75767	SEQ ID NO:678
679	tyrosinase	UniProtKB: P14679	SEQ ID NO:679
680	tyrosinase	UniProtKB: U3M8N0	SEQ ID NO:680

681	tyrosinase	UniProtKB: U3M9D5	SEQ ID NO:681
682	tyrosinase	UniProtKB: U3M9J2	SEQ ID NO:682
683	TYRP1	UniProtKB: P17643	SEQ ID NO:683
684	TYRP2	UniProtKB: P40126	SEQ ID NO:684
685	UPA	UniProtKB: Q96NZ9	SEQ ID NO:685
686	VEGFR1	UniProtKB: B5A924	SEQ ID NO:686
687	WT1	UniProtKB: A0A0H5AUY0	SEQ ID NO:687
688	WT1	UniProtKB: P19544	SEQ ID NO:688
689	WT1	UniProtKB: Q06250	SEQ ID NO:689
690	XAGE1	UniProtKB: Q9HD64	SEQ ID NO:690
691	IL-10	UniProtKB: P22301	SEQ ID NO:691
692	IL-5	UniProtKB: P05113	SEQ ID NO:692
693	M-CSF	UniProtKB: P09603	SEQ ID NO:693
694	TGFbeta1	UniProtKB: P01137	SEQ ID NO:694
695	Caspase_8	UniProtKB: Q14790	SEQ ID NO:695
696	SERPINB5	UniProtKB: P36952	SEQ ID NO:696
697	calreticulin	UniProtKB: B4DHR1	SEQ ID NO:697
698	calreticulin	UniProtKB: B4E2Y9	SEQ ID NO:698
699	calreticulin	UniProtKB: P27797	SEQ ID NO:699
700	calreticulin	UniProtKB: Q96L12	SEQ ID NO:700
701	N-myc	UniProtKB: P04198	SEQ ID NO:701

[0150] Additionally, the antigens (including the sequences/fragments/epitopes shown in Column 4) described in Table 1 can be cloned into the LAMP Constructs described herein either individually, or in combination with one another. For example, the names pp65, gB, IE1, MTRII, US28, IGFBP2, IL10, UL144, UL141, US11, HOS, IE2, TERT, Survivin, Tetanus, NY-ESO-1, HER2, HER3, HVEM, HPV16E6, HPV18E6, HPV16E7, HPV18E7, EBNA1, EBNA trunc, gp350, LMP2, GCP3, Middle S, X Protein, TIGIT, TEM8, TEM1, HER2 ECD+TM, CEA, TARP, PROSTEIN, PSMA, BIRC4, MUCIN-1, MUCIN-1 iso, CD40-L, WT-1, WT-1 trunc., PRAME, LAGE-1, and/or MAGE A3 refer to the proteins described in Table 1 and are explicitly intended to refer generically not only to the full-length sequences shown in Column 1 of Table 1, but also, and preferably, the sequences/fragments/epitopes as described in Figures 19 and 20 and in the fourth Column of Table 1. Thus, each one of the sequences shown in Column 1 of Table 1, including the epitopes/fragments described in Column 4 of Table 1 can be used to generate a LAMP Construct. To illustrate different possible combinations, but in no way limiting the disclosure, the combinations of antigens (including the sequences shown in Column 1 of Table 1 and/or the sequences/fragments/epitopes described in Column 4 of Table 1) can be cloned into the LAMP Constructs as follows: (a) pp65 and at least one of gB, IE1, MTRII, US28, IGFBP2, IL10, UL144, UL141, US11, HOS, IE2, TERT, Survivin, Tetanus, NY-ESO-1, HER2, HER3, HVEM, HPV16E6, HPV18E6, HPV16E7, HPV18E7, EBNA1, EBNA trunc, gp350, LMP2, GCP3, Middle S, X Protein, TIGIT, TEM8, TEM1, HER2 ECD+TM, CEA, TARP, PROSTEIN, PSMA, BIRC4, MUCIN-1, MUCIN-1 iso, CD40-L, WT-1, WT-1 trunc., PRAME, LAGE-1, and/or MAGE A3; (b) gB and at least one of pp65, IE1, MTRII, US28, IGFBP2, IL10, UL144, UL141, US11, HOS, IE2, TERT, Survivin, Tetanus, NY-ESO-1, HER2, HER3, HVEM, HPV16E6, HPV18E6, HPV16E7, HPV18E7, EBNA1, EBNA trunc, gp350, LMP2, GCP3, Middle S, X Protein, TIGIT, TEM8, TEM1, HER2 ECD+TM, CEA, TARP, PROSTEIN, PSMA, BIRC4, MUCIN-1, MUCIN-1 iso, CD40-L, WT-1, WT-1 trunc., PRAME, LAGE-1, and/or MAGE A3; (c) IE1 and at least one of pp65, gB, MTRII, US28, IGFBP2, IL10, UL144, UL141, US11, HOS, IE2, TERT, Survivin, Tetanus, NY-ESO-1, HER2, HER3, HVEM, HPV16E6, HPV18E6, HPV16E7, HPV18E7, EBNA1, EBNA trunc, gp350, LMP2, GCP3, Middle S, X Protein, TIGIT, TEM8, TEM1, HER2 ECD+TM, CEA, TARP, PROSTEIN, PSMA, BIRC4, MUCIN-1, MUCIN-1 iso, CD40-L, WT-1, WT-1 trunc., PRAME, LAGE-1, and/or MAGE A3; (d) MTRII, and at least one of pp65, gB, IE1, US28, IGFBP2, IL10, UL144, UL141, US11, HOS, IE2, TERT, Survivin, Tetanus, NY-ESO-1, HER2, HER3, HVEM, HPV16E6, HPV18E6, HPV16E7, HPV18E7, EBNA1, EBNA trunc, gp350, LMP2, GCP3, Middle S, X Protein, TIGIT, TEM8, TEM1, HER2 ECD+TM, CEA, TARP, PROSTEIN, PSMA, BIRC4, MUCIN-1, MUCIN-1 iso, CD40-L, WT-1, WT-1 trunc., PRAME, LAGE-1, and/or MAGE A3; (e) US28 and at least one of pp65, gB, IE1, MTRII, IGFBP2, IL10, UL144, UL141, US11, HOS, IE2, TERT, Survivin, Tetanus, NY-ESO-1, HER2, HER3, HVEM, HPV16E6, HPV18E6, HPV16E7, HPV18E7, EBNA1, EBNA trunc, gp350, LMP2, GCP3, Middle S, X Protein, TIGIT, TEM8, TEM1, HER2 ECD+TM, CEA, TARP, PROSTEIN, PSMA, BIRC4, MUCIN-1, MUCIN-1 iso, CD40-L, WT-1, WT-1 trunc., PRAME, LAGE-1, and/or MAGE A3; (f) IGFBP2 and at least one of pp65, gB, IE1,

MTRII, US28, IL10, UL144, UL141, US11, HOS, IE2, TERT, Survivin, Tetanus, NY-ESO-1, HER2, HER3, HVEM, HPV16E6, HPV18E6, HPV16E7, HPV18E7, EBNA1, EBNA trunc, gp350, LMP2, GCP3, Middle S, X Protein, TIGIT, TEM8, TEM1, HER2 ECD+TM, CEA, TARP, PROSTEIN, PSMA, BIRC4, MUCIN-1, MUCIN-1 iso, CD40-L, WT-1, WT-1 trunc., PRAME, LAGE-1, and/or MAGE A3; (g) IL10 and at least one of pp65, gB, IE1, MTRII, US28, IGFBP2, UL144, UL141, US11, HOS, IE2, TERT, Survivin, Tetanus, NY-ESO-1, HER2, HER3, HVEM, HPV16E6, HPV18E6, HPV16E7, HPV18E7, EBNA1, EBNA trunc, gp350, LMP2, GCP3, Middle S, X Protein, TIGIT, TEM8, TEM1, HER2 ECD+TM, CEA, TARP, PROSTEIN, PSMA, BIRC4, MUCIN-1, MUCIN-1 iso, CD40-L, WT-1, WT-1 trunc., PRAME, LAGE-1, and/or MAGE A3; (h) UL144 and at least one of pp65, gB, IE1, MTRII, US28, IGFBP2, IL10, UL141, US11, HOS, IE2, TERT, Survivin, Tetanus, NY-ESO-1, HER2, HER3, HVEM, HPV16E6, HPV18E6, HPV16E7, HPV18E7, EBNA1, EBNA trunc, gp350, LMP2, GCP3, Middle S, X Protein, TIGIT, TEM8, TEM1, HER2 ECD+TM, CEA, TARP, PROSTEIN, PSMA, BIRC4, MUCIN-1, MUCIN-1 iso, CD40-L, WT-1, WT-1 trunc., PRAME, LAGE-1, and/or MAGE A3; (i) UL141 and at least one of pp65, gB, IE1, MTRII, US28, IGFBP2, IL10, UL144, US11, HOS, IE2, TERT, Survivin, Tetanus, NY-ESO-1, HER2, HER3, HVEM, HPV16E6, HPV18E6, HPV16E7, HPV18E7, EBNA1, EBNA trunc, gp350, LMP2, GCP3, Middle S, X Protein, TIGIT, TEM8, TEM1, HER2 ECD+TM, CEA, TARP, PROSTEIN, PSMA, BIRC4, MUCIN-1, MUCIN-1 iso, CD40-L, WT-1, WT-1 trunc., PRAME, LAGE-1, and/or MAGE A3; (j) US11 and at least one of pp65, gB, IE1, MTRII, US28, IGFBP2, IL10, UL144, UL141, HOS, IE2, TERT, Survivin, Tetanus, NY-ESO-1, HER2, HER3, HVEM, HPV16E6, HPV18E6, HPV16E7, HPV18E7, EBNA1, EBNA trunc, gp350, LMP2, GCP3, Middle S, X Protein, TIGIT, TEM8, TEM1, HER2 ECD+TM, CEA, TARP, PROSTEIN, PSMA, BIRC4, MUCIN-1, MUCIN-1 iso, CD40-L, WT-1, WT-1 trunc., PRAME, LAGE-1, and/or MAGE A3; (k) IE2 and at least one of pp65, gB, IE1, MTRII, US28, IGFBP2, IL10, UL144, UL141, US11, HOS, TERT, Survivin, Tetanus, NY-ESO-1, HER2, HER3, HVEM, HPV16E6, HPV18E6, HPV16E7, HPV18E7, EBNA1, EBNA trunc, gp350, LMP2, GCP3, Middle S, X Protein, TIGIT, TEM8, TEM1, HER2 ECD+TM, CEA, TARP, PROSTEIN, PSMA, BIRC4, MUCIN-1, MUCIN-1 iso, CD40-L, WT-1, WT-1 trunc., PRAME, LAGE-1, and/or MAGE A3; (l) TERT and at least one of pp65, gB, IE1, MTRII, US28, IGFBP2, IL10, UL144, UL141, US11, HOS, IE2, Survivin, Tetanus, NY-ESO-1, HER2, HER3, HVEM, HPV16E6, HPV18E6, HPV16E7, HPV18E7, EBNA1, EBNA trunc, gp350, LMP2, GCP3, Middle S, X Protein, TIGIT, TEM8, TEM1, HER2 ECD+TM, CEA, TARP, PROSTEIN, PSMA, BIRC4, MUCIN-1, MUCIN-1 iso, CD40-L, WT-1, WT-1 trunc., PRAME, LAGE-1, and/or MAGE A3; (m) Survivin and at least one of pp65, gB, IE1, MTRII, US28, IGFBP2, IL10, UL144, UL141, US11, HOS, IE2, TERT, Tetanus, NY-ESO-1, HER2, HER3, HVEM, HPV16E6, HPV18E6, HPV16E7, HPV18E7, EBNA1, EBNA trunc, gp350, LMP2, GCP3, Middle S, X Protein, TIGIT, TEM8, TEM1, HER2 ECD+TM, CEA, TARP, PROSTEIN, PSMA, BIRC4, MUCIN-1, MUCIN-1 iso, CD40-L, WT-1, WT-1 trunc., PRAME, LAGE-1, and/or MAGE A3; (n) Tetanus and at least one of pp65, gB, IE1, MTRII, US28, IGFBP2, IL10, UL144, UL141, US11, HOS, IE2, TERT, Survivin, NY-ESO-1, HER2, HER3, HVEM, HPV16E6, HPV18E6, HPV16E7,

HPV18E7, EBNA1, EBNA trunc, gp350, LMP2, GCP3, Middle S, X Protein, TIGIT, TEM8, TEM1, HER2 ECD+TM, CEA, TARP, PROSTEIN, PSMA, BIRC4, MUCIN-1, MUCIN-1 iso, CD40-L, WT-1, WT-1 trunc., PRAME, LAGE-1, and/or MAGE A3; (o) NY-ESO-1 and at least one of pp65, gB, IE1, MTRII, US28, IGFBP2, IL10, UL144, UL141, US11, HOS, IE2, TERT, Survivin, Tetanus, HER2, HER3, HVEM, HPV16E6, HPV18E6, HPV16E7, HPV18E7, EBNA1, EBNA trunc, gp350, LMP2, GCP3, Middle S, X Protein, TIGIT, TEM8, TEM1, HER2 ECD+TM, CEA, TARP, PROSTEIN, PSMA, BIRC4, MUCIN-1, MUCIN-1 iso, CD40-L, WT-1, WT-1 trunc., PRAME, LAGE-1, and/or MAGE A3; (p) HER2 and at least one of pp65, gB, IE1, MTRII, US28, IGFBP2, IL10, UL144, UL141, US11, HOS, IE2, TERT, Survivin, Tetanus, NY-ESO-1, HER3, HVEM, HPV16E6, HPV18E6, HPV16E7, HPV18E7, EBNA1, EBNA trunc, gp350, LMP2, GCP3, Middle S, X Protein, TIGIT, TEM8, TEM1, HER2 ECD+TM, CEA, TARP, PROSTEIN, PSMA, BIRC4, MUCIN-1, MUCIN-1 iso, CD40-L, WT-1, WT-1 trunc., PRAME, LAGE-1, and/or MAGE A3; (q) HER3 and at least one of pp65, gB, IE1, MTRII, US28, IGFBP2, IL10, UL144, UL141, US11, HOS, IE2, TERT, Survivin, Tetanus, NY-ESO-1, HER2, HVEM, HPV16E6, HPV18E6, HPV16E7, HPV18E7, EBNA1, EBNA trunc, gp350, LMP2, GCP3, Middle S, X Protein, TIGIT, TEM8, TEM1, HER2 ECD+TM, CEA, TARP, PROSTEIN, PSMA, BIRC4, MUCIN-1, MUCIN-1 iso, CD40-L, WT-1, WT-1 trunc., PRAME, LAGE-1, and/or MAGE A3; (r) HVEM and at least one of pp65, gB, IE1, MTRII, US28, IGFBP2, IL10, UL144, UL141, US11, HOS, IE2, TERT, Survivin, Tetanus, NY-ESO-1, HER2, HER3, HPV16E6, HPV18E6, HPV16E7, HPV18E7, EBNA1, EBNA trunc, gp350, LMP2, GCP3, Middle S, X Protein, TIGIT, TEM8, TEM1, HER2 ECD+TM, CEA, TARP, PROSTEIN, PSMA, BIRC4, MUCIN-1, MUCIN-1 iso, CD40-L, WT-1, WT-1 trunc., PRAME, LAGE-1, and/or MAGE A3; (s) HOS and at least one of pp65, gB, IE1, MTRII, US28, IGFBP2, IL10, UL144, UL141, US11, IE2, TERT, Survivin, Tetanus, NY-ESO-1, HER2, HER3, HVEM, HPV16E6, HPV18E6, HPV16E7, HPV18E7, EBNA1, EBNA trunc, gp350, LMP2, GCP3, Middle S, X Protein, TIGIT, TEM8, TEM1, HER2 ECD+TM, CEA, TARP, PROSTEIN, PSMA, BIRC4, MUCIN-1, MUCIN-1 iso, CD40-L, WT-1, WT-1 trunc., PRAME, LAGE-1, and/or MAGE A3; (t) HPV16E6 and at least one of pp65, gB, IE1, MTRII, US28, IGFBP2, IL10, UL144, UL141, US11, HOS, IE2, TERT, Survivin, Tetanus, NY-ESO-1, HER2, HER3, HVEM, HPV18E6, HPV16E7, HPV18E7, EBNA1, EBNA trunc, gp350, LMP2, GCP3, Middle S, X Protein, TIGIT, TEM8, TEM1, HER2 ECD+TM, CEA, TARP, PROSTEIN, PSMA, BIRC4, MUCIN-1, MUCIN-1 iso, CD40-L, WT-1, WT-1 trunc., PRAME, LAGE-1, and/or MAGE A3; (u) HPV18E6 and at least one of pp65, gB, IE1, MTRII, US28, IGFBP2, IL10, UL144, UL141, US11, HOS, IE2, TERT, Survivin, Tetanus, NY-ESO-1, HER2, HER3, HVEM, HPV16E6, HPV16E7, HPV18E7, EBNA1, EBNA trunc, gp350, LMP2, GCP3, Middle S, X Protein, TIGIT, TEM8, TEM1, HER2 ECD+TM, CEA, TARP, PROSTEIN, PSMA, BIRC4, MUCIN-1, MUCIN-1 iso, CD40-L, WT-1, WT-1 trunc., PRAME, LAGE-1, and/or MAGE A3; (v) HPV16E7 and at least one of pp65, gB, IE1, MTRII, US28, IGFBP2, IL10, UL144, UL141, US11, HOS, IE2, TERT, Survivin, Tetanus, NY-ESO-1, HER2, HER3, HVEM, HPV16E6, HPV18E6, HPV18E7, EBNA1, EBNA trunc, gp350, LMP2, GCP3, Middle S, X Protein, TIGIT, TEM8, TEM1, HER2 ECD+TM, CEA, TARP, PROSTEIN, PSMA,

BIRC4, MUCIN-1, MUCIN-1 iso, CD40-L, WT-1, WT-1 trunc., PRAME, LAGE-1, and/or MAGE A3; (w) HPV18E7 and at least one of pp65, gB, IE1, MTRII, US28, IGFBP2, IL10, UL144, UL141, US11, HOS, IE2, TERT, Survivin, Tetanus, NY-ESO-1, HER2, HER3, HVEM, HPV16E6, HPV18E6, HPV16E7, EBNA1, EBNA trunc, gp350, LMP2, GCP3, Middle S, X Protein, TIGIT, TEM8, TEM1, HER2 ECD+TM, CEA, TARP, PROSTEIN, PSMA, BIRC4, MUCIN-1, MUCIN-1 iso, CD40-L, WT-1, WT-1 trunc., PRAME, LAGE-1, and/or MAGE A3; (x) EBNA1 and at least one of pp65, gB, IE1, MTRII, US28, IGFBP2, IL10, UL144, UL141, US11, HOS, IE2, TERT, Survivin, Tetanus, NY-ESO-1, HER2, HER3, HVEM, HPV16E6, HPV18E6, HPV16E7, HPV18E7, EBNA1, EBNA trunc, gp350, LMP2, GCP3, Middle S, X Protein, TIGIT, TEM8, TEM1, HER2 ECD+TM, CEA, TARP, PROSTEIN, PSMA, BIRC4, MUCIN-1, MUCIN-1 iso, CD40-L, WT-1, WT-1 trunc., PRAME, LAGE-1, and/or MAGE A3; (y) EBNA1 trunc and at least one of pp65, gB, IE1, MTRII, US28, IGFBP2, IL10, UL144, UL141, US11, HOS, IE2, TERT, Survivin, Tetanus, NY-ESO-1, HER2, HER3, HVEM, HPV16E6, HPV18E6, HPV16E7, HPV18E7, EBNA1, gp350, LMP2, GCP3, Middle S, X Protein, TIGIT, TEM8, TEM1, HER2 ECD+TM, CEA, TARP, PROSTEIN, PSMA, BIRC4, MUCIN-1, MUCIN-1 iso, CD40-L, WT-1, WT-1 trunc., PRAME, LAGE-1, and/or MAGE A3; (z) gp350 and at least one of pp65, gB, IE1, MTRII, US28, IGFBP2, IL10, UL144, UL141, US11, HOS, IE2, TERT, Survivin, Tetanus, NY-ESO-1, HER2, HER3, HVEM, HPV16E6, HPV18E6, HPV16E7, HPV18E7, EBNA1, EBNA trunc, LMP2, GCP3, Middle S, X Protein, TIGIT, TEM8, TEM1, HER2 ECD+TM, CEA, TARP, PROSTEIN, PSMA, BIRC4, MUCIN-1, MUCIN-1 iso, CD40-L, WT-1, WT-1 trunc., PRAME, LAGE-1, and/or MAGE A3; (aa) LMP2 and at least one of pp65, gB, IE1, MTRII, US28, IGFBP2, IL10, UL144, UL141, US11, HOS, IE2, TERT, Survivin, Tetanus, NY-ESO-1, HER2, HER3, HVEM, HPV16E6, HPV18E6, HPV16E7, HPV18E7, EBNA1, EBNA trunc, gp350, GCP3, Middle S, X Protein, TIGIT, TEM8, TEM1, HER2 ECD+TM, CEA, TARP, PROSTEIN, PSMA, BIRC4, MUCIN-1, MUCIN-1 iso, CD40-L, WT-1, WT-1 trunc., PRAME, LAGE-1, and/or MAGE A3; (ab) GCP3 and at least one of pp65, gB, IE1, MTRII, US28, IGFBP2, IL10, UL144, UL141, US11, HOS, IE2, TERT, Survivin, Tetanus, NY-ESO-1, HER2, HER3, HVEM, HPV16E6, HPV18E6, HPV16E7, HPV18E7, EBNA1, EBNA trunc, gp350, LMP2, Middle S, X Protein, TIGIT, TEM8, TEM1, HER2 ECD+TM, CEA, TARP, PROSTEIN, PSMA, BIRC4, MUCIN-1, MUCIN-1 iso, CD40-L, WT-1, WT-1 trunc., PRAME, LAGE-1, and/or MAGE A3; (ac) Middle S and at least one of pp65, gB, IE1, MTRII, US28, IGFBP2, IL10, UL144, UL141, US11, HOS, IE2, TERT, Survivin, Tetanus, NY-ESO-1, HER2, HER3, HVEM, HPV16E6, HPV18E6, HPV16E7, HPV18E7, EBNA1, EBNA trunc, gp350, LMP2, GCP3, X Protein, TIGIT, TEM8, TEM1, HER2 ECD+TM, CEA, TARP, PROSTEIN, PSMA, BIRC4, MUCIN-1, MUCIN-1 iso, CD40-L, WT-1, WT-1 trunc., PRAME, LAGE-1, and/or MAGE A3; (ad) X Protein and at least one of pp65, gB, IE1, MTRII, US28, IGFBP2, IL10, UL144, UL141, US11, HOS, IE2, TERT, Survivin, Tetanus, NY-ESO-1, HER2, HER3, HVEM, HPV16E6, HPV18E6, HPV16E7, HPV18E7, EBNA1, EBNA trunc, gp350, LMP2, GCP3, Middle S, TIGIT, TEM8, TEM1, HER2 ECD+TM, CEA, TARP, PROSTEIN, PSMA, BIRC4, MUCIN-1, MUCIN-1 iso, CD40-L, WT-1, WT-1 trunc., PRAME, LAGE-1, and/or MAGE A3; (ae) TIGIT and at least one of pp65, gB,

IE1, MTRII, US28, IGFBP2, IL10, UL144, UL141, US11, HOS, IE2, TERT, Survivin, Tetanus, NY-ESO-1, HER2, HER3, HVEM, HPV16E6, HPV18E6, HPV16E7, HPV18E7, EBNA1, EBNA trunc, gp350, LMP2, GCP3, Middle S, X Protein, TEM8, TEM1, HER2 ECD+TM, CEA, TARP, PROSTEIN, PSMA, BIRC4, MUCIN-1, MUCIN-1 iso, CD40-L, WT-1, WT-1 trunc., PRAME, LAGE-1, and/or MAGE A3; (af) TEM8 and at least one of pp65, gB, IE1, MTRII, US28, IGFBP2, IL10, UL144, UL141, US11, HOS, IE2, TERT, Survivin, Tetanus, NY-ESO-1, HER2, HER3, HVEM, HPV16E6, HPV18E6, HPV16E7, HPV18E7, EBNA1, EBNA trunc, gp350, LMP2, GCP3, Middle S, X Protein, TIGIT, TEM1, HER2 ECD+TM, CEA, TARP, PROSTEIN, PSMA, BIRC4, MUCIN-1, MUCIN-1 iso, CD40-L, WT-1, WT-1 trunc., PRAME, LAGE-1, and/or MAGE A3; (ag) TEM1 and at least one of pp65, gB, IE1, MTRII, US28, IGFBP2, IL10, UL144, UL141, US11, HOS, IE2, TERT, Survivin, Tetanus, NY-ESO-1, HER2, HER3, HVEM, HPV16E6, HPV18E6, HPV16E7, HPV18E7, EBNA1, EBNA trunc, gp350, LMP2, GCP3, Middle S, X Protein, TIGIT, TEM8, HER2 ECD+TM, CEA, TARP, PROSTEIN, PSMA, BIRC4, MUCIN-1, MUCIN-1 iso, CD40-L, WT-1, WT-1 trunc., PRAME, LAGE-1, and/or MAGE A3; (ah) HER2 ECD+TM and at least one of pp65, gB, IE1, MTRII, US28, IGFBP2, IL10, UL144, UL141, US11, HOS, IE2, TERT, Survivin, Tetanus, NY-ESO-1, HER2, HER3, HVEM, HPV16E6, HPV18E6, HPV16E7, HPV18E7, EBNA1, EBNA trunc, gp350, LMP2, GCP3, Middle S, X Protein, TIGIT, TEM8, TEM1, CEA, TARP, PROSTEIN, PSMA, BIRC4, MUCIN-1, MUCIN-1 iso, CD40-L, WT-1, WT-1 trunc., PRAME, LAGE-1, and/or MAGE A3; (ai) CEA and at least one of pp65, gB, IE1, MTRII, US28, IGFBP2, IL10, UL144, UL141, US11, HOS, IE2, TERT, Survivin, Tetanus, NY-ESO-1, HER2, HER3, HVEM, HPV16E6, HPV18E6, HPV16E7, HPV18E7, EBNA1, EBNA trunc, gp350, LMP2, GCP3, Middle S, X Protein, TIGIT, TEM8, TEM1, HER2 ECD+TM, TARP, PROSTEIN, PSMA, BIRC4, MUCIN-1, MUCIN-1 iso, CD40-L, WT-1, WT-1 trunc., PRAME, LAGE-1, and/or MAGE A3; (aj) TARP and at least one of pp65, gB, IE1, MTRII, US28, IGFBP2, IL10, UL144, UL141, US11, HOS, IE2, TERT, Survivin, Tetanus, NY-ESO-1, HER2, HER3, HVEM, HPV16E6, HPV18E6, HPV16E7, HPV18E7, EBNA1, EBNA trunc, gp350, LMP2, GCP3, Middle S, X Protein, TIGIT, TEM8, TEM1, HER2 ECD+TM, CEA, PROSTEIN, PSMA, BIRC4, MUCIN-1, MUCIN-1 iso, CD40-L, WT-1, WT-1 trunc., PRAME, LAGE-1, and/or MAGE A3; (ak) PROSTEIN and at least one of pp65, gB, IE1, MTRII, US28, IGFBP2, IL10, UL144, UL141, US11, HOS, IE2, TERT, Survivin, Tetanus, NY-ESO-1, HER2, HER3, HVEM, HPV16E6, HPV18E6, HPV16E7, HPV18E7, EBNA1, EBNA trunc, gp350, LMP2, GCP3, Middle S, X Protein, TIGIT, TEM8, TEM1, HER2 ECD+TM, CEA, TARP, PSMA, BIRC4, MUCIN-1, MUCIN-1 iso, CD40-L, WT-1, WT-1 trunc., PRAME, LAGE-1, and/or MAGE A3; (al) PSMA and at least one of pp65, gB, IE1, MTRII, US28, IGFBP2, IL10, UL144, UL141, US11, HOS, IE2, TERT, Survivin, Tetanus, NY-ESO-1, HER2, HER3, HVEM, HPV16E6, HPV18E6, HPV16E7, HPV18E7, EBNA1, EBNA trunc, gp350, LMP2, GCP3, Middle S, X Protein, TIGIT, TEM8, TEM1, HER2 ECD+TM, CEA, TARP, PROSTEIN, BIRC4, MUCIN-1, MUCIN-1 iso, CD40-L, WT-1, WT-1 trunc., PRAME, LAGE-1, and/or MAGE A3; (am) BIRC4 and at least one of pp65, gB, IE1, MTRII, US28, IGFBP2, IL10, UL144, UL141, US11, HOS, IE2, TERT, Survivin, Tetanus, NY-ESO-1, HER2, HER3, HVEM,

HPV16E6, HPV18E6, HPV16E7, HPV18E7, EBNA1, EBNA trunc, gp350, LMP2, GCP3, Middle S, X Protein, TIGIT, TEM8, TEM1, HER2 ECD+TM, CEA, TARP, PROSTEIN, PSMA, MUCIN-1, MUCIN-1 iso, CD40-L, WT-1, WT-1 trunc., PRAME, LAGE-1, and/or MAGE A3; (an) MUCIN-1 and at least one of pp65, gB, IE1, MTRII, US28, IGFBP2, IL10, UL144, UL141, US11, HOS, IE2, TERT, Survivin, Tetanus, NY-ESO-1, HER2, HER3, HVEM, HPV16E6, HPV18E6, HPV16E7, HPV18E7, EBNA1, EBNA trunc, gp350, LMP2, GCP3, Middle S, X Protein, TIGIT, TEM8, TEM1, HER2 ECD+TM, CEA, TARP, PROSTEIN, PSMA, BIRC4, MUCIN-1 iso, CD40-L, WT-1, WT-1 trunc., PRAME, LAGE-1, and/or MAGE A3; (ao) MUCIN-1 iso and at least one of pp65, gB, IE1, MTRII, US28, IGFBP2, IL10, UL144, UL141, US11, HOS, IE2, TERT, Survivin, Tetanus, NY-ESO-1, HER2, HER3, HVEM, HPV16E6, HPV18E6, HPV16E7, HPV18E7, EBNA1, EBNA trunc, gp350, LMP2, GCP3, Middle S, X Protein, TIGIT, TEM8, TEM1, HER2 ECD+TM, CEA, TARP, PROSTEIN, PSMA, BIRC4, MUCIN-1, CD40-L, WT-1, WT-1 trunc., PRAME, LAGE-1, and/or MAGE A3; (ap) CD40-L and at least one of pp65, gB, IE1, MTRII, US28, IGFBP2, IL10, UL144, UL141, US11, HOS, IE2, TERT, Survivin, Tetanus, NY-ESO-1, HER2, HER3, HVEM, HPV16E6, HPV18E6, HPV16E7, HPV18E7, EBNA1, EBNA trunc, gp350, LMP2, GCP3, Middle S, X Protein, TIGIT, TEM8, TEM1, HER2 ECD+TM, CEA, TARP, PROSTEIN, PSMA, BIRC4, MUCIN-1, MUCIN-1 iso, WT-1, WT-1 trunc., PRAME, LAGE-1, and/or MAGE A3; (aq) WT-1 and at least one of pp65, gB, IE1, MTRII, US28, IGFBP2, IL10, UL144, UL141, US11, HOS, IE2, TERT, Survivin, Tetanus, NY-ESO-1, HER2, HER3, HVEM, HPV16E6, HPV18E6, HPV16E7, HPV18E7, EBNA1, EBNA trunc, gp350, LMP2, GCP3, Middle S, X Protein, TIGIT, TEM8, TEM1, HER2 ECD+TM, CEA, TARP, PROSTEIN, PSMA, BIRC4, MUCIN-1, MUCIN-1 iso, CD40-L, WT-1 trunc., PRAME, LAGE-1, and/or MAGE A3; (ar) WT-1 trunc and at least one of pp65, gB, IE1, MTRII, US28, IGFBP2, IL10, UL144, UL141, US11, HOS, IE2, TERT, Survivin, Tetanus, NY-ESO-1, HER2, HER3, HVEM, HPV16E6, HPV18E6, HPV16E7, HPV18E7, EBNA1, EBNA trunc, gp350, LMP2, GCP3, Middle S, X Protein, TIGIT, TEM8, TEM1, HER2 ECD+TM, CEA, TARP, PROSTEIN, PSMA, BIRC4, MUCIN-1, MUCIN-1 iso, CD40-L, WT-1, PRAME, LAGE-1, and/or MAGE A3; (as) PRAME and at least one of pp65, gB, IE1, MTRII, US28, IGFBP2, IL10, UL144, UL141, US11, HOS, IE2, TERT, Survivin, Tetanus, NY-ESO-1, HER2, HER3, HVEM, HPV16E6, HPV18E6, HPV16E7, HPV18E7, EBNA1, EBNA trunc, gp350, LMP2, GCP3, Middle S, X Protein, TIGIT, TEM8, TEM1, HER2 ECD+TM, CEA, TARP, PROSTEIN, PSMA, BIRC4, MUCIN-1, MUCIN-1 iso, CD40-L, WT-1, WT-1 trunc., LAGE-1, and/or MAGE A3; (at) LAGE-1 and at least one of pp65, gB, IE1, MTRII, US28, IGFBP2, IL10, UL144, UL141, US11, HOS, IE2, TERT, Survivin, Tetanus, NY-ESO-1, HER2, HER3, HVEM, HPV16E6, HPV18E6, HPV16E7, HPV18E7, EBNA1, EBNA trunc, gp350, LMP2, GCP3, Middle S, X Protein, TIGIT, TEM8, TEM1, HER2 ECD+TM, CEA, TARP, PROSTEIN, PSMA, BIRC4, MUCIN-1, MUCIN-1 iso, CD40-L, WT-1, WT-1 trunc., PRAME, and/or MAGE A3; and/or (au) MAGE A3 and at least one of pp65, gB, IE1, MTRII, US28, IGFBP2, IL10, UL144, UL141, US11, HOS, IE2, TERT, Survivin, Tetanus, NY-ESO-1, HER2, HER3, HVEM, HPV16E6, HPV18E6, HPV16E7, HPV18E7, EBNA1, EBNA trunc, gp350, LMP2, GCP3, Middle S, X

Protein, TIGIT, TEM8, TEM1, HER2 ECD+TM, CEA, TARP, PROSTEIN, PSMA, BIRC4, MUCIN-1, MUCIN-1 iso, CD40-L, WT-1, WT-1 trunc., PRAME, and/or LAGE-1. The order of the combination of antigens as described above in a particular LAMP construct can vary as this list describes what a LAMP Construct comprises and not necessarily to describe the arrangement of the antigens within a particular construct. Moreover, it is specifically envisioned that these antigens can be combined within a single LAMP Construct, or can be delivered in a composition comprising multiple LAMP Constructs.

Assembly of Sequences Encoding Improved LAMP Constructs

[0151] Procedures for constructing improved LAMP Constructs comprising the antigen of interest are well known in the art (see e.g., Williams, et al., J. Cell Biol. 111: 955, 1990). DNA sequences encoding the desired segments can be obtained from readily available recombinant DNA materials such as those available from the American Type Culture Collection, 12301 Parklawn Drive, Rockville, Md. 20852, U.S.A., or from DNA libraries that contain the desired DNA.

[0152] For example, the DNA segments corresponding to the desired domain sequences can be assembled with appropriate control and signal sequences using routine procedures of recombinant DNA methodology. See, e.g., as described in U.S. Pat. No. 4,593,002, and Langford, et al., Molec. Cell. Biol. 6: 3191, 1986.

[0153] A DNA sequence encoding a protein or polypeptide can be synthesized chemically or isolated by one of several approaches. The DNA sequence to be synthesized can be designed with the appropriate codons for the desired amino acid sequence. In general, one will select preferred codons for the intended host in which the sequence will be used for expression. The complete sequence may be assembled from overlapping oligonucleotides prepared by standard methods and assembled into a complete coding sequence. See, e.g., Edge, Nature 292: 756, 1981; Nambair, et al. Science 223: 1299, 1984; Jay, et al., J. Biol. Chem. 259: 6311, 1984.

[0154] In one aspect, one or more of the nucleic acids encoding the domain sequences of the improved LAMP Construct are isolated individually using the polymerase chain reaction (M. A. Innis, et al., In PCR Protocols: A Guide to Methods and Applications, Academic Press, 1990). The domains are preferably isolated from publicly available clones known to contain them, but they may also be isolated from genomic DNA or cDNA libraries. Preferably, isolated fragments are bordered by compatible restriction endonuclease sites which allow an improved LAMP Construct encoding the cancer antigen sequence to be constructed. This technique is well known to those of skill in the art. Domain sequences may be fused directly to each other (e.g., with no intervening sequences), or inserted into one another (e.g., where domain sequences are discontinuous), or may be separated by intervening sequences (e.g., such as linker sequences).

[0155] The basic strategies for preparing oligonucleotide primers, probes and DNA libraries, as well as their screening by nucleic acid hybridization, are well known to those of ordinary skill in the art. See, e.g., Sambrook, et al., 1989, supra; Perbal, 1984, supra. The construction of an appropriate genomic DNA or cDNA

library is within the skill of the art. See, e.g., Perbal, 1984, *supra*. Alternatively, suitable DNA libraries or publicly available clones are available from suppliers of biological research materials, such as Clontech and Stratagene, as well as from public depositories such as the American Type Culture Collection.

[0156] Selection may be accomplished by expressing sequences from an expression library of DNA and detecting the expressed peptides immunologically. Clones which express peptides that bind to MHC II molecules and to the desired antibodies/T cell receptors are selected. These selection procedures are well known to those of ordinary skill in the art (see, e.g., Sambrook, et al., 1989, *supra*).

[0157] Once a clone containing the coding sequence for the desired polypeptide sequence has been prepared or isolated, the sequence can be cloned into any suitable vector, preferably comprising an origin of replication for maintaining the sequence in a host cell.

Nucleic Acid Delivery Vehicles

[0158] In one aspect, a vaccine composition comprising an improved LAMP Construct is introduced into a cell. The cell may be a host cell for replicating the nucleic acid or for expressing the improved LAMP Construct. Preferably, the host cell for expressing the improved LAMP Construct is an antigen presenting cell (described further below).

[0159] In preferred embodiments, the improved LAMP Construct further comprises a polynucleotide sequence for insertion into a target cell and an expression control sequence operably linked thereto to control expression of the polynucleotide sequence (e.g., transcription and/or translation) in the cell. Examples include plasmids, phages, autonomously replicating sequences (ARS), centromeres, and other sequences which are able to replicate or be replicated *in vitro* or in a host cell (e.g., such as a bacterial, yeast, or insect cell) and/or target cell (e.g., such as a mammalian cell, preferably an antigen presenting cell) and/or to convey the sequences encoding the improved LAMP Construct to a desired location within the target cell.

[0160] Recombinant expression vectors may be derived from micro-organisms which readily infect animals, including man, horses, cows, pigs, llamas, giraffes, dogs, cats or chickens. Preferred vectors include those which have already been used as live vaccines, such as vaccinia. These recombinants can be directly inoculated into a host, conferring immunity not only to the microbial vector, but also to express foreign antigens. Preferred vectors contemplated herein as live recombinant vaccines include RNA viruses, adenovirus, herpesviruses, poliovirus, and vaccinia and other pox viruses, as taught in Flexner, *Adv. Pharmacol.* 21: 51, 1990, for example.

[0161] Expression control sequences include, but are not limited to, promoter sequences to bind RNA polymerase, enhancer sequences or negative regulatory elements to bind to transcriptional activators and repressors, respectively, and/or translation initiation sequences for ribosome binding. For example, a bacterial expression vector can include a promoter such as the lac promoter and for transcription initiation, the Shine-Dalgarno sequence and the start codon AUG (Sambrook, et al., 1989, *supra*). Similarly, a eukaryotic expression

vector preferably includes a heterologous, homologous, or chimeric promoter for RNA polymerase II, a downstream polyadenylation signal, the start codon AUG, and a termination codon for detachment of a ribosome.

[0162] Expression control sequences may be obtained from naturally occurring genes or may be designed. Designed expression control sequences include, but are not limited to, mutated and/or chimeric expression control sequences or synthetic or cloned consensus sequences. Vectors that contain both a promoter and a cloning site into which a polynucleotide can be operatively linked are well known in the art. Such vectors are capable of transcribing RNA in vitro or in vivo, and are commercially available from sources such as Stratagene (La Jolla, Calif.) and Promega Biotech (Madison, Wis.).

[0163] In order to optimize expression and/or transcription, it may be necessary to remove, add or alter 5' and/or 3' untranslated portions of the vectors to eliminate extra, or alternative translation initiation codons or other sequences that may interfere with, or reduce, expression, either at the level of transcription or translation. Alternatively, consensus ribosome binding sites can be inserted immediately 5' of the start codon to enhance expression. A wide variety of expression control sequences--sequences that control the expression of a DNA sequence operatively linked to it--may be used in these vectors to express the DNA sequences of this invention. Such useful expression control sequences include, for example, the early or late promoters of SV40, CMV, vaccinia, polyoma, adenovirus, herpes virus and other sequences known to control the expression of genes of mammalian cells, and various combinations thereof.

[0164] In one aspect, the improved LAMP Construct comprises an origin of replication for replicating the vector. Preferably, the origin functions in at least one type of host cell which can be used to generate sufficient numbers of copies of the sequence for use in delivery to a target cell. Suitable origins therefore include, but are not limited to, those which function in bacterial cells (e.g., such as *Escherichia* sp., *Salmonella* sp., *Proteus* sp., *Clostridium* sp., *Klebsiella* sp., *Bacillus* sp., *Streptomyces* sp., and *Pseudomonas* sp.), yeast (e.g., such as *Saccharomyces* sp. or *Pichia* sp.), insect cells, and mammalian cells. In one preferred aspect, an origin of replication is provided which functions in the target cell into which the nucleic acid delivery vehicle is introduced (e.g., a mammalian cell, such as a human cell). In another aspect, at least two origins of replication are provided, one that functions in a host cell and one that functions in a target cell.

[0165] The improved LAMP Construct may alternatively, or additionally, comprise sequences to facilitate integration of at least a portion of the nucleic acid deliver vector into a target cell chromosome. For example, the improved LAMP Construct may comprise regions of homology to target cell chromosomal DNA. In one aspect, the delivery vector comprises two or more recombination sites which flank a nucleic acid sequence encoding the improved LAMP Construct.

[0166] The vector may additionally comprise a detectable and/or selectable marker to verify that the vector has been successfully introduced in a target cell and/or can be expressed by the target cell. These markers

can encode an activity, such as, but not limited to, production of RNA, peptide, or protein, or can provide a binding site for RNA, peptides, proteins, inorganic and organic compounds or compositions and the like.

[0167] Examples of detectable/selectable markers genes include, but are not limited to: DNA segments that encode products which provide resistance against otherwise toxic compounds (e.g., antibiotics); DNA segments that encode products which are otherwise lacking in the recipient cell (e.g., tRNA genes, auxotrophic markers); DNA segments that encode products which suppress the activity of a gene product; DNA segments that encode products which can be readily identified (e.g., phenotypic markers such as beta-galactosidase, a fluorescent protein (GFP, CFP, YFP, BFP, RFP, EGFP, EYFP, EBFP, dsRed, mutated, modified, or enhanced forms thereof, and the like), and cell surface proteins); DNA segments that bind products which are otherwise detrimental to cell survival and/or function; DNA segments that otherwise inhibit the activity of other nucleic acid segments (e.g., antisense oligonucleotides); DNA segments that bind products that modify a substrate (e.g., restriction endonucleases); DNA segments that can be used to isolate or identify a desired molecule (e.g., segments encoding specific protein binding sites); primer sequences; DNA segments, which when absent, directly or indirectly confer resistance or sensitivity to particular compounds; and/or DNA segments that encode products which are toxic in recipient cells.

[0168] The marker gene can be used as a marker for conformation of successful gene transfer and/or to isolate cells expressing transferred genes and/or to recover transferred genes from a cell. For example, in one aspect, the marker gene is used to isolate and purify antigen presenting cells expressing the improved LAMP Constructs.

[0169] Substantially similar genes may be provided, e.g., genes with greater than about 50%, greater than about 70%, greater than 80%, greater than about 90%, and preferably, greater than about 95% identity to a known gene. Substantially similar domain sequences may initially be identified by selecting a sequence which specifically hybridizes to a domain sequence of interest under stringent hybridization conditions. Performing assays to determine the suitability of homologous, variant, or modified domain sequences is merely a matter of screening for sequences which express the appropriate activity. Such screening is routine in the art.

[0170] The improved LAMP Construct may be provided as naked nucleic acids or in a delivery vehicle associated with one or more molecules for facilitating entry of a nucleic acid into a cell. Suitable delivery vehicles include, but are not limited to: liposomal formulations, polypeptides, polysaccharides, lipopolysaccharides, viral formulations (e.g., including viruses, viral particles, artificial viral envelopes and the like), cell delivery vehicles, and the like.

Lipid-Based Formulations

[0171] Delivery vehicles designed to facilitate intracellular delivery of the improved LAMP Constructs must interact with both non-polar and polar environments (in or on, for example, the plasma membrane, tissue fluids, compartments within the cell, and the like). Therefore, preferably, delivery vehicles

are designed to contain both polar and non-polar domains or a translocating sequence for translocating an improved LAMP Construct into a cell.

[0172] Compounds having polar and non-polar domains are termed amphiphiles. Cationic amphiphiles have polar groups that are capable of being positively charged at, or around, physiological pH for interacting with negatively charged polynucleotides such as DNA.

[0173] The improved LAMP Constructs described herein can be provided in formulations comprising lipid monolayers or bilayers to facilitate transfer of the vectors across a cell membrane. Liposomes or any form of lipid membrane, such as planar lipid membranes or the cell membrane of an intact cell, e.g., a red blood cell, can be used. Liposomal formulations can be administered by any means, including administration intravenously or orally.

[0174] Liposomes and liposomal formulations can be prepared according to standard methods and are well known in the art, see, e.g., Remington's; Akimaru, 1995, Cytokines Mol. Ther. 1: 197-210; Alving, 1995, Immunol. Rev. 145: 5-31; Szoka, 1980, Ann. Rev. Biophys. Bioeng. 9: 467; U.S. Pat. No. 4,235,871; U.S. Pat. No. 4,501,728; and U.S. Pat. No. 4,837,028. In one aspect, the liposome comprises a targeting molecule for targeting a liposome:improved LAMP Construct complex to a particular cell type. In a particularly preferred aspect, a targeting molecule comprises a binding partner (e.g., a ligand or receptor) for a biomolecule (e.g., a receptor or ligand) on the surface of a blood vessel or a cell found in a target tissue.

[0175] Liposome charge is an important determinant in liposome clearance from the blood, with negatively charged liposomes being taken up more rapidly by the reticuloendothelial system (Juliano, 1975, Biochem. Biophys. Res. Commun. 63: 651) and thus having shorter half-lives in the bloodstream. Incorporating phosphatidylethanolamine derivatives enhances the circulation time by preventing liposomal aggregation. For example, incorporation of N-(omega-carboxy)acylamidophosphatidylethanolamines into large unilamellar vesicles of L-alpha-distearoylphosphatidylcholine dramatically increases the in vivo liposomal circulation lifetime (see, e.g., Ahl, 1997, Biochim. Biophys. Acta 1329: 370-382). Liposomes with prolonged circulation half-lives are typically desirable for therapeutic and diagnostic uses. For a general discussion of pharmacokinetics, see, e.g., Remington's, Chapters 37-39, Lee, et al., In Pharmacokinetic Analysis: A Practical Approach (Technomic Publishing AG, Basel, Switzerland 1996).

[0176] Typically, liposomes are prepared with about 5 to 15 mole percent negatively charged phospholipids, such as phosphatidylglycerol, phosphatidylserine or phosphatidyl-inositol. Added negatively charged phospholipids, such as phosphatidylglycerol, also serve to prevent spontaneous liposome aggregation, and thus minimize the risk of undersized liposomal aggregate formation. Membrane-rigidifying agents, such as sphingomyelin or a saturated neutral phospholipid, at a concentration of at least about 50 mole percent, and 5 to 15 mole percent of monosialylganglioside can also impart desirably liposome properties, such as rigidity (see, e.g., U.S. Pat. No. 4,837,028).

[0177] Additionally, the liposome suspension can include lipid-protective agents which protect lipids against free-radical and lipid-peroxidative damages on storage. Lipophilic free-radical quenchers, such as alpha-tocopherol and water-soluble iron-specific chelators, such as ferrioxianine, are preferred.

[0178] The improved LAMP Constructs of the invention can include multilamellar vesicles of heterogeneous sizes. For example, vesicle-forming lipids can be dissolved in a suitable organic solvent or solvent system and dried under vacuum or an inert gas to form a thin lipid film. If desired, the film can be redissolved in a suitable solvent, such as tertiary butanol, and then lyophilized to form a more homogeneous lipid mixture which is in a more easily hydrated powderlike form. This film is covered with an aqueous solution of the peptide or polypeptide complex and allowed to hydrate, typically over a 15 to 60 minute period with agitation. The size distribution of the resulting multilamellar vesicles can be shifted toward smaller sizes by hydrating the lipids under more vigorous agitation conditions or by adding solubilizing detergents such as deoxycholate. The hydration medium preferably comprises the nucleic acid at a concentration which is desired in the interior volume of the liposomes in the final liposome suspension.

[0179] Following liposome preparation, the liposomes can be sized to achieve a desired size range and relatively narrow distribution of liposome sizes. One preferred size range is about 0.2 to 0.4 microns, which allows the liposome suspension to be sterilized by filtration through a conventional filter, typically a 0.22 micron filter. Filter sterilization can be carried out on a high throughput basis if the liposomes have been sized down to about 0.2 to 0.4 microns. Several techniques are available for sizing liposome to a desired size (see, e.g., U.S. Pat. No. 4,737,323).

[0180] Suitable lipids include, but are not limited to, DOTMA (Felgner, et al., 1987, Proc. Natl. Acad. Sci. USA 84: 7413-7417), DOGS or TransfectainTM (Behr, et al., 1989, Proc. Natl. Acad. Sci. USA 86: 6982-6986), DNERIE or DORIE (Felgner, et al., Methods 5: 67-75), DC-CHOL (Gao and Huang, 1991, BBRC 179: 280-285), DOTAPTM (McLachlan, et al., 1995, Gene Therapy 2: 674-622), LipofectamineTM, and glycerolipid compounds (see, e.g., EP901463 and WO98/37916).

[0181] Other molecules suitable for complexing with the improved LAMP Constructs include cationic molecules, such as, polyamidoamine (Haensler and Szoka, 1993, Bioconjugate Chem. 4: 372-379), dendritic polysine (WO 95/24221), polyethylene irinine or polypropylene h-nine (WO 96/02655), polylysine (U.S. Pat. No. 5,595,897; FR 2 719 316), chitosan (U.S. Pat. No. 5,744,166), DNA-gelatin coarcervates (see, e.g., U.S. Pat. No. 6,207,195; U.S. Pat. No. 6,025,337; U.S. Pat. No. 5,972,707) or DEAE dextran (Lopata, et al., 1984, Nucleic Acid Res. 12: 5707-5717).

Viral-Based Gene Delivery Vehicles

[0182] In one aspect, the improved LAMP Construct delivery vehicle comprises a virus or viral particle. In this aspect, preferably, the improved LAMP Construct comprises a viral vector. Viral vectors, such as retroviruses, adenoviruses, adeno-associated viruses and herpes viruses, are often made up of two

components, a modified viral genome and a coat structure surrounding it (see, e.g., Smith et al., 1995, *Ann. Rev. Microbiol.* 49: 807-838), although sometimes viral vectors are introduced in naked form or coated with proteins other than viral proteins. Most current vectors have coat structures similar to a wild-type virus. This structure packages and protects the viral nucleic acid and provides the means to bind and enter target cells.

[0183] Preferably, viral vectors comprising the improved LAMP Constructs described herein are modified from wild-type viral genomes to disable the growth of the virus in a target cell while enabling the virus to grow in a host cell (e.g., such as a packaging or helper cell) used to prepare infectious particles. Vector nucleic acids generally essential cis-acting viral sequences for replication and packaging in a helper line and expression control sequences for regulating the expression of a polynucleotide being delivered to a target cell. Other viral functions are expressed in trans in specific packaging or helper cell lines as are known in the art.

[0184] Preferred improved LAMP Constructs are viral vectors derived from a virus selected from the group consisting of herpes viruses, cytomegaloviruses, foamy viruses, lentiviruses, Semliki forrest virus, AAV (adeno-associated virus), poxviruses, adenoviruses and retroviruses. Such viral vectors are well known in the art.

[0185] In one preferred aspect, a viral vector used is an adenoviral vector. The adenoviral genome consists of a linear double-stranded DNA molecule of approximately 36 kb carrying more than about thirty genes necessary to complete the viral replication cycle. The early genes are divided into 4 regions (E1 to E4) that are essential for viral replication with the exception of the E3 region, which is believed to modulate the anti-viral host immune response. The E1 region (E1A and E1B) encodes proteins responsible for the regulation of transcription of the viral genome. Expression of the E2 region genes (E2A and E2B) leads to the synthesis of the polypeptides needed for viral replication. The proteins encoded by the E3 region prevent cytolysis by cytotoxic T cells and tumor necrosis factor (Wold and Gooding, 1991, *Virology* 184: 1-8). The proteins encoded by the E4 region are involved in DNA replication, late gene expression and splicing and host cell shut off (Halbert, et al., 1985, *J. Virol.* 56: 250-257). The late genes generally encode structural proteins contributing to the viral capsid. In addition, the adenoviral genome carries at cis-acting 5' and 3' ITRs (Inverted Terminal Repeat) and packaging sequences essential for DNA replication. The ITRs harbor origins of DNA replication while the encapsidation region is required for the packaging of adenoviral DNA into infectious particles.

[0186] Adenoviral vectors can be engineered to be conditionally replicative (CRAd vectors) in order to replicate selectively in specific cells (e.g., such as proliferative cells) as described in Heise and Kim (2000, *J. Clin. Invest.* 105: 847-851). In another aspect, an adenoviral vector is replication-defective for the E1 function (e.g., by total or partial deletion or mutagenesis of E1). The adenoviral backbone of the vector may comprise additional modifications (deletions, insertions or mutations in one or more viral genes). An example of an E2 modification is illustrated by the thermosensitive mutation localized on the DBP (DNA Binding Protein) encoding gene (Ensinger et al., 1972, *J. Virol.* 10: 328-339). The adenoviral sequence may also be deleted of all or part of the E4 region (see, e.g., EP 974 668; Christ, et al., 2000, *Human Gene Ther.* 11: 415-

427; Lusky, et al., 1999, J. Virol. 73: 8308-8319). Additional deletions within the non-essential E3 region may allow the size of the polynucleotide being delivered to be increased (Yeh, et al., 1997, FASEB Journal 11: 615-623). However, it may be advantageous to retain all or part of the E3 sequences coding for polypeptides (e.g., such as gp19k) allowing the virus to escape the immune system (Gooding, et al., 1990, Critical Review of Immunology 10: 53-71) or inflammatory reactions (EP 00440267.3).

[0187] Second generation vectors retaining the ITRs and packaging sequences and comprising substantial genetic modifications to abolish the residual synthesis of the viral antigens also may be used in order to improve long-term expression of the expressed gene in the transduced cells (see, e.g., WO 94/28152; Lusky, et al., 1998, J. Virol 72: 2022-2032).

[0188] The improved LAMP Constructs being introduced into the cell may be inserted in any location of the viral genome, with the exception of the cis-acting sequences. Preferably, it is inserted in replacement of a deleted region (E1, E3 and/or E4), preferably, within a deleted E1 region.

[0189] Adenoviruses can be derived from any human or animal source, in particular canine (e.g. CAV-1 or CAV-2 Genbank ref. CAVIGENOM and CAV77082, respectively), avian (Genbank ref. AAVEDSDNA), bovine (such as BAV3; Reddy, et al., 1998, J. Virol. 72: 1394-1402), murine (Genbank ref. ADRMUSMAVI), ovine, feline, porcine or simian sources or alternatively, may be a hybrid virus. Any serotype can be employed. However, the human adenoviruses of the C sub-group are preferred, especially adenoviruses 2 (Ad2) and 5 (Ad5). Such viruses are available, for example, from the ATCC.

[0190] Adenoviral particles or empty adenoviral capsids also can be used to transfer improved LAMP Constructs by a virus-mediated coinfection process as described in U.S. Pat. No. 5,928,944. This process can be accomplished in the presence of cationic agent(s) such as polycarbones or lipid vesicles comprising one or more lipid layers.

[0191] Adenoviral particles may be prepared and propagated according to any conventional technique in the field of the art (e.g., WO 96/17070) using a complementation cell line or a helper virus, which supplies in trans the missing viral genes necessary for viral replication. The cell lines 293 (Graham et al., 1977, J. Gen. Virol. 36: 59-72) and PERC6 (Fallaux et al., 1998, Human Gene Therapy 9: 1909-1917) are commonly used to complement E1 deletions. Other cell lines have been engineered to complement defective vectors (Yeh, et al., 1996, J. Virol. 70: 559-565; Kroughak and Graham, 1995, Human Gene Ther. 6: 1575-1586; Wang, et al., 1995, Gene Ther. 2: 775-783; Lusky, et al., 1998, J. Virol. 72: 2022-203; EP 919627 and WO 97/04119). The adenoviral particles can be recovered from the culture supernatant but also from the cells after lysis and optionally further purified according to standard techniques (e.g., chromatography, ultracentrifugation, as described in WO 96/27677, WO 98/00524 WO 98/26048 and WO 00/50573).

[0192] Cell-type specific targeting may be achieved with vectors derived from adenoviruses having a broad host range by the modification of viral surface proteins. For example, the specificity of infection of adenoviruses is determined by the attachment to cellular receptors present at the surface of permissive cells. In

this regard, the fiber and penton present at the surface of the adenoviral capsid play a critical role in cellular attachment (Defer, et al., 1990, J. Virol. 64: 3661-3673). Thus, cell targeting of adenoviruses can be carried out by genetic modification of the viral gene encoding fiber and/or penton, to generate modified fiber and/or penton capable of specific interaction with unique cell surface receptors. Examples of such modifications are described in Wickarn, et al., 1997, J. Virol. 71: 8221-8229; Arriberg, et al., 1997, Virol. Chem 268: 6866-6869; Roux, et al., 1989, Proc. Natl. Acad. Sci. USA 86: 9079-9083; Miller and Vile, 1995, FASEB J. 9: 190-199; WO 93/09221, and in WO 95/28494.

[0193] In a particularly preferred aspect, adeno-associated viral sequences are used as vectors. Vectors derived from the human parvovirus AAV-2 (adeno-associated virus type 2) are among the most promising gene delivery vehicles currently being developed. Several of the features of this system for packaging a single-stranded DNA suggest it as a possible alternative to naked DNA for delivery. A primary attractive feature, in contrast to other viral vectors such as vaccinia or adenovirus, is that AAV vectors do not express any viral genes. The only viral DNA sequences included in the vaccine construct are the 145 bp inverted terminal repeats (ITR). Thus, as in immunization with naked DNA, the only gene expressed is that of the antigen, or antigen chimera. Additionally, AAV vectors are known to transduce both dividing and non-dividing cells, such as human peripheral blood monocyte-derived dendritic cells, with persistent transgene expression, and with the possibility of oral and intranasal delivery for generation of mucosal immunity. Moreover, the amount of DNA required appears to be much less by several orders of magnitude, with maximum responses at doses of 10^{10} to 10^{11} particles or copies of DNA in contrast to naked DNA doses of 50 ug or about 10^{15} copies.

[0194] In one aspect, AAV vectors are packaged by co-transfection of a suitable cell line (e.g., human 293 cells) with the DNA contained in the AAV ITR chimeric protein encoding constructs and an AAV helper plasmid ACG2 containing the AAV coding region (AAV rep and cap genes) without the ITRs. The cells are subsequently infected with the adenovirus Ad5. Vectors can be purified from cell lysates using methods known in the art (e.g., such as cesium chloride density gradient ultracentrifugation) and are validated to ensure that they are free of detectable replication-competent AAV or adenovirus (e.g., by a cytopathic effect bioassay). AAV titer may be determined by quantitative PCR with virus DNA samples prepared after digestion with proteinase K. Preferably, vector titers produced by such a method are approximately 5×10^{12} to 1×10^{13} DNase resistant particles per ml.

[0195] In other aspects, retroviral vectors are used. Retroviruses are a class of integrative viruses which replicate using a virus-encoded reverse transcriptase, to replicate the viral RNA genome into double stranded DNA which is integrated into chromosomal DNA of the infected cells (e.g., target cells). Such vectors include those derived from murine leukemia viruses, especially Moloney (Gilboa, et al., 1988, Adv. Exp. Med. Biol. 241: 29) or Friend's FB29 strains (WO 95/01447). Generally, a retroviral vector is deleted of all or part of the viral genes gag, pol and env and retains 5' and 3' LTRs and an encapsidation sequence. These elements may be modified to increase expression level or stability of the retroviral vector. Such modifications include the

replacement of the retroviral encapsidation sequence by one of a retrotransposon such as VL30 (see, e.g., U.S. Pat. No. 5,747,323). Preferably, the improved LAMP Construct is inserted downstream of the encapsidation sequence, preferably in opposite direction relative to the retroviral genome. Cell specific targeting may be achieved by the conjugation of antibodies or antibody fragments to the retroviral envelope protein as is known in the art.

[0196] Retroviral particles are prepared in the presence of a helper virus or in an appropriate complementation (packaging) cell line which contains integrated into its genome the retroviral genes for which the retroviral vector is defective (e.g. gag/pol and env). Such cell lines are described in the prior art (Miller and Rosman, 1989, *BioTechniques* 7: 980; Danos and Mulligan, 1988, *Proc. Natl. Acad. Sci. USA* 85: 6460; Markowitz, et al., 1988, *Virol.* 167: 400). The product of the env gene is responsible for the binding of the viral particle to the viral receptors present on the surface of the target cell and, therefore determines the host range of the retroviral particle. In the context of the invention, it is advantageous to use a packaging cell line, such as the PA317 cells (ATCC CRL 9078) or 293EI6 (WO97/35996) containing an amphotropic envelope protein, to allow infection of human and other species' target cells. The retroviral particles are preferably recovered from the culture supernatant and may optionally be further purified according to standard techniques (e.g. chromatography, ultracentrifugation).

[0197] Other suitable viruses include poxviruses. The genome of several members of poxyiridae has been mapped and sequenced. A poxyiral vector may be obtained from any member of the poxyiridae, in particular canarypox, fowlpox and vaccinia virus. Suitable vaccinia viruses include, but are not limited to, the Copenhagen strain (Goebel, et al., 1990, *Virol.* 179: 247-266; Johnson, et al., 1993, *Virol.* 196: 381-401), the Wyeth strain and the modified Ankara (MVA) strain (Antoine, et al., 1998, *Virol.* 244: 365-396). The general conditions for constructing a vaccinia virus vector are known in the art (see, e.g., EP 83 286 and EP 206 920; Mayr et al., 1975, *Infection* 3: 6-14; Sutter and Moss, 1992, *Proc. Natl. Acad. Sci. USA* 89: 10847-10851). Preferably, the polynucleotide of interest is inserted within a non-essential locus such as the noncoding intergenic regions or any gene for which inactivation or deletion does not significantly impair viral growth and replication.

[0198] Poxyiral particles are prepared as described in the art (Piccini, et al., 1987, *Methods of Enzymology* 153: 545-563; U.S. Pat. No. 4,769,330; U.S. Pat. No. 4,772,848; U.S. Pat. No. 4,603,112; U.S. Pat. No. 5,100,587 and U.S. Pat. No. 5,179,993). Generally, a donor plasmid is constructed, amplified by growth in *E. coli* and isolated by conventional procedures. Then, it is introduced into a suitable cell culture (e.g. chicken embryo fibroblasts) together with a poxvirus genome, to produce, by homologous recombination, poxyiral particles. These can be recovered from the culture supernatant or from the cultured cells after a lysis step (e.g., chemical lysis, freezing/thawing, osmotic shock, sonication and the like). Consecutive rounds of plaque purification can be used to remove contaminating wild type virus. Viral particles can then be purified using the

techniques known in the art (e.g., chromatographic methods or ultracentrifugation on cesium chloride or sucrose gradients).

[0199] The use of vaccinia as a live virus vaccine in the global campaign to eradicate smallpox made vaccinia an obvious choice for development as a live recombinant vaccine vector. Live recombinant vaccinia viruses expressing close to 100 different foreign proteins have been reported, and a number of these are effective experimental vaccines (reviewed by Moss and Flexner, 1987). Vaccinia is particularly versatile as an expression vector because of its large genomic size, capability of accepting at least 25,000 base pairs of foreign DNA, and its ability to infect most eukaryotic cell types, including insect cells (*ibid.*). Unlike other DNA viruses, poxviruses replicate exclusively in the cytoplasm of infected cells, reducing the possibility of genetic exchange of recombinant viral DNA with the host chromosome. Recombinant vaccinia vectors have been shown to properly process and express proteins from a variety of sources including man, other mammals, parasites, RNA and DNA viruses, bacteria and bacteriophage.

[0200] The expression of DNA encoding a foreign protein is controlled by host virus regulatory elements, including upstream promoter sequences and, where necessary, RNA processing signals. Insertion of foreign DNA into nonessential regions of the vaccinia virus genome has been carried out by homologous recombination (Panicali, et al., *Proc. Nat'l. Acad. Sci, USA*, 79: 4927, 1982; Mackett, et al., *Proc. Nat'l. Acad. Sci. USA*, 79: 7415, 1982).

[0201] Expression of cancer antigens by the improved LAMP Construct may occur because of transcriptional regulatory elements at or near the site of insertion or by more precise genetic engineering. Plasmid vectors that greatly facilitate insertion and expression of foreign genes have been constructed (Mackett, et al., *J. Virol*, 49: 857, 1982). These vectors contain an expression site, composed of a vaccinia transcriptional promoter and one or more unique restriction endonuclease sites for insertion of the foreign coding sequence flanked by DNA from a nonessential region of the vaccinia genome. The choice of promoter determines both the time (e.g., early or late) and level of expression, whereas the flanking DNA sequence determines the site of homologous recombination.

[0202] Only about one in a thousand virus particles produced by this procedure is a recombinant. Although recombinant virus plaques can be identified by DNA hybridization, efficient selection procedures have been developed. By using segments of nonessential vaccinia virus thymidine kinase (TK) gene as flanking sequences, the foreign gene recombines into the TK locus and by insertion inactivates the TK gene. Selection of TK virus is achieved by carrying out the virus plaque assay in TK cells in the presence of 5-bromodeoxyuridine. Phosphorylation of the nucleoside analogue and consequent lethal incorporation into viral DNA occurs only in cells infected with TK+ parental virus. Depending on the efficiency of the transfection and recombination, up to 80 of the plaques are desired recombinants, and the rest are spontaneous TK mutants.

[0203] Plasmid vectors that contain the *E. coli* beta-galactosidase gene, as well as an expression site for a second gene, permit an alternative method of distinguishing recombinant from parental virus (Chakrabarti,

et al., Mol. Cell. Biol., 5: 3403, 1985). Plaques formed by such recombinants can be positively identified by the blue color that forms upon addition of an appropriate indicator. By combining both TK selection and beta-galactosidase expression, recombinant virus is readily and quickly isolated. The recombinants are then amplified by propagation in suitable cell lines and expression of the inserted gene is checked by appropriate enzymological, immunological or physical procedures.

[0204] An upper limit to the amount of genetic information that can be added to the vaccinia virus genome is not yet known. However, the addition of nearly 25,000 base pairs of foreign DNA had no apparent deleterious effect on virus yield (Smith, et al., Gene, 25:21, 1983). Were it necessary, large segments of the vaccinia virus genome could be deleted to provide additional capacity (Moss, et al., J. Virol. 40: 387, 1981).

[0205] Viral capsid molecules may include targeting moieties to facilitate targeting and/or entry into cells. Suitable targeting molecules, include, but are not limited to: chemical conjugates, lipids, glycolipids, hormones, sugars, polymers (e.g. PEG, polylysine, PEI and the like), peptides, polypeptides (see, e.g., WO 94/40958), vitamins, antigens, lectins, antibodies and fragments thereof. Preferably, such targeting molecules recognize and bind to cell-specific markers, tissue-specific markers, cellular receptors, viral antigens, antigenic epitopes or tumor-associated markers.

[0206] Compositions comprising an improved LAMP Construct based on viral particles may be formulated in the form of doses of between 10 and 10^{14} i.u. (infectious units), and preferably, between 10 and 10^{11} i.u. The titer may be determined by conventional techniques. The doses of LAMP Constructs are preferably comprised between 0.01 and 10 mg/kg, more especially between 0.1 and 2 mg/kg.

Self-Replicating RNA

[0207] Self-replicating RNA virus vectors can also be constructed using the improved LAMP Constructs as described herein. For example, alphaviruses, flaviviruses, measles virus and rhabdoviruses can be used to generate self-replicating RNA virus vaccines. Preferred strains of self-replicating RNA viruses include, but are not limited to rabies virus (RABV), vesicular stomatitis virus (VSV), West Nile virus, Kunjin virus, Semliki Forest virus (SFV), Sindbis virus (SIN) and/or Venezuelan equine encephalitis virus (VEE).

[0208] Self-replicating RNA viruses express the native antigen upon delivery into tissue, thus mimicking live attenuated vaccines without having the risk of reversion to pathogenicity. They also stimulate the innate immune system, thus potentiating responses. See, e.g., Ljungberg, K. “*Self-replicating alphavirus RNA vaccines*,” Expert Rev Vaccines (2):177-94 (2015); Lundstrom, K., “*Oncolytic Alphaviruses in Cancer Immunotherapy*”, Vaccines 5:9 (2017); Lundstrom, K. “*Replicon RNA Viral Vectors as Vaccines*,” Vaccines 4:39 (2016) (hereby incorporated by reference in their entirety). Use of self-replicating vaccines comprising the improved LAMP Constructs described herein can also be used in prime-boost protocols.

[0209] Moreover, self-replicating RNA viruses can also be encapsulated by liposomes, as described herein, to improve delivery and targeting. Immunization with self-replicating RNA viruses comprising the

improved LAMP Constructs described herein may provide higher transient expression levels of antigens resulting in generation of neutralizing antibody responses and protection against lethal challenges under safe conditions.

Cell-Based Delivery Vehicles

[0210] The improved LAMP Constructs according to the invention can be delivered to target cells by means of other cells ("delivery cells") which comprise the constructs. Methods for introducing constructs into cells are known in the art and include microinjection of DNA into the nucleus of a cell (Capechi, et al., 1980, Cell 22: 479-488); transfection with CaP₀₄ (Chen and Okayama, 1987, Mol. Cell Biol. 7: 2745-2752), electroporation (Chu, et al., 1987, Nucleic Acid Res. 15: 1311-1326); lipofection/liposome fusion (Feigner, et al., 1987, Proc. Natl. Acad. Sci. USA 84: 7413-7417) and particle bombardment (Yang, et al., 1990, Proc. Natl. Acad. Sci. USA 87: 9568-9572). Suitable cells include autologous and non-autologous cells, and may include xenogenic cells. Delivery cells may be induced to deliver their contents to the target cells by inducing their death (e.g., by providing inducible suicide genes to these cells).

Accessory Molecules

[0211] The compositions comprising the improved LAMP Constructs according to the invention may comprise one or more accessory molecules for facilitating the introduction of an improved LAMP Construct into a cell and/or for enhancing a particular therapeutic effect and/or enhancing antibody production.

[0212] In addition, the composition comprising the improved LAMP Construct according to the present invention may include one or more stabilizing substance(s), such as lipids, nuclease inhibitors, hydrogels, hyaluronidase (WO 98/53853), collagenase, polymers, chelating agents (EP 890362), in order to inhibit degradation within the animal/human body and/or improve transfection/infection of the vector into a target cell. Such substances may be used alone or in combination (e.g., cationic and neutral lipids).

[0213] It has also been shown that adenovirus proteins are capable of destabilizing endosomes and enhancing the uptake of DNA into cells. The mixture of adenoviruses to solutions containing a lipid-complexed DNA vector or the binding of DNA to polylysine covalently attached to adenoviruses using protein cross-linking agents may substantially improve the uptake and expression of an improved LAMP Construct (see, e.g., Curiel, et al., 1992, Am. J. Respir. Cell. Mol. Biol. 6: 247-252).

Host Cells

[0214] Improved LAMP Constructs according to the invention can be expressed in a variety of host cells, including, but not limited to: prokaryotic cells (e.g., E. coli, Staphylococcus sp., Bacillus sp.); yeast cells (e.g., Saccharomyces sp.); insect cells; nematode cells; plant cells; amphibian cells (e.g., Xenopus); avian cells;

and mammalian cells (e.g., human cells, mouse cells, mammalian cell lines, primary cultured mammalian cells, such as from dissected tissues).

[0215] The molecules can be expressed in host cells isolated from an organism, host cells which are part of an organism, or host cells which are introduced into an organism. In one aspect, improved LAMP Constructs are expressed in host cells *in vitro*, e.g., in culture. In another aspect, improved LAMP Constructs are expressed in a transgenic organism (e.g., a transgenic mouse, rat, rabbit, pig, primate, etc.) that comprises somatic and/or germline cells comprising nucleic acids encoding the improved LAMP Constructs. Methods for constructing transgenic animals are well known in the art and are routine.

[0216] Improved LAMP Constructs also can be introduced into cells *in vitro*, and the cells (e.g., such as stem cells, hematopoietic cells, lymphocytes, and the like) can be introduced into the host organism. The cells may be heterologous or autologous with respect to the host organism. For example, cells can be obtained from the host organism, improved LAMP Constructs introduced into the cells *in vitro*, and then reintroduced into the host organism.

Antigen Presenting Cells

[0217] In a preferred aspect of the invention, an improved LAMP Construct as described herein is introduced into a natural or engineered antigen presenting cell.

[0218] The term "antigen presenting cell" (APC) as used herein intends any cell which presents on its surface an antigen in association with a major histocompatibility complex molecule, preferably a class II molecule, or portion thereof. Examples of suitable APCs are discussed in detail below and include, but are not limited to, whole cells such as macrophages, dendritic cells, B cells, hybrid APCs, and foster antigen presenting cells. Methods of making hybrid APCs are described and known in the art.

[0219] Dendritic cells (DCs) are potent antigen-presenting cells. It has been shown that DCs provide all the signals required for T cell activation and proliferation. These signals can be categorized into two types. The first type, which gives specificity to the immune response, is mediated through interaction between the T-cell receptor/CD3 ("TCR/CD3") complex and an antigenic peptide presented by a major histocompatibility complex ("MHC" defined above) class I or II protein on the surface of APCs. This interaction is necessary, but not sufficient, for T cell activation to occur. In fact, without the second type of signals, the first type of signals can result in T cell anergy. The second type of signals, called co-stimulatory signals, is neither antigen-specific nor MHC-restricted, and can lead to a full proliferation response of T cells and induction of T cell effector functions in the presence of the first type of signals.

[0220] Several molecules have been shown to enhance co-stimulatory activity. These include, but are not limited to, heat stable antigen (HSA), chondroitin sulfate-modified MHC invariant chain (Ii-CS), intracellular adhesion molecule I (ICAM-1), and B7 co-stimulatory molecule on the surface of APCs and its counter-receptor CD28 or CTLA-4 on T cells.

[0221] Other important co-stimulatory molecules are CD40, CD54, CD80, CD86. As used herein, the term "co-stimulatory molecule" encompasses any single molecule or combination of molecules which, when acting together with a peptide/MHC complex bound by a TCR on the surface of a T cell, provides a co-stimulatory effect which achieves activation of the T cell that binds the peptide. The term thus encompasses B7, or other co-stimulatory molecule(s) on an APC, fragments thereof (alone, complexed with another molecule(s), or as part of a fusion protein) which, together with peptide/MHC complex, binds to a cognate ligand and result in activation of the T cell when the TCR on the surface of the T cell specifically binds the peptide. Co-stimulatory molecules are commercially available from a variety of sources, including, for example, Beckman Coulter.

[0222] In one aspect of the invention, the method described in Romani et al., *J. Immunol. Methods* 196: 135-151, 1996, and Bender et al, *J. Immunol. Methods* 196: 121-135, 1996, are used to generate both immature and mature dendritic cells from the peripheral blood mononuclear cells (PBMCs) of a mammal, such as a murine, simian or human. Briefly, isolated PBMCs are pre-treated to deplete T- and B-cells by means of an immunomagnetic technique. Lymphocyte-depleted PBMC are then cultured for in RPMI medium 9 e.g., about 7 days), supplemented with human plasma (preferably autologous plasma) and GM-CSF/IL-4, to generate dendritic cells. Dendritic cells are nonadherent when compared to their monocyte progenitors. Thus, on approximately day 7, non-adherent cells are harvested for further processing.

[0223] The dendritic cells derived from PBMC in the presence of GM-CSF and IL-4 are immature, in that they can lost the nonadherence property and revert back to macrophage cell fate if the cytokine stimuli are removed from the culture. The dendritic cells in an immature state are very effective in processing native protein antigens for the MHC class II restricted pathway (Romani, et al., *J. Exp. Med.* 169:1169, 1989). Further maturation of cultured dendritic cells is accomplished by culturing for 3 days in a macrophage-conditioned medium (CM), which contains the necessary maturation factors. Mature dendritic cells are less able to capture new proteins for presentation but are much better at stimulating resting T cells (both CD4 and CD8) to grow and differentiate.

[0224] Mature dendritic cells can be identified by their change in morphology, such as the formation of more motile cytoplasmic processes; by their nonadherence; by the presence of at least one of the following markers: CD83, CD68, HLA-DR or CD86; or by the loss of Fc receptors such as CD 115 (reviewed in Steinman, *Annu. Rev. Immunol.* 9: 271, 1991). Mature dendritic cells can be collected and analyzed using typical cytofluorography and cell sorting techniques and devices, such as FACScan and FACStar. Primary antibodies used for flow cytometry are those specific to cell surface antigens of mature dendritic cells and are commercially available. Secondary antibodies can be biotinylated Igs followed by FITC- or PE-conjugated streptavidin.

[0225] Alternatively, others have reported that a method for upregulating (activating) dendritic cells and converting monocytes to an activated dendritic cell phenotype. This method involves the addition of calcium ionophore to the culture media convert monocytes into activated dendritic cells. Adding the calcium

21 ionophore A23187, for example, at the beginning of a 24-48 hour culture period resulted in uniform activation and dendritic cell phenotypic conversion of the pooled "monocyte plus DC" fractions: characteristically, the activated population becomes uniformly CD 14 (Leu M3) negative, and upregulates HLA-DR, HLA-DQ, ICAM-1, 137.1, and 137.2. Furthermore, this activated bulk population functions as well on a small numbers basis as a further purified. Specific combination(s) of cytokines have been used successfully to amplify (or partially substitute) for the activation/conversion achieved with calcium ionophore: these cytokines include but are not limited to G-CSF, GM-CSF, IL-2, and IL-4. Each cytokine when given alone is inadequate for optimal upregulation.

[0226] The second approach for isolating APCs is to collect the relatively large numbers of precommitted APCs already circulating in the blood. Previous techniques for isolating committed APCs from human peripheral blood have involved combinations of physical procedures such as metrizamide gradients and adherence/nonadherence steps (Freudenthal et al. PNAS 87: 7698-7702, 1990); Percoll gradient separations (Mehta-Damani, et al., J. Immunol. 153: 996-1003, 1994); and fluorescence activated cell sorting techniques (Thomas et al., J. Immunol. 151: 6840-52, 1993).

[0227] There are many other methods routine in the art for isolating professional antigen presenting cells (or their precursors) and that such methods and others which may be developed are not limiting and are encompassed within the scope of the invention.

[0228] In one embodiment, the APCs and therefore the cells presenting one or more antigens are autologous. In another embodiment, the APCs presenting the antigen are allogeneic, i.e., derived from a different subject.

[0229] As discussed herein, improved LAMP Constructs can be introduced into APCs using the methods described above or others known in the art, including, but not limited to, transfection, electroporation, fusion, microinjection, viral-based delivery, or cell based delivery. Arthur et al., Cancer Gene Therapy 4(1): 17-25, 1997, reports a comparison of gene transfer methods in human dendritic cells.

[0230] Known, partial and putative human leukocyte antigen (HLA), the genetic designation for the human MHC, amino acid and nucleotide sequences, including the consensus sequence, are published (see, e.g., Zemmour and Parham, Immunogenetics 33: 310-320, 1991), and cell lines expressing HLA variants are known and generally available as well, many from the American Type Culture Collection ("ATCC"). Therefore, using PCR, MHC class II-encoding nucleotide sequences are readily operatively linked to an expression vector of this invention that is then used to transform an appropriate cell for expression therein.

[0231] Professional APCs can be used, such as macrophages, B cells, monocytes, dendritic cells, and Langerhans cells. These are collected from the blood or tissue of 1) an autologous donor; 2) a heterologous donor having a different HLA specificity than the host to be treated; or 3) from a xenogeneic donor of a different species using standard procedures (Coligan, et. al., Current Protocols in Immunology, sections 3 and 14, 1994).

The cells may be isolated from a normal host or a patient having an infectious disease, cancer, autoimmune disease, or allergy.

[0232] Professional APCs may be obtained from the peripheral blood using leukopheresis and "FICOLL/HYPAQUE" density gradient centrifugation (stepwise centrifugation through Ficoll and discontinuous Percoll density gradients). Procedures are utilized which avoid the exposure of the APCs to antigens which could be internalized by the APCs, leading to activation of T cells not specific for the antigens of interest.

[0233] Cells which are not naturally antigen presenting can be engineered to be antigen presenting by introducing sequences encoding appropriate molecules. For example, nucleic acid sequences encoding MHC class II molecules, accessory molecules, co-stimulatory molecules and antigen processing assisting molecules can be introduced after direct synthesis, cloning, purification of DNA from cells containing such genes, and the like. One expedient means to obtain genes for encoding the molecules used in the improved LAMP Constructs and methods described herein is by polymerase chain reaction (PCR) amplification on selected nucleic acid templates with selected oligonucleotide primer pairs. For example, epithelial cells, endothelial cells, tumor cells, fibroblasts, activated T cells, eosinophils, keratinocytes, astrocytes, microglial cells, thymic cortical epithelial cells, Schwann cells, retinal pigment epithelial cells, myoblasts, vascular smooth muscle cells, chondrocytes, enterocytes, thyrocytes and kidney tubule cells can be used. These may be primary cells recently explanted from a host and not extensively passaged in cell culture to form an established cell line, or established cell lines that are relatively homogeneous and capable of proliferating for many generations or indefinitely.

[0234] Cells that are not professional APCs are isolated from any tissue of an autologous donor; a heterologous donor or a xenogeneic donor, where they reside using a variety of known separation methods (Darling, *Animal Cells: Culture and Media*. J. Wiley, New York, 1994; Freshney, *Culture of Animal Cells*. Alan R. Liss, Inc., New York, 1987). Non-autologous cells, e.g., heterologous or xenogeneic cells, can be engineered *ex vivo* to express HLA class I and class II molecules that match known human HLA specificities. These cells can then be introduced into a human subject matching the HLA specificity of the engineered cells. The cells are further engineered *ex vivo* to express one or more LAMP Constructs according to the invention.

[0235] The engineered cells are maintained in cell culture by standard cell culture methods (Darling, *Animal Cells: Culture and Media*". J. Wiley, New York, 1994; Freshney, *Culture of Animal Cells*". Alan R. Liss, Inc., New York, 1987). Cell lines for use in the present invention are obtained from a variety of sources (e.g., ATCC Catalogue of Cell Lines & Hybridomas, American Type Culture Collection, 8th edition, 1995), or are produced using standard methods (Freshney, *Culture of Immortalized Cells*, Wiley-Liss, New York, 1996). Non-transformed cell lines are preferred for use in human subjects.

[0236] In one aspect, CD34+ precursors that are differentiating under the influence of GM-CSF into dendritic cells are obtained from the body of a subject and nucleic acids encoding LAMP Constructs according to the invention are introduced into the cells, which are then injected into the subject. Utilizing the improved

LAMP Constructs as described herein will enhance the association of peptides derived from a particular antigen with MHC class II molecules on the transduced antigen presenting cells, resulting in significantly more potent systemic T cell dependent immune responses and/or antibody production. While the antigen presenting cells transfected in this strategy are preferably autologous cells, any MHC class II cells that effectively present antigen in the host may be used as described above.

Peptide Vaccines

[0237] Also within the scope of this invention are peptide vaccines encoded by the improved LAMP Construct. Preferably, the antigen is processed within the compartment/organelle (or subsequent compartment/organelle to which it is delivered) to generate an epitope bound to an MHC class II molecule capable of modulating an immune response.

[0238] The peptide vaccines encoded by the improved LAMP Constructs may also may be bound in a membranous structure to facilitate its administration to the body of an organism. For example, the peptide vaccine encoded by the improved LAMP Construct may be incorporated into liposomes, as described in U.S. Pat. No. 4,448,765.

[0239] When a protein or polypeptide is to be used as an immunogen, it may be produced by expression of any one or more of the improved LAMP Constructs described herein in a recombinant cell or it may be prepared by chemical synthesis. For example, the Merrifield technique (Journal of American Chemical Society, vol. 85, pp. 2149-2154, 1968), can be used.

Methods of Producing Antibodies using LAMP Constructs

[0240] The improved LAMP Constructs as polynucleotides, the encoded proteins of the improved LAMP Constructs, and/or cells (such as antigen presenting cells which express the improved LAMP Constructs described herein) can be used to generate antibodies by methods well known by the skilled artisan, such as, for example, methods described in the art. See, for instance, Sutcliffe et al., *supra*; Wilson et al., *supra*; Chow et al., Proc. Natl. Acad. Sci. USA 82:910-914 (1985); and Bittle et al., J. Gen. Virol. 66:2347-2354 (1985). If *in vivo* immunization is used, animals may be immunized with a protein encoded by the improved LAMP Construct and/or a polynucleotide comprising the improved LAMP Construct comprising an antigen as described herein. Priming with improved LAMP Constructs as polynucleotides, the encoded proteins of the improved LAMP Constructs, and/or cells (such as antigen presenting cells which express the improved LAMP Constructs described herein) followed by boosting with an antigen is a preferred embodiment of the invention. In further preferred embodiments, priming with an improved LAMP Construct as described herein followed by boosting with an antigen is specifically contemplated and can be used to generate an even more robust immune response, especially in view of antibody repertoire diversity and titer.

[0241] The improved LAMP Construct comprising the antigen may be injected into the non-human vertebrate to raise antibodies. Preparation and injection of LAMP Constructs into non-human vertebrates can be accomplished according to principles of immunization of animals that are well known to those skilled in the art.

[0242] The use of an improved LAMP Construct to effectively present the antigen involves, in one aspect, the antigen being processed by LAMP in Antigen Presenting Cells after endocytosis and fusion of the endosome with a lysosome. The endosome then merges with an exocytic vesicle from the Golgi apparatus containing class II MHC molecules, to which the resultant peptides bind. The MHC-peptide complex then trafficks to the plasma membrane where the antigen is available for display to CD4⁺ T cells.

[0243] Animals such as rabbits, rats, mice, llamas, camels, and/or cows can be immunized with the improved LAMP Construct comprising an antigen and/or a polynucleotide encoding the improved LAMP Construct comprising an antigen. Additional animals suitable for immunization include, non-human mammals, such as a rodent (e.g. a guinea pig, a hamster, a rat, a mouse), murine (e.g. a mouse), canine (e.g. a dog), feline (e.g. a cat), equine (e.g. a horse), a primate, simian (e.g. a monkey or ape), a monkey (e.g. marmoset, baboon, rhesus macaque), an ape (e.g. gorilla, chimpanzee, orangutan, gibbon).

[0244] For instance, intraperitoneal and/or intradermal injection of emulsions containing about 100 micrograms of an improved LAMP Construct comprising an antigen or carrier protein and Freund's adjuvant or any other adjuvant known for stimulating an immune response may be used. Several booster injections (such as with the recombinant antigen protein) may be needed, for instance, at intervals of about two weeks, to provide a useful titer of an anti-antigen antibody which can be detected, for example, by ELISA assay using free antigen adsorbed, directly or indirectly (e.g., via a biotinylated AviTag), to a solid surface. The titer of anti-antigen antibodies in serum from an immunized animal may be increased by selection of anti-antibodies, for instance, by adsorption to the antigen on a solid support and elution of the selected antibodies according to methods well known in the art.

[0245] Alternatively, a polynucleotide encoding the improved LAMP Construct comprising an antigen can also be directly introduced into animals. See, for example, U.S. patent numbers 5,676,954; 6,875,748; 5,661,133; Sahin et al., *Nat Rev Drug Discov*, 2014 Oct;13(10):759-80; Kariko et al., *Mol Ther*, 2008 Nov;16(11):1833-40; Kariko et al., *Nucleic Acid Res*, 2011, Nov;39(21):e142; US Patent number 6,511,832. In one example, an improved LAMP Construct comprising an antigen is directly injected into a non-human vertebrate. Injection into the animals can occur via intramuscular, intradermal, intranasal, subcutaneous, intravenous, intratracheal, and intrathecal deliveries. Follow-on boosting with a recombinant antigen can also be include in generating the antibodies.

[0246] Additionally, antibodies generated by the disclosed methods can be affinity matured using display technology, such as for example, phage display, yeast display or ribosome display. In one example, single chain antibody molecules ("scFvs") displayed on the surface of phage particles are screened to identify

those scFvs that immunospecifically bind to the antigen and/or the starting protein. The present invention encompasses both scFvs and portions thereof that are identified to immunospecifically bind to the antigen and/or the starting protein. Such scFvs can routinely be "converted" to immunoglobulin molecules by inserting, for example, the nucleotide sequences encoding the VH and/or VL domains of the scFv into an expression vector containing the constant domain sequences and engineered to direct the expression of the immunoglobulin molecule.

[0247] Recombinant expression of the raised antibodies (including scFvs and other molecules comprising, or alternatively consisting of, antibody fragments or variants thereof (e.g., a heavy or light chain of an antibody of the invention or a portion thereof or a single chain antibody of the invention)) using the improved LAMP Construct comprising an antigen and/or a polynucleotide encoding the improved LAMP Construct comprising an antigen of the invention, requires construction of an expression vector(s) containing a polynucleotide that encodes the antibody or fragment or variant thereof. Once a polynucleotide encoding an antibody molecule (e.g., a whole antibody, a heavy or light chain of an antibody, or variant or portion thereof (preferably, but not necessarily, containing the heavy or light chain variable domain)), of the invention has been obtained, the vector(s) for the production of the antibody molecule may be produced by recombinant DNA technology using techniques well known in the art. Thus, methods for preparing an antibody by expressing a polynucleotide containing an antibody encoding nucleotide sequence are described herein. Methods which are well known to those skilled in the art can be used to construct expression vectors containing the antibody coding sequences and appropriate transcriptional and translational control signals. These methods include, for example, *in vitro* recombinant DNA techniques, synthetic techniques, and *in vivo* genetic recombination and are described herein. The invention, thus, provides replicable vectors comprising a nucleotide sequence encoding the anti-antigen antibody obtained and isolated as described herein (e.g., a whole antibody, a heavy or light chain of an antibody, a heavy or light chain variable domain of an antibody, or a portion thereof, or a heavy or light chain CDR, a single chain Fv, or fragments or variants thereof), operably linked to a promoter. Such vectors may include the nucleotide sequence encoding the constant region of the antibody molecule (see, e.g., PCT Publication WO 86/05807; PCT Publication WO 89/01036; and U.S. Patent No. 5,122,464) and the variable domain of the antibody may be cloned into such a vector for expression of the entire heavy chain, the entire light chain, or both the entire heavy and light chains.

[0248] The expression vector(s) can be transferred to a host cell by conventional techniques and the transfected cells are then cultured by conventional techniques to produce either the anti-antigen antibody. Thus, the invention includes host cells containing polynucleotide(s) encoding the anti-antigen antibody (e.g., whole antibody, a heavy or light chain thereof, or portion thereof, or a single chain antibody of the invention, or a fragment or variant thereof), operably linked to a heterologous promoter. In preferred embodiments, for the expression of entire antibody molecules, vectors encoding both the heavy and light chains may be co-expressed in the host cell for expression of the entire immunoglobulin molecule, as detailed below.

[0249] A variety of host-expression vector systems may be utilized to express anti-antigen antibody. Such host-expression systems represent vehicles by which the coding sequences of interest may be produced and subsequently purified, but also represent cells which may, when transformed or transfected, with the appropriate nucleotide coding sequences, express the anti-antigen antibody. These include, but are not limited to, microorganisms such as bacteria (e.g., *E. coli*, *B. subtilis*) transformed with recombinant bacteriophage DNA, plasmid DNA or cosmid DNA expression vectors containing sequences; yeast (e.g., *Saccharomyces*, *Pichia*) transformed with recombinant yeast expression vectors containing coding sequences; insect cell systems infected with recombinant virus expression vectors (e.g., baculovirus) containing coding sequences; plant cell systems infected with recombinant virus expression vectors (e.g., cauliflower mosaic virus, CaMV; tobacco mosaic virus, TMV) or transformed with recombinant plasmid expression vectors (e.g., Ti plasmid) containing coding sequences; or mammalian cell systems (e.g., COS, CHO, BHK, 293, 3T3 cells) harboring recombinant expression constructs containing promoters derived from the genome of mammalian cells (e.g., metallothionein promoter) or from mammalian viruses (e.g., the adenovirus late promoter; the vaccinia virus 7.5K promoter). Preferably, bacterial cells such as *Escherichia coli*, and more preferably, eukaryotic cells, are used for the expression of the anti-antigen antibody. For example, mammalian cells such as Chinese hamster ovary cells (CHO), in conjunction with a vector such as the major intermediate early gene promoter element from human cytomegalovirus is an effective expression system (Foecking et al., *Gene* 45:101 (1986); Cockett et al., *Bio/Technology* 8:2 (1990)).

[0250] In bacterial systems, a number of expression vectors may be advantageously selected depending upon the intended use. For example, when a large quantity of a protein is to be produced (for either antibody production or encoded polypeptides of the improved LAMP Construct), vectors which direct the expression of high levels of fusion protein products that are readily purified may be desirable. Such vectors include, but are not limited to, the *E. coli* expression vector pUR278 (Ruther et al., *EMBO* 1. 2:1791 (1983)), in which the coding sequence may be ligated individually into the vector in frame with the lac Z coding region so that a fusion protein is produced; pIN vectors (Inouye & Inouye, *Nucleic Acids Res.* 13:3101-3109 (1985); Van Heeke & Schuster, *J. Biol. Chem.* 24:5503-5509 (1989)); and the like. pGEX vectors may also be used to express foreign polypeptides as fusion proteins with glutathione S-transferase (GST). In general, such fusion proteins are soluble and can easily be purified from lysed cells by adsorption and binding to matrix glutathione agarose beads followed by elution in the presence of free glutathione. The pGEX vectors are designed to include thrombin or Factor Xa protease cleavage sites so that the cloned target gene product can be released from the GST moiety.

[0251] In an insect system, *Autographa californica* nuclear polyhedrosis virus (AcNPV) may be used as a vector to express an anti-antigen antibody or the encoded polypeptides of the improved LAMP Construct. The virus grows in *Spodoptera frugiperda* cells. Coding sequences may be cloned individually into non-

essential regions (for example, the polyhedrin gene) of the virus and placed under control of an AcNPV promoter (for example, the polyhedrin promoter).

[0252] In mammalian host cells, a number of viral-based expression systems may be utilized express an anti-antigen antibody or the encoded polypeptides of the improved LAMP Construct. In cases where an adenovirus is used as an expression vector, the coding sequence of interest may be ligated to an adenovirus transcription/translation control complex, e.g., the late promoter and tripartite leader sequence. This chimeric gene may then be inserted in the adenovirus genome by *in vitro* or *in vivo* recombination.

[0253] Insertion in a non-essential region of the viral genome (e.g., region EI or E3) will result in a recombinant virus that is viable and capable of expressing the anti-antigen antibody or the encoded polypeptides of the improved LAMP Construct in infected hosts (e.g., see Logan & Shenk, Proc. Natl. Acad. Sci. USA 81:355-359 (1984)).

[0254] Specific initiation signals may also be required for efficient translation of inserted coding sequences. These signals include the ATG initiation codon and adjacent sequences. Furthermore, the initiation codon must be in phase with the reading frame of the desired coding sequence to ensure translation of the entire insert. These exogenous translational control signals and initiation codons can be of a variety of origins, both natural and synthetic. The efficiency of expression may be enhanced by the inclusion of appropriate transcription enhancer elements, transcription terminators, etc. (see, e.g., Bittner et al., Methods in Enzymol. 153:51-544 (1987)).

[0255] In addition, a host cell strain may be chosen which modulates the expression of the inserted sequences, or modifies and processes the gene product in the specific fashion desired. Such modifications (e.g., glycosylation) and processing (e.g., cleavage) of protein products may be important for the function of the protein. Different host cells have characteristic and specific mechanisms for the post-translational processing and modification of proteins and gene products. Appropriate cell lines or host systems can be chosen to ensure the correct modification and processing of the foreign protein expressed, to this end, eukaryotic host cells which possess the cellular machinery for proper processing of the primary transcript, glycosylation, and phosphorylation of the gene product may be used. Such mammalian host cells include, but are not limited to, CHO, VERY, BHK, Hela, COS, NSO, MDCK, 293, 3T3, W138, and in particular, breast cancer cell lines such as, for example, BT483, Hs578T, HTB2, BT20 and T47D, and normal mammary gland cell line such as, for example, CRL703O and HsS78Bst.

[0256] For long-term, high-yield production of recombinant proteins, stable expression is preferred. For example, cell lines which stably express the express an anti-antigen antibody or the encoded polypeptides of the improved LAMP Construct may be engineered. Rather than using expression vectors which contain viral origins of replication, host cells can be transformed with a polynucleotide controlled by appropriate expression control elements (e.g., promoter, enhancer, sequences, transcription terminators, polyadenylation sites, etc.), and a selectable marker. Following the introduction of the foreign polynucleotide, engineered cells may be

allowed to grow for 1-2 days in an enriched media, and then are switched to a selective media. The selectable marker in the recombinant plasmid confers resistance to the selection and allows cells to stably integrate the plasmid into their chromosomes and grow to form foci which in turn can be cloned and expanded into cell lines. This method may advantageously be used to engineer cell lines which express the anti-antigen antibody or the encoded polypeptides of the improved LAMP Construct.

[0257] A number of selection systems may be used, including but not limited to, the herpes simplex virus thymidine kinase (Wigler et al., Cell 11:223 (1977)), hypoxanthineguanine phosphoribosyltransferase (Szybalska & Szybalski, Proc. Natl. Acad. Sci. USA 48:202 (1992)), and adenine phosphoribosyltransferase (Lowy et al., Cell 22:8 17 (1980)) genes can be employed in tk-, hgp^{rt}- or ap^{rt}- cells, respectively. Also, antimetabolite resistance can be used as the basis of selection for the following genes: dhfr, which confers resistance to methotrexate (Wigler et al., Natl. Acad. Sci. USA 77:357 (1980); O'Hare et al., Proc. Natl. Acad. Sci. USA 78:1527 (1981)); gpt, which confers resistance to mycophenolic acid (Mulligan & Berg, Proc. Natl. Acad. Sci. USA 78:2072 (1981)); neo, which confers resistance to the aminoglycoside G-418 (Goldspiel et al., Clinical Pharmacy, 12: 488-505 (1993); Wu and Wu, Biotherapy 3:87-95 (1991); Tolstoshev, Ann. Rev. Pharmacol. Toxicol. 32:573-596 (1993); Mulligan, Science 260:926-932 (1993); and Morgan and Anderson, Ann. Rev. Biochem. 62: 191-217 (1993); TIB TECH 11(5):155-2 15 (May; 1993)); and hyg^{ro}, which confers resistance to hygromycin (Santerre et al., Gene 30:147 (1984)). Methods commonly known in the art of recombinant DNA technology may be routinely applied to select the desired recombinant clone, and such methods are described, for example; in Ausubel et al. (eds.), Current Protocols in Molecular Biology, John Wiley & Sons, NY (1993); Kriegler, Gene Transfer and Expression, A Laboratory Manual, Stockton Press, NY (1990); and in Chapters 12 and 13, Dracopoli et al. (eds), Current Protocols in Human Genetics, John Wiley & Sons, NY (1994); Colberre-Garapin et al., J. Mol. Biol. 150:1 (1981).

[0258] The expression levels of either an anti-antigen antibody or the encoded polypeptides of the improved LAMP Construct can be increased by vector amplification (for a review, see Bebbington and Hentschel, *The Use Of Vectors Based On Gene Amplification For The Expression Of Cloned Genes In Mammalian Cells In DNA Cloning*, Vol.3. (Academic Press, New York, 1987)). When a marker in the vector system expressing an anti-antigen antibody or the encoded polypeptides of the improved LAMP Construct is amplifiable, an increase in the level of inhibitor present in the host cell culture will increase the number of copies of the marker gene. Since the amplified region is associated with the coding sequence, production of the anti-antigen antibody express or the encoded polypeptides of the improved LAMP Construct will also increase (Crouse et al., Mol. Cell. Biol. 3:257 (1983)).

[0259] Other elements that can be included in vector sequences include heterologous signal peptides (secretion signals), membrane anchoring sequences, introns, alternative splice sites, translation start and stop signals, inteins, biotinylation sites and other sites promoting post-translational modifications, purification tags, sequences encoding fusions to other proteins or peptides, separate coding regions separated by internal

ribosome reentry sites, sequences encoding “marker” proteins that, for example, confer selectability (e.g., antibiotic resistance) or sortability (e.g., fluorescence), modified nucleotides, and other known polynucleotide cis-acting features not limited to these examples.

[0260] The host cell may be co-transfected with two expression vectors of the invention, for example, the first vector encoding a heavy chain derived polypeptide and the second vector encoding a light chain derived polypeptide. The two vectors may contain identical selectable markers which enable equal expression of heavy and light chain polypeptides. Alternatively, a single vector may be used which encodes, and is capable of expressing, both heavy and light chain polypeptides. In such situations, the light chain is preferably placed before the heavy chain to avoid an excess of toxic free heavy chain (Proudfoot, Nature 322:52 (1986); Kohler, Proc. Natl. Acad. Sci. USA 77:2 197 (1980)). The coding sequences for the heavy and light chains may comprise cDNA or genomic DNA or synthetic DNA sequences.

[0261] Once an anti-antigen antibody or the encoded polypeptides of the improved LAMP Construct has been produced by recombinant expression, it may be purified by any method known in the art for purification of a protein, for example, by chromatography (e.g., ion exchange, affinity (particularly by Protein A affinity and immunoaffinity for the specific antigen), and sizing column chromatography), centrifugation, differential solubility, or by any other standard technique for the purification of proteins. Further, an anti-antigen antibody or the encoded polypeptides of the improved LAMP Construct may be fused to heterologous polypeptide sequences described herein or otherwise known in the art to facilitate purification.

[0262] In one example, the anti-antigen antibody or the encoded polypeptides of the improved LAMP Construct may be fused with the constant domain of immunoglobulins (IgA, IgE, IgG, IgM), or portions thereof (CH1, CH2, CH3, or any combination thereof and portions thereof), or albumin (including but not limited to recombinant human albumin or fragments or variants thereof (see, e.g., U.S. Patent No. 5,876,969, issued March 2, 1999, EP Patent 0 413 622, and U.S. Patent No. 5,766,883, issued June 16, 1998), resulting in chimeric polypeptides. Such fusion proteins may facilitate purification and may increase half-life *in vivo*. This has been shown for chimeric proteins consisting of the first two domains of the human CD4-polypeptide and various domains of the constant regions of the heavy or light chains of mammalian immunoglobulins. See, e.g., EP 394,827; Trauneker et al., Nature, 331:84-86 (1988). Enhanced delivery of an antigen across the epithelial barrier to the immune system has been demonstrated for antigens (e.g., insulin) conjugated to an FcRn binding partner such as IgG or Fc fragments (see, e.g., PCT Publications WO 96/22024 and WO 99/04813). IgG Fusion proteins that have a disulfide-linked dimeric structure due to the IgG portion disulfide bonds have also been found to be more efficient in binding and neutralizing other molecules than monomeric polypeptides or fragments thereof alone. See, e.g., Fountoulakis et al., J. Biochem., 270:3958-3964 (1995). Nucleic acids encoding the anti-antigen antibody or the encoded polypeptides of the improved LAMP Construct described herein can also be recombined with a gene of interest as an epitope tag (e.g., the hemagglutinin ("HA") tag or flag tag) to aid in detection and purification of the expressed polypeptide. For example, a system described by

Janknecht et al. allows for the ready purification of non-denatured fusion proteins expressed in human cell lines (Janknecht et al., 1991, Proc. Natl. Acad. Sci. USA 88:8972- 897). In this system, the gene of interest is subcloned into a vaccinia recombination plasmid such that the open reading frame of the gene is translationally fused to an amino-terminal tag consisting of six histidine residues. The tag serves as a matrix-binding domain for the fusion protein. Extracts from cells infected with the recombinant vaccinia virus are loaded onto Ni²⁺-nitriloacetic acid-agarose column and histidine-tagged proteins can be selectively eluted with imidazole-containing buffers.

Administration

[0263] Vaccine material according to this invention may contain the immune stimulatory improved LAMP Constructs described herein or may be recombinant microorganisms, or antigen presenting cells which express the immune stimulatory improved LAMP Constructs. Preparation of improved LAMP Constructs containing vaccine material according to this invention and administration of such improved LAMP Constructs for immunization of individuals are accomplished according to principles of immunization that are well known to those skilled in the art.

[0264] Large quantities of these materials may be obtained by culturing recombinant or transformed cells containing replicons that express the improved LAMP Constructs described herein. Culturing methods are well-known to those skilled in the art and are taught in one or more of the documents cited above. The improved LAMP Construct vaccines are generally produced by culture of recombinant or transformed cells and formulated in a pharmacologically acceptable solution or suspension, which is usually a physiologically-compatible aqueous solution, or in coated tablets, tablets, capsules, suppositories or ampules, as described in the art, for example in U.S. Pat. No. 4,446,128, incorporated herein by reference. Administration may be any suitable route, including oral, rectal, intranasal or by injection where injection may be, for example, transdermal, subcutaneous, intramuscular or intravenous.

[0265] The improved LAMP Constructs are administered to a mammal in an amount sufficient to induce an immune response in the mammal. A minimum preferred amount for administration is the amount required to elicit antibody formation to a concentration at least 4 times that which existed prior to administration. A typical initial dose for administration would be 10-5000 micrograms when administered intravenously, intramuscularly or subcutaneously, or 10⁵ to 10¹¹ plaque forming units of a recombinant vector, although this amount may be adjusted by a clinician doing the administration as commonly occurs in the administration of vaccines and other agents which induce immune responses. A single administration may usually be sufficient to induce immunity, but multiple administrations may be carried out to assure or boost the response.

[0266] The improved LAMP Construct vaccines may be tested initially in a non-human mammal (e.g., a mouse or primate). For example, assays of the immune responses of inoculated mice can be used to demonstrate greater antibody, T cell proliferation, and cytotoxic T cell responses to the improved LAMP

Constructs than to wild type antigen. Improved LAMP Constructs can be evaluated in Rhesus monkeys to determine whether the vaccine formulation that is highly effective in mice will also elicit an appropriate monkey immune response. In one aspect, each monkey receives a total of 5 mg DNA per immunization, delivered IM and divided between 2 sites, with immunizations at day 0 and at weeks 4, 8, and 20, with additional doses optional. Antibody responses, ADCC, CD4+ and CD8+ T-cell cytokine production, CD4+ and CD8+ T-cell antigen-specific cytokine staining can be measured to monitor immune responses to the vaccine.

[0267] Further description of suitable methods of formulation and administration according to this invention may be found in U.S. Pat. No. 4,454,116 (constructs), U.S. Pat. No. 4,681,762 (recombinant bacteria), and U.S. Pat. 4,592,002 and 4,920,209 (recombinant viruses).

Cancer Immunotherapy: Candidates for Prevention and Treatment

[0268] The improved LAMP Constructs described herein comprising at least one cancer antigen described in Table 1 can be used to treat patients who have cancer and/or a hyperproliferative disorder. Examples include patients with documented Epstein-Barr virus associated lymphomas, patients with HPV associated cervical carcinomas, patients with chronic HCV, or patients with a defined re-arrangement or mutation in an oncogene or tumor suppressor gene. Further preferred embodiments include patients having hyperproliferative disorders, including cancer, resulting from CMV infection.

[0269] In preferred embodiments, cancers that can be treated using the improved LAMP Constructs described herein include, but are not limited to all stages of progression, including hyperplasia of an adenocarcinoma, sarcoma, skin cancer, melanoma, bladder cancer, brain cancer (including glioblastoma multiforme), breast cancer, uterine cancer, ovarian cancer, prostate cancer, lung cancer (including, but not limited to NSCLC, SCLC, squamous cell cancer), colorectal cancer, anal cancer, rectal cancer, cervical cancer, liver cancer, head and neck cancer, oral cancer, salivary gland cancer, esophageal cancer, pancreas cancer, pancreatic ductal adenocarcinoma (PDA), renal cancer, stomach cancer, kidney cancer, multiple myeloma or cerebral cancer.

[0270] It is envisioned that therapy with an improved LAMP Construct, such as in the case of a vaccine composition comprising the improved LAMP Construct, could be utilized at any period during the course of the individual's cancer, once it is identified. It is also possible that in high risk patients, vaccination in order to prevent the subsequent emergence of a cancer. Protein based LAMP Construct vaccines as well as cell therapy (e.g, dendritic cell therapy comprising LAMP Constructs) are also envisioned.

Procedure for Therapy

[0271] In one embodiment, the improved LAMP Constructs could be injected into the patient at any suitable time during the course of their malignancy. For example, the improved LAMP Construct comprising at least one cancer antigen described in Table 1 would be injected at a stage when the tumor burden was low.

In an alternative embodiment in which the improved LAMP Construct is introduced into the individual's antigen presenting cells (such as, for example, dendritic cells), precursors to the antigen presenting cells or mature antigen presenting cells are drawn either from the individual's bone marrow or peripheral blood by vena puncture. These cells are established in culture followed by transduction with the improved LAMP Construct. Once transduction had occurred, these antigen presenting cells are injected back into the patient.

[0272] In a particularly preferred embodiment, the invention provides a method of treatment for a cancer patient having low tumor burden, such as early in the disease, after resection of a neoplastic tumor, or when the burden of tumor cells is otherwise reduced. In this method, a cell population containing autologous stem cells capable of differentiation into antigen presenting cells which will express MHC class II molecules is obtained from the patient. These cells are cultured and transformed by introducing an improved LAMP Construct to deliver the cancer antigen to be associated with an MHC class II molecule either within the compartment/organelle or within another compartment/organelle to which the antigen is delivered.

[0273] The transfected stem cell population is then reintroduced into the patient, where the stem cells differentiate into antigen presenting cells which express MHC class II molecules complexed with T_h epitopes from the antigen. The immune response to the antigen will be enhanced by enhanced stimulation of the helper T cell population.

[0274] More generally, in one embodiment, this invention provides a vaccine composition comprising the improved LAMP Construct for modulating an immune response in a mammal to an antigen (i.e., stimulating, enhancing, or reducing such a response).

Kits

[0275] The invention further comprises kits to facilitate performing the methods described herein. In one aspect, a kit comprises an improved LAMP Construct as described herein and a cell for receiving the improved LAMP Construct. The kit may additionally comprise one or more nucleic acids for engineering the cell into a professional APC. In one aspect, however, the cell is a professional APC. The cell may or may not express co-stimulatory molecules. In a preferred aspect, when the cell does not express co-stimulatory molecules, the antigen encoded by the improved LAMP Construct is an autoantigen. In another aspect, a panel of cells is provided expressing different MHC molecules (e.g., known to be expressed in human beings). In a further aspect, the kit comprises reagents to facilitate entry of the improved LAMP Constructs into a cell (e.g., lipid-based formulations, viral packaging materials, cells, and the like). In still a further aspect, one or more T cell lines specific for the antigen encoded by the improved LAMP Construct is provided, to verify the ability of the improved LAMP Construct to elicit, modulate, or enhance an immune response.

EXAMPLES

[0276] The invention will now be further illustrated with reference to the following examples. It will be appreciated that what follows is by way of example only and that modifications to detail may be made while still falling within the scope of the invention.

Example 1 – Construction of LAMP Constructs

[0277] The improved LAMP Constructs illustrated in Figure 1 can be constructed using standard molecular biology techniques well known to the skilled artisan. For example, plasmids comprising the polynucleotides can be designed to generate the different structures ILC-1 to ILC-6 shown in Figure 1. The LAMP domains illustrated in Figure 1 can be derived from the amino acid sequences shown in Figures 3-10. Preferably the LAMP domains are derived from the human LAMP proteins shown in Figures 3-10. The boundaries of each domain can be derived from Figure 2A and Figure 2B. It is envisioned that the corresponding domains can also be cloned from the orthologous sequences by identifying the equivalent domains when compared to the human sequence. The cancer antigens can be cloned into the described LAMP Constructs either individually or in combination as described in Table 1.

Example 2 - Immune Response Evaluation of Mice to LAMP Constructs

[0278] The ability of the improved LAMP Constructs as described in Example 1 can be tested for their ability to modulate an immune response. For example, Female BALB/c mice can be immunized i.d with 50ug of the improved LAMP Constructs and 5ug of GMCSF in 100ul PBS using nanopass on day 0, 14 and 28. Experiment will then be terminated 4 weeks after the last dose.

[0279] Splenocytes (3x10⁵/well) are stimulated with antigenic protein (10ug/ml) in T cell media (RPMI with 10% heat inactivated FBS, 1% penicillin/streptomycin, and 1X 2-ME), supernatants are collected 72h after. Supernatants are diluted (400ul supernatant + 200ul T cell media) and cytokines are evaluated by ELISA. IL-10 or IL-4 production can be measured via ELISPOT assay.

Example 3 – Improved Antigen Presentation using LAMP Constructs

[0280] Survivin is the smallest member of the Inhibitor of Apoptosis (IAP) family of proteins, involved in inhibition of apoptosis and regulation of cell cycle. These functional attributes make Survivin a unique protein exhibiting divergent functions i.e. regulating cell proliferation and cell death. Expression of Survivin in tumors correlates with not only inhibition of apoptosis and a decreased rate of cell death, but also resistance to chemotherapy and aggressiveness of tumors [1-6]. Therefore, Survivin is an important target for cancer vaccines and therapeutics [7-9]. Survivin has also been found to be prominently expressed on both human and embryonic stem cells and many somatic stem cell types indicating its yet unexplored role in stem cell generation and maintenance.

[0281] Cancer is a heterogeneous group of diseases where abnormal cell growth with potential to invade other body parts takes control of normal homeostasis and becomes fatal if not timely and rightly treated. Immunotherapy specifically targets tumor cells thereby avoiding collateral damage to non-tumor cells and inducing anti-tumor response. This anti-tumor response also has the potential to eradicate tumor at distant sites in the body which may not be possible by surgical resection. Induction or enhancement of anti-tumor immune response is a formidable challenge in cancer because tumor cells use multiple evasion strategies and avoid being detected or eliminated by immune cells.

[0282] The aim of this project is to evaluate *in vivo* immune response of all new generation of LAMP Constructs injected by I.D. in BALB/c mice. Specifically, mice were immunized with 50 µg of the tested constructs defined in the legend of Figure 1 by intradermal injection. No adjuvants were added at this experiment. Six mice per group were administrated with vaccines every 7 days with total three dose in one month. Immune response was monitored 14 days after the last immunization.

[0283] The tested LAMP constructs were generated as described herein and the sequence of each tested construct is shown in **Figure 19**. Survivin protein was purchased from MyBiosource (San Diego, CA). Survivin peptides were from GenScript (Piscataway, NJ). Anti-survivin and m-IgGk-BP-HRP were bought from Santa Cruz Biotechnology (Dallas, TX), and mouse Monoclonal anti-LAMP-1/CD107a were from OriGene Technologies (Rockville, MD). ELISPOT antibody pairs for IFN γ were from Biolegend. Fluorescently coupled CD3, CD4, CD8, CD44, CD62L, IFN γ , TNF α , granzyme B, CD69 monoclonal antibodies and Zombie aqua fixable viability kit were purchased from BioLegend (San Diego, CA). Goat anti-mouse IgG2a-HRP and goat anti-mouse IgG-HRP were purchased from Southern Biotechnologies (Birmingham, AL). Streptavidin-HRP was purchased from Thermo Fisher (Waltham, MA). SureBlue TMB microwell peroxidase substrate and TMB stop solution were purchased from KPL (Gaithersburg, MD).

[0284] 50 µg of each construct was used in a total volume of 100 µl per mouse per dose for Pharmajet. Mice were immunized with the vaccine by *i.d.* delivery on days 0, 7, and 14. Mice were bled on days 28 for serum collection. Serum was collected and stored in -30°C. Spleens were collected on day 28 at the termination of experiment and processed for ELISPOT and FACS to evaluate survivin specific T cell responses.

[0285] **Measurement of plasma survivin-specific total IgG by ELISA.** The murine antibody response to survivin was assessed by indirect ELISA. ELISA plates (MaxiSorp) were coated with 2 µg/ml survivin (1-142) protein in carbonate-bicarbonate buffer overnight and then blocked with 2% BSA in PBS. Plasma samples were diluted 1:100 in blocking buffer. Samples were detected with goat anti-mouse IgG-HRP (Southern Biotech, Birmingham, AL). Reaction was developed with SureBlue TMB Substrate and stopped with TMB Stop Solution from KPL (Gaithersburg, MD). Plates were read (OD450) by using Epoch ELISA reader (BioTek, Winooski, VT).

[0286] **Evaluation of antigen-specific T cell response.** To assess antigen-specific T cell response in the vaccinated mice, splenocytes from vaccinated mice were evaluated for antigen-specific IFN γ production by

Enzyme-linked immunospot (ELISPOT). For ELISPOT assays, 96-well nitrocellulose plates (Millipore), were coated overnight at 4°C with 100 µl/well of capture monoclonal antibody in PBS. The plates were washed three times with 200 µl/well PBS and blocked with 200 µl /well T cell media for at least 2 hrs at room temperature. Splenocytes were plated at 3×10^5 cells/well and co-cultured with 2 µg/ml pooled peptides of Survivin (Table 2) or concavalin A (0.125 µg/ml) or medium alone in a total volume of 200 µl/well T cell media (RPMI-1640 with L-Glutamine and HEPES (ATCC), 1% penicillin, 1% streptomycin, and 5×10^{-5} M β -ME) at 3×10^5 cells/well for 48h at 37°C in 5% CO₂. The plates were washed two times with 200 µl/well PBS and two times with 200 µl/well PBS-T (0.05% Tween/PBS). Diluted detection antibodies (50 µl/well in PBS-T/0.5%BSA) were added and plates were incubated for 2 hrs with shaking at room temperature. Plates were washed four times with PBS. Streptavidin-alkaline phosphatase diluted in PBS (50 µl/well) were added and incubated for 2 h. Plates were washed with PBS four times and developed with 50 µl/well of 3-Amino-9-Ethylcarbazole (AEC, BD Bioscience) substrate for 10 min. Color development was stopped by washing under running tap water. After drying 72h at room temperature in dark, colored spots were counted using an AID ELISPOT High-Resolution Reader System and AID ELISPOT Software version 3.5 (Autoimmun Diagnostika GmbH).

Table 2. Pooled peptides from Genscript

Pooled P1	Sur1-15, Sur11-25, Sur 21-35, Sur31-45, sur 41-55
Pooled P2	Sur51-65, sur61-75, sur71-85, sur81-95
Pooled P3	Sur91-105, sur 101-115, sur111-125, sur121-135, sur131-142
Pooled P4	Sur31-45, sur41-55 and sur51-65

[0287] **Western blots.** 293T cells were transfected with the tested constructs using lipofectamine 2000 reagents (Invitrogen). Transfected cells were washed with PBS and suspended in 200 µl of RIPA lysis buffer with halt proteinase inhibitors (Thermo Scientific, Waltham, MA). Lysates were centrifuges (700 g for 15 minutes at 4°C), followed by measurement of protein concentration in the clarified supernatants using Pierce BCA protein Assay kit (ThermoFisher Scientific, Waltham, MA). 10 µg of protein was electrophoresed in pre-cast (4-20%) SDS-PAGE gels (BioRad, Hercules, California), and transferred onto nitrocellulose membranes (BioRad) and immunoblotted with mAbs to hLAMP. Membranes were blocked with Detection™ block buffer (KPL) and probed with rabbit anti-human LAMP (Sino Biological Inc., Beijing, China) or anti-survivin antibody and goat anti-rabbit-HRP antibody, and then developed with TMB (KPL).

[0288] **Flow cytometry.** Cells were first labelled with Zombie aqua fixable viability dye in PBS (1:500 dilution), followed by surface antibodies (1:100 dilution) in staining buffer (4% FBS, 2% rat serum, 2% mouse serum in PBS). For intracellular staining cells were stained with Zombie aqua, followed by surface staining, fixation with 4% paraformaldehyde, and stained with intracellular antibody in permeabilization buffer (PBS with 1% FCS 0.1% saponin). Samples were analyzed on a CytoFlex flow cytometer (Beckman Coulter) and analyzed using Kaluza software (Beckman Coulter).

[0289] **Statistics.** Two-Way ANOVA test was performed using GraphPad Prism 6.0 software or R file to evaluate the statistical significance. Each mouse's RPMI result was deducted from the results of the antigen activation.

[0290] **Vaccines, and immunizations.** Control, Survivin+Complete LAMP, Survivin-ILC-1 Construct, Survivin-ILC-2, Survivin-ILC-3, and Survivin-ILC-4 Construct vaccines were used in a total volume of 25µl per mouse per dose. Mice were immunized with the vaccine by ID delivery on days 0, 7, and 14. Mice were bled on days -13, and 28 for serum collection. Serum was collected and stored in -30°C. Spleens were collected on day 28 and processed for ELISPOT/ELISA assays.

[0291] **Figure 14: Validation of the plasmids:** 293T cells were transfected with the plasmids for 3 days. Transfected cells were lysed, and then electrophoresed in pre-cast SDS-PAGE gel. The proteins were transferred to nitrocellulose membranes and immunoblotted with mAbs to human LAMP (OriGene, #TA337108) or survivin Santa Cruz #17779). Molecular weight of LAMP = 100KD, Survivin = 16KD. Figure 13 shows that all tested LAMP constructs produced appropriately sized protein.

[0292] **Figures 15 and 16: Tested LAMP Constructs induce Th1 effector T cells producing IFN γ .** Female BALB/c mice were immunized i.d with 50 µg of the indicated constructs in 100 µl PBS via Pharmajet device on day 0, 7 and 14. Experiment was terminated 14 days after the last dose. Splenocytes (3×10^5 /well) were stimulated with survivin pooled peptides (4 µg/ml) in T cell media (RPMI with 10% heat inactivated FBS, 1% penicillin/streptomycin, and 1X β -ME), for 48 h. A. IFN γ production by spots. B. IFN γ production induced by all pooled peptides (bar figure from A). n= 6 per group. Two way ANOVA (R file) was used for statistical analysis. Figure 14 shows that all tested LAMP constructs induced a robust T cell response as shown by IFN γ production.

[0281] We unexpectedly found that after 3 dose of the improved LAMP Constructs (one week apart), a robust Th1 type response elicited by tested LAMP Constructs, especially ILC-4 where the hinge sequence was replaced by Survivin gene. More interestingly, improved LAMP Construct ILC-4 appears to recognize the Survivin epitopes from N-terminal to C-terminal, and induce T cell response against human Survivin peptide sequence which is 100% identical to the mouse. We also found longer (72hrs) stimulation of frozen-thawed splenocyte cells with Survivin peptides, ILC-4 showed significant higher IFN γ production than the first generation of LAMP-Survivin (see Figure 19). Specifically, **Figure 16** shows that the all improved LAMP Constructs tested showed higher T cell response with ILC-4 having the best activity as this constructed elicited a significantly higher T cell response against all Survivin peptides pools. Moreover, contrary to what was known in the art, removal of the second homology domain of the luminal domain created an improved LAMP construct that elicited a more robust immune response as compared to the complete LAMP construct (see, results for ILC-2 and ILC-3). Frozen splenocytes (4×10^5 /well) were stimulated with pooled peptides 4 (4 µg/ml) in T cell media (RPMI with 10% heat inactivated FBS, 1% penicillin/streptomycin, and 1X β -ME), for 48 h. n=6 per group. Two way ANOVA was used for statistical analysis. *p<0.05, **p<0.01, ***p<0.005, ****p<0.0001

[0293] **Figure 17. CD4 T cells are the major source of IFN γ producing cells.** Female BALB/c mice were immunized i.d with 50 μ g of the indicated vaccines in 100 μ l PBS via Pharmajet device on day 0, 7 and 14. Experiment was terminated 14 days after the last dose. Splenocytes (1×10^6 /well) were stimulated with pooled peptides 1 (4 μ g/ml) in T cell media (RPMI with 10% heat inactivated FBS, 1% penicillin/streptomycin, and 1X β -ME) over night, followed by adding monensin and brefeldin A and culturing for additional 5h. Cells were harvested and stained by Zombie, surface marker, and intracellular staining according to ITI staining protocol. Cells are gated on memory CD4 T cells (CD4+CD44+CD62L-) or CD8 T cells (CD8+CD44+CD62L-). Data is representative of one mouse in each group. While there is an increase in CD8 effector memory cells in vaccinated mice with the various constructs, IFN γ production is more pronounced in the CD4 T cell population.

[0294] **Figure 18: Improved LAMP Constructs produced stronger Survivin-specific total IgG response in BALB/c mice.** Female BALB/c mice were immunized i.d with 50 μ g of the indicated vaccines in 100 μ l PBS via Pharmajet device on day 0, 7 and 14. Experiment was terminated 14 days after the last dose. Mice were bled on days 28. Serum was separated and stored in -30°C. Total IgG and IgG2a were determined in serum by ELISA. Briefly, ELISA plates were coated with 2 μ g/ml Survivin (1-142aa), blocked with PBS/2%BSA, serum (1:100 dilution in blocking buffer) were evaluated by HRP-conjugated goat anti mouse IgG (1:6000) and IgG2a (1:11000). n=6 mice per group. **p<0.01, ***p<0.005, ****p<0.0001. Importantly and contrary to what was known in the art, **Figure 18** shows that fragments of the luminal domain worked better than use of the complete luminal domain (i.e., compare complete LAMP construct with constructs ILC-2 and ILC-3). Unexpectedly, insertion of the antigen between the two homology domains of the luminal domain generated the strongest antibody response (see, ILC-4).

[0295] **References relied on in this section.**

1. Kami K, Doi R, Koizumi M, Toyoda E, Mori T, Ito D, et al. Survivin expression is a prognostic marker in pancreatic cancer patients. *Surgery*. 2004;136(2):443-8. doi: 10.1016/j.surg.2004.05.023. PubMed PMID: 15300213.
2. Zhang SQ, Qiang SY, Yang WB, Jiang JT, Ji ZZ. [Expression of survivin in different stages of carcinogenesis and progression of breast cancer]. *Ai Zheng*. 2004;23(6):697-700. PubMed PMID: 15191674.
3. Zhang X, Zhong L, Hu K, Li Q. [Expression of survivin and its correlation with apoptosis in non-small cell lung cancer]. *Zhongguo Fei Ai Za Zhi*. 2004;7(2):138-41. doi: 10.3779/j.issn.1009-3419.2004.02.14. PubMed PMID: 21215009.
4. Kishi H, Igawa M, Kikuno N, Yoshino T, Urakami S, Shiina H. Expression of the survivin gene in prostate cancer: correlation with clinicopathological characteristics, proliferative activity and apoptosis. *J Urol*. 2004;171(5):1855-60. doi: 10.1097/01.ju.0000120317.88372.03. PubMed PMID: 15076293.

5. Asanuma K, Tsuji N, Endoh T, Yagihashi A, Watanabe N. Survivin enhances Fas ligand expression via up-regulation of specificity protein 1-mediated gene transcription in colon cancer cells. *J Immunol.* 2004;172(6):3922-9. PubMed PMID: 15004200.
6. Miyachi K, Sasaki K, Onodera S, Taguchi T, Nagamachi M, Kaneko H, et al. Correlation between survivin mRNA expression and lymph node metastasis in gastric cancer. *Gastric Cancer.* 2003;6(4):217-24. doi: 10.1007/s10120-003-0255-2. PubMed PMID: 14716515.
7. Badana AK, Chintala M, Gavara MM, Naik S, Kumari S, Kappala VR, et al. Lipid rafts disruption induces apoptosis by attenuating expression of LRP6 and survivin in triple negative breast cancer. *Biomed Pharmacother.* 2017;97:359-68. doi: 10.1016/j.biopha.2017.10.045. PubMed PMID: 29091885.
8. Cai JP, Wang YD, Zhang X, Xue HZ. [Expression of P16 and survivin in liver cancer and their clinical significance]. *Zhonghua Gan Zang Bing Za Zhi.* 2017;25(10):778-80. doi: 10.3760/cma.j.issn.1007-3418.2017.10.013. PubMed PMID: 29108210.
9. Cho HJ, Kim HR, Park YS, Kim YH, Kim DK, Park SI. Prognostic value of survivin expression in stage III non-small cell lung cancer patients treated with platinum-based therapy. *Surg Oncol.* 2015;24(4):329-34. doi: 10.1016/j.suronc.2015.09.001. PubMed PMID: 26690822.
10. Godinho RM, Matassoli FL, Lucas CG, Rigato PO, Goncalves JL, Sato MN, et al. Regulation of HIV-Gag expression and targeting to the endolysosomal/secretory pathway by the luminal domain of lysosomal-associated membrane protein (LAMP-1) enhance Gag-specific immune response. *PLoS One.* 2014;9(6):e99887. doi: 10.1371/journal.pone.0099887. PubMed PMID: 24932692; PubMed Central PMCID: PMC4059647.

Example 4: Therapeutic Treatment of LAMP Constructs

[0296] Female BALB/c mice can be inoculated s.c with syngeneic 7000 4T1 mammary carcinoma cells on day 0. Vaccine 50ug and 5ug of GMCSF in 100ul PBS is given i.d using nanopass once the tumors are palpable. Primary tumors are measured with a caliper and tumor volume is calculated using the formula $p/6 \times (\text{length} \times \text{width})^2$. Average tumor volume as a function of days after tumor inoculation can be measured. A Kaplan-Meier plot can be used to show overall survival at the point of termination.

Example 5 – Prime/Boost Protocol

[0297] Herpesvirus entry mediator (HVEM), also known as tumor necrosis factor receptor superfamily member 14 (TNFRSF14) or CD270, is a human cell surface receptor of the TNF-receptor superfamily. In recent years, HVEM has been found highly expressed on hematopoietic cells and a variety of parenchymal cells, such as breast, melanoma, colorectal, and ovarian cancer cells, as well as gut epithelium. HVEM is a bidirectional protein, either inhibiting or stimulating T cells, through binding to BTLA or LIGHT (TNFSF14).

[0298] We generated a DNA vaccine encoding HVEM-LAMP to generate an antibody which could block the inhibitory function of HVEM for tumor therapeutic applications. We hypothesized that LAMP will promote the antibody response by enhancing the affinity of HVEM specific antibodies and/or expanding the repertoire of B cell epitopes in the HVEM protein. In this study, we compared the immunogenicity of HVEM encoding plasmid with and without LAMP (SEQ ID NO: 158 and SEQ ID NO:159). Plasmids encoding HVEM-LAMP and HVEM and recombinant HVEM protein were designed as described herein.

[0299] Goat anti-mouse IgG-HRP was purchased from Southern Biotechnologies (Birmingham, AL). SureBlue TMB microwell peroxidase substrate and TMB stop solution were purchased from KPL (Gaithersburg, MD). ELISPOT plates were ordered from EMD Millipore (Billerica, MA, Cat. No. MAIPS4510). IFN- γ antibody pair used in ELISPOT was purchased from BioLegend (San Diego, CA) and clones AN18 and R46A2 were used as coating and detection, respectively. Streptavidin-HRP and AEC substrate were purchased from BD Biosciences (San Jose, CA).

[0300] Six to eight week old female Balb/c mice were purchased from Harlan Laboratories (Frederick, MA) and maintained at animal facility in Immunomic Therapeutics, Inc. (Rockville, MA). Mice (n=6) were treated with 10 μ g/dose of HVEM-LAMP, HVEM, or LAMP vector control by electroporation IM delivery at days 0, 7, and 14. On day 35, mice were boosted with 5 μ g HVEM protein in the presence of Alum by i.p. injection. On day 28 and 49, mice were bled and sera were isolated for antibody detection. Mice were sacrificed on day 56 and splenocytes were tested for IFN- γ production by ELISPOT.

[0301] ELISA procedure was followed by Su et al., J of Immunol Res; (10):1-15 (2016). Plates were coated with 5 μ g/ml HVEM protein. Data were analyzed by using Microsoft Excel and Prism 6 software.

[0302] The primary aim of this study was to compare the antibody profiles between HVEM-LAMP and HVEM. On day 28, HVEM-LAMP vaccinated mice produced significant higher level of HVEM specific IgG antibody than that of the HVEM group (**Figure 11**). After a protein boost, the HVEM specific antibody was increased about 1000-fold in HVEM immunized mice and the mean titer was changed from 100 to 108000. This result indicates that the immune memory was induced by the HVEM DNA plasmid. Although HVEM DNA alone only induced a minimal antibody response, protein boost rapidly recalled the immune memory. On the other hand, HVEM-LAMP group again exhibited a significant higher titer than the HVEM and LAMP groups, the mean titer is 5 folds of the HVEM group, indicating the power of LAMP in enhancing antibody response (**Figure 12**).

[0303] Additionally serum samples (Day 49) from HVEM+LAMP or HVEM alone immunized/HVEM protein boosted mice were pooled and tested for peptide mapping. Twelve peptides were found to be bound to the pooled serum (mouse IgG reaction) and seven of the twelve peptides showed strong binding affinity. HVEM+LAMP alters the binding affinity of peptides 17, 24, 25, and 28 as compared to HVEM alone as shown in **Figure 13**. These changes may have physiological effects in protecting tumor growth.

[0304] In conclusion, data from this study suggest that two constructs were expressed *in vivo* and LAMP significantly improved the humoral immune response.

Example 6: Production of an Antibody from a Polypeptide

[0305] Anti-antigen antibodies can be prepared by a variety of standard methods of raising antibodies using animal injection. (See, Current Protocols, Chapter 2.) For example, cells expressing an improved LAMP Construct comprising a cancer antigen described herein is administered to a non-human vertebrate to induce the production of sera containing polyclonal antibodies. In a preferred method, a preparation of the LAMP/antigen protein is prepared and purified to render it substantially free of natural contaminants. Such a preparation is then introduced into the non-human vertebrate to produce polyclonal antisera of greater specific activity.

[0306] In the most preferred method, the anti-antigen antibodies of the present invention are monoclonal antibodies (or protein binding fragments thereof). Such monoclonal antibodies can be prepared using hybridoma technology. (Kohler et al., Nature 256:495 (1975); Kohler et al., Eur. J. Immunol. 6:511 (1976); Kohler et al., Eur. J. Immunol. 6:292 (1976); Hammerling et al., in: Monoclonal Antibodies and T-Cell Hybridomas, Elsevier, N.Y., pp. 563-681 (1981).) In general, such procedures involve immunizing a non-human vertebrate animal (preferably a rabbit, mouse, cow, camel, llama) with an improved LAMP Construct comprising an antigen, the encoded polypeptide of an improved LAMP Construct comprising an antigen or, more preferably, with an improved LAMP Construct-expressing cell. Such cells may be cultured in any suitable tissue culture medium; however, it is preferable to culture cells in Earle's modified Eagle's medium supplemented with 10% fetal bovine serum (inactivated at about 56 degrees C), and supplemented with about 10 g/l of nonessential amino acids, about 1,000 U/ml of penicillin, and about 100 ug/ml of streptomycin.

[0307] The splenocytes of such non-human vertebrate host (e.g, mice) are extracted and fused with a suitable myeloma cell line. Any suitable myeloma cell line may be employed in accordance with the present invention; however, it is preferable to employ the parent myeloma cell line (SP20), available from the ATCCTM. After fusion, the resulting hybridoma cells are selectively maintained in HAT medium, and then cloned by limiting dilution as described by Wands et al. (Gastroenterology 80:225-232 (1981).) The hybridoma cells obtained through such a selection are then assayed to identify clones which secrete antibodies capable of binding the antigen.

[0308] It will be appreciated that Fab and F(ab')₂ and other fragments of the anti-antigen antibodies may be used according to the methods disclosed herein. Such fragments are typically produced by proteolytic cleavage, using enzymes such as papain (to produce Fab fragments) or pepsin (to produce F(ab')₂ fragments). Alternatively, secreted protein-binding fragments can be produced through the application of recombinant DNA technology or through synthetic chemistry.

[0309] For *in vivo* use of antibodies in humans, it may be preferable to use "humanized" chimeric monoclonal antibodies. Such antibodies can be produced using genetic constructs derived from hybridoma cells producing the monoclonal antibodies described above. Methods for producing chimeric antibodies are known in the art. (See, for review, Morrison, Science 229:1202 (1985); Oi et al., BioTechniques 4:214 (1986); Cabilly et al., U.S. Pat. No. 4,816,567; Taniguchi et al., EP 171496; Morrison et al., EP 173494; Neuberger et al., WO 8601533; Robinson et al., WO 8702671; Boulianne et al., Nature 312:643 (1984); Neuberger et al., Nature 314:268 (1985).)

Example 7: Use of Polynucleotides to Generate Polyclonal and Monoclonal Antibodies

[0310] Methods of directly injecting polynucleotides into animals are well described in the art. See, for example, U.S. patent numbers 5,676,954; 6,875,748; 5,661,133. For example, a polynucleotide encoding an improved LAMP Construct comprising an antigen can be injected into the quadriceps muscles of restrained awake mice (female 6-12 week old BALB/c or Nude, nu/nu, from Harlan Sprague Dawley, Indianapolis, Ind.). In one embodiment, 50 µg of a polynucleotide in 50 µl solution using a disposable sterile, plastic insulin syringe and 28G ½ needle (Becton-Dickinson, Franklin Lakes, N.J., Cat. No. 329430) fitted with a plastic collar cut from a micropipette tip can be used to inject the mice, as described in Hartikka, J., et al., Hum. Gene Ther. 7:1205-1217 (1996)).

[0311] Alternatively, 6-week old Sprague Dawley female mice (body weight 20-25 grams) can be given 5000 ppm ZnOSO₄ in their drinking water beginning 24 hours prior to injection. This amount of zinc has been shown to be able to activate the metallothionein promoter. Each mouse is then injected intravenously through a tail vein puncture with a 25 gauge needle with 30 µg of a polynucleotide encoding an improved LAMP Construct comprising an antigen complexed with 150 µg liposome (Lipofection TM) in a total volume of 30 µl. Animal care should be maintained throughout the study and should be performed in compliance with the "Guide for the Use and Care of Laboratory Animals", Institute of Laboratory Animal Resources, Commission on Life Sciences, National Research Council, National Academy Press.

[0312] After the injected polynucleotide encoding the improved LAMP Construct comprising an antigen is delivered into the cells in the animal, the antigen is delivered to the endosome/lysosome, processed and presented to the immune system. The improved LAMP Construct comprising an antigen can then stimulate the production of antibodies specific to the antigen. These antibodies can be isolated and used as a polyclonal mixture or further isolated into single species or monoclonals. The process of the immune response and production of antibodies against foreign antigens *in vivo* are well known in the art.

[0313] In a third animal model, Balb/c 3T3 A31 cells are transfected by electroporation with a polynucleotide encoding an improved LAMP Construct comprising an antigen. G418 resistant clones expressing LAMP Construct comprising an antigen are identified by their ability to bind human RBC. To generate polyclonal antibodies, Balb/c mice are immunized twice intraperitoneally, at an interval of 14 days,

with 10^7 cells comprising the improved LAMP Construct comprising an antigen. After a final boost, the immune serum is collected, IgG is purified by protein G Sepharose and passed over an antigen column prepared by coupling 1.0 mg purified antigen to cyanogen bromide activated Sepharose CL-4B. Bound IgG can be eluted with 0.1 M glycine buffer pH 2.5 and neutralized with 0.1 volumes of 0.1 M Tris pH 8.0. To generate a monoclonal antibody (mAb), Balb/c mice are immunized with LAMP Construct comprising an antigen and hybridomas are generated by fusing immune spleen cells with the SP2 myeloma following standard methods (28). A positive well reacting specifically with an antigen can be identified by enzyme-linked immunosorbent assays as described in the art. The hybridoma is cloned three times by limiting dilution to produce an antibody.

Example 8: Immunization of an Improved LAMP Construct Comprising an Antigen

[0314] Methods of raising antibodies in mammals are well known in the art. In one example, polyclonal antiserum against a LAMP Construct comprising an antigen is raised by immunization of pathogen free rabbits with a total of 500 μ g of an improved LAMP Construct comprising an antigen over a period of two months. For example, the improved LAMP Construct comprising an antigen can be dissolved in PBS and emulsified with an equal volume of Freund's adjuvant. After the final booster, the serum of the rabbits can be separated to determine the titer of the polyclonal antiserum.

[0315] In an additional animal model, groups of 5 mice (C57BL/6J; Jackson Labs) can be subcutaneously immunized with 5 μ g of endotoxin-free LAMP Construct comprising an antigen emulsified in alum. Three weeks later, mice are bled and the presence of anti-antigen specific antibodies can be determined by titering the sera by ELISA (direct binding of antibodies in sera to wild type BPTI or APP-KI coated, directly or indirectly (via a biotinylated tag and streptavidin), on the wells).

[0316] To obtain monoclonal antibodies, 4-6 week old Balb/c mice can be immunized with an improved LAMP Construct comprising an antigen (for example 4 times with 2 week intervals with 10-100 μ g/injection dissolved in Freund's complete adjuvant for the first injection, and Freund's incomplete adjuvant for subsequent immunizations). Splenocytes are isolated and fused with a fusion cell line such as Sp2/0 myeloma cells, followed by limiting dilution. Growing clones are screened using for example an enzyme-linked immunosorbent assay (ELISA). 96 cells plates are coated with an improved LAMP Construct comprising an antigen or with a control protein. The culture supernatant is added, followed by washing and addition of a labeled anti-mouse antibody for detection. After limited dilution cloning of the anti-antigen antibody producing stable hybridomas are obtained. From each cell, supernatant is collected and by affinity chromatography using protein A sepharose columns monoclonal antibodies can be purified.

Example 9 - LAMP Constructs with IGFBP-2

[0317] Cancer vaccine development has been pursued for more than 4 decades. However, despite numerous clinical studies of a variety of cancer vaccine formulations, therapeutic cancer vaccination has had

overall clinical benefit of about 20%^{1, 2, 3, 4, 5}. Obstacles to improve efficacy have included a) poor immunogenicity of self-proteins that are cancer associated antigens, b) induction of regulatory T cells⁶, and c) low immune response obtained by vaccination. Recent reports suggest a correlation of vaccine-induced Th1 immune infiltrate in tumor microenvironment with improved clinical response in many tumors^{7, 8, 9, 10, 11}.

[0318] Insulin-like growth factor binding protein 2 (IGFBP-2) is a self-protein elevated during progression of many human tumors. IGFBP-2 overexpression is correlated with high-grade gliomas with poor prognosis¹² and is an independent indicator of malignancy in breast cancer patients¹³. IGFBP2 is associated with metastasis and poor survival in lung cancer patients¹⁴. IGFBP2 overexpression is also correlated with advanced disease in adrenal cancer¹⁵, bladder cancer¹⁶, gastric cancer¹⁷, ovarian cancer^{18, 19}, and prostate cancer^{20, 21}.

MATERIALS AND METHODS

[0319] **Mice.** Six to eight week old female C57BL/6 albino mice were purchased from Envigo and maintained at animal facility in Immunomic Therapeutics, Inc. (Rockville, MA).

[0320] **Reagents and antibodies.** Control vector Control, IGFBP2 (1-328)-no LAMP, and IGFBP2 (39-328)-ILC-1 Construct were made as described herein using standard protocols. Anti-mouse rabbit IGFBP2 PoAb was from MyBiosource (San Diego, CA), goat anti-rabbit IgG-FITC was from e-biosciences (San Diego, CA), rabbit anti-human LAMP was from Sino Biological (Beijing, China). Goat anti-rabbit-HRP, goat anti-mouse IgG1-HRP and goat anti-mouse IgG2a-HRP were purchased from Southern Biotechnologies (Birmingham, AL). Streptavidin-HRP were purchased from Thermo Fisher (Waltham, MA). SureBlue TMB microwell peroxidase substrate and TMB stop solution were purchased from KPL (Gaithersburg, MD). ELISPOT antibody pairs for IFN γ , and IL-10 was from BioLegend. Cytokine ELISA kits were from R&D systems.

[0321] **Vaccines, and immunizations.** Control, IGFBP2 (39-328)-ILC-1 Construct, and IGFBP2 (1-328)-no LAMP vaccines were used in a total volume of 20 μ l per mouse per dose. Mice were immunized with the vaccine by IM delivery via electroporation on days 0, 7, and 14. Mice were bled on days -13, and 28 for serum collection. Serum was collected and stored in -30°C. Spleens were collected on day 28 and processed for ELISPOT/ELISA assays.

[0322] **Measurement of serum IGFBP-2-specific IgG by ELISA.** The murine antibody response to IGFBP-2 was assessed by indirect ELISA. ELISA plates (MaxiSorp) were coated with 5 μ g/ml IGFBP2 (39-328) protein in carbonate bicarbonate buffer overnight and then blocked with 2% BSA in PBS. Serum samples were diluted (1:100, 1:300, 1:900, 1:2700, 1:8100, 1:24300, 1:72900, 1:218700) in PBS-T. Samples were detected with 1:6000 goat anti-mouse IgG-HRP (Southern Biotech, Birmingham, AL), followed by Streptavidin-HRP (Thermo Fisher Scientific, Rockford, IL). Reaction was developed with SureBlue TMB Substrate and stopped with TMB Stop Solution from KPL (Gaithersburg, MD). Plates were read (OD450) by using Epoch ELISA reader (BioTek, Winooski, VT). Average background (PBS only) was calculated, and samples which

have OD450 value more than 2 * average background were considered as positive. The dilutions of such samples are determined as the endpoint titers.

[0323] **Evaluation of antigen-specific T cell response.** To assess antigen-specific T cell response in the vaccinated mice, splenocytes from vaccinated mice were evaluated for antigen-specific IFN γ , and IL-10 by Enzyme-linked immunospot (ELISPOT).

[0324] Splenocytes were depleted of RBCs and co-cultured in flat bottom 96-well plates in 200 μ l/well T cell media (RPMI-1640 with L-Glutamine and HEPES (ATCC), 1% penicillin, 1% streptomycin, and 5 x 10⁻⁵M 2-ME) at 4x10⁵ cells/well and 10 μ g/ml IGFBP2 (39-328) protein or concavalin A (0.25 μ g/ml) or medium alone for 72h at 37°C in 5%CO₂. Plates were centrifuged at 1600 rpm for 6 minutes and supernatants were collected and stored at -30°C.

[0325] For ELISPOT assays were performed as described herein. Briefly, 96-well nitrocellulose plates (Millipore), were activated with 30 μ l of 35% ethanol for one minute, washed with PBS twice, and coated overnight at 4°C with 50 μ l/well of capture monoclonal antibody in PBS. The plates were washed three times with 200 μ l/well PBS and blocked with 200 μ l/well T cell media for at least 2hrs at room temperature. Splenocytes were plated at 4x10⁵ cells/well and co-cultured with 10 μ g/ml IGFBP2 (39-328) protein or 10 μ g/ml peptide pools or concavalin A (0.25 μ g/ml) or medium alone in a total volume of 200 μ l/well T cell media for 48h at 37°C in 5%CO₂. The plates were washed, diluted detection antibodies (50 μ l/well) were added and plates were incubated for 2hrs at room temperature on shaker. Plates were washed four times with PBS. Streptavidin-HRP diluted in PBS (50 μ l/well) were added and incubated for 1h. Plates were washed with PBS and developed with 50 μ l/well AEC development solution for up to 30 min. Color development was stopped by washing under running tap water. After drying 24-72h at room temperature in dark, colored spots were counted using an AID ELISPOT High-Resolution Reader System and AID ELISPOT Software version 3.5 (Autoimmun Diagnostika GmbH).

[0326] **Evaluation of intracellular cytokine.** To determine the cells responsible for production of cytokines intracellular staining was performed. Splenocytes were depleted of RBCs stored in refrigerator for 24h. Next day splenocytes were co-cultured in flat bottom 96-well plates in 200 μ l/well T cell media (RPMI-1640 with L-Glutamine and HEPES (ATCC), 1% penicillin, 1% streptomycin, and 5 x 10⁻⁵M 2-ME) at 3x10⁶ cells/well and 20 μ g/ml IGFBP2 (39-328) protein or peptide pool or medium alone. A mixture of Brafeldin A and monensin (X1000) was added to each well in 20 μ l volume (0.22 μ l per well for 20 μ l volume; prepare a stock for all the wells) one hour later. PMA/ionomycin activation cocktail was added to positive control wells along with BFA and Monensin (Two wells were set-up; one for IgG control and other one for cytokine staining). Cells were incubated for total of 6h at 37°C in 5%CO₂.

[0327] Cells were washed with 200 μ l PBS. Cells were stained with 50 μ l of diluted Zombie aqua dye (1:500 dilution of zombie aqua in PBS) and incubated for 20 min at room temperature protected from light. Cells were washed once with 2%serum in PBS. 20 μ l of purified anti-mouse CD16/32mAb (clone 2.4G2;

1ug/20ul) was added to the cells and cells were incubated at 4°C for 10mins. Cells were centrifuged (2000 rpm, 6 min), supernatant was decanted, and extracellular antibodies were added in PBS supplemented with 2% serum. The antibodies were 0.3 ul of each / well. Abs were added in a volume of 50µl/well, incubated for 30 min in 4°C (the CD3 clone 17A2 can activate T cells so 4°C temperature is important).

[0328] Cells were washed with PBS + protein (2% FCS), fixed and permeabilized with 100µl of CytoFix/CytoPerm solution at 4°C for 30 mins (mixed thoroughly with the multichannel when adding the fix buffer to reduce aggregates and doublets formation). Cells were washed with 200µl Perm/Wash buffer (1X) twice (2000 rpm, 6 min). Cells were stained with the intracellular staining Ab at 0.5µl Ab/well in Perm buffer. One of the PMA/ionomycin wells were stained with the isotype controls. After 1h (or overnight) incubation cells were washed twice with perm buffer, and cells were acquired by flow cytometer. While acquisition the events/second were less than 8000. Acquired >10⁶ cells per sample. The acquired data were analyzed using Kaluza analysis software. Dead cells and doublets were gated out.

[0329] **Statistics.** Statistical analyses were performed by using Prism 6 software (GraphPad Software, La Jolla, CA). Data were analyzed by one-way ANOVA followed by Tukey's test for multiple comparisons. *p* values below 0.05 were considered to indicate a statistically significant difference.

[0330] **Results. Figure 21:** IGFBP2 (39-328)-ILC-1 Construct induced significantly higher IFN γ producing effector T cells at the dose of 10ug IM/EP immunization. Peptide pool 1 induced the IFN γ response similar to IGFBP-2 full length protein indicating dominant epitope in peptide pool 1. Splenocytes (4x10⁵/well) were stimulated with IGFBP-2 protein (10ug/ml) or peptide pool (10ug/ml) in T cell media (RPMI with 10% heat inactivated FBS, 1% penicillin/streptomycin, and 1X 2-ME), for 48h. Values in dot plot are experimental – media for each mouse. N=7 mice per group. **Figure 21A.** Dot plot to show recall with IGFBP2 full length (10ug/ml) and **Figure 21B.** Dot plot to show recall with peptide pool 1 (10ug/ml). * indicates *p*<0.05.

[0331] **Figure 22.** IGFBP2 (39-328)-ILC-1 Construct induced IFN γ and/or TNF α producing CD4+ and CD8+ effector memory T cells at the dose of 10ug IM/EP immunization. Splenocytes (4x10⁵/well) were stimulated with IGFBP-2 protein (10ug/ml) or peptide pool 1 (5ug/ml) in T cell media (RPMI with 10% heat inactivated FBS, 1% penicillin/streptomycin, and 1X 2-ME), for 6hr. Cells were stained for intracellular cytokines as described and analyzed as shown below. Representative data from each group.

[0332] **Figure 23: IGFBP-2-specific IgG production in C57BL/6 albino mice immunized with IGFBP2 (39-328)-ILC-1 Construct by IM/EP.** Female C57BL/6 albino mice were immunized IM/EP with 10ug of the indicated vaccines in 20µl PBS on day 0, 7, and 14. Mice were bleed on days -6, 28. Serum was separated and stored in -30°C. IgG were determined in plasma by ELISA. Briefly, ELISA plates were coated with 5µg/ml IGFBP-2 (39-328) in carbonate bicarbonate buffer, blocked with 2%BSA, serum (1:100 dilution in PBS-T) were evaluated by HRP-conjugated goat anti mouse IgG (1:6000). Average background (PBS only) was calculated, and samples which have OD450 value more than 2 * average background are considered as positive. The dilutions of such samples are determined as the endpoint titers.

[0333] Reference relied upon in this Example.

1. Melero, I. *et al.* Therapeutic vaccines for cancer: an overview of clinical trials. *Nat Rev Clin Oncol* **11**, 509-524 (2014).
2. Obeid, J., Hu, Y. & Slingluff, C.L., Jr. Vaccines, Adjuvants, and Dendritic Cell Activators--Current Status and Future Challenges. *Semin Oncol* **42**, 549-561 (2015).
3. Pol, J. *et al.* Trial Watch: Peptide-based anticancer vaccines. *Oncoimmunology* **4**, e974411 (2015).
4. Speiser, D.E. & Romero, P. Molecularly defined vaccines for cancer immunotherapy, and protective T cell immunity. *Semin Immunol* **22**, 144-154 (2010).
5. Thomas, A. & Giaccone, G. Why has active immunotherapy not worked in lung cancer? *Ann Oncol* **26**, 2213-2220 (2015).
6. Ebert, L.M. *et al.* A cancer vaccine induces expansion of NY-ESO-1-specific regulatory T cells in patients with advanced melanoma. *PLoS One* **7**, e48424 (2012).
7. Galon, J. *et al.* Type, density, and location of immune cells within human colorectal tumors predict clinical outcome. *Science* **313**, 1960-1964 (2006).
8. Fridman, W.H., Pages, F., Sautes-Fridman, C. & Galon, J. The immune contexture in human tumours: impact on clinical outcome. *Nat Rev Cancer* **12**, 298-306 (2012).
9. Kenter, G.G. *et al.* Vaccination against HPV-16 oncoproteins for vulvar intraepithelial neoplasia. *N Engl J Med* **361**, 1838-1847 (2009).
10. Madan, R.A., Bilusic, M., Heery, C., Schlom, J. & Gulley, J.L. Clinical evaluation of TRICOM vector therapeutic cancer vaccines. *Semin Oncol* **39**, 296-304 (2012).
11. Disis, M.L. *et al.* Concurrent trastuzumab and HER2/neu-specific vaccination in patients with metastatic breast cancer. *J Clin Oncol* **27**, 4685-4692 (2009).
12. Moore, L.M. *et al.* IGFBP2 is a candidate biomarker for Ink4a-Arf status and a therapeutic target for high-grade gliomas. *Proc Natl Acad Sci U S A* **106**, 16675-16679 (2009).
13. Busund, L.T. *et al.* Significant expression of IGFBP2 in breast cancer compared with benign lesions. *J Clin Pathol* **58**, 361-366 (2005).
14. Hu, Q. *et al.* Is insulin-like growth factor binding protein 2 associated with metastasis in lung cancer? *Clin Exp Metastasis* **31**, 535-541 (2014).
15. Boulle, N., Logie, A., Gicquel, C., Perin, L. & Le Bouc, Y. Increased levels of insulin-like growth factor II (IGF-II) and IGF-binding protein-2 are associated with malignancy in sporadic adrenocortical tumors. *J Clin Endocrinol Metab* **83**, 1713-1720 (1998).

16. Miyake, H., Hara, I., Yamanaka, K., Muramaki, M. & Eto, H. Prognostic significance of insulin-like growth factor (IGF) binding protein-2 to IGF-binding protein-3 ratio in patients undergoing radical cystectomy for invasive transitional cell carcinoma of the bladder. *BJU Int* **95**, 987-991 (2005).
17. Shi, L.H., Zhu, X.Q., Zhao, G.H., Xia, Y.B. & Zhang, Y.S. Expression of insulin-like growth factor binding protein-2 in gastric carcinoma and its relationship with cell proliferation. *World J Gastroenterol* **12**, 6285-6289 (2006).
18. Lee, E.J. *et al.* Insulin-like growth factor binding protein 2 promotes ovarian cancer cell invasion. *Mol Cancer* **4**, 7 (2005).
19. Lukanova, A. *et al.* Risk of ovarian cancer in relation to prediagnostic levels of C-peptide, insulin-like growth factor binding proteins-1 and -2 (USA, Sweden, Italy). *Cancer Causes Control* **14**, 285-292 (2003).
20. Degraff, D.J., Aguiar, A.A. & Sikes, R.A. Disease evidence for IGFBP-2 as a key player in prostate cancer progression and development of osteosclerotic lesions. *Am J Transl Res* **1**, 115-130 (2009).
21. Shariat, S.F. *et al.* Association of preoperative plasma levels of insulin-like growth factor I and insulin-like growth factor binding proteins-2 and -3 with prostate cancer invasion, progression, and metastasis. *J Clin Oncol* **20**, 833-841 (2002).

Example 10: LAMP Constructs Comprising CMV pp65 and gB

[0334] Glioblastoma multiforme (GBM) brain cancer is an aggressive human brain cancer with 5 year survival rates below 10% (Schuessler A *et al.* 2014). Current treatment includes surgical removal of the tumor and radiation, however successful treatment increases the median survival to only about 15 months. Several clinical trials are currently being evaluated for GBM, including immunotherapy. Interestingly, it was recently found that GBM tumors express CMV antigens including the antigen pp65. The role of CMV in GBM is unclear because CMV is not an oncogenic virus, however from a therapeutic perspective, the presence of CMV antigens provides a unique opportunity to exploit pre-existing antiviral immunity for immune-based GBM treatment. A recent report showed that autologous immunotherapy using DC transfected with LAMP-pp65 mRNA in a unique protocol significantly improved GBM patient' survival. Specifically, Dr. Duane A. Mitchell from University of Florida, has shown that autologous DCs generated *ex vivo*, pulsed with LAMP-pp65 mRNA and injected back into GBM patients significantly improved the survival of GBM patients. The protocol for pp65-transfected DC also required pre-conditioning of the injection site by injection of Tetanus/Diphtheria vaccine 24h before DC injection (Mitchell DA *et al.* 2015).

[0335] Here, we compare pp65+ILC-1 LAMP construct with gB+ ILC-1 LAMP vaccine using PharmaJet and ID/EP.

[0336] MATERIALS AND METHODS

[0337] **Reagents.** Plasmid constructs Control, pp65+ILC-1 LAMP construct, and gB+ ILC-1 LAMP were constructed as described herein. pp65 and gB peptides for ELISPOT were purchased from JPT (70%

purity). RBC lysis buffer was purchased from TonboBio and filtered through 0.22µm filter. ConA (Sigma) was used at 2.5ug/ml. Antibodies for IFN γ ELISPOT were purchased from eBioscience or Biolegend. IL-10 ELISPOT reagents, SA-ALP and BCIP/NBT plus were purchased from MabTech. Ab Titers were evaluated using HRP anti- mouse antibodies from Southern Biotech. Lysate of cells infected by CMV was purchased from Virusys. The lysate was confirmed by the manufacturing company to be non-infective.

[0338] **Immunization and Plasma Collection.** Six to eight week old male BALB/C mice bred and maintained at animal facility in Immunomic Therapeutics, Inc. Mice were immunized with the vaccine by either ID (Pharmajet) or ID via electroporation on days 0, 7, and 14. Mice were sacrificed on Day 26.

[0339] **ELISPOT.** ELISPOT was carried out as described herein, with the exception of cell number: the cells were seeded at 2×10^5 splenocytes per well. Spleens from sacrificed mice were flushed with medium, red blood cells were lysed and then the cells were counted using a cellometer. 2×10^5 splenocytes were seeded per well of ELISPOT and incubated with medium (RPMI with HEPES + 10% HI equal Fetal + NaP + β ME + P/S), duplicate of PP65 and gB peptides (1 µg/ml of each peptide) or ConA (2.5 ug/ml). Results are shown after averaging the duplicate and reducing the value from RPMI well for each mouse.

[0340] **Antibody titers.** Antibodies titers were evaluated using a lysate of cells infected by CMV. Total IgG and IgG2a were evaluated. The results were only calculated for total IgG and only the 1:100 OD result was compared.

[0341]

[0342] **Results.** **Figure 24** shows that IFN γ was induced with both pp65 and gB peptides. Additionally, serum Ab were tested from the last bleed. When lysate from CMV-transfected cells was used, similar IgG titers are seen for both immunizations. Specifically, **Figure 25** shows that total IgG (left) and IgG2a (right) antibodies titer at in serum of immunized mice against CMV-transfected cell lysate. Statistical analysis was done in GraphPad prism, using Mann Whitney test. IgG2a CMV-lysate Ag – P = 0.041

Example 11. LAMP Constructs comprising PSMA

[0343] Prostate cancer is the most frequently diagnosed cancer in men, and the second most common cause of cancer death in men in the US¹. For localized disease, surgery and radiation continue to be curative treatments but have adverse effects such as urinary symptoms and sexual dysfunction that can negatively affect quality of life. For metastatic disease, chemotherapy as initial treatment now appears to extend survival compared with androgen deprivation therapy alone (ADT)². ADT is associated with a) decreased bone mineral density and an increased risk of osteoporotic fragility fractures, b) development of castration resistant prostate cancer (CRPC). Methods to harness the immune system to recognize and kill prostate cancer cells are being exploited. One such attempt has led to Sipuleucel-T, a FDA approved, autologous cellular immunotherapy that targets prostatic acid phosphatase (PAP) for the treatment of asymptomatic or minimally symptomatic

metastatic CRPC (mCRPC)³. Additional immunotherapies for prostate cancer are under development including a number of vaccine candidates, as well as approaches using targeted monoclonal antibodies^{4, 5}.

[0344] Several tumor-associated antigens (TAAs) have been identified that represent promising targets for T cell- or antibody-based immunotherapy. The group of molecules preferentially expressed in normal and malignant prostate tissues comprises prostate-specific membrane antigen (PSMA), prostein, prostate-specific antigen (PSA), prostatic acid phosphatase (PAP), prostate stem cell antigen (PSCA), T cell receptor gamma alternate reading frame protein (TARP), transient receptor potential (trp)-p8 and six-transmembrane epithelial antigen of the prostate 1 (STEAP1).

[0345] Human Prostate Specific Membrane Antigen (PSMA), also known as folate hydrolase I (FOLH1), is a 750-amino acid type II membrane glycoprotein, which is primarily expressed in normal human prostate epithelium and is upregulated in prostate cancer, including metastatic disease. Mouse homolog of PSMA (Folh1) is not expressed in the mouse prostate, but primarily expressed in the brain and kidney. Mouse Folh1 encodes for a 752-amino acid protein, with 86% identity and 91% similarity to the human PSMA amino acid sequence⁶. PSMA is considered an important clinical biomarker of prostate because it is expressed many fold higher on prostate cells than cells of other tissues^{7, 8, 9}. A strong correlation between increased PSMA expression and prostate cancer progression has been indicated¹⁰. Elevated PSMA expression is also associated with other malignancy including kidney and bladder cancer¹¹. Elevated PSMA expression has been observed on tumor neovasculature, but not normal vasculature suggesting a role for PSMA in angiogenesis¹². PSMA being a membrane protein is an attractive target to develop antibodies against it for diagnostic and therapeutic purposes¹³. Several therapeutic anti-PSMA mAbs have been developed, and many of these have been used in radioimmunotherapy for targeting cytotoxic radionucleotides, specifically to PSMA expressing cells¹⁴. Some anti-PSMA mAbs have been demonstrated to mediate a therapeutic effect by promoting an antibody-dependent cellular cytotoxicity (ADCC) effect that kills prostate cancer cells^{4, 14, 15}.

[0346] **MATERIALS AND METHODS**

[0347] **Mice.** Six to eight week old female C57BL/6 albino mice were purchased from Envigo and maintained at animal facility in Immunomic Therapeutics, Inc. (Rockville, MA).

[0348] **Reagents and antibodies.** Control and PSMA-ILC-1 LAMP Constructs were made as described herein. Human PSMA PepMix (185 peptides, 15mers with 11aa overlap) was from JPT (Acton, MA). Mouse anti-human PSMA Alexa Flour 488, Goat (Fab)2 anti-mouse IgG-Fc PE were from abcam (Cambridge, MA), rabbit anti-human LAMP was from Sino Biological (Beijing, China). Goat anti-rabbit-HRP, goat anti-mouse IgG1-HRP and goat anti-mouse IgG2a-HRP were purchased from Southern Biotechnologies (Birmingham, AL). Streptavidin-HRP were purchased from Thermo Fisher (Waltham, MA). SureBlue TMB microwell peroxidase substrate and TMB stop solution were purchased from KPL (Gaithersburg, MD). ELISPOT antibody pairs for IFN γ was from BioLegend.

[0349] **Vaccines, and immunizations.** Control vector, PSMA-ILC-1 LAMP Construct was used in a total volume of 20µl per mouse per dose. Mice were immunized with the vaccine by ID via electroporation on days 0, and 21. Serum was collected and stored in -30°C. Spleens were collected on day 34 for ELISPOT/ELISA assays.

[0350] **Evaluation of antigen-specific T cell response.** To assess antigen-specific T cell response in the vaccinated mice, splenocytes from vaccinated mice were evaluated for antigen-specific IFN γ and IL-10 by Enzyme-linked immunospot (ELISPOT). Splenocytes were depleted of RBCs and co-cultured in flat bottom 96-well plates in 200µl/well T cell media (RPMI-1640 with L-Glutamine and HEPES (ATCC), 1% penicillin, 1% streptomycin, and 5 x 10⁻⁵M 2-ME) at 4x10⁵ cells/well and 10µg/ml IGFBP2 (39-328) protein or concavalin A (0.25µg/ml) or medium alone for 72h at 37°C in 5%CO₂. Plates were centrifuged at 1600 rpm for 6 minutes and supernatants were collected and stored at -30°C.

[0351] For ELISPOT assays were performed as described herein. Briefly, 96-well nitrocellulose plates (Millipore), were activated with 30µl of 35% ethanol for one minute, washed with PBS twice, and coated overnight at 4°C with 50µl/well of capture monoclonal antibody in PBS. The plates were washed three times with 200µl/well PBS and blocked with 200µl/well T cell media for at least 2hrs at room temperature. Splenocytes were plated at 3x10⁵ cells/well and co-cultured with 10, 5, 2, 1, 0.1, 0.01µg/ml PSMA JPT peptide mix for PSMA or concavalin A (0.25µg/ml) or medium alone in a total volume of 200µl/well T cell media for 48h at 37°C in 5%CO₂. The plates were washed, diluted detection antibodies (50µl/well) were added and plates were incubated for 2hrs at room temperature on shaker. Plates were washed four times with PBS. Streptavidin-HRP diluted in PBS (50µl/well) were added and incubated for 1h. Plates were washed with PBS and developed with 50µl/well AEC development solution for up to 30 min. Color development was stopped by washing under running tap water. After drying 24-72h at room temperature in dark, colored spots were counted using an AID ELISPOT High-Resolution Reader System and AID ELISPOT Software version 3.5 (Autoimmun Diagnostika GmbH).

[0352] **Measurement of serum PSMA-specific IgG/IgG2a and Prostein-specific IgG/IgG2a by ELISA.** The murine antibody response to PSMA was assessed by indirect ELISA. ELISA plates (MaxiSorp) were coated with 5µg/ml of PSMA protein in carbonate bicarbonate buffer overnight and then blocked with 2% BSA in PBS. Serum samples were diluted (1:100, 1:300, 1:900, 1:2700, 1:8100, 1:24300, 1:72900, 1:218700) in PBS-T. Samples were detected with 1:6000 goat anti-mouse IgG-HRP or 1:11000 goat anti mouse IgG2a-HRP (Southern Biotech, Birmingham, Al), followed by Streptavidin-HRP (Thermo Fisher Scientific, Rockford, IL). Reaction was developed with SureBlue TMB Substrate and stopped with TMB Stop Solution from KPL (Gaithersburg, MD). Plates were read (OD450) by using Epoch ELISA reader (BioTek, Winooski, VT). Average background (PBS only) was calculated, and samples which have OD450 value more than 2 * average background were considered as positive. The dilutions of such samples are determined as the endpoint titers.

[0353] **Evaluation of intracellular cytokine.** To determine the cells responsible for production of cytokines intracellular staining was performed. Splenocytes were depleted of RBCs stored in refrigerator for 24h. Next day splenocytes were co-cultured in flat bottom 96-well plates in 200ul/well T cell media (RPMI-1640 with L-Glutamine and HEPES (ATCC), 1% penicillin, 1% streptomycin, and 5×10^{-5} M 2-ME) at 3×10^6 cells/well and 2ug/ml PSMA (JPT peptide mix) or medium alone. A mixture of Brافeldin A and monensin (X1000) was added to each well in 20ul volume (0.22ul per well for 20ul volume; prepare a stock for all the wells) one hour later. PMA/ionomycin activation cocktail was added to positive control wells along with BFA and Monensin (Two wells were set-up; one for IgG control and other one for cytokine staining). Cells were incubated for total of 6h at 37°C in 5%CO₂.

[0354] **Live/Dead staining (no protein in this step):** Cells were washed with 200ul PBS (no protein to this wash). Cells were stained with 50ul of diluted Zombie aqua dye (1:500 dilution of zombie aqua in PBS) and incubated for 20 min at room temperature protected from light (no protein in this step). Cells were washed once with 2%serum in PBS.

[0355] **Fc block:** 20ul of purified anti-mouse CD16/32mAb (clone 2.4G2; 1ug/20ul) was added to the cells and cells were incubated at 4°C for 10mins.

[0356] **Surface staining:** cells were centrifuged (2000 rpm, 6 min), supernatant was decanted, and extracellular antibodies were added in PBS supplemented with 2% serum. The antibodies were 0.3 ul of each / well. Abs were added in a volume of 50ul/well, incubated for 30 min in 4°C (the CD3 clone 17A2 can activate T cells so 4°C temperature is important).

[0357] **Fixation and permeabilization:** Cells were washed with PBS + protein (2% FCS), fixed and permeabilized with 100ul of CytoFix/CytoPerm solution at 4°C for 30 mins (mixed thoroughly with the multichannel when adding the fix buffer to reduce aggregates and doublets formation). Cells were washed with 200ul Perm/Wash buffer (1X) twice (2000 rpm, 6 min)

[0358] **Intracellular staining:** Cells were stained with the intracellular staining Ab at 0.5ul Ab/well in Perm buffer. One of the PMA/ionomycin wells were stained with the isotype controls. After 1h (or overnight) incubation cells were washed twice with perm buffer, and cells were acquired by flow cytometer. While acquisition the events/second were less than 8000. Acquired $>10^6$ cells per sample.

[0359] The acquired data were analyzed using Kaluza analysis software. Dead cells and doublets were gated out.

[0360] **Statistics.** Statistical analyses were performed by using Prism 6 software (GraphPad Software, La Jolla, CA). Data were analyzed by one-way ANOVA followed by Tukey's test for multiple comparisons. *p* values below 0.05 were considered to indicate a statistically significant difference.

[0361] **Figure 26** shows that the PSMA-ILC-1 LAMP Construct induced significantly higher IFN γ producing effector T cells at the dose of 20ug ID/EP immunization. Splenocytes (3×10^5 /well) were stimulated with PSMA peptide mix from JPT (2, 1, 0.1, 0.01, 0.001ug/ml) in T cell media (RPMI with 10% heat inactivated

FBS, 1% penicillin/streptomycin, and 1X 2-ME), for 48h. Values in dot plot are experimental – media for each mouse. N=7 mice per group. Dot plot to show recall with PSMA.

[0362] **Figure 27** shows that PSMA-ILC-1 LAMP Construct induced IFN γ producing CD4 $^{+}$ and CD8 $^{+}$ effector memory T cells at the dose of 20 μ g ID/EP immunization. Splenocytes (3×10^5 /well) were stimulated with PSMA peptides (JPT; 2 μ g/ml) in T cell media (RPMI with 10% heat inactivated FBS, 1% penicillin/streptomycin, and 1X 2-ME) for 6h. Cells were stained for intracellular cytokines as described and analyzed as shown below. Data from individual mice is shown.

[0363] **Figure 28** shows the total IgG and IgG2A production in C57BL/6 mice immunized with PSMA-ILC-1 LAMP Construct by immunization via ID/EP. IgG were determined in plasma by ELISA. Briefly, ELISA plates were coated with 5 μ g/ml of PSMA in carbonate bicarbonate buffer, blocked with 2%BSA, serum (1:100 dilution in PBS-T) were evaluated by HRP-conjugated goat anti mouse IgG (1:6000).

[0364] Variations, modifications, and other implementations of what is described herein will occur to those of ordinary skill in the art without departing from the spirit and scope of the invention and the claims. All of the patents, patent applications, international applications, and references identified are expressly incorporated herein by reference in their entireties.

[0365] The reference to any prior art in this specification is not, and should not be taken as, an acknowledgement or any form of suggestion that such prior art forms part of the common general knowledge.

THE CLAIMS DEFINING THE INVENTION ARE AS FOLLOWS:

1. A LAMP Construct comprising two homology domains of a luminal domain of a LAMP protein, and an antigenic domain, wherein the antigen domain is placed between the first homology domain of the LAMP protein and the second homology domain of the LAMP protein, and wherein the antigenic domain comprises one or more of: at least one epitope of pp65, at least one epitope of gB, and at least one epitope of IE1.
2. The LAMP Construct of claim 1, wherein the antigenic domain comprises at least one epitope of pp65 and at least one epitope of IE1, or at least one epitope of gB.
3. The LAMP Construct of claim 1 or 2, wherein the LAMP protein is selected from LAMP-1, LAMP2, LAMP-3, LIMP 2, Macrosailin, Endolyn, LAMP5 or LIMBIC.
4. The LAMP Construct of claim 1 or 2, wherein the LAMP Protein comprises an amino acid sequence selected from any one of SEQ ID NO:1-113, or comprises an amino acid sequence at least 90%, at least 95%, at least 96%, at least 97%, at least 98% or at least 99% identical to SEQ ID NO:1-113.
5. The LAMP Construct of any one of claims 1-4, wherein the LAMP Protein is LAMP-1.
6. The LAMP Construct of any one of claims 1-5, wherein the LAMP Construct comprises LAMP-1 Homology Domain 1 and LAMP-1 Homology Domain 2.
7. The LAMP Construct of claim 6, wherein the LAMP-1 Homology Domain 1 comprises
(a) the amino acid sequence of residues 29-194 of SEQ ID NO: 1, or
(b) a variant of (a) wherein said variant comprises an amino acid sequence at least 95% or at least 97% identical to the amino acid sequence of (a); and/or
wherein the LAMP-1 Homology Domain 2 comprises residues 228-381 of SEQ ID NO: 1.
8. The LAMP Construct of any one of claims 1-7, wherein the LAMP Construct further comprises a Transmembrane Domain and/or a cytosolic tail of a LAMP Protein.
9. The LAMP Construct of claim 8, wherein the Transmembrane Domain comprises residues 383-405 of SEQ ID NO: 1 and/or wherein the cytosolic tail comprises residues 406-417 of SEQ ID NO: 1.

10. The LAMP Construct of any one of claims 1-9, wherein the LAMP Construct further comprises a signal sequence, optionally wherein the signal sequence is derived from a LAMP protein.
11. The LAMP Construct of any one of claims 1-10, wherein the antigenic domain comprises more than one epitope and wherein the epitopes of the antigenic domain are separated by linkers, optionally wherein the linkers are selected from the amino acid sequence GPGPG or PMGLP.
12. The LAMP Construct of any one of claims 1-11, wherein the at least one pp65 epitope comprises the amino acid sequence of SEQ ID NO: 114, or comprises an amino acid sequence at least 95%, at least 96%, at least 97%, at least 98% or at least 99% identical to SEQ ID NO: 114; and/or wherein the at least one gB epitope comprises the amino acid sequence of SEQ ID NO: 117, or comprises an amino acid sequence at least 95%, at least 96%, at least 97%, at least 98% or at least 99% identical to SEQ ID NO: 117; and/or wherein the at least one 1E1 epitope comprises the amino acid sequence of SEQ ID NO: 121, or comprises an amino acid sequence at least 95%, at least 96%, at least 97%, at least 98% or at least 99% identical to SEQ ID NO: 121.
13. The LAMP Construct of any one of claims 1-11, wherein the at least one pp65 epitope comprises one or more of: LLQTGIHVRVSQPSL, ALPLKMLNIPSINVH, DQYVKVYLESFCEDV, IIKPGKISHIMLDVAFTSH, PQYSEHPTFTSQYRIQGKL, PPWQAGILARNLVPMV, or KYQEFFWDANDIYRIFA; and/or wherein the at least one gB epitope comprises one or more of: TTSAQTRSVYSQHVT, QLIPDDYSNTHSTRYV, VSVFETSGGLVFWQ, or NSAYEYVDYLFKRMIDLS; and/or wherein the at least one 1E1 epitope comprises one or more of: VLAELVKQIKVRVDMVRHRIKEHMLKKYTQ, IVPEDKREMWMACIKELH, KDELRRKMMYMCYRNIEFFTKNSAFPKTT, SVMKRRIEEICMKVFAQYI, AIAEESDEEEAIVAY, or VKSEPVSEIEEVAPEEEEDG.
14. The LAMP Construct of any one of claims 1-11, wherein the Construct comprises one or more of SEQ ID NO: 115, 116, 119, 120, 122, or 123.
15. The LAMP Construct of any one of claims 1-11, wherein the antigenic domain comprises one or more of SEQ ID NO: 114, SEQ ID NO: 117, or SEQ ID NO: 121.
16. A polynucleotide encoding the LAMP Construct of any one of claims 1-15.
17. The polynucleotide of claim 16, wherein the polynucleotide is RNA.

18. The polynucleotide of claim 16, wherein the polynucleotide is a viral vector, optionally a self-replicating RNA viral vector.
19. A host cell comprising the polynucleotide of any one of claims 16-18.
20. An antigen presenting cell comprising the polynucleotide of any one of claims 16-18.
21. The antigen presenting cell of claim 20, wherein the cell is a dendritic cell.
22. A pharmaceutical composition comprising polynucleotides encoding a mixture of LAMP Constructs, wherein the mixture of LAMP constructs collectively comprises pp65, IE1, and gB antigens, wherein each LAMP Construct of the mixture comprises two homology domains of a luminal domain of a LAMP protein, and an antigenic domain, wherein the antigenic domain is placed between the first homology domain of the LAMP protein and the second homology domain of the LAMP protein, wherein the antigenic domain comprises one or more of: at least one epitope of pp65, at least one epitope of gB, and at least one epitope of IE1.
23. The pharmaceutical composition of claim 22, wherein the antigenic domain of one LAMP Construct comprises at least one epitope of pp65 and at least one epitope of IE1 and the antigenic domain of a second LAMP Construct comprises at least one epitope of gB.
24. A method of treating a subject having a disease or a disorder characterized by the expression of one or more epitope of pp65, gB, or IE1, wherein the method comprises administering to the subject the LAMP Construct of any one of claims 1-15, the polynucleotide of any one of claims 16-18, the host cell of claim 19, the antigen presenting cell of claim 20 or 21, or the pharmaceutical composition of claim 22 or 23 in an amount sufficient to reduce or treat the disease or disorder.
25. A method of treating a subject having glioblastoma multiforme characterized by the expression of one or more epitope of pp65, gB, or IE1, wherein the method comprises administering to the subject the LAMP Construct of any one of claims 1-15, the polynucleotide of any one of claims 16-18, the host cell of claim 19, the antigen presenting cell of claim 20 or 21, or the pharmaceutical composition of claim 22 or 23 in an amount sufficient to treat the glioblastoma.
26. The method of claim 24 or 25, wherein the method comprises a priming step and/or at least one boosting step, optionally wherein more than one antigenic domain is used to prime and/or boost.

27. The method of claim 26, wherein the LAMP Construct of any one of claims 1-15, the polynucleotide of any one of claims 16-18, the host cell of claim 19, the antigen presenting cell of claim 20 or 21, or the pharmaceutical composition of claim 22 or 23 is administered in the priming step and/or in the boosting step.

Figure 1

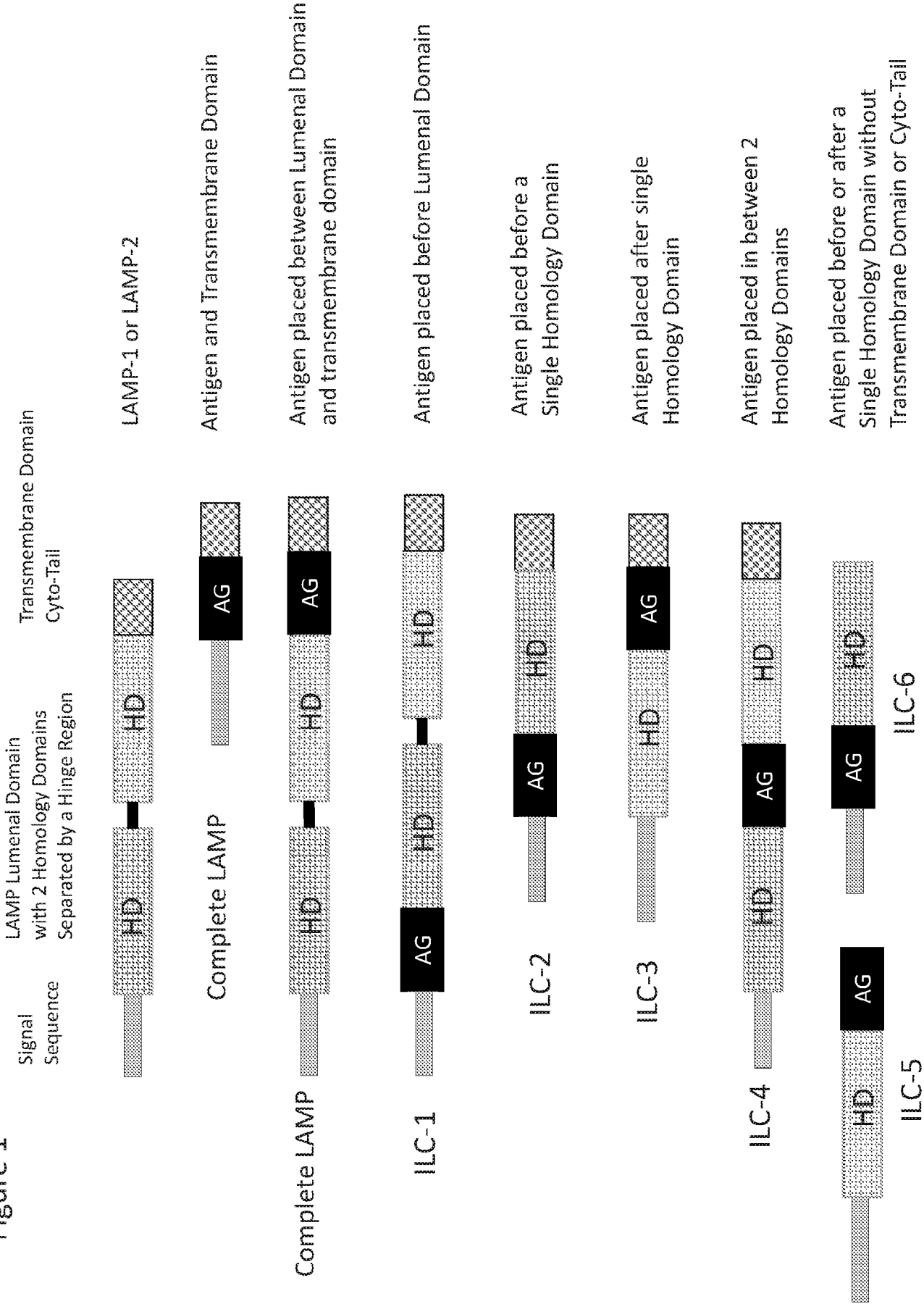


Figure 2A

Gene Name Accession No.	Alternative Names	SEQ ID NO.	Orthologs	Signal Seq.	Luminal Domain			Transmembrane Domain	Cytoplasmic Tail
					First Homologous domain	Hinge Region	Second Homologous Domain		
h. LAMP-1 NP_005552.3	CD107a; LAMPA; LGP120	1	SEQ ID NO: 6-24	1-28	29-194	195-227	228 to 381 or 382	382 or 383 to 405	406-417
h. LAMP-2 NP_002285.1	CD107b; LAMPB; LGP110	2	SEQ ID NO:25-43	1-28	29-192	193-228	229-375	376-399	400-410
h. LAMP-3 NP_055213.2	CD208; DC LAMP; DC- LAMP; DCLAMP; TSC403	3	SEQ ID NO:44-55	1-27	28-219	220-234	235-381	382-402	403-416
LIMP-2 Q14108	AMRF; EPM4; LGP85; CD36L2; HLGP85; LIMPII; SR-BII; SCARB2	4	SEQ ID NO:56-66	*5-27 Transm em. *Unclea vable	28-433			434-459	460-478
h. Endolyn NP_006007.2	Sialomucin CD164 MUC-24	5	SEQ ID NO:73-79	1-23	24-162			163-183	184-197
Macrosialin NP_001242.2	CD68	80	SEQ ID NO: 81-92	1-21	22-319			320-344	345-354

Replacement Sheet

Figure 2A cont.

LAMP5 NP_036393	BD-LAMP	93	SEQ ID NO: 94-101	1-29	30-235	236-256	257-280
h. LIMBIC NP_002329.2	LSAMP IGLON3	67	SEQ ID NO: 68-72 and 102-113	1-28	29-315	316-338	No tail

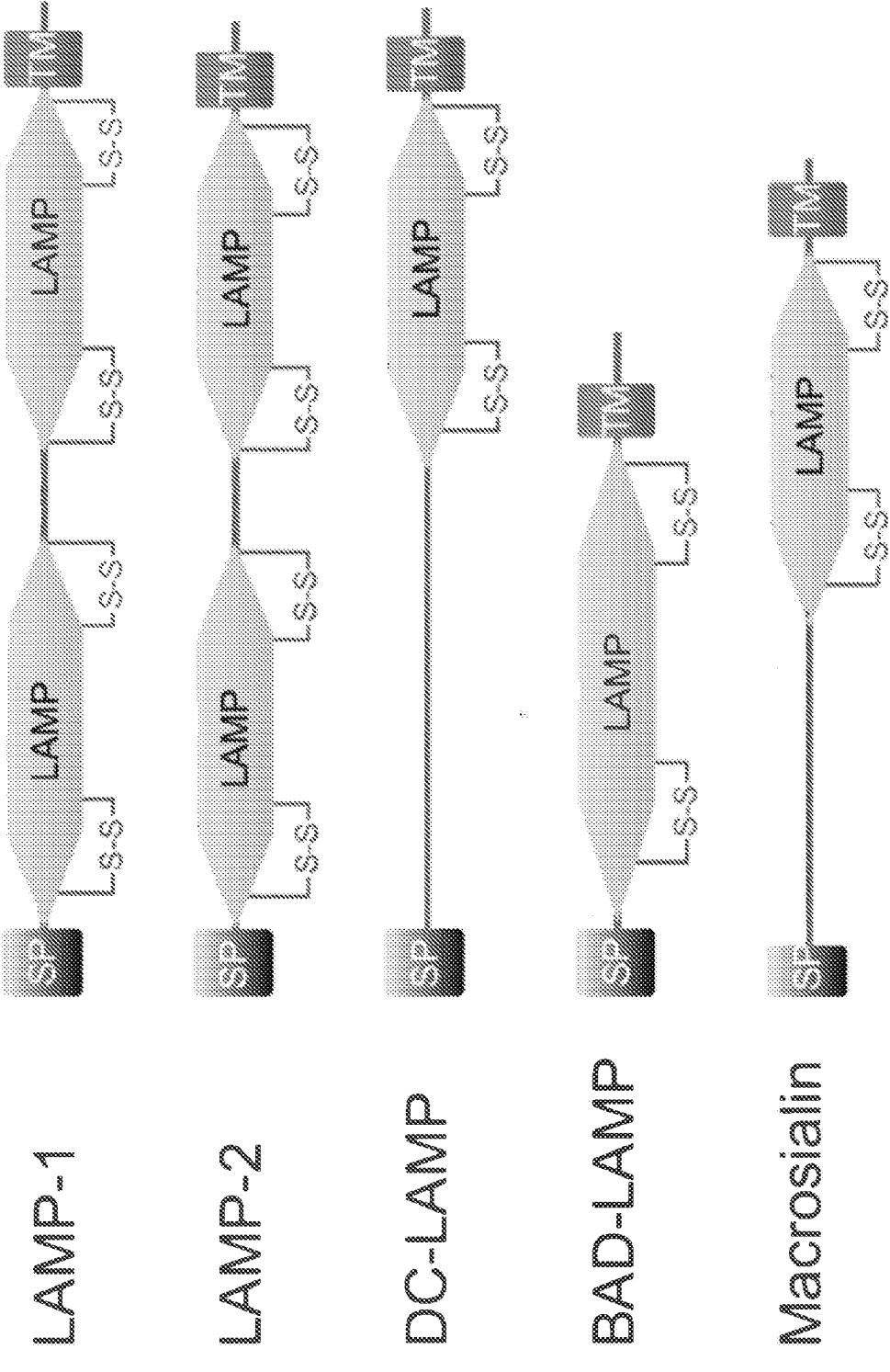


FIGURE 2B

FIGURE 3: HUMAN LAMP-1 ALIGNMENT WITH ORTHOLOGOUS SEQUENCES

	SIGNAL SEQUENCE	LAMP HOMOLGY DOMAIN 1	
		1	
SEQIDNO: 1	MAAPGSARRPLLLLLLLLLLGLIMH-CASAAMFMVKNGN-GTACIMANFSAAFSVNYDTKS		58
SEQIDNO: 6	MAAPGAR-RPLL---LLLLAGLAH--GASALFEVK--NN-GTTCIMASFSASFLTYYETAN		52
SEQIDNO: 7	-----MARAAG-VCWTLTMGCVFA-AHAVTFEVT DGN--STCIKELNASFSISYNTTN		50
SEQIDNO: 8	--MSWRQVKMPVYWMVMLLIGVVQ--VATAVQFEVKDGKTNITCILADLSINFSVSYNVSS		58
SEQIDNO: 9	MAAPGSARRPLLLLLLLLLLGLVH-CASAAMFMVKNGN-GTACIMANFSAFVSFVNYDTKS		58
SEQIDNO: 10	MAAPGSARRSLLL-LLLLLLGLTH-CASAAMFIVKNGN-GTACIMANFSAAFSVNYDTKS		57
SEQIDNO: 11	MAAPGGARPRPL--LLLLLAGLVH--GAAAVFVVKDAN-GTACIMANFSAAFASYETRS		55
SEQIDNO: 12	MEAPGGARRPLLLL---LLGLVH--GASAVFVVRNSN-GTACIMANFSAFVSFVYESKS		54
SEQIDNO: 13	MAAPGGARRRPLLL--LLFAGLVH--GASAVFVVKNGN-GTACIMADFSATFLTSDYTRS		55
SEQIDNO: 14	MAAPGAR-RPLL---LLLLAGLAH--SAPALFEVKDNN-GTACIMASFSASFLTYYDAGH		53
SEQIDNO: 15	-----MGGAA--RAVLLGFL---QASSSFVDVDST-GKVCIIANLTVAFSVEYKSSG		46
SEQIDNO: 16	MAAPGGAWRRPLLLL-LLLLGLAR--GASAVFVSDGN-GTACIMADFAAFEISYDSRS		56
SEQIDNO: 17	MAEPGGARTPQRLL--LLLLGLIH--VASSIFVVKNGT-GTACIMANFSATFSMNYTTKS		55
SEQIDNO: 18	-----MARALL--AAVLLGFL---QASSSFVDVDST-GKVCIIANLTVAFSVEYKSNG		47
SEQIDNO: 19	-----MARGLLA--AAALLGFL---QASSSFVVDSS-GKVCILADLTVAFSVEYKTNV		48
SEQIDNO: 20	MVSSSSCRRGLLL--AAVLLGFL---QASSTFEVRDKT-GKICILANFSAEFTVDYSTKA		54
SEQIDNO: 21	MKSFPSPVALFI-VCSAVLADT---QAVVTLEVKEGN--STCIKAESAVFSITYNTTN		53
SEQIDNO: 22	MKRSHALVVL-I-IAWFSLSGC----IQAVSLEVKEGN--STCIKANLSAYFSITYNTSS		52
SEQIDNO: 23	MTRTCPFVVG-I-AC-FAILGCVTVVQSQVTLEVTEGN--STCIKAELSASFISITYDTAN		55
SEQIDNO: 24	-----		0

	LAMP HOMOLGY DOMAIN 1	
	2	
SEQIDNO: 1	GPKNMTFDLPSDATVVLNRSSCGKENTSDPSLVIAFGRGH--TLTLNFTRNATRYSVQLM	116
SEQIDNO: 6	GSQIVNISLPASAEVLKNGSSCGKENVSDPSLTITFGRGY--LLTLNFTKNTRYSVQHM	110
SEQIDNO: 7	GTSVSVFALPASASVSE-RSSCGS-AAVPELALVFGDTHHTLSLLFSRDQRLYRVSNI	108
SEQIDNO: 8	KMELATFVLPSEAVTNINKSSCGVENTTAPVLAIQFGSNH--SLSIHFARNTRYEVAEL	116
SEQIDNO: 9	GPKNMTFDLPSDATVVLNRSSCGKENTSDPSLVIAFGRGH--TLTLNFTRNATRYSVQLM	116
SEQIDNO: 10	GPKNMTFDLPSDAKVVLNRSSCGKENTSDPSLVIAFGRGQ--TLTLNFTRNATRYSVQLM	115
SEQIDNO: 11	GPKNVTFDLPSDA-VVLNRSSCGKENTSDPSLMIAFGKGH--GLTLNFTRNATRYSVQLM	112
SEQIDNO: 12	GYKNASFELPATA-EVQNTSSCGRENTSNPSLQIAFGRGH--VLALNFTRNATLYSVPLL	111
SEQIDNO: 13	GPQNSFELPAGA-EVSNSSCGKENASDSSLVITFGRGH--TLTLIFTRNATRYEVQLM	112
SEQIDNO: 14	VSKVSNMTLPASAEVLKNSSSCGEKNASEPTLAITFEGGY--LLKLTFTKNTRYSVQHM	111
SEQIDNO: 15	QKQFAHFFLPQNATSQ-SHSSCGEGNTSHPILALSFGAGH--LISLNFSTLDKYQVEEL	103
SEQIDNO: 16	GAKNITFSLPASA-QVLNRSSCGKENTSDSSLVIAFGRGH--TLTLNFTRNATRYSVQLM	113
SEQIDNO: 17	GLESTTFRLPQNA-SVMNRSSCGKENTSNPILEIGFGGGH--TLTMNFSSTTQSYQVELL	112
SEQIDNO: 18	QKQFAHFFLPQNATSQ-SHSSCGEGNTSHPILALSFGAGH--LLSLNFSKTLDKYQVEEL	104
SEQIDNO: 19	KKEFVHFPLPQNASVD-SQSSCGKDNASHPIVLDFGGGH--SLSLNFSADKYQVEEL	105
SEQIDNO: 20	KVERKTFQLPSSAHINKESSCGKEKETSQVLVVEFGTGN--SLTFTFEKSNDFYHVSNL	112
SEQIDNO: 21	DTRTVSVFLPNSTTVDSANSSCGS-NGSTPGLMAKFGPGH--YFGMNFSTNGSLYSVDTL	110
SEQIDNO: 22	STRTAQFILPDSATVDPDSSTCGG-NGSSPWLVAVFGAGH--ALGLGFSTNGSFYSVANL	109
SEQIDNO: 23	GTRTMVPLPGSAVVG-ASSCGG-DGRSPWLVALFGDGH--ALGLGFSSNDSLYSVAKL	111
SEQIDNO: 24	-----	0

FIGURE 3 cont.

Replacement Sheet

LAMP HOMOLOGY DOMAIN 1

3

```

SEQIDNO:1  SFVYNLSDETHLFPNASSK-EIKT-VESITDIRADIDKKYRCVSGTQVHMNN-VTVTLHDA 173
SEQIDNO:6  YFTYNLSDTEHFPNAISK-EIYT-MDSTTDIKADINKAYRCVSDIRVYMKN-VTVVLRDA 167
SEQIDNO:7  SLQYNLSDGDIFFQSSSAGVQSVMASVSELSARLNSTYRCVSSSSISLSAAVNLTLSGV 168
SEQIDNO:8  VMSYNLSDKIIFFNASENGTKTV-STNKTAFLAENDTVYKCMNPHLIRMDN-ANATFHDI 174
SEQIDNO:9  SFVYNLSDTHLFPNASSK-EIKT-VESITDIRADIDKKYRCVSGTQVHMNN-VTVTLHDA 173
SEQIDNO:10 SFVYNLSDTHLFPNASSK-EIKT-VESITDIRADIDKKYRCVSGTQVHMNN-VTVTLHDA 172
SEQIDNO:11 SFIYNLSDTQIFFPNASSK-ETKT-VESATDIRADINKKYRCVSNTQIHMHN-VTVTFHDV 169
SEQIDNO:12 SFVYNLSDSDLFPNASSK-DIKT-VGSTTDIKADIDKKYRCVSDSKVPMGN-VTVTLQDA 168
SEQIDNO:13 RFAYNLSDTDTFPNSSST-GVKT-VESATDIKADINKTYRCVSETQVNMDN-VTVTLRDA 169
SEQIDNO:14 YFTYNLSDAQFFFPNASSK-GPDT-VDSTTDIKADINKTYRCVSDIRVYMKN-VTIVLWDA 168
SEQIDNO:15 TFHYNLSDETLFPNASEG-KVMV-ATQKSVIQARIGTEYRCINSKYVRMKH-VNITFSNV 160
SEQIDNO:16 TLVYNLSDAEFFFSASSK-GTKT-VAASTDIRADLNTKYRCVSNSQVHLLN-VTVTLGNA 170
SEQIDNO:17 SFSYNLSDATLFPNASKGEES-VKSKTDIQADIHKKYRCVSSNRITMSN-VTIVLSDV 170
SEQIDNO:18 TFHYNLSDETLFPNASEG-KVME-VTQKSVIQARIGTEYRCINSKYIYIRH-VNITFSNV 161
SEQIDNO:19 VFHYNLSDATLFPNSSTG-GMKT-VSHKSIIQAHMGTQYRCINSKHINMKN-VNVTFSNV 162
SEQIDNO:20 TFSYNLSDSSFFPNSSG--GQRE-VSRAGDIQANINTTYRCRSNHRVNMN-VTVLFSNV 168
SEQIDNO:21 FLRYNLSDASLFPEANSSGVPDFELASVGIWAPTNTTYRCLSPTTITR-PSVTFSEM 169
SEQIDNO:22 TLQYNLSDASVFPDANSSGVVTV-VSSSVGIWAAVNTTYRCLSSVLFQVGG-ATVTFSDM 167
SEQIDNO:23 TLQYNLSDVSNFPEANSTDVVTVE-TTSVGMVARVNTTYRCISASPVIVGG-ATVTFSNV 169
SEQIDNO:24 ----- 0

```

LAMP HOMOLOGY DOMAIN 1

Hinge Region

4

```

SEQIDNO:1  TIQAYLSNSSFSRGETRCEQDRPSPTTAPPAP-----PSP-SP---SPVFKSPS 218
SEQIDNO:6  TIQAYLSSGNFSKEETHCTQDGPSTTGP-----PSP-SP---PLVPTNPT 209
SEQIDNO:7  QMEAYMSSANLSADESVCSADQPSTTVAPPPSTT-----TSPPPIPPVPE 213
SEQIDNO:8  RLEAYLKQSNFSQKVSTCSEDITPTSAPA-FV--T-----T-----TAPVPAP-VPDPP 219
SEQIDNO:9  TIQAYLSNSSFSRGETRCEQDRPSPTTAPPAP-----PSP-SP---SPVPESPS 218
SEQIDNO:10 TIQAYLSNSSFSREETRCEQDRPSPTTAPPAP-----PSP-SP---SPVPESPS 217
SEQIDNO:11 TIQAYLANSNFSKEETRCEQDGFPPTTAPPPP-----PHP-SP---SPAPESPS 214
SEQIDNO:12 TIQAYLWNNFSQAESRCRQDMPSTTAPPAPFPV-----PSPSP-SP---PPKPESPS 219
SEQIDNO:13 AIQAYLSSSNFSREETRCEQDLPT-----P-----TTPPQP-AP---TPAPASPA 210
SEQIDNO:14 TIQAYLPSSNFSKEETRCQDQPSPTTGP-----PSP-SP---PLVPTNPS 210
SEQIDNO:15 TLEAYPTNDFTSANKTECREDMVSTTTVAPTTPKH-----ATSQVPTTSPAPTAAPSSPA 215
SEQIDNO:16 TIQAYLANNSFSQQETRCEQDKPSP-----PTP-----TAPPTP-TP---TPAPTSPV 214
SEQIDNO:17 TIQAYLSNNTFSKEETRCSDTPSPSPVPTTHPTT-----IPVPTP-TPTRPPTPAEIPP 224
SEQIDNO:18 TLEAYPTNGTFSTNKTECEDMVSTTTVAPTTPKH-----ITSQVPATSPAPTAAPSNPA 216
SEQIDNO:19 TLEAYLTNGTSLVNKTECAEDRVSTTTMVPTTPKQ-----TTSQSPTTGPAPTS-PPNPT 216
SEQIDNO:20 TLEAYLPNNAFSKNDSVCAEDKTSTVA--PPTTTH-----IPTTTS LAPPT-PPPTDTPK 220
SEQIDNO:21 KLEAYMPGNDFSPAERVCAADQTTTGAPTTTT-----SAATP-TT-PSPTPAGTPE 218
SEQIDNO:22 RLEAYMPGNDLSPRESFCAADQTTTAPPTTTAAP---TTTAATTM-AP-PAPTTPGTPV 221
SEQIDNO:23 TMEAFMTGEDLSPNESVCTADQSFTTAPPPPPS-----TTTAA-PA-PVPTPPGTPS 219
SEQIDNO:24 -----MVQICRVQSWFVGVTPLLI FATVLHQGFATVAP-PTFAPHKEPGRPE 46

```

* ;

*

FIGURE 3 cont.

Replacement Sheet

	Hinge	LAMP HOMOLGY DOMAIN 2	
	1	2	
SEQIDNO:1	VDKYNVSGTNGT-CLLASMGQLQNLITYE-RKDNTTVTRLLNINPNKTSASGSCGAHLVTL		276
SEQIDNO:6	VSKYNVTGNNGT-CLLASMGQLQNLITYL-KKDNKTVTRAFNISPNDT-SSGSCGINLVTL		266
SEQIDNO:7	RGNYSVTDGNGTVCVLALMGLQNLITYT-TTQNSQSVSELMNLQPNQTTVSGSCGVTESSL		272
SEQIDNO:8	VVQYSVNRSSSEP-CLLAKVGLQMNITYT-TKDGNKGSYVFNIESKGVTVDGNCNTNTTAYL		277
SEQIDNO:9	VDKYNVSGTNGT-CLLASMGQLQNLITYE-RKDNTTVTRLLNINPNKTSASGSCGAHLVTL		276
SEQIDNO:10	VDKYNVSGTNGT-CLLASMGQLQNLITYE-RKDNTTVTRLLNINPNKTLASGSCGAHLVTL		275
SEQIDNO:11	VHKYNVSGANGT-CLLASMGQLQNLITYK-KKDNTTVVKVVSINPNKTTAGGSCGAQLVTL		272
SEQIDNO:12	VSRYNVSDGNAT-CLLASMGQLQNLITYV-HRDNATVTRVFNINPNKTKPSGHCGAQQVTL		277
SEQIDNO:13	VFRYNVSGSNGT-CLLASMGQLQNLITYR-RVDNKTVTREFNVPNKTTFFGGNCSATLATL		268
SEQIDNO:14	VSKYNVTGDNGT-CLLASMGQLQNLITYM-KKDNTTVTRAFNINPSDK-YSGTCGAQLVTL		267
SEQIDNO:15	VGKYNVTGANGT-CVLASMGQLQNLITYV-KKDEKMGDLLNFIPHNTSASGMCESTSAFL		273
SEQIDNO:16	VSRYNVSGANGT-CLLASMGQLQNLITYR-TKDNTTVTRGLNINPNKTTFFGGSCSAQLVTL		272
SEQIDNO:17	IFKYNVSDANGT-CLLASMGQLQNLITYA-KKDNSSARI IWNINPNKTVAGGSCSPQVAIL		282
SEQIDNO:18	VGKYNVTGANGT-CVLASMGQLQNLITYL-KKDGTGLDLLNFVPHNTNASGTCENTSAFL		274
SEQIDNO:19	VGKYNVTGPNGT-CVLAYMGLQNLITYQ-QKDEKMGDLLNFVPHNTTSSGRCDNTSALL		274
SEQIDNO:20	IGRYNVTGLHGI-CLLATMGLQVNVITYS-TKNKTSKSELLNLPP-TAEVSGTCENSSITL		277
SEQIDNO:21	QGSYSVKNASGTVCLMAKMGVQLNVSYFSQSQNKTQVQLLNLTLPNLTSSTGSLCGGTNATL		278
SEQIDNO:22	RGTYSVVNGNDTTCLLAQMGLQNLNVSYFSRSQNKTQVSLVNLTLPNLTNSTGSCCKGSATL		281
SEQIDNO:23	QGSYSVSNNGTVCLLARMALQNLISHFSASQNKTQEVVNLLPNQTTSSGSCDPTSATL		279
SEQIDNO:24	RGYYNVTNHNGTICLMAYMGLQNLISYNSTSQKKVVQDVNMNLQPNLTKHSGLCDSDIASL		106
	.	*** :*:***: :	.. * * *

LAMP HOMOLGY DOMAIN 2

SEQIDNO:1	ELHS-EGTVLLFQFGMNASSSRFFLQGIQLNTTLP-DARDPAFKAANGSLRALQATVGN	334
SEQIDNO:6	KVEN-K-NRALELQFGMNASSSLFFLQGVRLNMTLP-DALVPTFSISNHSILKALQATVGN	323
SEQIDNO:7	RLSD--ETTNLTFSFTMNSTTQKYLSAVSVSALWP-DMS-VVFEAGNTSLSALQCSVGR	328
SEQIDNO:8	SLST-GS-IDLRNFNLTNSSLLEVFLYLDGVSLSTGLPADANDTHFEAANSSLYNMQTNVHK	335
SEQIDNO:9	ELHS-EGSTVLLFQFGMNASSSRFFLQGIQLNTTLP-DARDPAFKAANGSLRALQATVGN	334
SEQIDNO:10	ELHS-EGSTVLLFQFGMNASSSRFFLQGIQLNTTLP-DARDPAFKAANGSLRALQATVGN	333
SEQIDNO:11	ELRS-ESVTLLEFQFGMNASTSRFFLQGIQLNMTLP-DARDPTFKAGNNSLRALQATIGN	330
SEQIDNO:12	ELQS-ERSTVLVFQFGMNASSGQYFLQGVLLNTTLP-DAREPAFSASNSSLRALQATLGN	335
SEQIDNO:13	ELHS-ENLLLLALQFVMNESSSRVFLQGVQLNLTLP-DAKEGSFTATNSSLRALQATAGN	326
SEQIDNO:14	KVGN-K-SRVLELQFGMNATSSSLFFLQGVQLNMTLP-DAIEPTFSTSNYSILKALQASVGN	324
SEQIDNO:15	NLAF-EK-TKITFHFVLNASSEKFFLQGVNVSTTLPSEAKAPTFEASNDMSSESRAVGN	331
SEQIDNO:16	ELQG-ESLRLALQFALNTSSSRVFLQGVQLNMTLP-DARDPSFSAANGSLRALQATAGN	330
SEQIDNO:17	ELQT-EN-STLAFSFGMNATSSKFFLREIRFHKFFP-DAKDPAFGAVNSSLRALQATVGN	339
SEQIDNO:18	NLAF-EK-TKITFHFVLNASSEKFFLQGVNVSTTLPSEAKAPMFEASNDMSSELRAVGN	332
SEQIDNO:19	NLTF-EK-TRVIFQFALNATAEKFFLQGVSVSTTLPSEAKNPKFEATNNSMSELRASVGN	332
SEQIDNO:20	NLTS-ES-TLSLFQFSQNTSTEKYFLQGIIVTANLPPEATEKNISYSNHTLNALKTSVGK	335
SEQIDNO:21	VLAQ-EETTIVLSFLFTVNSTSNKYHLSGITLQANWT-DMM-SPFSASNTSLDYLRSSLGH	335
SEQIDNO:22	ILTQ-Q-TTILIFTFSLNSTSSKYHLSGLSLQANWS-DMA-AAFSASNASLSYLIRSTFGH	337
SEQIDNO:23	VLTQ-ANATNLSFLFTLNSTSNRYHLTGLSVVAAWS-DMT-APFNSTSNSSLDYQRGSLGR	336
SEQIDNO:24	NLTVDVAVKTNLTFFVTMNSTSNKYHLSEVTVSAAWP-EMK-EPVSVHNSSLDYLRGTGVY	164
	:	: : * * : . * : . : . * : : .

FIGURE 3 cont.

Replacement Sheet

	LAMP HOMOLOGY DOMAIN 2	Trans. Domain	
	3	4	
SEQIDNO: 1	SYKCNAAEEHVRVTKAFSVNIFKVWVQAFKVEGGQFGSVEECQLDENSM	LIPIAVGGALAG	394
SEQIDNO: 6	SYKCNTEEEHIFVSKMLSLNVFSVQVQAFKVDSDRFGSVEECVQDGNM	MLIPIAVGGALAG	383
SEQIDNO: 7	SYVCSAQQOMLSVTPVFSINTFRLQLQPFNITANRFSTAEECRVDQEN	MLIPIIVGAALAG	388
SEQIDNO: 8	SFKCNSKQTLQITDPFTVNTYHLQVQAFNSD-NTFASAVECSLDENG	MLVPIVGAALAG	394
SEQIDNO: 9	SYKCNAAEEHVRVTKAFSVNIFKVWVQAFKVEGGQFGSVEECVLDEN	NMLIPIAVGGALAG	394
SEQIDNO: 10	SYKCNAAEEHVRVTKAFSVNIFKVWVQAFKVEGGQFGSVEECLLDEN	NMLIPIAVGGALAG	393
SEQIDNO: 11	SYKCNAGEHVQVTEAFSVNIIKVWVQAFQVQGDKFGSVEECQLDEN	SMLIPIAVGGALAG	390
SEQIDNO: 12	SYKCNSEEHVRVTPAFSLSIFKVWVQAFQVKGDKFGSVEECLLDQDS	MMLIPIAVGGALAG	395
SEQIDNO: 13	SYKCNAEQRLRVTSFSLNMFVRWLQAFRVGDGDKFGPVEECQLDEN	SMLIPIAVGGALAG	386
SEQIDNO: 14	SYKCNSEEHIFVSKALALNVFSVQVQAFRVESDRFGSVEECVQDGN	NMLIPIAVGGALAG	384
SEQIDNO: 15	SYKCSAEENFQVTDKALVNVFNQVQAFKVDGDKDFGAMEECQLDEN	NMLIPIIVGAALAG	391
SEQIDNO: 16	SYKCRSEQRLQVTEAFALNVFQVRVQAFRVGDGDKFGPAEECQLDEN	SMLIPIAVGGALAG	390
SEQIDNO: 17	SYKCNAAEENVHVTDFGSVNIFRVRVQAFKVEGDGDKFGSVEECLL	DENNMLIPIAVGGALAG	399
SEQIDNO: 18	SYKCSAEENLQVTDKALVNVFNQVQAFKVDGDKDFGAVEECQLDEN	NMLIPIIVGAALAG	392
SEQIDNO: 19	SYKCSSEENLQVTDQALVNVFNQVQVIFKIDGDKFGPVEECQLDEN	NMLIPIIVGAALAG	392
SEQIDNO: 20	SYKCIAEESIWIISGKAAVNIFNIQLQAFKIPGDKFGAVEECQLDEN	NMLIPIIVGAALAG	395
SEQIDNO: 21	SYMCNAEQTLFVVSTFSLNMFELQVQPFVGTSTQFASAEVCQIDQD	QMLIPIIVGAALAG	395
SEQIDNO: 22	SYMCNAEQILAVTPVFSNLNTFSLQIQPFVGTTNQFAAAEECQMDQD	QMLIPIIVGASLAG	397
SEQIDNO: 23	SYMCISEQTLVVDQNFSLNTFQLQVQPFGITRQGFQAEECQLDQDN	NMLIPIVVGALAG	396
SEQIDNO: 24	SYFCRDEQTLNVAQNLSINTFQLQVQPFQAVKGDQFGAAEECQLDE	DDMLIPIVVGALAG	224
	*: * : . : . : . : * * * . * * : **: ** *:***		

Cytoplasmic Tail

SEQIDNO: 1	LVLIVLIAAYLVGRKRSHAGYQTI	417
SEQIDNO: 6	LVLIVLIAAYLIGRKRSHAGYQTI	406
SEQIDNO: 7	LVLIVLVAYLIGRKRTHAGYQTI	411
SEQIDNO: 8	LVLIVLIAAYLIGRKRSHAGYQTI	417
SEQIDNO: 9	LVLIVLIAAYLVGRKRSHAGYQTI	417
SEQIDNO: 10	LVLIVLIAAYLVGRKRSHAGYQT-	415
SEQIDNO: 11	LVLIVLIAAYLIGRKRSHAGYQTI	413
SEQIDNO: 12	LVLVVLIAAYLIGRKRSHAGYQT-	417
SEQIDNO: 13	LVLIVLLAYLIGRKRSHAGYQTI	409
SEQIDNO: 14	LVLIVLIAAYLIGRKRSHAGYQTI	407
SEQIDNO: 15	LVLIVLIAAYLIGRKRSHAGYQTI	414
SEQIDNO: 16	LVLVLMAYLVGRKRSHAGYQTI	413
SEQIDNO: 17	LVLIVLIAAYLIGRKRSHAGYQTI	422
SEQIDNO: 18	LVLIVLIAAYLIGRKRSHAGYQTI	415
SEQIDNO: 19	LVLIVLIAAYLIGRKRSHAGYQTI	415
SEQIDNO: 20	LVLIVLIAAYLIGRKRSHAGYQTI	418
SEQIDNO: 21	LVLIVLIAAYLIGRKRSHAGYQTI	418
SEQIDNO: 22	LVLIVLIAAYLIGRKRSHAGYQTI	420
SEQIDNO: 23	LVLIVLIAAYLIGRKRSHAGYQTI	419
SEQIDNO: 24	LVLIVLLAYLIGRKRSHAGYQSI	247
	::::***:***:*****:	

FIGURE 3 cont.

Replacement Sheet

LAMP-1					
Accession No.	Species	SEQ ID NO:	Accession No.	Species	SEQ ID NO:
NP_005552.3	<i>H. sapiens</i>	1	NP_990614.1	<i>G. gallus</i>	15
NP_034814.2	<i>M. musculus</i>	6	NP_001011507.1	<i>S. scrofa</i>	16
NP_955996.1	<i>D. rerio</i>	7	XP_001374132.1	<i>M. domestica</i>	17
NP_001087042.1	<i>X. laevis</i>	8	XP_003203252.1	<i>M. gallopavo</i>	18
NP_001233491.1	<i>P. troglodytes</i>	9	XP_002191607.2	<i>T. guttate</i>	19
XP_001087801.1	<i>M. mulatta</i>	10	XP_003218797.1	<i>A. carolinensis</i>	20
XP_534193.2	<i>C. lupus familiaris</i>	11	XP_004067118.1	<i>O. latipes</i>	21
XP_002723509.1	<i>O. cuniculus</i>	12	XP_003969941.1	<i>T. rubripes</i>	22
NP_001068592.1	<i>B. taurus</i>	13	NP_001158846.1	<i>S. salar</i>	23
NP_036989.1	<i>R. norvegicus</i>	14	XP_003452974.1	<i>O. niloticus</i>	24

FIGURE 4: HUMAN LAMP-2 ALIGNMENT WITH ORTHOLOGOUS SEQUENCES

SEQIDNO:2	-----	0
SEQIDNO:25	-----	0
SEQIDNO:26	-----	0
SEQIDNO:27	-----	0
SEQIDNO:28	-----	0
SEQIDNO:29	-----	0
SEQIDNO:30	-----	0
SEQIDNO:31	-----	0
SEQIDNO:32	-----	0
SEQIDNO:33	-----	0
SEQIDNO:34	-----	0
SEQIDNO:35	-----	0
SEQIDNO:36	-----	0
SEQIDNO:37	MAMKNFTLQQERDTSVALIIRTYVRAFLKVYTKVPKPQRCHNQW---QSLNIEGIEGIEI	57
SEQIDNO:38	-----	0
SEQIDNO:39	-----MECREGEVTRCKQKNNLFSGIN-DDISGAKQ	30
SEQIDNO:40	-----	0
SEQIDNO:41	-----	0
SEQIDNO:42	-----	0
SEQIDNO:43	-----	0

SEQIDNO:2	-----	0
SEQIDNO:25	-----	0
SEQIDNO:26	-----	0
SEQIDNO:27	-----	0
SEQIDNO:28	-----	0
SEQIDNO:29	-----	0
SEQIDNO:30	-----	0
SEQIDNO:31	-----	0
SEQIDNO:32	-----	0
SEQIDNO:33	-----	0
SEQIDNO:34	-----	0
SEQIDNO:35	-----	0
SEQIDNO:36	-----	0
SEQIDNO:37	VKGSKWR---SALETIIITIQVKRK-----SQVQKYHPFSLHSECQKTNQE	99
SEQIDNO:38	-----	0
SEQIDNO:39	AKQRQCTPQKPPKRATATLPLQRPPRGIPGPAPAAVAAVAADRITPSGSHQTRPPEAAR	90
SEQIDNO:40	-----	0
SEQIDNO:41	-----	0
SEQIDNO:42	-----	0
SEQIDNO:43	-----	0

FIGURE 4 cont.

Replacement Sheet

SEQIDNO:2	-----MVCF	4
SEQIDNO:25	-----M	1
SEQIDNO:26	-----MGDT	4
SEQIDNO:27	-----	0
SEQIDNO:28	-----MVCF	4
SEQIDNO:29	-----MVCF	4
SEQIDNO:30	-----MVCF	4
SEQIDNO:31	-----MVCF	4
SEQIDNO:32	-----MVCF	4
SEQIDNO:33	-----MVCF	4
SEQIDNO:34	-----MVCF	4
SEQIDNO:35	-----MVCF	4
SEQIDNO:36	-----MR	2
SEQIDNO:37	G---TGGVATVIADCECLLWPSIPFSTLAQKVNLGSCFAFSIIGYSVFALFIYLPNMLDF	156
SEQIDNO:38	-----	0
SEQIDNO:39	DERPVRDPRNRAAAPSGHWRRAGGPQRHR-----HHR-----HRRHGPAPLRR	133
SEQIDNO:40	-----	0
SEQIDNO:41	-----	0
SEQIDNO:42	-----	0
SEQIDNO:43	-----	0

SIGNAL SEQUENCE

LAMP HOMOMOLOGY DOMAIN 1

1

SEQIDNO:2	-RL---FPVPGSGLVLVCLVLGAVR--SYALELNLTDSSENATCLYAKWQMNFTVRYETT	57
SEQIDNO:25	-CL---SPVKGAKLILIFLFLGAVQ--SNALIVNLTDG-KGTCLYAEWEMNFTITYETT	53
SEQIDNO:26	GAM---ERCACPAAVLLLSLVL---MG---ATAFEVEIKDDKNATCIYAKLSVNITVQYETD	57
SEQIDNO:27	-----MAVRGFLPLLFILLSGIVHADDMMTSPLPS-----TAELEK	35
SEQIDNO:28	-RL---FPVPGSGLVLVCLVLGAVQ--SYALELNLTDSGKATCLYAKWQMNFTVRYETT	57
SEQIDNO:29	-RL---FPVPGSGLVLVCLVLGAVQ--SYALELNLTDSGKATCLYAKWQMNFTVRYETT	57
SEQIDNO:30	-RL---FPVPGSGLVLVCLVLGAVR--SHALELNEADSAIN-----	39
SEQIDNO:31	-RL---SPAPGSGLVLLCLVLGAVS--SYALEVNVTDSEKATCLYAKWQMNFTIQYNTT	57
SEQIDNO:32	-RL---SPVPGSGLVLLCLVLGAVS--SYALELNLTDSSEKALCLYAKWQMNFTIPYETT	57
SEQIDNO:33	-RL---APVPGSGFLLCLVLGAVS--SYALELNLTDSSEKATCLYAKWQMNFTIRYETT	57
SEQIDNO:34	-RL---SPVPGSGFLLCLVLGAVS--SYALELNLTDSSEKATCLYAKWQMNFTIRYETT	57
SEQIDNO:35	-RL---APVPGSGFLLCLVLGTVS--SYALELNLTDSSEKATCLYAKWQMNFTIRYETT	57
SEQIDNO:36	-LL---SPVTGSKLVLLFLFLGAVR--SDALKLNLTDS-KGTCLYAEWEMNFTITYEAL	54
SEQIDNO:37	IELAELMLSTETQLLEPTRVCCGICQ--SYALELNLTDSKNATCLYSKWQMTFTINYETT	214
SEQIDNO:38	--MAPPRCPAGLALLLLLLGACGFFQ--SYAVEVDVKDASNFTCLYQWMMKFLIKYETN	56
SEQIDNO:39	LLLRPPP-PAA-----AAARFLGFFQ--SYAVEVDIKDASNATCLYADWMMRFLIKYESN	185
SEQIDNO:40	--M---ERCACPAALLLSLVL---MG---AMAFDVEIKDDKNATCIYAKLSVNITVQYETN	51
SEQIDNO:41	-----MF-RCAFLILFLALGNELHLSHGTEVSVNNTENKLCLYANLMVNFVSVTYEVG	51
SEQIDNO:42	-----MKVSHATAGLVVWFVVLGCIDAVT----L-EVKESNTTCIKADLSASFIIYNTT	50
SEQIDNO:43	-----	0

FIGURE 4 cont.

Replacement Sheet

LAMP HOMOLGY DOMAIN 1

2

SEQIDNO:2	NKTYKTVTISDH--GTVTYNGSICGDDQNGPKIAVQFGPGFS--WIANFTKAA--STYSI	111
SEQIDNO:25	NQTNKTITIAVP--DKATHDGSSCGDDRNSAKIMIQFGFAVS-WAVNFTKEA---SHYSI	107
SEQIDNO:26	TSSSKNITFPVP--SDVTNGSSCGSDGKAPLLVINFGNSQS--WSLNFTRNN---STYSG	111
SEQIDNO:27	---T-----ANLP--LVIQTTSSTTSTTTT-SRP---SSTSTHSTLTTEPAA-----	73
SEQIDNO:28	NKTYKTVTISDR--GTVTYNGSICGDDQNGPKIAVQFGPGFS--WIANFSKAA---STYSI	111
SEQIDNO:29	NKTYKTVTISDR--GTVTYNGSICGDDQNGPKIAVQFGPGFS--WIANFSKAA---STYSI	111
SEQIDNO:30	CSKCKTVTISDH--GTVTYNGSICGDDQNGPKIAVQFGPGFS--WIANFTKAA---STYSI	93
SEQIDNO:31	SKNFKTATISDF--STATYNGSVCGNDQNNPKIVVQFGSGFS--WIVNFTKKE---SAYLI	111
SEQIDNO:32	SKSYKTVTISNF--GTPTYNGSICGDNQNGSRIAVQFGSGFS--WIVNFTKSV---SVYSI	111
SEQIDNO:33	DKHNKTVPISDL--GAATYNGSFCGDDQNGPKIAVQFGSGFS--WIVNFTKEAASPSTYLV	114
SEQIDNO:34	NNSHKTVSISDF--GAATYNGSFCGDDHNDPQIVMQFGSGFS--WIVNFAKES---SSYLI	111
SEQIDNO:35	DKHNKTVTISDF--DAAAYNGSVCGDDQNGPKIAVQFGSGFS--WIVNFTKEASSTSTYLV	114
SEQIDNO:36	K-VNETVTITVP--DKVTYNGSSCGDDKNGAKIMIQYGSTLS--WAVNFTKEA---SQYFI	107
SEQIDNO:37	GNETKNVTITVP--ENVTYDGSSCGDNQTVQIAVQFGLGYS--WHLNFTKKN---NSYSF	269
SEQIDNO:38	SSDYKNASLDLT--STVTHNGSICGSDTQAALLAVQFGDGHs--WSINFTKNN---ETYRA	110
SEQIDNO:39	SGDYKTTTLNLS--SSVTHNGSVCGNDTQAALVAVQFEGHs--WSINITKNN---ETYQG	239
SEQIDNO:40	TSSTKNVTFVLP--SEVTNGSSCGSNGKAPILVINFGNGHs--WSLNFTRND---SMYSG	105
SEQIDNO:41	VNKNETVIFVLP--ENVTEGSTCDNTTSTLKL--SFGHGHs--WTVEFTKKN---KTYQV	103
SEQIDNO:42	HAER-TVQVLLPNSTTVDTANSTCGKDGSSPRLVAVFGSGY--TLGLNFSTNG---TLYQV	105
SEQIDNO:43	-----	0

LAMP HOMOLGY DOMAIN 1

3

SEQIDNO:2	DSVSFSYNTGDNTTFPDAEDKGI-LTVDELLAIKIPLNDLFRCNLSLSTLEKNDVVQHYWD	170
SEQIDNO:25	HDIVLSYNTSDSTVFPGAVAKGV-HTVKNPENFKVPLDVIFKCNsvLTYNLTPVVQKYWG	166
SEQIDNO:26	SALIFTYNTNDTILFPDALRKLIS-STAMFLGPVPLNSTYKCIISREVVVSENVQTIIYD	170
SEQIDNO:27	-----KTTTARTTIVTTSa---PTSTQSTSSSSTSATVTTLAP	107
SEQIDNO:28	DSISFSYNTGDNTTFPDAEDKGI-ITVDELLAIKIPLNDLFRCNLSLSTLEKNDVVQNYWD	170
SEQIDNO:29	DSISFSYNTGDNTTFPDAEDKGI-ITVDELLAIKIPLNDLFRCNLSLSTLEKNDVVQNYWD	170
SEQIDNO:30	DSISFSYNTGDNTTFPDAEDKGI-LTVDELLAIKIPLNDLFRCNLSLSTLEKNDVVQHYWD	152
SEQIDNO:31	DSISFSYNLSDNATFPDAKEKGI-LTVHDLVGFRIPLNNIFRCNLSLSTLEKNGVVQYYWD	170
SEQIDNO:32	DSISFSYNTGDNTTFPDAKDKGI-LTVNESVAFKIPLNDIFRCNLSLSSLVKNGVVQNYWD	170
SEQIDNO:33	DTISFSYNTNDNKTFPDAKEKEV-FTVNNRVALKIPLNDIFRCNLSLSTLENRDVVQHYWD	173
SEQIDNO:34	NSISFSYNTSDTTTFPDAKKKGV-LTVNDSVGFQVPLNDIFRCNLSLSTLEKNDVVQHYWD	170
SEQIDNO:35	DSISFSYNTNDNATFPDAKEGV-FTVNNRVALKIPLNDIFRCNLSLSTLEKSDVVQHYWD	173
SEQIDNO:36	NNITLSYNTNDTKTFPGAVPKGI-LTVIIPVGSQPLGVIFKCSSVLTfNLSPVVQHYWG	166
SEQIDNO:37	DTIVFTYNTSDNETFPEAKEKGQVLSVFEFRYARIPLNKIFRCHSEESLIGDKATHHYWE	329
SEQIDNO:38	EFITFTYNTNDTAVFPDARRQGPVTIVVKDAMHPIQLNNVFVCHHTTSLEAENVQTIFWN	170
SEQIDNO:39	DFITLTYNNDTAVFPDAKRKGPITVLVRDPSRPIQLNTVFVCHNSFVIEAENTTQIFWN	299
SEQIDNO:40	GALIFTYNTNDSTLFPDALKEGLIS-STAAFLGPIPLNSTYKCIISREVVVSENVQTIIISD	164
SEQIDNO:41	DTIVFSYNLSDSSVFPNSTSKETKFVTVKSIITNVSVDTYYSCKSENVLTVESVIQTLVD	163
SEQIDNO:42	SSLTLQYNLSDTSVFPNATISGVVTLVSASVGIEANVNNTTYKASPTVIDVATAKVNFTD	165
SEQIDNO:43	-----MTQIGGVQPVFLA	13

FIGURE 4 cont.

Replacement Sheet

	LAMP HOMOLOGY DOMAIN 1	Hinge Region	
	4		
SEQIDNO: 2	VLVQAFVQNGTVSTNEFLCDEKTS---TVAPTIHTTVPS-----PTTTPT--PKEKPE		219
SEQIDNO: 25	IHLQAFVQNGTVSKNEQVCEEDQTP--TTVAPIIHTTAPSTTTTLTPTSTPTPTPTPT		224
SEQIDNO: 26	VKLEAFMANGTLGK-EIICDADKPS---PVPSPTQPST-----TASTAIPAPTSKPLDKPT		222
SEQIDNO: 27	TTTGHNTTNSTTEPPTTTGHNTNS--TTDAPTTHHTNAT----VAPTPPPTTSPVPKPT		161
SEQIDNO: 28	VLVQAFVQNGTVSTNEFLCDEKTS---TVAPTIHTTVPS-----PTTTPT--PKEKPE		219
SEQIDNO: 29	VLVQAFVQNGTVSTNEFLCDEKTS---TVAPTIHTTVPS-----PTTTPT--PKEKPE		219
SEQIDNO: 30	VLVQAFVQNGTVSTNEFLCDKDKTS---TVAPTIVHTTVPS-----PTTTPT--RIP---		198
SEQIDNO: 31	VHVQAFVQNGTVSTKEFLCEKDKTS---TTVPTISTTTPS-----PTTTPT--PKEKPE		220
SEQIDNO: 32	VHVQAFVQNGTVSTNEYLCEKDNTT--TTVAPIVPTTVPSPTTTSSPTTTPS--PKEKPD		226
SEQIDNO: 33	VHVQAFVQNGTVSTTEFLCDKDKTV--TTAVPIVPTTLPS-----PT-----KPV		216
SEQIDNO: 34	VHVQAFVQNGTVSTKEFLCDKDKTL--TTTVFVIPTSVPS-----PTTTPT--PKEKPE		220
SEQIDNO: 35	VHVQAFVQNGTVSTTEFLCDKDKTV--TTAMPIVPTTAPS-----PT-----KPV		216
SEQIDNO: 36	IHLQAFVQNGTVSKHEQVCKEDKTA--TTVAPIIHTTVPSPTTTTLTPTSI----PVPTPT		220
SEQIDNO: 37	TVVQAFIQNGTISKKEFICKDRAS--TTVAPVTTQVPS-----TTATVPVQDKPY		379
SEQIDNO: 38	VTMQPFVQNGTISKKESRCYADTPTAAPTVLPTVANVTAS--TTISPAPTAPKPAENPV		229
SEQIDNO: 39	VTMQAFVQNGTVSKKESRCPADTPTSEPTVPPTIANVTASTTTLSAPTAPKPVENPV		359
SEQIDNO: 40	VKLEAFMQNGTLGK-EVSCDADKPS--PTPT-TNPST-----TASTTTPTPTSKPLDNPT		215
SEQIDNO: 41	VALQAFVINGSKSDTDVCSADMTS---TTVAPTT-----TV----TSTAAPTSTPTLPTPT		213
SEQIDNO: 42	MRLEAYMPGNELSPNETVCFADQTS---TTPSPTTVSTTAV----PTQT-----P--PGTPQ		213
SEQIDNO: 43	VTVHLIL-----ATV--LHQTF--AT---VTPEVTTA----VPHK-----E--PGRPD		48

	Hinge	LAMP HOMOLOGY DOMAIN 2	
	1	2	
SEQIDNO: 2	AGTYSVNNG--NDTCLLATMGLQLNITQ-----DKVASVININPNTHSTGSCRSHTAL		271
SEQIDNO: 25	VGNYSIRNG--NTTCLLATMGLQLNITE-----EKVPFIFNINPATNFTGSCQPQSAQ		276
SEQIDNO: 26	MGNYSVSDA--SGICLLASMGLQINTSLL--SEGKNIWRPFNIDPLGIKNGTCTNQTGT		278
SEQIDNO: 27	VGNYSVKTD--NVSDCLLAKMGLQFSFKIS----GNASLQTVNLDPNVTKVNGTCGSGGSD		216
SEQIDNO: 28	AGTYSVNNG--NDTCLLATMGLQLNITQ-----DKVASVININPNTHSTGSCRSHTAL		271
SEQIDNO: 29	AGTYSVNNG--NETCLLATMGLQLNITQ-----DKVASVININPNTHSTGSCRSHTAL		271
SEQIDNO: 30	-----PXVASVININPNTHSTGSCRSHTAL		224
SEQIDNO: 31	VGSYSVNNS--NGTCLLATMGLQLNITH-----NKVASVININPNTHSTGSCQPQTAL		272
SEQIDNO: 32	VGSYLVKNG--SDTCLLATMGLQLNVTH-----DKVASVININPNVTGYSGSCHPQTAL		278
SEQIDNO: 33	VGSYSVNNS--NGTCLLATMGLQLNITH-----DKVASVININPNTHSTGSCQPQTAL		268
SEQIDNO: 34	TGSYSVTSS--NGTCLLANMGLQLNITQ-----DKVASVININPNTHSTGSCQPQTAL		272
SEQIDNO: 35	VGSYSVNNS--NGTCLLATMGLQLNITH-----DKVASVININPNTHSTGSCQPQTAL		268
SEQIDNO: 36	VGNYSISNG--NATCLLATMGLQLNITE-----EKVPFIFNINPATNFTGSCQPQTAQ		272
SEQIDNO: 37	PGKYAVKNG--NDTCLLATMGLQLNVTQ-----NKVSVININPNVTDFGSCSNETA		431
SEQIDNO: 38	TGNYSILKTG--NKTCLLATVGLQLNISQ-----DK-PLLINIDPKTHADGTCGNTSAT		280
SEQIDNO: 39	TGNYSILKSG--NKTCLLATVGLQLNVSQ-----EK-PLLININPKTTVADGACGNTTAT		410
SEQIDNO: 40	TGNYSVSDV--NGTCLLASMGLQINTSLL--SEGKNIWTA FNIDPTAMSKNGTCSNQTGT		271
SEQIDNO: 41	TGKYSIAPDVNSTACLMATFGLQIGYKQG----D--KEETINLVPNITEVGGACGANSS--		266
SEQIDNO: 42	QGNYSVKDA--NDTICLLAKMGLQLNVSYSY--SQNKTVQDVLNLPNVTNSTGSCGASSAT		270
SEQIDNO: 43	QGDYQVTSS--NGTVCFLLASMGLQLNITFNSTSQNKTLQEVINIQPNRTKSSGSCDTSSAL		107

. *: * * *

FIGURE 4 cont.

Replacement Sheet

LAMP HOMOMLOGY DOMAIN 2

SEQIDNO:2	LRLNS-STIKYLDVFVAVKNE---NRFYLKEVNI SMY-LVNGSV-FSIANNNLSYWDAP	324
SEQIDNO:25	LRLNN-SQIKYLDIFI FAVKNE---KRFYLKEVNVV MY-LANGSA-FNISKNLSFWDAP	329
SEQIDNO:26	LILTE--NRTIIEFTFALKNK----NH FYLEE VNITLI ---NGSAFSSRQNQNLSTWEAS	329
SEQIDNO:27	SSLFLT S--KDTIVHFVFTNDS---QK FRLHALTLFVD-LGNG-NIFNDSNTNLSLWEAS	269
SEQIDNO:28	LRLNS-STIKYLDVFVAVKNE----NRFYLKEVNVSMY-LVNGSV-FSIANNNLSYWDAP	324
SEQIDNO:29	LRLNS-STIKYLDVFVAVKNE----NRFYLKEVNVSMY-LVNGSV-FSIANNNLSYWDAP	324
SEQIDNO:30	LRLNS-STIKYLDVFVAVKNE----NRFYLKEVNI SMY-LVNGSV-FSIANNNLSYWDAP	277
SEQIDNO:31	LRLNS-SNIKYLDVFVAVKNE-----NRFYLKEVNVSMY-LVNGSV-FSIANNNLSYWDAP	325
SEQIDNO:32	LRLNS-SNIKYLDVFVAVKNE----NRFYLKEVNVSMY-LANGSV-FSFANNNLSYWDAP	331
SEQIDNO:33	LRLSS-SNIKYLDVFVAVKNE----NRFYLKEVNVSMI-LVNGSV-YSISNTNLSYWDAP	321
SEQIDNO:34	LRLSG-SNIKYLDVFVAVKND----NRFYLKEVNVSVY-LVNGSV-FSIANNNLSYWDAP	325
SEQIDNO:35	LRLSS-SNIKYLDVFVAVKNE----NRFYLKEVNVSMI-LVNGSV-YSISNTNLSYWDAP	321
SEQIDNO:36	LRLNN-SQIKYLDIFI FAVKNE----KRFYLKEVNVNMY-LANGSA-FHVSNNNLSFWDAP	325
SEQIDNO:37	LRLSG-SNVKYIDIFI FAVKNG----NRFYLKEVNV SIS-FVNASD-LNVANNNLSYWDAP	484
SEQIDNO:38	LKLND-GNRTLIDFTFIV-NASASVQKFYLR EVNVTLLN YQNGSVILSADNNNLSKWDAS	338
SEQIDNO:39	LKLND-GNSTLIGFTFAVKNTSASVQKFYLR EVNVTLLNRLNGSVISSADNSNLSKWDAP	469
SEQIDNO:40	LILTD--NSTVIEFTLALKNK----NH FYLKEVNVALI ---NGSASSTRQNQNLSAWEAS	322
SEQIDNO:41	--DLILTS--DTITIMFTFSNDG---KKFHLHALKVTVK-PATG-DPVI AVNNNMSIWAAA	318
SEQIDNO:42	LVLTLQ-TQSTILTFNFTLNSTT---NKYHLSGVTLIAN-WFDS-AHFMSMNNLSLNYLRST	324
SEQIDNO:43	LTLTTDAEKTNLTFVFALNTTS---NKYHLS EVLSAA-LSDMKETFVAQHSLDYLGRGT	163

LAMP HOMOMLOGY DOMAIN 2

Trans. Domain

	3	4	
SEQIDNO:2	LGSSYMCNKEQTVSVSGAFQINTFDLRVQPFNVTKGKYSTAQDCSADD-DN	LVPIAVGA	383
SEQIDNO:25	LGSSYMCNKEQVLSVSRAFAQINTFNLKVQPFNVTKGQYSTAQECSLDDD-TILIP	PIIVGA	388
SEQIDNO:26	VDSSYMCHKEQQIKVSEDLFINAFDVRVQPFQVNGTGFATAEDCFAD-Q-NFIV	PIVVGA	387
SEQIDNO:27	VGSSYMCNRKEQSYNISDKLTLNTELFQVQPFQVKNKSFSTAHECSLDDT-SLI	PIIVGA	328
SEQIDNO:28	LGSSYMCNKEQTVSVSGAFQINTFDLRVQPFNVTKGKYSTAEECSADSDLNFLI	PVAVGV	384
SEQIDNO:29	LGSSYMCNKEQTVSVSGAFQINTFDLRVQPFNVTKGKYSTAQDCSADD-DNFL	PIAVGA	383
SEQIDNO:30	LGSSYMCNKEQTVSVSGAFQINTFDLRVQPFNVTKGKYSTAEECSADSDLNFLI	PVAVGV	337
SEQIDNO:31	LGSSYMCNKEQTVSVSGAFQINTFDLRVQPFNVMEGKYSTAQECSLDDD-TILIP	PIIVGA	384
SEQIDNO:32	LGSSYMCNKEQTVSVSGEFQINTFDLRVQPFNVKDGKYSTAQDCRADD-DNFL	PIAVGA	390
SEQIDNO:33	LGSSYMCNKEQTVSVSGAFQINTFDLRVQPFVTEGKYSTAQECSLDDD-TILIP	PIIVGA	388
SEQIDNO:34	LGSSYMCNKEQTVSVSGAFQINTFNLRVQPFVMEGKYSTAQDCSADD-DNFL	PIAVGA	384
SEQIDNO:35	LGSSYMCNKEQTVSVSGALQINTFDLRVQPFVTEGKYSTAEECSADSDLNFLI	PVAVGV	381
SEQIDNO:36	LGSSYMCNKEQVVSVSRTFAQINTFNLKVQPFNVTKGEYSTAQDCSADDED-NFL	PIAVGA	384
SEQIDNO:37	LGSSYMCNKEQTLALADSLQINTFNLRVQPFVVGKYSTAEDCSADDD-NFIV	PIAVGA	543
SEQIDNO:38	LGNSYMCNRKEQTLLEINENLQVHTFNLWVQPFVLVKNKFSIAEECFADSDLNFLI	PVAVGM	398
SEQIDNO:39	LGSSYMCNRKEQTLQINENVQVHTFNLWIQPFVLEANKFATAEECIADSDLNFLI	PIAVGV	529
SEQIDNO:40	VGSSYMCHKEQQIKVSEDLVINSFDVRVQLFGVKNETFATAQQCSLDDD-SIVI	PIVVGA	381
SEQIDNO:41	VGSSYMCNKEQTLNVTDTLTLYTFELRVQPFQVNGKEFATAHECSLDDT-SILI	PIIVGA	377
SEQIDNO:42	LGYSYMCNAEQTLFVTPSFSLNTEFLQVQPFQVKSGRFATAEECQMDQN-QMI	PIIVGA	383
SEQIDNO:43	LGFSYMCRRERQTLGVTPDFAINTFQVQVQPFQVTKQFAAAEECQLDKD-DMLI	PIIVGA	222
	: **** *	: : * *	: * *

FIGURE 4 cont.

Replacement Sheet

Cytoplasmic Tail

SEQIDNO:2 ALAGVLIIVLLAYFISLKHHH-AGYEQF 410
 SEQIDNO:25 GLSGLIIVIVIAAYLIGRRKTY-AGYQTL 415
 SEQIDNO:26 ALGVLVVLVMVAYFIGRRKQSSAGYEQM 415
 SEQIDNO:27 ALAGLIFIVVIAYVIGRRRTY-VGYQTL 355
 SEQIDNO:28 ALGFLIIVVFISYMIIGRRKSR-TGYQSV 411
 SEQIDNO:29 ALAGVLILVLLAYFIGLKRHH-AGYEQF 410
 SEQIDNO:30 ALGFLIIVVFISYMIIGRRKSR-TGYQSV 364
 SEQIDNO:31 GLSGLIIVIVIAAYLIGRRKSY-AGYQTL 411
 SEQIDNO:32 ALAGVLILVLLAYFIGLKRHH-AGYEQF 417
 SEQIDNO:33 GLSGLIIVIVIAAYLIGRRKSY-AGYQTL 407
 SEQIDNO:34 ALAGVLILVLLAYFIGLKRHH-AGYEQF 411
 SEQIDNO:35 ALGFLIIVVFISYMIIGRRKSR-TGYQSV 408
 SEQIDNO:36 ALGGVLILVLLAYFIGLKRHH-TGYEQF 411
 SEQIDNO:37 ALGGLVILVLMAYFVGRKRRRA-TGYEQF 570
 SEQIDNO:38 ALGFLIILVFISYIIIGRRKSR-TGYQSV 425
 SEQIDNO:39 ALGFLIILVFISYIIIGRRKSR-TGYQSV 556
 SEQIDNO:40 ALAGLIVIVIAAYLIGRRKGY-SGYQTL 408
 SEQIDNO:41 ALAGLILIVVIAYVIGRRKTY-VGYQTL 404
 SEQIDNO:42 ALAGLVLTITLIAYLIGKRRSH-AGYQAI 410
 SEQIDNO:43 ALAALVLIVLSAYLIGRKRSH-AGYQSI 249
 .*. :.: . :*.:* :. **: .

LAMP-2					
Accession No.	Species	SEQ ID NO:	Accession No.	Species	SEQ ID NO:
NP_002285.1	<i>H. sapiens</i>	2	NP_001231184.1	<i>S. scrofa</i>	34
NP_034815.2	<i>M. musculus</i>	25	XP_004022401.1	<i>O. aries</i>	35
NP_001087881.1	<i>X. laevis</i>	26	NP_058764.2	<i>R. norvegicus</i>	36
NP_001013551.1	<i>D. rerio</i>	27	XP_001510101.2	<i>O. anatinus</i>	37
XP_003918270.1	<i>P. Anubis</i>	28	NP_001001749.1	<i>G. gallus</i>	38
XP_001084005.2	<i>M. mulatta</i>	29	XP_002191794.1	<i>T. guttata</i>	39
XP_003317709.1	<i>P. troglodytes</i>	30	NP_001116192.2	<i>X. tropicalis</i>	40
XP_005641822.1	<i>C. lupus familiaris</i>	31	NP_001133282.1	<i>S. salar</i>	41
XP_001493687.3	<i>E. caballus</i>	32	XP_003445830.1	<i>O. niloticus</i>	42
NP_001029742.1	<i>B. Taurus</i>	33	XP_003961835.1	<i>T. rubripes</i>	43

FIGURE 5: HUMAN LAMP-3 ALIGNMENT WITH ORTHOLOGOUS SEQUENCES

	SIGNAL SEQUENCE	LAMP HOMOLOGY DOMAIN 1		
SEQIDNO:3	MPRQLSAAAAALFASLAVILHD	GSQMRAKAPPETRDYSQPTAAATVQDIKKPV-QQP	55	
SEQIDNO:44	MPRQLSAAAAALFASLAVILHD----	GSQMRAKAPPETRDYSQPSAAATVQDIKKPV-QQP	55	
SEQIDNO:45	MPRQLSAAAVLFASLAVILHD----	GSQMRAKAFPKTRDYSQPTAAATGQDIKKPV-QQP	55	
SEQIDNO:46	MPRQLSAAAVLFASLAVILHD----	GSQMRAKAFPKTRDYSQPTAAATGQDIKKPV-QQP	55	
SEQIDNO:47	MSWQLSAAVALFVSLALILHY----	GSQIRAKMFPETVDFQ-PTTAATVRATAKPFL-HL	54	
SEQIDNO:48	MSWRLSAVLVSFVSLAVFLHY-----	GHHMKAKVFPEITDSSSPTTAATVQATAEPSLWKP	56	
SEQIDNO:49	-----	-----	0	
SEQIDNO:50	MAWQLSAVVVLFVSLAVILYY----	GSHVRANVFPEITDYSQPTTAATIQTRAQPSLSQP	56	
SEQIDNO:51	MSWQIPAVVMSFMALVAIWYYDSHYNSHMQAKVFPEITGYSSPTTG---	QATVKPSLLQP	57	
SEQIDNO:52	MSWQISAVVLFVSLAVIWYDS-----	HMKANVFPEITGYSSPTTG---	QATVKPSLLQP	53
SEQIDNO:53	MPGQTSAAVAVL-LCLAVILH-----	GYQIREKEFPEARGYLQYTATTTEQITAKPPL-PL	53	
SEQIDNO:54	MPGQISAAVAVLFLSLTVILH-----	GYQIREKEFPKARGYLQYTATSAEQITTKPPL-QL	54	
SEQIDNO:55	-----	-----	0	
LAMP HOMOLOGY DOMAIN 1				
SEQIDNO:3	AKQAPHQTLAARFMDGHITFQTAATVKIP-----	TTTPATTKNTATTSPITY	102	
SEQIDNO:44	AKQAPHQTLAARFMDGHITFQTAATVKIP-----	TTTPATTKNTATTSPITY	102	
SEQIDNO:45	ANQAPHQTLAARLMDGHITFQTAATIKTP-----	TTTPVTTKNTPTTSPIIY	102	
SEQIDNO:46	ANQAPHQTLAARLMDGHITFQTAATIKTP-----	TTTPVTTKNTPTTSPIIY	102	
SEQIDNO:47	TNQVPSQTLAARSMGDGHIASQRAATTSSSEPPTHTTTVKTLVTTSLVTANSTPSSSPIIY		114	
SEQIDNO:48	TNHTPHKTLAAKSTDGHVTSQIATTVTDSETLTHTTTITTLAATSLAATNSTPSTSPPTH		116	
SEQIDNO:49	-----	-----	0	
SEQIDNO:50	TNQVPHKTLATRSMDGQVTSQTAATTVNPETPVTHTTIKTAAATSLVTNSTLSTSPITN		116	
SEQIDNO:51	TNYVPHKTAAARSTDGHVTSQTVAKTSSSETLTNTTTIDVLATTSPVTTKSTLPTTPTTH		117	
SEQIDNO:52	TNHVPCNTAAAKSTDGHVTSQTVAKTSSPETLTNTTTIEVLVTTSPVTTQSTLPTTPTTH		113	
SEQIDNO:53	TNQTSATLASRSKDDYIQTAAEYS---TFE----	DTAHITMKTAPVTTKSLPISSTSY	107	
SEQIDNO:54	INQRSHITLASRFKDDYIQMAAEYS--AIE----	NTAHITMKTVPVTTKSLPPISSASY	108	
SEQIDNO:55	-----	-----MDRVSLSTILLY	14	
LAMP HOMOLOGY DOMAIN 1				
SEQIDNO:3	TLVT-----TQATPNNSHTAPPVTEVTVGPSLVPSLPPTI---TPPAHTTGTSSSTV		152	
SEQIDNO:44	TLVT-----TQATPNNSHTAPPVTEVTVGPSLVPSLPPTI---TPPAHTTGTSSSTV		152	
SEQIDNO:45	TLVT-----TQATSNNSHTAPPLTKVTVGPSLVPSLPPTI---TPPAHTTGTSSSTV		152	
SEQIDNO:46	TLVT-----TQATSNNSHTAPPLTKVTVGPSLVPSLPPTI---TPPAHTTGTSSSTV		152	
SEQIDNO:47	TLVT-----TIVTPNNSHTAAPVTEATIGPSADPGSLPTTS--TPLAHTTRTNPSTL		164	
SEQIDNO:48	TLFT-----TLATPNTSHMAAPVTEAAISPSAGLSLLPTI---IPPAHTTGTSSSTL		166	
SEQIDNO:49	-----	-----	0	
SEQIDNO:50	TLLT-----TLATPDNTHTTTTPVTEATIGPSAGPGSPPTTITTTSSAYTTGTSSSTV		168	
SEQIDNO:51	TLVT-----TLATPNKSHVTFPVTEAKVGLSVGPSSPPVTV---NPTAHTTGNRPSTA		167	
SEQIDNO:52	TLVT-----TLATPSKSHVTFPVTEAKAGLSIGPSSPPVTI---NPAHTTGNRPSTA		163	
SEQIDNO:53	TFV-----RTNNSHMTASSTEDTIGSGSITHL-----	FPPTTRASLAIV	146	
SEQIDNO:54	TFV-----RSNNAHMTASSTDDTIGSGSIAHL-----	PVPTTRASLAIV	147	
SEQIDNO:55	GLLYINDAYSENTEFAOPSNTTTPAPNTTTTHVTSNTTTLAP-----	NTTT	59	

FIGURE 5 cont.

Replacement Sheet

LAMP HOMOLOGY DOMAIN 1

```

SEQIDNO:3      SHTTGNTTQPSNQTTLPATLSIALHKSTTGQKPVQF---THAPGTTAAAHNTTTRTAAPAS 209
SEQIDNO:44     SHTTGNTTQPSNQTTLPATLSIALHKSTTGQKPVQF---THAPGTTAAAHNTTTRTAAPAS 209
SEQIDNO:45     NHTTGNATQPSNQTTLPATLSIALHKSTTGQKPVQF---THAPGTTAAAHNTTTRTAAPAS 209
SEQIDNO:46     NHTTGNATQPSNQTTLPATLSIALHKSTTGQKPVQF---THAPGTTAAAHNTTTRTAAPAS 209
SEQIDNO:47     SHKTRKTTTHFGNQTTLPATLSTSTHKSTSSHKSQAS---THAPGTTAAAHNTTQTASPAT 221
SEQIDNO:48     SPTAGKTTQPSNQTTLPATLSTSPHNSTASQKPTHF---NHTPGPTTGAHNTTQTASPAT 223
SEQIDNO:49     -----MTQSSRSVLLMLSSLHCLGSSLESNPKDPSVLAEAPGQN-----KRDSDSL 48
SEQIDNO:50     SHTTGKTTQLSNQTTLPATLSTSPHNSTTSQNPAHS---THTPGPTTGT CNTTQTASPAT 225
SEQIDNO:51     SHTTGKTTQLSNQTTLPATLSTSPHNITTSQKPTQF---THTPGPTTATYNTTQTASPAT 224
SEQIDNO:52     SHTTGKTTQLSNQTTLPATLSTSPHNITTSQKPTQF---THTPGPTTAAANTTHTASPAT 220
SEQIDNO:53     NHITGRSTQLGGQTTLPKALFTPSHESSTTQRP TLS---TI-VSELTPTGKDRSTTSVP 202
SEQIDNO:54     NYITGRATQLGGQTTLPKFTFTASHKSTTNQRPTLS---TNVLGTSTPTHKDRSTTSPVP 204
SEQIDNO:55     THVTSNTTTLA-----PNTTTHITSNTTTTLPNTT---TTLAPNTTTTHSVTTTKTAST 111

```

Hinge

LAMP HOMOLOGY DOMAIN 2

```

1
SEQIDNO:3      TVPGPTLAPQPSVKTGIYQVLN-GSRLCIKAEMGIQLIVQDKESVSPRRYFNIDPNAT 268
SEQIDNO:44     TVPGPTLAPQPSVKTGIYQVLN-GSRLCIKAEMGIQLIVQDKESVSGHRTITLSS--K 266
SEQIDNO:45     TVPGSTLAPQPSVKTGIYQVLN-GSRLCIKAEMGIQLIVQDKESVSPRRYFNIDPNAT 268
SEQIDNO:46     TVPGSTLAPQPSIKTGIYQVLN-GSRLCIKAEMGIQLIVQDKESVSPRRYFNIDPNAT 268
SEQIDNO:47     PASGPTLAPQPSPKTGIYQVLN-GSRLCIKAEMGIELMVQDTKSVFSPQRYFNIDPNAT 280
SEQIDNO:48     IAPGPTLAPQPSAKTGIYQVLN-GSKLCIKAEMGIELTVQDTQSVFSPQRYFNIDPNTT 282
SEQIDNO:49     VPQMPVLQPKETAPPLVYTIIRNPQGVKCVRASFGVEFVVREN----KKKYFYNLTNSA 104
SEQIDNO:50     TAPGPTLAPQPSAKTGMYQILN-GSKLCIKAEMGIQLTVQDTKSASPPQGYFNIDPNTT 284
SEQIDNO:51     IAPRPTLAPQPLSPKTGIYQVHN-GSKLCIKAEMGIQLTVQDSVSVFSPQRYFNIDPNAT 283
SEQIDNO:52     IAPRPTLAPQPLSPKTGLYQVLN-GSKLCIKAEMGIQLTVQDSVSVFSPQRYFNIDPNAT 279
SEQIDNO:53     LVRPRTFVTWSSPAKIGTYEVLN-GSRLCIKAEMGIALIVQEKGLDSATQRHFNIDPSLT 261
SEQIDNO:54     LVRPRTLVTWSSPAKIGTYEVLN-GSRLCIKAEMGIALIVQEKDLDSATQRYFNIDPSLT 263
SEQIDNO:55     TTPTPTLEPKPSPPETGNYTVKI-KNEFCIEALMGLELELTNS---TKTQYFYNIVPSQI 167

```

LAMP HOMOLOGY DOMAIN 2

```

2
SEQIDNO:3      QASGNCGTRK----SNLLLNFGGGFVNLTFTKDEGSYYISEVGAYLTVS----DPETIY 319
SEQIDNO:44     SLGGCLARNEHSPHPLFLFFKGPSPSVTQAEDEESYYISEVGAYLTVS----DPETIY 321
SEQIDNO:45     QASGNCGTRN----SNLLLNFGGGFVNLTFTKDEGSYYISEVGACLTVS----DPETIY 319
SEQIDNO:46     QASGNCGTRN----SNLLLNFGGGFVNLTFTKDEGSYYISEVGACLTVS----DPETIY 319
SEQIDNO:47     QTSNGCGSQK----SNLLLNFGGGFVNLTFLKDENSYYINEVGAYLTVS----NPEKIY 331
SEQIDNO:48     QASGNCGSRK----SKLLLNFGGGFVNLTFTKDENSYYVSGVGAYLTVS----NPEKVV 333
SEQIDNO:49     RATGYCANQK---TVLSLEFSGGNLEFTFIKDGQSYVKTVKGSLRAAPPCKNCPSKIY 160
SEQIDNO:50     QVSGICGSRK----SNLLLNFGGGFVNLTFTKDENSYYISEVGAYLTVS----NPEKTY 335
SEQIDNO:51     QASGNCGSRK----SNLLLNFGGGFVNLTFTKGEKSYYYISEVEAYLTVS----NPAKVV 334
SEQIDNO:52     QASGNCGSRK----SNLLLNFGGGFVNLTFTKDENSYYISEVEAYLTVS----NPAKVV 330
SEQIDNO:53     HASGKCGSQN----SNLFLNFGGGSVNVTFTKEENLYYVSEVGAYLTIS----NTEKTY 312
SEQIDNO:54     HASGKCDQSK----SNLFLNFGGGSVNITFTKEENLYYISEVGAYLTIS----NTEKTY 314
SEQIDNO:55     NSNGTCEKSK---ANLNLTFANSYINVFVAQDDNSYYLDNVTVYFNLTV----RSESWY 218

```

FIGURE 5 cont.

Replacement Sheet

LAMP HOMOLGY DOMAIN 2		
	3	4
SEQIDNO: 3	QGIKHAVVMFQTAVGHSFKCVSEQSLQLSAHLQVKTIDVQLQAFDFEDDHFGNVDECSSD	379
SEQIDNO: 44	QGIKHAVVMFQTAVGHSFKCVSEQSLQLSAHLQVKTIDVQLQAFDFEDDHFGNVDECSSD	381
SEQIDNO: 45	QGMKHAVVMFQTAVGHSFKCVSEQSLQLSAHLQVKTIDVQLQAFDFEDDHFGNVDECSSD	379
SEQIDNO: 46	QGMKHAVVMFQTAVGHSFKCVSEQSLQLSAHLQVKTIDVQLQAFDFEDDHFGNVDECSSD	379
SEQIDNO: 47	QGMKSSVVMFETGVGHSFKCVSEQSLQLSTHLQLKTMNVQVQAFDFEDDHFGNVDECSSD	391
SEQIDNO: 48	QGMKNAVVMFETMIGHHSFKCVSEQSLQLSPHLQLKTMNVQVQAFDFEDDHFGNVDECSSD	393
SEQIDNO: 49	VGLVDNEKLFKAKNGLSFNCKSETMLILADYFRLKLVPLQIQAFDLVNGAFGKEVECWAD	220
SEQIDNO: 50	QGMKSPVVMFETVIGHHSFKCVSEQSLQLSTHLQLKTMNVQVQAFDFEDDHFGNVDECSSD	395
SEQIDNO: 51	QGLKHAMMMFETVVGHSFKCVSEQSLQLSTYLQLKTMNVQVQAFDFEDDHFGNADECISD	394
SEQIDNO: 52	QGMKYAMMMFETVVGHSFKCVSEQSLQLSNHLQLKTMNVQVQAFDFEDDHFGNADECISD	390
SEQIDNO: 53	QGKS-TMMMFETVVGHSFKCVSEQSLQLSAQLQMKTMNIHLQAFDFEGDSFGIVDECLSD	371
SEQIDNO: 54	QGKNTLMFETVVGHSFKCVSEQSLQLSAQLQMKTMNIHLQAFDFEGDSFGIVDECLSD	374
SEQIDNO: 55	GNAT-NQKLLKTENGYSVKCKNTPKIQLGDTMNLVMTNVKLQVFNFKDNSFGKETTCYD	277
	. : : : * * . : * . : : : : * . : : . . * * * *	

Trns Memb. Cyto. Tail

SEQIDNO: 3	YIV-LPV-IGAIVVGLCLMGMGVYKIRLRCSGGYQRI	416
SEQIDNO: 44	YTIV-LPV-IGAIVVGLCLMGMGVYKIRLRCSGGYQRI	418
SEQIDNO: 45	YTIV-LPV-IGAIVVGLCLVIGGVYKIRLRCSGGYQRI	416
SEQIDNO: 46	YTIV-LPV-IGAIVVGLCLVGMGVYKIRLRCSGGYQRI	416
SEQIDNO: 47	YTVV-LPV-IGAIVLGLCAVGLIVYGIHLRRESSGYQRI	428
SEQIDNO: 48	YTIV-LPV-IGAIVLGLCAVGLIVYGIRLRKRESSEYQRI	430
SEQIDNO: 49	YNKRMIPIILGAVAAICLIATILTYVLVREHRNQGYEQI	259
SEQIDNO: 50	YTVV-LPV-IGAIVLGLFAVGLIVYGVRVRREASGYQRI	432
SEQIDNO: 51	RNRREIPVAVGLSIAVLLAVLLTACLVTTRKRPSRGYERM	433
SEQIDNO: 52	RNRREIPVAVGLSIAVLLAVLLTACLVTTRKRPSRGYERM	429
SEQIDNO: 53	YTVV-LPV-VGIIVVLCVVGIGIYKIRQRQSSAYQRI	408
SEQIDNO: 54	YTVV-LPM-VAIIVVVICVVGISVYKIRQRHQSSAYQRI	411
SEQIDNO: 55	HNFG-LMI-AGIVIVVIVVLGVIIYFIWHKRKSSGYQRI	314
	. : : . : : : . * : :	

LAMP-3					
Accession No.	Species	SEQ ID NO:	Accession No.	Species	SEQ ID NO:
NP_055213.2	<i>H. sapiens</i>	3	XP_001496333.1	<i>E. caballus</i>	50
XP_001155195.3	<i>P. troglodytes</i>	44	NP_001095605.1	<i>B. Taurus</i>	51
XP_003894825.1	<i>P. Anubis</i>	45	XP_004003158.1	<i>O. aries</i>	52
NP_001028044.1	<i>M. mulatta</i>	46	NP_001012015.1	<i>R. norvegicus</i>	53
XP_848889.2	<i>C. lupus familiaris</i>	47	NP_796330.2	<i>M. musculus</i>	54
XP_003358746.1	<i>S. scrofa</i>	48	XP_002936919.2	<i>X. tropicalis</i>	55
XP_001342688.2	<i>D. rerio</i>	49			

FIGURE 6: HUMAN LIMP-2 ALIGNMENT WITH ORTHOLOGOUS SEQUENCES

		SIGNAL SEQUENCE	
SEQIDNO: 4	-----	MGRCCFYTAGTLS	13
SEQIDNO: 56	-----	MGRCCFYTAGTLS	13
SEQIDNO: 57	-----	MGRCCFYTAGTLS	13
SEQIDNO: 58	-----	MGRCCFYTVGTLS	13
SEQIDNO: 59	-----	MGRCCFYAVGTLS	13
SEQIDNO: 60	-----	MGRCCFYTAGTLS	13
SEQIDNO: 61	-----	MTRRSCTIYATGIVC	15
SEQIDNO: 62	-----	MARCCFYTAGTLS	13
SEQIDNO: 63	-----	MRSCLCLVTGVLA	13
SEQIDNO: 64	-----	MVKWAVFGTAAVS	13
SEQIDNO: 65	MQLDDILHINNCKADCSSLSTTPNPKTDLVNMNGPKHKFCTKLSSTYLKWWITIV--VA		58
SEQIDNO: 66	-----	MYGRSNRLCAKLSSAFLRKWWFVIA--FA	27

LAMP HOMOLOGY DOMAIN

SEQIDNO: 4	LLLLVTSVTLLVARVFQKAVDQSIIEKKIVLRNGTEAFDSWEKPPLPVYTQFYFFNVTNPE	73
SEQIDNO: 56	LLLLVTSVTLLVARVFQKAVDQSIIEKKIVLRNGTEAFDSWEKPPLPVYTQFYFFNVTNPE	73
SEQIDNO: 57	LLLLVTSVTLLVARVFQKAVDQSIIEKKIVLRNGTEAFDSWEKPPLPVYTQFYFFNVTNPE	73
SEQIDNO: 58	LLLLVTSIALLLVARVFQKAVDQTIIEKNIVLRNGSETFDSWKKPPLPVYAQFYFFNVTNPE	73
SEQIDNO: 59	LLLLVTSITLLVARVFQKAVDQTIIEKNIVLRNGSETFDSWKKPPLPVYTQFYFFNVTNPE	73
SEQIDNO: 60	LLLLVTSVTLLVARVFQKAVDQTIIEKNMVLQNGTKVENSWEKPPLPVYIQFYFFNVTNPE	73
SEQIDNO: 61	AHLLILGIALLLAQVFQTMIEKERIKKEITLAENSRVLDGWINPPPPVYMQFYFFNVTNPD	75
SEQIDNO: 62	LLLLVTSVTLLVARVFQKAVDQTIIEKNMVLQNGTKVFDSEKPPLPVYIQFYFFNVTNPE	73
SEQIDNO: 63	LTLIASISLLVAHVFTVVDLQVKQGTVLKNGTETFEAWEDPPPPVYMQFYFFNVTNPL	73
SEQIDNO: 64	VTLLIVSIVLLTHTFMDIVEGQVKQAIVLKNESEVFEDWANPPPPVYMQFYFFNVTNPL	73
SEQIDNO: 65	AALIIG--GIVVACEFTVLIDAVVDRMVALRPGAKTFGWWAKPPVEPRISLYIYNVTNAD	116
SEQIDNO: 66	LSLLVL--GALVTFGFTAFTIRTIIDHQVALRVGGQSFGWWSRPPVEPIIRIFVYNVTNAD	85
	*:: ::: * : ::: .* . : * ** :.:****	

LAMP HOMOLOGY DOMAIN

SEQIDNO: 4	EILRGE-TPRVEEVGPYTYRELNRNKANIQFGDNGTTISAVSNKAYVFERDQSVGDPKIDL	132
SEQIDNO: 56	EILRGE-TPRVEEVGPYTYRELNRNKANIQFGDNGTTISAVSNKAYVFERDQSVGDPKIDL	132
SEQIDNO: 57	EILRGE-TPRVEEVGPYTYRELNRKANVQFGDNGTTISAVSNKAYVFERDQSVGDPKIDL	132
SEQIDNO: 58	EILRGE-IPRLEEVPYTYRELNRKADIQFGDNGTTISAVSNKAYVFERDQSVGDPKIDL	132
SEQIDNO: 59	EILNGE-TPRLEEVPYTYRELNRKDDIQFGDNGTTISAVSNKAYVFERDQSVGDPKIDL	132
SEQIDNO: 60	EILQGE-IPLLEEVPYTYRELNRNKANIQFGDNGTTISAVTNKAYVFERDQSVGDPKIDL	132
SEQIDNO: 61	EFLAGKEKAKVTQMGPYTYREYRPRENVTYLENGTKIFATNPKSFVFLRNMSAGDPEVDR	135
SEQIDNO: 62	EILQGE-IPLLEEVPYTYRELNRKANVQFGDNGTTISAVTNKAYIFERNQSVGDPTVDL	132
SEQIDNO: 63	EVLQGA-TPLVEEKGPYTYREYRPRVHVQFLDNGTKVSALNPKTYVFEPEKSVGNPEVDL	132
SEQIDNO: 64	EVLSGE-KPFVDEIGPYTYREYRPRENITFSVNGTEVSAVTPKTYVFEPEKSIGDPKVDL	132
SEQIDNO: 65	DFLSNGSKAIVDEVGPYVYSETWEKVNIVENDNGTL-SYNLRKIYSFREDLSVG-PEDDV	174
SEQIDNO: 66	EFLNNGTKPILDELGPYVYVQTEKVNIEKNPNGTI-SYNQKRVYIFNEDLSGG-LEDDV	143
	:. * . : : *** . * : : : : *** : : * : * * *	

FIGURE 6 cont.

Replacement Sheet

LAMP HOMOLOGY DOMAIN

```

SEQIDNO: 4      IRTLNIPVLTVIEWSQ-V-HFLREIEEAMLKAYQQKLFVTHTVDELLWGYKDEILSLIHV 190
SEQIDNO: 56     IRTLNIPVLTVIEWSQ-V-RFLREIEEAMLKAYQQKLFVTHTVDELLWGYKDEILSLIHV 190
SEQIDNO: 57     IRTLNIPVLTVIEWSQ-V-HFLREIEEAMLKAYQQKLFVTHTVDELLWGYKDEILSLIHV 190
SEQIDNO: 58     IRTLNIPAVTAMEWAH-L-HFFRELIEALLKAYQQTLFVTHTVDELLWGYKDEILSLINV 190
SEQIDNO: 59     LRTLNIPALTAMEWTQ-L-PLLRDIEEALLKAYRQKLFVTHTVDELLWGYKDEILSLINT 190
SEQIDNO: 60     IRTINIPLLTVVDLAQ-L-TLLRELIEAMLKAYQQKLFVIHTVHELLWGYKDEILSLVHI 190
SEQIDNO: 61     VTTVNIPMIAVMNELNSYSFFVRTAVSMYMGSMGMGLFMNRTVHEILWGFKDPLLTKLHA 195
SEQIDNO: 62     IRTINIPLLTVVEMAQ-Q-PFLREIEEAMLKAYQQTLFVTHTVHELLWGYKDEVLSLVHI 190
SEQIDNO: 63     IRTINVPVAVTAMEWTR-A-TSLQFATEVLLLLLYQESLFTVRTVHELLWGYKDKLLSTIHV 190
SEQIDNO: 64     IRTVINIPLVTILEMTK-DSSLLRPFIIAALKTYKEGMFVTRTVDELLWGYKDAVLSILHP 191
SEQIDNO: 65     VIVFNIPMLSATSQSKHAARFLRLAMASIMDILKIKPFVQVSVGQLLWGYEDPLLKLAKD 234
SEQIDNO: 66     VIVFNIPMLSATSQSKHAARFLRLAMASIMDILKIKPFVEVSVGQLLWGYEDPLLKLAKD 203
                : . * : * : : . . . : : * : * : : * : * : : * : * : :

```

LAMP HOMOLOGY DOMAIN

```

1
SEQIDNO: 4      FRPDI----SPYFGLFYEKNGTNDGDYVFLTGEDSYLNFETKIVEWNGKTSLDWWITDKCN 246
SEQIDNO: 56     FRPDI----SPYFGLFYEKNGTNDGDYVFLTGEDSYLNFETKIVEWNGKTSLDWWITDKCN 246
SEQIDNO: 57     FRPDI----SPYFGLFYEKNGTNDGDYVFLTGEDSYLNFETKIVEWNGKTSLDWWITDKCN 246
SEQIDNO: 58     FKPEI----SPYFGLYYGKNGTNDGDYVFLTGEDSYLNFETKIVEWNGKTSLDWWITDKCN 246
SEQIDNO: 59     FKHDV----SPYFGLFYGKNGTNDGDYVFLTGEDSYLNFETKIVEWNGKTSLDWWITDKCN 246
SEQIDNO: 60     FKPDV----SPNFGFLFYERNGTNDGEYVFLTGEDSYLNFETKIVEWNGKTSLDWWITDKCN 246
SEQIDNO: 61     MRPEV----DEHFGLMYNKNGTHEGEFVFHTGEKNYMNYGKIDTWNGISQMNWWSNQS 251
SEQIDNO: 62     FRPDV----SPNFGFLFYERNGTNDGEYVFLTGEDSYLNFETKIVEWNGKTSLDWWITDKCN 246
SEQIDNO: 63     LHPEI----DPVFGFFNKMNGTDDGEYVFLSGEMNYLNFSTRIVEWKGKESLNWWTTTKCN 246
SEQIDNO: 64     FKKNI----SDTFGLFYKMNTTDDGEYIFLSGEKDYLEFTQIAEWKGQKALNWWTTTTCN 247
SEQIDNO: 65     VVPKEQKLPYEEFGLLYGKNGTSSDRVTVNTGVDDIRRYGIIDNFNGRTHLPHWTTDACN 294
SEQIDNO: 66     VVPKEQKLPYEEFGLMYGKNSTSKDVTVTWTVGDDITQYGIIDKYNGRSHQTHWLSEQC 263
                . . . * : * * . . . : * . . : * : * * : * . . *

```

LAMP HOMOLOGY DOMAIN

```

2
SEQIDNO: 4      MINGTDGDSFHPLITKDEVLYVFPSDFCRSVYITFSDYES-VQGLPAFRYKVP AEILANT 305
SEQIDNO: 56     MINGTDGDSFHPLITKDEVLYVFPSDFCRSVYITFSDYES-VQGLPAFRYKVP AEILANT 305
SEQIDNO: 57     MINGTDGDSFHPLITKDEVLYVFPSDFCRSVYITFSDYES-VQGLPAFRYKVP AEILANT 305
SEQIDNO: 58     MINGTDGDSFHPLIDKDEILYVFPSEFCRSVYITFSDFKS-VQGLPAFRYKVP GEVLANT 305
SEQIDNO: 59     MINGTDGDTFHPLITRDEVLYVFPSDFCRSVYITFSDFES-VQGLPALRYKVP AEILANT 305
SEQIDNO: 60     MINGTDGDSFHPLISKDEVLYLFFPSDLCRSVHITFSSFEN-VEGLPAFRYKVP AEILANT 305
SEQIDNO: 61     MINGTDGDSVFHTFSLRKELLYIFAADLCRSIHLGYVRDME-VKGIPAFRFPSPDV LAP 310
SEQIDNO: 62     MINGTDGDSFHPLISKDETLYIFPSDFCRSVYITFSSFEN-VEGLPAFRYKVP AEILANS 305
SEQIDNO: 63     MINGTDGTSFHPLISKDENIYIFSSDFCRSLYLVYDSSGS-VAGVPTYRFVPS PMVFANT 305
SEQIDNO: 64     MINGTDGTSFHPLLNKDDTIYMFSSDLCRSIYAVYESSN-IKDISVFRESPPASVFANV 306
SEQIDNO: 65     TLAGTDGSIFFPHIDHRIHLHYVDKDLRLLFLVFEKEVMTSNEVPGYRET PPEWVFADV 354
SEQIDNO: 66     RLNGTDGSIFFPRITKNSTLHVYEDKDLRLLPLSFEKEVTVRGGVGKGYRET PPDVFASV 323
                : **** * : : . : : : : : : : : : : : : : : : : : : : : : : :

```

FIGURE 6 cont.

Replacement Sheet

LAMP HOMOLGY DOMAIN

```

          3         4         5
SEQIDNO: 4  ---SDNAGFCIPE-GNCLGSGVLNVSIKNGAPIIMSFPHFYQADERFVSAIEGMHP-NK 360
SEQIDNO: 56 ---SDNAGFCIPE-GNCLGSGVLNVSIKNGAPIIMSFPHFYQADERFVSAIEGMHP-NK 360
SEQIDNO: 57 ---SDNAGFCIPE-GNCLGSGVLNVSIKNGAPIIMSFPHFYQADERFVSAIEGMHP-NK 360
SEQIDNO: 58 ---SDNAGFCVPK-GNCLGSGVLNISICKNGAPIIISFPHFYEADKKFVSAIDGMRP-NK 360
SEQIDNO: 59 ---SDNAGFCIPK-GNCLGSGVLNVSVCKNGAPIIMSFPHFYQADEKFVSAIGGMHP-NK 360
SEQIDNO: 60 ---SENAGFCIPE-GNCMDSGVLNISICKNGAPIIMSFPHFYQADEKFVSAIKGMHP-NK 360
SEQIDNO: 61 DENPANAGFCVPA-GDCLGKGVLVSVCRQGAPIVVSFPHFYQADERYINAIEGMNP-NE 368
SEQIDNO: 62 ---SENAGFCIPE-GNCMDAGVLNVSIKNGAPIIMSFPHFYQADEKFVSAIKGMRP-NK 360
SEQIDNO: 63 TVNPDNAGFCVFP-GNCPGAGVLNVSIKQGAPIFLSAPHFYQADQKFVSDIEGMHP-TK 363
SEQIDNO: 64 SVNPNQKGFVPE-GNCLPSGVLNVSIKQGAPIVLSSPHFYQADENVINSIRGMKP-VK 364
SEQIDNO: 65 DSHFDNMCFCPAGKPCSNGLEFNVSLCQYDSPIMLSFPHFYLADES LRTQVEGISPPMK 414
SEQIDNO: 66 DKNPNMCMCYCPAG-PPCAPHGLFNVSLCQYDSPILLSFPHFYMAQT LRTAVEGISPPEK 382
          *  : *      *  *:::***: .:***: *  **** *:  .  : *: *  :

```

LAMP HOMOLGY DOMAIN

```

SEQIDNO: 4  EDHETFDINPLTGIILKAAKRFQINIVVKLLDDFVETGDIRTMVFPVMYLNESVHIDKE 420
SEQIDNO: 56 EDHETFDINPLTGIILKAAKRFQINIVVKLLDDFVETGDIRTMVFPVMYLNESVHIDKE 420
SEQIDNO: 57 EDHETFDINPLTGIILKAAKRFQINIVVKLLDDFVETGDIRTMVFPVMYLNESVHIDKE 420
SEQIDNO: 58 DYHETFDINPLTGIILRAAKRFQINIVVKLLDDFIETGNIRTMVFPVMYLNESVHIDKD 420
SEQIDNO: 59 EYHETFDINPLTGIILRAAKRFQINIVVRKLLDDFVETGNIQTLVFPVMYLNESVHIDKE 420
SEQIDNO: 60 EEHESFVDINPLTGIILRGAKRFQINTYVRKLLDDFVETGDIRTMVFPVMYLNESVHIDKE 420
SEQIDNO: 61 EEHETYLDINPTTGVPPIRACKRAQLNIIKRVRGFENTKFLNETIFPIMYVNETATIDDE 428
SEQIDNO: 62 EEHESFVDINPLTGIILRGAKRFQINTYVRKLLDDFVETGNIQTLVFPVMYLNESVHIDKE 420
SEQIDNO: 63 EYHETFDINPLTGLVLQAARKFQINIHVRKLPFEFFETGNIRTLIFPVMYLNESVHIDKE 423
SEQIDNO: 64 EHHMTFLDLNPLTGLTQAARKFQINIVVRKINVYLITQDIQTLFFPVMHNLNESVHIDKE 424
SEQIDNO: 65 EKHQFFFDVQPKMGTTLRVARQINLAVSQVFDIKQVANFPDIIFFPILWFEEGIDNLPD 474
SEQIDNO: 66 DKHQFLFIDVQPDGMTALRAPARIQINLAVSQVVDIKQVANFPDIVFPILWFEEGIDSLPD 442
          : *  :.***: *  ::  *  *:*  :::  .  :  .***: :.*

```

Trans. Domain

Cytoplasmic Tail

```

SEQIDNO: 4  TASRLKSMINTTLLITNI----PYIIMALGVFFGLVFTWLACKGQGSMDDEGTADERAPLI 476
SEQIDNO: 56 TASRLKSMINTTLLITNI----PYIIMALGVFFGLVFTWLACKGQGSMDDEGTADERAPLI 476
SEQIDNO: 57 TASRLKSVINTTLLITNI----PYIIMALGVFFGLVFTWLACKGQGSMDDEGTADERAPLI 476
SEQIDNO: 58 TASRLKSVINTTLLITNI----PYIIMALGVFFGLVFTWLACRGQGSMDDEGTADERAPLI 476
SEQIDNO: 59 TASRLKSVINTTLLITNI----PYIIMALGVFFGLVFTWLACRGQGSMDDEGTADERAPLI 476
SEQIDNO: 60 TANQLKSVINTTLLITNI----PYIIMALGVFFGLVFTWLACRGQGSMDDEGTADERAPLI 476
SEQIDNO: 61 SAAQMRMLLLIVTVVSNF----PVIILALGVILVVLIFLVCRNRQRKNEVKRIDFTEAF 484
SEQIDNO: 62 TASQLKSVINTTLLITNI----PYIIMALGVFFGLVFTWLACRGQGSMDDEGTADERAPLI 476
SEQIDNO: 63 SANKLKHVLEASVVTGI----PFVIMAIGIVFGIVFSVLVCRAQGAREESTEEERSPLI 479
SEQIDNO: 64 SAGRLRSILFQGRVVANI----PFIIMGLGIIILAFLETTLSCLQKRSRDEGTEEEERGPI 480
SEQIDNO: 65 EVTDL--MRFAEQVPPKIRVALIVGLCALGVILLLLSTF--CLIRNSHRQSTLHLEGSNY 530
SEQIDNO: 66 EILD--MKVATNIPPRAKFIITIALFGLGGFLFVAVI--CLVRKSHRQSTLHLEGSNY 498
          :  :      :      :  :.*  :.  :  *  :  :

```

FIGURE 6 cont.

Replacement Sheet

```

SEQIDNO: 4      RT----- 478
SEQIDNO: 56     RT----- 478
SEQIDNO: 57     RT----- 478
SEQIDNO: 58     RT----- 478
SEQIDNO: 59     RT----- 478
SEQIDNO: 60     RT----- 478
SEQIDNO: 61     HSFATTKDETAYTQVSNQAEDSPENRNNQPLRNGSYIAMSFVEAQKC 531
SEQIDNO: 62     RT----- 478
SEQIDNO: 63     RT----- 481
SEQIDNO: 64     RAS----- 483
SEQIDNO: 65     LATA-----QVDMNKKQNKDNQPARY----- 551
SEQIDNO: 66     LATA-----SVDQAKKKAKMDNGMSSKSN----- 522
                  :

```

LIMP-2					
Accession No.	Species	SEQ ID NO:	Accession No.	Species	SEQ ID NO:
NP_005497.1	<i>H. sapiens</i>	4	NP_775366.1	<i>D. rerio</i>	61
XP_517214.2	<i>P. troglodytes</i>	56	NP_446453.1	<i>R. norvegicus</i>	62
XP_001096458.1	<i>M. mulatta</i>	57	XP_420593.1	<i>G. gallus</i>	63
XP_005639134.1	<i>C. lupus familiaris</i>	58	NP_001016557.1	<i>X. tropicalis</i>	64
NP_001095623.1	<i>B. Taurus</i>	59	NP_726504.2	<i>D. Melanogaster</i>	65
NP_031670.1	<i>M. musculus</i>	60	XP_314345.2	<i>A.gambiae</i>	66

FIGURE 7: HUMAN LIMBIC/SLAMP ALIGNMENT WITH ORTHOLOGOUS SEQUENCES

SIGNAL SEQUENCE		LAMP HOMOLOGY DOMAIN	
		1	
SEQIDNO: 67	-MVRVQPDRLQLPLV-LLRLCL-LPTGLPVRSDFNRGTDNITVRQGDTAILRCVVED	57	
SEQIDNO: 68	-MVRVQPDRLQLPLV-LLRLCL-LPTGLPVRSDFNRGTDNITVRQGDTAILRCVVED	57	
SEQIDNO: 69	-MGARVQPDRLQLPLV-LLRLCL-LPTGLPVRSDFNRGTDNITVRQGDTAILRCVVED	57	
SEQIDNO: 70	-MVGRVQPDRLQLPLV-LLRLCL-LPTGLPVRSDFNRGTDNITVRQGDTAILRCVVED	57	
SEQIDNO: 71	-MVGRSQSDRNQLPLF-LLRLCL-LPTGLPVRSGDFNRSTDNMTVRQGDTAILRCFVED	57	
SEQIDNO: 72	----MSCLWIHSVFIPGFF--LLF-GFEGFPVISVESQRSTDNITVRQGDITVIRCYVDD	53	
SEQIDNO: 102	-MVGRVQPDRLQLPLV-LLRLCL-LPTGLPVRSDFNRGTDNITVRQGDTAILRCVVED	57	
SEQIDNO: 103	-MVGRVQPDRLQLPLV-LLRLCL-LPTGLPVRSDFNRGTDNITVRQGDTAILRCVVED	57	
SEQIDNO: 104	-MVARVQPDRLQLPLV-LLRLCL-LPTGLPVRSDFNRGTDNITVRQGDTAILRCVVED	57	
SEQIDNO: 105	-MVARVQPDRLQLPLV-LLRLCL-LPTGLPVRSDFNRGTDNITVRQGDTAILRCVVED	57	
SEQIDNO: 106	-----MSFAGEAA-----SQILNKAEPFISRSEAFKFAVGDTITLPCEVAS	42	
SEQIDNO: 107	-----MRPCLLHSIWMLGFVLCCLSLQGLPVRSGDFNRSTDNITVRQGDTAILRCFVED	54	
SEQIDNO: 108	-MLGARRPPRSQPLV-LLRLCL-LPTGLPVRSDFNRGTDNITVRQGDTAILRCVVED	57	
SEQIDNO: 109	-MVGRVHPDRKQLPLV-LLRLCL-LPTGLPVRGVDFTRGTDNITVRQGDTAILRCYVED	57	
SEQIDNO: 110	-MVARAQPDRLQLPLV-LLRLCL-LPTGLPVRSDFTRGTDNITVRQGDTAILRCFVED	57	
SEQIDNO: 111	----MRTYW-LHSIWVL-GFFLSLF-SLQGLPVRSDFTRGTDNITVRQGDTAILRCYVED	54	
SEQIDNO: 112	-----MRPCLLHSIWMLGFVLCCLSLQGLPVRSGDFNRSTDNITVRQGDTAILRCFVED	54	
SEQIDNO: 113	MQVGRKSCWRQ---LQASFFRLCL-IPFGFPVRSDMQRATDNITVRQGDTAILRCYVDD	57	
		:	:: :.. *** : * * .
		LAMP HOMOLOGY DOMAIN	
		2	
SEQIDNO: 67	KN-SKVAWLNRSGIIFAGHDKWSLDPVELEKRHSLEYSRLRIQKVDVYDEGSYTCVQQTQ	116	
SEQIDNO: 68	KN-SKVAWLNRSGIIFAGHDKWSLDPVELEKRHSLEYSRLRIQKVDVYDEGSYTCVQQTQ	116	
SEQIDNO: 69	KN-SKVAWLNRSGIIFAGHDKWSLDPVELEKRHSLEYSRLRIQKVDVYDEGSYTCVQQTQ	116	
SEQIDNO: 70	KN-SKVAWLNRSGIIFAGHDKWSLDPVELEKRHSLEYSRLRIQKVDVYDEGSYTCVQQTQ	116	
SEQIDNO: 71	KS-SKVAWLNRSGIIFAVDDKWSLDPVELEKRSPFEYSRLRIQKVDVSDGPGYICSVQTN	116	
SEQIDNO: 72	KV-SKVAWLNRSGIIFAGEDKWSLDPVELVTQGGLEYSLRIQKVDVDFDEGPYTCVQTK	112	
SEQIDNO: 102	KN-SKVAWLNRSGIIFAGHDKWSLDPVELEKRHSLEYSRLRIQKVDVYDEGSYTCVQQTQ	116	
SEQIDNO: 103	KN-SKVAWLNRSGIIFAGHDKWSLDPVELEKRHSLEYSRLRIQKVDVYDEGSYTCVQQTQ	116	
SEQIDNO: 104	KN-SKVAWLNRSGIIFAGHDKWSLDPVELEKRHSLEYSRLRIQKVDVYDEGSYTCVQQTQ	116	
SEQIDNO: 105	KN-SKVAWLNRSGIIFAGHDKWSLDPVELEKRHSLEYSRLRIQKVDVYDEGSYTCVQQTQ	116	
SEQIDNO: 106	PGTYVLAWKRGIAILTAGSVKVTDPDRVRLVN---GYSLQIRDAVPQDAGDYICQIAML	98	
SEQIDNO: 107	RS-SKVAWLNRSGIIFAGDDKWSLDPVELEKRHSLEYSRLRIQKVDVSDGPGYTCVQTK	113	
SEQIDNO: 108	KN-SKVAWLNRSGIIFAGHDKWSLDPVELEKRHSLEYSRLRIQKVDVYDEGSYTCVQQTQ	116	
SEQIDNO: 109	KS-SKVAWLNRSGIIFAGHDKWSLDPVELEKRHSLEYSRLRIQKVDVYDEGSYTCVQQTQ	116	
SEQIDNO: 110	RS-SKVAWLNRSGIIFAGEDKWSLDPVELEKRSPLEYSLRIQKVDVYDEGSYTCVQQTQ	116	
SEQIDNO: 111	RS-SKVAWLNRSGIIFAGEDKWSLDPVELEKRNPLEYSLRIQKVDVYDEGSYTCVQQTQ	113	
SEQIDNO: 112	RS-SKVAWLNRSGIIFAGDDKWSLDPVELEKRHSLEYSRLRIQKVDVSDGPGYTCVQTK	113	
SEQIDNO: 113	KV-SKVAWLNRSGIIFAGQDKWSLDPVDLVTKGQLEYSLRIQKVDVYDEGSYTCVQTK	116	
		: ** . * : * * : **** * . ***: :.. * * * * .:	

FIGURE 7 cont.

Replacement Sheet

LAMP HOMOLGY DOMAIN

3

```

SEQIDNO: 67 HEPKTSQVYLIVQVPPKISNISS--DVTVNEGSNVTLCMANGRPEPVITWRHLTP---T 171
SEQIDNO: 68 HEPKTSQVYLIVQVPPKISNISS--DVTVNEGSNVTLCMANGRPEPVITWRHLTP---T 171
SEQIDNO: 69 HEPKTSQVYLIVQVPPKISNISS--DVTVNEGSNVTLCMANGRPEPVITWRHLTP---T 171
SEQIDNO: 70 HEPKTSQVYLIVQVPPKISNISS--DVTVNEGSNVTLCMANGRPEPVITWRHLTP---L 171
SEQIDNO: 71 QHTKTMQVYLIVQVPPKISNISA--DITVNEGSNVTLMCIAYGRPEPMITWRHLTP---T 171
SEQIDNO: 72 QQSKTSQVYLIVQVPAIIYKVE--DITVNEGSNVALTCLANGRPDPAITWRLLNP---S 167
SEQIDNO: 102 HEPKTSQVYLIVQVPPKISNISS--DVTVNEGSNVTLCMANGRPEPVITWRHLTP---L 171
SEQIDNO: 103 HEPKTSQVYLIVQVPPKISNISS--DVTVNEGSNVTLCMANGRPEPVITWRHLTP---T 171
SEQIDNO: 104 HEPKTSQVYLIVQVPPKISNISS--DVTVNEGSNVTLCMANGRPEPVITWRHLTP---T 171
SEQIDNO: 105 HEPKTSQVYLIVQVPPKISNISS--DVTVNEGSNVTLCMANGRPEPVITWRHLTP---T 171
SEQIDNO: 106 DPR-EITHSVEILVPPKITHVTSGGHLQVRKGSVRLECSATGNPMPNITWRKNNLLPN 157
SEQIDNO: 107 QHTKTTQVYLIVQVPPKISNISA--DITVNEGSNVTLMCIAYGRPEPMITWRHLTP---T 168
SEQIDNO: 108 HEPKTSQVYLIVQVPPKISNISS--DVTVNEGSNVTLCMANGRPEPVITWRHLTP---T 171
SEQIDNO: 109 HQPKTSQVYLIVQVPPKISNISS--DVTVNEGSNVTLCMANGRPEPVITWRHLTP---T 171
SEQIDNO: 110 HHPKTSQVYLIVQVPPKISNISS--DITVNEGSNVTLCMANGRPEPVITWRHLTP---T 171
SEQIDNO: 111 HHPKTSQVYLIVQVPPKISNISS--DITVNEGSNVTLCMANGRPEPVITWRHLTP---T 168
SEQIDNO: 112 QHTKTTQVYLIVQVPPKISNISA--DITVNEGSNVTLMCIAYGRPEPMITWRHLTP---T 168
SEQIDNO: 113 QQPKTSQVYLIVQVPASIQVSN---DITVNEGSNVTLSCLANGRPDPAITWRLLNP---S 171
. : : * * * : : . : * : * * * * * * * * * * * * * * * *

```

LAMP HOMOLGY DOMAIN

4

```

SEQIDNO: 67 GREFEGEEEEYLEILGITREQSGKYECKAANEVSSADVQVKVTVNYPPTITESKS 230
SEQIDNO: 68 GREFEGEEEEYLEILGITREQSGKYECKAANEVSSADVQVKVTVNYPPTITESKS-NEAT 230
SEQIDNO: 69 GREFEGEEEEYLEILGITREQSGKYECKAANEVSSADVQVKVTVNYPPTITESKS-NEAT 230
SEQIDNO: 70 GREFEGEEEEYLEILGITREQSGKYECKAANEVSSADVQVKVTVNYPPTITESKS-NEAT 230
SEQIDNO: 71 ARDFEGEEEFLEIQGITREQSGRYECKAANEVASADVQVRVTVNYPPIITESNS-NEAT 230
SEQIDNO: 72 AEALDV-GEYLEISGVVRSQAGRYECKASNDVSTPDVKYVNVVVNYPPIKDVRS-SETA 225
SEQIDNO: 102 GREFEGEEEEYLEILGITREQSGKYECKAANEVSSADVQVKVTVNYPPTITESKS-NEAT 230
SEQIDNO: 103 GREFEGEEEEYLEILGITREQSGKYECKAANEVSSADVQVKVTVNYPPTITESKS-NEAT 230
SEQIDNO: 104 GRELEGELEEYLEILGITREQSGKYECKAANEVSSADVQVKVTVNYPPTITESKS-NEAT 230
SEQIDNO: 105 GREFEGEEEEYLEILGITREQSGKYECKAANEVSSADVQVKVTVNYPPTITESKS-NEAT 230
SEQIDNO: 106 GEEQFT-NPVYVIENMDRHKGGTYICTANNGVGQVATSQIILHVLVYPPEISVENPTVYSG 216
SEQIDNO: 107 ARDFEGEEEFLEIQGITREQSGRYECKAANEVASADVQVRVTVNYPPIITESKS-NEAT 227
SEQIDNO: 108 GREFEGEEEEYLEILGITREQSGKYECKAANEVSSADVQVKVTVNYPPTITESKS-NEAT 230
SEQIDNO: 109 GREFEGEEEEYLEILGITREQSGKYECKAANEVSSADVQVKVTVNYPPTITESKS-NEAT 230
SEQIDNO: 110 GKEFEGEEEEYLEILGITREQSGKYECKAANEVASADVQVRVTVNYPPTITESKS-NEAA 230
SEQIDNO: 111 GKEFEGEEEEYLEILGITREQSGKYECKAANEVASADVQVRVTVNYPPTITESKS-NEAA 227
SEQIDNO: 112 ARDFEGEEEFLEIQGITREQSGRYECKAANEVASADVQVRVTVNYPPIITESKS-NEAT 227
SEQIDNO: 113 AEPLDG-EEYLDIIGIMRTQAGRYECKASNDVATPDVKYVNVIVNYPPTIKKTQS-SETP 229
. . * . : * : * * * * * * * * * * * * * * * * * * * * * * * * * *

```

LAMP HOMOMLOGY DOMAIN

Trns Memb.

SEQIDNO:67	VAANKLGVTNASIVLFRPGSVRGINGSISLAVPLWLLAASLLCCL-SKC-----	338
SEQIDNO:68	VAANKLGVTNASIVLFRPGSVRGINGSISLAVPLWLLAASLLCCL-SKC-----	338
SEQIDNO:69	VAANKLGVTNASIVLFRPGSVRGINGSISLAVPLWLLAASLLCCL-SKC-----	338
SEQIDNO:70	VAANKLGVTNASIVLFSKYAKTEPDSMQVIE-FLHIDKISRHPL-KVNPIQK-----	341
SEQIDNO:71	VAANKLGITNTSLYLYI-GPGTPIDNATSLAASLWLMANILLCLF-CTC-----	337
SEQIDNO:72	VATNRLGVHNASVFLYKPGMGRDINSAGCICQSLWLLLLCVSSAL-LQC-----	333
SEQIDNO:102	VAANKLGVTNASIVLFRPGSVRGINGSISLAVPLWLLAASLFCCL-SKC-----	338
SEQIDNO:103	VAANNLGVTNASIVLFRPGSVRGINGSISLAVPLWLLAASLLCCL-SKC-----	338
SEQIDNO:104	VAANNLGVTNASIVLFRPGSVRGINGSISLAVPLWLLAASLLCCL-SKC-----	338
SEQIDNO:105	VAANNLGMTNASIVLFRPGSVRGINGSISLAVPLWLLAASLLCCL-SKC-----	338
SEQIDNO:106	IADNQLGKTRKTVTTLTGPKPTAVF---RSVPNSQWKDKYNISWIVDSHSPIEEFKLYYRQ	333
SEQIDNO:107	VAANKLGITNTSLYLYI-GPGTPIDSATSLAASLWLMANLLFCLF-CTC-----	334
SEQIDNO:108	VAANNLGVTNASIVLFRPGSVRGINGSISLAVPLWLLAASLLCCL-SKC-----	338
SEQIDNO:109	VAANKLGVTNASILIFRPGSVRGINGSISLAVPLWLLAASLFCCL-SKC-----	338
SEQIDNO:110	VAANKLGVTNASLYLYRPGTGRVDNGSVSLAVPLWLLAASLLCCL-SKC-----	338
SEQIDNO:111	VAANKLGVTNASLYLYRPGTGRVDNGSMSLAVPLWLLAASLLCCL-SKC-----	335
SEQIDNO:112	VAANKLGITNTSLYLYI-GPGTPIDSATSLAASLWLMANLLFCLF-CTC-----	334
SEQIDNO:113	VASNRLGVQNASLYLYRPGTGRDINGSACVSQSLWLLLLASACLF-LKC-----	337
	: * *.** . : : *	

FIGURE 7 cont.

Replacement Sheet

```

SEQIDNO:67 ----- 338
SEQIDNO:68 ----- 338
SEQIDNO:69 ----- 338
SEQIDNO:70 ----- 341
SEQIDNO:71 ----- 337
SEQIDNO:72 ----- 333
SEQIDNO:102 ----- 338
SEQIDNO:103 ----- 338
SEQIDNO:104 ----- 338
SEQIDNO:105 ----- 338
SEQIDNO:106 MTFSIGQLQLQTDWRDIVLPAPFPYSHHYTQGMSYLRGLEPDQQYEARVQSRNRYGWSD 393
SEQIDNO:107 ----- 334
SEQIDNO:108 ----- 338
SEQIDNO:109 ----- 338
SEQIDNO:110 ----- 338
SEQIDNO:111 ----- 335
SEQIDNO:112 ----- 334
SEQIDNO:113 ----- 337

```

```

SEQIDNO:67 ----- 338
SEQIDNO:68 ----- 338
SEQIDNO:69 ----- 338
SEQIDNO:70 ----- 341
SEQIDNO:71 ----- 337
SEQIDNO:72 ----- 333
SEQIDNO:102 ----- 338
SEQIDNO:103 ----- 338
SEQIDNO:104 ----- 338
SEQIDNO:105 ----- 338
SEQIDNO:106 FSESFLFTTSNTGKWMGQCCTNPG 417
SEQIDNO:107 ----- 334
SEQIDNO:108 ----- 338
SEQIDNO:109 ----- 338
SEQIDNO:110 ----- 338
SEQIDNO:111 ----- 335
SEQIDNO:112 ----- 334
SEQIDNO:113 ----- 337

```

LIMBIC/LSAMP					
Accession No.	Species	SEQ ID NO:	Accession No.	Species	SEQ ID NO:
NP_002329.2	<i>H. sapiens</i>	67	NP_001192297.1	<i>B. Taurus</i>	105
XP_516662.2	<i>P. troglodytes</i>	68	XP_312298.5	<i>A.gambiae</i>	106
XP_002716722.1	<i>O. cuniculus</i>	69	NP_001096385.1	<i>X.tropicalis</i>	107
NP_780757.1	<i>M. musculus</i>	70	XP_003434117.1	<i>C. lupus familiaris</i>	108
NP_001086181.1	<i>X. laevis</i>	71	XP_001362972.1	<i>M. domestica</i>	109
NP_001034921.1	<i>D. rerio</i>	72	NP_990205.1	<i>G. gallus</i>	110
NP_058938.1	<i>R. norvegicus</i>	102	XP_002190582.1	<i>T. guttate</i>	111
XP_001502710.1	<i>E. caballus</i>	103	NP_001096385.1	<i>X. tropicalis</i>	112
NP_001231626.1	<i>S. scrofa</i>	104	XP_003449349.1	<i>O. niloticus</i>	113

FIGURE 8: HUMAN ENDOLYN ALIGNMENT WITH ORTHOLOGOUS SEQUENCES

	SIGNAL SEQUENCE	LAMP HOMOLOGY DOMAIN
SEQIDNO: 5	MSRLSRSLIWAATCLGVLCVLSADKNTTQH	PNVTTNAPISNVTISAP --- V-TSLPLV 53
SEQIDNO: 73	MSGSSRRLIWAATCLAVLCVLSAQPNTTLAPNVTEVPT	-----TT-----TKVVPTTQM 50
SEQIDNO: 74	MSRLSRSLIWAATCLAVLCVLSAENPTPH-TNVTSLAPTSNITSAP	-----V-TSLPLV 53
SEQIDNO: 75	MLGLSRQLLWAVGCLAALCVLTAANKSTIL-PPSTTPWLSPTTQT	-----TSAPPKTL 54
SEQIDNO: 76	MSGLSRPLLLAVGCLAALCVITAAGNTTTLA-PNVTTASS-PPPTTTTVPVSPPTLSPLPV 58	
SEQIDNO: 77	MSGLSRPLLLAVGYLAALCVITAARNTTVT-PNVTTFSS-PPPTTATVPVSPPTLTTPPV 58	
SEQIDNO: 78	MSGLSRQLCWAAACLAALCALTAQAQSFSSD-PNGTTTTTQATTDAAT	-----TRVTTAAPA 55
SEQIDNO: 79	MSGASRGLFWAATCLAALCLSAAQSNS-SASPNVTDEPT	-----TT-----SKVVPTTLT 49
	* * * * * * * * * *	:

	LAMP HOMOLOGY DOMAIN							
	1	2	3	4	5	6	7	8
SEQIDNO: 5	TTPAPETCEGRNSCVSCVSVV-NNTCFWIECKD--ESYCSHNSTVSDCQVGNNTDFCS 110							
SEQIDNO: 73	PTVLPETCASFNSCVSCVNATFTNNITCFWLHCQEANKTYCAN-EPLSNCSQVNRTDLCS 109							
SEQIDNO: 74	TTPAPETCEGRNSCVSCFNASTV-NNTCFWIECKD--ESYCSHNSTVSDCQVGNNTDFCS 110							
SEQIDNO: 75	PTPAPEICENRNSCISCFDA----NNTCFWIECKG--KSYCSDNSTVSDCHVNGTDFCS 108							
SEQIDNO: 76	TTPAPDICGSRNSCVSCVDG----NATCFWIECKG--KSYCSDNSTAGDCKVNTTGFC 112							
SEQIDNO: 77	TTPAPDICGSRNSCISCVDG----NATCFWIECKG--KSYCSDNSTVSDCKVNTTGFC 112							
SEQIDNO: 78	TTPAPDPCDNRNSCVSCVNTSVD-ATACSWIECKE--KSYCSHNSTVSDCQVNSTQLCS 112							
SEQIDNO: 79	TTKPPETCESFNSCVSCVNATLTNNITCVWLDCHAEANKTYCSS-ELVSNCTQKTSTDSCS 108							
	* *	:	* *	:	* *	:	* *	:

	LAMP HOMOLOGY DOMAIN
SEQIDNO: 5	VST-ATVEVTANSTAKPTVQPSSTT-SKVTTSCTTNTTNTVPTSPVRKSTFDAASFIG 168
SEQIDNO: 73	VIPPTPVPT-NSTAKPTTRPSSPTPTPSVVTSGATTNTTLTPTSQPERKSTFDAASFIG 168
SEQIDNO: 74	VPT-ATLVPTANSTAKPTVQPSSTT-SKTVTTSCTTNTTNTVPTSPVRKSTFDAASFIG 168
SEQIDNO: 75	GPT-VTPLPT-NSTAKTTTLPSFSSA-STTATTSCTTNTTLAPTTPMRKSTFDAASFIG 165
SEQIDNO: 76	VPT-TTPTPT-NSTAKTTTLPSSTTT-STTATTSCTTNTTLSPTIQPTRKSTFDAASFIG 169
SEQIDNO: 77	VPT-TTPTPT-NSTAKTTTLPSSTTT-STTATTSCTTNTTLAPTTPMRKSTFDAASFIG 169
SEQIDNO: 78	APE-PTMMPT-NSTAKTTTPSSSTA-TTATTSCTTNTLSPTSQGRKSTFDAASFIG 169
SEQIDNO: 79	VIP-TTPVPT-NSTAKPTTRPSSPTPTPSVVTSGATTNTTNTVPTSPVRKSTFDAASFIG 166
	* * * * * * * * * *

Trns Memb. Cytoplasmic Tail

SEQIDNO: 5	GIVLVLGQAVIFFLYKFCKSKERNYHTL 197
SEQIDNO: 73	GIVLVLGQAVIFFLYKFCKSKERNYHTL 197
SEQIDNO: 74	GIVLVLGQAVIFFLYKFCKSKERNYHTL 197
SEQIDNO: 75	GIVLVLGQAVIFFLYKFCKSKERNYHTL 194
SEQIDNO: 76	GIVLVLGQAVIFFLYKFCKSKERNYHTL 198
SEQIDNO: 77	GIVLVLGQAVIFFLYKFCKSKERNYHTL 198
SEQIDNO: 78	GIVLVLGQAVIFFLYKFCKSKERNYHTL 198
SEQIDNO: 79	GIVLVLGQAVIFFLYKFCKSKERNYHTL 195

FIGURE 8 cont.

Replacement Sheet

Endolyn					
Accession No.	Species	SEQ ID NO:	Accession No.	Species	SEQ ID NO:
NP_006007.2	<i>H. sapiens</i>	5	NP_001039506.1	<i>B. taurus</i>	76
NP_058594.1	<i>M. musculus</i>	73	XP_004011265.1	<i>O. aries</i>	77
XP_001091286.1	<i>M. mulatta</i>	74	XP_532256.2	<i>C. lupus familiaris</i>	78
XP_001924661.2	<i>S. scrofa</i>	75	NP_114000.1	<i>R. norvegicus</i>	79

FIGURE 9: HUMAN MACROSAILIN ALIGNMENT WITH ORTHOLOGOUS SEQUENCES

	SIGNAL SEQUENCE	LAMP HOMOLOGY DOMAIN 1	
		1	
SEQIDNO: 80	MRLAVLFSGALLGL-LAAQGTGND	CPHKKSATLLPSETVPTVTEST	55
SEQIDNO: 81	MRLAVLFSGALLGL-LAAQGTGND	CPHKKSATLLPSETVPTVTEST	55
SEQIDNO: 82	MRLAVFFSGALLGL-LAAQGTGND	CPHKKSATLLPSETVPTTATESTPS	58
SEQIDNO: 83	MRLPVCL--ILLGP-LIAQGT	EDCPHKKAVTLLPSETMTPTATESTAS	56
SEQIDNO: 84	MRLAVLFLGALLGL-LAAQGTGND	CPHKKSATLLPSETVPTTATEST	55
SEQIDNO: 85	MRFPVCL--TLLVL-LVAQGT	GKDCPHKKAATLLPSETETPTTGSTAS	56
SEQIDNO: 86	MRPAVFFLGLVGL-LAAQGT	RSDCPHKKSATLLPSETVPTTATESTGS	58
SEQIDNO: 87	MRLAVLFSGALLGL-LAAQGTGND	CPHKKSATLLPSETVPTTATESTAS	58
SEQIDNO: 88	MRLFVLFLA-LLGL-HAA		27
SEQIDNO: 89	MTLAVLFLGALLGL-LAESTTSH		22
SEQIDNO: 90	MRLAVLFSGALLGL-LAAQGTGND	CPHKKSATLLPSETVPTTATEST	55
SEQIDNO: 91	MRLSLLSGILLGL-LAEQAG	GDKCPQEKSVTLVPSETVTTIATERSTSPETTSSGS	58
SEQIDNO: 92	-----MGLTLFLPAQGSQCRAN	CPHKKSATLVPSSETVPTTATSG	49

:

LAMP HOMOLOGY DOMAIN 1

SEQIDNO: 80	SHKTTTHRTTT-----TGTTSHGPTTATHNP	TTTSHGNVTVHPTSNSTATSQGPSTAT	108
SEQIDNO: 81	SHKTTTHRTTT-----TGTASHGPTTATHNP	TTTSHGNVTVHPTSNSTATSQGPSTAT	108
SEQIDNO: 82	SHRTTWRISTTTHTNTTGTTSSESPTATHSPA		92
SEQIDNO: 83	SHGNVTVH-----T-----SSGPTTVTHNPA		77
SEQIDNO: 84	SHKTTTHRTTT-----TGTTSHRPTTATHNP	TTTSHRNATVHPTSNSTATSQGPSTAT	108
SEQIDNO: 85	SHRPTTTS-----HRPTTSHRPTTSHRPT		85
SEQIDNO: 86	AETT-----SHAPNTTTHQ		72
SEQIDNO: 87	SHRTTT-----GTTSDHPTTATHNP		79
SEQIDNO: 88	NPHTT-----SHSTATPGTTSRPTTAT		50
SEQIDNO: 89	--RTTTPR-----TTTTTSHGPTTVTHNPA		47
SEQIDNO: 90	SHKTTTHRTTT-----TGTTSHRPTTATHNP	TTTSHRNATVHPTSNSTATSQGPSTAT	108
SEQIDNO: 91	--TATTYRTS-----TAATTPHS		80
SEQIDNO: 92	DHGTTTSHETTTSQGTSTHGTSTPHTTTTGHGTT	TGHQN-----TSH	91

LAMP HOMOLOGY DOMAIN 1

SEQIDNO: 80	HSPATTSHGNATVHPT-SNSTATSPG		154
SEQIDNO: 81	HSPATTSHGNATVHPT-SNSTATSPG		154
SEQIDNO: 82	---TTTSHQNTTVHPT-SNITATSPG		135
SEQIDNO: 83	---TTTSHGNATISHATVSPPT	---NG-TATSPRSST--VGPHPGPPPPSP--SPRSK	124
SEQIDNO: 84	HRPATTSHGNATVHPT-SNSTATSPG		154
SEQIDNO: 85	HRPTTSHGNATV-----SP-----TTNSPGEST	--VGPHPGPPPPSPSPSPST	128
SEQIDNO: 86	-APTTPGHRNTTIHPTTSNSTSNTTGTG	GKPHSTSY--TQPGPGPRPPPPSPGPGPQ	129
SEQIDNO: 87	---TTTSHGNTTVHPTTSNSTVTSFG		124
SEQIDNO: 88	---PTTGHGNVTVHPTTSNTTNTTTTGTS	---PGFST--STPHPGPPPPPPSPSPGSR	102
SEQIDNO: 89	---TTTSHGNATVHPT-SSSTATSPG		91
SEQIDNO: 90	HRPATTSHGNATVHPT-SNSTATSPG		154
SEQIDNO: 91	--YSTTSEGTAVTHGTTTSPRN		123
SEQIDNO: 92	--STTTSHGTSTPHKTTTRHPTTSHGTTTSHG	TSTGHWTARPTIRPGPPPPPP---SPG	145

*

* * * *

FIGURE 9 cont.

Replacement Sheet

LAMP HOMOMLOGY DOMAIN

2

```
SEQIDNO: 80      ETIGDYPWTWNGSQPCVHLQAQIQIRVMYTTQGGG-----EAWGISVLNPNK-TKVQ 204
SEQIDNO: 81      ETIGDYTWTWNGSQPCVHLQAQIQIRVMYTTQGGG-----EAWGISVLNPNK-TKVQ 204
SEQIDNO: 82      EAIGDYTWSNGSQPCVRLQAQIQIRVLYPTQGGG-----EAWGISVLNPNR-TKAQ 185
SEQIDNO: 83      GALGNYTWANGSQPCVQLQAQIQIRILYPIQGGRVKLKWGLKRAWGISVLNPNK-TKVQ 183
SEQIDNO: 84      ETIGDYMWTNGSQPCVHLQAQIQIRVMYTTQGGG-----EAWGISVLNPNK-TKVQ 204
SEQIDNO: 85      GALGNYTWTWNGSQPCVQLQAQIQIRILYLTQGGK-----KAWGLSVLNPNK-TKVQ 178
SEQIDNO: 86      DAIGDYTWTTSQPCCARLQARIQIGVVYPTQAGG-----QAWGISVLNPNS-TKPW 179
SEQIDNO: 87      EAIGDYYWTWNGSQPCVRLQAQIQIRVLYPTLGGG-----KAWGISVLNPNK-TKAQ 174
SEQIDNO: 88      EAVGNYTWTWNGSQPCVQLQAQIQIRVLYPTQGGG-----QAWGMSVLNPNR-TKAQ 152
SEQIDNO: 89      EAIGDYTWTWNGSQPCVQLQAQIQIRVLYPTQGGG-----EAWGISVLNPNK-TKAL 141
SEQIDNO: 90      ETIGDYMWTNGSQPCVHLQAQIQIRVMYTTQGGG-----EAWGISVLNPNK-TKVQ 204
SEQIDNO: 91      GAVGDYIGANGSQLCVHLRAQIQRMLVLYQASGGG-----KLWGI FVLNPNR-TMAQ 173
SEQIDNO: 92      KAVGNYSVTFGNSQPCRLLRAEIQLRWLVLYQAQEAGEAPPVSG-----AASFPPRP RPVA 199
                :*:.*:*** *:**:*.*:**:
```

LAMP HOMOMLOGY DOMAIN

```

3
SEQIDNO: 80  GSCEGAHPHLLLSF----PYGHLSTFGFMQDLQQ--KWVYLSYMAVEYNVSFPHAAQWTF 258
SEQIDNO: 81  GSCEGAHPHLLLSF----PYGHLSTFGFMQDLQQ--KAVYLSYMAVEYNVSFPHAAQWTF 258
SEQIDNO: 82  GGCEGTHSHLLLSF----PSGQLSFGEFKQDPLQ--SAVYLYMAVEYNVSFPQAVQWTF 239
SEQIDNO: 83  GGCDGTHPHLSLSF----PYGQLTFGEFKQDLHQSPSTVYLDYMAVEYNVSFPQAAQWTFM 239
SEQIDNO: 84  GSCEGAHPHLLLSF----PYGHLSTFGFMQDLQQ--RVVYLSYMAVEYNVSFPHAAQWTF 258
SEQIDNO: 85  GGDCSAHPHLLLSF----PYGQLTFGEFKQDRHQSHSTVYLYMAVEYNVSFPQAAQWTF 234
SEQIDNO: 86  GDCDGAHPHLLLSF----PFGQLSFGFTQEPQQ--GSVYLDYLAQYNVSFPQAAQWTF 233
SEQIDNO: 87  GGCA--HPHLLLSF----PYGQLSFGFKQEPQLQ--STVYLYNIAVEYNVSFPQAAQWTF 226
SEQIDNO: 88  GGCEGPRPHLLLSF----PYGQLSFGFKQDPGQGQSAVYLSYLAVEYNVSFPQARWTF 208
SEQIDNO: 89  GGCEGAHPHVRLSF----PYGQLTFGEFKQQPQE--STVYLYMAVEYNVSFPRAAQWTF 195
SEQIDNO: 90  GSCEGAHPHLLLSF----PYGHLSTFGFMQDLQQ--RVVYLSYMAVEYNVSFPHAAQWTF 258
SEQIDNO: 91  GNCEANHSSLLLSF----PNGKLIFGEFKQDSIK--KIVYLSHLATEFNVSFPSATRWIF 227
SEQIDNO: 92  GEGDGRSRTVPASAMTVEGGSRAFGAM----- 228

```

LAMP HOMOMLOGY DOMAIN

```

4
SEQIDNO: 80 AQNASLRDLQAPLGQSFSCSNSSIILSPAVHLDLLSLRLQAAQLPHTGVFGQSFSCPSDR 318
SEQIDNO: 81 AQNASLRDLQAPLGRSFSCSNSSIILSPAVHLDLLSLRLQAAQLPHTGVFGQSFSCPSDR 318
SEQIDNO: 82 VQNSSLRLDLQTPLGHSFSCRNASIIIVSPALHLDLLSLKLQAAQLSPSGAFGPSFSCPNDK 299
SEQIDNO: 83 AQNSSLRELQAPLGQSFCCGNASIVLSPAVHLDLLSLRLQAAQLPDKGHFGPCFSCNRDQ 299
SEQIDNO: 84 AQNASLRDLQAPLGQSFSCSNSSIILSPAVHLDLLSLRLQAAQLPHTGVFGQSFSCPSDR 318
SEQIDNO: 85 AQNSSLQELQAPLGQSFCCGNASIVLSPAIHLDLLSLRLQAAQLPDKGHFGPCFSCASDQ 294
SEQIDNO: 86 GQNASLRALQAPLGQSFSCRNASIIILTPALRLDLHLHLKLQAAQLPPSGAFGPSFSCPSEH 293
SEQIDNO: 87 VQNSSLRLDLQAPLGQRFSCRNASIALSPAFHLDLLSLKLQAAQLTPTGAFGPSFSCPSDQ 286
SEQIDNO: 88 AQNASLRDLQAPLGQSFSCRNASIAVSPALHLDLLSLRVQAAQLPRTGIFGPSFSCPADH 268
SEQIDNO: 89 VQNSSLRLDLQTPVGRSYSCRNASIIILSTAFHLDLLSLKLQAAQLPPTGNFGGPSFSCPSDQ 255
SEQIDNO: 90 AQNASLRDLQAPLGQSFSCSNSSIILSPAVHLDLLSLRLQAAQLPHTGVFGQSFSCPSDR 318
SEQIDNO: 91 VENSLLQDLQTPLGHSFSCNRNRSIALSPDIHLDLLSLQLQAAQLSSSGAFGAAFSCSADL 287
SEQIDNO: 92 -LGAEVRSRAPSLGRAGKTRL--RIHQPVVVLQ-----HTYYV----- 263

```

FIGURE 9 cont.

Replacement Sheet

Trans. Domain Cyto Tail

```

SEQIDNO: 80  -SILLPLIIGLILLGLLALVLIATFCIIRRRPSAYQAL 354
SEQIDNO: 81  -SILLPLIIGLILLGLLALVLIATFCIIRRRPSAYQAL 354
SEQIDNO: 82  -SILLPLIIGLILLGLLTLVLVTFCIIRRRPPTYQPL 335
SEQIDNO: 83  -SILLPLIIGLVLLGLLTLVLIAFCITRRRQSTYQPL 335
SEQIDNO: 84  -SILLPLIIGLVLLGLLALVLIATFCIVRRRPSAYQAL 354
SEQIDNO: 85  -SILLPLIIGLVLLGLLTLVLIAFCVTRRRQSTYQPL 330
SEQIDNO: 86  -FNLLPLIVGVISLGLLALALVTFCIIRRRPPTYQPL 329
SEQIDNO: 87  -SILLPLIIGLILLGLFALVLITFCVIRRRPPTYQAL 322
SEQIDNO: 88  PSILVPLIIGLILVGLLALVLVAFCIARRRPSAYQAL 305
SEQIDNO: 89  -TILLPLIIGLIFLGLLILVLVTFCIIRRRPPAYQPL 291
SEQIDNO: 90  -SILLPLIIGLVLLGLLALVLIATFCIVRRRPSAYQAL 354
SEQIDNO: 91  -NILVPLVVGVLVLLTLLIIVLSAFCISRRRPPAYQPL 323
SEQIDNO: 92  ----- 263

```

Macrosailin					
Accession No.	Species	SEQ ID NO:	Accession No.	Species	SEQ ID NO:
NP_001242.2	<i>H. sapiens</i>	80	XP_849733.1	<i>C. lupus familiaris</i>	86
XP_003315403.1	<i>P. troglodytes</i>	81	NP_001093232.1	<i>E. caballus</i>	87
NP_001039367.1	<i>B. taurus</i>	82	XP_002719034.1	<i>O. aries</i>	88
BAA23738.1	<i>M. musculus</i>	83	XP_003131995.1	<i>S. scrofa</i>	89
XP_014974003.1	<i>M. mulatta</i>	84	XP_003912313.1	<i>P. anubis</i>	90
NP_001026808.1	<i>R. norvegicus</i>	85	XP_001369761.1	<i>M. domestica</i>	91
			XP_001517723.2	<i>O. anatinus</i>	92

FIGURE 10: HUMAN LAMP5 ALIGNMENT WITH ORTHOLOGOUS SEQUENCES

	SIGNAL SEQUENCE	LAMP HOMOLOGY DOMAIN	
		1	
SEQIDNO: 93	MDLQGRGVPSIDRLRVLLMLEHTMAQIMAEQVENLSGLSTNPEKDI	FVVRENGTTCLMA	60
SEQIDNO: 94	MDLRGRAVPSIDRLRVLLMLEHTMAQIMAEQVENLSGLSTNPEKDI	FVVRENGTTCLMA	60
SEQIDNO: 95	MDLQGRAVPSVDRRLRVLLMLEHTMAQIMAEQVENLSGLSTNPEKDI	FVVRENGTTCLMA	60
SEQIDNO: 96	MDLRGRAVPSVYRLRVLLMLEHTMAQIMAEQVENLSGLSTNPEKDI	FVVRENGTTCLMA	60
SEQIDNO: 97	MDLRRRALLGVDGLRVLLMLEHTVTRIMAEQVENLSGLSTNPEKDI	FVVRENGTTCLMA	60
SEQIDNO: 98	MDLRVRTLLGGDRRLRILLMFHVMVQTVAEQVENLSGLSTNPEKDI	FVVRENGTTCLMA	60
SEQIDNO: 99	MDLRGRALLGGDRRLRILLMFHAMAQTVAEQVENLSGLSTNPEKDI	FVVRENGTTCLMA	60
SEQIDNO: 100	-----MAAGRLPGLLFLHAAARLAAEQVENLSGLSPNPEKDI	FVVRENRTTCLMA	52
SEQIDNO: 101	---MDYRACTSALRMPVLELLCTFSCNLAEQVENLSGLSSNPDKNI	FAIRENGTTCLMA	58
	. : *::: . ***** **;*::** *****		
		LAMP HOMOLOGY DOMAIN	
		2	
SEQIDNO: 93	EFAAKFIVPYDVWASNYVDLITEQADIALTRGAEVKGRCGHSQSE	LQVFWVDRAYALKML	120
SEQIDNO: 94	EFAAKFIVPYDVWASNYVDLITEQADIALTRGAEVKGRCGHSQSE	LQVFWVDRAYALKML	120
SEQIDNO: 95	EFAAKFIVPYDVWASNYVDLITEQADIALTRGAEVKGRCGHSQSE	LQVFWVDRAYALKML	120
SEQIDNO: 96	EFAAKFIVPYDVWASNYVDLITEQADISLTRGAEVKGHCGHNESE	LQVFWVDRAYALKML	120
SEQIDNO: 97	EFAAKFIVPYDVWASNYVDLITEQADISLTRGAEVKGHCGHDESE	LQVFWVDRAYALKML	120
SEQIDNO: 98	EFAAKFIVPYDVWASNYVDLITEQAEISLTRGAEVKGHCGHNESE	LEVFWVDHAYTLKML	120
SEQIDNO: 99	EFAAKFIVPYDVWASNYVDLITEQAEISLTRGAEVKGRCGHNESE	LQVFWVDRAYTLKML	120
SEQIDNO: 100	EFAAKFVVPYDVWASNYVDLITEQADIPLSRGAEMKGKCGTNESE	LEISWLERAYTLKLF	112
SEQIDNO: 101	EFSARILVPYEVPSNEVDWDLEEASIQLPDTEIRGKCWNNESEL	HLSWLDKAYTLKLF	118
	::*:*: * ** *::* * *::*:*** :***: *::*:***:::		
		LAMP HOMOLOGY DOMAIN	
SEQIDNO: 93	FVK-----ESHNMSKGPEATWRLSKVQFVYDSSEKTHF		153
SEQIDNO: 94	FVK-----ESHNMSKGPEATWRLSKVQFVYDSSEKTHF		153
SEQIDNO: 95	FVK-----ESHNTSKGPEATWRLSKVQFVYDSSEKTHF		153
SEQIDNO: 96	FVK-----ESRNASKGPEATWRLSKVQFVYDSSEKTHF		153
SEQIDNO: 97	FLK-----ESHNTPKGPEATWKLSKVQFVYDSSEKTHF		153
SEQIDNO: 98	FVK-----ESHNTSKGPEATWNLNVHVFVYDSSEKTHF		153
SEQIDNO: 99	FVK-----ESHNTSKGLEATWKLSKVQFVYDSSEKTHF		153
SEQIDNO: 100	FLKVRGCPRLGRGCAALRGPDQPCPPQEGHNTSRGPEAFWRLSRI	QFSYDTSERTYF	172
SEQIDNO: 101	FSK-----EGQDA--SKRSWKMSKIQFLYDPSEHTIF		149
	* * *::: . . *::*:** **;* * *		

FIGURE 10 cont.

Replacement Sheet

LAMP HOMOLGY DOMAIN

3

```

SEQIDNO: 93  KDAVSAGKHTANSHHLSALVTPAGKSYECQAQQTISLASSDPQKTVMILSAVHIQPFDI 213
SEQIDNO: 94  KDAVSAGKHTANSHHLSALVTPAGKSYECQAQQTISLASSDLQKTVMILSAVHIQPFDI 213
SEQIDNO: 95  KDAVSAGKHTANSHHLSALVTPAGKSYECQAQQTISLASSDPQKMVTMILSAVHIQPFDI 213
SEQIDNO: 96  KDAVSAGKHTANSHRLSALVTPAGKSYECQAQQTISLASSDPQKTVMILSAVHIQPFDI 213
SEQIDNO: 97  KDAVSAGKHTANSHHLSALVTPAGKSYECQAQQTISLASSDPQKTVMILSAVHIQPFDI 213
SEQIDNO: 98  KAPVKVNKYIASSHHLSALVTPAGMSYECQAQQTISLASSDPQKTVMILSAVHIQPFDI 213
SEQIDNO: 99  KDAVSAGKHTANSHHLSALVTPAGMSYECQAQQTISLASSDPQKTVMILSAVHIQPFDI 213
SEQIDNO: 100 KDAVSPGKHTASSHRLSALVTPAGKSYECQAQQTISLISSDHQKSVQLLLSEVRIQPFDI 232
SEQIDNO: 101 KSGARPGRHTANSHHLSLMVTPAGMSYECQATQRISTLTDHQQIVVLYLSEVHLQPFDI 209
* . . .: *.**:* :***** ***: * * * * *: * * * : * * *:*****

```

Trans. Domain

Cyto Tail

4

```

SEQIDNO: 93  ISDFVFSEEHKCPVDEREQLEETLPLILGLILGLVIMVTLAIYHVHHKMTANQVQIPRDR 273
SEQIDNO: 94  ISDFVFSEEHKCPVDEREQLEETLPLILGLILGLVIMVTLAIYHVHHKMTANQVQIPRDR 273
SEQIDNO: 95  ISDFVFSEEHKCPVDEREQLEETLPLILGLILGLVIVVTLTIYHVHHKMTANQVQIPRDR 273
SEQIDNO: 96  ISDFVFSEEHKCPVDEREQLEETLPLILGLILGLVIVVTLAIYHIHHKMTANQVQIPRDR 273
SEQIDNO: 97  ISDFVFSEEHKCPVDEREQLEETLPLILGLILGLVIVVTLVIYHIHHKMTANQVQIPRDR 273
SEQIDNO: 98  ISDFVFSEEHKCPVDEQEQLLEETLPLILGLILGLVIVITLVIYHIHHKMTANQVQIPRDR 273
SEQIDNO: 99  ISDFVFSEEHKCPVDEREQLEETLPLILGLILGLVIVITLVIYHIHHKMTANQVQIPRDR 273
SEQIDNO: 100 TADFVFSEEHKCPVDQREQLEETLPLILGLILGLVIVITLCVYHIHHKLTANQVQIPRDR 292
SEQIDNO: 101 KSDVFVYSEYKCPDQKQLEETLPLILGLTLGVAILIIVAVYHIHHKMTANQVQIPRDR 269
:***:***:***.*: :***** ***: .: : :*:***:*****

```

```

SEQIDNO: 93  SQYKHM 280
SEQIDNO: 94  SQYKHM 280
SEQIDNO: 95  SQYKHM 280
SEQIDNO: 96  SQYKHM 280
SEQIDNO: 97  SQYKHM 280
SEQIDNO: 98  SQYKHM 280
SEQIDNO: 99  SQYKHM 280
SEQIDNO: 100 SQYKHM 299
SEQIDNO: 101 SLYKHM 276
* *****

```

LAMP5

Accession No.	Species	SEQ ID NO:	Accession No.	Species	SEQ ID NO:
NP_036393.1	<i>H. sapiens</i>	93	NP_001076887.1	<i>B. taurus</i>	97
XP_514512.3	<i>P. troglodytes</i>	94	NP_083806.2	<i>M. musculus</i>	98
NP_001181627.1	<i>M. mulatta</i>	95	NP_001014205.1	<i>R. norvegicus</i>	99
XP_850634.1	<i>C. lupus familiaris</i>	96	XP_004935300.1	<i>G. gallus</i>	100
			NP_001090781.1	<i>X. tropicalis</i>	101

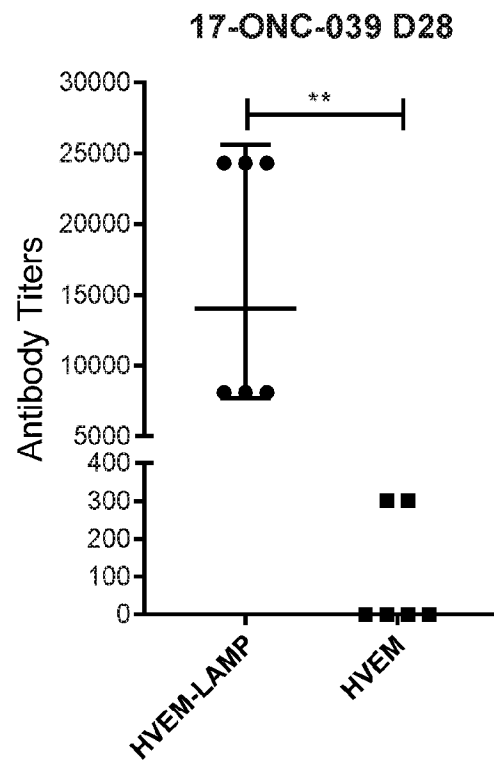


Figure 11 HVEM specific IgG antibody (day 28)

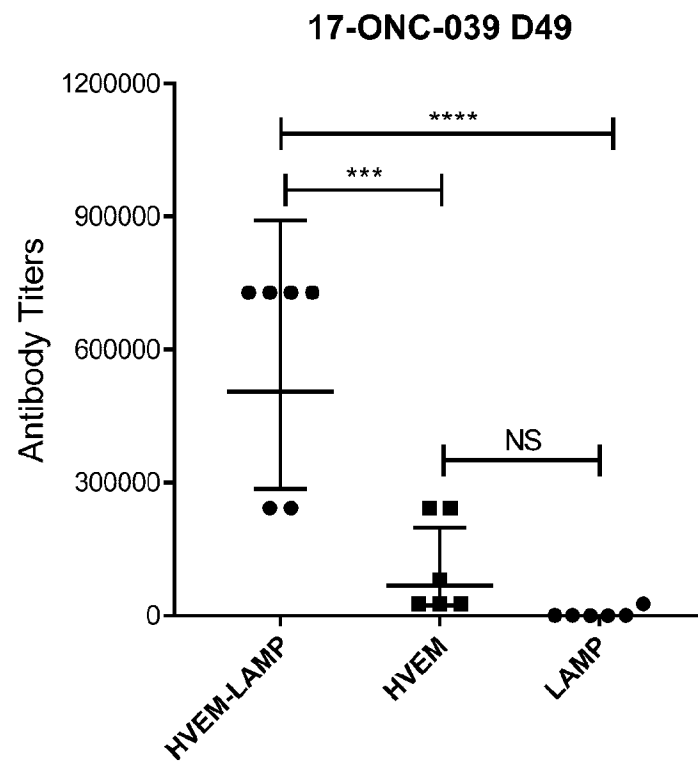


Figure 13

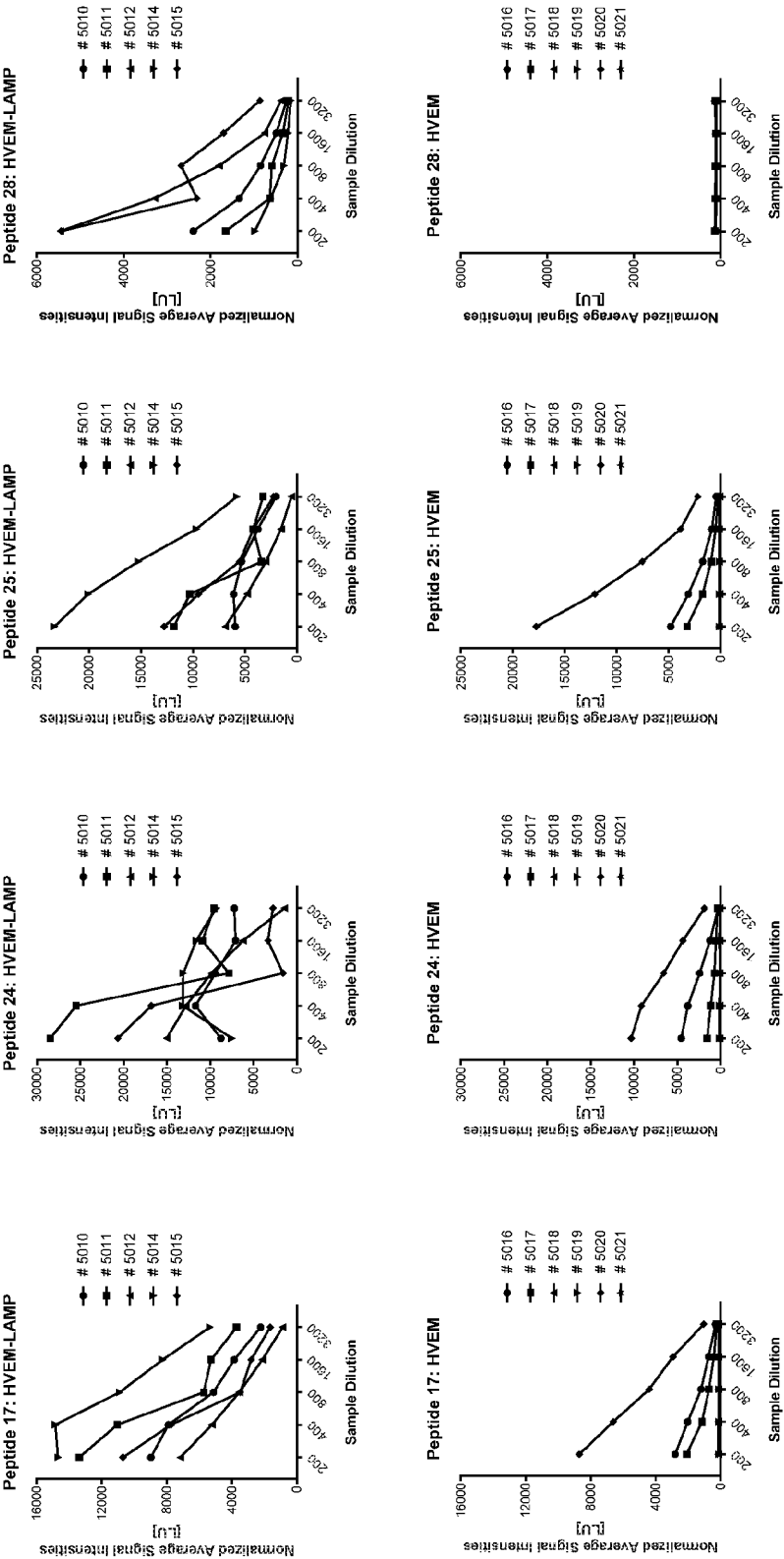


Figure 14

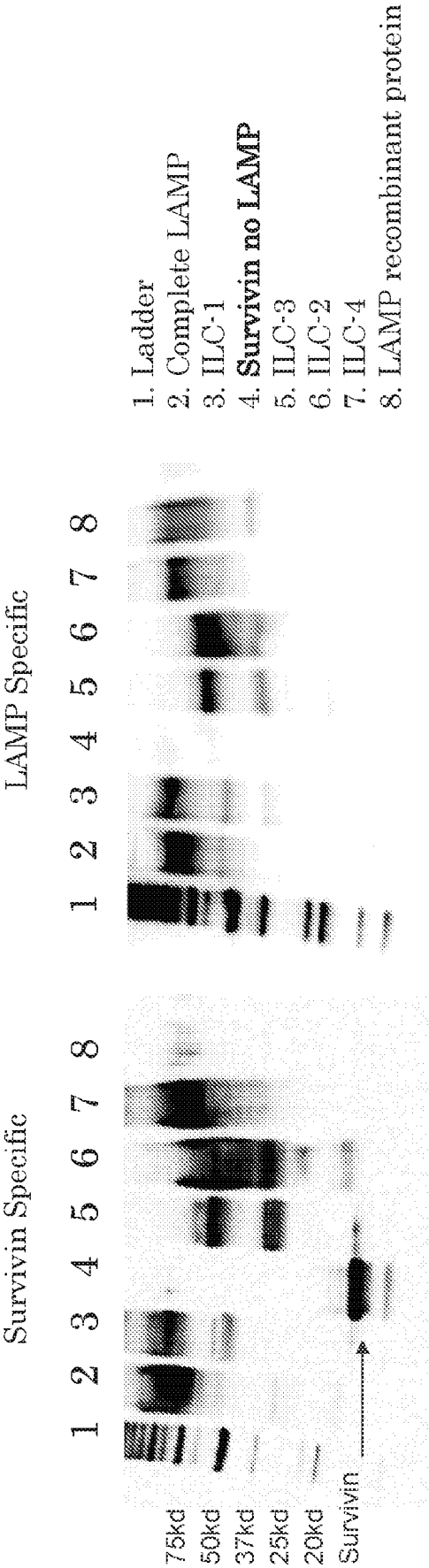


Figure 15

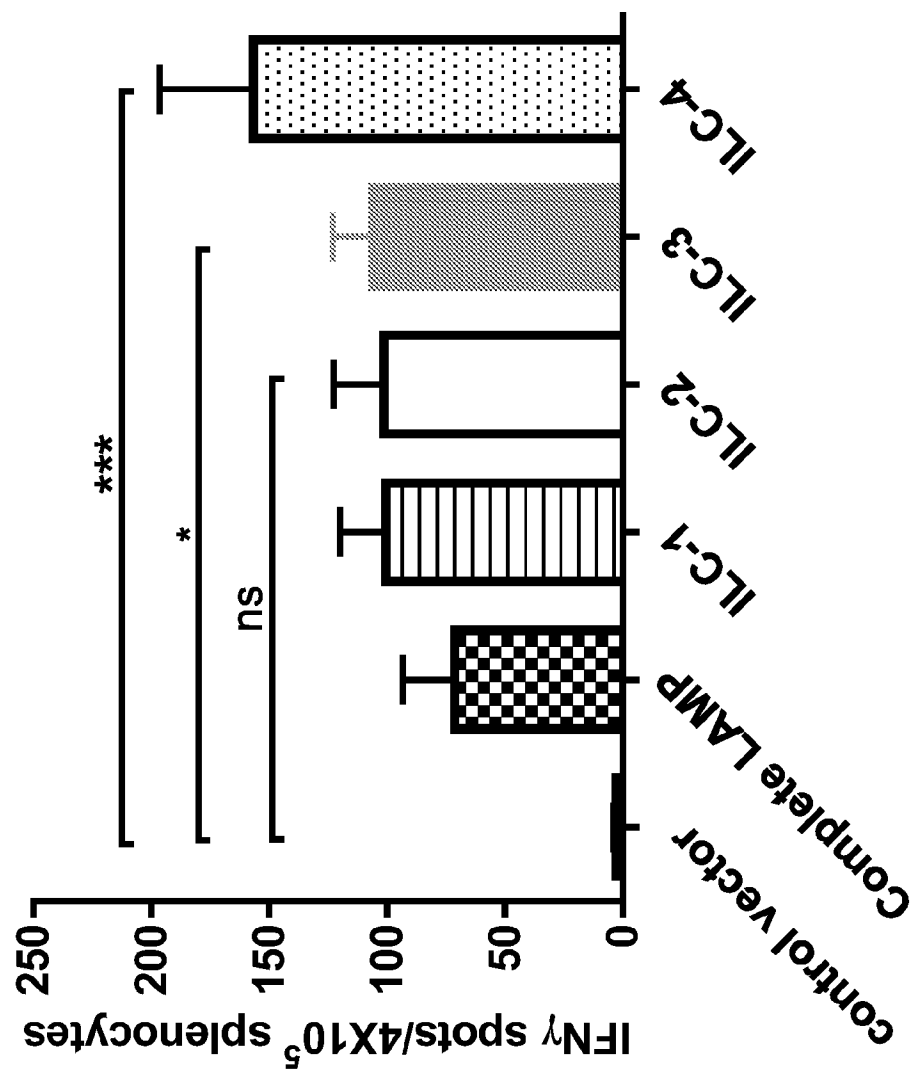


Figure 16

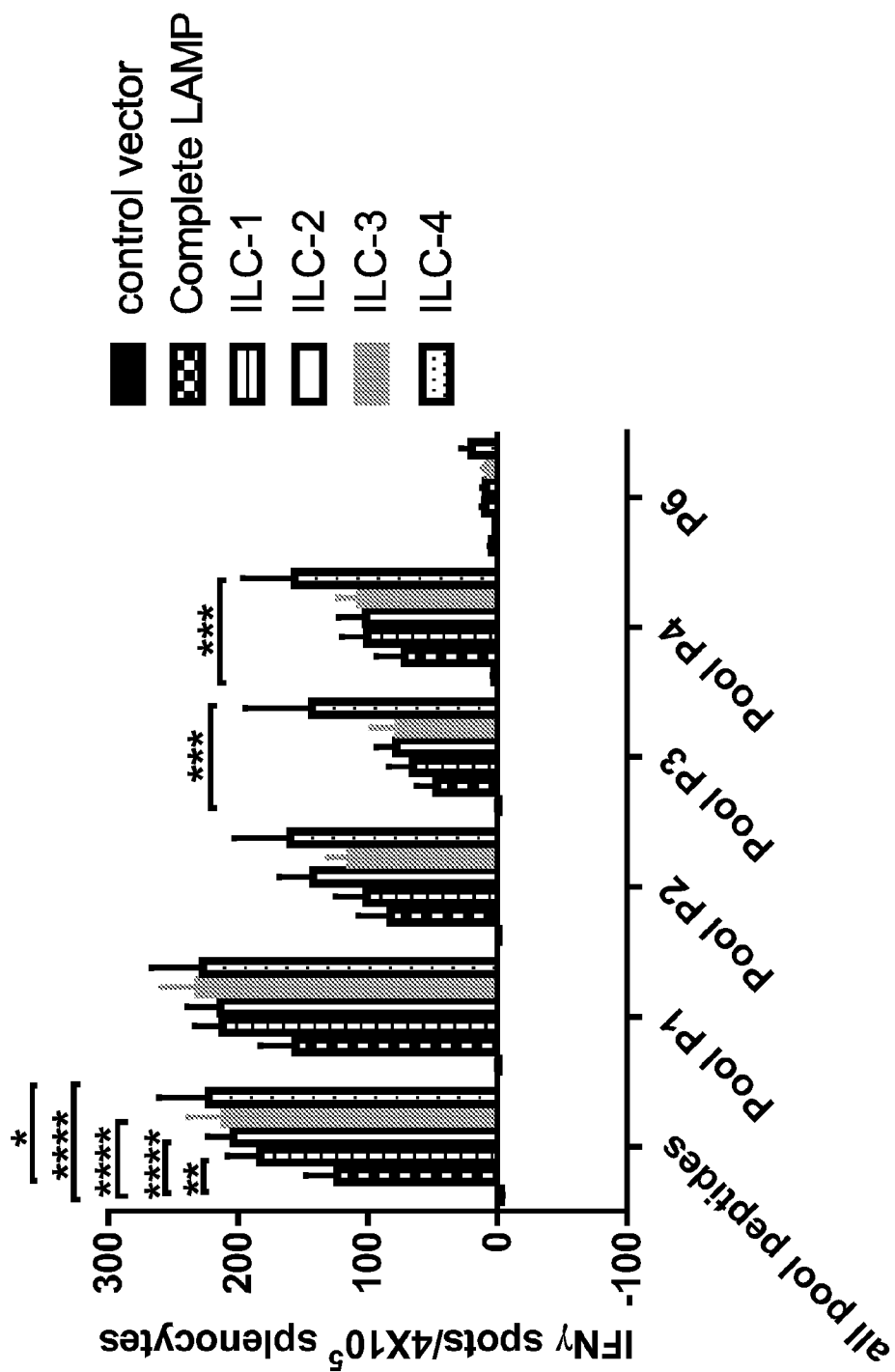


Figure 17

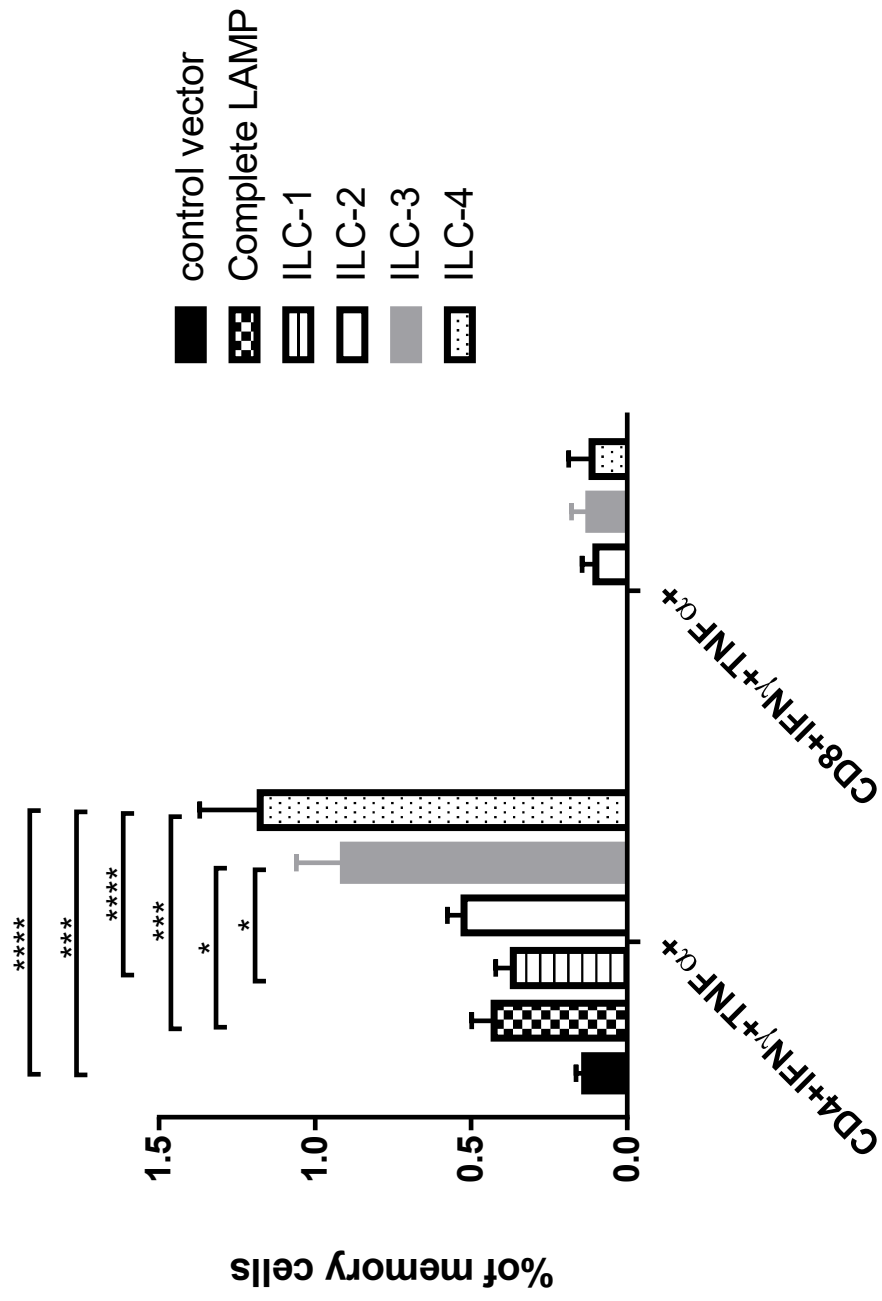


Figure 18

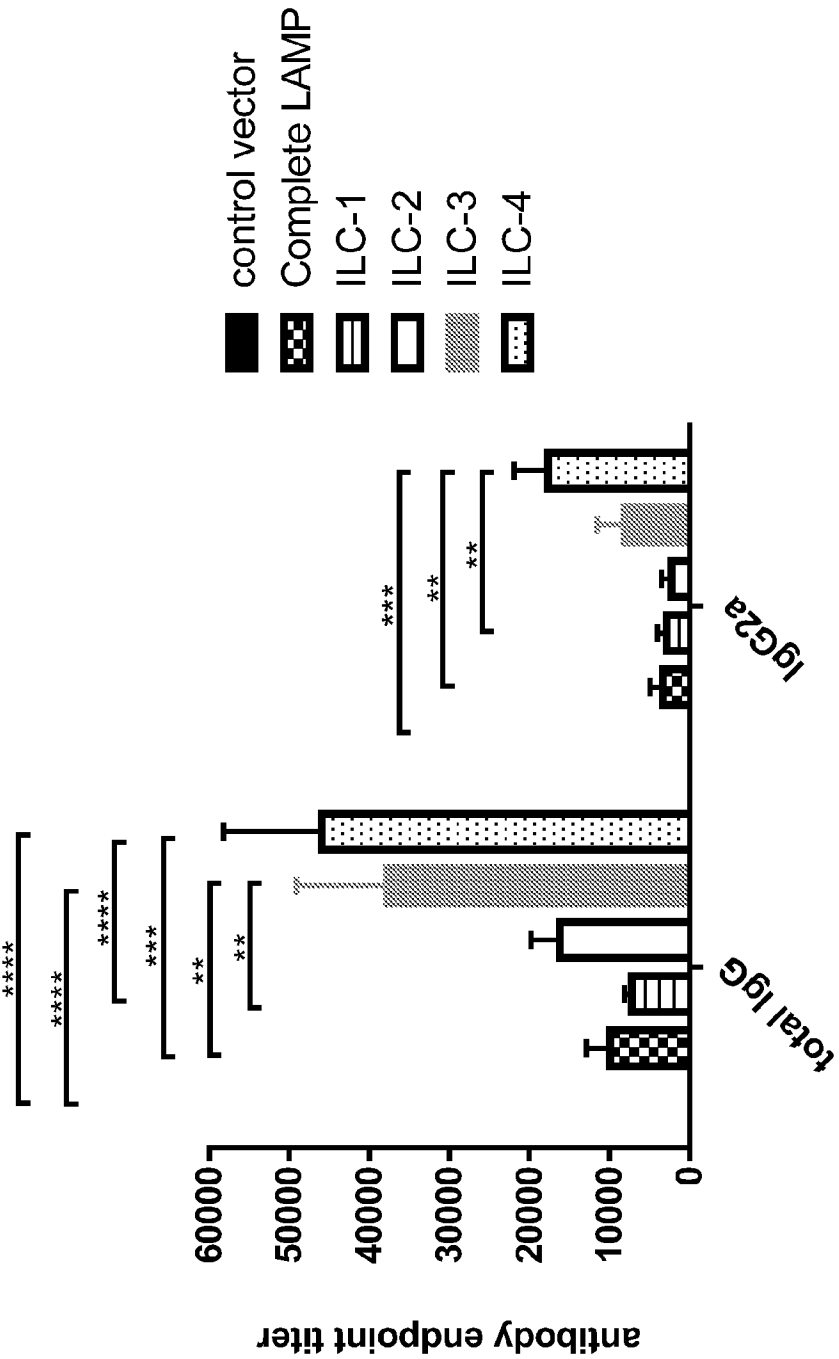


Figure 19

Survivin – Example of a Complete LAMP Construct (SEQ ID NO:193)

maprsarrpIIIIIIIIIIgImhcasaaMFMVKNGNGTACIMANFSAAFSVNYDTKSGPKNMTLDLPDATVVLNRSSCGKENTSDP
 SLVIAFGRGHTLTlnftrnatrysvqlmsfvynlsdthlfpnasskeiktvesitdiradidkkyrcvsgtqvhmnnvtvtlh
 datiqaylsnssfsrgetrceqdrpspttappappspspvpkpsvdkynvsgtngtcllasmglqlnltyerkdnttvtr
 llninpnktsasgscgaHLVtLeHsegtTVLLFqFGMNASSSRFFLQGIQLNTILPDARDPAFKAANGSLRALQATVGNSYK
 CNAEEHVRVTKAfSVNIFKVVWQAFKVEGGQFGSVEECLLDENSLE**MGAPTLPPAWQPFLKDHRIStfKNWPFLEGCACT**
TPERMAEAGFIHCPTENEPDLAQCFfCFKELEGWEPDDDPiEEHKKHSSGCAFLSVKKQFEELtLGEFLKDRERAKNKIA
KETNNKKKEFEETAKKVRRAIEQLAAMDEFTLIPIAVGGALAGLVLIvLIAYLVGRKRSHAGYQTI

Survivin – Example of a ILC-1 Construct (SEQ ID NO:194)

maprsarrpIIIIIIIIIIgImhcasaa**MGAPTLPPAWQPFLKDHRIStfKNWPFLEGCACTPERMAEAGFIHCPTENEPDLAQCFfCF**
FKELEGWEPDDDPiEEHKKHSSGCAFLSVKKQFEELtLGEFLKDRERAKNKIAKETNNKKKEFEETAKKVRRAIEQLAAM
DAMFMVKNNGTACIMANFSAAFSVNYDTKSGPKNMTLDLPDATVVLNRSSCGKENTSDPSLVIAFGRGHTLTlnftrn
 ATRYSVQLMSFVYNLSdthlfpnasskeiktvesitdiradidkkyrcvsgtqvhmnnvtvtlhdatiqaylsnssfsrgetr
 ceqdrpspttappappspspvpkpsvdkynvsgtngtcllasmglqlnltyerkdnttvtrllninpnktsasgscgaH
 LVtLeHsegtTVLLFqFGMNASSSRFFLQGIQLNTILPDARDPAFKAANGSLRALQATVGNSYKNAEEHVRVTKAfSVNIF
 KVVWQAFKVEGGQFGSVEECLLDENSMLIPIAVGGALAGLVLIvLIAYLVGRKRSHAGYQTI

Survivin – Example of a ILC-2 Construct (SEQ ID NO:195)

maprsarrpIIIIIIIIIIgImhcasaa**MGAPTLPPAWQPFLKDHRIStfKNWPFLEGCACTPERMAEAGFIHCPTENEPDLAQCFfCF**
KELEGWEPDDDPiEEHKKHSSGCAFLSVKKQFEELtLGEFLKDRERAKNKIAKETNNKKKEFEETAKKVRRAIEQLAAMDA
 MFMVKNGNGTACIMANFSAAFSVNYDTKSGPKNMTLDLPDATVVLNRSSCGKENTSDPSLVIAFGRGHTLTlnftrnat
 RYSVQLMSFVYNLSdthlfpnasskeiktvesitdiradidkkyrcvsgtqvhmnnvtvtlhdatiqaylsnssfsrgetrce
 QDLIPIAVGGALAGLVLIvLIAYLVGRKRSHAGYQTI

Survivin – Example of a ILC-3 Construct (SEQ ID NO:196)

maprsarrpIIIIIIIIIIgImhcasaaAMFMVKNNGTACIMANFSAAFSVNYDTKSGPKNMTLDLPDATVVLNRSSCGKENTSDP
 SLVIAFGRGHTLTlnftrnatrysvqlmsfvynlsdthlfpnasskeiktvesitdiradidkkyrcvsgtqvhmnnvtvtlh
 datiqaylsnssfsrgetrceQDLE**MGAPTLPPAWQPFLKDHRIStfKNWPFLEGCACTPERMAEAGFIHCPTENEPDLAQ**
CFfCFKELEGWEPDDDPiEEHKKHSSGCAFLSVKKQFEELtLGEFLKDRERAKNKIAKETNNKKKEFEETAKKVRRAIEQLAA
MDEFTLIPIAVGGALAGLVLIvLIAYLVGRKRSHAGYQTI

Survivin – Example of a ILC-4 Construct (SEQ ID NO:197)

maprsarrpIIIIIIIIIIgImhcasaaAMFMVKNNGTACIMANFSAAFSVNYDTKSGPKNMTLDLPDATVVLNRSSCGKENTSDP
 SLVIAFGRGHTLTlnftrnatrysvqlmsfvynlsdthlfpnasskeiktvesitdiradidkkyrcvsgtqvhmnnvtvtlh
 datiqaylsnssfsrgetrceQDLE**MGAPTLPPAWQPFLKDHRIStfKNWPFLEGCACTPERMAEAGFIHCPTENEPDLA**
QCfCFKELEGWEPDDDPiEEHKKHSSGCAFLSVKKQFEELtLGEFLKDRERAKNKIAKETNNKKKEFEETAKKVRRAIEQ
LAAMDEFTCLLASMGLQLNLtyerkdnttvtrllninpnktsasgscgaHLVtLeHsegtTVLLFqFGMNASSSRFFLQ
 IQLNTILPDARDPAFKAANGSLRALQATVGNSYKNAEEHVRVTKAfSVNIFKVVWQAFKVEGGQFGSVEECLLDENSMLIPIAVGGALAGLVLIvLIAYLVGRKRSHAGYQTI

Figure 20

>SEQIDNO:114; pp65; Accession No.: ABQ23593; Amino Acids 1-561

MESRGRRCPEMISVLGPISGHVLKAVFSRGDTPVLPHETRLLQTGIHVRVSPSLILVSQYTPDSTPCHRGDNQLQ
VQHTYFTGSEVENVSVNVHNPTGRSICPSQEPMSIYVYALPLKMLNIPSINVHYPSSAAERKHRHLPVADAVIHAS
GKQMWQARLTVSGLAWTRQQNQWKEPDVYYTSAFVFPTKDVALRHVVCAHELVCSEMENTRATKMQVIGDQYVKVYL
ESFCEDVPSGKLFMHVTLGSDVEEDLTMTTRNPQPFMRPHERNGFTVLCPKNMIKPGKISHIMLDVAFTSHEHFG
LCPKSIPGLSISGNLLMNGQQIFLEVQAIRETVELRQYDPVAALFFFDIDLLQRPQYSEHPTFTSQYRIQGKLE
YRHTWDRHDEGAAQGGDDVWTSGSDSDEELVTTERKTPRVTGGGAMAGASTSAGRKRKSASSATACTSGVMTRGRL
KAESTVAPEEDTDESDNEIHNPAVFTWPPWQAGILARNLVPMTATVQGQNLKYQEFFWDANDIYRIFAEELEGVWQ
PAAQPKRRRRHRQDALPGPCIASTPKKHRG

Representative pp65 LAMP Construct Insert: pp65 epitopes (highlighted above) separated by a GPGPG linker (SEQ ID NO:115)

LLQTGIHVRVSPSLGPGPGALPLKMLNIPSINVHGP GPGDQYVKVYLESFCEVDVGP GPGI IKPGKISHIMLDVAF
TSHGPGPGPQYSEHPTFTSQYRIQGKLGPGGPPWQAGILARNLVPMTGPGPKYQEFFWDANDIYRIFA

Representative pp65 LAMP Construct Insert: pp65 epitopes (highlighted above) separated by a PMGLP linker (SEQ ID NO:116)

LLQTGIHVRVSPSLPMGLPALPLKMLNIPSINVHMPMGLPDQYVKVYLESFCEVDVPMGLPI IKPGKISHIMLDVAF
TSHPMGLPPQYSEHPTFTSQYRIQGKLPMGLPPPWQAGILARNLVPMTMGLPKYQEFFWDANDIYRIFA

>SEQIDNO:117; gB; Amino Acids 1-906 of Accession No. P06473 Human herpesvirus 5 strain AD169

MESRIWCLVVCVNLICIVCLGAAVSSSSTSHATSSTHNGSHTSRTTSAQTRSVYSQHVTSSSEAVSHRANETIYNTTL
KYGDVVGVTNTTKYPYRVCSMAQGTDLIRFERNICTSMKPINEDLDEGIMVVYKRNIVAHFTKVRVYQKVLTFRRS
YAYIYTTYLLGSNTEYVAPPMWEIHHINKFAQCYSSYSRVIGGTVEFVAYHRDSYENKTMQLIPDDYSNTHSTRYVT
VKDQWHSRGSTWLYRETCNLNCLMTITTARSKYPYHFFATSTGDVVYISPFYNGTNRNASYFGENADKFFIFPNYT
IVSDFGRPNAAPEHRLVAFLE RADSVISWDIQDEKNVTCQLTFWEASERTIRSEAEDSYHFSSAKMTATFLSKKQ
EVNMSDSALDCVRDEAINKLQQIFNTSYNQTYEKGNSVVFETSGGLVVFQGIKQKSLVELERLANRSSLNITHR
TRRSTSDNNTTHLSSMESVHNLVYAQLQFTYDTRLGYINRALAQIAEAWCVDQRRTELVFKELSKINPSAILSAY
NKP IAA RFMGDVLGLASCVTINQTSVKVLRDMNVKESPGRCYSRPVVFIFNFANSSYVQYQGLGEDNEILLGNHRTE
ECQLPSLKIFIAGNSAYEYVDYLFKRMIDLSSISTVDSMIALDIDPLENTDFRVLELYSQKELRSSNVFDLEEIMR
EFNSYKQRVKYVEDKVVDPLPPYLKGLDDLMSGLGAAGKAVGVAIGAVGGAVASVVEGVATFLKNPFGAFTIILVA
IAVVIITYLIYTRQRRCTQPLQNLFPYLV SADGTTVTSGSTKDTSLQAPPSYEE SVYNSGRKGPGPPSSDASTAA
PPYTNEQAYQMLLALARLDAEQRAQQNGTDSL DGGTGTQDKGQKPNLLDRLRHRKNGYRHLKDSDEEENV

>SEQIDNO:118; gB fragment of Accession No. P06473 Human herpesvirus 5 strain AD169

VSSSSTSHATSSTHNGSHTSR TTTSAQTRSVYSQHVTSSSEAVSHRANETIYNTTLKYGDVVGVTNTTKYPYRVCSMAQ
GTDLIRFERNICTSMKPINEDLDEGIMVVYKRNIVAHFTKVRVYQKVLTFRRSYAYIYTTYLLGSNTEYVAPPMW
EIIHHINKFAQCYSSYSRVIGGTVEFVAYHRDSYENKTMQLIPDDYSNTHSTRYVTVKDQWHSRGSTWLYRETCNLN
CLMTITTARSKYPYHFFATSTGDVVYISPFYNGTNRNASYFGENADKFFIFPNYTIVSDFGRPNAAPEHRLVAFLE
RADSVISWDIQDEKNVTCQLTFWEASERTIRSEAEDSYHFSSAKMTATFLSKKQEVNMSDSALDCVRDEAINKLQQ
IFNTSYNQTYEKGNSVVFETSGGLVVFQGIKQKSLVELERLANRSSLNITHRTRRSTSDNNTTHLSSMESVHNL
VYAQLQFTYDTRLGYINRALAQIAEAWCVDQRRTELVFKELSKINPSAILSAYNKP IAA RFMGDVLGLASCVTIN
QTSVKVLRDMNVKESPGRCYSRPVVFIFNFANSSYVQYQGLGEDNEILLGNHRTEECQLPSLKIFIAGNSAYEYVDY
LFKRMIDLSSISTVDSMIALDIDPLENTDFRVLELYSQKELRSSNVFDLEEIMREFNSYKQRVKYVEDKVVDPLPP
YLKGLDDLMSGLGAAGKAVGVAIGAVGGAVASVVEGVATFLKNPTRQRRCTQPLQNLFPYLV SADGTTVTSGSTK
DTSLQAPPSYEE SVYNSGRKGPGPPSSDASTAAPPYTNEQAYQMLLALARLDAEQRAQQNGTDSL DGGTGTQDKGQ
KPNLLDRLRHRKNGYRHLKDSDEEENV

FIGURE 20 cont.

Replacement Sheet

SEQ ID NO:119: Representative gB LAMP Construct Insert: gB epitopes (highlighted above) separated by a GPGPG linker

T TSAQTRSVYSQHVTGPGPGQLIPDDYSNTHSTRYVGP GPGVSVFETSGGLVVFVWQGP GPGNSAYEYVDYLFKRMI
DLS

SEQ ID NO:120: Representative gB LAMP Construct Insert: gB epitopes (highlighted above) separated by a PMGLP linker

T TSAQTRSVYSQHVT^{PMGLP}QLIPDDYSNTHSTRYV^{PMGLP}VSVFETSGGLVVFVWQ^{PMGLP}NSAYEYVDYLFKRMI
DLS

>SEQIDNO:121; IE1; Amino Acids 1-491 of Accession No. P13202 Human herpesvirus 5 strain AD169

MESSAKRKMDPDNPDEGPSSKVPETPVTKATTF LQTMLRKEVNSQLSLGDPLFPPELAEESLKTFEQVTEDCNEN
PEKD^{VLAELVKQIKVRVDMVRHRIKEHMLKKYTQ}TEEKFTGAFNMMGGCLQNALDILDKVHEPF EEMKCIGLTMQS
MYENY^IVPEDKREMWMACIKELH^DVSKGAANKLGGALQAKARAK^KDELRRKMMYMCYRNIEFFTKNSAFPKTTNGC
SQAMAALQNLPCSPDEIMAYAQKIFKILDEERDKVLTHIDHIFMDILTTCTVETMCNEYKVTSDACMMTMYGGISL
LSEFCRVLCCYVLEETSVMLAKRPLITKPEVI^{SVMKRRIEEICMKVFAQYI}LGADPLRVCSPSVDDLRAIAEESDE
^{EEAIVAY}TLATAGVSSSDSLVSPPESPVPATIP LSSVIVAENSDQEESQSD EEEEEGAQEEREDTVS^{VKSEPVSE}
^{IEEVAPEEEEDG}AEEPTASGGKSTHPMVTRSKADQ

SEQ ID NO:122: Representative IE1 LAMP Construct Insert: IE1 epitopes (highlighted above) separated by a GPGPG linker

VLAELVKQIKVRVDMVRHRIKEHMLKKYTQ^{GPGPG}GIVPEDKREMWMACIKELH^{GPGPG}KDELRRKMMYMCYRNIEF
FTKNSAFPKTT^{GPGPG}SVMKRRIEEICMKVFAQYI^{GPGPG}PAIAEESDEEEAIVAY^{GPGPG}VKSEPVSEIEEVAPEE
EEDG

SEQ ID NO:123: Representative IE1 LAMP Construct Insert: IE1 epitopes (highlighted above) separated by a PMGLP linker

VLAELVKQIKVRVDMVRHRIKEHMLKKYTQ^{PMGLP}I^VVPEDKREMWMACIKELH^{PMGLP}KDELRRKMMYMCYRNIEF
FTKNSAFPKTT^{PMGLP}SVMKRRIEEICMKVFAQYI^{PMGLP}PAIAEESDEEEAIVAY^{PMGLP}VKSEPVSEIEEVAPEE
EEDG

>SEQIDNO:124; Morphological transforming region II; Amino acids 1-79 of AAA66543 Human betaherpesvirus 5

MLSVMVSSSLVLIVFFLGASEEAKPATTTTIKNTKPQCRPEDYATRLQDLRVTFHRVKPTLVGHVGTVYCDGLSFP
RVG

>SEQIDNO:125; Representative Morphological transforming region II LAMP Construct Insert

ATTTTIKNTKPQCRPEDYATRLQDLRVTFHRVKPTLVGHVGTVYCDGLSFP RVG

>SEQIDNO:126; US28; Amino Acids 1-364 of AMJ53524 Human betaherpesvirus 5

MTPTTTTAEALTTEFDYDEDATPCVFTDVLNQSKPVTFLYGVVFLFGSIGNFLVIFTITWRRRIQCSGDVYFINLA
AADLLFVCTLP LWMQYLLDHNSLASVPCTLLTACFYVAMFASLCFITEIALDRYYAIVYMRYPVKQACLF SIFWW
IFAVIIAIPHFMVVTKKDNQCMTDYDYLEVSYPIILNVELMLGAFVIPLSVISYCYRISRIVAVSQSRHKGRIVR
VLIAVVLVFIIFWLPYHLTLFVDTLKLKWISSSCEFEFSRLKRALILTESLAFCHCCLNPLLYVFGTKFRQELHC
LLAEFRQRLFSRDVSWYHSMFSR RSPSRRETSSDTLSDEVCRVSQIIP

>SEQIDNO:127; Representative US28 LAMP Construct Insert

FIGURE 20 cont.

Replacement Sheet

MTPTTTTAAELTTEFDYDEDATPCVF TDVLNQSKPVTTWRRRIQCSGDDHNSLEIALDRYYAIVMYRYPVKQTKKD
NQCMDYDYLEVSYPRISRIVAVSQSRHKGRIVRDTLKLKWISSSCEFEFSLKRGTKFRQELHCLLAEFRQLFS
RDVSWYHSMFSRRSSPSRRETSSDTLSDEVCRVSIIP

**>SEQIDNO:128 NP_000588.2 insulin-like growth factor-binding protein 2
isoform a precursor [Homo sapiens]**

MLPRVGC PALPLPPPPLLP LLLLLLGGASGGGGGARA EVLFRCPPTPERLAACGPPPVAPPA AVAAGGARM
PCAELVREPGCGCCSVCARLEGEACGVYTPRCGQGLRCYPHPGSELPLQALVMGEGTCEKRRDAEYGASPEQVADN
GDDHSEGG LVENHVDSTMNMLGGGGSAGRKPLKSGMKELAVFREKVTEQHRQMGKGKHHLGLLEPKLRPPPART
PCQQELDQVLERISTMRLPDERGP LEHLYSLHIPNCDKHGLYNLQCKMSLNQRGECWCVNPN TGKLIQGAPTIRG
DPECHLFYNEQQEARGVHTQRMQ

**>SEQIDNO:129 sp|P17150|IL10H_HCMVA Viral interleukin-10 homolog OS=Human
cytomegalovirus (strain AD169) GN=UL111A PE=1 SV=2**

MLSVMVSSSLVLIVFFLGASEEAKPATTTIKNTKPCRPEDYATRLQDLRVTFHRVKPTLQREDDYSVWLDGTVVK
GCWGCSVMDWLLRRYLEIVFPAGDHVYPGLKTELHSMRSTLESYKDMRQCPLLGC GDKSVISRLSQAERKSDNG
TRKGLSELDTLFSRLEEYLHSRK

**>SEQ ID NO:130 - Representative HCMVA Viral interleukin-10 LAMP Construct
Insert**

ATTTIKNTKPCRPEDYATRLQDLRVTFHRVKPTLQREDDYSVWLDGTVVKGCGWGCSVMDWLLRRYLEIVFPAGDH
VYPGLKTELHSMRSTLESYKDMRQCPLLGC GDKSVISRLSQAERKSDNGTRKGLSELDTLFSRLEEYLHSRK

**>SEQ ID NO:131; sp|F5HAM0|UL144_HCMVM Membrane glycoprotein UL144 OS=Human
cytomegalovirus (strain Merlin) GN=UL144 PE=3 SV=1**

MKPLVMLICFGVILLQLGVTKVCQHNEVQLGNECCPPCGLGQRVTKVCTERTSVTCTPCPN GTYVSGLYNCTDCTQ
CNVTQVMIRNCTSTNNTVCAPKNHTYFSTPGVQH KQRQNH TAHTV KQKSGRHTLAWLSL FIFLVGIILLILY
LIAAYRSERCQQCCSIGKIFYRTL

**>SEQIDNO:132: Representative HCMVM Membrane glycoprotein UL144 LAMP
Construct Insert**

KVCQHNEVQLGNECCPPCGLGQRVTKVCTERTSVTCTPCPN GTYVSGLYNCTDCTQCNVTQVMIRNCTSTNNTVCA
PKNHTYFSTPGVQH KQRQNH TAHTV KQKSGRHTAAYRSERCQQCCSIGKIFYRTL

**>SEQ ID NO:133; sp|Q6RJQ3|UL141_HCMVM Protein UL141 OS=Human cytomegalovirus
(strain Merlin) GN=UL141 PE=1 SV=1**

MCRRESLRTLPLWLFVLLSCPRLL EYSSSSFPFATADIAEKMWAENYETTSPAPVLVAEGEQVTIPCTVMTHSWPM
VSIRARFCRSHDGSDELILD AVKGHRLMNGLQYRLPYATWNFSQLHLGQIFSLTFNVSTDTAGMYECVLRNYSHGL
IMQRFVILTQLETLSRPDEPCCTPALGRYSLGDQIWSPTPWRLRNHDCGMYRGFQRNYFYIGRADAEDCWKPACPD
EEPDRCWTVIQRYRLPGDCYRSQPHPPKFLPVT PAPPADIDTGMSPWATRGIAAFLGFWSIFTVCFLCYLCYLQCC
GRWCPTPGRGRRGEGYRRLPTYDSYPGVKKMKR

> SEQ ID NO:134: Representative HCMVM Protein UL141 LAMP Construct Insert

DIAEKMWAENYETTSPAPVLVAEGEQVTIPCTVMTHSWPMVSIRARFCRSHDGSDELILD AVKGHRLMNGLQYRLP
YATWNFSQLHLGQIFSLTFNVSTDTAGMYECVLRNYSHGLIMQRFVILTQLETLSRPDEPCCTPALGRYSLGDQIW
SPTPWRLRNHDCGMYRGFQRNYFYIGRADAEDCWKPACDEEPDRCWTVIQRYRLPGDCYRSQPHPPKFLPVT P
PADIDTGMSPWATRYLQCCGRWCPTPGRGRRGEGYRRLPTYDSYPGVKKMKR

**>SEQIDNO:135: sp|P09727|US11_HCMVA Unique short US11 glycoprotein OS=Human
cytomegalovirus (strain AD169) GN=US11 PE=1 SV=1**

FIGURE 20 cont.

Replacement Sheet

MNLVMLILALWAPVAGSMPELSLTLEFDEPPPLVETEPLPPLSDVSEYRVEYSEARCVLRSGGRLEALWTLRGNLSV
PTPTPRVYYQTLEGYADRVPTFVEDVSESLVAKRYWLRDYRVPQRTKLVLFYFSPCHQCQTYTVECEPRCLVPWVP
LWSSLEDIERLLFEDRRLMAYYALTIKSAQYTLMMVAVIQVFWGLYVKGWLHRHFPWMFSDQW

>SEQIDNO:136: Representative HCMVA Unique short US11 glycoprotein LAMP Construct Insert

MPELSLTLEFDEPPPLVETEPLPPLSDVSEYRVEYSEARCVLRSGGRLEALWTLRGNLSVPTPTPRVYYQTLEGYAD
RVPTFVEDVSESLVAKRYWLRDYRVPQRTKLVLFYFSPCHQCQTYTVECEPRCLVPWVPLWSSLEDIERLLFEDRR
LMAYYALTIKSAQYHRHFPWMFSDQW

>SEQIDNO:137: tr|A0A0G2TM81|A0A0G2TM81_HCMV Envelope glycoprotein H OS=Human cytomegalovirus GN=UL75 PE=3 SV=1

MRPGLPSYLIVLAVCLLSHLLSPRYGAEVSEPLDKAFHLLLNTYGRPIRFLRENATQCTYNSSLRNSTVVRENAI
SFNFFQSYNQYYVFHMPRCLEFAGPLAEQFLNQVDLTETLERYQQRNLNTYALVSKDLASYRSFSQQLKAQDSLGEQP
TTVPPPIDLSIPHVWMPPTTPHGWTESHHTTSGLHRPHFNQTCILFDGHDLLFSTVTPCLHQGFYLIDELRYVKIT
LTEDFFVVTVSIDDDTPMLLIFGHLPRVLFKAPYQRDNFILRQTEKHELLVLVKKDQLNRHSYLKDPDFLDAALDF
NYLDLSALLRNSFHRYAVDVLKSGRCQMLDRRTVEMAFAYALALFAAARQEEAGAQVSVPRALDRQAALLQIQEFM
ITCLSQTTPRTTLLLYPTAVDLAKRALWTPNQITDITSLVRLVYILSKQNQQHLIPQWALRQIADFALKLHKTHLA
SFLSAFARQELYLMGSLVHSMVHTTERREIFIVETGLCSLAELSHFTQLLAHPHHEYLSDLTPCSSSGRRDHS
ERLTRLFPDATVPTTPTALSILSTMQPSLTETFPDLFCPLGESFSALTVEHVSYYVTNQYLIKGISYPVSTTV
VGQSLIITQDTSQSKCELTRNMHTTHSITAALNISLENCAFCQSALLEYDDTQGVINIMYMHDSDDVLFALDPYNE
VVVSSPRTHYLMLLKNGTVLEVTDVVVDATDSRLLMMSVYALSIIIGIYLLYRMLKTC

>SEQIDNO:138 HCMV Envelope glycoprotein H fragment

VSEPLDKAFHLLLNTYGRPIRFLRENATQCTYNSSLRNSTVVRENAISFNFFQSYNQYYVFHMPRCLEFAGPLAEQF
LNQVDLTETLERYQQRNLNTYALVSKDLASYRSFSQQLKAQDSLGEQPPTVPPPIDLSIPHVWMPPTTPHGWTE
TTSGLHRPHFNQTCILFDGHDLLFSTVTPCLHQGFYLIDELRYVKITLTEDFFVVTVSIDDDTPMLLIFGHLPRVL
FKAPYQRDNFILRQTEKHELLVLVKKDQLNRHSYLKDPDFLDAALDFNYLDLSALLRNSFHRYAVDVLKSGRCQML
DRRTVEMAFAYALALFAAARQEEAGAQVSVPRALDRQAALLQIQEFMITCLSQTTPRTTLLLYPTAVDLAKRALWT
PNQITDITSLVRLVYILSKQNQQHLIPQWALRQIADFALKLHKTHLASFLSAFARQELYLMGSLVHSMVHTTERR
EIFIVETGLCSLAELSHFTQLLAHPHHEYLSDLTPCSSSGRRDHSLERLTRLFPDATVPTTPTALSILSTMQPS
LTETFPDLFCPLGESFSALTVEHVSYYVTNQYLIKGISYPVSTTVVGQSLIITQDTSQSKCELTRNMHTTHSIT
AALNISLENCAFCQSALLEYDDTQGVINIMYMHDSDDVLFALDPYNEVVVSSPRTHYLMLLKNGTVLEVTDVVVDA
TDSRRMLKTC

>SEQIDNO:139 Representative HCMV Envelope glycoprotein epitopes (highlighted above)LAMP Construct Insert separated by a GPGPG linker

TYNSSLRNSTVVRENAISFNFFQSYNQYYVFHMPRGPGDGLTETLERYQQRNLNTYALVSKDLASYRSFSGPGPGS
HTTSGLHRPHFNQTCILFDGPGPQLNRHSYLKDPDFLDAALDF

>SEQIDNO:140 Representative HCMV Envelope glycoprotein epitopes (highlighted above)LAMP Construct Insert separated by a PMGLP linker

TYNSSLRNSTVVRENAISFNFFQSYNQYYVFHMPRPMGLPDLTETLERYQQRNLNTYALVSKDLASYRSFS^{PMGLP}
HTTSGLHRPHFNQTCILFD^{PMGLP}QLNRHSYLKDPDFLDAALDF

>SEQIDNO:141: sp|Q6SWP7|VIE2_HCMVT Viral transcription factor IE2 OS=Human cytomegalovirus (strain Towne) GN=UL122 PE=1 SV=1

MESSAKRKMDDPNPDEGPSSKVPREPETPVTKATTFLQTMLRKEVNSQLSLGDPLFPPELAEEESLKTFFERVTEDCNEN
PEKDVLAELGDILAQAVNHAGIDSSSTGPTLTTHSCSVSSAPLNKPTPTSVAVTNTPLPGASATPELSPRKKPRKT
TRPFKVIKPPVPAPIMPLIKQEDIKPEPFTIQRNKIIDTAGCIVISDSEEEQGEVETRGTASSPSTGSG
TPRVTSPTHPLSQMNHPPPLPDPLGRPDEDSSSSSSSSSSASDSESESEEMKCSSGGGASVTS^{RRGRVKIDEVSRMFR}NTNRSLEYKN

FIGURE 20 cont.

Replacement Sheet

LPFTIPSMHQVLDEAIKACKTMQVNNKGIQIIYTRNHEVKSEVDAVRCRLGTMCNLA LSTPFLMEHTMPVTHPPEV
 AQRADACNEGKAAWSLKLHQLCPRSSDYRNMIHAATPVDLLGALNLCPLMQKFPKQVMVRIESTNQGGF
 MLPIYETAAKAYAVGQFEQPTETPPEDLDLTLAIEAAIQDLRNKSQ

>SEQIDNO:142: Representative Viral transcription factor IE2 LAMP Construct
 Insert with IE2 epitopes (highlighted above) separated by a GPGPG linker
 RRGVVKIDEVSRMFRGPGPGGIQIIYTRNHEVKSEGPGPLSTPFLMEHTMPVTHPPEVA

>SEQIDNO:143: Representative Viral transcription factor IE2 LAMP Construct
 Insert with IE2 epitopes (highlighted above) separated by a PMGLP linker
 RRGVVKIDEVSRMFRPMGLPGIQIIYTRNHEVKSEPMGLPLSTPFLMEHTMPVTHPPEVA

>SEQIDNO:144 NP_937983.2 telomerase reverse transcriptase isoform 1 [Homo sapiens]

MPRAPRCRAVRSLRSHYREVLPATFVRRLGPGQWRLVQRGDPAAFRALVAQCLVCPWDARPPPAAPSFQVSC
 LKELVARVLQRLCERGAKNVLAFFGALLDGARGGPPEAFTTSVRSYLPNTVTDALRGSGAWGLLLRRVGDDVLVHL
 LARCALFVLVAPSCAYQVCGPPLYQLGAATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGSSA
 SRSLPLPKRPRRGAAPEPERTPVGQGSWAHPGTRGPPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVGRQHH
 AGPPSTSRPPRPWDTPCPPVYAETKHFYSSGDKEQLRPSFLLSSLRPSLTGARRLVETIFLGSRPWMPGTPRRLP
 RLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCP LRAAVTPAAGVCAREKPQGSVAAPPEEDTDPRRLVQLLRQHS
 SPWQVYGFVRACLRLVPPGLWGSRHNERFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRSPGVGCVPA
 EHLREEILAKFLHWMSSVYVVELLRSEFFYVTETTFQKNRLFFYRKS VWSKLQSIGIRQHLKRVQLRELSEAEVRQ
 HREARPAALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKALF SVLN YERARRPGLLGASVLGLD
 DIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTIPQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFK
 SHVSTLTDLQPYMRQFVAHLQETSPLRDAVVEIQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGS
 ILSTLLCSLCYGD MENKLFAGIRRDG LLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNLRKTVVNFVDE
 ALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTFNRGFKAGRNMRRLKFGVLRLLKCHSLFLD
 LQVNSLQTVCTNIYKILLQAYRFHACVLQLPFHQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGP
 LPSEAVQWLCHQAFLLKLTRHRVTYVPLLGLSLRTAQTLRSRKLPGTTLTALEAAANPALPSDFKTILD

>SEQIDNO:145: telomerase reverse transcriptase short fragment 1 168-1132
 amino acids that can be inserted into the Improved and Complete LAMP
 Constructs Described herein

YQVCGPPLYQLGAATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGSSASRSLPLPKRPRRGAA
 PEPERTPVGQGSWAHPGTRGPPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVGRQHHAGPPSTSRPPRPWD
 TPCPPVYAETKHFYSSGDKEQLRPSFLLSSLRPSLTGARRLVETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLE
 LLGNHAQCPYGVLLKTHCP LRAAVTPAAGVCAREKPQGSVAAPPEEDTDPRRLVQLLRQHS SPWQVYGFVRACLRR
 LVPPGLWGSRHNERFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRSPGVGCVPAEHLREEILAKFLHW
 LMSVYVVELLRSEFFYVTETTFQKNRLFFYRKS VWSKLQSIGIRQHLKRVQLRELSEAEVRQHREARPAALLTSRLRF
 IPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKALF SVLN YERARRPGLLGASVLGLDDI HRAWRTFVLRVRA
 QDPPPELYFVKVDVTGAYDTIPQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQ
 FVAHLQETSPLRDAVVEIQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTLLCSLCYGD MEN
 KLFAGIRRDG LLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNLRKTVVNFVDEALGGTAFVQMPAHGL
 FPWCGLLLDTRTLEVQSDYSSYARTSIRASLTFNRGFKAGRNMRRLKFGVLRLLKCHSLFLDLQVNSLQTVCTNIYK
 ILLQAYRFHACVLQLPFHQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL
 KLTRHRVTYVPLLGLSLRTAQTLRSRKLPGTTLTALEAAANPALPSDFKTILD

>SEQIDNO:146: telomerase reverse transcriptase fragment 2 that can be
 inserted into the Improved and Complete LAMP Constructs Described herein

MPRAPRCRAVRSLRSHYREVLPATFVRRLGPGQWRLVQRGDPAAFRALVAQCLVCPWDARPPPAAPSFQVSC
 LKELVARVLQRLCERGAKNVLAFFGALLDGARGGPPEAFTTSVRSYLPNTVTDALRGSGAWGLLLRRVGDDGPPLY

FIGURE 20 cont.

Replacement Sheet

QLGAATQARPPPHASGPRRRRLGCERAWNHHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRRGAAPEPERTVPG
 QGSWAHPGRTRGSPDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVGRQHHAGPPSTSRPPRPWDTPCPPVYAET
 KHFLYSSGDKEQLRPSFLLSSLRPSLTGARRLVETIFLGSRPWMPGTFRRLPRLPQRYWQMRPLFLELLGNHAQCP
 YGVLLKTHCPLRAAVTPAAGVCAREKPPQGSVAAPPEEDTDPRLRVQLLRQHSSPWQVYGFVRACLRLVPPGLWGS
 RHNERFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEILAKFLHWLMSVYVVEL
 LRSFFYVTETTFQKNRLFFYRKSVMWSKLQSIGIRQHLKRVQLRELSEAEVRQHREARPALLTSRLRFIPKPDGLRP
 IVNMDYVVGARTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPELYF
 VKVAITGAYDTIPQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLPYMRQFVAHLQETS
 PLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQENKLFAGIRRDGLLLRLVDDFLVTPHLTHAKT
 FLRTLVRGVPEYGCVVNLRKTVVNFVEDEALDTRTLEVQSDYSSYARTSIRASLTFNRGFKAGRNMRRKLFGLR
 LKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVLQLPFHQVWKNPTFFLRVISDTASLCYSILKAKNAGMS
 LGAKGAAGPLPSEAVQWLCHQAFLLKLTRHRVTYVPLLGSRLTAQTQLSRKLPGTTLTALEAAANPALPSDFKTIIL
 D

**>SEQIDNO:147 Survivin; Amino Acids 1-142 of Accession Number NP_001125727;
 baculoviral IAP repeat-containing protein 5**

MGAPTLPAPWQPFLLKDHRISTFKNWPFLGCACTPERMAEAGFIHCPTENEPDLAQCFFCFKELEGWEPDDDDPIEE
 HKKHSSGCAFLSVKKQFEELTLGEFLKLDREKAKNKIAKETNNKKKEFEETAKKVRRAIEQLAAMD

>SEQIDNO:148 1A9_A Chain A, Tetanus Neurotoxin C Fragment

MKNLDCWVDNEEDIDVILKKSTILNLDINNDIISDISGFNSSVITYPDAQLVPGINGKAIHLVNNESEVIVHKAM
 DIEYNDMFNNFTVSFWLRVPKVSASHLEQYGTNEYSIISMKKHSLSIGSGWSVSLKGNLIWTLKDSAGEVRQIT
 FRDLDPKFNAYLANKWVFIITNDRLSSANLYINGVLMGSAEITGLGAIREDDNNITLKLDRCNNNNQYVSIDKFRI
 FCKALNPKEIEKLYTSYLSITFLRDFWGNPLRYDTEYLLIPVASSSKDVQLKNITDYMILTANAPSYTNGKLNIIYR
 RLYNGLKFIKRYTPNNEIDSFVKSDFIKLYVSYNNEHIVGPKDGNAFNNLDRILRVGYNAPGIPLYKKMEAV
 KLRDLKITYSVQLKLYDDKNASLGLVGTHTNGQIGNDPNRDILIASNWFNHLKDKILGCDWYFVPTDEGWNTD

**> Representative Tetanus Neurotoxin C LAMP Construct Insert: Tetanus
 Neurotoxin C epitopes (highlighted above) separated by a GPGPG linker (SEQ
 ID NO:149)**

PGINGKAIHLVNNESESGPGPGFNNFTVSFWLRVPKVSASHLEQYGTGPGPGYVSIDKFRIFFCKALNPKEIEKLYT
 SYLSGPGPGILRVGYNAPGIPLYKKMEAVKLRDLK

**> Representative Tetanus Neurotoxin C LAMP Construct Insert: Tetanus
 Neurotoxin C epitopes (highlighted above) separated by a PMGLP linker (SEQ
 ID NO:150)**

PGINGKAIHLVNNESESPMGLPFNNFTVSFWLRVPKVSASHLEQYGTGPMGLPYVSIDKFRIFFCKALNPKEIEKLYT
 SYLSPMGLPILRVGYNAPGIPLYKKMEAVKLRDLK

>NP_001318.1 cancer/testis antigen 1 [Homo sapiens] (SEQ ID NO:151)

MQAEGRGTTGGSTGDADGPGPGIPDGPGGNAGGPGGAGATGGRGPRGAGAARASGPGGGAPRGPHGGAASGLNGCC
 RCGARGPESRLLEFYLAMPFATPMEAEELARRSLAQDAPPLVPVGVLLKEFTVSGNILTIRLTAADHRQLQLSISSC
 LQQLSLLMWITQCFLPVFLAQPPSGQRR

NY-ESO-1 1-155 of SEQ ID NO:151 (SEQ ID NO: 167)

MQAEGRGTTGGSTGDADGPGPGIPDGPGGNAGGPGGAGATGGRGPRGAGAARASGPGGGAPRGPHGGAASGLNGCC
 RCGARGPESRLLEFYLAMPFATPMEAEELARRSLAQDAPPLVPVGVLLKEFTVSGNILTIRLTAADHRQLQLSISSC
 LQQQRR

FIGURE 20 cont.

Replacement Sheet

NY-ESO-1 80-155 of SEQ ID NO:151 (SEQ ID NO: 168)

ARGPESRLLEFYLAMPFATPMEAEELARRSLAQDAPPLPVPGVLLKEFTVSGNILTIRLTAADHRQLQLSISSCLQQ
QRR

>AAA75493.1 HER2 receptor [Homo sapiens] (SEQ ID NO:152)

MELAALCRWGILLALLPPGAASTQVCTGTDMKRLRPASPETHLDMRLHLYQGCVVQGNLELTLYLPTNASLSFLQD
IQEVQGYVLIHNNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPGGLRELQLRSLTEILKGG
VLIQRNPQLCYQDTILWKDIFHKNNQLALTIDTNRSRACHPCSPMCKGSRGWGESSEDCQSLTRTVCAAGGCARCK
GPLPTDCCHEQCAAGCTGPKHSDCLACLFHNSGICELHCPALVTYNTDTFESMPNPEGRTYTFGASCVTACPYNYL
STDVGSCTLVCPHNNQEVTAEDGTQRCEKSKPCARVCYGLGMEHLREVRAVTSANIQEFAGCKKIFGSLAFLPES
FDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLPLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLR
SLRELGSGLALIHNNHLCFVHTVTPWDQLFRNPHQALLHTANRPEDECVGEGGLACHQLCARGHCWGPPTQCVNCS
QFLRGQECVEECRVLQGLPREYVNAHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPFFCVARCPSGVKPDL
SYMPIWKFPDEEGACQPCPINCETHSCVDLDDKGCPAEQASPLTSIVSAVVGILLVVVLGVVFGILIKRRQQKIRK
YTMRRLLQETELVEPLTPSGAMPNQAQMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRNTS
PKANKEILDEAYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCCLLDHVRENRRGLSGDQLLNWCMQIAKGMSYL
EDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEHADGGKVPKWMMALESILRRRFTHQSDVWSYGVT
WELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVV
IQNEDLGPASPLDSTFYRSLLEDDDMGDLVDAEYLVLPQQGFFCPDPAPGAGGMVHRRHRSSTRSGGDLTLGLE
PSEEEAPRSPLAPSEGAGSDVFDGDLGMGAAGLQSLPHTDPSPQLQRYSEDPTVPLPSETDGIVAPLTCSPQPEYV
NQPDVRPQPPSPREGPLPAARPAGATLERAKTSLPGKNGVVKDVFAFGGAVENPEYLTTPQGGAAPQPHPPAFSPA
FDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV

**Representative HER2 Construct (SEQ ID NO:153) comprising amino acids 23-652
and 690-1255 of SEQ ID NO:152**

TQVCTGTDMKRLRPASPETHLDMRLHLYQGCVVQGNLELTLYLPTNASLSFLQDIQEVQGYVLIHNNQVRQVPLQRL
LRIVRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFH
KNNQLALTIDTNRSRACHPCSPMCKGSRGWGESSEDCQSLTRTVCAAGGCARCKGPLPTDCCHEQCAAGCTGPKHS
DCLACLFHNSGICELHCPALVTYNTDTFESMPNPEGRTYTFGASCVTACPYNYLSTDVGSCTLVCPHNNQEVTAED
GTQRCEKSKPCARVCYGLGMEHLREVRAVTSANIQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFET
LEEITGYLYISAWPDSLPLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHNNHLCFVH
TVPWDQLFRNPHQALLHTANRPEDECVGEGGLACHQLCARGHCWGPPTQCVNCSQFLRGQECVEECRVLQGLPREY
VNAHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPFFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINC
THSCVDLDDKGCPAEQASPLTLQETELVEPLTPSGAMPNQAQMRILKETELRKVKVLGSGAFGTVYKGIWIPDG
ENVKIPVAIAVLRNTSPKANKEILDEAYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCCLLDHVRENRRGLSG
QDQLLNWCMQIAKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEHADGGKVPKWMMALESIL
RRRFTHQSDVWSYGVTWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWMIDSECRPRFRE
LVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDAEYLVLPQQGFFCPDPAPGAGGMVHRRH
RSSTRSGGDLTLGLEPSEEEAPRSPLAPSEGAGSDVFDGDLGMGAAGLQSLPHTDPSPQLQRYSEDPTVPLPSE
TDGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTSLPGKNGVVKDVFAFGGAVENPEYLT
TPQGGAAPQPHPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV

**Second Representative HER2 Construct (SEQ ID NO:154) comprising amino acids
23-632 of SEQ ID NO:152.**

TQVCTGTDMKRLRPASPETHLDMRLHLYQGCVVQGNLELTLYLPTNASLSFLQDIQEVQGYVLIHNNQVRQVPLQRL
LRIVRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFH

FIGURE 20 cont.

Replacement Sheet

KNNQLALTIDTNRSRACHPCSPMCKGSRGWGESSEDCQSLTRTVCAAGGCARCKGPLPTDCCHEQCAAGCTGPKHS
 DCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRTYTFGASCVTACPYNYLSTDVGSCTLVCPHNLQEVTAED
 GTQRCEKCSKPCARVCYGLGMEHLREVRAVTSANIQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFET
 LEEITGYLYISAWPDSLPLDSVFNQLQVIRGRILHNGAYSLLTQGLGISWLGLRSLRELGSGLALIHNNHLCFVH
 TVPWDQLFRNPHQALLHTANRPEDECVGEGLAGLQCLARGHCWGPGPTQCVNCSQFLRGQECVEECRVLQGLPREY
 VNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPFFCVARCPSGVKPDLSPYIWKFPDEEGACQPCPINC
 TH

**>NP_001973.2 receptor tyrosine-protein kinase erbB-3 isoform 1 precursor
 [Homo sapiens] (SEQ ID NO:155)**

MRANDALQVLGLLFLARGSEVGNQAVCPGTLNGLSVTGDAENQYQTLTKLYERCEVVMGNLEIVLTGHNADLSF
 LQWIREVTGYVLVAMNEFSTLPLPNLRVVRGTQVYDYGKFAIFVMLNYNTNSSHALLRQLRLTQLTEILSGGVYIEKN
 DKLCHMDTIDWRDIVRDRDAEIVVKDNGRSCPPCHEVCKGRCWGPGESEDCQTLTKTICAPQCNGHCFGNPNQCCH
 DECAGGCSGPQDTCFACRHFNDSGACVPRCPQLVYNKLTQLEPNPHTKYQYGGVCVASCPHNFVVDQTSVCRA
 CPPDKMEVDKNGLKMCEPCGGGLCPKACEGTGSGSRFQTVDSNIDGFVNCTKILGNLDFLITGLNGDPWHKIPALD
 PEKLNVFRTVREITGYLNIQSWPPHMHNFVFSNLTTIGGRSLYNRGFSLLIMKNLNVTSLGFRSLKEISAGRIYI
 SANRQLCYHHSNLNWKVLRGPTTEERLDIKHNRPRRDCVAEGKVCDFLCSSGGCWGPGPGQCLSCRNYSRGGVCVTH
 CNFLNGEPREFAEAEFCFSCHPECQPMEGTATCNGSGSDTCAQCAHFRDGPCHVSSCPHGVLAGKPIYKYPDVQN
 ECRPCHENCTQGCKGPELQDCLGQTLVLIGKTHLTALTVIAGLVVIFMMLGGTFLYWRGRRIQNKRAMRRYLERG
 ESIEPLDPSEKANKVLARIFKETELRKLKVLGSGVFGTVHKGWVWIEPEGESIKIPVCIKVIEDKSGRQSFQAVTDHM
 LAIGSLDHAHIVRLLGLCPGSSSLQVLTQYLPGLSLLDHVRQHRGALGPQLLLNWGVQIAKGMYYLEEHGMVHRNLA
 ARNVLLKSPSQVQVADFGVADLLPPDDKQLLYSEAKPIKWMALESIHFQKGYTHQSDVWSYGVTVWELMTFGAEPY
 AGLRLAEVDDLLEKGERLAQPQICTIDVYVMVMVKCWMIDENIRPTFKELANEFTRMARDPPRYLVIKRESGPGIAP
 GPEPHGLTNKKLEEEVELEPELDLDDLEAEEDNLATTTLGSALESLPVGTLNRPGRSQSLSPSSGYMPMNQGNLGE
 SCQESAVSGSSERCPRPVSLHPMPRGCLASESSEGHVTGSEAELEQKVSMSRCSRSPRPRGDSAYHSQRHSL
 TPVTPSPGLEEEDVNGYVMPDTHLKGTPSSREGTLSSVGLSSVLGTEEEDEDEEYEMNRRRRHSPHPPRPSS
 LEELGYEYMDVGSLSASLSTQSCPLHPVPIMPTAGTTPDEDEYEMNRQRDGGGPGGDYAAAGACPASEQGYEEM
 RAFQGPQHQAAPHVHYARLKTLSLEATDSAFDNPDYWHSRLFPKANAQRT

**Representative HER3 Construct (SEQ ID NO:156) comprising amino acids 20-643,
 665-1201, and 1209-1342 of SEQ ID NO:155**

SEVGNQAVCPGTLNGLSVTGDAENQYQTLTKLYERCEVVMGNLEIVLTGHNADLSFLQWIREVTGYVLVAMNEFS
 TLPLPNLRVVRGTQVYDYGKFAIFVMLNYNTNSSHALLRQLRLTQLTEILSGGVYIEKNDKLCHMDTIDWRDIVRDR
 AEIVVKDNGRSCPPCHEVCKGRCWGPGESEDCQTLTKTICAPQCNGHCFGNPNQCCHDECAGGCSGPQDTCFACR
 HFNDSGACVPRCPQLVYNKLTQLEPNPHTKYQYGGVCVASCPHNFVVDQTSVCVRACPPDKMEVDKNGLKMCEPC
 GGLCPKACEGTGSGSRFQTVDSNIDGFVNCTKILGNLDFLITGLNGDPWHKIPALDPEKLNVFRTVREITGYLNI
 QSWPPHMHNFVFSNLTTIGGRSLYNRGFSLLIMKNLNVTSLGFRSLKEISAGRIYISANRQLCYHHSNLNWKVLR
 GPTTEERLDIKHNRPRRDCVAEGKVCDFLCSSGGCWGPGPGQCLSCRNYSRGGVCVTHCNFLNGEPREFAEAEFCFS
 CHPECQPMEGTATCNGSGSDTCAQCAHFRDGPCHVSSCPHGVLAGKPIYKYPDVQNECRPCHENCTQGCKGPELQ
 DCLGQTLVLIGKTHLTQYWRGRRIQNKRAMRRYLERGESIEPLDPSEKANKVLARIFKETELRKLKVLGSGVFGTVH
 KGVWIEPEGESIKIPVCIKVIEDKSGRQSFQAVTDHMLAIGSLDHAHIVRLLGLCPGSSSLQVLTQYLPGLSLLDHVR
 QHRGALGPQLLLNWGVQIAKGMYYLEEHGMVHRNLAARNVLLKSPSQVQVADFGVADLLPPDDKQLLESEAKTPIK
 WMALESIHFQKGYTHQSDVWSYGVTVWELMTFGAEPYAGLRLAEVDDLLEKGERLAQPQICTIDVYVMVMVKCWMIDE
 NIRPTFKELANEFTRMARDPPRYLVIKRESGPGIAPGPEPHGLTNKKLEEEVELEPELDLDDLEAEEDNLATTTLG
 SALSLESLPVGTLNRPGRSQSLSPSSGYMPMNQGNLGESEAVSGSSERCPRPVSLHPMPRGCLASESSEGHVTGS
 EAELEQKVSMSRCSRSPRPRGDSAYHSQRHSLTPVTPSPGLEEEDVNGYVMPDTHLKGTPSSREGTLSSV
 GLSSVLGTEEEDEDEEYEMNPHPPRPSLEELGYEYMDVGSLSASLSTQSCPLHPVPIMPTAGTTPDEDEYEM
 NRQRDGGGPGGDYAAAGACPASEQGYEEMRAFGQGPQHQAAPHVHYARLKTLSLEATDSAFDNPDYWHSRLFPKANA
 QRT

FIGURE 20 cont.

Replacement Sheet

Second Representative Construct of HER3 (SEQ ID NO:157) comprising amino acids 20-643 of SEQ ID NO:155

SEVGN SQAVCPGTLNGLSVTGDAENQYQTLTKLYERCEVVMGNLEIVLTGHNADLSFLQWIREVTGYVLVAMNEFS
 TLPLPNLRVVRGTQVYDVGKFAIFVMLNYNTNSSHALRQLRLTQLTEILSGGVYIEKNDKLCHMDTIDWRDIVRDRD
 AEIVVKDNGRSCPPCHEVCKGRCWGPSEDCQTLTKTICAPQCNGHCFGNPNQCCHDECAGGCSGPQDTCFACR
 HFND SGACVPRCPQPLVYNKLTFLQLEPNPHTKYQYGGVCVASCPHNFVVDQTSVVRACPPDKMEVDKNGLKMCEPC
 GGLCPKACEGTGSGSRFQTV DSSNIDGFVNCTKILGNLDFLITGLNGDPWHKIPALDPEKLNVFRTVREITGYLNI
 QSWPPHMHNF SVFSNLTTIGGRSLYNRGFSLIMKNLNVTS LGFRSLKEISAGRIYISANRQLCYHHSNLTWKVLR
 GPTEERLDIKHNRPRRD CVAEGKVC DPLCSSGGCWGP GPGQCLSCRNYSRGGVCVTHCNFLNGEPREFAEAECS
 CHPECQPMEGTATCNGSGSDTCAQCAHFRDGP HCVSSCPHGVLAGKPIYKYPDVQNECRPCHENCTQGCKGPELQ
 DCLGQTLVLIGKTHLT

>NP_003811.2 tumor necrosis factor receptor superfamily member 14 isoform 1 precursor [Homo sapiens] (SEQ ID NO:158)

MEPPGDWGPPPWRSTPKTDVLRVLVLYLTFLGAPCYAPALPSCKEDEYPVGSECCPKCSPGYRVKEACGELTGTVCE
 PCPPGTYYIAHLNGLSKCLQCQMCDPAMGLRASRNC SRTENAVCGCSPGHFCIVQDGDHCAACRAYATSSPGQRVQK
 GGTESQDTLCQNCPPGTTFSPNGTLEECQHQT KCSWLVT KAGAGTSSSHVWWF LSGSLVIVIVCSTVGLIICVKRR
 KPRGDVVKVIVSVQRKRQEAEGEATVIEALQAPPDVTTVAVEETIPSTGRSPNH

Representative HVEM Construct (SEQ ID NO:159) comprising amino acids 39-202 of SEQ ID NO:158

LPSCKEDEYPVGSECCPKCSPGYRVKEACGELTGTVCEPCPPGTYYIAHLNGLSKCLQCQMCDPAMGLRASRNC SRT
 ENAVCGCSPGHFCIVQDGDHCAACRAYATSSPGQRVQKGGTESQDTLCQNCPPGTTFSPNGTLEECQHQT KCSWLVT
 KAGAGTSSSHV

HPV Constructs**Representative HPV 16 E6-E7 Construct (SEQ ID NO:164) separated by a GPGPG linker**

MHQKRTAMFQDPQESGRKLPQLCTELQTTIHDIILECVYCKQQLLRREYVDRDLCIVYRDGNPYAVCDKCLKFYSK
 ISEYRHYCYSLYGTTLEQQYNKPLCDLLIRCINCQKPLQRHLDDKKQRFHNIIRGRWTGRCMSCCRSSRTRRETQ~~LG~~
 GPGMHGDTPTLHEYMLDLQPETDLYGYGQLNDSSEEEDEIDGPAGQAEPDRAHYNIIVTFCKCDSTLRLCVQSTH
 VDIRTLEDLLMGTLGIVCPICSQKP

Representative HPV 18 E6-E7 Construct (SEQ ID NO:165) separated by a GPGPG linker

MARFEDPTRSGYKLPDLCTELNTSLQDIEITCVYCKTVLELTFEFDLFFVYRDSIPHAACHKCIDFYSRIRELR
 HYSDSVYGD TLEKLTNTGLYNLLIRCLRCQKPLLRLHNEKRRFHNIAGHYRGQCHSCCNRARQERLQRRRETQ~~VGP~~
 GPGMHGPKATLQDIVLHLEPQNEIPVDLLGHGQLSDSEEENDEIDGVNHQHLPARRAEPQRHTMLCMCKCEARIE
 LVVESSADDLRAFQQLFLNTLSFVCPWCASQQ

Representative HPV 16 E6 - linker - HPV 18 E6 - linker - HPV 16 E7 - linker - HPV 18 E7 Construct (SEQ ID NO:166)

MHQKRTAMFQDPQESGRKLPQLCTELQTTIHDIILECVYCKQQLLRREYVDRDLCIVYRDGNPYAVCDKCLKFYSK
 ISEYRHYCYSLYGTTLEQQYNKPLCDLLIRCINCQKPLQRHLDDKKQRFHNIIRGRWTGRCMSCCRSSRTRRETQ~~LG~~
 GPGMARFEDPTRSGYKLPDLCTELNTSLQDIEITCVYCKTVLELTFEFDLFFVYRDSIPHAACHKCIDFYSRIR
 ELRHYSDSVYGD TLEKLTNTGLYNLLIRCLRCQKPLLRLHNEKRRFHNIAGHYRGQCHSCCNRARQERLQRRRETQ
 V~~GPGPG~~

Replacement Sheet

VNHQHLPARRAEPQRHTMLCMCKCEARIELVVESSADDLRAFQQLFLNTLSFVCPWCASQQ

Sequences used to create the above constructs

HPV 16 E6 (SEQ ID NO:160) Human papillomavirus type 16

MHQKRTAMFQDPQESGRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDRDLCIVYRDGNFYAVCDKCLKFYSK
 ISEYRHYCYSLYGTTLEQQYNKPLCDLLIRCINCQKPLQRHLDKKQRFHNIRGRWTGRCMSCCRSSRTRRETQL

HPV 18 E6 (SEQ ID NO: 161) Human papillomavirus type 18

MARFEDPTRSGYKLPDLCTELNTSLQDIEITCVYCKTVLELTEVF EKDLFVVYRDSIPHAACHKCIDFYSRIRELR
HYSDSVYGDITLEKLTNTGLYNLLIRCLRCQKPLLRHLNEKRRFHNIAGHYRGQCHSCCNRRARQERLQRRRETQV

HPV 16 E7 (SEQ ID NO: 162) Human papillomavirus type 16

MHGDTPTLHEYMLDLQPETTDLYGYGQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCKCDSTLRLCVQSTHVDI
RTLEDLLMGTLGIVCPICSQKP

HPV 18 E7 (SEQ ID NO:163) Human papillomavirus type 18

MHGPKATLQDIVLHLEPQNEIPVDLLGHGQLSDSEEENDEIDGVNHQHLPARRAEPQRHTMLCMCKCEARIELVV
ESSADDLRAFQQLFLNTLSFVCPWCASQQ

EBV Antigens

EBV EBNA1 full length nuclear antigen EBNA-1 [Human gammaherpesvirus 4] (SEQ ID NO: 169)

MSDEGPGTGPNGNLGEKGDTSIGPESSGGSGPQRRGGDNHGRGRGRGRGRGGGRPGAPGGS GSGPRHRDGVRRPQKR
PSCIGCKGTHGGTGAGAGAGGAGAGGAGAGGGAGAGGGAGGAGGAGGAGAGGGAGAGGGAGGAGAGGGAGAGC
GAGGAGAGGGAGGAGGAGAGGGAGAGGGAGGAGAGGGAGGAGAGGGAGAGGAGGAGGAGAGGGAGGAGAGC
GAGAGGAGAGGAGAGGAGAGGAGGAGAGGAGGAGAGGAGGAGAGGGAGGAGAGGGAGGAGAGGAGGAGAGGAGC
AGGAGGAGAGGGAGAGGAGAGGGGRGRGSGRGRGSGRGRGSGRGRGSGRRRGRGRERARGSRERARGRGRGRGEKR
PRSPSSQSSSSGSPRRPPPPGRRPFFHPVGEADYFEYHQEGGPDGEPDVPPGAIEQQPADDPGEGPSTGPRQGQDG
GRRKKGGWFGKHRGQGSNPKFENIAEGLRALLARSHVERTTDEGTWVAGVFVYGSKTSLYNLRRTALAI PQCR
LTPLSRLPFGMAPGPGPQPGLRESIVCYFMVFLQTHIFAEVLKDAIKDLVMTKPAPTCNIRVTVC SFDDGVDLPP
WFPPMVEGAAAEGDDGDDGDEGGDGDEGEEGOE

EBV EBNA1 truncated nuclear antigen EBNA-1 [Human gammaherpesvirus 4] (SEQ ID NO: 170)

MSDEGPGTGPNGLGEKGDTSGPEGSGGSGPQRRGGDNHGRGRGRGRGRGGGRPGAPGSGSGPRHRDGVRRPQKR
PSCIGCKGTHRGRGSGGRGRGSGGRRGRGRERARGGSRRERARGRGRGRGEKRPSPSSQSSSSGSPRRPPPPGR
RPFHFHPVGEADYFEYHQEGGPDGEPDVPPGAIEQQPADDPGEGPSTGPRGQGDGGRKKGGWFGKHRGQGGSNPKF
ENIAEGLRALLARSHVERTTDEGTWVAGVFVYGGSKTSLYNLRRGTALAIQCRLTPLSRLPFGMAGPGPGPQGPL
RESIVCYFMVFLQTHIFAEVLKDAIKDLVMTKPAPTCNIRVTVCSFDDGVDLPPWFPPMVEGAAAEGDDGDDGDEG
GDGDEGEEOE

EBV gp350 ECD glycoprotein 350 [Human gammaherpesvirus 4] (SEQ ID NO: 171)

MEAAALLVCQYTIQSLIHILTGEDPGFFNVEIPEFFPYPTCNVCTADVNVTINFDVGGKKHQDLDFGQLTPHTKAVY
QPRGAFGGSENA TNLFLELLGAGELALTMRSKKLPINVTTGEEQQVSLESVDVYFQDVF GTMWCHHAEMQNVPVYL
IPETVPYIKWDNCNSTNITAVVRAOGLDVTLP LSLPTSAQDSNFSVKTEMLGNEIDIECIMEDGEISQVLP GDNKE

FIGURE 20 cont.

Replacement Sheet

NITCSGYESHVPSGGILTSTSPVATPIPGTGYAYSLRLTPRPVSRFLGNNISILYVFYSGNGPKASGGDYCIQSNIV
 FSDEIPASQDMPTNTTDITYVGDNATYSVPMVTSEDANSPNVTVTAFWAWPNNTETDFKCKWLTSGTPSGCENIS
 GAFASNRTFDITVSGLGTA PKTLIITRTATNATTTTHKVIFSKAPESTTTSTPLNTTGFA DPNTTTGLPSSTHVPT
 NLTA PASTGPTVSTADVTSPTPAGTTSGASPVTPSPSPWDNGTESKAPDMTSSTSPVTTPTPNATSPTPAVTTPTP
 NATSPTPAVTTPTPNATSPTLGKTSPTS AVTTPTPNATSPTLGKTSPTS AVTTPTPNATSPTLGKTSPTS AVTTPT
 PNATGPTVGETSPQANATNHTLGGTSPTPVVT SQPNATSAVTTGQHNI TSSSTSSMSLRPSSNPETLSPSTSDNS
 TSHMPLLTSAHPTGGENITQVTPASISTHHVSTSSPAPRPGTT SQASGPGNSSTSTKPGEVNVTKGTPPQNATSPQ
 APSGQKTAVPTVTSTGGKANSTTGGKHTTGHGARTSTEPTTDYGGDSITPRPRYNATTYLPSTSSKLRPRWFTS
 PPVTTAQATVPVPPTSQPRFSNLS

EBV LMP2 membrane protein LMP-2A [Human gammaherpesvirus 4] (SEQ ID NO: 172)
 MGSLEMVPMGAGPPSPGGDPDGYDGGNNSQYPSASGSSGNTPTPNDEERESNEEPPPPYEDPYWNGDRHSDYQP
 LGTQDQSLYLGLQHDGNDGLPPPPYSPRDDSSQHIYEEAGRGSMPVCLPVIVAPYLFWLAAIAASCFTASVSTV
 TATGLALSLLLLAAVASSYAAAQRKLLTPVTVLTAVVTFFAICLTWRIEDPPFNSSLFALLAAAGGLQGIYVLVML
 VLLILAYRRRWRLTVCGGIMFLACVLVLIVDAVLQLSPLLGA VTTVVSMTLLLLAFVLWLSSPGGLGTLGAALLTL
 AAALALLASLILGTLNLTTFLLMLLWTLVLLICSSSCSSCPLSKILLARLFYALALLLASALIAGGSILQTNF
 KSLSSTEFIPNLF CMLLLIVAGILFILAILTEWGSNRTYGPVFMCLGGLLTMVAGAVWLTVMSTLLSAWILTAG
 FLIFLIGFALFGVIRCCRYCCYCYCTLESEERPPTPYRNTV

GCP3 glypican-3 isoform 2 precursor [Homo sapiens] (SEQ ID NO: 173)
 AQPPPPPPDATCHQVRSFFQRLQPLKWPETPVPGSDLQVCLPKGPTCCSRKMEEKYQLTARLNMEQLLQSASME
 LKFLIIQNAAVFQEA FEIVVRHAKNYTNAMFKNNYPSLTPQAFEFVGEFFTDVSLYILGSDINVDDMVNELFDSL
 FVIY TQLMNPGLPDSALDINECLRGARRDLKVFGNFPKLIMTQVSKSLQVTRIFLQALNLGIEVINTTDHLKFSK
 CGRMLTRMWYCSYQGLMMVKPCGGYCNVVMQGC MAGVVEIDKYWREYILSLEELVNGMYRIYDMENVLLGLFSTI
 HDSIQYVQKNAGKLT TIGKLC AHSQQRQYRSAYYPEDLFDKVKLVKVAHVEHEETLSSRRREL IQKLKSFISFYS
 ALPGYICSHSPVAENDTLCWNGQELVERY SQKAARNGMKNQFNHELKMKGPEPVVSQIIDKLKHINQLLR TMSMP
 KGRVLDKNLDEEGFESGDCGDDDEDECIGSGDGMIVKNQLRFLAELAYDLDDVDDAPGNSQQATPKDNEISTFHN
 L GNVHSPLK

Middle S Protein (HBV) middle envelope protein [Hepatitis B virus] (SEQ ID NO: 174)
 MQWNSTTFHQTLQDPRVRGLYFPAGGSSSGTVNPVLTTASPLSSIFSRIGDPALNMENITSGTIPQSLDSWWTSLN
 FLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRDYQGMPLVCPLIPGSSTTSTGPCRTCMTTAQGTSMYP
 SCCCTKPSDGNCTCIPSSWAFGKFLWEWASARYWGPSX

X Protein (HBV) X protein [Hepatitis B virus] (SEQ ID NO: 175)
 MAARLCCQLDPARDVLCLRPVGAESRGRPLSGPLGALPSPSPSAVPADHGAHLSLRGLPVCA FSSAGPCALRFTSA
 RRMETTVNAHQILPKVLHKRTFGLSAMSTTDLEAYFKDCVFKDW

TIGIT hypothetical protein, partial [Homo sapiens] 99% homology to TIGIT
 isoform 6, partial [Pongo abeliii] (SEQ ID NO: 176)
 MMTGTIETTGNISA EKGSII LQCHLSSTTAQVTQVNWEQQDQLLAICNADLGWHISPSFKDRVAPGPGLGLTLQS
 LTVNDTGEYFCIYHTYPDGTYTGRIFLEVLESSVAEHGARFQIP

TEM8 anthrax toxin receptor 1 isoform 1 precursor [Homo sapiens] (SEQ ID NO: 177)
 EDGGPACYGGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIRQGLEE
 LQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALT D GELHEDLFFYSEREANRSRDLGAIVYCVGVKDFN
 ETQLARIADSKDHVPVNDG FQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRNGNFRHARNVDRVLC SFK
 INDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFISSSVITTTTHCS DGS

FIGURE 20 cont.

Replacement Sheet

TEM1 endosialin precursor [Homo sapiens] (SEQ ID NO: 178)

QDPWAAEPRAACGPSSCYALFPRRTFLEAWRACRELGGDLATPRTPEEAQRVDSL VGAGPASRLWIGLQRQARQ
CQLQRPLRGFTWTTGDQDTAFTNWAQPASGGPCPAQRCVALEASGEHRWLEGSCTLAVDGYLCQFGFEGACPALQD
EAGQAGPAVYTTTFHLVSTEFEWLFPFGSVAAVQCQAGRASLLCVKQPEGGVGWSRAGPLCLGTGCS PDNNGGCEHE
CVEEVDGHVSCRCTEGFRLAADGRSCEDPCAQAPCEQQCEPGGPQGYSCHCRLGFRPAEDDPHRCVDTDECQIAGV
CQQMCVNYVGGFECYCSEGHELEADGISCSPAGAMGAQASQDLGDELDDGEDEDEDEAWKAFNGGWTEMPGILW
MEPTQPPDFALAYRPSFPEDREPQIPYPEPTWPPPLSAPRVPHYSSVLSVTRPVVVSATHEPTLPSAHQPPVIPATH
PALSRDHQIPVIAANYPDLP SAYQPGILSVSHAQPPAHQPPMISTKYPELFP AHQSPMFPDTRVAGTQTTHLPG
IPPNHAPLVTTLGAQLPPQAPDALVLRQTATQLPIIPTAQPSLTTTSRSPVSPAHQISVPAATQPAALPTLLPSQS
PTNQTSPISPTHPSKAPQIPREDGPSK LALWLPSPAPTAAPTALGEAGLAHSQRDDRWLYCTRCGPHAPNKRI
TDCYRWVIHAGSKSPTEPMPPRGS LTGVQTCRTSV

HER2 ECD+TM v-erb-b2 erythroblastic leukemia viral oncogene homolog 2,
neuro/glioblastoma derived oncogene homolog, partial [synthetic construct]
(SEQ ID NO: 179)

TQVCTGTDMKRLRPASPETHLDMRLHLYQGCQVVGQNL ELYLPTNASLSFLQDIQEVQGYVLI AHNQVRQVPLQR
LRIVRGTLQFEDNYALAVLDNGDPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFH
KNNQLALTLIDTNRSRACHPCSPMCKGSRWGESSDCQSLTRTV CAGGCARCKGPLPTDCCHEQCAAGCTGPKHS
DCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEG RYTFGASCVTACPYNYLSTDVGSCTLVCP LHNQEVTAED
GTQRCEKCSKPCARVCYGLGMEHLREVRAVTSANIQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFET
LEEITGYLYISAWPDSLPLDSVFQNLQVIRGRILHNGAYS LTLQGLGISWLGLRSLRELGSGLALIH HNTLHLCFVH
TVPWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGP GPTQCVNCSQFLRGQECVEECRVLQGLPREY
VNARHCLPCHPECQPQNGSVTCFGPEADQC VACAHYKDPFFCVARCPSGVKPDL SYMPIWKFPDEEGACQPCP INC
THSCVDLDDKGCPAEQRASPLTSIVSAVVGILLVVVLGVVFGILI

CEA carcinoembryonic antigen-related cell adhesion molecule 5 isoform 1
preproprotein [Homo sapiens] (SEQ ID NO: 180)

KLTIESTPFNVAEGKEVLLLVHNLPQH LFGYSWYKGERVDGNRQIIIGYVIGTQQATPGPAYSGREIIYPNASLLIQ
NIIQNDTGFTLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWVWNNQSLP
VSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAPTISPLNTSYRSGENLNLSCHAA
SNPPAQYSWFVNGTFQOSTQELFIPNITVNNSGSYTCQAHNSDTGLNRTT VTITVYAEPPKPFITSNNSNPVEDE
DAVALTCEPEIQNTTYLWVWNNQSLPVSPRLQLSNDNRTLTL LSVTRNDVGPYECGIQNKLSVDHSDP VILNVLYG
PDDPTISPSYTYRPGVNL SLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQANN SASGHSRTT
VKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWVWNGQSLPVSPRLQLSNGNRTLTLFNVTRNDA
RAYVCGIQNSVSANRSDPVTLDVLYGPDTP IISPPDSSYLSGANLNLSCHSASNPS PQYSWRINGIPQQHTQVLF I
AKITPNNNGTYACFVSNLATGRNNSIVKSITVSASGTSPGLSA

TARP TCR gamma alternate reading frame protein isoform 2 [Homo sapiens] (SEQ ID NO: 181)

MKTNDTYMKFSWLTVP EKSLDKEHRCIVRHENNKNGVDQEIIFFPIKTDVITMDPKDNCSKDANDTLLLQLTNTSA

PROSTEIN solute carrier family 45 member 3 [Homo sapiens] (SEQ ID NO: 182)

MVQRLWVSRLLRHRKAQLPPLLLLEVGVEEKSASDHWRGRYGRRRPLAGLLCPDPRPTPLEALLSDLFRDPD HCRQA
DWDTSALAPYLGTEEC EEAALGPTEPAEGLSAPSLSPHCCPCRARLAFRNLGALLPRLHQLCCRMPTLRRLVGE
GLYQGVPR AEPGTEARRHYDEGVRRLVQRFGTRASVAVVTASYHREKQVFLPKYRGDTGGASSEDSLMTSFLPGPK
PGAPFPNGHV GAGGSGLLPPPPALCGASACDVSVRVVVGEPTEARVVPGRGICLDLAILDSAFLLSQVAPSLFMGS
IVQLSQSVTFDKSDLAKYSA

PSMA prostate-specific membrane antigen [Homo sapiens] (SEQ ID NO: 183)

Replacement Sheet

MWNLLHETDSAVATARRPRWLCKSSNEATNITPKHNMKAFLDELKAENIKKFLYNFTQIPHLAGTEQNFQLAKQIQ
SQWKEFGLDSVELAHYDVLSSYPNKTHPNYISIINEDGNEIFNTSLFEP PPPGYENVSDIVPPFSAFSPQGMPEGD
LVVYNYARTEDFFKLERDMKINCSCGKIVIARYGKVFRGNKVKNQLAGAKGVILYSDPADYFAPGVKSYDPGWNLP
GGGVQRGNILNLNGAGDPLTPGYPANEYAYRRGIAEAVGLPSIPVHPIGYYDAQKLEKMGGSAPPDSSWRGSLKV
PYNVGPGFTGNFSTQVKVMHIHSTNEVTRIYNVIGTLRGAVEPDRYVILGGHRDSWVFGGIDPQSGAAVVHEIVRS
FGTLKKEGWRPRRTILFASWDAEEFGLLGSTEWAEENSRLQLQERGVAYINADSSIEGNYTLRVDCTPLMYSLVHNL
TKELKSPDEGFEGKSLYESWTKKSPSPEFGMPRISKLGSGNDFEVFFQRLGIASGRARYTKNWETNKFSGYPLYH
SVYETIELVEKFYDPMFKYHLTVAQVRGGMVFELANSIVLPFDCRDYAVVLRKYADKIYSISMKHPQEMKTYSVSF
DSLFSAVKNFTEIASKFSERLQDFDKSNPIVLRMMNDQLMFLERAFIDPLGLPDRPFYRHVIYAPSSHNKYAGESF
PGIYDALFDIESKVDPSKAWGEVKRQIYVAAFTVQAAAETLSEVA

BIRC4 survivin-beta [Homo sapiens] (SEQ ID NO: 184)

MGAPTLPPAWQPFLKDHRISTFKNWPFLGCACTPERMAEAGFIHCPTENEPDLAQCFCCFKELEGWEPDDDP IGP
GTVAYACNTSTLGGRGGRITREEHKKHSSGCAFLSVKKQFEELTLGEFLKLDREERAKNKIAKETNNKKKEFEETAK
KVRRAIEQLAAMD

MUCIN-1 mucin [Homo sapiens] (SEQ ID NO: 185)

TGSGHASSTPGGEKETSATQRSSVPSSTEKNAVSMTSSVLSSHSPGSGSSTTQGQDVT LAPATEPASGSAATWGQD
VTSVPVTRPALGSTTPPAHDVTSAPDNKPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAP
PAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTRPAPG
STAPPAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTR
PAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTR
PDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGVTS
VTSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAP
PAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTRPAPG
STAPPAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTR
PAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTR
PDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGVTS
VTSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAP
PAHGVTSAPDNRPALGSTAPPVHNVTASGSASGSASTLVHNGTSARATTTTPASKSTPFSIPSHHSDTPTTLASHS
TKTDASSTHHSSVPLTSSNHSTSPQLSTGVSFFFLSFHISNLQFNSSLED PSTDYYQELQORDISEMFLQIYKQGG
FLGLSNIKFRPGSVVVQLTLAFREGTINVHDVETQFNQYKTEAASRYNLTISDVSVDVPPFSAQSAGAVPG

MUCIN-1 isoform mucin-1 isoform 11 precursor [Homo sapiens] (SEQ ID NO: 186)

TSGSHASSTPGGEKETSATQRSSVPSSTEKNALSTGVSFFFLSFHISNLQFNSSLEDPSTDYYQELQRDISEMFLQ
IYKQGGLGLSNIKFRPGSVVVQLTLAFREGTINVHDVETQFNQYKTEAASRYNLTISDVSVDVPPFSAQSAG
VPGWGIALLVLCVLVALAIVYLIALAVCQCRRKNYGQLDIFPARDTYHPMSEYPTYHTHGRYVPPSSSTRSPYEK
VSAGNGGSSLSYTNPAVAATSANL

CD40 Ligand [Homo sapiens] (SEQ ID NO: 187)

MKIFMYLLTVFLITQMIGSALFAVYLHRRLDKIEDERNLHEDFVFMKTIQRCNTGERSLSLLNCEEIKSQFEGFVK
 DIMLNKEETKKENSFEMQKGDQNPQIAAHVISEASSKTTSVLQWAEKGYTMSNNLVTLENGKQLTVKRQGLYYIY
 AQVTFCSNREASSQAPFIASLCLKSPGRFERILLRAANTHSSAKPCGQQSIHLGGVFELQPGASVFNVTDPSSQVS
 HGTGFTSFGLLKL

WT-1 Wilms tumor protein isoform D [Homo sapiens] (SEQ ID NO: 188)

MGSDVRDLNALLPAVP SLGGGGGCGALPVSGAAQWAPVLDFAAPPASAYGSLGGFAPPPAPPPPPPPPHSFIKQEP
SWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFPGPPPSQASSGQARMFPNAPYLPSCLESQPAIRNQGYSTV
TFDGTSPSYGHTPSHHAAQFPNHSFKHEDPMGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSSDNLYQ
MTSOLECMTWNOMNLGAILKGVAAGSSSSVKWTEGOSNHSTGYESDNHHTPILCGAOYRIHTHGVFRGIODVRRVP

FIGURE 20 cont.

Replacement Sheet

GVAPTLVRSASETSEKRPFMCAYPGCNKRYFKLSHLQMHSRKHTGEKPYQCDFKDCERRFSRSDQLKRHQRRHTGV
KPFQCKTCQRKFSRSDHLKTHTRHTGKTSEKPFSCRWPSCQKKFARSDDELVRHHNMHQRNMTKLQLAL

WT-1 truncated Wilms tumor protein isoform D [Homo sapiens] (SEQ ID NO: 189)
MGSDVRDLNALLPAVPSLGGGGGCALPVSGAAQWAPVLDFAAPPASAYGSLGGPAPPPAPPPPPPPPHSFIKQEP
SWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFGPPPPSQASSGQARMFPNAPYLPSCLESQPAIRNQGYSTV
TFDGTSPSYGHTPSHHAAQFPNHSFKHEDPMGQQGSLGEQQYSVPPPVYGCHTPTDSTGTSQALLLRTPYSSDNLYQ
MTSQLECMTWNQMNLGATLKGVAAGSSSSSVKWTEGQSNHSTGYESDNHTTPILCGAQYRIHTHGVFRGIQDVRVP
GVAPTLVRSASETSEKRP

PRAME preferentially expressed antigen of melanoma [Homo sapiens] (SEQ ID NO: 190)
MERRRLWGSIQSRYISMSVWTSPPRRLVELAGQSLLKDEALAIAALELLPRELFPPLFMAAFDGRHSQTLKAMVQAW
PFTCLPLGLVMKGQHLHLETFKAVLDGLDVLLAQEVPRRWKLQVLDLRKNSHQDFWTVWSGNRASLYSFPEPEAA
QPMTKKRKVDGLSTEAEQFPFIPVEVLVDLFLKEGACDELF SYLIEKVKKKNVLRLOCKKLIKIFAMPMQDIKMILK
MVQLDSIEDLEVTCTWKLP TLAKFSPYLGQMINLRRLLSHIHASSYISPEKEEQYIAQFTSQFLSLQCLQALYVD
SLFFLRGRDLQLLRHVMNPLETSLITNCRLESGDVMHLSQSPSVSQLSVLSLSGVMLTDVSPEPLQALLERASATL
QDLVFDECGITDDQLLALLPSLSHCSQLTTLSFYGNSISISALQSLQLHLIGLSNLTHVLYPVPLESYEDIHGT LH
LERLAYLHARLRELLCELGRPSMVWLSANPCPHCGDRTFYDPEPILCPCFMPN

LAGE-1 cancer/testis antigen 2, isoform CRA_a [Homo sapiens] (SEQ ID NO: 191)
MQAEGQGTGGSTGDADGPGGPGIPDGPGGNAGGPGEAGATGGRGPRGAGAARASGPRGGAPRGPHGGAASAQDGRG
PCGARRPDSRLLQLHITMFFSSPMEAEVRRILSRDAAPLPRPGAVLKDFITVSGNLLFMSVRDQDREGAGMRVVG
WGLGSASPEGQKARDLRTPKHVSEQRPGTPGPPPEGAQGDGCRGVAFNVMFSAPHI

MAGE A3 melanoma-associated antigen 3 [Homo sapiens] (SEQ ID NO: 192)
MPLEQRSQHCKPEEGLEARGEALGLVGAQAPATEEQEAASSSSTLVEVTLGEPVAAESPDPPQSPQGASSLPTTMN
YPLWSQSYEDSSNQEEEGPSTFPDLESEFQAALSRKVAELVHFLLLKYRAREPVTKAEMLGSVVGNWQYFFPVIFS
KASSSLQLVFGIELMEVDPIGHLYIFATCLGLSYDGLLDNQIMPKAGLLIIVLAIAREGDCAPEEKIWEELSVL
EVFEGREDSILGDPKKLLTQHFVQENYLEYRQVPGSDPACYEFLWGPRALVETSYVKVLHMMVKISGGPHISYPPL
HEWVLREGEE

FIGURE 21

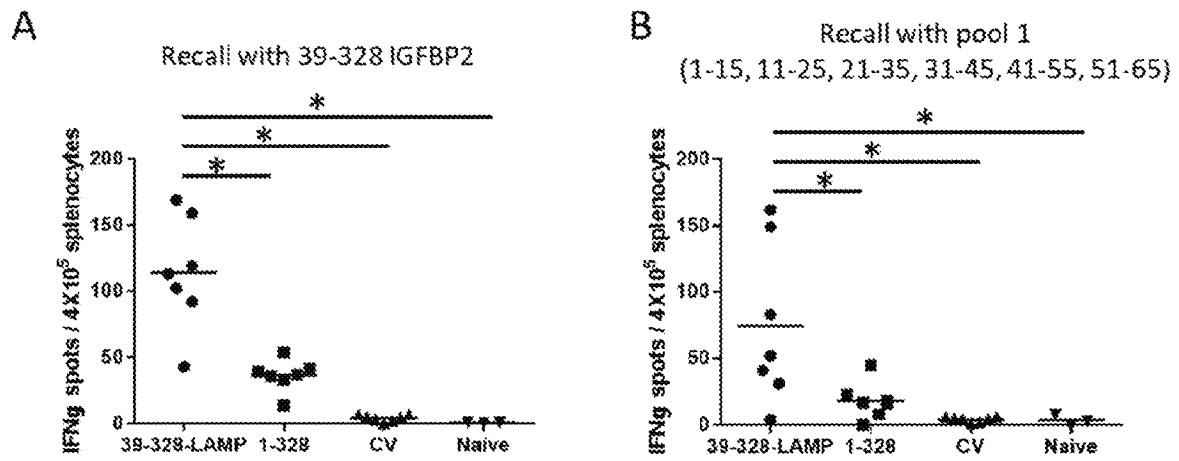
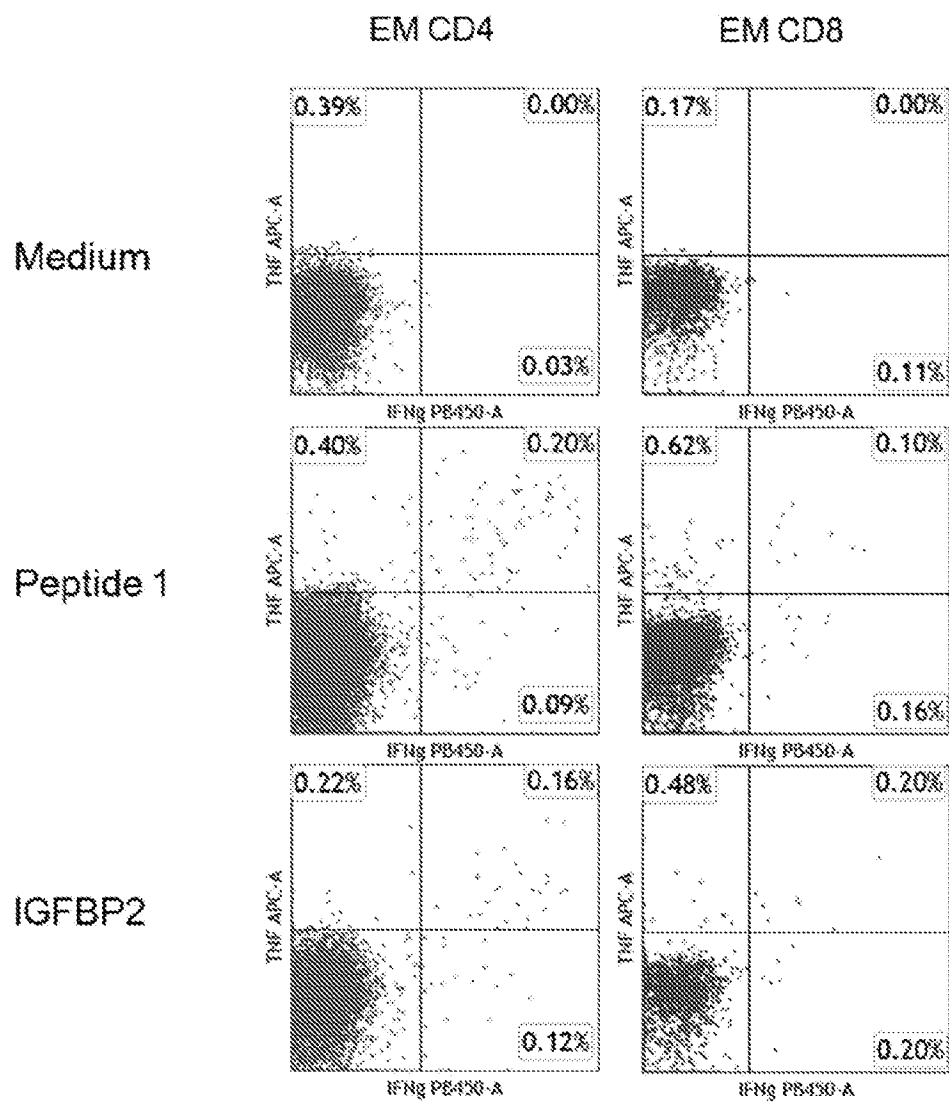


FIGURE 22



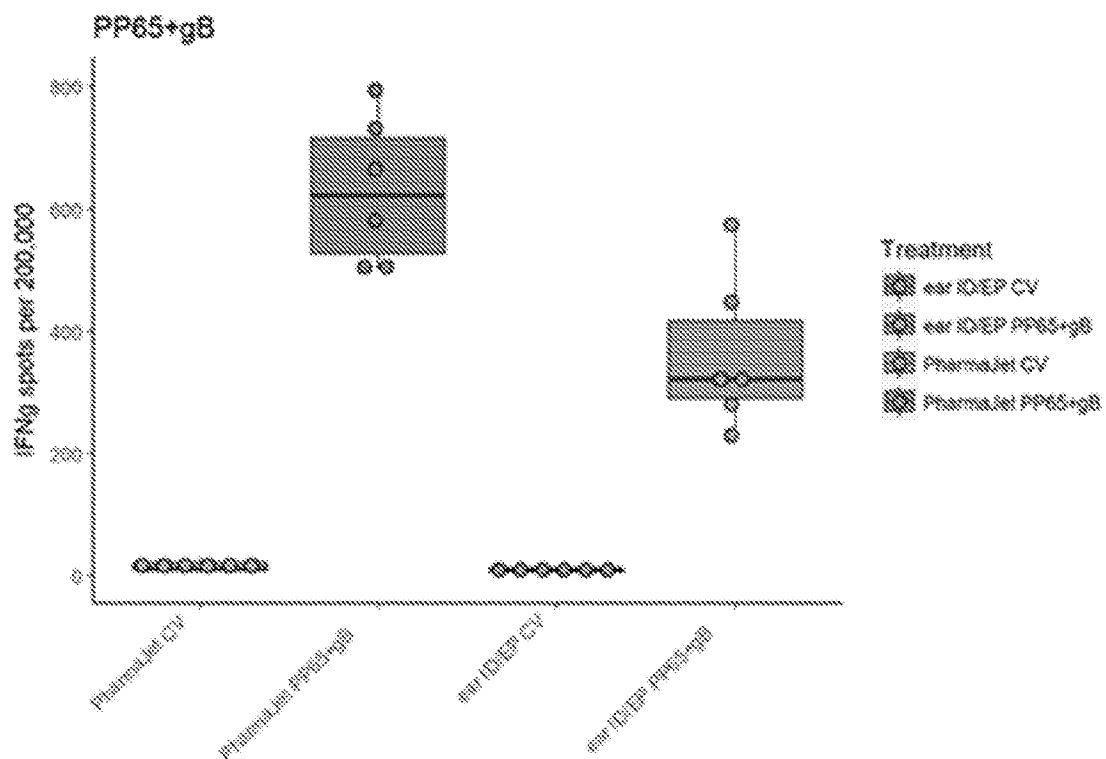
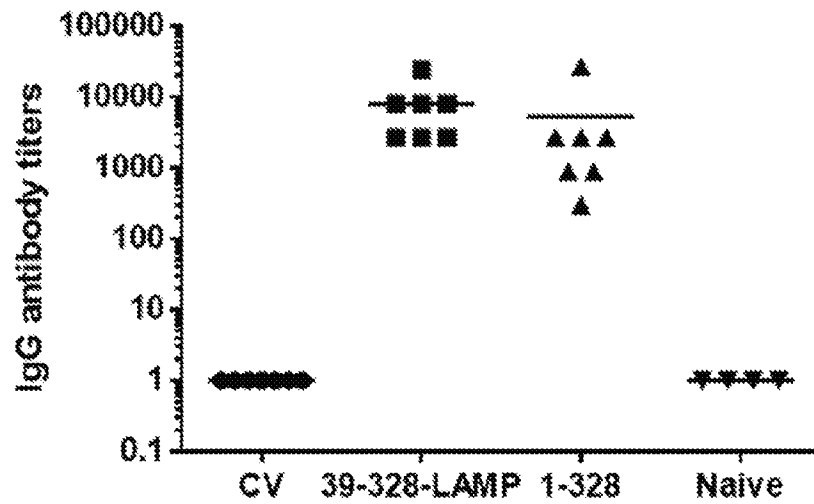


FIGURE 27

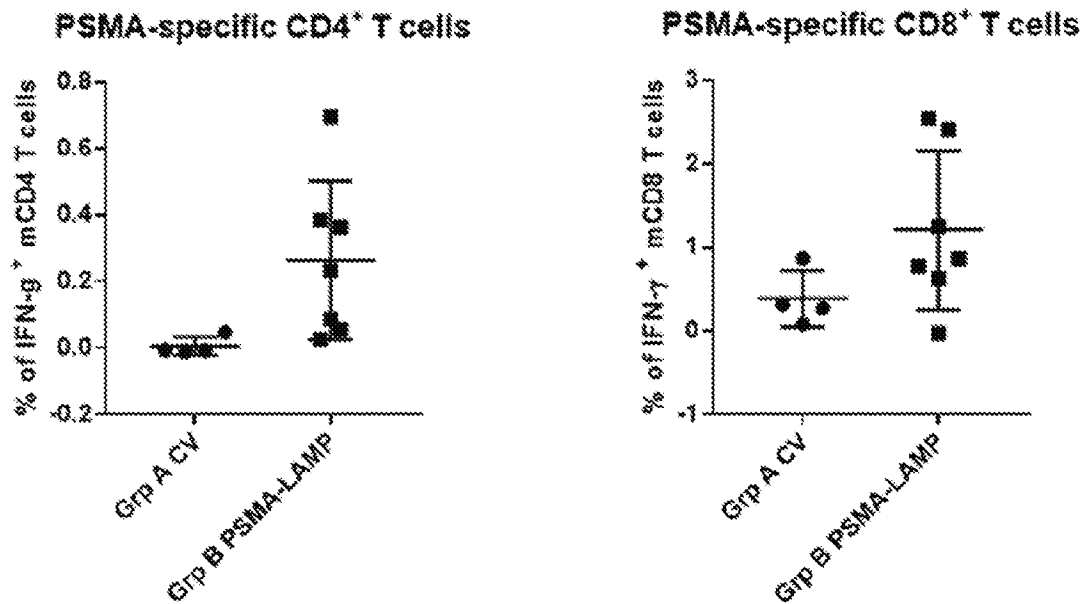
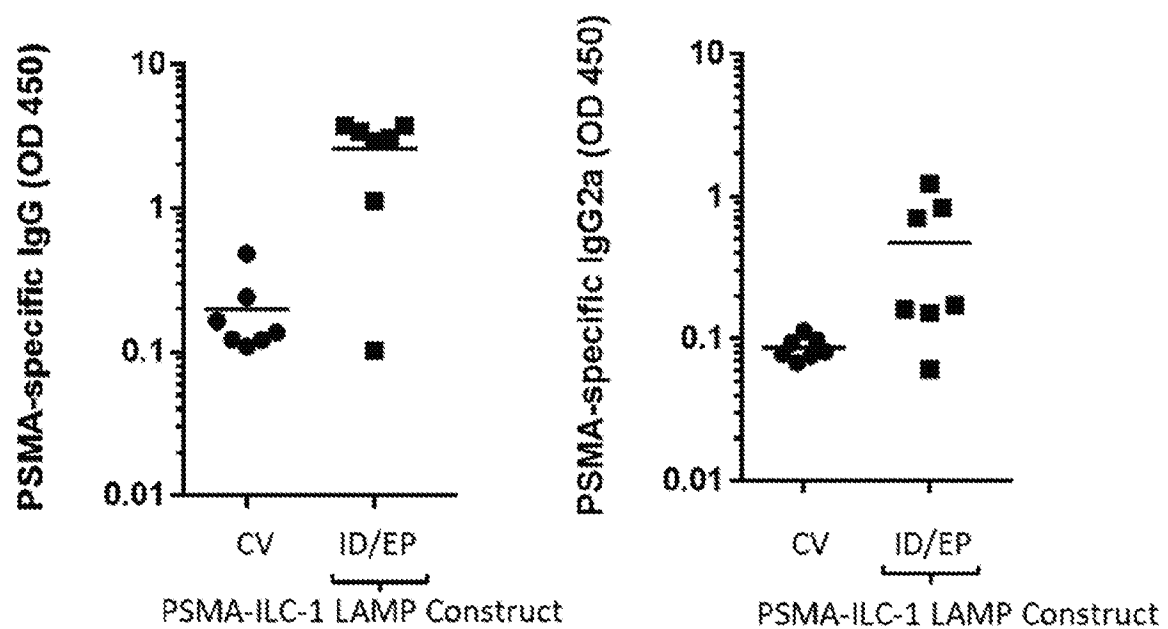


FIGURE 28



ITI-08-PCT_Sequence_Listing_ST25.txt
SEQUENCE LISTING

<110> Immunomic Therapeutics, Inc

<120> IMPROVED LAMP CONSTRUCTS COMPRISING CANCER ANTIGENS

<130> ITI-08-PCT

<150> US 62/500,053

<151> 2017-05-02

<150> US 62/561,760

<151> 2017-09-22

<160> 701

<170> PatentIn version 3.5

<210> 1

<211> 417

<212> PRT

<213> Homo sapiens

<400> 1

Met	Ala	Ala	Pro	Gly	Ser	Ala	Arg	Arg	Pro	Leu	Leu	Leu	Leu	Leu	Leu	1	5	10	15
Leu	Leu	Leu	Leu	Gly	Leu	Met	His	Cys	Ala	Ser	Ala	Ala	Met	Phe	Met	20	25	30	
Val	Lys	Asn	Gly	Asn	Gly	Thr	Ala	Cys	Ile	Met	Ala	Asn	Phe	Ser	Ala	35	40	45	
Ala	Phe	Ser	Val	Asn	Tyr	Asp	Thr	Lys	Ser	Gly	Pro	Lys	Asn	Met	Thr	50	55	60	
Phe	Asp	Leu	Pro	Ser	Asp	Ala	Thr	Val	Val	Leu	Asn	Arg	Ser	Ser	Cys	65	70	75	80
Gly	Lys	Glu	Asn	Thr	Ser	Asp	Pro	Ser	Leu	Val	Ile	Ala	Phe	Gly	Arg	85	90	95	
Gly	His	Thr	Leu	Thr	Leu	Asn	Phe	Thr	Arg	Asn	Ala	Thr	Arg	Tyr	Ser	100	105	110	
Val	Gln	Leu	Met	Ser	Phe	Val	Tyr	Asn	Leu	Ser	Asp	Thr	His	Leu	Phe	115	120	125	
Pro	Asn	Ala	Ser	Ser	Lys	Glu	Ile	Lys	Thr	Val	Glu	Ser	Ile	Thr	Asp	130	135	140	

ITI-08-PCT_Sequence_Listing_ST25.txt

Ile	Arg	Ala	Asp	Ile	Asp	Lys	Lys	Tyr	Arg	Cys	Val	Ser	Gly	Thr	Gln
145					150					155					160
Val	His	Met	Asn	Asn	Val	Thr	Val	Thr	Leu	His	Asp	Ala	Thr	Ile	Gln
				165					170					175	
Ala	Tyr	Leu	Ser	Asn	Ser	Ser	Phe	Ser	Arg	Gly	Glu	Thr	Arg	Cys	Glu
			180					185					190		
Gln	Asp	Arg	Pro	Ser	Pro	Thr	Thr	Ala	Pro	Pro	Ala	Pro	Pro	Ser	Pro
		195					200					205			
Ser	Pro	Ser	Pro	Val	Pro	Lys	Ser	Pro	Ser	Val	Asp	Lys	Tyr	Asn	Val
	210					215					220				
Ser	Gly	Thr	Asn	Gly	Thr	Cys	Leu	Leu	Ala	Ser	Met	Gly	Leu	Gln	Leu
225					230					235					240
Asn	Leu	Thr	Tyr	Glu	Arg	Lys	Asp	Asn	Thr	Thr	Val	Thr	Arg	Leu	Leu
				245					250					255	
Asn	Ile	Asn	Pro	Asn	Lys	Thr	Ser	Ala	Ser	Gly	Ser	Cys	Gly	Ala	His
			260					265					270		
Leu	Val	Thr	Leu	Glu	Leu	His	Ser	Glu	Gly	Thr	Thr	Val	Leu	Leu	Phe
		275					280					285			
Gln	Phe	Gly	Met	Asn	Ala	Ser	Ser	Ser	Arg	Phe	Phe	Leu	Gln	Gly	Ile
	290					295					300				
Gln	Leu	Asn	Thr	Ile	Leu	Pro	Asp	Ala	Arg	Asp	Pro	Ala	Phe	Lys	Ala
305					310					315					320
Ala	Asn	Gly	Ser	Leu	Arg	Ala	Leu	Gln	Ala	Thr	Val	Gly	Asn	Ser	Tyr
				325					330					335	
Lys	Cys	Asn	Ala	Glu	Glu	His	Val	Arg	Val	Thr	Lys	Ala	Phe	Ser	Val
			340					345					350		
Asn	Ile	Phe	Lys	Val	Trp	Val	Gln	Ala	Phe	Lys	Val	Glu	Gly	Gly	Gln
		355					360					365			
Phe	Gly	Ser	Val	Glu	Glu	Cys	Leu	Leu	Asp	Glu	Asn	Ser	Met	Leu	Ile
	370					375					380				
Pro	Ile	Ala	Val	Gly	Gly	Ala	Leu	Ala	Gly	Leu	Val	Leu	Ile	Val	Leu
385					390					395					400
Ile	Ala	Tyr	Leu	Val	Gly	Arg	Lys	Arg	Ser	His	Ala	Gly	Tyr	Gln	Thr
				405					410					415	

Ile

ITI-08-PCT_Sequence_Listing_ST25.txt

<210> 2

<211> 410

<212> PRT

<213> Homo sapiens

<400> 2

Met Val Cys Phe Arg Leu Phe Pro Val Pro Gly Ser Gly Leu Val Leu
1 5 10 15

Val Cys Leu Val Leu Gly Ala Val Arg Ser Tyr Ala Leu Glu Leu Asn
20 25 30

Leu Thr Asp Ser Glu Asn Ala Thr Cys Leu Tyr Ala Lys Trp Gln Met
35 40 45

Asn Phe Thr Val Arg Tyr Glu Thr Thr Asn Lys Thr Tyr Lys Thr Val
50 55 60

Thr Ile Ser Asp His Gly Thr Val Thr Tyr Asn Gly Ser Ile Cys Gly
65 70 75 80

Asp Asp Gln Asn Gly Pro Lys Ile Ala Val Gln Phe Gly Pro Gly Phe
85 90 95

Ser Trp Ile Ala Asn Phe Thr Lys Ala Ala Ser Thr Tyr Ser Ile Asp
100 105 110

Ser Val Ser Phe Ser Tyr Asn Thr Gly Asp Asn Thr Thr Phe Pro Asp
115 120 125

Ala Glu Asp Lys Gly Ile Leu Thr Val Asp Glu Leu Leu Ala Ile Arg
130 135 140

Ile Pro Leu Asn Asp Leu Phe Arg Cys Asn Ser Leu Ser Thr Leu Glu
145 150 155 160

Lys Asn Asp Val Val Gln His Tyr Trp Asp Val Leu Val Gln Ala Phe
165 170 175

Val Gln Asn Gly Thr Val Ser Thr Asn Glu Phe Leu Cys Asp Lys Asp
180 185 190

Lys Thr Ser Thr Val Ala Pro Thr Ile His Thr Thr Val Pro Ser Pro
195 200 205

Thr Thr Thr Pro Thr Pro Lys Glu Lys Pro Glu Ala Gly Thr Tyr Ser
210 215 220

Val Asn Asn Gly Asn Asp Thr Cys Leu Leu Ala Thr Met Gly Leu Gln
225 230 235 240

ITI-08-PCT_Sequence_Listing_ST25.txt

Leu Asn Ile Thr Gln Asp Lys Val Ala Ser Val Ile Asn Ile Asn Pro
245 250 255

Asn Thr Thr His Ser Thr Gly Ser Cys Arg Ser His Thr Ala Leu Leu
260 265 270

Arg Leu Asn Ser Ser Thr Ile Lys Tyr Leu Asp Phe Val Phe Ala Val
275 280 285

Lys Asn Glu Asn Arg Phe Tyr Leu Lys Glu Val Asn Ile Ser Met Tyr
290 295 300

Leu Val Asn Gly Ser Val Phe Ser Ile Ala Asn Asn Asn Leu Ser Tyr
305 310 315 320

Trp Asp Ala Pro Leu Gly Ser Ser Tyr Met Cys Asn Lys Glu Gln Thr
325 330 335

Val Ser Val Ser Gly Ala Phe Gln Ile Asn Thr Phe Asp Leu Arg Val
340 345 350

Gln Pro Phe Asn Val Thr Gln Gly Lys Tyr Ser Thr Ala Gln Asp Cys
355 360 365

Ser Ala Asp Asp Asp Asn Phe Leu Val Pro Ile Ala Val Gly Ala Ala
370 375 380

Leu Ala Gly Val Leu Ile Leu Val Leu Leu Ala Tyr Phe Ile Gly Leu
385 390 395 400

Lys His His His Ala Gly Tyr Glu Gln Phe
405 410

<210> 3

<211> 416

<212> PRT

<213> Homo sapiens

<400> 3

Met Pro Arg Gln Leu Ser Ala Ala Ala Ala Leu Phe Ala Ser Leu Ala
1 5 10 15

Val Ile Leu His Asp Gly Ser Gln Met Arg Ala Lys Ala Phe Pro Glu
20 25 30

Thr Arg Asp Tyr Ser Gln Pro Thr Ala Ala Ala Thr Val Gln Asp Ile
35 40 45

Lys Lys Pro Val Gln Gln Pro Ala Lys Gln Ala Pro His Gln Thr Leu
50 55 60

ITI-08-PCT_Sequence_Listing_ST25.txt

Ala	Ala	Arg	Phe	Met	Asp	Gly	His	Ile	Thr	Phe	Gln	Thr	Ala	Ala	Thr	65	70	75	80
Val	Lys	Ile	Pro	Thr	Thr	Thr	Pro	Ala	Thr	Thr	Lys	Asn	Thr	Ala	Thr	85	90	95	
Thr	Ser	Pro	Ile	Thr	Tyr	Thr	Leu	Val	Thr	Thr	Gln	Ala	Thr	Pro	Asn	100	105	110	
Asn	Ser	His	Thr	Ala	Pro	Pro	Val	Thr	Glu	Val	Thr	Val	Gly	Pro	Ser	115	120	125	
Leu	Ala	Pro	Tyr	Ser	Leu	Pro	Pro	Thr	Ile	Thr	Pro	Pro	Ala	His	Thr	130	135	140	
Thr	Gly	Thr	Ser	Ser	Ser	Thr	Val	Ser	His	Thr	Thr	Gly	Asn	Thr	Thr	145	150	155	160
Gln	Pro	Ser	Asn	Gln	Thr	Thr	Leu	Pro	Ala	Thr	Leu	Ser	Ile	Ala	Leu	165	170	175	
His	Lys	Ser	Thr	Thr	Gly	Gln	Lys	Pro	Val	Gln	Pro	Thr	His	Ala	Pro	180	185	190	
Gly	Thr	Thr	Ala	Ala	Ala	His	Asn	Thr	Thr	Arg	Thr	Ala	Ala	Pro	Ala	195	200	205	
Ser	Thr	Val	Pro	Gly	Pro	Thr	Leu	Ala	Pro	Gln	Pro	Ser	Ser	Val	Lys	210	215	220	
Thr	Gly	Ile	Tyr	Gln	Val	Leu	Asn	Gly	Ser	Arg	Leu	Cys	Ile	Lys	Ala	225	230	235	240
Glu	Met	Gly	Ile	Gln	Leu	Ile	Val	Gln	Asp	Lys	Glu	Ser	Val	Phe	Ser	245	250	255	
Pro	Arg	Arg	Tyr	Phe	Asn	Ile	Asp	Pro	Asn	Ala	Thr	Gln	Ala	Ser	Gly	260	265	270	
Asn	Cys	Gly	Thr	Arg	Lys	Ser	Asn	Leu	Leu	Leu	Asn	Phe	Gln	Gly	Gly	275	280	285	
Phe	Val	Asn	Leu	Thr	Phe	Thr	Lys	Asp	Glu	Glu	Ser	Tyr	Tyr	Ile	Ser	290	295	300	
Glu	Val	Gly	Ala	Tyr	Leu	Thr	Val	Ser	Asp	Pro	Glu	Thr	Ile	Tyr	Gln	305	310	315	320
Gly	Ile	Lys	His	Ala	Val	Val	Met	Phe	Gln	Thr	Ala	Val	Gly	His	Ser	325	330	335	

ITI-08-PCT_Sequence_Listing_ST25.txt

Phe Lys Cys Val Ser Glu Gln Ser Leu Gln Leu Ser Ala His Leu Gln
340 345 350

Val Lys Thr Thr Asp Val Gln Leu Gln Ala Phe Asp Phe Glu Asp Asp
355 360 365

His Phe Gly Asn Val Asp Glu Cys Ser Ser Asp Tyr Thr Ile Val Leu
370 375 380

Pro Val Ile Gly Ala Ile Val Val Gly Leu Cys Leu Met Gly Met Gly
385 390 395 400

Val Tyr Lys Ile Arg Leu Arg Cys Gln Ser Ser Gly Tyr Gln Arg Ile
405 410 415

<210> 4

<211> 478

<212> PRT

<213> Homo sapiens

<400> 4

Met Gly Arg Cys Cys Phe Tyr Thr Ala Gly Thr Leu Ser Leu Leu Leu
1 5 10 15

Leu Val Thr Ser Val Thr Leu Leu Val Ala Arg Val Phe Gln Lys Ala
20 25 30

Val Asp Gln Ser Ile Glu Lys Lys Ile Val Leu Arg Asn Gly Thr Glu
35 40 45

Ala Phe Asp Ser Trp Glu Lys Pro Pro Leu Pro Val Tyr Thr Gln Phe
50 55 60

Tyr Phe Phe Asn Val Thr Asn Pro Glu Glu Ile Leu Arg Gly Glu Thr
65 70 75 80

Pro Arg Val Glu Glu Val Gly Pro Tyr Thr Tyr Arg Glu Leu Arg Asn
85 90 95

Lys Ala Asn Ile Gln Phe Gly Asp Asn Gly Thr Thr Ile Ser Ala Val
100 105 110

Ser Asn Lys Ala Tyr Val Phe Glu Arg Asp Gln Ser Val Gly Asp Pro
115 120 125

Lys Ile Asp Leu Ile Arg Thr Leu Asn Ile Pro Val Leu Thr Val Ile
130 135 140

Glu Trp Ser Gln Val His Phe Leu Arg Glu Ile Ile Glu Ala Met Leu
145 150 155 160

ITI-08-PCT_Sequence_Listing_ST25.txt

Lys Ala Tyr Gln Gln Lys Leu Phe Val Thr His Thr Val Asp Glu Leu
 165 170 175
 Leu Trp Gly Tyr Lys Asp Glu Ile Leu Ser Leu Ile His Val Phe Arg
 180 185 190
 Pro Asp Ile Ser Pro Tyr Phe Gly Leu Phe Tyr Glu Lys Asn Gly Thr
 195 200 205
 Asn Asp Gly Asp Tyr Val Phe Leu Thr Gly Glu Asp Ser Tyr Leu Asn
 210 215 220
 Phe Thr Lys Ile Val Glu Trp Asn Gly Lys Thr Ser Leu Asp Trp Trp
 225 230 235 240
 Ile Thr Asp Lys Cys Asn Met Ile Asn Gly Thr Asp Gly Asp Ser Phe
 245 250 255
 His Pro Leu Ile Thr Lys Asp Glu Val Leu Tyr Val Phe Pro Ser Asp
 260 265 270
 Phe Cys Arg Ser Val Tyr Ile Thr Phe Ser Asp Tyr Glu Ser Val Gln
 275 280 285
 Gly Leu Pro Ala Phe Arg Tyr Lys Val Pro Ala Glu Ile Leu Ala Asn
 290 295 300
 Thr Ser Asp Asn Ala Gly Phe Cys Ile Pro Glu Gly Asn Cys Leu Gly
 305 310 315 320
 Ser Gly Val Leu Asn Val Ser Ile Cys Lys Asn Gly Ala Pro Ile Ile
 325 330 335
 Met Ser Phe Pro His Phe Tyr Gln Ala Asp Glu Arg Phe Val Ser Ala
 340 345 350
 Ile Glu Gly Met His Pro Asn Gln Glu Asp His Glu Thr Phe Val Asp
 355 360 365
 Ile Asn Pro Leu Thr Gly Ile Ile Leu Lys Ala Ala Lys Arg Phe Gln
 370 375 380
 Ile Asn Ile Tyr Val Lys Lys Leu Asp Asp Phe Val Glu Thr Gly Asp
 385 390 395 400
 Ile Arg Thr Met Val Phe Pro Val Met Tyr Leu Asn Glu Ser Val His
 405 410 415
 Ile Asp Lys Glu Thr Ala Ser Arg Leu Lys Ser Met Ile Asn Thr Thr
 420 425 430
 Leu Ile Ile Thr Asn Ile Pro Tyr Ile Ile Met Ala Leu Gly Val Phe

ITI-08-PCT_Sequence_Listing_ST25.txt

435 440 445
 Phe Gly Leu Val Phe Thr Trp Leu Ala Cys Lys Gly Gln Gly Ser Met
 450 455 460
 Asp Glu Gly Thr Ala Asp Glu Arg Ala Pro Leu Ile Arg Thr
 465 470 475
 <210> 5
 <211> 197
 <212> PRT
 <213> Homo sapiens
 <400> 5
 Met Ser Arg Leu Ser Arg Ser Leu Leu Trp Ala Ala Thr Cys Leu Gly
 1 5 10 15
 Val Leu Cys Val Leu Ser Ala Asp Lys Asn Thr Thr Gln His Pro Asn
 20 25 30
 Val Thr Thr Leu Ala Pro Ile Ser Asn Val Thr Ser Ala Pro Val Thr
 35 40 45
 Ser Leu Pro Leu Val Thr Thr Pro Ala Pro Glu Thr Cys Glu Gly Arg
 50 55 60
 Asn Ser Cys Val Ser Cys Phe Asn Val Ser Val Val Asn Thr Thr Cys
 65 70 75 80
 Phe Trp Ile Glu Cys Lys Asp Glu Ser Tyr Cys Ser His Asn Ser Thr
 85 90 95
 Val Ser Asp Cys Gln Val Gly Asn Thr Thr Asp Phe Cys Ser Val Ser
 100 105 110
 Thr Ala Thr Pro Val Pro Thr Ala Asn Ser Thr Ala Lys Pro Thr Val
 115 120 125
 Gln Pro Ser Pro Ser Thr Thr Ser Lys Thr Val Thr Thr Ser Gly Thr
 130 135 140
 Thr Asn Asn Thr Val Thr Pro Thr Ser Gln Pro Val Arg Lys Ser Thr
 145 150 155 160
 Phe Asp Ala Ala Ser Phe Ile Gly Gly Ile Val Leu Val Leu Gly Val
 165 170 175
 Gln Ala Val Ile Phe Phe Leu Tyr Lys Phe Cys Lys Ser Lys Glu Arg
 180 185 190
 Asn Tyr His Thr Leu

ITI-08-PCT_Sequence_Listing_ST25.txt

195

<210> 6
 <211> 406
 <212> PRT
 <213> Mus musculus

<400> 6

Met Ala Ala Pro Gly Ala Arg Arg Pro Leu Leu Leu Leu Leu Ala
 1 5 10 15

Gly Leu Ala His Gly Ala Ser Ala Leu Phe Glu Val Lys Asn Asn Gly
 20 25 30

Thr Thr Cys Ile Met Ala Ser Phe Ser Ala Ser Phe Leu Thr Thr Tyr
 35 40 45

Glu Thr Ala Asn Gly Ser Gln Ile Val Asn Ile Ser Leu Pro Ala Ser
 50 55 60

Ala Glu Val Leu Lys Asn Gly Ser Ser Cys Gly Lys Glu Asn Val Ser
 65 70 75 80

Asp Pro Ser Leu Thr Ile Thr Phe Gly Arg Gly Tyr Leu Leu Thr Leu
 85 90 95

Asn Phe Thr Lys Asn Thr Thr Arg Tyr Ser Val Gln His Met Tyr Phe
 100 105 110

Thr Tyr Asn Leu Ser Asp Thr Glu His Phe Pro Asn Ala Ile Ser Lys
 115 120 125

Glu Ile Tyr Thr Met Asp Ser Thr Thr Asp Ile Lys Ala Asp Ile Asn
 130 135 140

Lys Ala Tyr Arg Cys Val Ser Asp Ile Arg Val Tyr Met Lys Asn Val
 145 150 155 160

Thr Val Val Leu Arg Asp Ala Thr Ile Gln Ala Tyr Leu Ser Ser Gly
 165 170 175

Asn Phe Ser Lys Glu Glu Thr His Cys Thr Gln Asp Gly Pro Ser Pro
 180 185 190

Thr Thr Gly Pro Pro Ser Pro Ser Pro Pro Leu Val Pro Thr Asn Pro
 195 200 205

Thr Val Ser Lys Tyr Asn Val Thr Gly Asn Asn Gly Thr Cys Leu Leu
 210 215 220

Ala Ser Met Ala Leu Gln Leu Asn Ile Thr Tyr Leu Lys Lys Asp Asn

ITI-08-PCT_Sequence_Listing_ST25.txt

225 230 235 240
 Lys Thr Val Thr Arg Ala Phe Asn Ile Ser Pro Asn Asp Thr Ser Ser
 245 250 255
 Gly Ser Cys Gly Ile Asn Leu Val Thr Leu Lys Val Glu Asn Lys Asn
 260 265 270
 Arg Ala Leu Glu Leu Gln Phe Gly Met Asn Ala Ser Ser Ser Leu Phe
 275 280 285
 Phe Leu Gln Gly Val Arg Leu Asn Met Thr Leu Pro Asp Ala Leu Val
 290 295 300
 Pro Thr Phe Ser Ile Ser Asn His Ser Leu Lys Ala Leu Gln Ala Thr
 305 310 315 320
 Val Gly Asn Ser Tyr Lys Cys Asn Thr Glu Glu His Ile Phe Val Ser
 325 330 335
 Lys Met Leu Ser Leu Asn Val Phe Ser Val Gln Val Gln Ala Phe Lys
 340 345 350
 Val Asp Ser Asp Arg Phe Gly Ser Val Glu Glu Cys Val Gln Asp Gly
 355 360 365
 Asn Asn Met Leu Ile Pro Ile Ala Val Gly Gly Ala Leu Ala Gly Leu
 370 375 380
 Val Leu Ile Val Leu Ile Ala Tyr Leu Ile Gly Arg Lys Arg Ser His
 385 390 395 400
 Ala Gly Tyr Gln Thr Ile
 405

<210> 7
 <211> 411
 <212> PRT
 <213> Danio rerio

<400> 7

Met Ala Arg Ala Ala Gly Val Cys Trp Thr Leu Leu Met Gly Cys Val
 1 5 10 15
 Phe Ala Ala His Ala Val Thr Phe Glu Val Thr Asp Gly Asn Ser Thr
 20 25 30
 Cys Ile Lys Gly Glu Leu Asn Ala Ser Phe Ser Ile Ser Tyr Asn Thr
 35 40 45
 Thr Asn Gly Thr Ser Val Ser Val Phe Ala Leu Pro Ala Ser Ala Ser

ITI-08-PCT_Sequence_Listing_ST25.txt

50	55	60													
Val	Ser	Glu	Arg	Ser	Ser	Cys	Gly	Ser	Ala	Ala	Val	Pro	Pro	Glu	Leu
65					70					75					80
Ala	Leu	Val	Phe	Gly	Asp	Thr	His	Thr	His	Thr	Leu	Ser	Leu	Leu	Phe
				85					90					95	
Ser	Arg	Asp	Gln	Arg	Leu	Tyr	Arg	Val	Ser	Asn	Ile	Ser	Leu	Gln	Tyr
			100					105					110		
Asn	Leu	Ser	Asp	Gly	Asp	Ile	Phe	Pro	Gln	Ser	Ser	Ser	Ala	Gly	Val
		115					120					125			
Gln	Ser	Val	Met	Ala	Ser	Val	Ser	Glu	Leu	Met	Ser	Ala	Arg	Leu	Asn
	130					135					140				
Ser	Thr	Tyr	Arg	Cys	Val	Ser	Ser	Ser	Ser	Ile	Ser	Leu	Ser	Ala	Ala
145					150					155					160
Val	Asn	Leu	Thr	Leu	Ser	Gly	Val	Gln	Met	Glu	Ala	Tyr	Met	Ser	Ser
				165				170						175	
Ala	Asn	Leu	Ser	Ala	Asp	Glu	Ser	Val	Cys	Ser	Ala	Asp	Gln	Pro	Ser
			180					185					190		
Thr	Thr	Val	Ala	Pro	Pro	Pro	Ser	Thr	Thr	Thr	Ser	Pro	Pro	Pro	Ile
		195					200					205			
Pro	Pro	Val	Pro	Glu	Arg	Gly	Asn	Tyr	Ser	Val	Thr	Asp	Gly	Asn	Gly
	210					215					220				
Thr	Val	Cys	Val	Leu	Ala	Leu	Met	Gly	Leu	Gln	Leu	Asn	Ile	Thr	His
225					230					235					240
Thr	Thr	Thr	Gln	Asn	Gln	Ser	Val	Ser	Glu	Leu	Met	Asn	Leu	Gln	Pro
			245						250					255	
Asn	Gln	Thr	Thr	Val	Ser	Gly	Ser	Cys	Gly	Val	Thr	Glu	Ser	Ser	Leu
			260					265					270		
Arg	Leu	Ser	Asp	Glu	Thr	Thr	Asn	Leu	Thr	Phe	Ser	Phe	Thr	Met	Asn
		275					280					285			
Ser	Thr	Thr	Gln	Lys	Tyr	Tyr	Leu	Ser	Ala	Val	Ser	Val	Ser	Ala	Leu
	290					295					300				
Trp	Pro	Asp	Met	Ser	Val	Val	Phe	Glu	Ala	Gly	Asn	Thr	Ser	Leu	Ser
305					310					315					320
Ala	Leu	Gln	Cys	Ser	Val	Gly	Arg	Ser	Tyr	Val	Cys	Ser	Ala	Gln	Gln
			325						330					335	

ITI-08-PCT_Sequence_Listing_ST25.txt

Met Leu Ser Val Thr Pro Val Phe Ser Ile Asn Thr Phe Arg Leu Gln
340 345 350

Leu Gln Pro Phe Asn Ile Thr Ala Asn Arg Phe Ser Thr Ala Glu Glu
355 360 365

Cys Arg Val Asp Gln Glu Asn Met Leu Ile Pro Ile Ile Val Gly Ala
370 375 380

Ala Leu Ala Gly Leu Val Leu Ile Val Leu Val Ala Tyr Leu Ile Gly
385 390 395 400

Arg Lys Arg Thr His Ala Gly Tyr Gln Thr Ile
405 410

<210> 8

<211> 417

<212> PRT

<213> Xenopus laevis

<400> 8

Met Ser Trp Arg Gln Val Lys Met Pro Val Tyr Trp Met Ala Val Met
1 5 10 15

Leu Leu Ile Gly Val Val Gln Val Ala Thr Ala Val Gln Phe Glu Val
20 25 30

Lys Asp Gly Lys Thr Asn Ile Thr Cys Ile Leu Ala Asp Leu Ser Ile
35 40 45

Asn Phe Ser Val Ser Tyr Asn Val Ser Ser Lys Met Glu Leu Ala Thr
50 55 60

Phe Val Leu Pro Ser Glu Ala Val Thr Asn Ile Asn Lys Ser Ser Cys
65 70 75 80

Gly Val Glu Asn Thr Thr Ala Pro Val Leu Ala Ile Gln Phe Gly Ser
85 90 95

Asn His Ser Leu Ser Ile His Phe Ala Arg Asn Asn Thr Arg Tyr Glu
100 105 110

Val Ala Glu Leu Val Met Ser Tyr Asn Leu Ser Asp Lys Ile Ile Phe
115 120 125

Pro Asn Ala Ser Glu Asn Gly Thr Lys Thr Val Ser Thr Asn Lys Thr
130 135 140

Ala Val Leu Ala Glu Asn Asp Thr Val Tyr Lys Cys Met Asn Pro His
145 150 155 160

ITI-08-PCT_Sequence_Listing_ST25.txt

```

Leu Ile Arg Met Asp Asn Ala Asn Ala Thr Phe His Asp Ile Arg Leu
      165                      170                      175

Glu Ala Tyr Leu Lys Gln Ser Asn Phe Ser Gln Lys Val Ser Thr Cys
      180                      185                      190

Ser Glu Asp Ile Thr Pro Thr Ser Ala Pro Ala Pro Val Thr Thr Thr
      195                      200                      205

Ala Pro Val Pro Ala Pro Val Pro Asp Pro Pro Val Val Gln Tyr Ser
      210                      215                      220

Val Asn Arg Ser Ser Glu Pro Cys Leu Leu Ala Lys Val Gly Leu Gln
225                      230                      235                      240

Met Asn Ile Thr Tyr Thr Thr Lys Asp Gly Lys Asn Gly Ser Tyr Val
      245                      250                      255

Phe Asn Ile Glu Ser Lys Gly Val Thr Val Asp Gly Asn Cys Thr Asn
      260                      265                      270

Thr Thr Ala Tyr Leu Ser Leu Ser Thr Gly Ser Ile Asp Leu Arg Phe
      275                      280                      285

Asn Phe Thr Leu Asn Ser Ser Leu Glu Val Phe Tyr Leu Asp Gly Val
      290                      295                      300

Ser Leu Ser Thr Gly Leu Pro Ala Asp Ala Asn Asp Thr His Phe Glu
305                      310                      315                      320

Ala Ala Asn Ser Ser Leu Asn Tyr Met Gln Thr Asn Val His Lys Ser
      325                      330                      335

Phe Lys Cys Asn Ser Lys Gln Thr Leu Gln Ile Thr Asp Pro Phe Thr
      340                      345                      350

Val Asn Thr Tyr His Leu Gln Val Gln Ala Phe Asn Ser Asp Asn Thr
      355                      360                      365

Phe Ala Ser Ala Val Glu Cys Ser Leu Asp Glu Asn Gly Met Leu Val
      370                      375                      380

Pro Ile Val Val Gly Ala Ala Leu Ala Gly Leu Val Leu Ile Val Leu
385                      390                      395                      400

Ile Ala Tyr Leu Ile Gly Arg Lys Arg Ser His Ala Gly Tyr Gln Thr
      405                      410                      415

```

Ile

<210> 9

ITI-08-PCT_Sequence_Listing_ST25.txt

<211> 417

<212> PRT

<213> Pan troglodytes

<400> 9

Met Ala Ala Pro Gly Ser Ala Arg Arg Pro Leu Leu Leu Leu Leu Leu
1 5 10 15

Leu Leu Leu Leu Gly Leu Val His Cys Ala Ser Ala Ala Met Phe Met
20 25 30

Val Lys Asn Gly Asn Gly Thr Ala Cys Ile Met Ala Asn Phe Ser Ala
35 40 45

Ser Phe Ser Val Asn Tyr Asp Thr Lys Ser Gly Pro Lys Asn Met Thr
50 55 60

Phe Asp Leu Pro Ser Asp Ala Thr Val Val Leu Asn Arg Ser Ser Cys
65 70 75 80

Gly Lys Glu Asn Thr Ser Asp Pro Ser Leu Val Ile Ala Phe Gly Arg
85 90 95

Gly His Thr Leu Thr Leu Asn Phe Thr Arg Asn Ala Thr Arg Tyr Ser
100 105 110

Val Gln Leu Met Ser Phe Val Tyr Asn Leu Ser Asp Thr His Leu Phe
115 120 125

Pro Asn Ala Ser Ser Lys Glu Ile Lys Thr Val Glu Ser Ile Thr Asp
130 135 140

Ile Arg Ala Asp Ile Asp Lys Lys Tyr Arg Cys Val Ser Gly Thr Gln
145 150 155 160

Val His Met Asn Asn Val Thr Val Thr Leu His Asp Ala Thr Ile Gln
165 170 175

Ala Tyr Leu Ser Asn Ser Ser Phe Ser Arg Gly Glu Thr Arg Cys Glu
180 185 190

Gln Asp Arg Pro Ser Pro Thr Thr Ala Pro Pro Ala Pro Pro Ser Pro
195 200 205

Ser Pro Ser Pro Val Pro Glu Ser Pro Ser Val Asp Lys Tyr Asn Val
210 215 220

Ser Gly Thr Asn Gly Thr Cys Leu Leu Ala Ser Met Gly Leu Gln Leu
225 230 235 240

Asn Leu Thr Tyr Glu Arg Lys Asp Asn Thr Thr Val Thr Arg Leu Leu

ITI-08-PCT_Sequence_Listing_ST25.txt

245 250 255

Asn Ile Asn Pro Asn Lys Thr Ser Ala Ser Gly Ser Cys Gly Ala His
260 265 270

Leu Val Thr Leu Glu Leu His Ser Glu Gly Ser Thr Val Leu Leu Phe
275 280 285

Leu Phe Gly Met Asn Ala Ser Ser Ser Arg Phe Phe Leu Gln Gly Ile
290 295 300

Gln Leu Asn Thr Thr Leu Pro Asp Ala Arg Asp Pro Ala Phe Lys Ala
305 310 315 320

Ala Asn Gly Ser Leu Arg Ala Leu Gln Ala Thr Val Gly Asn Ser Tyr
325 330 335

Lys Cys Asn Ala Glu Glu His Val Arg Val Thr Lys Ala Phe Ser Val
340 345 350

Asn Ile Phe Lys Val Trp Val Gln Ala Phe Lys Val Glu Gly Gly Gln
355 360 365

Phe Gly Ser Val Glu Glu Cys Val Leu Asp Glu Asn Asn Met Leu Ile
370 375 380

Pro Ile Ala Val Gly Gly Ala Leu Ala Gly Leu Val Leu Ile Val Leu
385 390 395 400

Ile Ala Tyr Leu Val Gly Arg Lys Arg Ser His Ala Gly Tyr Gln Thr
405 410 415

Ile

<210> 10

<211> 415

<212> PRT

<213> Macaca mulatta

<400> 10

Met Ala Ala Pro Gly Ser Ala Arg Arg Ser Leu Leu Leu Leu Leu Leu
1 5 10 15

Leu Leu Leu Gly Leu Thr His Cys Ala Ser Ala Ala Met Phe Ile Val
20 25 30

Lys Asn Gly Asn Gly Thr Ala Cys Ile Met Ala Asn Phe Ser Ala Ala
35 40 45

Phe Ser Val Asn Tyr Asp Thr Lys Ser Gly Pro Lys Asn Met Thr Phe
50 55 60

ITI-08-PCT_Sequence_Listing_ST25.txt

Asp	Leu	Pro	Ser	Asp	Ala	Lys	Val	Val	Leu	Asn	Ser	Ser	Ser	Cys	Gly	65	70	75	80
Lys	Glu	Asn	Thr	Ser	Asp	Pro	Ser	Leu	Val	Ile	Ala	Phe	Gly	Arg	Gly	85	90	95	
Gln	Thr	Leu	Thr	Leu	Asn	Phe	Thr	Arg	Asn	Ala	Thr	Arg	Tyr	Ser	Val	100	105	110	
Gln	Leu	Met	Ser	Phe	Val	Tyr	Asn	Leu	Ser	Asp	Thr	His	Leu	Phe	Pro	115	120	125	
Asn	Ala	Ser	Ser	Lys	Glu	Ile	Lys	Thr	Val	Glu	Ser	Ile	Thr	Asp	Ile	130	135	140	
Arg	Ala	Asp	Ile	Asp	Lys	Lys	Tyr	Arg	Cys	Val	Ser	Gly	Thr	Gln	Val	145	150	155	160
His	Met	Asn	Asn	Val	Thr	Val	Thr	Leu	His	Asp	Ala	Thr	Ile	Gln	Ala	165	170	175	
Tyr	Leu	Ser	Asn	Ser	Ser	Phe	Ser	Arg	Glu	Glu	Thr	Arg	Cys	Glu	Gln	180	185	190	
Asp	Arg	Pro	Ser	Pro	Thr	Thr	Ala	Pro	Pro	Ala	Pro	Pro	Ser	Pro	Ser	195	200	205	
Pro	Ser	Pro	Val	Pro	Glu	Ser	Pro	Ser	Val	Asp	Lys	Tyr	Asn	Val	Ser	210	215	220	
Gly	Thr	Asn	Gly	Thr	Cys	Leu	Leu	Ala	Ser	Met	Gly	Leu	Gln	Leu	Asn	225	230	235	240
Leu	Thr	Tyr	Glu	Arg	Lys	Asp	Asn	Thr	Thr	Val	Thr	Arg	Leu	Leu	Asn	245	250	255	
Ile	Asn	Pro	Asn	Lys	Thr	Leu	Ala	Ser	Gly	Ser	Cys	Gly	Ala	His	Leu	260	265	270	
Val	Thr	Leu	Glu	Leu	His	Ser	Glu	Gly	Ser	Thr	Val	Leu	Leu	Phe	Gln	275	280	285	
Phe	Gly	Met	Asn	Ala	Ser	Ser	Ser	Arg	Phe	Phe	Leu	Gln	Gly	Ile	Gln	290	295	300	
Leu	Asn	Thr	Thr	Leu	Pro	Asp	Ala	Arg	Asp	Pro	Ala	Phe	Lys	Ala	Ala	305	310	315	320
Asn	Ser	Ser	Leu	Arg	Ala	Leu	Gln	Ala	Thr	Val	Gly	Asn	Ser	Tyr	Lys	325	330	335	

ITI-08-PCT_Sequence_Listing_ST25.txt

Cys Asn Ala Glu Glu His Val Arg Val Thr Lys Ala Phe Ser Val Asn
340 345 350

Ile Phe Lys Val Trp Val Gln Ala Phe Lys Val Glu Gly Gly Gln Phe
355 360 365

Gly Ser Val Glu Glu Cys Leu Leu Asp Glu Asn Asn Met Leu Ile Pro
370 375 380

Ile Ala Val Gly Gly Ala Leu Ala Gly Leu Val Leu Ile Val Leu Ile
385 390 395 400

Ala Tyr Leu Val Gly Arg Lys Arg Ser His Ala Gly Tyr Gln Thr
405 410 415

<210> 11

<211> 413

<212> PRT

<213> Canis lupus familiaris

<400> 11

Met Ala Ala Phe Gly Gly Ala Arg Pro Arg Pro Leu Leu Leu Leu Leu
1 5 10 15

Leu Ala Gly Leu Val His Gly Ala Ala Val Phe Val Val Lys Asp
20 25 30

Ala Asn Gly Thr Ala Cys Ile Met Ala Asn Phe Ser Ala Ala Phe Leu
35 40 45

Ala Ser Tyr Glu Thr Arg Ser Gly Pro Lys Asn Val Thr Phe Asp Leu
50 55 60

Pro Ser Asp Ala Val Val Leu Asn Ser Ser Ser Cys Gly Lys Glu Asn
65 70 75 80

Thr Ser Asp Pro Ser Leu Met Ile Ala Phe Gly Lys Gly His Gly Leu
85 90 95

Thr Leu Asn Phe Thr Arg Asn Ala Thr Arg Tyr Ser Val Gln Leu Met
100 105 110

Ser Phe Ile Tyr Asn Leu Ser Asp Thr Gln Ile Phe Pro Asn Ala Ser
115 120 125

Ser Lys Glu Thr Lys Thr Val Glu Ser Ala Thr Asp Ile Arg Ala Asp
130 135 140

Ile Asn Lys Lys Tyr Arg Cys Val Ser Asn Thr Gln Ile His Met His
145 150 155 160

ITI-08-PCT_Sequence_Listing_ST25.txt

```

Asn Val Thr Val Thr Phe His Asp Val Thr Ile Gln Ala Tyr Leu Ala
      165                      170                      175

Asn Ser Asn Phe Ser Lys Glu Glu Thr Arg Cys Glu Gln Asp Gly Pro
      180                      185                      190

Phe Pro Thr Thr Ala Pro Pro Pro Pro Pro His Pro Ser Pro Ser Pro
      195                      200                      205

Ala Pro Glu Ser Pro Ser Val His Lys Tyr Asn Val Ser Gly Ala Asn
      210                      215                      220

Gly Thr Cys Leu Leu Ala Ser Met Gly Leu Gln Leu Asn Val Thr Tyr
225                      230                      235                      240

Lys Lys Lys Asp Asn Thr Thr Val Val Lys Val Val Ser Ile Asn Pro
      245                      250                      255

Asn Lys Thr Thr Ala Gly Gly Ser Cys Gly Ala Gln Leu Val Thr Leu
      260                      265                      270

Glu Leu Arg Ser Glu Ser Val Thr Leu Leu Ala Phe Gln Phe Gly Met
      275                      280                      285

Asn Ala Ser Thr Ser Arg Phe Phe Leu Gln Gly Ile Gln Leu Asn Met
      290                      295                      300

Thr Leu Pro Asp Ala Arg Asp Pro Thr Phe Lys Ala Gly Asn Asn Ser
305                      310                      315                      320

Leu Arg Ala Leu Gln Ala Thr Ile Gly Asn Ser Tyr Lys Cys Asn Ala
      325                      330                      335

Gly Glu His Val Gln Val Thr Glu Ala Phe Ser Val Asn Ile Ile Lys
      340                      345                      350

Val Trp Val Gln Ala Phe Gln Val Gln Gly Asp Lys Phe Gly Ser Val
      355                      360                      365

Glu Glu Cys Gln Leu Asp Glu Asn Ser Met Leu Ile Pro Ile Ala Val
      370                      375                      380

Gly Gly Ala Leu Ala Gly Leu Val Leu Ile Val Leu Ile Ala Tyr Leu
385                      390                      395                      400

Ile Gly Arg Lys Arg Ser His Ala Gly Tyr Gln Thr Ile
      405                      410

```

```

<210> 12
<211> 417
<212> PRT
<213> Oryctolagus cuniculus

```

ITI-08-PCT_Sequence_Listing_ST25.txt

<400> 12

```

Met Glu Ala Pro Gly Gly Ala Arg Arg Pro Leu Leu Leu Leu Leu Leu
1          5          10          15

Leu Gly Leu Val His Gly Ala Ser Ala Val Phe Val Val Arg Asn Ser
          20          25          30

Asn Gly Thr Ala Cys Ile Met Ala Asn Phe Ser Ala Val Phe Ser Val
          35          40          45

Ile Tyr Glu Ser Lys Ser Gly Tyr Lys Asn Ala Ser Phe Glu Leu Pro
          50          55          60

Ala Thr Ala Glu Val Gln Asn Thr Ser Ser Cys Gly Arg Glu Asn Thr
65          70          75          80

Ser Asn Pro Ser Leu Gln Ile Ala Phe Gly Arg Gly His Val Leu Ala
          85          90          95

Leu Asn Phe Thr Arg Asn Ala Thr Leu Tyr Ser Val Pro Leu Leu Ser
          100          105          110

Phe Val Tyr Asn Leu Ser Asp Ser Asp Leu Phe Pro Asn Ala Ser Ser
          115          120          125

Lys Asp Ile Lys Thr Val Gly Ser Thr Thr Asp Ile Lys Ala Asp Ile
          130          135          140

Asp Lys Arg Tyr Arg Cys Val Ser Asp Ser Lys Val Pro Met Gly Asn
145          150          155          160

Val Thr Val Thr Leu Gln Asp Ala Thr Ile Gln Ala Tyr Leu Trp Asn
          165          170          175

Asn Ser Phe Ser Gln Ala Glu Ser Arg Cys Arg Gln Asp Met Pro Ser
          180          185          190

Pro Thr Thr Ala Pro Pro Ala Pro Pro Val Pro Pro Ser Pro Pro Ser
          195          200          205

Pro Ser Pro Pro Pro Lys Pro Glu Ser Pro Ser Val Ser Arg Tyr Asn
          210          215          220

Val Ser Asp Gly Asn Ala Thr Cys Leu Leu Ala Ser Met Gly Leu Gln
225          230          235          240

Leu Asn Leu Thr Tyr Val His Arg Asp Asn Ala Thr Val Thr Arg Val
          245          250          255

Phe Asn Ile Asn Pro Asn Lys Thr Lys Pro Ser Gly His Cys Gly Ala

```

ITI-08-PCT_Sequence_Listing_ST25.txt

260

265

270

Gln Gln Val Thr Leu Glu Leu Gln Ser Glu Arg Ser Thr Val Leu Val
275 280 285

Phe Gln Phe Gly Met Asn Ala Ser Ser Gly Gln Tyr Phe Leu Gln Gly
290 295 300

Val Leu Leu Asn Thr Thr Leu Pro Asp Ala Arg Glu Pro Ala Phe Ser
305 310 315 320

Ala Ser Asn Ser Ser Leu Arg Ala Leu Gln Ala Thr Leu Gly Asn Ser
325 330 335

Tyr Lys Cys Asn Ser Glu Glu His Val Arg Val Thr Pro Ala Phe Ser
340 345 350

Leu Ser Ile Phe Lys Val Trp Val Gln Ala Phe Gln Val Lys Gly Asp
355 360 365

Lys Phe Gly Ser Val Glu Glu Cys Leu Leu Asp Gln Asp Ser Met Leu
370 375 380

Ile Pro Ile Ala Val Gly Gly Ala Leu Ala Gly Leu Val Leu Val Val
385 390 395 400

Leu Ile Ala Tyr Leu Ile Gly Arg Lys Arg Ser His Ala Gly Tyr Gln
405 410 415

Thr

<210> 13

<211> 409

<212> PRT

<213> Bos taurus

<400> 13

Met Ala Ala Pro Gly Gly Ala Arg Arg Arg Pro Leu Leu Leu Leu Leu
1 5 10 15

Phe Ala Gly Leu Val His Gly Ala Ser Ala Val Phe Val Val Lys Asn
20 25 30

Gly Asn Gly Thr Ala Cys Ile Met Ala Asp Phe Ser Ala Thr Phe Leu
35 40 45

Thr Ser Tyr Asp Thr Arg Ser Gly Pro Gln Asn Lys Ser Phe Glu Leu
50 55 60

Pro Ala Gly Ala Glu Val Ser Asn Ser Ser Ser Cys Gly Lys Glu Asn
65 70 75 80

ITI-08-PCT_Sequence_Listing_ST25.txt

Ala	Ser	Asp	Ser	Ser	Leu	Val	Ile	Thr	Phe	Gly	Arg	Gly	His	Thr	Leu	85	90	95
Thr	Leu	Ile	Phe	Thr	Arg	Asn	Ala	Thr	Arg	Tyr	Glu	Val	Gln	Leu	Met	100	105	110
Arg	Phe	Ala	Tyr	Asn	Leu	Ser	Asp	Thr	Asp	Thr	Phe	Pro	Asn	Ser	Ser	115	120	125
Ser	Thr	Gly	Val	Lys	Thr	Val	Glu	Ser	Ala	Thr	Asp	Ile	Lys	Ala	Asp	130	135	140
Ile	Asn	Lys	Thr	Tyr	Arg	Cys	Val	Ser	Glu	Thr	Gln	Val	Asn	Met	Asp	145	150	155
Asn	Val	Thr	Val	Thr	Leu	Arg	Asp	Ala	Ala	Ile	Gln	Ala	Tyr	Leu	Ser	165	170	175
Ser	Ser	Asn	Phe	Ser	Arg	Glu	Glu	Thr	Arg	Cys	Glu	Gln	Asp	Leu	Pro	180	185	190
Thr	Pro	Thr	Thr	Pro	Pro	Gln	Pro	Ala	Pro	Thr	Pro	Ala	Pro	Ala	Ser	195	200	205
Pro	Ala	Val	Phe	Arg	Tyr	Asn	Val	Ser	Gly	Ser	Asn	Gly	Thr	Cys	Leu	210	215	220
Leu	Ala	Ser	Met	Gly	Leu	Gln	Leu	Asn	Val	Thr	Tyr	Arg	Arg	Val	Asp	225	230	235
Asn	Lys	Thr	Val	Thr	Arg	Glu	Phe	Asn	Val	Asn	Pro	Asn	Lys	Thr	Thr	245	250	255
Phe	Gly	Gly	Asn	Cys	Ser	Ala	Thr	Leu	Ala	Thr	Leu	Glu	Leu	His	Ser	260	265	270
Glu	Asn	Leu	Leu	Leu	Leu	Ala	Leu	Gln	Phe	Val	Met	Asn	Glu	Ser	Ser	275	280	285
Ser	Arg	Val	Phe	Leu	Gln	Gly	Val	Gln	Leu	Asn	Leu	Thr	Leu	Pro	Asp	290	295	300
Ala	Lys	Glu	Gly	Ser	Phe	Thr	Ala	Thr	Asn	Ser	Ser	Leu	Arg	Ala	Leu	305	310	315
Gln	Ala	Thr	Ala	Gly	Asn	Ser	Tyr	Lys	Cys	Asn	Ala	Glu	Gln	Arg	Leu	325	330	335
Arg	Val	Thr	Ser	Ser	Phe	Ser	Leu	Asn	Met	Phe	Arg	Val	Trp	Leu	Gln	340	345	350

ITI-08-PCT_Sequence_Listing_ST25.txt

Ala Phe Arg Val Asp Gly Asp Lys Phe Gly Pro Val Glu Glu Cys Gln
355 360 365

Leu Asp Glu Asn Ser Met Leu Ile Pro Ile Ala Val Gly Gly Ala Leu
370 375 380

Ala Gly Leu Val Leu Ile Val Leu Leu Ala Tyr Leu Ile Gly Arg Lys
385 390 395 400

Arg Ser His Ala Gly Tyr Gln Thr Ile
405

<210> 14

<211> 407

<212> PRT

<213> Rattus norvegicus

<400> 14

Met Ala Ala Pro Gly Ala Arg Arg Pro Leu Leu Leu Leu Leu Ala
1 5 10 15

Gly Leu Ala His Ser Ala Pro Ala Leu Phe Glu Val Lys Asp Asn Asn
20 25 30

Gly Thr Ala Cys Ile Met Ala Ser Phe Ser Ala Ser Phe Leu Thr Thr
35 40 45

Tyr Asp Ala Gly His Val Ser Lys Val Ser Asn Met Thr Leu Pro Ala
50 55 60

Ser Ala Glu Val Leu Lys Asn Ser Ser Ser Cys Gly Glu Lys Asn Ala
65 70 75 80

Ser Glu Pro Thr Leu Ala Ile Thr Phe Gly Glu Gly Tyr Leu Leu Lys
85 90 95

Leu Thr Phe Thr Lys Asn Thr Thr Arg Tyr Ser Val Gln His Met Tyr
100 105 110

Phe Thr Tyr Asn Leu Ser Asp Thr Gln Phe Phe Pro Asn Ala Ser Ser
115 120 125

Lys Gly Pro Asp Thr Val Asp Ser Thr Thr Asp Ile Lys Ala Asp Ile
130 135 140

Asn Lys Thr Tyr Arg Cys Val Ser Asp Ile Arg Val Tyr Met Lys Asn
145 150 155 160

Val Thr Ile Val Leu Trp Asp Ala Thr Ile Gln Ala Tyr Leu Pro Ser
165 170 175

ITI-08-PCT_Sequence_Listing_ST25.txt

```

Ser Asn Phe Ser Lys Glu Glu Thr Arg Cys Pro Gln Asp Gln Pro Ser
    180                      185                      190

Pro Thr Thr Gly Pro Pro Ser Pro Ser Pro Pro Leu Val Pro Thr Asn
    195                      200                      205

Pro Ser Val Ser Lys Tyr Asn Val Thr Gly Asp Asn Gly Thr Cys Leu
    210                      215                      220

Leu Ala Ser Met Ala Leu Gln Leu Asn Ile Thr Tyr Met Lys Lys Asp
    225                      230                      235                      240

Asn Thr Thr Val Thr Arg Ala Phe Asn Ile Asn Pro Ser Asp Lys Tyr
    245                      250                      255

Ser Gly Thr Cys Gly Ala Gln Leu Val Thr Leu Lys Val Gly Asn Lys
    260                      265                      270

Ser Arg Val Leu Glu Leu Gln Phe Gly Met Asn Ala Thr Ser Ser Leu
    275                      280                      285

Phe Phe Leu Gln Gly Val Gln Leu Asn Met Thr Leu Pro Asp Ala Ile
    290                      295                      300

Glu Pro Thr Phe Ser Thr Ser Asn Tyr Ser Leu Lys Ala Leu Gln Ala
    305                      310                      315                      320

Ser Val Gly Asn Ser Tyr Lys Cys Asn Ser Glu Glu His Ile Phe Val
    325                      330                      335

Ser Lys Ala Leu Ala Leu Asn Val Phe Ser Val Gln Val Gln Ala Phe
    340                      345                      350

Arg Val Glu Ser Asp Arg Phe Gly Ser Val Glu Glu Cys Val Gln Asp
    355                      360                      365

Gly Asn Asn Met Leu Ile Pro Ile Ala Val Gly Gly Ala Leu Ala Gly
    370                      375                      380

Leu Val Leu Ile Val Leu Ile Ala Tyr Leu Ile Gly Arg Lys Arg Ser
    385                      390                      395                      400

His Ala Gly Tyr Gln Thr Ile
    405

```

```

<210> 15
<211> 414
<212> PRT
<213> Gallus gallus

```

```

<400> 15

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Met	Gly	Gly	Ala	Ala	Arg	Ala	Val	Leu	Leu	Gly	Phe	Leu	Gln	Ala	Ser	1	5	10	15
Ser	Ser	Phe	Asp	Val	Arg	Asp	Ser	Thr	Gly	Lys	Val	Cys	Ile	Ile	Ala	20	25	30	
Asn	Leu	Thr	Val	Ala	Phe	Ser	Val	Glu	Tyr	Lys	Ser	Ser	Gly	Gln	Lys	35	40	45	
Gln	Phe	Ala	His	Phe	Phe	Leu	Pro	Gln	Asn	Ala	Thr	Ser	Gln	Ser	His	50	55	60	
Ser	Ser	Cys	Gly	Glu	Gly	Asn	Thr	Ser	His	Pro	Ile	Leu	Ala	Leu	Ser	65	70	75	80
Phe	Gly	Ala	Gly	His	Leu	Ile	Ser	Leu	Asn	Phe	Ser	Lys	Thr	Leu	Asp	85	90	95	
Lys	Tyr	Gln	Val	Glu	Glu	Leu	Thr	Phe	His	Tyr	Asn	Leu	Ser	Asp	Glu	100	105	110	
Thr	Leu	Phe	Pro	Asn	Ala	Thr	Glu	Gly	Lys	Val	Met	Val	Ala	Thr	Gln	115	120	125	
Lys	Ser	Val	Ile	Gln	Ala	Arg	Ile	Gly	Thr	Glu	Tyr	Arg	Cys	Ile	Asn	130	135	140	
Ser	Lys	Tyr	Val	Arg	Met	Lys	His	Val	Asn	Ile	Thr	Phe	Ser	Asn	Val	145	150	155	160
Thr	Leu	Glu	Ala	Tyr	Pro	Thr	Asn	Asp	Thr	Phe	Ser	Ala	Asn	Lys	Thr	165	170	175	
Glu	Cys	Arg	Glu	Asp	Met	Val	Ser	Thr	Thr	Thr	Val	Ala	Pro	Thr	Thr	180	185	190	
Pro	Lys	His	Ala	Thr	Ser	Gln	Val	Pro	Thr	Thr	Ser	Pro	Ala	Pro	Thr	195	200	205	
Ala	Ala	Pro	Ser	Ser	Pro	Ala	Val	Gly	Lys	Tyr	Asn	Val	Thr	Gly	Ala	210	215	220	
Asn	Gly	Thr	Cys	Val	Leu	Ala	Ser	Met	Gly	Leu	Gln	Leu	Asn	Ile	Thr	225	230	235	240
Tyr	Val	Lys	Lys	Asp	Glu	Lys	Met	Gly	Leu	Asp	Leu	Leu	Asn	Phe	Ile	245	250	255	
Pro	His	Asn	Thr	Ser	Ala	Ser	Gly	Met	Cys	Glu	Ser	Thr	Ser	Ala	Phe	260	265	270	
Leu	Asn	Leu	Ala	Phe	Glu	Lys	Thr	Lys	Ile	Thr	Phe	His	Phe	Val	Leu				

ITI-08-PCT_Sequence_Listing_ST25.txt

275

280

285

Asn Ala Ser Ser Glu Lys Phe Phe Leu Gln Gly Val Asn Val Ser Thr
290 295 300

Thr Leu Pro Ser Glu Ala Lys Ala Pro Thr Phe Glu Ala Ser Asn Asp
305 310 315 320

Ser Met Ser Glu Ser Arg Ala Thr Val Gly Asn Ser Tyr Lys Cys Ser
325 330 335

Ala Glu Glu Asn Phe Gln Val Thr Asp Lys Ala Leu Val Asn Val Phe
340 345 350

Asn Val Gln Val Gln Ala Phe Lys Val Asp Gly Asp Lys Phe Gly Ala
355 360 365

Met Glu Glu Cys Gln Leu Asp Glu Asn Asn Met Leu Ile Pro Ile Ile
370 375 380

Val Gly Ala Ala Leu Ala Gly Leu Val Leu Ile Val Leu Ile Ala Tyr
385 390 395 400

Leu Ile Gly Arg Lys Arg Ser His Ala Gly Tyr Gln Thr Ile
405 410

<210> 16

<211> 413

<212> PRT

<213> Sus scrofa

<400> 16

Met Ala Ala Pro Gly Gly Ala Trp Arg Arg Pro Leu Leu Leu Leu Leu
1 5 10 15

Leu Leu Leu Gly Leu Ala Arg Gly Ala Ser Ala Val Phe Val Val Ser
20 25 30

Asp Gly Asn Gly Thr Ala Cys Ile Met Ala Asp Phe Ala Ala Ala Phe
35 40 45

Glu Ile Ser Tyr Asp Ser Arg Ser Gly Ala Lys Asn Thr Thr Phe Ser
50 55 60

Leu Pro Ala Ser Ala Gln Val Leu Asn Ser Ser Ser Cys Gly Lys Glu
65 70 75 80

Asn Thr Ser Asp Ser Ser Leu Val Ile Ala Phe Gly Arg Gly His Thr
85 90 95

Leu Thr Leu Ser Phe Thr Arg Asn Ala Thr Arg Tyr Ser Val Gln Leu

ITI-08-PCT_Sequence_Listing_ST25.txt

100	105	110															
Met	Thr	Leu	Val	Tyr	Asn	Leu	Ser	Asp	Ala	Glu	Phe	Phe	Pro	Ser	Ala		
	115						120					125					
Ser	Ser	Lys	Gly	Thr	Lys	Thr	Val	Ala	Ala	Ser	Thr	Asp	Ile	Arg	Ala		
	130						135					140					
Asp	Leu	Asn	Thr	Lys	Tyr	Arg	Cys	Val	Ser	Asn	Ser	Gln	Val	His	Leu		
145					150					155					160		
Leu	Asn	Val	Thr	Val	Thr	Leu	Gly	Asn	Ala	Thr	Ile	Gln	Ala	Tyr	Leu		
				165					170					175			
Ala	Asn	Asn	Ser	Phe	Ser	Gln	Gln	Glu	Thr	Arg	Cys	Glu	Gln	Asp	Lys		
			180					185					190				
Pro	Ser	Pro	Pro	Thr	Pro	Thr	Ala	Pro	Pro	Thr	Pro	Thr	Pro	Thr	Pro		
		195					200					205					
Ala	Pro	Thr	Ser	Pro	Val	Val	Ser	Arg	Tyr	Asn	Val	Ser	Gly	Ala	Asn		
	210					215					220						
Gly	Thr	Cys	Leu	Leu	Ala	Ser	Met	Gly	Leu	Gln	Leu	Asn	Val	Thr	Tyr		
225					230					235					240		
Arg	Thr	Lys	Asp	Asn	Thr	Thr	Val	Thr	Arg	Gly	Leu	Asn	Ile	Asn	Pro		
				245					250					255			
Asn	Lys	Thr	Thr	Phe	Gly	Gly	Ser	Cys	Ser	Ala	Gln	Leu	Val	Thr	Leu		
			260					265					270				
Glu	Leu	Gln	Gly	Glu	Ser	Leu	Arg	Leu	Leu	Ala	Leu	Gln	Phe	Ala	Leu		
		275					280					285					
Asn	Thr	Ser	Ser	Ser	Arg	Val	Phe	Leu	Gln	Gly	Val	Gln	Leu	Asn	Met		
	290					295					300						
Thr	Leu	Pro	Asp	Ala	Arg	Asp	Pro	Ser	Phe	Ser	Ala	Ala	Asn	Ser	Ser		
305					310					315					320		
Leu	Arg	Ala	Leu	Gln	Ala	Thr	Ala	Gly	Asn	Ser	Tyr	Lys	Cys	Arg	Ser		
				325					330					335			
Glu	Gln	Arg	Leu	Gln	Val	Thr	Glu	Ala	Phe	Ala	Leu	Asn	Val	Phe	Gln		
			340					345					350				
Val	Arg	Val	Gln	Ala	Phe	Arg	Val	Asp	Gly	Asp	Lys	Phe	Gly	Pro	Ala		
		355					360					365					
Glu	Glu	Cys	Gln	Leu	Asp	Glu	Asn	Ser	Met	Leu	Ile	Pro	Ile	Ala	Val		
	370					375					380						

ITI-08-PCT_Sequence_Listing_ST25.txt

Gly Gly Ala Leu Ala Gly Leu Val Leu Val Val Leu Met Ala Tyr Leu
385 390 395 400

Val Gly Arg Lys Arg Ser His Ala Gly Tyr Gln Thr Ile
405 410

<210> 17

<211> 422

<212> PRT

<213> Monodelphis domestica

<400> 17

Met Ala Glu Pro Gly Gly Ala Arg Thr Pro Gln Arg Leu Leu Leu Leu
1 5 10 15

Leu Leu Gly Leu Ile His Val Ala Ser Ser Ile Phe Val Val Lys Asn
20 25 30

Gly Thr Gly Thr Ala Cys Ile Met Ala Asn Phe Ser Ala Thr Phe Ser
35 40 45

Met Asn Tyr Thr Thr Lys Ser Gly Leu Glu Ser Thr Thr Phe Arg Leu
50 55 60

Pro Gln Asn Ala Ser Val Met Asn Ser Ser Ser Cys Gly Lys Glu Asn
65 70 75 80

Thr Ser Asn Pro Ile Leu Glu Ile Gly Phe Gly Gly Gly His Thr Leu
85 90 95

Thr Met Asn Phe Ser Ser Thr Thr Gln Ser Tyr Gln Val Glu Leu Leu
100 105 110

Ser Phe Ser Tyr Asn Leu Ser Asp Ala Thr Leu Phe Pro Asn Ala Ser
115 120 125

Lys Gly Ser Glu Glu Ser Ser Val Lys Ser Lys Thr Asp Ile Gln Ala
130 135 140

Asp Ile His Lys Lys Tyr Arg Cys Val Ser Ser Asn Arg Ile Thr Met
145 150 155 160

Ser Asn Val Thr Ile Val Leu Ser Asp Val Thr Ile Gln Ala Tyr Leu
165 170 175

Ser Asn Asn Thr Phe Ser Lys Glu Glu Thr Arg Cys Ser Gln Asp Thr
180 185 190

Pro Ser Pro Ser Pro Val Pro Thr Thr His Pro Thr Thr Ile Pro Val
195 200 205

ITI-08-PCT_Sequence_Listing_ST25.txt

```

Pro Thr Pro Thr Pro Thr Arg Pro Pro Thr Pro Ala Glu Ile Pro Pro
 210                215                220

Ile Phe Lys Tyr Asn Val Ser Asp Ala Asn Gly Thr Cys Leu Leu Ala
225                230                235                240

Ser Met Gly Leu Gln Leu Asn Ile Thr Tyr Ala Lys Lys Asp Asn Ser
                245                250                255

Ser Ala Arg Ile Ile Trp Asn Ile Asn Pro Asn Lys Thr Val Ala Gly
                260                265                270

Gly Ser Cys Ser Pro Gln Val Ala Ile Leu Glu Leu Gln Thr Glu Asn
                275                280                285

Ser Thr Leu Ala Phe Ser Phe Gly Met Asn Ala Thr Thr Ser Lys Phe
 290                295                300

Phe Leu Arg Glu Ile Arg Phe His Lys Phe Phe Pro Asp Ala Lys Asp
305                310                315                320

Pro Ala Phe Gly Ala Val Asn Ser Ser Leu Lys Glu Leu Gln Ala Thr
                325                330                335

Val Gly Asn Ser Tyr Lys Cys Asn Ala Glu Glu Asn Val His Val Thr
                340                345                350

Asp Gly Phe Ser Val Asn Ile Phe Arg Val Arg Val Gln Ala Phe Lys
                355                360                365

Val Glu Gly Asp Lys Phe Gly Ser Val Glu Glu Cys Leu Leu Asp Glu
 370                375                380

Asn Asn Met Leu Ile Pro Ile Ala Val Gly Gly Ala Leu Ala Gly Leu
385                390                395                400

Val Leu Ile Val Leu Ile Ala Tyr Leu Ile Gly Arg Lys Arg Ser His
                405                410                415

Ala Gly Tyr Gln Thr Ile
                420

```

```

<210> 18
<211> 415
<212> PRT
<213> Meleagris gallopavo

```

```

<400> 18

```

```

Met Ala Arg Ala Leu Leu Ala Ala Val Leu Leu Gly Phe Leu Gln Ala
 1                5                10                15

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Ser	Ser	Ser	Phe	Asp	Val	Arg	Asp	Ser	Thr	Gly	Lys	Val	Cys	Ile	Ile	20	25	30
Ala	Asn	Leu	Thr	Val	Ala	Phe	Ser	Val	Glu	Tyr	Lys	Ser	Asn	Gly	Gln	35	40	45
Lys	Gln	Phe	Ala	His	Phe	Phe	Leu	Pro	Gln	Asn	Ala	Thr	Ser	Gln	Ser	50	55	60
His	Ser	Ser	Cys	Gly	Glu	Gly	Asn	Thr	Ser	His	Pro	Ile	Leu	Ala	Leu	65	70	75
Ser	Phe	Gly	Ala	Gly	His	Leu	Leu	Ser	Leu	Asn	Phe	Ser	Lys	Thr	Leu	85	90	95
Asp	Lys	Tyr	Gln	Val	Glu	Glu	Leu	Thr	Phe	His	Tyr	Asn	Leu	Ser	Asp	100	105	110
Glu	Thr	Leu	Phe	Pro	Asn	Ala	Ser	Glu	Gly	Lys	Val	Met	Glu	Val	Thr	115	120	125
Gln	Lys	Ser	Val	Ile	Gln	Ala	Arg	Ile	Gly	Thr	Glu	Tyr	Arg	Cys	Ile	130	135	140
Asn	Ser	Lys	Tyr	Ile	Tyr	Ile	Arg	His	Val	Asn	Ile	Thr	Phe	Ser	Asn	145	150	155
Val	Thr	Leu	Glu	Ala	Tyr	Pro	Thr	Asn	Gly	Thr	Phe	Ser	Thr	Asn	Lys	165	170	175
Thr	Glu	Cys	Ser	Glu	Asp	Met	Val	Ser	Thr	Thr	Thr	Val	Ala	Pro	Thr	180	185	190
Thr	Pro	Lys	His	Ile	Thr	Ser	Gln	Val	Pro	Ala	Thr	Ser	Pro	Ala	Pro	195	200	205
Thr	Ala	Ala	Pro	Ser	Asn	Pro	Ala	Val	Gly	Lys	Tyr	Asn	Val	Thr	Gly	210	215	220
Ala	Asn	Gly	Thr	Cys	Val	Leu	Ala	Ser	Met	Gly	Leu	Gln	Leu	Asn	Ile	225	230	235
Thr	Tyr	Leu	Lys	Lys	Asp	Gly	Lys	Thr	Gly	Leu	Asp	Leu	Leu	Asn	Phe	245	250	255
Val	Pro	His	Asn	Thr	Asn	Ala	Ser	Gly	Thr	Cys	Glu	Asn	Thr	Ser	Ala	260	265	270
Phe	Leu	Asn	Leu	Ala	Phe	Glu	Lys	Thr	Lys	Ile	Thr	Phe	His	Phe	Val	275	280	285

ITI-08-PCT_Sequence_Listing_ST25.txt

Leu Asn Ala Ser Ser Glu Lys Phe Phe Leu Gln Gly Val Asn Val Ser
290 295 300

Thr Thr Leu Pro Ser Glu Ala Lys Ala Pro Met Phe Glu Ala Ser Asn
305 310 315 320

Asp Ser Met Ser Glu Leu Arg Ala Thr Val Gly Asn Ser Tyr Lys Cys
325 330 335

Ser Ala Glu Glu Asn Leu Gln Val Thr Asp Lys Ala Leu Val Asn Val
340 345 350

Phe Asn Val Gln Val Gln Ala Phe Lys Val Asp Gly Asp Lys Phe Gly
355 360 365

Ala Val Glu Glu Cys Gln Leu Asp Glu Asn Asn Met Leu Ile Pro Ile
370 375 380

Ile Val Gly Ala Ala Leu Ala Gly Leu Val Leu Ile Val Leu Ile Ala
385 390 395 400

Tyr Leu Ile Gly Arg Lys Arg Ser His Ala Gly Tyr Gln Thr Ile
405 410 415

<210> 19

<211> 415

<212> PRT

<213> Taeniopygia guttata

<400> 19

Met Ala Arg Gly Leu Leu Ala Ala Ala Ala Leu Leu Gly Phe Leu Gln
1 5 10 15

Ala Ser Ser Ser Phe Glu Val Lys Asp Ser Ser Gly Lys Val Cys Ile
20 25 30

Leu Ala Asp Leu Thr Val Ala Phe Ser Val Glu Tyr Lys Thr Asn Val
35 40 45

Gln Lys Glu Phe Val His Phe Phe Leu Pro Gln Asn Ala Ser Val Asp
50 55 60

Ser Gln Ser Ser Cys Gly Lys Asp Asn Ala Ser His Pro Ile Leu Val
65 70 75 80

Leu Asp Phe Gly Gly Gly His Ser Leu Ser Leu Asn Phe Ser Glu Ser
85 90 95

Ala Asp Lys Tyr Gln Val Glu Glu Leu Val Phe His Tyr Asn Leu Ser
100 105 110

ITI-08-PCT_Sequence_Listing_ST25.txt

Asp	Ala	Thr	Leu	Phe	Pro	Asn	Ser	Ser	Thr	Gly	Gly	Met	Lys	Thr	Val	115	120	125	
Ser	His	Lys	Ser	Ile	Ile	Gln	Ala	His	Met	Gly	Thr	Gln	Tyr	Arg	Cys	130	135	140	
Ile	Asn	Ser	Lys	His	Ile	Asn	Met	Lys	Asn	Val	Asn	Val	Thr	Phe	Ser	145	150	155	160
Asn	Val	Thr	Leu	Glu	Ala	Tyr	Leu	Thr	Asn	Gly	Thr	Leu	Ser	Val	Asn	165	170	175	
Lys	Thr	Glu	Cys	Ala	Glu	Asp	Arg	Val	Ser	Thr	Thr	Thr	Met	Val	Pro	180	185	190	
Thr	Thr	Pro	Lys	Gln	Thr	Thr	Ser	Gln	Ser	Pro	Thr	Thr	Gly	Pro	Ala	195	200	205	
Pro	Thr	Ser	Pro	Pro	Asn	Pro	Thr	Val	Gly	Lys	Tyr	Asn	Val	Thr	Gly	210	215	220	
Pro	Asn	Gly	Thr	Cys	Val	Leu	Ala	Tyr	Met	Gly	Leu	Gln	Leu	Asn	Ile	225	230	235	240
Thr	Tyr	Gln	Gln	Lys	Asp	Glu	Lys	Met	Gly	Leu	Asp	Leu	Leu	Asn	Phe	245	250	255	
Val	Pro	His	Asn	Thr	Thr	Ser	Ser	Gly	Arg	Cys	Asp	Asn	Thr	Ser	Ala	260	265	270	
Leu	Leu	Asn	Leu	Thr	Phe	Glu	Lys	Thr	Arg	Val	Ile	Phe	Gln	Phe	Ala	275	280	285	
Leu	Asn	Ala	Thr	Ala	Glu	Lys	Phe	Phe	Leu	Gln	Gly	Val	Ser	Val	Ser	290	295	300	
Thr	Thr	Leu	Pro	Ser	Glu	Ala	Lys	Asn	Pro	Lys	Phe	Glu	Ala	Thr	Asn	305	310	315	320
Asn	Ser	Met	Ser	Glu	Leu	Arg	Ala	Ser	Val	Gly	Asn	Ser	Tyr	Lys	Cys	325	330	335	
Ser	Ser	Glu	Glu	Asn	Leu	Gln	Val	Thr	Asp	Gln	Ala	Leu	Val	Asn	Val	340	345	350	
Phe	Asn	Val	Gln	Val	Gln	Ile	Phe	Lys	Ile	Asp	Gly	Asp	Lys	Phe	Gly	355	360	365	
Pro	Val	Glu	Glu	Cys	Gln	Leu	Asp	Glu	Asn	Asn	Met	Leu	Ile	Pro	Ile	370	375	380	
Ile	Val	Gly	Ala	Ala	Leu	Ala	Gly	Leu	Val	Leu	Ile	Val	Leu	Ile	Ala				

ITI-08-PCT_Sequence_Listing_ST25.txt

385 390 395 400

Tyr Leu Ile Gly Arg Lys Arg Ser His Ala Gly Tyr Gln Thr Ile
405 410 415

<210> 20
<211> 418
<212> PRT
<213> Anolis carolinensis

<400> 20

Met Val Ser Ser Ser Ser Cys Arg Arg Gly Leu Leu Leu Ala Ala Val
1 5 10 15

Leu Leu Gly Phe Leu Gln Ala Ser Ser Thr Phe Glu Val Arg Asp Lys
20 25 30

Thr Gly Lys Ile Cys Ile Leu Ala Asn Phe Ser Ala Glu Phe Thr Val
35 40 45

Asp Tyr Ser Thr Lys Ala Lys Val Glu Arg Lys Thr Phe Gln Leu Pro
50 55 60

Ser Ser Ala His Ile Asn Lys Glu Ser Ser Ser Cys Gly Lys Glu Lys
65 70 75 80

Glu Thr Ser Gln Val Leu Val Val Glu Phe Gly Thr Gly Asn Ser Leu
85 90 95

Thr Phe Thr Phe Glu Lys Ser Asn Asp Phe Tyr His Val Ser Asn Leu
100 105 110

Thr Phe Ser Tyr Asn Leu Ser Asp Ser Ser Phe Phe Pro Asn Ser Ser
115 120 125

Gly Gly Gln Arg Glu Val Ser Arg Ala Gly Asp Ile Gln Ala Asn Ile
130 135 140

Asn Thr Thr Tyr Arg Cys Arg Ser Asn His Arg Val Asn Met Thr Asn
145 150 155 160

Val Thr Val Leu Phe Ser Asn Val Thr Leu Glu Ala Tyr Leu Pro Asn
165 170 175

Asn Ala Phe Ser Lys Asn Asp Ser Val Cys Ala Glu Asp Lys Thr Ser
180 185 190

Thr Val Ala Pro Pro Ile Thr Thr His Ile Pro Thr Thr Thr Ser Leu
195 200 205

Ala Pro Pro Thr Pro Pro Pro Thr Asp Thr Pro Lys Ile Gly Arg Tyr

ITI-08-PCT_Sequence_Listing_ST25.txt

210

215

220

Asn Val Thr Gly Leu His Gly Ile Cys Leu Leu Ala Thr Met Gly Leu
225 230 235 240

Gln Val Asn Val Thr Tyr Ser Thr Lys Asn Lys Thr Ser Lys Ser Glu
245 250 255

Leu Leu Asn Leu Pro Pro Thr Ala Glu Val Ser Gly Thr Cys Glu Asn
260 265 270

Ser Ser Ile Thr Leu Asn Leu Thr Ser Glu Ser Thr Ser Leu Ser Phe
275 280 285

Gln Phe Ser Gln Asn Thr Ser Thr Glu Lys Tyr Phe Leu Gln Gly Ile
290 295 300

Ile Val Thr Ala Asn Leu Pro Pro Glu Ala Thr Glu Lys Asn Ile Ser
305 310 315 320

Tyr Ser Asn His Thr Leu Asn Ala Leu Lys Thr Ser Val Gly Lys Ser
325 330 335

Tyr Lys Cys Ile Ala Glu Glu Ser Ile Trp Ile Ser Gly Lys Ala Ala
340 345 350

Val Asn Ile Phe Asn Ile Gln Leu Gln Ala Phe Lys Ile Pro Gly Asp
355 360 365

Lys Phe Gly Ala Val Glu Glu Cys Gln Leu Asp Glu Asn Asn Met Leu
370 375 380

Ile Pro Ile Ile Val Gly Ala Ala Leu Ala Gly Leu Val Leu Ile Val
385 390 395 400

Leu Ile Ala Tyr Leu Ile Gly Arg Lys Arg Ser His Ala Gly Tyr Gln
405 410 415

Thr Ile

<210> 21

<211> 418

<212> PRT

<213> Oryzias latipes

<400> 21

Met Lys Ser Phe Pro Ser Phe Val Ala Leu Phe Ile Val Cys Ser Ala
1 5 10 15

Val Leu Ala Asp Thr Gln Ala Val Val Thr Leu Glu Val Lys Glu Gly
20 25 30

ITI-08-PCT_Sequence_Listing_ST25.txt

Asn	Ser	Thr	Cys	Ile	Lys	Ala	Glu	Phe	Ser	Ala	Val	Phe	Ser	Ile	Thr	35	40	45
Tyr	Asn	Thr	Thr	Asn	Asp	Thr	Arg	Thr	Val	Ser	Val	Phe	Leu	Pro	Asn	50	55	60
Ser	Thr	Thr	Val	Asp	Ser	Ala	Asn	Ser	Ser	Cys	Gly	Ser	Asn	Gly	Ser	65	70	75
Thr	Pro	Gly	Leu	Met	Ala	Lys	Phe	Gly	Pro	Gly	His	Tyr	Phe	Gly	Met	85	90	95
Asn	Phe	Ser	Thr	Asn	Gly	Ser	Leu	Tyr	Ser	Val	Asp	Thr	Leu	Phe	Leu	100	105	110
Arg	Tyr	Asn	Leu	Ser	Asp	Ala	Ser	Leu	Phe	Pro	Glu	Ala	Asn	Ser	Ser	115	120	125
Gly	Pro	Val	Asp	Phe	Glu	Leu	Ser	Ala	Ser	Val	Gly	Ile	Trp	Ala	Pro	130	135	140
Thr	Asn	Thr	Thr	Tyr	Arg	Cys	Leu	Ser	Pro	Thr	Thr	Ile	Thr	Ile	Thr	145	150	155
Arg	Pro	Ser	Val	Thr	Phe	Ser	Glu	Met	Lys	Leu	Glu	Ala	Tyr	Met	Pro	165	170	175
Gly	Asn	Asp	Phe	Ser	Pro	Ala	Glu	Arg	Val	Cys	Ala	Ala	Asp	Gln	Thr	180	185	190
Thr	Thr	Gly	Ala	Pro	Thr	Thr	Thr	Thr	Ser	Ala	Ala	Thr	Pro	Thr	Thr	195	200	205
Pro	Ser	Pro	Thr	Pro	Ala	Gly	Thr	Pro	Glu	Gln	Gly	Ser	Tyr	Ser	Val	210	215	220
Lys	Asn	Ala	Ser	Gly	Thr	Val	Cys	Leu	Met	Ala	Lys	Met	Gly	Val	Gln	225	230	235
Leu	Asn	Val	Ser	Tyr	Phe	Ser	Gln	Ser	Gln	Asn	Lys	Thr	Val	Gln	Glu	245	250	255
Leu	Leu	Asn	Leu	Thr	Pro	Asn	Leu	Thr	Ser	Ser	Ser	Gly	Leu	Cys	Gly	260	265	270
Gly	Thr	Asn	Ala	Thr	Leu	Val	Leu	Ala	Gln	Glu	Glu	Thr	Thr	Val	Leu	275	280	285
Ser	Phe	Leu	Phe	Thr	Val	Asn	Ser	Thr	Ser	Asn	Lys	Tyr	His	Leu	Ser	290	295	300

ITI-08-PCT_Sequence_Listing_ST25.txt

Gly Ile Thr Leu Gln Ala Asn Trp Thr Asp Met Met Ser Pro Phe Ser
305 310 315 320

Ala Ser Asn Thr Ser Leu Asp Tyr Leu Arg Ser Ser Leu Gly His Ser
325 330 335

Tyr Met Cys Asn Ala Glu Gln Thr Leu Phe Val Val Ser Thr Phe Ser
340 345 350

Ile Asn Met Phe Glu Leu Gln Val Gln Pro Phe Gly Val Thr Ser Thr
355 360 365

Gln Phe Ala Ser Ala Glu Val Cys Gln Ile Asp Gln Asp Gln Met Leu
370 375 380

Ile Pro Ile Ile Val Gly Ala Ala Leu Ala Gly Leu Val Leu Ile Val
385 390 395 400

Leu Ile Ala Tyr Leu Ile Gly Arg Lys Arg Ser His Ala Gly Tyr Gln
405 410 415

Thr Ile

<210> 22

<211> 420

<212> PRT

<213> Takifugu rubripes

<400> 22

Met Lys Arg Ser His Ala Leu Val Val Leu Ile Ile Ala Trp Phe Ser
1 5 10 15

Leu Ser Gly Cys Ile Gln Ala Val Ser Leu Glu Val Lys Glu Gly Asn
20 25 30

Ser Thr Cys Ile Lys Ala Asn Leu Ser Ala Tyr Phe Ser Ile Thr Tyr
35 40 45

Asn Thr Ser Ser Ser Thr Arg Thr Ala Gln Phe Ile Leu Pro Asp Ser
50 55 60

Ala Thr Val Asp Pro Asp Ser Ser Thr Cys Gly Gly Asn Gly Ser Ser
65 70 75 80

Pro Trp Leu Val Ala Val Phe Gly Ala Gly His Ala Leu Gly Leu Gly
85 90 95

Phe Ser Thr Asn Gly Ser Phe Tyr Ser Val Ala Asn Leu Thr Leu Gln
100 105 110

Tyr Asn Leu Ser Asp Ala Ser Val Phe Pro Asp Ala Asn Ser Ser Gly

115 120 125

Page 36

ITI-08-PCT_Sequence_Listing_ST25.txt

Ile Val Leu Ile Ala Tyr Leu Ile Gly Arg Lys Lys Ser His Ala Gly
405 410 415

Tyr Gln Thr Ile
420

<210> 23
<211> 419
<212> PRT
<213> Salmo salar

<400> 23

Met Thr Arg Thr Cys Pro Phe Val Val Gly Ile Ala Cys Phe Ala Ile
1 5 10 15

Leu Gly Cys Val Thr Val Val Gln Ser Gln Val Thr Leu Glu Val Thr
20 25 30

Glu Gly Asn Ser Thr Cys Ile Lys Ala Glu Leu Ser Ala Ser Phe Ser
35 40 45

Ile Thr Tyr Asp Thr Ala Asn Gly Thr Arg Thr Val Met Val Pro Leu
50 55 60

Pro Gly Ser Ala Val Val Gly Val Ala Ser Ser Cys Gly Gly Asp Gly
65 70 75 80

Arg Ser Pro Trp Leu Val Ala Leu Phe Gly Asp Gly His Ala Leu Gly
85 90 95

Leu Gly Phe Ser Ser Asn Asp Ser Leu Tyr Ser Val Ala Lys Leu Thr
100 105 110

Leu Gln Tyr Asn Leu Ser Asp Val Ser Asn Phe Pro Glu Ala Asn Ser
115 120 125

Thr Asp Val Val Thr Val Glu Thr Thr Ser Val Gly Met Val Ala Arg
130 135 140

Val Asn Thr Thr Tyr Arg Cys Ile Ser Ala Ser Pro Val Ile Val Gly
145 150 155 160

Gly Ala Thr Val Thr Phe Ser Asn Val Thr Met Glu Ala Phe Met Thr
165 170 175

Gly Glu Asp Leu Ser Pro Asn Glu Ser Val Cys Thr Ala Asp Gln Ser
180 185 190

Phe Thr Thr Ala Pro Pro Pro Pro Pro Ser Thr Thr Thr Ala Ala Pro
195 200 205

ITI-08-PCT_Sequence_Listing_ST25.txt

Ala Pro Val Pro Thr Pro Pro Gly Thr Pro Ser Gln Gly Ser Tyr Ser
 210 215 220

Val Ser Asn Ser Asn Gly Thr Val Cys Leu Leu Ala Arg Met Ala Leu
 225 230 235 240

Gln Leu Asn Ile Ser His Phe Ser Ala Ser Gln Asn Lys Thr Ile Gln
 245 250 255

Glu Val Val Asn Leu Leu Pro Asn Gln Thr Thr Ser Ser Gly Ser Cys
 260 265 270

Asp Pro Thr Ser Ala Thr Leu Val Leu Thr Gln Ala Asn Ala Thr Asn
 275 280 285

Leu Ser Phe Leu Phe Thr Leu Asn Ser Thr Ser Asn Arg Tyr His Leu
 290 295 300

Thr Gly Leu Ser Val Val Ala Ala Trp Ser Asp Met Thr Ala Pro Phe
 305 310 315 320

Asn Thr Ser Asn Ser Ser Leu Asp Tyr Gln Arg Gly Ser Leu Gly Arg
 325 330 335

Ser Tyr Met Cys Ile Ser Glu Gln Thr Leu Val Val Asp Gln Asn Phe
 340 345 350

Ser Leu Asn Thr Phe Gln Leu Gln Val Gln Pro Phe Gly Ile Thr Arg
 355 360 365

Gly Gln Phe Ala Gln Ala Glu Glu Cys Gln Leu Asp Gln Asp Asn Met
 370 375 380

Leu Ile Pro Ile Val Val Gly Ala Ala Leu Ala Gly Leu Val Leu Ile
 385 390 395 400

Val Leu Ile Ala Tyr Leu Ile Gly Arg Lys Arg Ser His Ala Gly Tyr
 405 410 415

Gln Thr Ile

<210> 24

<211> 247

<212> PRT

<213> Oreochromis niloticus

<400> 24

Met Val Gln Ile Cys Arg Val Gln Ser Trp Phe Val Gly Val Thr Pro
 1 5 10 15

ITI-08-PCT_Sequence_Listing_ST25.txt

Leu Leu Ile Phe Ala Thr Val Leu His Gln Gly Phe Ala Thr Val Ala
 20 25 30
 Pro Pro Thr Pro Ala Pro His Lys Glu Pro Gly Arg Pro Glu Arg Gly
 35 40 45
 Tyr Tyr Asn Val Thr Asn His Asn Gly Thr Ile Cys Leu Met Ala Tyr
 50 55 60
 Met Gly Leu Gln Leu Asn Ile Ser Tyr Asn Ser Thr Ser Gln Lys Lys
 65 70 75 80
 Val Val Gln Asp Val Met Asn Leu Gln Pro Asn Leu Thr Lys His Ser
 85 90 95
 Gly Leu Cys Asp Ser Asp Ile Ala Ser Leu Asn Leu Thr Val Asp Ala
 100 105 110
 Val Lys Thr Asn Leu Thr Phe Val Phe Thr Met Asn Ser Thr Ser Asn
 115 120 125
 Lys Tyr His Leu Ser Glu Val Thr Val Ser Ala Ala Trp Pro Glu Met
 130 135 140
 Lys Glu Pro Val Ser Val His Asn Ser Ser Leu Asp Tyr Leu Arg Gly
 145 150 155 160
 Thr Val Gly Tyr Ser Tyr Phe Cys Arg Asp Glu Gln Thr Leu Asn Val
 165 170 175
 Ala Gln Asn Leu Ser Ile Asn Thr Phe Gln Leu Gln Val Gln Pro Phe
 180 185 190
 Ala Val Lys Gly Asp Gln Phe Gly Ala Ala Glu Glu Cys Gln Leu Asp
 195 200 205
 Glu Asp Asp Met Leu Ile Pro Ile Val Val Gly Ala Ala Leu Ala Gly
 210 215 220
 Leu Val Val Ile Val Leu Leu Ala Tyr Leu Ile Gly Arg Lys Arg Ser
 225 230 235 240
 His Ala Gly Tyr Gln Ser Ile
 245

<210> 25
 <211> 415
 <212> PRT
 <213> Mus musculus

<400> 25

ITI-08-PCT_Sequence_Listing_ST25.txt

```

Met Cys Leu Ser Pro Val Lys Gly Ala Lys Leu Ile Leu Ile Phe Leu
1      5      10      15

Phe Leu Gly Ala Val Gln Ser Asn Ala Leu Ile Val Asn Leu Thr Asp
      20      25      30

Ser Lys Gly Thr Cys Leu Tyr Ala Glu Trp Glu Met Asn Phe Thr Ile
      35      40      45

Thr Tyr Glu Thr Thr Asn Gln Thr Asn Lys Thr Ile Thr Ile Ala Val
      50      55      60

Pro Asp Lys Ala Thr His Asp Gly Ser Ser Cys Gly Asp Asp Arg Asn
65      70      75      80

Ser Ala Lys Ile Met Ile Gln Phe Gly Phe Ala Val Ser Trp Ala Val
      85      90      95

Asn Phe Thr Lys Glu Ala Ser His Tyr Ser Ile His Asp Ile Val Leu
      100     105     110

Ser Tyr Asn Thr Ser Asp Ser Thr Val Phe Pro Gly Ala Val Ala Lys
      115     120     125

Gly Val His Thr Val Lys Asn Pro Glu Asn Phe Lys Val Pro Leu Asp
      130     135     140

Val Ile Phe Lys Cys Asn Ser Val Leu Thr Tyr Asn Leu Thr Pro Val
145     150     155     160

Val Gln Lys Tyr Trp Gly Ile His Leu Gln Ala Phe Val Gln Asn Gly
      165     170     175

Thr Val Ser Lys Asn Glu Gln Val Cys Glu Glu Asp Gln Thr Pro Thr
      180     185     190

Thr Val Ala Pro Ile Ile His Thr Thr Ala Pro Ser Thr Thr Thr Thr
      195     200     205

Leu Thr Pro Thr Ser Thr Pro Thr Pro Thr Pro Thr Pro Thr Pro Thr
      210     215     220

Val Gly Asn Tyr Ser Ile Arg Asn Gly Asn Thr Thr Cys Leu Leu Ala
225     230     235     240

Thr Met Gly Leu Gln Leu Asn Ile Thr Glu Glu Lys Val Pro Phe Ile
      245     250     255

Phe Asn Ile Asn Pro Ala Thr Thr Asn Phe Thr Gly Ser Cys Gln Pro
      260     265     270

Gln Ser Ala Gln Leu Arg Leu Asn Asn Ser Gln Ile Lys Tyr Leu Asp

```

ITI-08-PCT_Sequence_Listing_ST25.txt

275

280

285

Phe Ile Phe Ala Val Lys Asn Glu Lys Arg Phe Tyr Leu Lys Glu Val
290 295 300

Asn Val Tyr Met Tyr Leu Ala Asn Gly Ser Ala Phe Asn Ile Ser Asn
305 310 315 320

Lys Asn Leu Ser Phe Trp Asp Ala Pro Leu Gly Ser Ser Tyr Met Cys
325 330 335

Asn Lys Glu Gln Val Leu Ser Val Ser Arg Ala Phe Gln Ile Asn Thr
340 345 350

Phe Asn Leu Lys Val Gln Pro Phe Asn Val Thr Lys Gly Gln Tyr Ser
355 360 365

Thr Ala Gln Glu Cys Ser Leu Asp Asp Asp Thr Ile Leu Ile Pro Ile
370 375 380

Ile Val Gly Ala Gly Leu Ser Gly Leu Ile Ile Val Ile Val Ile Ala
385 390 395 400

Tyr Leu Ile Gly Arg Arg Lys Thr Tyr Ala Gly Tyr Gln Thr Leu
405 410 415

<210> 26

<211> 415

<212> PRT

<213> Xenopus laevis

<400> 26

Met Gly Asp Thr Gly Ala Met Glu Arg Cys Ala Cys Pro Ala Ala Val
1 5 10 15

Leu Leu Leu Ser Leu Val Leu Met Gly Ala Thr Ala Phe Glu Val Glu
20 25 30

Ile Lys Asp Asp Lys Asn Ala Thr Cys Ile Tyr Ala Lys Leu Ser Val
35 40 45

Asn Ile Thr Val Gln Tyr Glu Thr Asp Thr Ser Ser Ser Lys Asn Ile
50 55 60

Thr Phe Pro Val Pro Ser Asp Val Thr Thr Asn Gly Ser Ser Cys Gly
65 70 75 80

Ser Asp Gly Lys Ala Pro Leu Leu Val Ile Asn Phe Gly Asn Ser Gln
85 90 95

Ser Trp Ser Leu Asn Phe Thr Arg Asn Asn Ser Thr Tyr Ser Gly Ser

ITI-08-PCT_Sequence_Listing_ST25.txt

100	105	110																	
Ala	Leu	Ile	Phe	Thr	Tyr	Asn	Thr	Asn	Asp	Thr	Ile	Leu	Phe	Pro	Asp				
	115						120					125							
Ala	Leu	Arg	Lys	Gly	Leu	Ile	Ser	Ser	Thr	Ala	Met	Phe	Leu	Gly	Pro				
	130					135					140								
Val	Pro	Leu	Asn	Ser	Thr	Tyr	Lys	Cys	Ile	Ser	Arg	Glu	Val	Val	Val				
145					150					155					160				
Ser	Glu	Asn	Val	Thr	Gln	Ile	Ile	Tyr	Asp	Val	Lys	Leu	Glu	Ala	Phe				
				165					170					175					
Met	Ala	Asn	Gly	Thr	Leu	Gly	Lys	Glu	Ile	Ile	Cys	Asp	Ala	Asp	Lys				
			180					185					190						
Pro	Ser	Pro	Val	Pro	Ser	Pro	Thr	Gln	Pro	Ser	Thr	Thr	Ala	Ser	Thr				
		195					200					205							
Ala	Ile	Pro	Ala	Pro	Thr	Ser	Lys	Pro	Leu	Asp	Lys	Pro	Thr	Met	Gly				
	210					215					220								
Asn	Tyr	Thr	Val	Ser	Asp	Ala	Ser	Gly	Ile	Cys	Leu	Leu	Ala	Ser	Met				
225					230					235					240				
Gly	Leu	Gln	Ile	Asn	Thr	Ser	Leu	Leu	Ser	Glu	Gly	Lys	Asn	Ile	Trp				
				245					250					255					
Arg	Pro	Phe	Asn	Ile	Asp	Pro	Leu	Gly	Ile	Lys	Thr	Asn	Gly	Thr	Cys				
			260					265					270						
Thr	Asn	Gln	Thr	Gly	Thr	Leu	Ile	Leu	Thr	Glu	Asn	Arg	Thr	Ile	Ile				
		275					280					285							
Glu	Phe	Thr	Phe	Ala	Leu	Lys	Asn	Lys	Asn	His	Phe	Tyr	Leu	Glu	Glu				
	290					295				300									
Val	Asn	Ile	Thr	Leu	Ile	Asn	Gly	Ser	Ala	Phe	Ser	Ser	Arg	Gln	Asn				
305					310					315					320				
Gln	Asn	Leu	Ser	Thr	Trp	Glu	Ala	Ser	Val	Asp	Ser	Ser	Tyr	Met	Cys				
				325					330					335					
His	Lys	Glu	Gln	Gln	Ile	Lys	Val	Ser	Glu	Asp	Leu	Phe	Ile	Asn	Ala				
			340					345					350						
Phe	Asp	Val	Arg	Val	Gln	Pro	Phe	Gly	Val	Asn	Asn	Gly	Thr	Phe	Ala				
	355						360					365							
Thr	Ala	Glu	Asp	Cys	Phe	Ala	Asp	Gln	Asn	Phe	Ile	Val	Pro	Ile	Val				
	370					375					380								

ITI-08-PCT_Sequence_Listing_ST25.txt

Val Gly Ala Ala Leu Gly Val Leu Val Val Leu Val Met Val Ala Tyr
385 390 395 400

Phe Ile Gly Arg Arg Lys Gln Ser Ser Ala Gly Tyr Glu Gln Met
405 410 415

<210> 27

<211> 355

<212> PRT

<213> Danio rerio

<400> 27

Met Ala Val Arg Gly Phe Leu Pro Leu Leu Phe Ile Leu Leu Ser Gly
1 5 10 15

Ile Val His Ala Asp Asp Met Met Thr Ser Pro Leu Pro Ser Thr Ala
20 25 30

Glu Leu Lys Thr Ala Asn Leu Pro Leu Val Ile Gln Thr Thr Ser Ser
35 40 45

Thr Thr Ser Thr Thr Thr Thr Ser Arg Pro Ser Ser Thr Ser Thr His
50 55 60

Ser Thr Leu Thr Thr Glu Pro Ala Ala Lys Thr Thr Thr Ala Arg Thr
65 70 75 80

Thr Val Thr Thr Ser Ala Pro Thr Ser Thr Gln Ser Thr Ser Ser Ser
85 90 95

Ser Thr Ser Ala Thr Val Thr Thr Leu Ala Pro Thr Thr Thr Gly His
100 105 110

Asn Thr Thr Asn Ser Thr Thr Glu Pro Pro Thr Thr Thr Gly His Asn
115 120 125

Thr Thr Asn Ser Thr Thr Asp Ala Pro Thr Thr Thr His Thr Asn Ala
130 135 140

Thr Val Ala Pro Thr Pro Pro Pro Thr Thr Pro Ser Val Pro Lys Pro
145 150 155 160

Thr Val Gly Asn Tyr Ser Val Lys Thr Asp Asn Val Ser Asp Cys Leu
165 170 175

Leu Ala Lys Met Gly Leu Gln Phe Ser Phe Lys Ile Ser Gly Asn Ala
180 185 190

Ser Leu Gln Thr Val Asn Leu Asp Pro Asn Val Thr Lys Val Asn Gly
195 200 205

ITI-08-PCT_Sequence_Listing_ST25.txt

Thr Cys Gly Ser Gly Gly Ser Asp Ser Ser Leu Phe Leu Thr Ser Lys
210 215 220

Asp Ile Thr Val His Phe Val Phe Thr Asn Asp Ser Gln Lys Phe Arg
225 230 235 240

Leu His Ala Leu Thr Leu Thr Val Asp Leu Gly Asn Gly Asn Ile Phe
245 250 255

Asn Asp Ser Asn Thr Asn Leu Ser Leu Trp Glu Ala Ser Val Gly Ser
260 265 270

Ser Tyr Met Cys Arg Lys Glu Gln Ser Tyr Asn Ile Ser Asp Lys Leu
275 280 285

Thr Leu Asn Thr Phe Glu Leu Gln Val Gln Pro Phe Asp Val Lys Lys
290 295 300

Asn Ser Phe Ser Thr Ala His Glu Cys Ser Leu Asp Asp Thr Ser Leu
305 310 315 320

Leu Ile Pro Ile Ile Val Gly Ala Ala Leu Ala Gly Leu Ile Phe Ile
325 330 335

Val Val Ile Ala Tyr Val Ile Gly Arg Arg Arg Thr Tyr Val Gly Tyr
340 345 350

Gln Thr Leu
355

<210> 28
<211> 411
<212> PRT
<213> Papio anubis

<400> 28

Met Val Cys Phe Arg Leu Phe Pro Val Pro Gly Ser Gly Leu Val Leu
1 5 10 15

Val Cys Leu Val Leu Gly Ala Val Gln Ser Tyr Ala Leu Glu Leu Asn
20 25 30

Leu Thr Asp Ser Gly Lys Ala Thr Cys Leu Tyr Ala Lys Trp Gln Met
35 40 45

Asn Phe Thr Val Arg Tyr Glu Thr Thr Asn Lys Thr Tyr Lys Thr Val
50 55 60

Thr Ile Ser Asp Arg Gly Thr Val Thr Tyr Asn Gly Ser Ile Cys Gly
65 70 75 80

ITI-08-PCT_Sequence_Listing_ST25.txt

Asp	Asp	Gln	Asn	Gly	Pro	Lys	Ile	Ala	Val	Gln	Phe	Gly	Pro	Gly	Phe	85	90	95
Ser	Trp	Ile	Ala	Asn	Phe	Ser	Lys	Ala	Ala	Ser	Thr	Tyr	Ser	Ile	Asp	100	105	110
Ser	Ile	Ser	Phe	Ser	Tyr	Asn	Thr	Gly	Asp	Asn	Thr	Thr	Phe	Pro	Asp	115	120	125
Ala	Glu	Asp	Lys	Gly	Ile	Ile	Thr	Val	Asp	Glu	Leu	Leu	Ala	Ile	Lys	130	135	140
Ile	Pro	Leu	Asn	Asp	Leu	Phe	Arg	Cys	Asn	Ser	Leu	Ser	Thr	Leu	Glu	145	150	155
Lys	Asn	Asp	Val	Val	Gln	Asn	Tyr	Trp	Asp	Val	Leu	Val	Gln	Ala	Phe	165	170	175
Val	Gln	Asn	Gly	Thr	Val	Ser	Thr	Asn	Glu	Phe	Leu	Cys	Asp	Glu	Asp	180	185	190
Lys	Thr	Ser	Thr	Val	Ala	Pro	Thr	Ile	His	Thr	Thr	Val	Pro	Ser	Pro	195	200	205
Thr	Thr	Thr	Pro	Thr	Pro	Lys	Glu	Lys	Pro	Glu	Ala	Gly	Thr	Tyr	Ser	210	215	220
Val	Asn	Asn	Gly	Asn	Asp	Thr	Cys	Leu	Leu	Ala	Thr	Met	Gly	Leu	Gln	225	230	235
Leu	Asn	Ile	Thr	Gln	Asp	Lys	Val	Ala	Ser	Val	Ile	Asn	Ile	Asn	Pro	245	250	255
Asn	Thr	Thr	His	Ser	Thr	Gly	Ser	Cys	Arg	Ser	His	Thr	Ala	Leu	Leu	260	265	270
Arg	Leu	Asn	Ser	Ser	Thr	Ile	Lys	Tyr	Leu	Asp	Phe	Val	Phe	Ala	Val	275	280	285
Lys	Asn	Glu	Asn	Arg	Phe	Tyr	Leu	Lys	Glu	Val	Asn	Val	Ser	Met	Tyr	290	295	300
Leu	Val	Asn	Gly	Ser	Val	Phe	Ser	Ile	Ala	Asn	Asn	Asn	Leu	Ser	Tyr	305	310	315
Trp	Asp	Ala	Pro	Leu	Gly	Ser	Ser	Tyr	Met	Cys	Asn	Lys	Glu	Gln	Thr	325	330	335
Val	Ser	Val	Ser	Gly	Ala	Phe	Gln	Ile	Asn	Thr	Phe	Asp	Leu	Arg	Val	340	345	350

ITI-08-PCT_Sequence_Listing_ST25.txt

Gln Pro Phe Asn Val Thr Gln Gly Lys Tyr Ser Thr Ala Glu Glu Cys
355 360 365

Ser Ala Asp Ser Asp Leu Asn Phe Leu Ile Pro Val Ala Val Gly Val
370 375 380

Ala Leu Gly Phe Leu Ile Ile Val Val Phe Ile Ser Tyr Met Ile Gly
385 390 395 400

Arg Arg Lys Ser Arg Thr Gly Tyr Gln Ser Val
405 410

<210> 29

<211> 410

<212> PRT

<213> Macaca mulatta

<400> 29

Met Val Cys Phe Arg Leu Phe Pro Val Pro Gly Ser Gly Leu Val Leu
1 5 10 15

Val Cys Leu Val Leu Gly Ala Val Gln Ser Tyr Ala Leu Glu Leu Asn
20 25 30

Leu Thr Asp Ser Gly Lys Ala Thr Cys Leu Tyr Ala Lys Trp Gln Met
35 40 45

Asn Phe Thr Val Arg Tyr Glu Thr Thr Asn Lys Thr Tyr Lys Thr Val
50 55 60

Thr Ile Ser Asp Arg Gly Thr Val Thr Tyr Asn Gly Ser Ile Cys Gly
65 70 75 80

Asp Asp Gln Asn Gly Pro Lys Ile Ala Val Gln Phe Gly Pro Gly Phe
85 90 95

Ser Trp Ile Ala Asn Phe Ser Lys Ala Ala Ser Thr Tyr Ser Ile Asp
100 105 110

Ser Ile Ser Phe Ser Tyr Asn Thr Gly Asp Asn Thr Thr Phe Pro Asp
115 120 125

Ala Glu Asp Lys Gly Ile Ile Thr Val Asp Glu Leu Leu Ala Ile Lys
130 135 140

Ile Pro Leu Asn Asp Leu Phe Arg Cys Asn Ser Leu Ser Thr Leu Glu
145 150 155 160

Lys Asn Asp Val Val Gln Asn Tyr Trp Asp Val Leu Val Gln Ala Phe
165 170 175

Val Gln Asn Gly Thr Val Ser Thr Asn Glu Phe Leu Cys Asp Glu Asp
180 185 190

Thr Thr Thr Pro Thr Pro Lys Glu Lys Pro Glu Ala Gly Thr Tyr Ser
210 215 220

Leu Asn Ile Thr Gln Asp Lys Val Ala Ser Val Ile Asn Ile Asn Pro
245 250 255

Arg Leu Asn Ser Ser Thr Ile Lys Tyr Leu Asp Phe Val Phe Ala Val
275 280 285

Leu Val Asn Gly Ser Val Phe Ser Ile Ala Asn Asn Asn Leu Ser Tyr
305 310 315 320

Trp Asp Ala Pro Leu Gly Ser Ser Tyr Met Cys Asn Lys Glu Gln Thr
325 330 335

Val Ser Val Ser Gly Ala Phe Gln Ile Asn Thr Phe Asp Leu Arg Val
340 345 350

Gln Pro Phe Asn Val Thr Gln Gly Lys Tyr Ser Thr Ala Gln Asp Cys
355 360 365

Ser Ala Asp Asp Asp Asn Phe Leu Val Pro Ile Ala Val Gly Ala Ala
370 375 380

Leu Ala Gly Val Leu Ile Leu Val Leu Leu Ala Tyr Phe Ile Gly Leu
385 390 395 400

Lys Arg His His Ala Gly Tyr Glu Gln Phe
405 410

<213> Pan troglodytes

<221> SITE

ITI-08-PCT_Sequence_Listing_ST25.txt

<222> (200)..(200)

<223> Xaa can be any naturally occurring amino acid

<400> 30

Met Val Cys Phe Arg Leu Phe Pro Val Pro Gly Ser Gly Leu Val Leu
1 5 10 15

Val Cys Leu Val Leu Gly Ala Val Arg Ser His Ala Leu Glu Leu Asn
20 25 30

Glu Ala Asp Ser Ala Ile Asn Cys Ser Lys Cys Lys Thr Val Thr Ile
35 40 45

Ser Asp His Gly Thr Val Thr Tyr Asn Gly Ser Ile Cys Gly Asp Asp
50 55 60

Gln Asn Gly Pro Lys Ile Ala Val Gln Phe Gly Pro Gly Phe Ser Trp
65 70 75 80

Ile Ala Asn Phe Thr Lys Ala Ala Ser Thr Tyr Ser Ile Asp Ser Ile
85 90 95

Ser Phe Ser Tyr Asn Thr Gly Asp Asn Thr Thr Phe Pro Asp Ala Glu
100 105 110

Asp Lys Gly Ile Leu Thr Val Asp Glu Leu Leu Ala Ile Lys Ile Pro
115 120 125

Leu Asn Asp Leu Phe Arg Cys Asn Ser Leu Ser Thr Leu Glu Lys Asn
130 135 140

Asp Val Val Gln His Tyr Trp Asp Val Leu Val Gln Ala Phe Val Gln
145 150 155 160

Asn Gly Thr Val Ser Thr Asn Glu Phe Leu Cys Asp Lys Asp Lys Thr
165 170 175

Ser Thr Val Ala Pro Thr Val His Thr Thr Val Pro Ser Pro Thr Thr
180 185 190

Thr Pro Thr Arg Ile Pro Pro Xaa Val Ala Ser Val Ile Asn Ile Asn
195 200 205

Pro Asn Thr Thr His Ser Thr Gly Ser Cys Arg Ser His Thr Ala Leu
210 215 220

Leu Arg Leu Asn Ser Ser Thr Ile Lys Tyr Leu Asp Phe Val Phe Ala
225 230 235 240

Val Lys Asn Glu Asn Arg Phe Tyr Leu Lys Glu Val Asn Ile Ser Met
245 250 255

ITI-08-PCT_Sequence_Listing_ST25.txt

Tyr Leu Val Asn Gly Ser Val Phe Ser Ile Ala Asn Asn Asn Leu Ser
260 265 270

Tyr Trp Asp Ala Pro Leu Gly Ser Ser Tyr Met Cys Asn Lys Glu Gln
275 280 285

Thr Val Ser Val Ser Gly Ala Phe Gln Ile Asn Thr Phe Asp Leu Arg
290 295 300

Val Gln Pro Phe Asn Val Thr Gln Gly Lys Tyr Ser Thr Ala Glu Glu
305 310 315 320

Cys Ser Ala Asp Ser Asp Leu Asn Phe Leu Ile Pro Val Ala Val Gly
325 330 335

Val Ala Leu Gly Phe Leu Ile Ile Val Val Phe Ile Ser Tyr Met Ile
340 345 350

Gly Arg Arg Lys Ser Arg Thr Gly Tyr Gln Ser Val
355 360

<210> 31

<211> 411

<212> PRT

<213> Canis lupus familiaris

<400> 31

Met Val Cys Phe Arg Leu Ser Pro Ala Pro Gly Ser Gly Leu Val Leu
1 5 10 15

Leu Cys Leu Val Leu Gly Ala Val Ser Ser Tyr Ala Leu Glu Val Asn
20 25 30

Val Thr Asp Ser Glu Lys Ala Thr Cys Leu Tyr Ala Lys Trp Gln Met
35 40 45

Asn Phe Thr Ile Gln Tyr Asn Thr Thr Ser Lys Asn Phe Lys Thr Ala
50 55 60

Thr Ile Ser Asp Phe Ser Thr Ala Thr Tyr Asn Gly Ser Val Cys Gly
65 70 75 80

Asn Asp Gln Asn Asn Pro Lys Ile Val Val Gln Phe Gly Ser Gly Phe
85 90 95

Ser Trp Ile Val Asn Phe Thr Lys Lys Glu Ser Ala Tyr Leu Ile Asp
100 105 110

Ser Ile Ser Phe Ser Tyr Asn Leu Ser Asp Asn Ala Thr Phe Pro Asp
115 120 125

ITI-08-PCT_Sequence_Listing_ST25.txt

Ala	Lys	Glu	Lys	Gly	Ile	Leu	Thr	Val	His	Asp	Leu	Val	Gly	Phe	Arg	130	135	140	
Ile	Pro	Leu	Asn	Asn	Ile	Phe	Arg	Cys	Asn	Ser	Leu	Ser	Thr	Leu	Glu	145	150	155	160
Lys	Asn	Gly	Val	Val	Gln	Tyr	Tyr	Trp	Asp	Val	His	Val	Gln	Ala	Phe	165	170	175	
Val	Gln	Asn	Gly	Thr	Val	Ser	Thr	Lys	Glu	Phe	Leu	Cys	Glu	Lys	Asp	180	185	190	
Lys	Thr	Ser	Thr	Thr	Val	Val	Pro	Thr	Ile	Ser	Thr	Thr	Thr	Pro	Ser	195	200	205	
Pro	Thr	Thr	Thr	Pro	Thr	Pro	Lys	Glu	Lys	Pro	Glu	Val	Gly	Ser	Tyr	210	215	220	
Ser	Val	Asn	Asn	Ser	Asn	Gly	Thr	Cys	Leu	Leu	Ala	Thr	Met	Gly	Leu	225	230	235	240
Gln	Leu	Asn	Ile	Thr	His	Asn	Lys	Val	Ala	Ser	Val	Ile	Asn	Ile	Asn	245	250	255	
Pro	Asn	Thr	Thr	Asp	Phe	Thr	Gly	Ser	Cys	Gln	Pro	Gln	Thr	Ala	Leu	260	265	270	
Leu	Arg	Leu	Asn	Ser	Ser	Asn	Ile	Lys	Tyr	Leu	Asp	Phe	Val	Phe	Ala	275	280	285	
Val	Lys	Asn	Glu	Asn	Arg	Phe	Tyr	Leu	Lys	Glu	Val	Asn	Val	Ser	Met	290	295	300	
Tyr	Leu	Val	Asn	Gly	Ser	Val	Phe	Ser	Ile	Ala	Asn	Asn	Asn	Leu	Ser	305	310	315	320
Tyr	Trp	Asp	Ala	Pro	Leu	Gly	Ser	Ser	Tyr	Met	Cys	Asn	Lys	Glu	Gln	325	330	335	
Thr	Val	Ser	Val	Ser	Gly	Ala	Phe	Gln	Ile	Asn	Thr	Phe	Asp	Leu	Arg	340	345	350	
Val	Gln	Pro	Phe	Asn	Val	Met	Glu	Gly	Lys	Tyr	Ser	Thr	Ala	Gln	Glu	355	360	365	
Cys	Ser	Leu	Asp	Asp	Asp	Thr	Ile	Leu	Ile	Pro	Ile	Ile	Val	Gly	Ala	370	375	380	
Gly	Leu	Ser	Gly	Leu	Ile	Ile	Val	Ile	Val	Ile	Ala	Tyr	Leu	Ile	Gly	385	390	395	400

ITI-08-PCT_Sequence_Listing_ST25.txt

Arg Arg Lys Ser Tyr Ala Gly Tyr Gln Thr Leu
405 410

<210> 32
<211> 417
<212> PRT
<213> Equus caballus

<400> 32

Met Val Cys Phe Arg Leu Ser Pro Val Pro Gly Ser Gly Leu Val Leu
1 5 10 15

Leu Cys Leu Val Leu Gly Ala Val Ser Ser Tyr Ala Leu Glu Leu Asn
20 25 30

Leu Thr Asp Ser Glu Lys Ala Leu Cys Leu Tyr Ala Lys Trp Gln Met
35 40 45

Asn Phe Thr Ile Pro Tyr Glu Thr Thr Ser Lys Ser Tyr Lys Thr Val
50 55 60

Thr Ile Ser Asn Phe Gly Thr Pro Thr Tyr Asn Gly Ser Ile Cys Gly
65 70 75 80

Asp Asn Gln Asn Gly Ser Arg Ile Ala Val Gln Phe Gly Ser Gly Phe
85 90 95

Ser Trp Ile Val Asn Phe Thr Lys Ser Val Ser Val Tyr Ser Ile Asp
100 105 110

Ser Ile Ser Phe Ser Tyr Asn Thr Gly Asp Asn Thr Thr Phe Pro Asp
115 120 125

Ala Lys Asp Lys Gly Ile Leu Thr Val Asn Glu Ser Val Ala Phe Lys
130 135 140

Ile Pro Leu Asn Asp Ile Phe Arg Cys Asn Ser Leu Ser Ser Leu Val
145 150 155 160

Lys Asn Gly Val Val Gln Asn Tyr Trp Asp Val His Val Gln Ala Phe
165 170 175

Val Gln Asn Gly Thr Val Ser Thr Asn Glu Tyr Leu Cys Glu Lys Asp
180 185 190

Asn Thr Thr Thr Thr Val Ala Pro Ile Val Pro Thr Thr Val Pro Ser
195 200 205

Pro Thr Thr Thr Ser Ser Pro Thr Thr Thr Pro Ser Pro Lys Glu Lys
210 215 220

ITI-08-PCT_Sequence_Listing_ST25.txt

Pro Asp Val Gly Ser Tyr Leu Val Lys Asn Gly Ser Asp Thr Cys Leu
225 230 235 240

Leu Ala Thr Met Gly Leu Gln Leu Asn Val Thr His Asp Lys Val Ala
245 250 255

Ser Val Ile Asn Ile Asn Pro Asn Val Thr Gly Tyr Ser Gly Ser Cys
260 265 270

His Pro Gln Thr Ala Leu Leu Arg Leu Asn Ser Ser Asn Ile Lys Tyr
275 280 285

Leu Asp Phe Val Phe Ala Val Lys Asn Glu Asn Arg Phe Tyr Leu Lys
290 295 300

Glu Val Asn Val Ser Met Tyr Leu Ala Asn Gly Ser Val Phe Ser Phe
305 310 315 320

Ala Asn Asn Asn Leu Ser Tyr Trp Asp Ala Pro Leu Gly Ser Ser Tyr
325 330 335

Met Cys Asn Lys Glu Gln Thr Val Ser Val Ser Gly Glu Phe Gln Ile
340 345 350

Asn Thr Phe Asp Leu Arg Val Gln Pro Phe Asn Val Lys Asp Gly Lys
355 360 365

Tyr Ser Thr Ala Gln Asp Cys Arg Ala Asp Asp Asp Asn Phe Leu Val
370 375 380

Pro Ile Ala Val Gly Ala Ala Leu Ala Gly Val Leu Ile Leu Val Leu
385 390 395 400

Leu Ala Tyr Phe Ile Gly Leu Lys Arg His His Ala Gly Tyr Glu Gln
405 410 415

Phe

<210> 33

<211> 407

<212> PRT

<213> Bos taurus

<400> 33

Met Val Cys Phe Arg Leu Ala Pro Val Pro Gly Ser Gly Phe Leu Leu
1 5 10 15

Leu Cys Leu Val Leu Gly Ala Val Ser Ser Tyr Ala Leu Glu Leu Asn
20 25 30

Leu Thr Asp Ser Ser Asn Ala Thr Cys Leu Tyr Ala Lys Trp Gln Met

ITI-08-PCT_Sequence_Listing_ST25.txt

35															
Asn	Phe	Thr	Ile	Arg	Tyr	Glu	Thr	Thr	Asp	Lys	His	Asn	Lys	Thr	Val
50						55					60				
Pro	Ile	Ser	Asp	Leu	Gly	Ala	Ala	Thr	Tyr	Asn	Gly	Ser	Phe	Cys	Gly
65					70					75					80
Asp	Asp	Gln	Asn	Gly	Pro	Lys	Ile	Ala	Val	Gln	Phe	Gly	Ser	Gly	Phe
				85					90					95	
Ser	Trp	Ile	Val	Asn	Phe	Thr	Lys	Glu	Ala	Ala	Ser	Pro	Ser	Thr	Tyr
			100					105					110		
Leu	Val	Asp	Thr	Ile	Ser	Phe	Ser	Tyr	Asn	Thr	Asn	Asp	Asn	Lys	Thr
		115						120				125			
Phe	Pro	Asp	Ala	Lys	Glu	Lys	Glu	Val	Phe	Thr	Val	Asn	Asn	Arg	Val
	130						135				140				
Ala	Leu	Lys	Ile	Pro	Leu	Asn	Asp	Ile	Phe	Arg	Cys	Asn	Ser	Leu	Ser
145					150					155					160
Thr	Leu	Glu	Asn	Arg	Asp	Val	Val	Gln	His	Tyr	Trp	Asp	Val	His	Val
				165					170					175	
Gln	Ala	Phe	Val	Gln	Asn	Gly	Thr	Val	Ser	Thr	Thr	Glu	Phe	Leu	Cys
			180					185					190		
Asp	Lys	Asp	Lys	Thr	Val	Thr	Thr	Ala	Val	Pro	Ile	Val	Pro	Thr	Thr
		195					200					205			
Leu	Pro	Ser	Pro	Thr	Lys	Pro	Val	Val	Gly	Ser	Tyr	Ser	Val	Val	Asn
	210					215					220				
Ser	Asn	Gly	Thr	Cys	Leu	Leu	Ala	Thr	Met	Gly	Leu	Gln	Leu	Asn	Ile
225					230					235					240
Thr	His	Asp	Lys	Val	Ala	Ser	Val	Phe	Asn	Ile	Asn	Pro	Asn	Thr	Thr
				245					250					255	
Asn	Ala	Thr	Gly	Ser	Cys	Gln	Pro	Gln	Thr	Ala	Leu	Leu	Arg	Leu	Ser
			260					265					270		
Ser	Ser	Asn	Ile	Lys	Tyr	Leu	Asp	Phe	Val	Phe	Ala	Val	Lys	Asn	Glu
		275					280					285			
Asn	Arg	Phe	Tyr	Leu	Lys	Glu	Val	Asn	Val	Ser	Met	Ile	Leu	Val	Asn
	290					295					300				
Gly	Ser	Val	Tyr	Ser	Ile	Ser	Asn	Thr	Asn	Leu	Ser	Tyr	Trp	Asp	Ala
305					310					315					320

ITI-08-PCT_Sequence_Listing_ST25.txt

Pro Leu Gly Ser Ser Tyr Met Cys Asn Lys Glu Gln Thr Val Ser Val
325 330 335

Ser Gly Ala Phe Gln Ile Asn Thr Phe Asp Leu Arg Val Gln Pro Phe
340 345 350

Ser Val Thr Glu Gly Lys Tyr Ser Thr Ala Gln Glu Cys Ser Leu Asp
355 360 365

Asp Asp Thr Ile Leu Ile Pro Ile Ile Val Gly Ala Gly Leu Ser Gly
370 375 380

Leu Ile Ile Val Ile Val Ile Ala Tyr Leu Ile Gly Arg Arg Lys Ser
385 390 395 400

Tyr Ala Gly Tyr Gln Thr Leu
405

<210> 34

<211> 411

<212> PRT

<213> Sus scrofa

<400> 34

Met Val Cys Phe Arg Leu Ser Pro Val Pro Gly Ser Gly Leu Leu Met
1 5 10 15

Leu Cys Leu Val Leu Gly Ala Val Ser Ser Tyr Ala Leu Glu Leu Asn
20 25 30

Leu Thr Asn Ser Glu Lys Ala Thr Cys Leu Tyr Ala Lys Trp Gln Met
35 40 45

Asn Phe Thr Ile Arg Tyr Glu Thr Thr Asn Asn Ser His Lys Thr Val
50 55 60

Ser Ile Ser Asp Phe Gly Ala Ala Thr Tyr Asn Gly Ser Phe Cys Gly
65 70 75 80

Asp Asp His Asn Asp Pro Gln Ile Val Met Gln Phe Gly Ser Gly Phe
85 90 95

Ser Trp Ile Val Asn Phe Ala Lys Glu Ser Ser Ser Tyr Leu Ile Asn
100 105 110

Ser Ile Ser Phe Ser Tyr Asn Thr Ser Asp Thr Thr Thr Phe Pro Asp
115 120 125

Ala Lys Lys Lys Gly Val Leu Thr Val Asn Asp Ser Val Gly Phe Gln
130 135 140

ITI-08-PCT_Sequence_Listing_ST25.txt

Val	Pro	Leu	Asn	Asp	Ile	Phe	Arg	Cys	Asn	Ser	Leu	Ser	Thr	Leu	Glu	145	150	155	160
Lys	Asp	Asn	Val	Val	Gln	His	Tyr	Trp	Asp	Val	His	Val	Gln	Ala	Phe	165	170	175	
Val	Gln	Asn	Gly	Thr	Val	Ser	Thr	Lys	Glu	Phe	Leu	Cys	Asp	Lys	Asp	180	185	190	
Lys	Thr	Leu	Thr	Thr	Thr	Val	Pro	Val	Ile	Pro	Thr	Ser	Val	Pro	Ser	195	200	205	
Pro	Thr	Thr	Thr	Pro	Thr	Pro	Lys	Glu	Lys	Pro	Glu	Thr	Gly	Ser	Tyr	210	215	220	
Ser	Val	Thr	Ser	Ser	Asn	Gly	Thr	Cys	Leu	Leu	Ala	Asn	Met	Gly	Leu	225	230	235	240
Gln	Leu	Asn	Ile	Thr	Gln	Asp	Lys	Val	Ala	Ser	Val	Ile	Asn	Ile	Asn	245	250	255	
Pro	Asn	Thr	Thr	Asn	Ala	Thr	Gly	Asn	Cys	His	Ser	Lys	Thr	Ala	Leu	260	265	270	
Leu	Arg	Leu	Ser	Gly	Ser	Asn	Ile	Lys	Tyr	Leu	Asp	Phe	Val	Phe	Ala	275	280	285	
Val	Lys	Asn	Asp	Asn	Arg	Phe	Tyr	Leu	Lys	Glu	Val	Asn	Val	Ser	Val	290	295	300	
Tyr	Leu	Val	Asn	Gly	Ser	Val	Phe	Ser	Ile	Ala	Asn	Asn	Asn	Leu	Ser	305	310	315	320
Tyr	Trp	Asp	Ala	Pro	Leu	Gly	Ser	Ser	Tyr	Met	Cys	Asn	Lys	Glu	Gln	325	330	335	
Thr	Val	Ser	Val	Ser	Gly	Ala	Phe	Gln	Ile	Asn	Thr	Phe	Asn	Leu	Arg	340	345	350	
Val	Gln	Pro	Phe	Ser	Val	Met	Glu	Gly	Lys	Tyr	Ser	Thr	Ala	Gln	Asp	355	360	365	
Cys	Ser	Ala	Asp	Asp	Asp	Asn	Phe	Ile	Val	Pro	Ile	Ala	Val	Gly	Ala	370	375	380	
Ala	Leu	Ala	Gly	Val	Leu	Ile	Leu	Val	Leu	Leu	Ala	Tyr	Phe	Ile	Gly	385	390	395	400
Leu	Lys	Arg	His	His	Ala	Gly	Tyr	Glu	Gln	Phe						405	410		

ITI-08-PCT_Sequence_Listing_ST25.txt

<210> 35

<211> 408

<212> PRT

<213> Ovis aries

<400> 35

Met Val Cys Phe Arg Leu Ala Pro Val Pro Gly Cys Gly Phe Leu Leu
1 5 10 15

Phe Cys Leu Val Leu Gly Thr Val Ser Ser Tyr Ala Leu Glu Leu Asn
20 25 30

Leu Thr Asp Ser Ser Lys Ala Thr Cys Leu Tyr Ala Lys Trp Gln Met
35 40 45

Asn Phe Thr Ile Arg Tyr Glu Thr Thr Asp Lys His Asn Lys Thr Val
50 55 60

Thr Ile Ser Asp Phe Asp Ala Ala Ala Tyr Asn Gly Ser Val Cys Gly
65 70 75 80

Asp Asp Gln Asn Gly Pro Lys Ile Ala Val Gln Phe Gly Ser Gly Phe
85 90 95

Ser Trp Ile Val Asn Phe Thr Lys Glu Ala Ser Ser Thr Ser Thr Tyr
100 105 110

Leu Val Asp Ser Ile Ser Phe Ser Tyr Asn Thr Asn Asp Asn Ala Thr
115 120 125

Phe Pro Asp Ala Lys Glu Lys Gly Val Phe Thr Val Asn Asn Arg Val
130 135 140

Ala Leu Lys Ile Pro Leu Asn Asp Ile Phe Arg Cys Asn Ser Leu Ser
145 150 155 160

Thr Leu Glu Lys Ser Asp Val Val Gln His Tyr Trp Asp Val His Val
165 170 175

Gln Ala Phe Val Gln Asn Gly Thr Val Ser Thr Thr Glu Phe Leu Cys
180 185 190

Asp Lys Asp Lys Thr Val Thr Thr Ala Met Pro Ile Val Pro Thr Thr
195 200 205

Ala Pro Ser Pro Thr Lys Pro Val Val Gly Ser Tyr Ser Val Val Asn
210 215 220

Ser Asn Gly Thr Cys Leu Leu Ala Thr Met Gly Leu Gln Leu Asn Ile
225 230 235 240

ITI-08-PCT_Sequence_Listing_ST25.txt

Thr His Asp Lys Val Ala Ser Val Phe Asn Ile Asn Pro Asn Thr Thr
245 250 255

Asn Ala Thr Gly Ser Cys Gln Pro Gln Thr Ala Leu Leu Arg Leu Ser
260 265 270

Ser Ser Asn Ile Lys Tyr Leu Asp Phe Val Phe Ala Val Lys Asn Glu
275 280 285

Asn Arg Phe Tyr Leu Lys Glu Val Asn Val Ser Met Ile Leu Val Asn
290 295 300

Gly Ser Val Tyr Ser Ile Ser Asn Thr Asn Leu Ser Tyr Trp Asp Ala
305 310 315 320

Pro Leu Gly Ser Ser Tyr Met Cys Asn Lys Glu Gln Thr Val Ser Val
325 330 335

Ser Gly Ala Leu Gln Ile Asn Thr Phe Asp Leu Arg Val Gln Pro Phe
340 345 350

Ser Val Thr Glu Gly Lys Tyr Ser Thr Ala Glu Glu Cys Ser Ala Asp
355 360 365

Ser Asp Leu Asn Phe Leu Ile Pro Val Ala Val Gly Val Ala Leu Gly
370 375 380

Phe Leu Ile Ile Val Val Phe Ile Ser Tyr Met Ile Gly Arg Arg Lys
385 390 395 400

Ser Arg Thr Gly Tyr Gln Ser Val
405

<210> 36

<211> 411

<212> PRT

<213> Rattus norvegicus

<400> 36

Met Arg Leu Leu Ser Pro Val Thr Gly Ser Lys Leu Val Leu Phe
1 5 10 15

Leu Phe Leu Gly Ala Val Arg Ser Asp Ala Leu Lys Leu Asn Leu Thr
20 25 30

Asp Ser Lys Gly Thr Cys Leu Tyr Ala Glu Trp Glu Met Asn Phe Thr
35 40 45

Ile Thr Tyr Glu Ala Leu Lys Val Asn Glu Thr Val Thr Ile Thr Val
50 55 60

ITI-08-PCT_Sequence_Listing_ST25.txt

Pro	Asp	Lys	Val	Thr	Tyr	Asn	Gly	Ser	Ser	Cys	Gly	Asp	Asp	Lys	Asn	65	70	75	80
Gly	Ala	Lys	Ile	Met	Ile	Gln	Tyr	Gly	Ser	Thr	Leu	Ser	Trp	Ala	Val	85	90	95	
Asn	Phe	Thr	Lys	Glu	Ala	Ser	Gln	Tyr	Phe	Ile	Asn	Asn	Ile	Thr	Leu	100	105	110	
Ser	Tyr	Asn	Thr	Asn	Asp	Thr	Lys	Thr	Phe	Pro	Gly	Ala	Val	Pro	Lys	115	120	125	
Gly	Ile	Leu	Thr	Val	Ile	Ile	Pro	Val	Gly	Ser	Gln	Leu	Pro	Leu	Gly	130	135	140	
Val	Ile	Phe	Lys	Cys	Ser	Ser	Val	Leu	Thr	Phe	Asn	Leu	Ser	Pro	Val	145	150	155	160
Val	Gln	His	Tyr	Trp	Gly	Ile	His	Leu	Gln	Ala	Phe	Val	Gln	Asn	Gly	165	170	175	
Thr	Val	Ser	Lys	His	Glu	Gln	Val	Cys	Lys	Glu	Asp	Lys	Thr	Ala	Thr	180	185	190	
Thr	Val	Ala	Pro	Ile	Ile	His	Thr	Thr	Val	Pro	Ser	Pro	Thr	Thr	Thr	195	200	205	
Leu	Thr	Pro	Thr	Ser	Ile	Pro	Val	Pro	Thr	Pro	Thr	Val	Gly	Asn	Tyr	210	215	220	
Thr	Ile	Ser	Asn	Gly	Asn	Ala	Thr	Cys	Leu	Leu	Ala	Thr	Met	Gly	Leu	225	230	235	240
Gln	Leu	Asn	Ile	Thr	Glu	Glu	Lys	Val	Pro	Phe	Ile	Phe	Asn	Ile	Asn	245	250	255	
Pro	Ala	Thr	Thr	Asn	Phe	Thr	Gly	Ser	Cys	Gln	Pro	Gln	Thr	Ala	Gln	260	265	270	
Leu	Arg	Leu	Asn	Asn	Ser	Gln	Ile	Lys	Tyr	Leu	Asp	Phe	Ile	Phe	Ala	275	280	285	
Val	Lys	Asn	Glu	Lys	Arg	Phe	Tyr	Leu	Lys	Glu	Val	Asn	Val	Asn	Met	290	295	300	
Tyr	Leu	Ala	Asn	Gly	Ser	Ala	Phe	His	Val	Ser	Asn	Asn	Asn	Leu	Ser	305	310	315	320
Phe	Trp	Asp	Ala	Pro	Leu	Gly	Ser	Ser	Tyr	Met	Cys	Asn	Lys	Glu	Gln	325	330	335	
Val	Val	Ser	Val	Ser	Arg	Thr	Phe	Gln	Ile	Asn	Thr	Phe	Asn	Leu	Lys				

ITI-08-PCT_Sequence_Listing_ST25.txt

340

345

350

Val Gln Pro Phe Asn Val Thr Lys Gly Glu Tyr Ser Thr Ala Gln Asp
355 360 365

Cys Ser Ala Asp Glu Asp Asn Phe Leu Val Pro Ile Ala Val Gly Ala
370 375 380

Ala Leu Gly Gly Val Leu Ile Leu Val Leu Leu Ala Tyr Phe Ile Gly
385 390 395 400

Leu Lys Arg His His Thr Gly Tyr Glu Gln Phe
405 410

<210> 37

<211> 570

<212> PRT

<213> Ornithorhynchus anatinus

<400> 37

Met Ala Met Lys Asn Phe Thr Leu Gln Gln Glu Arg Asp Thr Ser Val
1 5 10 15

Ala Leu Ile Ile Arg Thr Tyr Val Arg Ala Phe Leu Lys Val Tyr Thr
20 25 30

Lys Val Pro Lys Pro Gln Arg Cys His Asn Gln Trp Gln Ser Leu Asn
35 40 45

Ile Glu Gly Ile Glu Gly Ile Glu Ile Val Lys Gly Ser Lys Trp Arg
50 55 60

Ser Ala Leu Glu Thr Ile Ile Thr Ile Gln Val Lys Arg Lys Ser Gln
65 70 75 80

Val Gln Lys Tyr His Pro Phe Ser Leu His Ser Glu Cys Gln Lys Thr
85 90 95

Asn Gln Glu Gly Thr Gly Gly Val Ala Thr Val Ile Ala Asp Glu Cys
100 105 110

Leu Leu Trp Pro Ser Ile Pro Phe Ser Thr Leu Ala Gln Lys Val Asn
115 120 125

Leu Gly Ser Cys Glu Ala Phe Ser Ile Ile Gly Tyr Ser Val Phe Ala
130 135 140

Leu Phe Ile Tyr Leu Lys Pro Asn Met Leu Asp Phe Ile Glu Leu Ala
145 150 155 160

Glu Leu Met Leu Ser Thr Glu Thr Gln Leu Leu Glu Pro Thr Arg Val

ITI-08-PCT_Sequence_Listing_ST25.txt

165

170

175

Cys Cys Gly Ile Cys Gln Ser Tyr Ala Leu Glu Ile Asn Leu Thr Asp
 180 185 190

Ser Lys Asn Ala Thr Cys Leu Tyr Ser Lys Trp Gln Met Thr Phe Thr
 195 200 205

Ile Asn Tyr Glu Thr Thr Gly Asn Glu Thr Lys Asn Val Thr Val Thr
 210 215 220

Val Pro Glu Asn Val Thr Tyr Asp Gly Ser Ser Cys Gly Asp Asn Gln
 225 230 235 240

Thr Val Pro Gln Ile Ala Val Gln Phe Gly Leu Gly Tyr Ser Trp His
 245 250 255

Leu Asn Phe Thr Lys Lys Glu Asn Asn Ser Tyr Ser Phe Asp Thr Ile
 260 265 270

Val Phe Thr Tyr Asn Thr Ser Asp Asn Glu Thr Phe Pro Glu Ala Lys
 275 280 285

Glu Lys Gly Gln Val Leu Ser Val Phe Glu Phe Arg Tyr Ala Arg Ile
 290 295 300

Pro Leu Asn Lys Ile Phe Arg Cys His Ser Glu Glu Ser Leu Ile Gly
 305 310 315 320

Asp Lys Ala Thr His His Tyr Trp Glu Thr Val Val Gln Ala Phe Ile
 325 330 335

Gln Asn Gly Thr Ile Ser Lys Glu Glu Phe Ile Cys Ser Lys Asp Arg
 340 345 350

Ala Ser Thr Thr Val Ala Pro Val Thr Thr Gln Val Val Pro Ser Thr
 355 360 365

Thr Ala Thr Pro Val Pro Gln Asp Lys Pro Tyr Pro Gly Lys Tyr Ala
 370 375 380

Val Lys Asn Gly Asn Asp Thr Cys Leu Leu Ala Thr Met Gly Leu Gln
 385 390 395 400

Leu Asn Val Thr Gln Asn Lys Val Asn Ser Val Ile Asn Ile Asn Pro
 405 410 415

Asn Val Thr Asp Phe Thr Gly Ser Cys Ser Asn Glu Thr Ala Glu Leu
 420 425 430

Arg Leu Ser Gly Ser Asn Val Lys Tyr Ile Asp Phe Ile Phe Ala Val
 435 440 445

ITI-08-PCT_Sequence_Listing_ST25.txt

Lys Asn Gly Asn Arg Phe Tyr Leu Lys Glu Val Asn Val Ser Ile Ser
450 455 460

Phe Val Asn Ala Ser Asp Leu Asn Val Ala Asn Asn Asn Leu Ser Tyr
465 470 475 480

Trp Asp Ala Pro Leu Gly Ser Ser Tyr Met Cys Asn Lys Glu Gln Thr
485 490 495

Leu Ala Leu Ala Asp Ser Leu Gln Ile Asn Thr Phe Asn Leu Arg Val
500 505 510

Gln Pro Phe Ser Val Val Ala Gly Lys Tyr Ser Thr Ala Glu Asp Cys
515 520 525

Ser Ala Asp Asp Asp Asn Phe Ile Val Pro Ile Ala Val Gly Ala Ala
530 535 540

Leu Gly Gly Leu Val Ile Leu Val Leu Met Ala Tyr Phe Val Gly Arg
545 550 555 560

Lys Arg Arg Ala Thr Gly Tyr Glu Gln Phe
565 570

<210> 38

<211> 425

<212> PRT

<213> Gallus gallus

<400> 38

Met Ala Pro Pro Arg Cys Pro Ala Gly Leu Ala Leu Leu Leu Leu Leu
1 5 10 15

Leu Gly Ala Cys Gly Phe Phe Gln Ser Tyr Ala Val Glu Val Asp Val
20 25 30

Lys Asp Ala Ser Asn Phe Thr Cys Leu Tyr Ala Gln Trp Met Met Lys
35 40 45

Phe Leu Ile Lys Tyr Glu Thr Asn Ser Ser Asp Tyr Lys Asn Ala Ser
50 55 60

Leu Asp Leu Thr Ser Thr Val Thr His Asn Gly Ser Ile Cys Gly Ser
65 70 75 80

Asp Thr Gln Ala Ala Leu Leu Ala Val Gln Phe Gly Asp Gly His Ser
85 90 95

Trp Ser Ile Asn Phe Thr Lys Asn Asn Glu Thr Tyr Arg Ala Glu Phe
100 105 110

ITI-08-PCT_Sequence_Listing_ST25.txt

Ile	Thr	Phe	Thr	Tyr	Asn	Thr	Asn	Asp	Thr	Ala	Val	Phe	Pro	Asp	Ala	115	120	125
Arg	Arg	Gln	Gly	Pro	Val	Thr	Ile	Val	Val	Lys	Asp	Ala	Met	His	Pro	130	135	140
Ile	Gln	Leu	Asn	Asn	Val	Phe	Val	Cys	His	His	Thr	Thr	Ser	Leu	Glu	145	150	155
Ala	Glu	Asn	Val	Thr	Gln	Ile	Phe	Trp	Asn	Val	Thr	Met	Gln	Pro	Phe	165	170	175
Val	Gln	Asn	Gly	Thr	Ile	Ser	Lys	Lys	Glu	Ser	Arg	Cys	Tyr	Ala	Asp	180	185	190
Thr	Pro	Thr	Ala	Ala	Pro	Thr	Val	Leu	Pro	Thr	Val	Ala	Asn	Val	Thr	195	200	205
Thr	Ala	Ser	Thr	Thr	Ile	Ser	Pro	Ala	Pro	Thr	Thr	Ala	Pro	Lys	Pro	210	215	220
Ala	Glu	Asn	Pro	Val	Thr	Gly	Asn	Tyr	Ser	Leu	Lys	Thr	Gly	Asn	Lys	225	230	235
Thr	Cys	Leu	Leu	Ala	Thr	Val	Gly	Leu	Gln	Leu	Asn	Ile	Ser	Gln	Asp	245	250	255
Lys	Pro	Leu	Leu	Ile	Asn	Ile	Asp	Pro	Lys	Thr	Thr	His	Ala	Asp	Gly	260	265	270
Thr	Cys	Gly	Asn	Thr	Ser	Ala	Thr	Leu	Lys	Leu	Asn	Asp	Gly	Asn	Arg	275	280	285
Thr	Leu	Ile	Asp	Phe	Thr	Phe	Ile	Val	Asn	Ala	Ser	Ala	Ser	Val	Gln	290	295	300
Lys	Phe	Tyr	Leu	Arg	Glu	Val	Asn	Val	Thr	Leu	Leu	Asn	Tyr	Gln	Asn	305	310	315
Gly	Ser	Val	Ile	Leu	Ser	Ala	Asp	Asn	Asn	Asn	Leu	Ser	Lys	Trp	Asp	325	330	335
Ala	Ser	Leu	Gly	Asn	Ser	Tyr	Met	Cys	Arg	Lys	Glu	Gln	Thr	Leu	Glu	340	345	350
Ile	Asn	Glu	Asn	Leu	Gln	Val	His	Thr	Phe	Asn	Leu	Trp	Val	Gln	Pro	355	360	365
Phe	Leu	Val	Lys	Glu	Asn	Lys	Phe	Ser	Ile	Ala	Glu	Glu	Cys	Phe	Ala	370	375	380

ITI-08-PCT_Sequence_Listing_ST25.txt

Asp Ser Asp Leu Asn Phe Leu Ile Pro Val Ala Val Gly Met Ala Leu
385 390 395 400

Gly Phe Leu Ile Ile Leu Val Phe Ile Ser Tyr Ile Ile Gly Arg Arg
405 410 415

Lys Ser Arg Thr Gly Tyr Gln Ser Val
420 425

<210> 39

<211> 556

<212> PRT

<213> Taeniopygia guttata

<400> 39

Met Glu Cys Arg Glu Gly Glu Val Thr Arg Cys Lys Gln Lys Asn Asn
1 5 10 15

Leu Phe Ser Gly Ile Asn Asp Asp Ile Ser Gly Ala Lys Gln Ala Lys
20 25 30

Gln Arg Gln Cys Thr Pro Gln Lys Pro Pro Lys Arg Ala Thr Ala Thr
35 40 45

Leu Pro Leu Gln Arg Pro Pro Arg Gly Ile Pro Gly Pro Ala Pro Ala
50 55 60

Ala Val Ala Ala Ala Val Ala Ala Asp Arg Ile Thr Pro Ser Gly Ser
65 70 75 80

His Gln Thr Arg Pro Pro Glu Ala Ala Arg Asp Glu Arg Pro Val Arg
85 90 95

Asp Pro Arg Asn Arg Ala Ala Ala Pro Ser Gly His Trp Arg Arg Ala
100 105 110

Gly Gly Pro Gln Arg His Arg His His Arg His Arg Arg His Gly Pro
115 120 125

Ala Pro Leu Arg Arg Leu Leu Leu Arg Pro Pro Pro Pro Ala Ala Ala
130 135 140

Ala Ala Arg Phe Leu Gly Phe Phe Gln Ser Tyr Ala Val Glu Val Asp
145 150 155 160

Ile Lys Asp Ala Ser Asn Ala Thr Cys Leu Tyr Ala Asp Trp Met Met
165 170 175

Arg Phe Leu Ile Lys Tyr Glu Ser Asn Ser Gly Asp Tyr Lys Thr Thr
180 185 190

ITI-08-PCT_Sequence_Listing_ST25.txt

Thr	Leu	Asn	Leu	Ser	Ser	Ser	Val	Thr	His	Asn	Gly	Ser	Val	Cys	Gly	195	200	205
Asn	Asp	Thr	Gln	Ala	Ala	Leu	Val	Ala	Val	Gln	Phe	Gly	Glu	Gly	His	210	215	220
Ser	Trp	Ser	Ile	Asn	Ile	Thr	Lys	Asn	Asn	Glu	Thr	Tyr	Gln	Gly	Asp	225	230	235
Phe	Ile	Thr	Leu	Thr	Tyr	Asn	Thr	Asn	Asp	Thr	Ala	Val	Phe	Pro	Asp	245	250	255
Ala	Lys	Arg	Lys	Gly	Pro	Ile	Thr	Val	Leu	Val	Arg	Asp	Pro	Ser	Arg	260	265	270
Pro	Ile	Gln	Leu	Asn	Thr	Val	Phe	Val	Cys	His	Asn	Ser	Phe	Val	Ile	275	280	285
Glu	Ala	Glu	Asn	Thr	Thr	Gln	Ile	Phe	Trp	Asn	Val	Thr	Met	Gln	Ala	290	295	300
Phe	Val	Gln	Asn	Gly	Thr	Val	Ser	Lys	Lys	Glu	Ser	Arg	Cys	Pro	Ala	305	310	315
Asp	Thr	Pro	Thr	Ser	Glu	Pro	Thr	Val	Pro	Pro	Thr	Ile	Ala	Asn	Val	325	330	335
Thr	Thr	Ala	Ser	Thr	Thr	Thr	Leu	Ser	Pro	Ala	Pro	Thr	Thr	Ala	Pro	340	345	350
Lys	Pro	Val	Glu	Asn	Pro	Val	Thr	Gly	Asn	Tyr	Ser	Leu	Lys	Ser	Gly	355	360	365
Asn	Lys	Thr	Cys	Phe	Leu	Ala	Thr	Val	Gly	Leu	Gln	Leu	Asn	Val	Ser	370	375	380
Gln	Glu	Lys	Pro	Leu	Leu	Ile	Asn	Ile	Asn	Pro	Lys	Thr	Thr	Val	Ala	385	390	395
Asp	Gly	Ala	Cys	Gly	Asn	Thr	Thr	Ala	Thr	Leu	Lys	Leu	Asn	Asp	Gly	405	410	415
Asn	Ser	Thr	Leu	Ile	Gly	Phe	Thr	Phe	Ala	Val	Lys	Asn	Thr	Ser	Ala	420	425	430
Ser	Val	Gln	Lys	Phe	Tyr	Leu	Arg	Glu	Val	Asn	Val	Thr	Leu	Leu	Asn	435	440	445
Arg	Leu	Asn	Gly	Ser	Val	Ile	Ser	Ser	Ala	Asp	Asn	Ser	Asn	Leu	Ser	450	455	460
Lys	Trp	Asp	Ala	Phe	Leu	Gly	Ser	Ser	Tyr	Met	Cys	Arg	Lys	Glu	Gln			

ITI-08-PCT Sequence Listing ST25.txt

465 470 475 480

Thr Leu Gln Ile Asn Glu Asn Val Gln Val His Thr Phe Asn Leu Trp
485 490 495

Ile Gln Pro Phe Leu Val Glu Ala Asn Lys Phe Ala Thr Ala Glu Glu
500 505 510

Cys Ile Ala Asp Ser Asp Leu Asn Phe Leu Ile Pro Ile Ala Val Gly
515 520 525

Val Ala Leu Gly Phe Leu Ile Ile Leu Val Phe Ile Ser Tyr Ile Ile
530 535 540

Gly Arg Arg Lys Ser Arg Thr Gly Tyr Gln Ser Val
545 550 555

<210> 40

<211> 408

<212> PRT

<213> *Xenopus tropicalis*

<400> 40

Met Glu Arg Cys Ala Cys Pro Ala Ala Leu Leu Leu Ser Leu Val
1 5 10 15

Leu Met Gly Ala Met Ala Phe Asp Val Glu Ile Lys Asp Asp Lys Asn
20 25 30

Ala Thr Cys Ile Tyr Ala Lys Leu Ser Val Asn Val Thr Val Gln Tyr
35 40 45

Glu Thr Asn Thr Ser Ser Thr Lys Asn Val Thr Phe Ser Val Pro Ser
50 55 60

Glu Val Thr Thr Asn Gly Ser Ser Cys Gly Ser Asn Gly Lys Ala Pro
65 70 75 80

Ile Leu Val Ile Asn Phe Gly Asn Gly His Ser Trp Ser Leu Asn Phe
85 90 95

Thr Arg Asn Asp Ser Met Tyr Ser Gly Gly Ala Leu Ile Phe Thr Tyr
100 105 110

Asn Thr Asn Asp Ser Thr Leu Phe Pro Asp Ala Leu Lys Glu Gly Leu
115 120 125

Ile Ser Ser Thr Ala Ala Phe Leu Gly Pro Ile Pro Leu Asn Ser Thr
130 135 140

Tyr Lys Cys Ile Ser Ser Glu Val Val Val Ser Glu Asn Val Thr Gln

ITI-08-PCT_Sequence_Listing_ST25.txt

```

145                150                155                160
Ile Ile Ser Asp Val Lys Leu Glu Ala Phe Met Gln Asn Gly Thr Leu
                165                170                175
Gly Lys Glu Val Ser Cys Asp Ala Asp Lys Pro Ser Pro Thr Pro Thr
                180                185                190
Thr Asn Pro Ser Thr Thr Ala Ser Thr Thr Thr Pro Thr Pro Thr Ser
                195                200                205
Lys Pro Leu Asp Asn Pro Thr Thr Gly Asn Tyr Ser Val Ser Asp Val
                210                215                220
Asn Gly Thr Cys Leu Leu Ala Ser Met Gly Leu Gln Ile Asn Thr Ser
225                230                235                240
Leu Leu Ser Glu Gly Lys Asn Ile Trp Thr Ala Phe Asn Ile Asp Pro
                245                250                255
Thr Ala Met Ser Lys Asn Gly Thr Cys Ser Asn Gln Thr Gly Thr Leu
                260                265                270
Ile Leu Thr Asp Asn Ser Thr Val Ile Glu Phe Thr Leu Ala Leu Lys
                275                280                285
Asn Lys Asn His Phe Tyr Leu Lys Glu Val Asn Val Ala Leu Ile Asn
                290                295                300
Gly Ser Ala Ser Ser Thr Arg Gln Asn Gln Asn Leu Ser Ala Trp Glu
305                310                315                320
Ala Ser Val Gly Ser Ser Tyr Met Cys His Lys Glu Gln Gln Ile Lys
                325                330                335
Val Ser Glu Asp Leu Val Ile Asn Ser Phe Asp Val Arg Val Gln Leu
                340                345                350
Phe Gly Val Lys Asn Glu Thr Phe Ala Thr Ala Gln Gln Cys Ser Leu
                355                360                365
Asp Asp Asp Ser Ile Val Ile Pro Ile Val Val Gly Ala Ala Leu Ala
                370                375                380
Gly Leu Ile Val Ile Ile Val Ile Ala Tyr Leu Ile Gly Arg Arg Lys
385                390                395                400
Gly Tyr Ser Gly Tyr Gln Thr Leu
                405

```

<210> 41
<211> 404

ITI-08-PCT_Sequence_Listing_ST25.txt

<212> PRT

<213> Salmo salar

<400> 41

```

Met Phe Arg Cys Ala Phe Leu Ile Leu Phe Leu Ala Leu Gly Asn Glu
1          5          10          15
Leu His Leu Ser His Gly Thr Glu Val Ser Val Asn Asn Thr Glu Asn
          20          25          30
Lys Leu Cys Leu Tyr Ala Asn Leu Met Val Asn Phe Ser Val Thr Tyr
          35          40          45
Glu Val Gly Val Asn Lys Asn Glu Thr Val Ile Phe Val Leu Pro Glu
          50          55          60
Asn Val Thr Thr Glu Gly Ser Thr Cys Asp Asn Thr Thr Ser Thr Leu
65          70          75          80
Lys Leu Ser Phe Gly His Gly His Ser Trp Thr Val Glu Phe Thr Lys
          85          90          95
Lys Asn Lys Thr Tyr Gln Val Asp Thr Ile Val Phe Ser Tyr Asn Leu
          100          105          110
Asn Asp Ser Ser Val Phe Pro Asn Ser Thr Ser Lys Glu Thr Lys Phe
          115          120          125
Val Thr Val Lys Ser Ile Ile Thr Asn Val Ser Val Asp Thr Tyr Tyr
          130          135          140
Ser Cys Lys Ser Glu Asn Val Leu Thr Val Glu Ser Val Ile Gln Thr
145          150          155          160
Leu Tyr Asp Val Ala Leu Gln Ala Phe Val Ile Asn Gly Ser Lys Ser
          165          170          175
Asp Thr Asp Thr Val Cys Ser Ala Asp Met Thr Ser Thr Thr Val Ala
          180          185          190
Pro Thr Thr Thr Val Thr Ser Thr Ala Ala Pro Thr Ser Thr Pro Thr
          195          200          205
Leu Pro Thr Pro Thr Thr Gly Lys Tyr Ser Ile Ala Pro Asp Val Asn
          210          215          220
Ser Thr Ala Cys Leu Met Ala Thr Phe Gly Leu Gln Ile Gly Tyr Lys
225          230          235          240
Gln Gly Asp Lys Glu Glu Thr Ile Asn Leu Val Pro Asn Ile Thr Glu
          245          250          255

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Val Gly Gly Ala Cys Gly Ala Asn Ser Ser Asp Leu Ile Leu Thr Ser
260 265 270

Asp Thr Ile Thr Ile Met Phe Thr Phe Ser Asn Asp Gly Lys Lys Phe
275 280 285

His Leu His Ala Leu Lys Val Thr Val Lys Pro Ala Thr Gly Asp Pro
290 295 300

Val Ile Ala Val Asn Asn Asn Met Ser Ile Trp Ala Ala Ala Val Gly
305 310 315 320

Ser Ser Tyr Met Cys Asn Lys Glu Gln Thr Leu Asn Val Thr Asp Thr
325 330 335

Leu Thr Leu Tyr Thr Phe Glu Leu Arg Val Gln Pro Phe Glu Val Asn
340 345 350

Lys Gly Glu Phe Ala Thr Ala His Glu Cys Ser Leu Asp Asp Thr Ser
355 360 365

Ile Leu Ile Pro Ile Ile Val Gly Ala Ala Leu Ala Gly Leu Ile Leu
370 375 380

Ile Val Val Ile Ala Tyr Val Ile Gly Arg Arg Lys Thr Tyr Val Gly
385 390 395 400

Tyr Gln Thr Leu

<210> 42

<211> 410

<212> PRT

<213> Oreochromis niloticus

<400> 42

Met Lys Val Ser His Ala Thr Ala Gly Leu Val Val Trp Phe Val Val
1 5 10 15

Leu Gly Cys Ile Asp Ala Val Thr Leu Glu Val Lys Glu Ser Asn Thr
20 25 30

Thr Cys Ile Lys Ala Asp Leu Ser Ala Ser Phe Ser Ile Ile Tyr Asn
35 40 45

Thr Thr His Ala Glu Arg Thr Val Gln Val Leu Leu Pro Asn Ser Thr
50 55 60

Thr Val Asp Thr Ala Asn Ser Thr Cys Gly Lys Asp Gly Ser Ser Pro
65 70 75 80

ITI-08-PCT_Sequence_Listing_ST25.txt

Arg	Leu	Val	Ala	Val	Phe	Gly	Ser	Gly	Tyr	Thr	Leu	Gly	Leu	Asn	Phe	85	90	95
Ser	Thr	Asn	Gly	Thr	Leu	Tyr	Gln	Val	Ser	Ser	Leu	Thr	Leu	Gln	Tyr	100	105	110
Asn	Leu	Ser	Asp	Thr	Ser	Val	Phe	Pro	Asn	Ala	Thr	Ile	Ser	Gly	Val	115	120	125
Val	Thr	Leu	Val	Ser	Ala	Ser	Val	Gly	Ile	Glu	Ala	Asn	Val	Asn	Thr	130	135	140
Thr	Tyr	Lys	Cys	Ala	Ser	Pro	Thr	Val	Ile	Asp	Val	Ala	Thr	Ala	Lys	145	150	155
Val	Asn	Phe	Thr	Asp	Met	Arg	Leu	Glu	Ala	Tyr	Met	Pro	Gly	Asn	Glu	165	170	175
Leu	Ser	Pro	Asn	Glu	Thr	Val	Cys	Phe	Ala	Asp	Gln	Thr	Ser	Thr	Thr	180	185	190
Pro	Ser	Pro	Thr	Thr	Val	Ser	Thr	Thr	Ala	Val	Pro	Thr	Gln	Thr	Pro	195	200	205
Pro	Gly	Thr	Pro	Gln	Gln	Gly	Asn	Tyr	Thr	Val	Lys	Asp	Ala	Asn	Asp	210	215	220
Thr	Ile	Cys	Leu	Leu	Ala	Lys	Met	Gly	Leu	Gln	Leu	Asn	Val	Ser	Tyr	225	230	235
Thr	Ser	Gln	Asn	Lys	Thr	Val	Gln	Asp	Val	Leu	Asn	Leu	Asn	Pro	Asn	245	250	255
Val	Thr	Asn	Ser	Thr	Gly	Ser	Cys	Gly	Ala	Ser	Ser	Ala	Thr	Leu	Val	260	265	270
Leu	Thr	Gln	Thr	Gln	Ser	Thr	Ile	Leu	Thr	Phe	Asn	Phe	Thr	Leu	Asn	275	280	285
Ser	Thr	Thr	Asn	Lys	Tyr	His	Leu	Ser	Gly	Val	Thr	Leu	Ile	Ala	Asn	290	295	300
Trp	Phe	Asp	Ser	Ala	His	Phe	Ser	Met	Ser	Asn	Asn	Ser	Leu	Asn	Tyr	305	310	315
Leu	Arg	Ser	Thr	Leu	Gly	Tyr	Ser	Tyr	Met	Cys	Asn	Ala	Glu	Gln	Thr	325	330	335
Leu	Phe	Val	Thr	Pro	Ser	Phe	Ser	Leu	Asn	Thr	Phe	Asp	Leu	Gln	Val	340	345	350
Gln	Pro	Phe	Gly	Val	Lys	Ser	Gly	Arg	Phe	Ala	Thr	Ala	Glu	Glu	Cys			

ITI-08-PCT_Sequence_Listing_ST25.txt

355

360

365

Gln Met Asp Gln Asn Gln Met Ile Ile Pro Ile Ile Val Gly Ala Ala
370 375 380

Leu Ala Gly Leu Val Leu Ile Thr Leu Ile Ala Tyr Leu Ile Gly Lys
385 390 395 400

Arg Arg Ser His Ala Gly Tyr Gln Ala Ile
405 410

<210> 43

<211> 249

<212> PRT

<213> Takifugu rubripes

<400> 43

Met Thr Gln Ile Gly Gly Val Gln Pro Val Phe Leu Ala Val Thr Val
1 5 10 15

His Leu Ile Leu Ala Thr Val Leu His Gln Thr Phe Ala Thr Val Thr
20 25 30

Pro Pro Val Thr Thr Ala Val Pro His Lys Glu Pro Gly Arg Pro Asp
35 40 45

Gln Gly Asp Tyr Gln Val Thr Ser Ser Asn Gly Thr Val Cys Phe Leu
50 55 60

Ala Ser Met Gly Leu Gln Leu Asn Ile Thr Phe Asn Ser Thr Ser Gln
65 70 75 80

Asn Lys Thr Leu Gln Glu Val Ile Asn Ile Gln Pro Asn Arg Thr Lys
85 90 95

Ser Ser Gly Ser Cys Asp Thr Ser Ser Ala Leu Leu Thr Leu Thr Thr
100 105 110

Asp Ala Glu Lys Thr Asn Leu Thr Phe Val Phe Ala Leu Asn Thr Thr
115 120 125

Ser Asn Lys Tyr His Leu Ser Glu Val Ser Leu Ser Ala Ala Leu Ser
130 135 140

Asp Met Lys Glu Thr Phe Val Ala Gln Asn His Ser Leu Asp Tyr Leu
145 150 155 160

Arg Gly Thr Leu Gly Phe Ser Tyr Met Cys Arg Glu Arg Gln Thr Leu
165 170 175

Gly Val Thr Pro Asp Phe Ala Ile Asn Thr Phe Gln Val Gln Val Gln

ITI-08-PCT_Sequence_Listing_ST25.txt

180

185

190

Pro Phe Gly Val Thr Gly Lys Gln Phe Ala Ala Ala Glu Glu Cys Gln
195 200 205

Leu Asp Lys Asp Asp Met Leu Ile Pro Ile Ile Val Gly Ala Ala Leu
210 215 220

Ala Ala Leu Val Leu Ile Val Leu Ser Ala Tyr Leu Ile Gly Arg Lys
225 230 235 240

Arg Ser His Ala Gly Tyr Gln Ser Ile
245

<210> 44

<211> 418

<212> PRT

<213> Pan troglodytes

<400> 44

Met Pro Arg Gln Leu Ser Ala Ala Ala Ala Leu Phe Ala Ser Leu Ala
1 5 10 15

Val Ile Leu His Asp Gly Ser Gln Met Arg Ala Lys Ala Phe Pro Glu
20 25 30

Thr Arg Asp Tyr Ser Gln Pro Ser Ala Ala Ala Thr Val Gln Asp Ile
35 40 45

Lys Lys Pro Val Gln Gln Pro Ala Lys Gln Ala Pro His Gln Thr Leu
50 55 60

Ala Ala Arg Phe Met Asp Gly His Ile Thr Phe Gln Thr Ala Ala Thr
65 70 75 80

Val Lys Thr Pro Thr Thr Thr Pro Ala Thr Thr Lys Asn Thr Ala Thr
85 90 95

Thr Ser Pro Ile Thr Tyr Thr Leu Val Thr Thr Gln Ala Thr Pro Asn
100 105 110

Asn Ser His Thr Ala Pro Pro Val Thr Glu Val Thr Val Gly Pro Ser
115 120 125

Leu Val Pro Tyr Ser Leu Pro Pro Thr Ile Thr Pro Pro Ala His Thr
130 135 140

Thr Gly Thr Ser Ser Ser Thr Val Ser His Thr Thr Gly Asn Thr Thr
145 150 155 160

Gln Pro Ser Asn Gln Thr Thr Leu Pro Ala Thr Leu Ser Ile Ala Leu

ITI-08-PCT_Sequence_Listing_ST25.txt

165 170 175

His Lys Ser Thr Thr Gly Gln Lys Pro Val Gln Pro Thr His Ala Pro
180 185 190

Gly Thr Thr Ala Ala Ala His Asn Thr Thr Arg Thr Ala Ala Pro Ala
195 200 205

Ser Thr Val Pro Gly Pro Thr Leu Ala Pro Gln Pro Ser Ser Val Lys
210 215 220

Thr Gly Ile Tyr Gln Val Leu Asn Gly Ser Arg Leu Cys Ile Lys Ala
225 230 235 240

Glu Met Gly Ile Gln Leu Ile Val Gln Asp Lys Glu Ser Val Ser Trp
245 250 255

Gly His Arg Thr Ile Thr Leu Ser Ser Lys Ser Leu Ser Gly Gly Cys
260 265 270

Leu Ala Arg Asn Glu His Ser Pro His Pro Leu Phe Leu Phe Phe Glu
275 280 285

Lys Gly Pro Pro Ser Val Thr Gln Ala Glu Asp Glu Glu Ser Tyr Tyr
290 295 300

Ile Ser Glu Val Gly Ala Tyr Leu Thr Val Ser Asp Pro Glu Thr Ile
305 310 315 320

Tyr Gln Gly Ile Lys His Ala Val Val Met Phe Gln Thr Ala Val Gly
325 330 335

His Ser Phe Lys Cys Val Ser Glu Gln Ser Leu Gln Leu Ser Ala His
340 345 350

Leu Gln Leu Lys Thr Thr Asp Val Gln Leu Gln Ala Phe Asp Phe Glu
355 360 365

Asp Asp His Phe Gly Asn Val Asp Glu Cys Ser Ser Asp Tyr Thr Ile
370 375 380

Val Leu Pro Val Ile Gly Ala Ile Val Val Gly Leu Cys Leu Met Gly
385 390 395 400

Met Gly Val Tyr Lys Ile Arg Leu Arg Cys Gln Ser Ser Gly Tyr Gln
405 410 415

Arg Ile

<210> 45

<211> 416

<212> PRT

ITI-08-PCT_Sequence_Listing_ST25.txt

<213> Papio anubis

<400> 45

```

Met Pro Arg Gln Leu Ser Ala Ala Ala Val Leu Phe Ala Ser Leu Ala
1          5          10          15

Val Ile Leu His Asp Gly Ser Gln Met Arg Ala Lys Ala Phe Pro Lys
          20          25          30

Thr Arg Asp Tyr Ser Gln Pro Thr Ala Ala Ala Thr Gly Gln Asp Ile
          35          40          45

Ala Lys Pro Val Gln Gln Pro Ala Asn Gln Ala Pro His Gln Thr Leu
          50          55          60

Ala Ala Arg Leu Met Asp Gly His Ile Thr Phe Gln Thr Ala Ala Thr
65          70          75          80

Ile Lys Thr Pro Thr Thr Thr Pro Val Thr Thr Lys Asn Thr Pro Thr
          85          90          95

Thr Ser Pro Ile Ile Tyr Thr Leu Val Thr Thr Gln Ala Thr Ser Asn
          100          105          110

Asn Ser His Thr Ala Pro Pro Leu Thr Lys Val Thr Val Gly Pro Ser
          115          120          125

Leu Ala Pro Tyr Ser Leu Pro Pro Thr Ile Thr Pro Pro Ala His Thr
          130          135          140

Thr Gly Thr Ser Ser Ser Thr Val Asn His Thr Thr Gly Asn Ala Thr
145          150          155          160

Gln Pro Ser Asn Gln Thr Thr Leu Pro Ala Thr Leu Ser Ile Ala Leu
          165          170          175

His Lys Ser Thr Thr Gly Gln Lys Pro Val Gln Pro Thr His Ala Pro
          180          185          190

Gly Thr Thr Ala Ala Ala His Asn Thr Thr Arg Thr Ala Ala Pro Ala
          195          200          205

Ser Thr Val Pro Gly Ser Thr Leu Ala Pro Gln Pro Ser Ser Val Lys
          210          215          220

Thr Gly Ile Tyr Gln Val Leu Asn Gly Ser Arg Leu Cys Ile Lys Ala
225          230          235          240

Glu Met Gly Ile Gln Leu Ile Val Gln Asp Lys Glu Ser Val Phe Ser
          245          250          255

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Pro Arg Arg Tyr Phe Asn Leu Asp Pro Asn Ala Thr Gln Ala Ser Gly
260 265 270

Asn Cys Gly Thr Arg Asn Ser Asn Leu Leu Leu Asn Phe Gln Gly Gly
275 280 285

Phe Val Asn Leu Thr Phe Thr Lys Asp Glu Gly Ser Tyr Tyr Ile Ser
290 295 300

Glu Val Gly Ala Cys Leu Thr Val Ser Asp Pro Glu Thr Ile Tyr Gln
305 310 315 320

Gly Met Lys His Ala Val Val Met Phe Gln Thr Ala Val Gly His Ser
325 330 335

Phe Lys Cys Val Ser Glu Gln Ser Leu Gln Leu Ser Ala His Leu Gln
340 345 350

Leu Lys Thr Thr Asn Val Gln Leu Gln Ala Phe Asp Phe Glu Asp Asp
355 360 365

His Phe Gly Asn Val Asp Glu Cys Ser Ser Asp Tyr Thr Ile Val Leu
370 375 380

Pro Val Ile Gly Ala Ile Val Val Gly Leu Cys Leu Val Gly Ile Gly
385 390 395 400

Val Tyr Lys Ile Arg Leu Arg Cys Gln Ser Ser Gly Tyr Gln Arg Ile
405 410 415

<210> 46

<211> 416

<212> PRT

<213> Macaca mulatta

<400> 46

Met Pro Arg Gln Leu Ser Ala Ala Ala Val Leu Phe Ala Ser Leu Ala
1 5 10 15

Val Ile Leu His Asp Gly Ser Gln Met Arg Ala Lys Ala Phe Pro Lys
20 25 30

Thr Arg Asp Tyr Ser Gln Pro Thr Ala Ala Ala Thr Gly Gln Asp Ile
35 40 45

Ala Lys Pro Val Gln Gln Pro Ala Asn Gln Ala Pro His Gln Thr Leu
50 55 60

Ala Ala Arg Leu Met Asp Gly His Ile Thr Phe Gln Thr Ala Ala Thr
65 70 75 80

ITI-08-PCT_Sequence_Listing_ST25.txt

Ile	Lys	Thr	Pro	Thr	Thr	Thr	Pro	Val	Thr	Thr	Lys	Asn	Thr	Pro	Thr	85	90	95
Thr	Ser	Pro	Ile	Ile	Tyr	Thr	Leu	Val	Thr	Thr	Gln	Ala	Thr	Ser	Asn	100	105	110
Asn	Ser	His	Thr	Ala	Pro	Pro	Leu	Thr	Lys	Val	Thr	Val	Gly	Pro	Ser	115	120	125
Leu	Ala	Pro	Tyr	Ser	Leu	Pro	Pro	Thr	Ile	Thr	Pro	Pro	Ala	His	Thr	130	135	140
Thr	Gly	Thr	Ser	Ser	Ser	Thr	Val	Asn	His	Thr	Thr	Gly	Asn	Ala	Thr	145	150	155
Gln	Pro	Ser	Asn	Gln	Thr	Thr	Leu	Pro	Ala	Thr	Leu	Ser	Ile	Ala	Pro	165	170	175
His	Lys	Ser	Thr	Thr	Gly	Gln	Lys	Pro	Val	Gln	Pro	Thr	His	Ala	Pro	180	185	190
Gly	Thr	Thr	Ala	Ala	Ala	His	Asn	Thr	Thr	Arg	Thr	Ala	Ala	Pro	Ala	195	200	205
Ser	Thr	Val	Pro	Gly	Ser	Thr	Leu	Ala	Pro	Gln	Pro	Ser	Ser	Ile	Lys	210	215	220
Thr	Gly	Ile	Tyr	Gln	Val	Leu	Asn	Gly	Ser	Arg	Leu	Cys	Ile	Lys	Ala	225	230	235
Glu	Met	Gly	Ile	Gln	Leu	Ile	Val	Gln	Asp	Lys	Glu	Ser	Val	Phe	Ser	245	250	255
Pro	Arg	Arg	Tyr	Phe	Asn	Leu	Asp	Pro	Asn	Ala	Thr	Gln	Ala	Ser	Gly	260	265	270
Asn	Cys	Gly	Thr	Arg	Asn	Ser	Asn	Leu	Leu	Leu	Asn	Phe	Gln	Gly	Gly	275	280	285
Phe	Val	Asn	Leu	Thr	Phe	Thr	Lys	Asp	Glu	Gly	Ser	Tyr	Tyr	Ile	Ser	290	295	300
Glu	Val	Gly	Ala	Cys	Leu	Thr	Val	Ser	Asp	Pro	Glu	Thr	Ile	Tyr	Gln	305	310	315
Gly	Met	Lys	His	Ala	Val	Val	Met	Phe	Gln	Thr	Val	Val	Gly	His	Ser	325	330	335
Phe	Lys	Cys	Val	Ser	Glu	Gln	Ser	Leu	Gln	Leu	Ser	Ala	His	Leu	Gln	340	345	350
Leu	Lys	Thr	Thr	Asn	Val	Gln	Leu	Gln	Ala	Phe	Asp	Phe	Glu	Asp	Asp			

ITI-08-PCT_Sequence_Listing_ST25.txt

355

360

365

His Phe Gly Asn Val Asp Glu Cys Ser Ser Asp Tyr Thr Ile Val Leu
370 375 380

Pro Val Ile Gly Ala Ile Val Val Gly Leu Cys Leu Val Gly Met Gly
385 390 395 400

Val Tyr Lys Ile Arg Leu Arg Cys Gln Ser Ser Gly Tyr Gln Arg Ile
405 410 415

<210> 47

<211> 428

<212> PRT

<213> Canis lupus familiaris

<400> 47

Met Ser Trp Gln Leu Ser Ala Ala Val Ala Leu Phe Val Ser Leu Ala
1 5 10 15

Leu Ile Leu His Tyr Gly Ser Gln Ile Arg Ala Lys Met Phe Pro Glu
20 25 30

Thr Val Asp Phe Gln Pro Thr Thr Ala Ala Thr Val Arg Ala Thr Ala
35 40 45

Lys Pro Phe Leu His Leu Thr Asn Gln Val Pro Ser Gln Thr Leu Ala
50 55 60

Ala Arg Ser Met Asp Gly His Ile Ala Ser Gln Arg Ala Ala Thr Thr
65 70 75 80

Ser Ser Ser Glu Pro Pro Thr Thr His Thr Thr Val Lys Thr Leu Val
85 90 95

Thr Thr Ser Leu Val Thr Ala Asn Ser Thr Pro Ser Ser Ser Pro Ile
100 105 110

Ile Tyr Thr Leu Val Thr Thr Ile Val Thr Pro Asn Asn Ser Asn Thr
115 120 125

Ala Ala Pro Val Thr Glu Ala Thr Ile Gly Pro Ser Ala Asp Pro Gly
130 135 140

Ser Leu Pro Thr Thr Ser Thr Pro Leu Ala His Thr Thr Arg Thr Asn
145 150 155 160

Pro Ser Thr Leu Ser His Lys Thr Arg Lys Thr Thr His Phe Gly Asn
165 170 175

Gln Thr Thr Leu Pro Ala Thr Leu Ser Thr Ser Thr His Lys Ser Thr

ITI-08-PCT_Sequence_Listing_ST25.txt

180	185	190															
Ser	Ser	His	Lys	Ser	Ala	Gln	Ser	Thr	His	Ala	Pro	Gly	Pro	Thr	Thr		
	195						200					205					
Ala	Ala	His	Asn	Thr	Thr	Gln	Thr	Ala	Ser	Pro	Ala	Thr	Pro	Ala	Ser		
	210					215					220						
Gly	Pro	Thr	Leu	Ala	Pro	Gln	Pro	Ser	Ser	Pro	Lys	Thr	Gly	Ile	Tyr		
225					230					235					240		
Gln	Val	Leu	Asn	Gly	Ser	Arg	Leu	Cys	Ile	Lys	Ala	Glu	Met	Gly	Ile		
				245					250					255			
Glu	Leu	Met	Val	Gln	Asp	Thr	Lys	Ser	Val	Phe	Ser	Pro	Gln	Arg	Tyr		
			260					265					270				
Phe	Asn	Ile	Asp	Pro	Asn	Ala	Thr	Gln	Thr	Ser	Gly	Asn	Cys	Gly	Ser		
	275						280					285					
Gln	Lys	Ser	Asn	Leu	Leu	Leu	Asn	Phe	Gln	Gly	Gly	Phe	Val	Asn	Leu		
	290					295					300						
Thr	Phe	Leu	Lys	Asp	Glu	Asn	Ser	Tyr	Tyr	Ile	Asn	Glu	Val	Gly	Ala		
305					310					315					320		
Tyr	Leu	Ala	Val	Ser	Asn	Pro	Glu	Lys	Ile	Tyr	Gln	Gly	Met	Lys	Ser		
				325					330					335			
Ser	Val	Val	Met	Phe	Glu	Thr	Gly	Val	Gly	His	Ser	Phe	Lys	Cys	Val		
			340					345					350				
Ser	Glu	Gln	Ser	Ile	Gln	Leu	Ser	Thr	His	Leu	Gln	Leu	Lys	Thr	Met		
	355						360					365					
Asn	Val	Gln	Phe	Gln	Ala	Phe	Asp	Phe	Glu	Asp	Asp	His	Phe	Gly	Asn		
	370					375					380						
Val	Asp	Glu	Cys	Ser	Ser	Asp	Tyr	Thr	Val	Val	Leu	Pro	Val	Ile	Gly		
385					390					395					400		
Ala	Ile	Val	Leu	Gly	Leu	Cys	Ala	Val	Gly	Leu	Ile	Val	Tyr	Gly	Ile		
				405					410					415			
His	Leu	Arg	Arg	Glu	Ser	Ser	Gly	Tyr	Gln	Arg	Ile						
			420					425									

<210> 48
 <211> 430
 <212> PRT
 <213> Sus scrofa

ITI-08-PCT_Sequence_Listing_ST25.txt

<400> 48

```

Met Ser Trp Arg Leu Ser Ala Val Leu Val Ser Phe Val Ser Leu Ala
1          5          10          15

Val Phe Leu His Tyr Gly His His Met Lys Ala Lys Val Phe Pro Glu
          20          25          30

Ile Thr Asp Ser Ser Ser Pro Thr Thr Ala Ala Thr Val Gln Ala Thr
          35          40          45

Ala Glu Pro Ser Leu Trp Lys Pro Thr Asn His Thr Pro His Lys Thr
          50          55          60

Leu Ala Ala Lys Ser Thr Asp Gly His Val Thr Ser Gln Ile Ala Thr
65          70          75          80

Thr Val Thr Asp Ser Glu Thr Leu Thr Thr His Thr Thr Ile Thr Thr
          85          90          95

Leu Ala Ala Thr Ser Leu Ala Ala Thr Asn Ser Thr Pro Ser Thr Ser
          100          105          110

Pro Thr Thr His Thr Leu Phe Thr Thr Leu Ala Thr Pro Asn Thr Ser
          115          120          125

His Met Ala Ala Pro Val Thr Glu Ala Ala Ile Ser Pro Ser Ala Gly
          130          135          140

Leu Ser Ser Leu Leu Pro Thr Ile Ile Pro Pro Ala His Thr Thr Gly
145          150          155          160

Thr Arg Ser Ser Thr Leu Ser Pro Thr Ala Gly Lys Thr Thr Gln Pro
          165          170          175

Ser Asn Gln Thr Thr Leu Pro Ala Thr Leu Ser Thr Ser Pro His Asn
          180          185          190

Ser Thr Ala Ser Gln Lys Pro Thr His Pro Asn His Thr Pro Gly Pro
          195          200          205

Thr Thr Gly Ala His Asn Thr Thr Gln Thr Ala Ser Pro Ala Thr Ile
          210          215          220

Ala Pro Gly Pro Thr Leu Ala Pro Gln Pro Ser Ser Ala Lys Thr Gly
225          230          235          240

Ile Tyr Gln Val Leu Asn Gly Ser Lys Leu Cys Ile Lys Ala Glu Met
          245          250          255

Gly Ile Glu Leu Thr Val Gln Asp Thr Gln Ser Val Phe Ser Pro Gln
          260          265          270

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Arg Tyr Phe Asn Ile Asp Pro Asn Thr Thr Gln Ala Ser Gly Asn Cys
275 280 285

Gly Ser Arg Lys Ser Lys Leu Leu Leu Asn Phe Gln Gly Gly Phe Val
290 295 300

Asn Leu Thr Phe Thr Lys Asp Glu Asn Ser Tyr Tyr Val Ser Gly Val
305 310 315 320

Gly Ala Tyr Leu Thr Val Ser Asn Pro Glu Lys Val Tyr Gln Gly Met
325 330 335

Lys Asn Ala Val Val Met Phe Glu Thr Met Ile Gly His Ser Phe Lys
340 345 350

Cys Val Ser Glu Gln Ser Ile Gln Leu Ser Pro His Leu Gln Leu Asn
355 360 365

Thr Met Asn Val Gln Leu Gln Ala Phe Asp Phe Glu Asp Asp His Phe
370 375 380

Gly Asn Val Asp Glu Cys Ser Ser Asp Tyr Thr Ile Val Leu Pro Val
385 390 395 400

Ile Gly Ala Ile Val Leu Gly Leu Cys Ala Val Gly Leu Ile Val Tyr
405 410 415

Gly Ile Arg Leu Lys Arg Glu Ser Ser Glu Tyr Gln Arg Ile
420 425 430

<210> 49

<211> 259

<212> PRT

<213> Danio rerio

<400> 49

Met Thr Gln Ser Ser Arg Ser Val Leu Leu Leu Met Leu Ser Ser Leu
1 5 10 15

His Cys Leu Gly Ser Ser Leu Glu Ser Asn Pro Lys Asp Pro Ser Val
20 25 30

Leu Ala Glu Ala Pro Gly Gln Asn Lys Arg Asp Ser Asp Ile Ser Leu
35 40 45

Val Pro Gln Met Pro Val Leu Gln Pro Lys Glu Thr Ala Pro Pro Leu
50 55 60

Val Thr Tyr Thr Ile Arg Asn Pro Gln Gly Lys Val Cys Val Arg Ala
65 70 75 80

ITI-08-PCT_Sequence_Listing_ST25.txt

Ser Phe Gly Val Glu Phe Val Val Arg Glu Asn Lys Lys Lys Tyr Tyr
85 90 95

Phe Asn Leu Thr Pro Asn Ser Ala Arg Ala Thr Gly Tyr Cys Ala Asn
100 105 110

Gln Lys Thr Val Leu Ser Leu Glu Phe Ser Gly Gly Asn Leu Glu Phe
115 120 125

Thr Phe Ile Lys Asp Gly Asp Gln Ser Tyr Val Lys Thr Val Lys Gly
130 135 140

Ser Leu Arg Ala Ala Pro Pro Cys Lys Asn Cys Pro Ser Lys Ile Tyr
145 150 155 160

Val Gly Leu Val Asp Asn Glu Lys Leu Phe Lys Ala Lys Asn Gly Leu
165 170 175

Ser Phe Asn Cys Lys Ser Glu Thr Met Leu Ile Leu Ala Asp Tyr Phe
180 185 190

Arg Leu Lys Leu Val Pro Leu Gln Ile Gln Ala Phe Asp Leu Val Asn
195 200 205

Gly Ala Phe Gly Lys Glu Val Glu Cys Trp Ala Asp Tyr Asn Lys Arg
210 215 220

Met Ile Pro Ile Ile Leu Gly Ala Val Ala Ala Ala Ile Cys Leu Ile
225 230 235 240

Ala Ile Leu Thr Tyr Val Leu Val Arg Glu His Arg Asn Gln Gly Tyr
245 250 255

Glu Gln Leu

<210> 50

<211> 432

<212> PRT

<213> Equus caballus

<400> 50

Met Ala Trp Gln Leu Ser Ala Val Val Val Leu Phe Val Ser Leu Ala
1 5 10 15

Val Ile Leu Tyr Tyr Gly Ser His Val Arg Ala Asn Val Phe Pro Glu
20 25 30

Ile Thr Asp Tyr Ser Gln Pro Thr Thr Ala Ala Thr Ile Gln Thr Arg
35 40 45

ITI-08-PCT_Sequence_Listing_ST25.txt

Ala	Gln	Pro	Ser	Leu	Ser	Gln	Pro	Thr	Asn	Gln	Val	Pro	His	Lys	Thr	50	55	60	
Leu	Ala	Thr	Arg	Ser	Met	Asp	Gly	Gln	Val	Thr	Ser	Gln	Thr	Ala	Ala	65	70	75	80
Thr	Thr	Val	Asn	Pro	Glu	Thr	Pro	Val	Thr	His	Thr	Thr	Ile	Lys	Thr	85	90	95	
Ala	Ala	Ala	Thr	Ser	Leu	Val	Thr	Thr	Asn	Ser	Thr	Leu	Ser	Thr	Ser	100	105	110	
Pro	Ile	Thr	Asn	Thr	Leu	Leu	Thr	Thr	Leu	Ala	Thr	Pro	Asp	Asn	Thr	115	120	125	
His	Thr	Thr	Thr	Pro	Val	Thr	Glu	Ala	Thr	Ile	Gly	Pro	Ser	Ala	Gly	130	135	140	
Pro	Gly	Ser	Pro	Pro	Thr	Thr	Ile	Thr	Thr	Thr	Ser	Ser	Ala	Tyr	Thr	145	150	155	160
Thr	Gly	Thr	Arg	Ser	Ser	Thr	Val	Ser	His	Thr	Thr	Gly	Lys	Thr	Thr	165	170	175	
Gln	Leu	Ser	Asn	Gln	Thr	Thr	Leu	Pro	Ala	Thr	Leu	Ser	Thr	Ser	Pro	180	185	190	
His	Asn	Ser	Thr	Thr	Ser	Gln	Asn	Pro	Ala	His	Ser	Thr	His	Thr	Pro	195	200	205	
Gly	Pro	Thr	Thr	Gly	Thr	Cys	Asn	Thr	Thr	Gln	Thr	Ala	Ser	Pro	Thr	210	215	220	
Thr	Thr	Ala	Pro	Gly	Pro	Thr	Leu	Ala	Pro	Gln	Pro	Ser	Ser	Ala	Lys	225	230	235	240
Thr	Gly	Met	Tyr	Gln	Ile	Leu	Asn	Gly	Ser	Lys	Leu	Cys	Ile	Lys	Ala	245	250	255	
Glu	Met	Gly	Ile	Gln	Leu	Thr	Val	Gln	Asp	Thr	Lys	Ser	Ala	Ser	Pro	260	265	270	
Pro	Gln	Gly	Tyr	Phe	Asn	Ile	Asp	Pro	Asn	Thr	Thr	Gln	Val	Ser	Gly	275	280	285	
Ile	Cys	Gly	Ser	Arg	Lys	Ser	Asn	Leu	Leu	Leu	Asn	Phe	Trp	Gly	Gly	290	295	300	
Phe	Val	Asn	Leu	Thr	Phe	Thr	Lys	Asp	Glu	Asn	Ser	Tyr	Tyr	Ile	Ser	305	310	315	320
Glu	Val	Gly	Ala	Tyr	Leu	Thr	Val	Ser	Asn	Pro	Glu	Lys	Thr	Tyr	Gln				

ITI-08-PCT_Sequence_Listing_ST25.txt

325 330 335

Gly Met Lys Ser Pro Val Val Met Phe Glu Thr Val Ile Gly His Ser
340 345 350

Phe Lys Cys Val Ser Glu Gln Ser Leu Glu Leu Ser Thr Gln Leu His
355 360 365

Leu Lys Thr Thr Asn Val Gln Leu Gln Ala Phe Asp Phe Glu Asp Asp
370 375 380

Asn Phe Gly Asn Val Asp Glu Cys Ser Ser Asp Tyr Thr Val Val Leu
385 390 395 400

Pro Val Ile Gly Ala Ile Val Leu Gly Leu Phe Ala Val Gly Leu Ile
405 410 415

Val Tyr Gly Val Arg Val Arg Arg Glu Ala Ser Gly Tyr Gln Arg Ile
420 425 430

<210> 51

<211> 433

<212> PRT

<213> Bos taurus

<400> 51

Met Ser Trp Gln Ile Pro Ala Val Val Met Ser Phe Met Ala Leu Val
1 5 10 15

Ala Ile Trp Tyr Tyr Asp Ser His Tyr Asn Ser His Met Gln Ala Lys
20 25 30

Val Phe Pro Glu Ile Thr Gly Tyr Ser Ser Pro Thr Thr Gly Gln Ala
35 40 45

Thr Val Lys Pro Ser Leu Leu Gln Pro Thr Asn Tyr Val Pro His Lys
50 55 60

Thr Ala Ala Ala Arg Ser Thr Asp Gly His Val Thr Ser Gln Thr Val
65 70 75 80

Ala Lys Thr Ser Ser Ser Glu Thr Leu Thr Thr Asn Thr Thr Ile Asp
85 90 95

Val Leu Ala Thr Thr Ser Pro Val Thr Thr Lys Ser Thr Leu Pro Thr
100 105 110

Thr Pro Thr Thr His Thr Leu Val Thr Thr Leu Ala Thr Pro Asn Lys
115 120 125

Ser His Val Thr Phe Pro Val Thr Glu Ala Lys Val Gly Leu Ser Val

ITI-08-PCT_Sequence_Listing_ST25.txt

130																	
Gly	Pro	Ser	Ser	Pro	Pro	Val	Thr	Val	Asn	Pro	Thr	Ala	His	Thr	Thr		
145					150					155						160	
Gly	Asn	Arg	Pro	Ser	Thr	Ala	Ser	His	Thr	Thr	Gly	Lys	Thr	Thr	Gln		
				165					170					175			
Leu	Ser	Asn	Gln	Thr	Thr	Leu	Pro	Ala	Thr	Leu	Ser	Thr	Ser	Pro	His		
			180					185					190				
Asn	Ile	Thr	Thr	Ser	Gln	Lys	Pro	Thr	Gln	Pro	Thr	His	Thr	Pro	Gly		
		195					200					205					
Pro	Thr	Thr	Ala	Thr	Tyr	Asn	Thr	Thr	Gln	Thr	Ala	Ser	Pro	Ala	Thr		
		210				215					220						
Ile	Ala	Pro	Arg	Pro	Thr	Leu	Ala	Pro	Gln	Pro	Leu	Ser	Pro	Lys	Thr		
225					230					235					240		
Gly	Ile	Tyr	Gln	Val	His	Asn	Gly	Ser	Lys	Leu	Cys	Ile	Lys	Ala	Glu		
				245					250					255			
Met	Gly	Ile	Gln	Leu	Thr	Val	Gln	Asp	Ser	Val	Ser	Val	Phe	Ser	Pro		
			260					265					270				
Gln	Lys	Tyr	Phe	Asn	Ile	Asp	Pro	Asn	Ala	Thr	Gln	Ala	Ser	Gly	Asn		
		275					280					285					
Cys	Gly	Ser	Arg	Lys	Ser	Asn	Leu	Leu	Leu	Asn	Phe	Gln	Gly	Gly	Phe		
	290					295					300						
Val	Asn	Leu	Thr	Phe	Thr	Lys	Gly	Glu	Lys	Ser	Tyr	Tyr	Ile	Ser	Glu		
305					310					315					320		
Val	Glu	Ala	Tyr	Leu	Thr	Val	Ser	Asn	Pro	Ala	Lys	Val	Tyr	Gln	Gly		
				325					330					335			
Leu	Lys	His	Ala	Met	Met	Met	Phe	Glu	Thr	Val	Val	Gly	His	Ser	Phe		
			340					345					350				
Lys	Cys	Val	Ser	Glu	Gln	Ser	Ile	Gln	Leu	Ser	Thr	Tyr	Leu	Gln	Leu		
		355					360					365					
Lys	Thr	Met	Asn	Val	Gln	Leu	Gln	Ala	Phe	Asp	Phe	Glu	Asp	Asp	His		
		370				375					380						
Phe	Gly	Asn	Ala	Asp	Glu	Cys	Ile	Ser	Asp	Arg	Asn	Arg	Arg	Glu	Ile		
385					390				395						400		
Pro	Val	Ala	Val	Gly	Leu	Ser	Ile	Ala	Val	Leu	Leu	Ala	Val	Leu	Leu		
				405					410					415			

ITI-08-PCT_Sequence_Listing_ST25.txt

Thr Ala Cys Leu Val Thr Arg Lys Arg Pro Ser Arg Gly Tyr Glu Arg
420 425 430

Met

<210> 52
<211> 429
<212> PRT
<213> Ovis aries

<400> 52

Met Ser Trp Gln Ile Ser Ala Val Val Leu Phe Phe Val Ser Leu Ala
1 5 10 15

Val Ile Trp Tyr Tyr Asp Ser His Met Lys Ala Asn Val Phe Pro Glu
20 25 30

Ile Thr Gly Tyr Ser Ser Pro Thr Thr Gly Gln Ala Thr Val Lys Pro
35 40 45

Ser Leu Leu Gln Pro Thr Asn His Val Pro Cys Asn Thr Ala Ala Ala
50 55 60

Lys Ser Thr Asp Gly His Val Thr Ser Gln Thr Val Ala Lys Thr Ser
65 70 75 80

Ser Pro Glu Thr Leu Thr Thr Asn Thr Thr Ile Glu Val Leu Val Thr
85 90 95

Thr Ser Pro Val Thr Thr Gln Ser Thr Leu Pro Thr Thr Pro Thr Thr
100 105 110

His Thr Leu Val Thr Thr Leu Ala Thr Pro Ser Lys Ser His Val Thr
115 120 125

Phe Pro Val Thr Glu Ala Lys Ala Gly Leu Ser Ile Gly Pro Ser Ser
130 135 140

Pro Pro Val Thr Ile Asn Pro Ala Ala His Thr Thr Gly Asn Arg Pro
145 150 155 160

Ser Thr Ala Ser His Thr Thr Gly Lys Thr Thr Gln Leu Ser Asn Gln
165 170 175

Thr Thr Leu Pro Ala Thr Leu Ser Thr Ser Pro His Asn Ile Thr Thr
180 185 190

Ser Gln Lys Pro Thr Gln Pro Thr His Thr Pro Gly Pro Thr Thr Ala
195 200 205

ITI-08-PCT_Sequence_Listing_ST25.txt

Ala Asn Asn Thr Thr His Thr Ala Ser Pro Ala Thr Ile Ala Pro Arg
210 215 220

Pro Thr Leu Ala Pro Gln Pro Leu Ser Pro Lys Thr Gly Leu Tyr Gln
225 230 235 240

Val Leu Asn Gly Ser Lys Leu Cys Ile Lys Ala Glu Met Gly Ile Gln
245 250 255

Leu Thr Val Gln Asp Ser Val Ser Val Phe Ser Pro Gln Lys Tyr Phe
260 265 270

Asn Ile Asp Pro Asn Ala Thr Gln Ala Ser Gly Asn Cys Gly Ser Arg
275 280 285

Lys Ser Asn Leu Leu Leu Asn Phe Gln Gly Gly Phe Val Asn Leu Thr
290 295 300

Phe Ile Lys Asp Glu Asn Ser Tyr Tyr Ile Ser Glu Val Glu Ala Tyr
305 310 315 320

Leu Thr Val Ser Asn Pro Ala Lys Val Tyr Gln Gly Met Lys Tyr Ala
325 330 335

Met Met Met Phe Glu Thr Val Val Gly His Ser Phe Lys Cys Val Ser
340 345 350

Glu Gln Ser Ile Gln Leu Ser Asn His Leu Gln Leu Lys Thr Val Asn
355 360 365

Val Gln Leu Gln Ala Phe Asp Phe Glu Asp Asp Arg Phe Gly Asn Ala
370 375 380

Asp Glu Cys Ile Ser Asp Arg Asn Arg Arg Glu Ile Pro Val Ala Val
385 390 395 400

Gly Leu Ser Ile Ala Val Leu Leu Ala Val Leu Leu Thr Ala Cys Leu
405 410 415

Val Thr Arg Lys Arg Pro Ser Arg Gly Tyr Glu Arg Met
420 425

<210> 53

<211> 408

<212> PRT

<213> Rattus norvegicus

<400> 53

Met Pro Gly Gln Thr Ser Ala Val Ala Val Leu Leu Cys Leu Ala Val
1 5 10 15

ITI-08-PCT_Sequence_Listing_ST25.txt

Ile	Leu	His	Gly	Tyr	Gln	Ile	Arg	Glu	Lys	Glu	Phe	Pro	Glu	Ala	Arg	20	25	30
Gly	Tyr	Leu	Gln	Tyr	Thr	Ala	Thr	Thr	Thr	Glu	Gln	Ile	Thr	Ala	Lys	35	40	45
Pro	Pro	Leu	Pro	Leu	Thr	Asn	Gln	Thr	Ser	His	Ala	Thr	Leu	Ala	Ser	50	55	60
Arg	Ser	Lys	Asp	Asp	Tyr	Ile	Gln	Thr	Ala	Ala	Glu	Thr	Ser	Thr	Phe	65	70	75
Glu	Asp	Thr	Ala	His	Ile	Thr	Met	Lys	Thr	Ala	Ile	Pro	Val	Thr	Thr	85	90	95
Lys	Ser	Leu	Leu	Pro	Ile	Ser	Ser	Thr	Ser	Tyr	Thr	Phe	Val	Arg	Thr	100	105	110
Asn	Asn	Ser	His	Met	Thr	Ala	Ser	Ser	Thr	Glu	Asp	Thr	Ile	Gly	Ser	115	120	125
Gly	Ser	Ile	Thr	His	Leu	Pro	Phe	Pro	Thr	Thr	Arg	Ala	Ser	Leu	Ala	130	135	140
Ala	Val	Asn	His	Ile	Thr	Gly	Arg	Ser	Thr	Gln	Leu	Gly	Gly	Gln	Thr	145	150	155
Thr	Leu	Pro	Lys	Ala	Leu	Phe	Thr	Pro	Ser	His	Glu	Ser	Thr	Thr	Thr	165	170	175
Gln	Arg	Pro	Thr	Leu	Ser	Thr	Ile	Val	Ser	Glu	Leu	Thr	Pro	Thr	Gly	180	185	190
Lys	Asp	Arg	Ser	Thr	Thr	Ser	Ser	Val	Pro	Leu	Val	Pro	Arg	Pro	Thr	195	200	205
Phe	Val	Thr	Trp	Ser	Ser	Pro	Ala	Lys	Ile	Gly	Thr	Tyr	Glu	Val	Leu	210	215	220
Asn	Gly	Ser	Arg	Leu	Cys	Ile	Lys	Ala	Glu	Met	Gly	Ile	Ala	Leu	Ile	225	230	235
Val	Gln	Glu	Lys	Gly	Leu	Asp	Ser	Ala	Thr	Gln	Arg	His	Phe	Asn	Ile	245	250	255
Asp	Pro	Ser	Leu	Thr	His	Ala	Ser	Gly	Lys	Cys	Gly	Ser	Gln	Asn	Ser	260	265	270
Asn	Leu	Phe	Leu	Asn	Phe	Gln	Gly	Gly	Ser	Val	Asn	Val	Thr	Phe	Thr	275	280	285
Lys	Glu	Glu	Asn	Leu	Tyr	Tyr	Val	Ser	Glu	Val	Gly	Ala	Tyr	Leu	Thr			

ITI-08-PCT_Sequence_Listing_ST25.txt

290

295

300

Ile Ser Asn Thr Glu Lys Thr Tyr Gln Gly Lys Ser Thr Met Met Met
305 310 315 320

Phe Glu Thr Val Val Gly His Ser Phe Lys Cys Val Ser Glu Gln Ser
325 330 335

Ile Gln Leu Ser Ala Gln Leu Gln Met Lys Thr Met Asn Ile His Leu
340 345 350

Gln Ala Phe Asp Phe Glu Gly Asp Ser Phe Gly Ile Val Asp Glu Cys
355 360 365

Leu Ser Asp Tyr Thr Val Val Leu Pro Val Val Gly Ile Ile Val Val
370 375 380

Val Leu Cys Val Val Gly Leu Gly Ile Tyr Lys Ile Arg Gln Arg Arg
385 390 395 400

Gln Ser Ser Ala Tyr Gln Arg Ile
405

<210> 54

<211> 411

<212> PRT

<213> Mus musculus

<400> 54

Met Pro Gly Gln Ile Ser Ala Val Ala Val Leu Phe Leu Ser Leu Thr
1 5 10 15

Val Ile Leu His Gly Tyr Gln Ile Arg Glu Lys Glu Phe Pro Lys Ala
20 25 30

Arg Gly Tyr Leu Gln Tyr Thr Ala Thr Ser Ala Glu Gln Ile Thr Thr
35 40 45

Lys Pro Leu Leu Gln Leu Ile Asn Gln Arg Ser His Ile Thr Leu Ala
50 55 60

Ser Arg Phe Lys Asp Asp Tyr Ile Gln Met Ala Ala Glu Thr Ser Ala
65 70 75 80

Ile Glu Asn Thr Ala His Ile Thr Met Lys Thr Val Thr Pro Val Thr
85 90 95

Thr Lys Ser Leu Pro Pro Ile Ser Ser Ala Ser Tyr Thr Phe Val Arg
100 105 110

Ser Asn Asn Ala His Met Thr Ala Ser Ser Thr Asp Asp Thr Ile Gly

115				120				125					
Ser	Ile	Ala	His	Leu	Pro	Val	Pro	Thr	Thr	Arg	Ala	Ser	Leu
				135					140				
Val	Asn	Tyr	Ile	Thr	Gly	Arg	Ala	Thr	Gln	Leu	Gly	Gly	Gln
				150					155				
Leu	Pro	Lys	Thr	Phe	Phe	Thr	Ala	Ser	His	Lys	Ser	Thr	Thr
				165					170				
Arg	Pro	Thr	Leu	Ser	Thr	Asn	Val	Leu	Gly	Thr	Ser	Thr	Pro
				180					185				
Lys	Asp	Arg	Ser	Thr	Thr	Ser	Pro	Val	Pro	Leu	Val	Pro	Arg
195					200				205				
Leu	Val	Thr	Trp	Ser	Ser	Pro	Ala	Lys	Ile	Gly	Thr	Tyr	Glu
				215					220				
Asn	Gly	Ser	Arg	Leu	Cys	Ile	Lys	Ala	Glu	Met	Gly	Leu	Ala
				230					235				
Val	Gln	Glu	Lys	Asp	Leu	Asp	Ser	Ala	Thr	Gln	Arg	Tyr	Phe
				245					250				
Asp	Pro	Ser	Leu	Thr	His	Ala	Ser	Gly	Lys	Cys	Asp	Ser	Gln
				260					265				
Asn	Leu	Phe	Leu	Asn	Phe	Gln	Gly	Gly	Ser	Val	Asn	Ile	Thr
275					280				285				
Lys	Glu	Glu	Asn	Leu	Tyr	Tyr	Ile	Ser	Glu	Val	Gly	Ala	Tyr
				295					300				
Ile	Ser	Asn	Thr	Glu	Lys	Thr	Tyr	Gln	Gly	Lys	Lys	Asn	Thr
				310					315				
Met	Phe	Glu	Thr	Val	Val	Gly	His	Ser	Phe	Lys	Cys	Val	Ser
				325					330				
Ser	Ile	Gln	Leu	Ser	Ala	Gln	Leu	Gln	Met	Lys	Thr	Met	Asn
				340					345				
Leu	Gln	Ala	Phe	Asp	Phe	Glu	Gly	Asp	Ser	Phe	Gly	Asn	Val
				355					360				
Cys	Leu	Ser	Asp	Tyr	Thr	Val	Val	Leu	Pro	Met	Val	Ala	Ile
				375					380				
Val	Val	Ile	Cys	Val	Val	Gly	Leu	Ser	Val	Tyr	Lys	Ile	Arg
				390					395				
												400	

ITI-08-PCT_Sequence_Listing_ST25.txt

Gln Arg His Gln Ser Ser Ala Tyr Gln Arg Ile
 405 410

<210> 55
 <211> 314
 <212> PRT
 <213> Xenopus tropicalis

<400> 55

Met Asp Arg Val Ser Leu Leu Ser Thr Ile Leu Leu Leu Tyr Gly Leu
 1 5 10 15

Leu Tyr Ile Asn Asp Ala Tyr Ser Glu Asn Thr Phe Ala Gln Pro Ser
 20 25 30

Asn Thr Thr Thr Pro Ala Pro Asn Thr Thr Thr Thr His Val Thr Ser
 35 40 45

Asn Thr Thr Thr Leu Ala Pro Asn Thr Thr Thr Thr His Val Thr Ser
 50 55 60

Asn Thr Thr Thr Leu Ala Pro Asn Thr Thr Thr Thr His Ile Thr Ser
 65 70 75 80

Asn Thr Thr Thr Leu Ala Pro Asn Thr Thr Thr Thr Leu Ala Pro Asn
 85 90 95

Thr Thr Thr Thr His Ser Val Thr Thr Thr Lys Thr Ala Ser Thr Thr
 100 105 110

Thr Pro Thr Pro Thr Leu Glu Pro Lys Pro Ser Pro Pro Glu Thr Gly
 115 120 125

Asn Tyr Thr Val Lys Ile Lys Asn Glu Phe Cys Ile Glu Ala Leu Met
 130 135 140

Gly Leu Glu Leu Glu Leu Thr Asn Ser Thr Lys Thr Gln Gln Tyr Phe
 145 150 155 160

Asn Ile Val Pro Ser Gln Ile Asn Ser Asn Gly Thr Cys Glu Lys Ser
 165 170 175

Lys Ala Asn Leu Asn Leu Thr Phe Ala Asn Ser Tyr Ile Asn Phe Val
 180 185 190

Phe Ala Gln Asp Asp Asn Ser Tyr Tyr Leu Asp Asn Val Thr Val Tyr
 195 200 205

Phe Asn Leu Thr Arg Ser Glu Ser Trp Tyr Gly Asn Ala Thr Asn Gln
 210 215 220

ITI-08-PCT_Sequence_Listing_ST25.txt

Lys Leu Leu Lys Thr Glu Asn Gly Tyr Ser Val Lys Cys Lys Asn Thr
225 230 235 240

Pro Lys Ile Gln Leu Gly Asp Thr Met Asn Leu Val Met Thr Asn Val
245 250 255

Lys Leu Gln Val Phe Asn Phe Lys Asp Asn Ser Phe Gly Lys Glu Thr
260 265 270

Thr Cys Lys Tyr Asp His Asn Phe Gly Leu Met Ile Ala Gly Ile Val
275 280 285

Ile Val Val Ile Val Val Leu Gly Val Ile Ile Tyr Phe Ile Trp His
290 295 300

Lys Arg Lys Ser Ser Gly Tyr Gln Arg Ile
305 310

<210> 56

<211> 478

<212> PRT

<213> Pan troglodytes

<400> 56

Met Gly Arg Cys Cys Phe Tyr Thr Ala Gly Thr Leu Ser Leu Leu Leu
1 5 10 15

Leu Val Thr Ser Val Thr Leu Leu Val Ala Arg Val Phe Gln Lys Ala
20 25 30

Val Asp Gln Ser Ile Glu Lys Lys Ile Val Leu Arg Asn Gly Thr Glu
35 40 45

Ala Phe Asp Ser Trp Glu Lys Pro Pro Leu Pro Val Tyr Thr Gln Phe
50 55 60

Tyr Phe Phe Asn Val Thr Asn Pro Glu Glu Ile Leu Arg Gly Glu Thr
65 70 75 80

Pro Arg Val Glu Glu Val Gly Pro Tyr Thr Tyr Arg Glu Leu Arg Asn
85 90 95

Lys Ala Asn Ile Gln Phe Gly Asp Asn Gly Thr Thr Ile Ser Ala Val
100 105 110

Ser Asn Lys Ala Tyr Val Phe Glu Arg Asp Gln Ser Val Gly Asp Pro
115 120 125

Lys Ile Asp Leu Ile Arg Thr Leu Asn Ile Pro Val Leu Thr Val Ile
130 135 140

ITI-08-PCT_Sequence_Listing_ST25.txt

Glu	Trp	Ser	Gln	Val	Arg	Phe	Leu	Arg	Glu	Ile	Ile	Glu	Ala	Met	Leu	145	150	155	160
Lys	Ala	Tyr	Gln	Gln	Lys	Leu	Phe	Val	Thr	His	Thr	Val	Asp	Glu	Leu	165	170	175	
Leu	Trp	Gly	Tyr	Lys	Asp	Glu	Ile	Leu	Ser	Leu	Ile	His	Val	Phe	Arg	180	185	190	
Pro	Asp	Ile	Ser	Pro	Tyr	Phe	Gly	Leu	Phe	Tyr	Glu	Lys	Asn	Gly	Thr	195	200	205	
Asn	Asp	Gly	Asp	Tyr	Val	Phe	Leu	Thr	Gly	Glu	Asp	Ser	Tyr	Leu	Asn	210	215	220	
Phe	Thr	Lys	Ile	Val	Glu	Trp	Asn	Gly	Lys	Thr	Ser	Leu	Asp	Trp	Trp	225	230	235	240
Ile	Thr	Asp	Lys	Cys	Asn	Met	Ile	Asn	Gly	Thr	Asp	Gly	Asp	Ser	Phe	245	250	255	
His	Pro	Leu	Ile	Thr	Lys	Asp	Glu	Val	Leu	Tyr	Val	Phe	Pro	Ser	Asp	260	265	270	
Phe	Cys	Arg	Ser	Val	Tyr	Ile	Thr	Phe	Ser	Asp	Tyr	Glu	Ser	Val	Gln	275	280	285	
Gly	Leu	Pro	Ala	Phe	Arg	Tyr	Lys	Val	Pro	Ala	Glu	Ile	Leu	Ala	Asn	290	295	300	
Thr	Ser	Asp	Asn	Ala	Gly	Phe	Cys	Ile	Pro	Glu	Gly	Asn	Cys	Leu	Gly	305	310	315	320
Ser	Gly	Val	Leu	Asn	Val	Ser	Ile	Cys	Lys	Asn	Gly	Ala	Pro	Ile	Ile	325	330	335	
Met	Ser	Phe	Pro	His	Phe	Tyr	Gln	Ala	Asp	Glu	Arg	Phe	Val	Ser	Ala	340	345	350	
Ile	Glu	Gly	Met	His	Pro	Asn	Lys	Glu	Asp	His	Glu	Thr	Phe	Val	Asp	355	360	365	
Ile	Asn	Pro	Leu	Thr	Gly	Ile	Ile	Leu	Lys	Ala	Ala	Lys	Arg	Phe	Gln	370	375	380	
Ile	Asn	Ile	Tyr	Val	Lys	Lys	Leu	Asp	Asp	Phe	Val	Glu	Thr	Gly	Asp	385	390	395	400
Ile	Arg	Thr	Met	Val	Phe	Pro	Val	Met	Tyr	Leu	Asn	Glu	Ser	Val	His	405	410	415	

ITI-08-PCT_Sequence_Listing_ST25.txt

Ile Asp Lys Glu Thr Ala Ser Arg Leu Lys Ser Met Ile Asn Thr Thr
420 425 430

Leu Ile Ile Thr Asn Ile Pro Tyr Ile Ile Met Ala Leu Gly Val Phe
435 440 445

Phe Gly Leu Val Phe Thr Trp Leu Ala Cys Lys Gly Gln Gly Ser Met
450 455 460

Asp Glu Gly Thr Ala Asp Glu Arg Ala Pro Leu Ile Arg Thr
465 470 475

<210> 57

<211> 478

<212> PRT

<213> Macaca mulatta

<400> 57

Met Gly Arg Cys Cys Phe Tyr Thr Ala Gly Thr Leu Ser Leu Leu Leu
1 5 10 15

Leu Val Thr Ser Val Thr Leu Leu Val Ala Arg Val Phe Gln Lys Ala
20 25 30

Val Asp Gln Ser Ile Glu Lys Lys Ile Val Leu Arg Asn Gly Thr Glu
35 40 45

Ala Phe Asp Ser Trp Glu Lys Pro Pro Leu Pro Val Tyr Thr Gln Phe
50 55 60

Tyr Phe Phe Asn Val Thr Asn Pro Glu Glu Ile Leu Arg Gly Glu Thr
65 70 75 80

Pro Arg Val Glu Glu Val Gly Pro Tyr Thr Tyr Arg Glu Leu Arg Asn
85 90 95

Lys Ala Asn Val Gln Phe Gly Asp Asn Gly Thr Thr Ile Ser Ala Val
100 105 110

Ser Asn Lys Ala Tyr Val Phe Glu Arg Asp Gln Ser Val Gly Asp Pro
115 120 125

Lys Ile Asp Leu Ile Arg Thr Leu Asn Ile Pro Val Leu Thr Val Ile
130 135 140

Glu Trp Ser Gln Val His Phe Leu Arg Glu Ile Ile Glu Ala Met Leu
145 150 155 160

Lys Ala Tyr Gln Gln Lys Leu Phe Val Thr His Thr Val Asp Glu Leu
165 170 175

ITI-08-PCT_Sequence_Listing_ST25.txt

```

Leu Trp Gly Tyr Lys Asp Glu Ile Leu Ser Leu Ile His Val Phe Arg
      180                      185                      190

Pro Asp Ile Ser Pro Tyr Phe Gly Leu Phe Tyr Glu Lys Asn Gly Thr
      195                      200                      205

Asn Asp Gly Asp Tyr Val Phe Leu Thr Gly Glu Asp Asn Tyr Leu Asn
      210                      215                      220

Phe Thr Lys Ile Val Glu Trp Asn Gly Lys Thr Ser Leu Asp Trp Trp
      225                      230                      235                      240

Ile Thr Asp Lys Cys Asn Met Ile Asn Gly Thr Asp Gly Asp Ser Phe
      245                      250                      255

His Pro Leu Ile Thr Lys Asp Glu Val Leu Tyr Val Phe Pro Ser Asp
      260                      265                      270

Phe Cys Arg Ser Val Tyr Ile Thr Phe Ser Asp Tyr Glu Ser Val Gln
      275                      280                      285

Gly Leu Pro Ala Phe Arg Tyr Lys Val Pro Ala Glu Ile Leu Ala Asn
      290                      295                      300

Thr Ser Asp Asn Ala Gly Phe Cys Ile Pro Glu Gly Asn Cys Leu Gly
      305                      310                      315                      320

Ser Gly Val Leu Asn Val Ser Ile Cys Lys Asn Gly Ala Pro Ile Ile
      325                      330                      335

Met Ser Phe Pro His Phe Tyr Gln Ala Asp Glu Arg Phe Val Ser Ala
      340                      345                      350

Ile Glu Gly Met His Pro Asn Lys Glu Asp His Glu Thr Phe Val Asp
      355                      360                      365

Ile Asn Pro Leu Thr Gly Ile Ile Leu Lys Ala Ala Lys Arg Phe Gln
      370                      375                      380

Ile Asn Ile Tyr Val Lys Lys Leu Asp Asp Phe Val Glu Thr Gly Asp
      385                      390                      395                      400

Ile Arg Thr Met Val Phe Pro Val Met Tyr Leu Asn Glu Ser Val Leu
      405                      410                      415

Ile Asp Lys Glu Thr Ala Ser Arg Leu Lys Ser Val Ile Asn Thr Thr
      420                      425                      430

Leu Ile Ile Thr Asn Ile Pro Tyr Ile Ile Met Ala Leu Gly Val Phe
      435                      440                      445

Phe Gly Phe Val Phe Thr Trp Leu Ala Cys Lys Gly Gln Gly Ser Met

```


ITI-08-PCT_Sequence_Listing_ST25.txt

450

455

460

Asp Glu Gly Thr Ala Asp Glu Arg Ala Pro Leu Ile Arg Thr
 465 470 475

<210> 58

<211> 478

<212> PRT

<213> Canis lupus familiaris

<400> 58

Met Gly Arg Cys Cys Phe Tyr Thr Val Gly Thr Leu Ser Leu Leu Leu
 1 5 10 15

Leu Val Thr Ser Ile Ala Leu Leu Val Ala Arg Val Phe Gln Lys Ala
 20 25 30

Val Asp Gln Thr Ile Glu Lys Asn Ile Val Leu Arg Asn Gly Ser Glu
 35 40 45

Thr Phe Asp Ser Trp Lys Lys Pro Pro Leu Pro Val Tyr Ala Gln Phe
 50 55 60

Tyr Phe Phe Asn Val Thr Asn Pro Glu Glu Ile Leu Arg Gly Glu Ile
 65 70 75 80

Pro Arg Leu Glu Glu Val Gly Pro Tyr Thr Tyr Arg Glu Leu Arg Asp
 85 90 95

Lys Ala Asp Ile Gln Phe Gly Asp Asn Gly Thr Thr Ile Ser Ala Val
 100 105 110

Ser Asn Lys Ala Tyr Val Phe Glu Arg Asn Gln Ser Val Gly Asp Pro
 115 120 125

Lys Thr Asp Leu Ile Arg Thr Leu Asn Ile Pro Ala Val Thr Ala Met
 130 135 140

Glu Trp Ala His Leu His Phe Phe Arg Glu Leu Ile Glu Ala Leu Leu
 145 150 155 160

Lys Ala Tyr Gln Gln Thr Leu Phe Val Thr His Thr Val Asp Glu Leu
 165 170 175

Leu Trp Gly Tyr Lys Asp Glu Ile Leu Ser Leu Ile Asn Val Phe Lys
 180 185 190

Pro Glu Ile Ser Pro Tyr Phe Gly Leu Tyr Tyr Gly Lys Asn Gly Thr
 195 200 205

Asn Asp Gly Asp Tyr Val Phe Leu Thr Gly Glu Asp Asn Tyr Leu Asn

ITI-08-PCT_Sequence_Listing_ST25.txt

210

215

220

Phe Ser Lys Ile Val Glu Trp Asn Gly Lys Thr Ser Leu Asp Trp Trp
 225 230 235 240

Thr Thr Asp Lys Cys Asn Met Ile Asn Gly Thr Asp Gly Asp Ser Phe
 245 250 255

His Pro Leu Ile Asp Lys Asp Glu Ile Leu Tyr Val Phe Pro Ser Glu
 260 265 270

Phe Cys Arg Ser Val Tyr Ile Thr Phe Ser Asp Phe Lys Ser Val Gln
 275 280 285

Gly Leu Pro Ala Phe Arg Tyr Lys Val Pro Gly Glu Val Leu Ala Asn
 290 295 300

Thr Ser Asp Asn Ala Gly Phe Cys Val Pro Lys Gly Asn Cys Leu Gly
 305 310 315 320

Ser Gly Val Leu Asn Ile Ser Ile Cys Lys Asn Gly Ala Pro Ile Ile
 325 330 335

Ile Ser Phe Pro His Phe Tyr Glu Ala Asp Lys Lys Phe Val Ser Ala
 340 345 350

Ile Asp Gly Met Arg Pro Asn Lys Asp Tyr His Glu Thr Phe Val Asp
 355 360 365

Ile Asn Pro Leu Thr Gly Ile Ile Leu Arg Ala Ala Lys Arg Phe Gln
 370 375 380

Ile Asn Val Tyr Val Lys Lys Leu Asp Asp Phe Ile Glu Thr Gly Asn
 385 390 395 400

Ile Arg Thr Met Val Phe Pro Val Met Tyr Ile Asn Glu Ser Val Leu
 405 410 415

Ile Asp Lys Asp Thr Ala Ser Arg Leu Lys Ser Val Ile Asn Thr Thr
 420 425 430

Leu Ile Ile Thr Asn Ile Pro Tyr Ile Val Met Ala Leu Gly Val Phe
 435 440 445

Phe Gly Leu Ile Phe Thr Trp Leu Ala Cys Arg Gly Gln Gly Ser Met
 450 455 460

Asp Glu Gly Thr Pro Asp Glu Arg Ala Pro Leu Ile Arg Thr
 465 470 475

<210> 59

<211> 478

ITI-08-PCT_Sequence_Listing_ST25.txt

<212> PRT

<213> Bos taurus

<400> 59

```

Met Gly Arg Cys Cys Phe Tyr Ala Val Gly Thr Leu Ser Leu Leu Leu
1          5          10          15

Leu Val Thr Ser Ile Thr Leu Leu Val Ala Arg Val Phe Gln Lys Ala
          20          25          30

Val Asp Gln Thr Ile Glu Lys Asn Ile Val Leu Arg Asn Gly Ser Glu
          35          40          45

Thr Phe Asp Ser Trp Lys Lys Pro Pro Leu Pro Val Tyr Thr Gln Phe
          50          55          60

Tyr Phe Phe Asn Val Thr Asn Pro Glu Glu Ile Leu Asn Gly Glu Thr
65          70          75          80

Pro Arg Leu Glu Glu Val Gly Pro Tyr Thr Tyr Arg Glu Leu Arg Asn
          85          90          95

Lys Asp Asp Ile Gln Phe Gly Asp Asn Gly Thr Thr Ile Ser Ala Val
          100          105          110

Ser Asn Lys Ala Tyr Val Phe Glu Arg Asp Lys Ser Val Gly Asp Pro
          115          120          125

Lys Ile Asp Leu Leu Arg Thr Leu Asn Ile Pro Ala Leu Thr Ala Met
          130          135          140

Glu Trp Thr Gln Leu Pro Leu Leu Arg Asp Ile Ile Glu Ala Leu Leu
145          150          155          160

Lys Ala Tyr Arg Gln Lys Leu Phe Val Thr His Thr Val Asp Glu Leu
          165          170          175

Leu Trp Gly Tyr Lys Asp Glu Ile Leu Ser Leu Ile Asn Thr Phe Lys
          180          185          190

His Asp Val Ser Pro Tyr Phe Gly Leu Phe Tyr Gly Lys Asn Gly Thr
          195          200          205

Asn Asp Gly Asp Tyr Val Phe Leu Thr Gly Glu Asp Asn Tyr Leu Asn
          210          215          220

Phe Ser Lys Ile Val Glu Trp Asn Gly Lys Thr Ser Leu Asp Trp Trp
225          230          235          240

Thr Ala Asp Glu Cys Asn Met Ile Asn Gly Thr Asp Gly Asp Thr Phe
          245          250          255

```

ITI-08-PCT_Sequence_Listing_ST25.txt

His Pro Leu Ile Thr Arg Asp Glu Val Leu Tyr Val Phe Pro Ser Asp
260 265 270

Phe Cys Arg Ser Val Tyr Ile Thr Phe Ser Asp Phe Glu Ser Val Gln
275 280 285

Gly Leu Pro Ala Leu Arg Tyr Lys Val Pro Ala Glu Ile Leu Ala Asn
290 295 300

Thr Ser Asp Asn Ala Gly Phe Cys Ile Pro Lys Gly Asn Cys Leu Gly
305 310 315 320

Ser Gly Val Leu Asn Val Ser Val Cys Lys Asn Gly Ala Pro Ile Ile
325 330 335

Met Ser Phe Pro His Phe Tyr Gln Ala Asp Glu Lys Phe Val Ser Ala
340 345 350

Ile Gly Gly Met His Pro Asn Lys Glu Tyr His Glu Thr Phe Val Asp
355 360 365

Ile Asn Pro Leu Thr Gly Ile Ile Leu Arg Ala Ala Lys Arg Phe Gln
370 375 380

Ile Asn Val Tyr Val Arg Lys Leu Asp Asp Phe Val Glu Thr Gly Asn
385 390 395 400

Ile Gln Thr Leu Val Phe Pro Val Met Tyr Ile Asn Glu Ser Val Leu
405 410 415

Ile Asp Lys Glu Thr Ala Ser Arg Leu Lys Ser Val Ile Asn Thr Thr
420 425 430

Leu Ile Val Thr Asn Ile Pro Tyr Ile Ile Met Ala Leu Gly Val Phe
435 440 445

Phe Gly Leu Ile Phe Thr Trp Leu Ala Cys Arg Gly Gln Gly Ser Thr
450 455 460

Asp Glu Gly Thr Ala Asp Glu Arg Ala Pro Leu Ile Arg Thr
465 470 475

<210> 60

<211> 478

<212> PRT

<213> Mus musculus

<400> 60

Met Gly Arg Cys Cys Phe Tyr Thr Ala Gly Thr Leu Ser Leu Leu Leu
1 5 10 15

ITI-08-PCT_Sequence_Listing_ST25.txt

Leu	Val	Thr	Ser	Val	Thr	Leu	Leu	Val	Ala	Arg	Val	Phe	Gln	Lys	Ala
			20					25					30		
Val	Asp	Gln	Thr	Ile	Glu	Lys	Asn	Met	Val	Leu	Gln	Asn	Gly	Thr	Lys
		35					40					45			
Val	Phe	Asn	Ser	Trp	Glu	Lys	Pro	Pro	Leu	Pro	Val	Tyr	Ile	Gln	Phe
	50					55					60				
Tyr	Phe	Phe	Asn	Val	Thr	Asn	Pro	Glu	Glu	Ile	Leu	Gln	Gly	Glu	Ile
65					70					75					80
Pro	Leu	Leu	Glu	Glu	Val	Gly	Pro	Tyr	Thr	Tyr	Arg	Glu	Leu	Arg	Asn
				85					90					95	
Lys	Ala	Asn	Ile	Gln	Phe	Gly	Glu	Asn	Gly	Thr	Thr	Ile	Ser	Ala	Val
			100					105					110		
Thr	Asn	Lys	Ala	Tyr	Val	Phe	Glu	Arg	Asn	Gln	Ser	Val	Gly	Asp	Pro
		115					120					125			
Asn	Val	Asp	Leu	Ile	Arg	Thr	Ile	Asn	Ile	Pro	Leu	Leu	Thr	Val	Val
		130				135					140				
Asp	Leu	Ala	Gln	Leu	Thr	Leu	Leu	Arg	Glu	Leu	Ile	Glu	Ala	Met	Leu
145					150					155					160
Lys	Ala	Tyr	Gln	Gln	Lys	Leu	Phe	Val	Ile	His	Thr	Val	His	Glu	Leu
			165						170					175	
Leu	Trp	Gly	Tyr	Lys	Asp	Glu	Ile	Leu	Ser	Leu	Val	His	Ile	Phe	Lys
			180					185					190		
Pro	Asp	Val	Ser	Pro	Asn	Phe	Gly	Leu	Phe	Tyr	Glu	Arg	Asn	Gly	Thr
		195					200					205			
Asn	Asp	Gly	Glu	Tyr	Val	Phe	Leu	Thr	Gly	Glu	Asp	Asn	Tyr	Leu	Asn
		210				215					220				
Phe	Ser	Lys	Ile	Val	Glu	Trp	Asn	Gly	Lys	Thr	Ser	Leu	Asp	Trp	Trp
225					230					235					240
Thr	Thr	Asp	Thr	Cys	Asn	Met	Ile	Asn	Gly	Thr	Asp	Gly	Asp	Ser	Phe
				245					250					255	
His	Pro	Leu	Ile	Ser	Lys	Asp	Glu	Val	Leu	Tyr	Leu	Phe	Pro	Ser	Asp
			260					265					270		
Leu	Cys	Arg	Ser	Val	His	Ile	Thr	Phe	Ser	Ser	Phe	Glu	Asn	Val	Glu
		275					280					285			

ITI-08-PCT_Sequence_Listing_ST25.txt

Gly Leu Pro Ala Phe Arg Tyr Lys Val Pro Ala Glu Ile Leu Ala Asn
290 295 300

Thr Ser Glu Asn Ala Gly Phe Cys Ile Pro Glu Gly Asn Cys Met Asp
305 310 315 320

Ser Gly Val Leu Asn Ile Ser Ile Cys Lys Asn Gly Ala Pro Ile Ile
325 330 335

Met Ser Phe Pro His Phe Tyr Gln Ala Asp Glu Lys Phe Val Ser Ala
340 345 350

Ile Lys Gly Met His Pro Asn Lys Glu Glu His Glu Ser Phe Val Asp
355 360 365

Ile Asn Pro Leu Thr Gly Ile Ile Leu Arg Gly Ala Lys Arg Phe Gln
370 375 380

Ile Asn Thr Tyr Val Arg Lys Leu Asp Asp Phe Val Glu Thr Gly Asp
385 390 395 400

Ile Arg Thr Met Val Phe Pro Val Met Tyr Leu Asn Glu Ser Val Leu
405 410 415

Ile Asp Lys Glu Thr Ala Asn Gln Leu Lys Ser Val Ile Asn Thr Thr
420 425 430

Leu Val Val Thr Asn Ile Pro Tyr Ile Ile Met Ala Leu Gly Val Phe
435 440 445

Phe Gly Leu Val Phe Thr Trp Leu Ala Cys Arg Gly Gln Gly Ser Met
450 455 460

Asp Glu Gly Thr Ala Asp Glu Arg Ala Pro Leu Ile Arg Thr
465 470 475

<210> 61
<211> 531
<212> PRT
<213> Danio rerio

<400> 61

Met Thr Arg Arg Ser Cys Thr Ile Tyr Ala Thr Gly Ile Val Cys Ala
1 5 10 15

His Leu Leu Ile Leu Gly Ile Ala Leu Leu Leu Ala Gln Val Phe Gln
20 25 30

Thr Met Ile Gln Glu Arg Ile Lys Lys Glu Ile Thr Leu Ala Glu Asn
35 40 45

ITI-08-PCT_Sequence_Listing_ST25.txt

Ser Arg Val Leu Asp Gly Trp Ile Asn Pro Pro Pro Pro Val Tyr Met
50 55 60

Gln Tyr Phe Phe Phe Asn Val Thr Asn Pro Asp Glu Phe Leu Ala Gly
65 70 75 80

Lys Glu Lys Ala Lys Val Thr Gln Met Gly Pro Tyr Thr Tyr Arg Glu
85 90 95

Tyr Arg Pro Arg Glu Asn Val Thr Tyr Leu Glu Asn Gly Thr Lys Ile
100 105 110

Phe Ala Thr Asn Pro Lys Ser Phe Val Phe Leu Arg Asn Met Ser Ala
115 120 125

Gly Asp Pro Glu Val Asp Arg Val Thr Thr Val Asn Ile Pro Met Ile
130 135 140

Ala Val Met Asn Glu Leu Asn Ser Tyr Ser Phe Phe Val Arg Thr Ala
145 150 155 160

Val Ser Met Tyr Met Gly Ser Met Gly Met Gly Leu Phe Met Asn Arg
165 170 175

Thr Val His Glu Ile Leu Trp Gly Phe Lys Asp Pro Leu Leu Thr Lys
180 185 190

Leu His Ala Met Arg Pro Glu Val Asp Glu His Phe Gly Leu Met Tyr
195 200 205

Asn Lys Asn Gly Thr His Glu Gly Glu Phe Val Phe His Thr Gly Glu
210 215 220

Lys Asn Tyr Met Asn Tyr Gly Lys Ile Asp Thr Trp Asn Gly Ile Ser
225 230 235 240

Gln Met Asn Trp Trp Ser Ser Asn Gln Ser Asn Met Ile Asn Gly Thr
245 250 255

Asp Gly Ser Val Phe His Thr Phe Leu Ser Arg Lys Glu Leu Leu Tyr
260 265 270

Ile Phe Ala Ala Asp Leu Cys Arg Ser Ile His Leu Gly Tyr Val Arg
275 280 285

Asp Met Glu Val Lys Gly Ile Pro Ala Phe Arg Phe Ala Pro Pro Ser
290 295 300

Asp Val Leu Ala Pro Pro Asp Glu Asn Pro Ala Asn Ala Gly Phe Cys
305 310 315 320

Val Pro Ala Gly Asp Cys Leu Gly Lys Gly Val Leu Lys Val Ser Val

ITI-08-PCT_Sequence_Listing_ST25.txt

325 330 335

Cys Arg Gln Gly Ala Pro Ile Val Val Ser Phe Pro His Phe Tyr Gln
340 345 350

Ala Asp Glu Arg Tyr Ile Asn Ala Ile Glu Gly Met Asn Pro Asn Glu
355 360 365

Glu Glu His Glu Thr Tyr Leu Asp Ile Asn Pro Thr Thr Gly Val Pro
370 375 380

Ile Arg Ala Cys Lys Arg Ala Gln Leu Asn Ile Ile Leu Lys Arg Val
385 390 395 400

Arg Gly Phe Pro Asn Thr Lys Phe Leu Asn Glu Thr Ile Phe Pro Ile
405 410 415

Met Tyr Val Asn Glu Thr Ala Thr Ile Asp Asp Glu Ser Ala Ala Gln
420 425 430

Met Arg Met Leu Leu Leu Ile Val Thr Val Val Ser Asn Phe Pro Val
435 440 445

Ile Ile Leu Ala Leu Gly Val Ile Leu Leu Val Val Leu Ile Phe Leu
450 455 460

Val Cys Arg Asn Arg Gln Arg Lys Asn Glu Val Lys Arg Ile Asp Phe
465 470 475 480

Thr Glu Ala Phe His Ser Phe Ala Thr Thr Lys Asp Glu Thr Ala Tyr
485 490 495

Thr Gln Val Ser Asn Gln Ala Glu Asp Ser Pro Glu Asn Arg Asn Asn
500 505 510

Gln Pro Leu Arg Asn Gly Ser Tyr Ile Ala Met Ser Pro Val Glu Ala
515 520 525

Gln Lys Cys
530

<210> 62
<211> 478
<212> PRT
<213> Rattus norvegicus

<400> 62

Met Ala Arg Cys Cys Phe Tyr Thr Ala Gly Thr Leu Ser Leu Leu Leu
1 5 10 15

Leu Val Thr Ser Val Thr Leu Leu Val Ala Arg Val Phe Gln Lys Ala

ITI-08-PCT_Sequence_Listing_ST25.txt

20	25	30																	
Val	Asp	Gln	Thr	Ile	Glu	Lys	Asn	Met	Val	Leu	Gln	Asn	Gly	Thr	Lys				
	35						40					45							
Val	Phe	Asp	Ser	Trp	Glu	Lys	Pro	Pro	Leu	Pro	Val	Tyr	Ile	Gln	Phe				
	50					55					60								
Tyr	Phe	Phe	Asn	Val	Thr	Asn	Pro	Glu	Glu	Ile	Leu	Gln	Gly	Glu	Ile				
65					70					75					80				
Pro	Leu	Leu	Glu	Glu	Val	Gly	Pro	Tyr	Thr	Tyr	Arg	Glu	Leu	Arg	Asn				
				85					90					95					
Lys	Ala	Asn	Val	Gln	Phe	Gly	Glu	Asn	Gly	Thr	Thr	Ile	Ser	Ala	Val				
			100					105					110						
Thr	Asn	Lys	Ala	Tyr	Ile	Phe	Glu	Arg	Asn	Gln	Ser	Val	Gly	Asp	Pro				
		115					120					125							
Thr	Val	Asp	Leu	Ile	Arg	Thr	Ile	Asn	Ile	Pro	Leu	Leu	Thr	Val	Val				
	130					135					140								
Glu	Met	Ala	Gln	Gln	Pro	Phe	Leu	Arg	Glu	Ile	Ile	Glu	Ala	Met	Leu				
145					150				155						160				
Lys	Ala	Tyr	Gln	Gln	Thr	Leu	Phe	Val	Thr	His	Thr	Val	His	Glu	Leu				
			165						170					175					
Leu	Trp	Gly	Tyr	Lys	Asp	Glu	Val	Leu	Ser	Leu	Val	His	Ile	Phe	Arg				
			180					185					190						
Pro	Asp	Val	Ser	Pro	Asn	Phe	Gly	Leu	Phe	Tyr	Glu	Arg	Asn	Gly	Thr				
		195					200					205							
Asn	Asp	Gly	Glu	Tyr	Val	Phe	Leu	Thr	Gly	Glu	Asp	Asn	Tyr	Leu	Asn				
	210					215					220								
Phe	Thr	Lys	Ile	Val	Glu	Trp	Asn	Gly	Lys	Thr	Ser	Leu	Asp	Trp	Trp				
225					230					235					240				
Thr	Thr	Asp	Thr	Cys	Asn	Met	Ile	Asn	Gly	Thr	Asp	Gly	Asp	Ser	Phe				
				245					250					255					
His	Pro	Leu	Ile	Ser	Lys	Asp	Glu	Thr	Leu	Tyr	Ile	Phe	Pro	Ser	Asp				
			260					265					270						
Phe	Cys	Arg	Ser	Val	Tyr	Ile	Thr	Phe	Ser	Ser	Phe	Glu	Asn	Val	Glu				
		275					280					285							
Gly	Leu	Pro	Ala	Phe	Arg	Tyr	Lys	Val	Pro	Ala	Glu	Ile	Leu	Ala	Asn				
	290					295					300								

ITI-08-PCT_Sequence_Listing_ST25.txt

Ser Ser Glu Asn Ala Gly Phe Cys Ile Pro Glu Gly Asn Cys Met Asp
305 310 315 320

Ala Gly Val Leu Asn Val Ser Ile Cys Lys Asn Gly Ala Pro Ile Ile
325 330 335

Met Ser Phe Pro His Phe Tyr Gln Ala Asp Glu Lys Phe Val Ser Ala
340 345 350

Ile Lys Gly Met Arg Pro Asn Lys Glu Glu His Glu Ser Phe Val Asp
355 360 365

Ile Asn Pro Leu Thr Gly Ile Ile Leu Arg Gly Ala Lys Arg Phe Gln
370 375 380

Ile Asn Thr Tyr Val Lys Lys Leu Asp Asp Phe Val Glu Thr Gly Asn
385 390 395 400

Ile Arg Thr Met Val Phe Pro Val Met Tyr Leu Asn Glu Ser Val Leu
405 410 415

Ile Asp Lys Glu Thr Ala Ser Gln Leu Lys Ser Val Ile Asn Thr Thr
420 425 430

Leu Ile Val Thr Asn Ile Pro Tyr Ile Ile Met Ala Leu Gly Val Phe
435 440 445

Phe Gly Leu Ile Phe Thr Trp Leu Ala Cys Arg Gly Gln Gly Ser Thr
450 455 460

Asp Glu Gly Thr Ala Asp Glu Arg Ala Pro Leu Ile Arg Thr
465 470 475

<210> 63

<211> 481

<212> PRT

<213> Gallus gallus

<400> 63

Met Arg Ser Leu Cys Leu Val Thr Val Gly Val Leu Ala Leu Thr Leu
1 5 10 15

Leu Ile Ala Ser Ile Ser Leu Leu Val Ala His Val Phe Gln Thr Val
20 25 30

Val Asp Leu Gln Val Lys Gln Gly Thr Val Leu Lys Asn Gly Thr Glu
35 40 45

Thr Phe Glu Ala Trp Glu Asp Pro Pro Pro Pro Val Tyr Met Gln Phe
50 55 60

ITI-08-PCT_Sequence_Listing_ST25.txt

Tyr	Phe	Phe	Asn	Val	Thr	Asn	Pro	Leu	Glu	Val	Leu	Gln	Gly	Ala	Thr	65	70	75	80
Pro	Leu	Val	Glu	Glu	Lys	Gly	Pro	Tyr	Thr	Tyr	Arg	Glu	Tyr	Arg	Pro	85	90	95	
Arg	Val	His	Val	Gln	Phe	Leu	Asp	Asn	Gly	Thr	Lys	Val	Ser	Ala	Leu	100	105	110	
Asn	Pro	Lys	Thr	Tyr	Val	Phe	Glu	Pro	Glu	Lys	Ser	Val	Gly	Asn	Pro	115	120	125	
Glu	Val	Asp	Leu	Ile	Arg	Thr	Ile	Asn	Val	Pro	Ala	Val	Thr	Ala	Met	130	135	140	
Glu	Trp	Thr	Arg	Ala	Thr	Ser	Leu	Gln	Phe	Ala	Thr	Glu	Val	Leu	Leu	145	150	155	160
Leu	Leu	Tyr	Gln	Glu	Ser	Leu	Phe	Thr	Val	Arg	Thr	Val	His	Glu	Leu	165	170	175	
Leu	Trp	Gly	Tyr	Lys	Asp	Lys	Leu	Leu	Ser	Thr	Ile	His	Val	Leu	His	180	185	190	
Pro	Glu	Ile	Asp	Pro	Val	Phe	Gly	Phe	Phe	Asn	Lys	Met	Asn	Gly	Thr	195	200	205	
Asp	Asp	Gly	Glu	Tyr	Val	Phe	Leu	Ser	Gly	Glu	Met	Asn	Tyr	Leu	Asn	210	215	220	
Phe	Ser	Arg	Ile	Val	Glu	Trp	Lys	Gly	Lys	Glu	Ser	Leu	Asn	Trp	Trp	225	230	235	240
Thr	Thr	Lys	Thr	Cys	Asn	Met	Ile	Asn	Gly	Thr	Asp	Gly	Thr	Ser	Phe	245	250	255	
His	Pro	Leu	Ile	Ser	Lys	Asp	Glu	Asn	Ile	Tyr	Ile	Phe	Ser	Ser	Asp	260	265	270	
Phe	Cys	Arg	Ser	Leu	Tyr	Leu	Val	Tyr	Asp	Ser	Ser	Gly	Ser	Val	Ala	275	280	285	
Gly	Val	Pro	Thr	Tyr	Arg	Phe	Val	Pro	Ser	Pro	Met	Val	Phe	Ala	Asn	290	295	300	
Thr	Thr	Val	Asn	Pro	Asp	Asn	Ala	Gly	Phe	Cys	Val	Pro	Pro	Gly	Asn	305	310	315	320
Cys	Pro	Gly	Ala	Gly	Val	Leu	Asn	Val	Ser	Ile	Cys	Lys	Gln	Gly	Ala	325	330	335	

ITI-08-PCT_Sequence_Listing_ST25.txt

Pro Ile Phe Leu Ser Ala Pro His Phe Tyr Gln Ala Asp Gln Lys Phe
340 345 350

Val Ser Asp Ile Glu Gly Met His Pro Thr Lys Glu Tyr His Glu Thr
355 360 365

Phe Val Asp Ile Asn Pro Leu Thr Gly Leu Val Leu Gln Ala Ala Lys
370 375 380

Arg Met Gln Ile Asn Ile His Val Arg Lys Leu Pro Glu Phe Phe Glu
385 390 395 400

Thr Gly Asn Ile Arg Thr Leu Ile Phe Pro Val Met Tyr Ile Asn Glu
405 410 415

Ser Val Leu Ile Asp Glu Ala Ser Ala Asn Lys Leu Lys His Val Leu
420 425 430

Leu Glu Ala Ser Val Val Thr Gly Ile Pro Phe Val Ile Met Ala Ile
435 440 445

Gly Ile Val Phe Gly Ile Val Phe Ser Val Leu Val Cys Arg Ala Gln
450 455 460

Gly Ala Arg Glu Glu Ser Thr Glu Glu Glu Arg Ser Pro Leu Ile Arg
465 470 475 480

Thr

<210> 64

<211> 483

<212> PRT

<213> *Xenopus tropicalis*

<400> 64

Met Val Lys Trp Ala Val Phe Gly Thr Ala Ala Val Ser Val Thr Leu
1 5 10 15

Leu Ile Val Ser Ile Val Leu Leu Leu Thr His Thr Phe Met Asp Ile
20 25 30

Val Glu Gly Gln Val Lys Gln Ala Ile Val Leu Lys Asn Glu Ser Glu
35 40 45

Val Phe Glu Asp Trp Ala Asn Pro Pro Pro Pro Val Tyr Met Gln Phe
50 55 60

Tyr Phe Phe Asn Val Thr Asn Pro Leu Glu Val Leu Ser Gly Glu Lys
65 70 75 80

Pro Phe Val Asp Glu Ile Gly Pro Tyr Thr Tyr Arg Glu Tyr Arg Pro

ITI-08-PCT_Sequence_Listing_ST25.txt

85

90

95

Arg Glu Asn Ile Thr Phe Ser Val Asn Gly Thr Glu Val Ser Ala Val
 100 105 110

Thr Pro Lys Thr Tyr Val Phe Glu Pro Glu Lys Ser Ile Gly Asp Pro
 115 120 125

Lys Val Asp Leu Ile Arg Thr Val Asn Ile Pro Leu Val Thr Ile Leu
 130 135 140

Glu Met Thr Lys Asp Ser Ser Leu Leu Arg Pro Phe Ile Ile Ala Ala
 145 150 155 160

Leu Lys Thr Tyr Lys Glu Gly Met Phe Val Thr Arg Thr Val Asp Glu
 165 170 175

Leu Leu Trp Gly Tyr Lys Asp Ala Val Leu Ser Ile Leu His Pro Phe
 180 185 190

Lys Lys Asn Ile Ser Asp Thr Phe Gly Leu Phe Tyr Lys Met Asn Thr
 195 200 205

Thr Asp Asp Gly Glu Tyr Ile Phe Leu Ser Gly Glu Lys Asp Tyr Leu
 210 215 220

Glu Phe Thr Gln Ile Ala Glu Trp Lys Gly Gln Lys Ala Leu Asn Trp
 225 230 235 240

Trp Thr Thr Glu Thr Cys Asn Met Ile Asn Gly Thr Asp Gly Thr Ser
 245 250 255

Phe His Pro Leu Leu Asn Lys Asp Asp Thr Ile Tyr Met Phe Ser Ser
 260 265 270

Asp Leu Cys Arg Ser Ile Tyr Ala Val Tyr Glu Ser Ser Glu Asn Ile
 275 280 285

Lys Asp Ile Ser Val Phe Arg Phe Ser Pro Pro Ala Ser Val Phe Ala
 290 295 300

Asn Val Ser Val Asn Pro Gln Asn Lys Gly Phe Cys Val Pro Glu Gly
 305 310 315 320

Asn Cys Leu Pro Ser Gly Leu Leu Asn Val Ser Ile Cys Lys Glu Gly
 325 330 335

Ala Pro Ile Val Leu Ser Ser Pro His Phe Tyr Gln Ala Asp Glu Asn
 340 345 350

Val Ile Asn Ser Ile Arg Gly Met Lys Pro Val Lys Glu His His Met
 355 360 365

ITI-08-PCT_Sequence_Listing_ST25.txt

Thr Phe Leu Asp Leu Asn Pro Leu Thr Gly Thr Leu Ile Gln Ala Ala
370 375 380

Lys Arg Ile Gln Val Asn Val Tyr Val Arg Lys Ile Asn Val Tyr Leu
385 390 395 400

Ile Thr Gln Asp Ile Gln Thr Leu Phe Phe Pro Val Met His Leu Asn
405 410 415

Glu Ser Val Leu Ile Asp Asp Lys Ser Ala Gly Arg Leu Arg Ser Ile
420 425 430

Leu Phe Gln Gly Arg Val Val Ala Asn Ile Pro Phe Ile Ile Met Gly
435 440 445

Leu Gly Ile Ile Leu Ala Phe Leu Phe Thr Thr Leu Ser Cys Leu Gln
450 455 460

Lys Arg Ser Arg Asp Glu Gly Thr Glu Glu Glu Arg Gly Pro Leu Ile
465 470 475 480

Arg Ala Ser

<210> 65

<211> 551

<212> PRT

<213> Drosophila melanogaster

<400> 65

Met Gln Leu Asp Asp Ile Leu His Ile Asn Asn Cys Lys Ala Asp Cys
1 5 10 15

Ser Ser Leu Ser Thr Thr Pro Asn Pro Lys Thr Asp Leu Val Asn Met
20 25 30

Asn Gly Pro Lys His Lys Phe Cys Thr Lys Leu Ser Ser Thr Tyr Leu
35 40 45

Arg Lys Trp Trp Ile Thr Ile Val Val Ala Ala Ala Leu Ile Ile Gly
50 55 60

Gly Ile Val Val Ala Cys Glu Phe Thr Val Leu Ile Asp Ala Val Val
65 70 75 80

Asp Arg Met Val Ala Leu Arg Pro Gly Ala Lys Thr Phe Gly Trp Trp
85 90 95

Ala Lys Pro Pro Val Glu Pro Arg Ile Ser Leu Tyr Ile Tyr Asn Val
100 105 110

ITI-08-PCT_Sequence_Listing_ST25.txt

Thr	Asn	Ala	Asp	Asp	Phe	Leu	Ser	Asn	Gly	Ser	Lys	Ala	Ile	Val	Asp	115	120	125	
Glu	Val	Gly	Pro	Tyr	Val	Tyr	Ser	Glu	Thr	Trp	Glu	Lys	Val	Asn	Ile	130	135	140	
Val	Glu	Asn	Asp	Asn	Gly	Thr	Leu	Ser	Tyr	Asn	Leu	Arg	Lys	Ile	Tyr	145	150	155	160
Ser	Phe	Arg	Glu	Asp	Leu	Ser	Val	Gly	Pro	Glu	Asp	Asp	Val	Val	Ile	165	170	175	
Val	Pro	Asn	Ile	Pro	Met	Leu	Ser	Ala	Thr	Ser	Gln	Ser	Lys	His	Ala	180	185	190	
Ala	Arg	Phe	Leu	Arg	Leu	Ala	Met	Ala	Ser	Ile	Met	Asp	Ile	Leu	Lys	195	200	205	
Ile	Lys	Pro	Phe	Val	Gln	Val	Ser	Val	Gly	Gln	Leu	Leu	Trp	Gly	Tyr	210	215	220	
Glu	Asp	Pro	Leu	Leu	Lys	Leu	Ala	Lys	Asp	Val	Val	Pro	Lys	Glu	Gln	225	230	235	240
Lys	Leu	Pro	Tyr	Glu	Glu	Phe	Gly	Leu	Leu	Tyr	Gly	Lys	Asn	Gly	Thr	245	250	255	
Ser	Ser	Asp	Arg	Val	Thr	Val	Asn	Thr	Gly	Val	Asp	Asp	Ile	Arg	Arg	260	265	270	
Tyr	Gly	Ile	Ile	Asp	Asn	Phe	Asn	Gly	Arg	Thr	His	Leu	Pro	His	Trp	275	280	285	
Thr	Thr	Asp	Ala	Cys	Asn	Thr	Leu	Ala	Gly	Thr	Asp	Gly	Ser	Ile	Phe	290	295	300	
Pro	Pro	His	Ile	Asp	His	Asp	Arg	Ile	Leu	His	Val	Tyr	Asp	Lys	Asp	305	310	315	320
Leu	Cys	Arg	Leu	Leu	Pro	Leu	Val	Phe	Glu	Lys	Glu	Val	Met	Thr	Ser	325	330	335	
Asn	Glu	Val	Pro	Gly	Tyr	Arg	Phe	Thr	Pro	Pro	Glu	Trp	Val	Phe	Ala	340	345	350	
Asp	Val	Asp	Ser	His	Pro	Asp	Asn	Met	Cys	Phe	Cys	Pro	Ala	Gly	Lys	355	360	365	
Pro	Ser	Cys	Ser	Pro	Asn	Gly	Leu	Phe	Asn	Val	Ser	Leu	Cys	Gln	Tyr	370	375	380	
Asp	Ser	Pro	Ile	Met	Leu	Ser	Phe	Pro	His	Phe	Tyr	Leu	Ala	Asp	Glu				

ITI-08-PCT_Sequence_Listing_ST25.txt

```

385          390          395          400
Ser Leu Arg Thr Gln Val Glu Gly Ile Ser Pro Pro Met Lys Glu Lys
          405          410          415

His Gln Phe Phe Phe Asp Val Gln Pro Lys Met Gly Thr Thr Leu Arg
          420          425          430

Val Arg Ala Arg Ile Gln Ile Asn Leu Ala Val Ser Gln Val Phe Asp
          435          440          445

Ile Lys Gln Val Ala Asn Phe Pro Asp Ile Ile Phe Pro Ile Leu Trp
          450          455          460

Phe Glu Glu Gly Ile Asp Asn Leu Pro Asp Glu Val Thr Asp Leu Met
465          470          475          480

Arg Phe Ala Glu Gln Val Pro Pro Lys Ile Arg Val Ala Leu Ile Val
          485          490          495

Gly Leu Cys Ala Leu Gly Val Ile Leu Leu Leu Leu Ser Thr Phe Cys
          500          505          510

Leu Ile Arg Asn Ser His Arg Gln Ser Thr Leu His Leu Glu Gly Ser
          515          520          525

Asn Tyr Leu Ala Thr Ala Gln Val Asp Met Asn Lys Lys Gln Asn Lys
          530          535          540

Asp Asn Gln Pro Ala Arg Tyr
545          550

```

```

<210> 66
<211> 522
<212> PRT
<213> Anopheles gambiae str. PEST

```

```

<400> 66

```

```

Met Tyr Gly Arg Ser Asn Arg Leu Cys Ala Lys Leu Ser Ser Ala Phe
1          5          10          15

Leu Arg Lys Trp Trp Phe Val Ile Ala Phe Ala Leu Ser Leu Leu Val
          20          25          30

Leu Gly Ala Leu Val Thr Phe Gly Phe Thr Ala Phe Ile Arg Thr Ile
          35          40          45

Ile Asp His Gln Val Ala Leu Arg Val Gly Gly Gln Ser Phe Gly Trp
          50          55          60

Trp Ser Arg Pro Pro Val Glu Pro Ile Ile Arg Ile Phe Val Tyr Asn

```


ITI-08-PCT_Sequence_Listing_ST25.txt

```

65          70          75          80
Val Thr Asn Ala Asp Glu Phe Leu Asn Asn Gly Thr Lys Pro Ile Leu
      85          90          95
Asp Glu Leu Gly Pro Tyr Val Tyr Val Gln Thr Trp Glu Lys Val Asn
      100         105         110
Ile Lys Glu Asn Pro Asn Gly Thr Ile Ser Tyr Asn Gln Lys Arg Val
      115         120         125
Tyr Ile Phe Asn Glu Asp Leu Ser Gly Gly Leu Glu Asp Asp Val Val
      130         135         140
Ile Val Pro Asn Ile Pro Met Leu Ser Ala Thr Ser Gln Ser Lys His
      145         150         155
Ala Ala Arg Phe Leu Arg Leu Ala Met Ala Ser Ile Met Asp Ile Leu
      165         170         175
Lys Ile Lys Pro Phe Val Glu Val Ser Val Gly Gln Leu Leu Trp Gly
      180         185         190
Tyr Glu Asp Pro Leu Leu Lys Leu Ala Lys Asp Val Val Pro Lys Glu
      195         200         205
Gln Lys Leu Pro Tyr Glu Glu Phe Gly Leu Met Tyr Gly Lys Asn Ser
      210         215         220
Thr Ser Lys Asp Thr Val Thr Val Trp Thr Gly Val Asp Asp Ile Thr
      225         230         235
Gln Tyr Gly Ile Ile Asp Lys Tyr Asn Gly Arg Ser His Gln Thr His
      245         250         255
Trp Leu Ser Glu Gln Cys Asn Arg Leu Asn Gly Thr Asp Gly Ser Ile
      260         265         270
Phe Pro Pro Arg Ile Thr Lys Asn Ser Thr Leu His Val Tyr Glu Lys
      275         280         285
Asp Leu Cys Arg Leu Leu Pro Leu Ser Phe Glu Lys Glu Val Thr Val
      290         295         300
Arg Gly Gly Val Lys Gly Tyr Arg Phe Thr Pro Ser Pro Asp Val Phe
      305         310         315
Ala Ser Val Asp Lys Asn Pro Asn Asn Met Cys Tyr Cys Pro Ala Gly
      325         330         335
Pro Pro Cys Ala Pro His Gly Leu Phe Asn Val Ser Leu Cys Gln Tyr
      340         345         350

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Asp Ser Pro Ile Leu Leu Ser Phe Pro His Phe Tyr Met Ala Asp Gln
355 360 365

Thr Leu Arg Thr Ala Val Glu Gly Ile Ser Pro Pro Glu Lys Asp Lys
370 375 380

His Gln Leu Phe Ile Asp Val Gln Pro Asp Met Gly Thr Ala Leu Arg
385 390 395 400

Ala Arg Ala Arg Ile Gln Ile Asn Leu Ala Val Ser Gln Val Val Asp
405 410 415

Ile Lys Gln Val Ala Asn Phe Pro Asp Ile Val Phe Pro Ile Leu Trp
420 425 430

Phe Glu Glu Gly Ile Asp Ser Leu Pro Asp Glu Ile Leu Asp Leu Met
435 440 445

Lys Val Ala Thr Asn Ile Pro Pro Arg Ala Lys Phe Ile Leu Thr Ile
450 455 460

Ala Leu Phe Gly Leu Gly Gly Phe Leu Phe Val Val Ala Val Ile Cys
465 470 475 480

Leu Val Arg Lys Ser His Arg Gln Ser Thr Leu His Leu Glu Gly Ser
485 490 495

Asn Tyr Leu Ala Thr Ala Ser Val Asp Gln Ala Lys Lys Lys Ala Lys
500 505 510

Met Asp Asn Gly Met Ser Ser Lys Ser Asn
515 520

<210> 67

<211> 338

<212> PRT

<213> Homo sapiens

<400> 67

Met Val Arg Arg Val Gln Pro Asp Arg Lys Gln Leu Pro Leu Val Leu
1 5 10 15

Leu Arg Leu Leu Cys Leu Leu Pro Thr Gly Leu Pro Val Arg Ser Val
20 25 30

Asp Phe Asn Arg Gly Thr Asp Asn Ile Thr Val Arg Gln Gly Asp Thr
35 40 45

Ala Ile Leu Arg Cys Val Val Glu Asp Lys Asn Ser Lys Val Ala Trp
50 55 60

ITI-08-PCT_Sequence_Listing_ST25.txt

Leu	Asn	Arg	Ser	Gly	Ile	Ile	Phe	Ala	Gly	His	Asp	Lys	Trp	Ser	Leu	65	70	75	80
Asp	Pro	Arg	Val	Glu	Leu	Glu	Lys	Arg	His	Ser	Leu	Glu	Tyr	Ser	Leu	85	90	95	
Arg	Ile	Gln	Lys	Val	Asp	Val	Tyr	Asp	Glu	Gly	Ser	Tyr	Thr	Cys	Ser	100	105	110	
Val	Gln	Thr	Gln	His	Glu	Pro	Lys	Thr	Ser	Gln	Val	Tyr	Leu	Ile	Val	115	120	125	
Gln	Val	Pro	Pro	Lys	Ile	Ser	Asn	Ile	Ser	Ser	Asp	Val	Thr	Val	Asn	130	135	140	
Glu	Gly	Ser	Asn	Val	Thr	Leu	Val	Cys	Met	Ala	Asn	Gly	Arg	Pro	Glu	145	150	155	160
Pro	Val	Ile	Thr	Trp	Arg	His	Leu	Thr	Pro	Thr	Gly	Arg	Glu	Phe	Glu	165	170	175	
Gly	Glu	Glu	Glu	Tyr	Leu	Glu	Ile	Leu	Gly	Ile	Thr	Arg	Glu	Gln	Ser	180	185	190	
Gly	Lys	Tyr	Glu	Cys	Lys	Ala	Ala	Asn	Glu	Val	Ser	Ser	Ala	Asp	Val	195	200	205	
Lys	Gln	Val	Lys	Val	Thr	Val	Asn	Tyr	Pro	Pro	Thr	Ile	Thr	Glu	Ser	210	215	220	
Lys	Ser	Asn	Glu	Ala	Thr	Thr	Gly	Arg	Gln	Ala	Ser	Leu	Lys	Cys	Glu	225	230	235	240
Ala	Ser	Ala	Val	Pro	Ala	Pro	Asp	Phe	Glu	Trp	Tyr	Arg	Asp	Asp	Thr	245	250	255	
Arg	Ile	Asn	Ser	Ala	Asn	Gly	Leu	Glu	Ile	Lys	Ser	Thr	Glu	Gly	Gln	260	265	270	
Ser	Ser	Leu	Thr	Val	Thr	Asn	Val	Thr	Glu	Glu	His	Tyr	Gly	Asn	Tyr	275	280	285	
Thr	Cys	Val	Ala	Ala	Asn	Lys	Leu	Gly	Val	Thr	Asn	Ala	Ser	Leu	Val	290	295	300	
Leu	Phe	Arg	Pro	Gly	Ser	Val	Arg	Gly	Ile	Asn	Gly	Ser	Ile	Ser	Leu	305	310	315	320
Ala	Val	Pro	Leu	Trp	Leu	Leu	Ala	Ala	Ser	Leu	Leu	Cys	Leu	Leu	Ser	325	330	335	

ITI-08-PCT_Sequence_Listing_ST25.txt

Lys Cys

<210> 68

<211> 338

<212> PRT

<213> Pan troglodytes

<400> 68

Met Val Arg Arg Val Gln Pro Asp Arg Lys Gln Leu Pro Leu Val Leu
1 5 10 15

Leu Arg Leu Leu Cys Leu Leu Pro Thr Gly Leu Pro Val Arg Ser Val
20 25 30

Asp Phe Asn Arg Gly Thr Asp Asn Ile Thr Val Arg Gln Gly Asp Thr
35 40 45

Ala Ile Leu Arg Cys Val Val Glu Asp Lys Asn Ser Lys Val Ala Trp
50 55 60

Leu Asn Arg Ser Gly Ile Ile Phe Ala Gly His Asp Lys Trp Ser Leu
65 70 75 80

Asp Pro Arg Val Glu Leu Glu Lys Arg His Ser Leu Glu Tyr Ser Leu
85 90 95

Arg Ile Gln Lys Val Asp Val Tyr Asp Glu Gly Ser Tyr Thr Cys Ser
100 105 110

Val Gln Thr Gln His Glu Pro Lys Thr Ser Gln Val Tyr Leu Ile Val
115 120 125

Gln Val Pro Pro Lys Ile Ser Asn Ile Ser Ser Asp Val Thr Val Asn
130 135 140

Glu Gly Ser Asn Val Thr Leu Val Cys Met Ala Asn Gly Arg Pro Glu
145 150 155 160

Pro Val Ile Thr Trp Arg His Leu Thr Pro Thr Gly Arg Glu Phe Glu
165 170 175

Gly Glu Glu Glu Tyr Leu Glu Ile Leu Gly Ile Thr Arg Glu Gln Ser
180 185 190

Gly Lys Tyr Glu Cys Lys Ala Ala Asn Glu Val Ser Ser Ala Asp Val
195 200 205

Lys Gln Val Lys Val Thr Val Asn Tyr Pro Pro Thr Ile Thr Glu Ser
210 215 220

Lys Ser Asn Glu Ala Thr Thr Gly Arg Gln Ala Ser Leu Lys Cys Glu

ITI-08-PCT_Sequence_Listing_ST25.txt

225 230 235 240
 Ala Ser Ala Val Pro Ala Pro Asp Phe Glu Trp Tyr Arg Asp Asp Thr
 245 250 255
 Arg Ile Asn Ser Ala Asn Gly Leu Glu Ile Lys Ser Thr Glu Gly Gln
 260 265 270
 Ser Ser Leu Thr Val Thr Asn Val Thr Glu Glu His Tyr Gly Asn Tyr
 275 280 285
 Thr Cys Val Ala Ala Asn Lys Leu Gly Val Thr Asn Ala Ser Leu Val
 290 295 300
 Leu Phe Arg Pro Gly Ser Val Arg Gly Ile Asn Gly Ser Ile Ser Leu
 305 310 315 320
 Ala Val Pro Leu Trp Leu Leu Ala Ala Ser Leu Leu Cys Leu Leu Ser
 325 330 335

Lys Cys

<210> 69
 <211> 338
 <212> PRT
 <213> Oryctolagus cuniculus

<400> 69

Met Gly Ala Arg Val Gln Pro Asp Arg Lys Gln Leu Pro Leu Val Leu
 1 5 10 15
 Leu Arg Leu Leu Cys Leu Leu Pro Thr Gly Leu Pro Val Arg Ser Val
 20 25 30
 Asp Phe Asn Arg Gly Thr Asp Asn Ile Thr Val Arg Gln Gly Asp Thr
 35 40 45
 Ala Ile Leu Arg Cys Val Val Glu Asp Lys Asn Ser Lys Val Ala Trp
 50 55 60
 Leu Asn Arg Ser Gly Ile Ile Phe Ala Gly His Asp Lys Trp Ser Leu
 65 70 75 80
 Asp Pro Arg Val Glu Leu Glu Lys Arg His Ser Leu Glu Tyr Ser Leu
 85 90 95
 Arg Ile Gln Lys Val Asp Val Tyr Asp Glu Gly Ser Tyr Thr Cys Ser
 100 105 110
 Val Gln Thr Gln His Glu Pro Lys Thr Ser Gln Val Tyr Leu Ile Val
 115 120 125

ITI-08-PCT_Sequence_Listing_ST25.txt

Gln Val Pro Pro Lys Ile Ser Asn Ile Ser Ser Asp Val Thr Val Asn
130 135 140

Glu Gly Ser Asn Val Thr Leu Val Cys Met Ala Asn Gly Arg Pro Glu
145 150 155 160

Pro Val Ile Thr Trp Arg His Leu Thr Pro Thr Gly Arg Glu Phe Glu
165 170 175

Gly Glu Glu Glu Tyr Leu Glu Ile Leu Gly Ile Thr Arg Glu Gln Ser
180 185 190

Gly Lys Tyr Glu Cys Lys Ala Ala Asn Glu Val Ser Ser Ala Asp Val
195 200 205

Lys Gln Val Lys Val Thr Val Asn Tyr Pro Pro Thr Ile Thr Glu Ser
210 215 220

Lys Ser Asn Glu Ala Thr Thr Gly Arg Gln Ala Ser Leu Lys Cys Glu
225 230 235 240

Ala Ser Ala Val Pro Ala Pro Asp Phe Glu Trp Tyr Arg Asp Asp Thr
245 250 255

Arg Ile Asn Ser Ala Asn Gly Leu Glu Ile Lys Ser Thr Glu Gly Gln
260 265 270

Ser Ser Leu Thr Val Thr Asn Val Thr Glu Glu His Tyr Gly Asn Tyr
275 280 285

Thr Cys Val Ala Ala Asn Lys Leu Gly Val Thr Asn Ala Ser Leu Val
290 295 300

Leu Phe Arg Pro Gly Ser Val Arg Gly Ile Asn Gly Ser Ile Ser Leu
305 310 315 320

Ala Val Pro Leu Trp Leu Leu Ala Ala Ser Leu Leu Cys Leu Leu Ser
325 330 335

Lys Cys

<210> 70
<211> 341
<212> PRT
<213> Mus musculus

<400> 70

Met Val Gly Arg Val Gln Pro Asp Arg Lys Gln Leu Pro Leu Val Leu
1 5 10 15

ITI-08-PCT_Sequence_Listing_ST25.txt

Leu Arg Leu Leu Cys Leu Leu Pro Thr Gly Leu Pro Val Arg Ser Val
 20 25 30
 Asp Phe Asn Arg Gly Thr Asp Asn Ile Thr Val Arg Gln Gly Asp Thr
 35 40 45
 Ala Ile Leu Arg Cys Val Val Glu Asp Lys Asn Ser Lys Val Ala Trp
 50 55 60
 Leu Asn Arg Ser Gly Ile Ile Phe Ala Gly His Asp Lys Trp Ser Leu
 65 70 75 80
 Asp Pro Arg Val Glu Leu Glu Lys Arg His Ala Leu Glu Tyr Ser Leu
 85 90 95
 Arg Ile Gln Lys Val Asp Val Tyr Asp Glu Gly Ser Tyr Thr Cys Ser
 100 105 110
 Val Gln Thr Gln His Glu Pro Lys Thr Ser Gln Val Tyr Leu Ile Val
 115 120 125
 Gln Val Pro Pro Lys Ile Ser Asn Ile Ser Ser Asp Val Thr Val Asn
 130 135 140
 Glu Gly Ser Asn Val Thr Leu Val Cys Met Ala Asn Gly Arg Pro Glu
 145 150 155 160
 Pro Val Ile Thr Trp Arg His Leu Thr Pro Leu Gly Arg Glu Phe Glu
 165 170 175
 Gly Glu Glu Glu Tyr Leu Glu Ile Leu Gly Ile Thr Arg Glu Gln Ser
 180 185 190
 Gly Lys Tyr Glu Cys Lys Ala Ala Asn Glu Val Ser Ser Ala Asp Val
 195 200 205
 Lys Gln Val Lys Val Thr Val Asn Tyr Pro Pro Thr Ile Thr Glu Ser
 210 215 220
 Lys Ser Asn Glu Ala Thr Thr Gly Arg Gln Ala Ser Leu Lys Cys Glu
 225 230 235 240
 Ala Ser Ala Val Pro Ala Pro Asp Phe Glu Trp Tyr Arg Asp Asp Thr
 245 250 255
 Arg Ile Asn Ser Ala Asn Gly Leu Glu Ile Lys Ser Thr Glu Gly Gln
 260 265 270
 Ser Ser Leu Thr Val Thr Asn Val Thr Glu Glu His Tyr Gly Asn Tyr
 275 280 285
 Thr Cys Val Ala Ala Asn Lys Leu Gly Val Thr Asn Ala Ser Leu Val

ITI-08-PCT_Sequence_Listing_ST25.txt

290

295

300

Leu Phe Ser Lys Tyr Ala Lys Thr Glu Pro Asp Ser Met Gln Val Ile
305 310 315 320

Glu Phe Leu His Ile Asp Leu Lys Ser Ile Arg His Pro Leu Lys Val
325 330 335

Asn Pro Ile Gln Lys
340

<210> 71

<211> 337

<212> PRT

<213> Xenopus laevis

<400> 71

Met Val Gly Arg Ser Gln Ser Asp Arg Asn Gln Leu Pro Leu Phe Leu
1 5 10 15

Leu Arg Leu Leu Cys Leu Leu Pro Thr Gly Leu Pro Val Arg Ser Gly
20 25 30

Asp Phe Asn Arg Ser Thr Asp Asn Met Thr Val Arg Gln Gly Asp Thr
35 40 45

Ala Ile Leu Arg Cys Phe Val Glu Asp Lys Ser Ser Lys Val Ala Trp
50 55 60

Leu Asn Arg Ser Gly Ile Ile Phe Ala Val Asp Asp Lys Trp Ser Leu
65 70 75 80

Asp Pro Arg Val Glu Leu Glu Lys Arg Ser Pro Phe Glu Tyr Ser Leu
85 90 95

Arg Ile Gln Lys Val Asp Val Ser Asp Glu Gly Pro Tyr Ile Cys Ser
100 105 110

Val Gln Thr Asn Gln His Thr Lys Thr Met Gln Val Tyr Leu Ile Val
115 120 125

Gln Val Pro Pro Lys Ile Ser Asn Ile Ser Ala Asp Ile Thr Val Asn
130 135 140

Glu Gly Ser Asn Val Thr Leu Met Cys Ile Ala Tyr Gly Arg Pro Glu
145 150 155 160

Pro Met Ile Thr Trp Arg His Leu Thr Pro Thr Ala Arg Asp Phe Glu
165 170 175

Gly Glu Glu Glu Phe Leu Glu Ile Gln Gly Ile Thr Arg Glu Gln Ser

ITI-08-PCT_Sequence_Listing_ST25.txt

180

185

190

Gly Arg Tyr Glu Cys Lys Ala Ala Asn Glu Val Ala Ser Ala Asp Val
195 200 205

Lys Gln Val Arg Val Thr Val Asn Tyr Pro Pro Ile Ile Thr Glu Ser
210 215 220

Asn Ser Asn Glu Ala Thr Thr Gly Lys Gln Ala Ile Leu Arg Cys Glu
225 230 235 240

Ala Ser Ala Val Pro Ala Pro Asp Phe Glu Trp Tyr Lys Asp Asp Thr
245 250 255

Arg Ile Asn Ser Ala Gln Gly Leu Glu Ile Arg Asn Thr Gly Ser Arg
260 265 270

Ser Val Leu Met Val Ala Asn Val Thr Glu Glu His Tyr Gly Asn Tyr
275 280 285

Thr Cys Val Ala Ala Asn Lys Leu Gly Ile Thr Asn Thr Ser Leu Tyr
290 295 300

Leu Tyr Ile Gly Pro Gly Thr Pro Ile Asp Asn Ala Thr Ser Leu Ala
305 310 315 320

Ala Ser Leu Trp Leu Met Ala Asn Ile Leu Leu Cys Leu Phe Cys Thr
325 330 335

Cys

<210> 72

<211> 333

<212> PRT

<213> Danio rerio

<400> 72

Met Ser Cys Leu Trp Ile His Ser Val Phe Ile Pro Gly Phe Phe Leu
1 5 10 15

Leu Phe Gly Phe Glu Gly Phe Pro Val Ile Ser Val Glu Ser Gln Arg
20 25 30

Ser Thr Asp Asn Ile Thr Ile Arg Gln Gly Asp Thr Thr Val Ile Arg
35 40 45

Cys Tyr Val Asp Asp Lys Val Ser Lys Val Ala Trp Leu Asn Arg Ser
50 55 60

Asn Ile Ile Phe Ala Gly Glu Asp Lys Trp Ser Leu Asp Pro Arg Val
65 70 75 80

ITI-08-PCT_Sequence_Listing_ST25.txt

Glu	Leu	Val	Thr	Gln	Gly	Gln	Leu	Glu	Tyr	Ser	Leu	Arg	Ile	Gln	Lys	85	90	95
Val	Asp	Val	Phe	Asp	Glu	Gly	Pro	Tyr	Thr	Cys	Ser	Ile	Gln	Thr	Lys	100	105	110
Gln	Gln	Ser	Lys	Thr	Ser	Gln	Val	Tyr	Leu	Ile	Val	Gln	Val	Pro	Ala	115	120	125
Ile	Ile	Tyr	Lys	Val	Ser	Glu	Asp	Ile	Thr	Val	Asn	Glu	Gly	Ser	Asn	130	135	140
Val	Ala	Leu	Thr	Cys	Leu	Ala	Asn	Gly	Arg	Pro	Asp	Pro	Ala	Ile	Thr	145	150	155
Trp	Arg	Leu	Leu	Asn	Pro	Ser	Ala	Glu	Ala	Leu	Asp	Val	Gly	Glu	Tyr	165	170	175
Leu	Glu	Ile	Ser	Gly	Val	Val	Arg	Ser	Gln	Ala	Gly	Arg	Tyr	Glu	Cys	180	185	190
Lys	Ala	Ser	Asn	Asp	Val	Ser	Thr	Pro	Asp	Val	Lys	Tyr	Val	Asn	Val	195	200	205
Val	Val	Asn	Tyr	Pro	Pro	Tyr	Ile	Lys	Asp	Val	Arg	Ser	Ser	Glu	Thr	210	215	220
Ala	Val	Gly	Gln	Ala	Gly	Val	Leu	His	Cys	Glu	Ala	Ser	Ala	Val	Pro	225	230	235
Gln	Pro	Glu	Phe	Glu	Trp	Tyr	Arg	Asp	Glu	Arg	Arg	Leu	Ser	Ser	Ser	245	250	255
Gln	Ser	Leu	Thr	Ile	Gln	Val	Ser	Gly	Ser	Arg	Thr	Val	Leu	Val	Val	260	265	270
Ala	Asn	Val	Thr	Glu	Glu	Asp	Tyr	Gly	Asn	Tyr	Thr	Cys	Val	Ala	Thr	275	280	285
Asn	Arg	Leu	Gly	Val	His	Asn	Ala	Ser	Val	Phe	Leu	Tyr	Lys	Pro	Gly	290	295	300
Met	Gly	Arg	Asp	Ile	Asn	Ser	Ala	Gly	Cys	Ile	Cys	Gln	Ser	Leu	Trp	305	310	315
Leu	Leu	Leu	Leu	Cys	Val	Ser	Ser	Ala	Leu	Leu	Gln	Cys				325	330	

<210> 73
 <211> 197
 <212> PRT

ITI-08-PCT_Sequence_Listing_ST25.txt

<213> Mus musculus

<400> 73

Met Ser Gly Ser Ser Arg Arg Leu Leu Trp Ala Ala Thr Cys Leu Ala
1 5 10 15

Val Leu Cys Val Ser Ala Ala Gln Pro Asn Ile Thr Thr Leu Ala Pro
20 25 30

Asn Val Thr Glu Val Pro Thr Thr Thr Thr Lys Val Val Pro Thr Thr
35 40 45

Gln Met Pro Thr Val Leu Pro Glu Thr Cys Ala Ser Phe Asn Ser Cys
50 55 60

Val Ser Cys Val Asn Ala Thr Phe Thr Asn Asn Ile Thr Cys Phe Trp
65 70 75 80

Leu His Cys Gln Glu Ala Asn Lys Thr Tyr Cys Ala Asn Glu Pro Leu
85 90 95

Ser Asn Cys Ser Gln Val Asn Arg Thr Asp Leu Cys Ser Val Ile Pro
100 105 110

Pro Thr Thr Pro Val Pro Thr Asn Ser Thr Ala Lys Pro Thr Thr Arg
115 120 125

Pro Ser Ser Pro Thr Pro Thr Pro Ser Val Val Thr Ser Ala Gly Thr
130 135 140

Thr Asn Thr Thr Leu Thr Pro Thr Ser Gln Pro Glu Arg Lys Ser Thr
145 150 155 160

Phe Asp Ala Ala Ser Phe Ile Gly Gly Ile Val Leu Val Leu Gly Val
165 170 175

Gln Ala Val Ile Phe Phe Leu Tyr Lys Phe Cys Lys Ser Lys Glu Arg
180 185 190

Asn Tyr His Thr Leu
195

<210> 74

<211> 197

<212> PRT

<213> Macaca mulatta

<400> 74

Met Ser Arg Leu Ser Arg Ser Leu Leu Trp Ala Val Thr Cys Leu Ala
1 5 10 15

ITI-08-PCT_Sequence_Listing_ST25.txt

Val Leu Cys Val Leu Ser Ala Glu Glu Asn Pro Thr Pro His Thr Asn
20 25 30

Val Thr Ser Leu Ala Pro Thr Ser Asn Ile Thr Ser Ala Pro Val Thr
35 40 45

Ser Leu Pro Leu Val Thr Thr Pro Ala Pro Glu Thr Cys Glu Gly Arg
50 55 60

Asn Ser Cys Val Ser Cys Phe Asn Ala Ser Thr Val Asn Thr Thr Cys
65 70 75 80

Phe Trp Ile Glu Cys Lys Asp Glu Ser Tyr Cys Ser His Asn Ser Thr
85 90 95

Val Ser Asp Cys Gln Val Gly Asn Thr Thr Asp Phe Cys Ser Val Pro
100 105 110

Thr Ala Thr Leu Val Pro Thr Ala Asn Ser Thr Ala Lys Pro Thr Val
115 120 125

Gln Pro Ser Pro Ser Thr Thr Ser Lys Thr Val Thr Thr Ser Gly Thr
130 135 140

Thr Asn Thr Thr Val Thr Pro Thr Ser Gln Pro Val Arg Lys Ser Thr
145 150 155 160

Phe Asp Ala Ala Ser Phe Ile Gly Gly Ile Val Leu Val Leu Gly Val
165 170 175

Gln Ala Val Ile Phe Phe Leu Tyr Lys Phe Cys Lys Ser Lys Glu Arg
180 185 190

Asn Tyr His Thr Leu
195

<210> 75
<211> 194
<212> PRT
<213> Sus scrofa

<400> 75

Met Leu Gly Leu Ser Arg Gln Leu Leu Trp Ala Val Gly Cys Leu Ala
1 5 10 15

Ala Leu Cys Val Leu Thr Ala Ala Lys Asn Ser Thr Ile Leu Pro Pro
20 25 30

Ser Thr Thr Thr Pro Trp Leu Ser Pro Pro Thr Thr Gln Thr Thr Ser
35 40 45

ITI-08-PCT_Sequence_Listing_ST25.txt

Ala Pro Pro Lys Thr Leu Pro Thr Pro Ala Pro Glu Ile Cys Glu Asn
50 55 60

Arg Asn Ser Cys Ile Ser Cys Phe Asp Ala Asn Asn Thr Cys Phe Trp
65 70 75 80

Ile Glu Cys Lys Gly Lys Ser Tyr Cys Ser Asp Asn Ser Thr Val Ser
85 90 95

Asp Cys His Val Val Asn Gly Thr Asp Phe Cys Ser Gly Pro Thr Val
100 105 110

Thr Pro Leu Pro Thr Asn Ser Thr Ala Lys Thr Thr Thr Leu Pro Ser
115 120 125

Pro Ser Ser Ala Ser Thr Thr Ala Thr Thr Ser Gly Thr Thr Asn Thr
130 135 140

Thr Leu Ala Pro Thr Thr Gln Pro Met Arg Lys Ser Thr Phe Asp Ala
145 150 155 160

Ala Ser Phe Ile Gly Gly Ile Val Leu Val Leu Gly Val Gln Ala Val
165 170 175

Ile Phe Phe Leu Tyr Lys Phe Cys Lys Ser Lys Glu Arg Asn Tyr His
180 185 190

Thr Leu

<210> 76

<211> 198

<212> PRT

<213> Bos taurus

<400> 76

Met Ser Gly Leu Ser Arg Pro Leu Leu Leu Ala Val Gly Cys Leu Ala
1 5 10 15

Ala Leu Cys Val Ile Thr Ala Ala Gly Asn Thr Thr Leu Ala Pro Asn
20 25 30

Val Thr Thr Ala Ser Ser Pro Pro Pro Thr Thr Thr Thr Val Pro Val
35 40 45

Ser Pro Thr Thr Leu Ser Pro Leu Pro Val Thr Thr Pro Ala Pro Asp
50 55 60

Ile Cys Gly Ser Arg Asn Ser Cys Val Ser Cys Val Asp Gly Asn Ala
65 70 75 80

ITI-08-PCT_Sequence_Listing_ST25.txt

Thr Cys Phe Trp Ile Glu Cys Lys Gly Lys Ser Tyr Cys Ser Asp Asn
85 90 95

Ser Thr Ala Gly Asp Cys Lys Val Val Asn Thr Thr Gly Phe Cys Ser
100 105 110

Val Pro Thr Thr Thr Pro Thr Pro Thr Asn Ser Thr Ala Lys Thr Thr
115 120 125

Thr Leu Pro Ser Thr Thr Thr Thr Ser Thr Thr Ala Thr Thr Ser Gly
130 135 140

Thr Thr Asn Thr Thr Leu Ser Pro Thr Ile Gln Pro Thr Arg Lys Ser
145 150 155 160

Thr Phe Asp Ala Ala Ser Phe Ile Gly Gly Ile Val Leu Val Leu Gly
165 170 175

Val Gln Ala Val Ile Phe Phe Leu Tyr Lys Phe Cys Lys Ser Lys Glu
180 185 190

Arg Asn Tyr His Thr Leu
195

<210> 77

<211> 198

<212> PRT

<213> Ovis aries

<400> 77

Met Ser Gly Leu Ser Arg Pro Leu Leu Leu Ala Val Gly Tyr Leu Ala
1 5 10 15

Ala Leu Cys Val Ile Thr Ala Ala Arg Asn Thr Thr Val Thr Pro Asn
20 25 30

Val Thr Thr Pro Ser Ser Pro Pro Pro Thr Thr Ala Thr Val Pro Val
35 40 45

Ser Pro Thr Thr Leu Thr Pro Pro Pro Val Thr Thr Pro Ala Pro Asp
50 55 60

Ile Cys Gly Ser Arg Asn Ser Cys Ile Ser Cys Val Asp Gly Asn Ala
65 70 75 80

Thr Cys Phe Trp Ile Glu Cys Lys Gly Lys Ser Tyr Cys Ser Asp Asn
85 90 95

Ser Thr Val Ser Asp Cys Lys Val Val Asn Thr Thr Gly Phe Cys Ala
100 105 110

ITI-08-PCT_Sequence_Listing_ST25.txt

Val Pro Thr Thr Thr Pro Thr Pro Thr Asn Ser Thr Ala Lys Thr Thr
115 120 125

Thr Leu Pro Ser Thr Thr Thr Thr Ser Thr Thr Ala Thr Thr Ser Gly
130 135 140

Thr Ala Asn Thr Thr Leu Thr Pro Thr Ile Gln Pro Met Arg Lys Ser
145 150 155 160

Thr Phe Asp Ala Ala Ser Phe Ile Gly Gly Ile Val Leu Val Leu Gly
165 170 175

Val Gln Ala Val Ile Phe Phe Leu Tyr Lys Phe Cys Lys Ser Lys Glu
180 185 190

Arg Asn Tyr His Thr Leu
195

<210> 78

<211> 198

<212> PRT

<213> Canis lupus familiaris

<400> 78

Met Ser Gly Leu Ser Arg Gln Leu Cys Trp Ala Ala Ala Cys Leu Ala
1 5 10 15

Ala Leu Cys Ala Leu Thr Ala Ala Gln Ser Phe Ser Ser Asp Pro Asn
20 25 30

Gly Thr Thr Thr Thr Thr Gln Ala Thr Thr Asp Ala Ala Thr Thr Arg
35 40 45

Val Thr Thr Ala Ala Pro Ala Thr Thr Pro Ala Pro Asp Pro Cys Asp
50 55 60

Asn Arg Asn Ser Cys Val Ser Cys Val Asn Thr Ser Val Asp Ala Thr
65 70 75 80

Ala Cys Ser Trp Ile Glu Cys Lys Glu Lys Ser Tyr Cys Ser His Asn
85 90 95

Thr Thr Val Ser Asp Cys Gln Val Val Asn Ser Thr Gln Leu Cys Ser
100 105 110

Ala Pro Glu Pro Thr Met Met Pro Thr Asn Ser Thr Ala Lys Thr Thr
115 120 125

Thr Gln Pro Ser Ser Ser Thr Ala Thr Thr Thr Ala Thr Thr Ser Gly
130 135 140

ITI-08-PCT_Sequence_Listing_ST25.txt

Thr Thr Asn Ile Thr Leu Ser Pro Thr Ser Gln Pro Gly Arg Lys Ser
145 150 155 160

Thr Phe Asp Ala Ala Ser Phe Ile Gly Gly Ile Val Leu Ile Leu Gly
165 170 175

Val Gln Ala Val Ile Phe Phe Leu Tyr Lys Phe Cys Lys Ser Lys Glu
180 185 190

Arg Asn Tyr His Thr Leu
195

<210> 79

<211> 195

<212> PRT

<213> Rattus norvegicus

<400> 79

Met Ser Gly Ala Ser Arg Gly Leu Phe Trp Ala Ala Thr Cys Leu Ala
1 5 10 15

Ala Leu Cys Leu Ser Ala Ala Gln Ser Asn Ser Ser Ala Ser Pro Asn
20 25 30

Val Thr Asp Pro Pro Thr Thr Thr Ser Lys Val Val Pro Thr Thr Leu
35 40 45

Thr Thr Thr Lys Pro Pro Glu Thr Cys Glu Ser Phe Asn Ser Cys Val
50 55 60

Ser Cys Val Asn Ala Thr Leu Thr Asn Asn Ile Thr Cys Val Trp Leu
65 70 75 80

Asp Cys His Glu Ala Asn Lys Thr Tyr Cys Ser Ser Glu Leu Val Ser
85 90 95

Asn Cys Thr Gln Lys Thr Ser Thr Asp Ser Cys Ser Val Ile Pro Thr
100 105 110

Thr Pro Val Pro Thr Asn Ser Thr Ala Lys Pro Thr Thr Arg Pro Ser
115 120 125

Ser Pro Thr Pro Thr Pro Ser Val Val Thr Ser Ala Gly Ala Thr Asn
130 135 140

Thr Thr Val Thr Pro Thr Ser Gln Pro Glu Arg Lys Ser Thr Phe Asp
145 150 155 160

Ala Ala Ser Phe Ile Gly Gly Ile Val Leu Val Leu Gly Val Gln Ala
165 170 175

ITI-08-PCT_Sequence_Listing_ST25.txt

Val Ile Phe Phe Leu Tyr Lys Phe Cys Lys Ser Lys Glu Arg Asn Tyr
180 185 190

His Thr Leu
195

<210> 80
<211> 354
<212> PRT
<213> Homo sapiens

<400> 80

Met Arg Leu Ala Val Leu Phe Ser Gly Ala Leu Leu Gly Leu Leu Ala
1 5 10 15

Ala Gln Gly Thr Gly Asn Asp Cys Pro His Lys Lys Ser Ala Thr Leu
20 25 30

Leu Pro Ser Phe Thr Val Thr Pro Thr Val Thr Glu Ser Thr Gly Thr
35 40 45

Thr Ser His Arg Thr Thr Lys Ser His Lys Thr Thr Thr His Arg Thr
50 55 60

Thr Thr Thr Gly Thr Thr Ser His Gly Pro Thr Thr Ala Thr His Asn
65 70 75 80

Pro Thr Thr Thr Ser His Gly Asn Val Thr Val His Pro Thr Ser Asn
85 90 95

Ser Thr Ala Thr Ser Gln Gly Pro Ser Thr Ala Thr His Ser Pro Ala
100 105 110

Thr Thr Ser His Gly Asn Ala Thr Val His Pro Thr Ser Asn Ser Thr
115 120 125

Ala Thr Ser Pro Gly Phe Thr Ser Ser Ala His Pro Glu Pro Pro Pro
130 135 140

Pro Ser Pro Ser Pro Ser Pro Thr Ser Lys Glu Thr Ile Gly Asp Tyr
145 150 155 160

Thr Trp Thr Asn Gly Ser Gln Pro Cys Val His Leu Gln Ala Gln Ile
165 170 175

Gln Ile Arg Val Met Tyr Thr Thr Gln Gly Gly Gly Glu Ala Trp Gly
180 185 190

Ile Ser Val Leu Asn Pro Asn Lys Thr Lys Val Gln Gly Ser Cys Glu
195 200 205

ITI-08-PCT_Sequence_Listing_ST25.txt

Gly Ala His Pro His Leu Leu Leu Ser Phe Pro Tyr Gly His Leu Ser
210 215 220

Phe Gly Phe Met Gln Asp Leu Gln Gln Lys Val Val Tyr Leu Ser Tyr
225 230 235 240

Met Ala Val Glu Tyr Asn Val Ser Phe Pro His Ala Ala Gln Trp Thr
245 250 255

Phe Ser Ala Gln Asn Ala Ser Leu Arg Asp Leu Gln Ala Pro Leu Gly
260 265 270

Gln Ser Phe Ser Cys Ser Asn Ser Ser Ile Ile Leu Ser Pro Ala Val
275 280 285

His Leu Asp Leu Leu Ser Leu Arg Leu Gln Ala Ala Gln Leu Pro His
290 295 300

Thr Gly Val Phe Gly Gln Ser Phe Ser Cys Pro Ser Asp Arg Ser Ile
305 310 315 320

Leu Leu Pro Leu Ile Ile Gly Leu Ile Leu Leu Gly Leu Leu Ala Leu
325 330 335

Val Leu Ile Ala Phe Cys Ile Ile Arg Arg Arg Pro Ser Ala Tyr Gln
340 345 350

Ala Leu

<210> 81

<211> 354

<212> PRT

<213> Pan troglodytes

<400> 81

Met Arg Leu Ala Val Leu Phe Ser Gly Ala Leu Leu Gly Leu Leu Ala
1 5 10 15

Ala Gln Gly Thr Gly Asn Asp Cys Pro His Lys Lys Ser Ala Thr Leu
20 25 30

Leu Pro Ser Phe Thr Val Thr Pro Thr Val Thr Glu Ser Thr Gly Thr
35 40 45

Thr Ser His Arg Thr Thr Lys Ser His Lys Thr Thr Thr His Arg Thr
50 55 60

Thr Thr Thr Gly Thr Ala Ser His Gly Pro Thr Thr Ala Thr His Asn
65 70 75 80

Pro Thr Thr Thr Ser His Gly Asn Val Thr Val His Pro Thr Ser Asn

ITI-08-PCT_Sequence_Listing_ST25.txt

85

90

95

Ser Thr Ala Thr Ser Gln Gly Pro Ser Thr Ala Thr His Ser Pro Ala
 100 105 110

Thr Thr Ser His Gly Asn Ala Thr Val His Pro Thr Ser Asn Ser Thr
 115 120 125

Ala Thr Ser Pro Gly Phe Thr Ser Ser Ala His Pro Glu Pro Pro Pro
 130 135 140

Pro Ser Pro Ser Pro Ser Pro Thr Ser Lys Glu Thr Ile Gly Asp Tyr
 145 150 155 160

Thr Trp Thr Asn Gly Ser Gln Pro Cys Val His Leu Gln Ala Gln Ile
 165 170 175

Gln Ile Arg Val Met Tyr Thr Thr Gln Gly Gly Gly Glu Ala Trp Gly
 180 185 190

Ile Ser Val Leu Asn Pro Asn Lys Thr Lys Val Gln Gly Ser Cys Glu
 195 200 205

Gly Ala His Pro His Leu Leu Leu Ser Phe Pro Tyr Gly His Leu Ser
 210 215 220

Phe Gly Phe Met Gln Asp Leu Gln Gln Lys Ala Val Tyr Leu Ser Tyr
 225 230 235 240

Met Ala Val Glu Tyr Asn Val Ser Phe Pro His Ala Ala Gln Trp Thr
 245 250 255

Phe Ser Ala Gln Asn Ala Ser Leu Arg Asp Leu Gln Ala Pro Leu Gly
 260 265 270

Arg Ser Phe Ser Cys Ser Asn Ser Ser Ile Ile Leu Ser Pro Ala Val
 275 280 285

His Leu Asp Leu Leu Ser Leu Arg Leu Gln Ala Ala Gln Leu Pro His
 290 295 300

Thr Gly Val Phe Gly Gln Ser Phe Ser Cys Pro Ser Asp Arg Ser Ile
 305 310 315 320

Leu Leu Pro Leu Ile Ile Gly Leu Ile Leu Leu Gly Leu Leu Ala Leu
 325 330 335

Val Leu Ile Ala Phe Cys Ile Ile Arg Arg Arg Pro Ser Ala Tyr Gln
 340 345 350

Ala Leu

ITI-08-PCT_Sequence_Listing_ST25.txt

<210> 82

<211> 335

<212> PRT

<213> Bos taurus

<400> 82

Met Arg Leu Ala Val Phe Phe Ser Gly Ala Leu Leu Gly Leu Leu Ala
1 5 10 15

Ala Gln Gly Thr Gly Asn Asp Cys Pro His Lys Lys Ser Ala Thr Leu
20 25 30

Leu Pro Ser Phe Thr Val Thr Pro Thr Ala Thr Glu Ser Thr Pro Ser
35 40 45

Pro Gly Thr Thr Ser His Arg Thr Thr Lys Ser His Arg Thr Thr Thr
50 55 60

Trp Arg Ile Ser Thr Thr Thr His Thr Thr Asn Thr Thr Gly Thr Thr
65 70 75 80

Ser Ser Glu Ser Pro Thr Ala Thr His Ser Pro Ala Thr Thr Thr Ser
85 90 95

His Gln Asn Thr Thr Val His Pro Thr Ser Asn Ile Thr Ala Thr Ser
100 105 110

Pro Gly Pro Ser Thr Arg Ser Pro His Pro Glu Pro Pro Pro Ser Pro
115 120 125

Ser Pro Ser Pro Gly Ser Lys Glu Ala Ile Gly Asp Tyr Thr Trp Ser
130 135 140

Asn Gly Ser Gln Pro Cys Val Arg Leu Gln Ala Gln Ile Gln Ile Arg
145 150 155 160

Val Leu Tyr Pro Thr Gln Gly Gly Gly Glu Ala Trp Gly Ile Ser Val
165 170 175

Leu Asn Pro Asn Arg Thr Lys Ala Gln Gly Gly Cys Glu Gly Thr His
180 185 190

Ser His Leu Leu Leu Ser Phe Pro Ser Gly Gln Leu Ser Phe Gly Phe
195 200 205

Lys Gln Asp Pro Leu Gln Ser Ala Val Tyr Leu Asn Tyr Met Ala Val
210 215 220

Glu Tyr Asn Val Ser Phe Pro Gln Ala Val Gln Trp Thr Phe Ser Val
225 230 235 240

ITI-08-PCT_Sequence_Listing_ST25.txt

Gln Asn Ser Ser Leu Arg Asp Leu Gln Thr Pro Leu Gly His Ser Phe
245 250 255

Ser Cys Arg Asn Ala Ser Ile Ile Val Ser Pro Ala Leu His Leu Asp
260 265 270

Leu Leu Ser Leu Lys Leu Gln Ala Ala Gln Leu Ser Pro Ser Gly Ala
275 280 285

Phe Gly Pro Ser Phe Ser Cys Pro Asn Asp Lys Ser Ile Leu Leu Pro
290 295 300

Leu Ile Ile Gly Leu Ile Leu Leu Gly Leu Leu Thr Leu Val Leu Val
305 310 315 320

Thr Phe Cys Ile Ile Arg Arg Arg Pro Pro Thr Tyr Gln Pro Leu
325 330 335

<210> 83

<211> 335

<212> PRT

<213> Mus musculus

<400> 83

Met Arg Leu Pro Val Cys Leu Ile Leu Leu Gly Pro Leu Ile Ala Gln
1 5 10 15

Gly Thr Glu Glu Asp Cys Pro His Lys Lys Ala Val Thr Leu Leu Pro
20 25 30

Ser Phe Thr Met Thr Pro Thr Ala Thr Glu Ser Thr Ala Ser Pro Thr
35 40 45

Thr Ser His Arg Pro Thr Thr Thr Ser His Gly Asn Val Thr Val His
50 55 60

Thr Ser Ser Gly Pro Thr Thr Val Thr His Asn Pro Ala Thr Thr Thr
65 70 75 80

Ser His Gly Asn Ala Thr Ile Ser His Ala Thr Val Ser Pro Thr Thr
85 90 95

Asn Gly Thr Ala Thr Ser Pro Arg Ser Ser Thr Val Gly Pro His Pro
100 105 110

Gly Pro Pro Pro Pro Ser Pro Ser Pro Arg Ser Lys Gly Ala Leu Gly
115 120 125

Asn Tyr Thr Trp Ala Asn Gly Ser Gln Pro Cys Val Gln Leu Gln Ala
130 135 140

ITI-08-PCT_Sequence_Listing_ST25.txt

Gln Ile Gln Ile Arg Ile Leu Tyr Pro Ile Gln Gly Gly Arg Lys Val
145 150 155 160

Lys Leu Lys Trp Gly Leu Lys Arg Ala Trp Gly Ile Ser Val Leu Asn
165 170 175

Pro Asn Lys Thr Lys Val Gln Gly Gly Cys Asp Gly Thr His Pro His
180 185 190

Leu Ser Leu Ser Phe Pro Tyr Gly Gln Leu Thr Phe Gly Phe Lys Gln
195 200 205

Asp Leu His Gln Ser Pro Ser Thr Val Tyr Leu Asp Tyr Met Ala Val
210 215 220

Glu Tyr Asn Val Ser Phe Pro Gln Ala Ala Gln Trp Thr Phe Met Ala
225 230 235 240

Gln Asn Ser Ser Leu Arg Glu Leu Gln Ala Pro Leu Gly Gln Ser Phe
245 250 255

Cys Cys Gly Asn Ala Ser Ile Val Leu Ser Pro Ala Val His Leu Asp
260 265 270

Leu Leu Ser Leu Arg Leu Gln Ala Ala Gln Leu Pro Asp Lys Gly His
275 280 285

Phe Gly Pro Cys Phe Ser Cys Asn Arg Asp Gln Ser Leu Leu Leu Pro
290 295 300

Leu Ile Ile Gly Leu Val Leu Leu Gly Leu Leu Thr Leu Val Leu Ile
305 310 315 320

Ala Phe Cys Ile Thr Arg Arg Arg Gln Ser Thr Tyr Gln Pro Leu
325 330 335

<210> 84

<211> 354

<212> PRT

<213> Macaca mulatta

<400> 84

Met Arg Leu Ala Val Leu Phe Leu Gly Ala Leu Leu Gly Leu Leu Ala
1 5 10 15

Ala Gln Gly Thr Gly Asn Asp Cys Pro His Lys Lys Ser Ala Thr Leu
20 25 30

Leu Pro Ser Phe Thr Val Thr Pro Thr Ala Thr Glu Ser Thr Gly Thr
35 40 45

ITI-08-PCT_Sequence_Listing_ST25.txt

```

Thr Ser His Arg Thr Thr Lys Ser His Lys Thr Thr Thr His Arg Thr
50                    55                    60

Thr Thr Thr Gly Thr Thr Ser His Arg Pro Thr Thr Ala Thr His Asn
65                    70                    75                    80

Pro Thr Thr Thr Ser His Arg Asn Ala Thr Val His Pro Thr Ser Asn
85                    90                    95

Ser Thr Ala Thr Ser Gln Gly Pro Ser Thr Ala Thr His Arg Pro Ala
100                   105                   110

Thr Thr Ser His Gly Asn Ala Thr Val His Pro Thr Ser Asn Ser Thr
115                   120                   125

Ala Thr Ser Pro Gly Leu Thr Ser Ser Ala His Pro Gly Pro Pro Pro
130                   135                   140

Pro Ser Pro Ser Pro Ser Pro Ala Ser Lys Glu Thr Ile Gly Asp Tyr
145                   150                   155                   160

Met Trp Thr Asn Gly Ser Gln Pro Cys Val His Leu Gln Ala Gln Ile
165                   170                   175

Gln Ile Arg Val Met Tyr Thr Thr Gln Gly Gly Gly Glu Ala Trp Gly
180                   185                   190

Ile Ser Val Leu Asn Pro Asn Lys Thr Lys Val Gln Gly Ser Cys Glu
195                   200                   205

Gly Ala His Pro His Leu Leu Leu Ser Phe Pro Tyr Gly His Leu Ser
210                   215                   220

Phe Gly Phe Met Gln Asp Leu Gln Gln Arg Val Val Tyr Leu Ser Tyr
225                   230                   235                   240

Met Ala Val Glu Tyr Asn Val Ser Phe Pro His Ala Ala Gln Trp Thr
245                   250                   255

Phe Ser Ala Gln Asn Ala Ser Leu Arg Asp Leu Gln Ala Pro Leu Gly
260                   265                   270

Gln Ser Phe Ser Cys Ser Asn Ser Ser Ile Ile Leu Ser Pro Ala Val
275                   280                   285

His Leu Asp Leu Leu Ser Leu Arg Leu Gln Ala Ala Gln Leu Pro His
290                   295                   300

Thr Gly Val Phe Gly Gln Ser Phe Ser Cys Pro Ser Asp Arg Ser Ile
305                   310                   315                   320

Leu Leu Pro Leu Ile Ile Gly Leu Val Leu Leu Gly Leu Leu Ala Leu

```

ITI-08-PCT_Sequence_Listing_ST25.txt

325 330 335

Val Leu Ile Ala Phe Cys Ile Val Arg Arg Arg Pro Ser Ala Tyr Gln
340 345 350

Ala Leu

<210> 85

<211> 330

<212> PRT

<213> Rattus norvegicus

<400> 85

Met Arg Phe Pro Val Cys Leu Thr Leu Leu Val Leu Leu Val Ala Gln
1 5 10 15

Gly Thr Gly Lys Asp Cys Pro His Lys Lys Ala Ala Thr Leu Leu Pro
20 25 30

Ser Phe Thr Glu Thr Pro Thr Thr Thr Gly Ser Thr Ala Ser Pro Thr
35 40 45

Thr Thr His Arg Pro Thr Thr Thr Ser His Arg Pro Thr Thr Thr Ser
50 55 60

His Arg Pro Thr Thr Thr Ser His Arg Pro Thr Thr Thr Ser His Arg
65 70 75 80

Pro Thr Thr Thr Ser His Arg Pro Thr Thr Thr Ser His Gly Asn Ala
85 90 95

Thr Val Ser Pro Thr Thr Asn Ser Pro Gly Phe Ser Thr Val Gly Pro
100 105 110

His Pro Gly Pro Pro Pro Pro Ser Pro Ser Pro Ser Pro Ser Ser Thr
115 120 125

Gly Ala Leu Gly Asn Tyr Thr Trp Thr Asn Gly Ser Gln Pro Cys Val
130 135 140

Gln Leu Gln Ala Gln Ile Gln Ile Arg Ile Leu Tyr Leu Thr Gln Gly
145 150 155 160

Gly Lys Lys Ala Trp Gly Leu Ser Val Leu Asn Pro Asn Lys Thr Lys
165 170 175

Val Gln Gly Gly Cys Asp Ser Ala His Pro His Leu Ala Leu Ser Phe
180 185 190

Pro Tyr Gly Gln Leu Thr Phe Gly Phe Lys Gln Asp Arg His Gln Ser
195 200 205

ITI-08-PCT_Sequence_Listing_ST25.txt

His Ser Thr Val Tyr Leu Asn Tyr Met Ala Val Glu Tyr Asn Val Ser
210 215 220

Phe Pro Gln Ala Ala Gln Trp Thr Phe Ser Ala Gln Asn Ser Ser Leu
225 230 235 240

Gln Glu Leu Gln Ala Pro Leu Gly Gln Ser Phe Cys Cys Gly Asn Thr
245 250 255

Ser Ile Val Leu Ser Pro Ala Ile His Leu Asp Leu Leu Ser Leu Arg
260 265 270

Leu Gln Ala Ala Gln Leu Pro Asp Lys Gly His Phe Gly Pro Cys Phe
275 280 285

Ser Cys Ala Ser Asp Gln Ser Leu Leu Leu Pro Leu Ile Ile Gly Leu
290 295 300

Val Leu Leu Gly Leu Leu Thr Leu Val Leu Ile Ala Phe Cys Val Thr
305 310 315 320

Arg Arg Arg Gln Ser Thr Tyr Gln Pro Leu
325 330

<210> 86

<211> 329

<212> PRT

<213> Canis lupus familiaris

<400> 86

Met Arg Pro Ala Val Phe Phe Leu Gly Ala Leu Val Gly Leu Leu Ala
1 5 10 15

Ala Gln Gly Thr Arg Ser Asp Cys Pro His Lys Lys Ser Ala Thr Leu
20 25 30

Leu Pro Ser Phe Thr Val Thr Pro Thr Ala Thr Glu Ser Thr Gly Ser
35 40 45

Pro Gly Thr Thr Ser His Ser Thr Thr Thr Ala Glu Thr Thr Ser His
50 55 60

Ala Pro Asn Thr Thr Thr His Gln Ala Pro Thr Thr Pro Gly His Arg
65 70 75 80

Asn Thr Thr Ile His Pro Thr Thr Ser Asn Ser Thr Ser Asn Thr Thr
85 90 95

Gly Thr Thr Gly Thr Gly Lys Pro His Thr Ser Thr Ser Tyr Thr Gln
100 105 110

ITI-08-PCT_Sequence_Listing_ST25.txt

Pro Gly Pro Gly Pro Arg Pro Pro Pro Pro Ser Pro Gly Pro Gly Pro
115 120 125

Gln Asp Ala Ile Gly Asp Tyr Thr Trp Thr Thr Gly Ser Gln Pro Cys
130 135 140

Ala Arg Leu Gln Ala Arg Ile Gln Ile Gly Val Val Tyr Pro Thr Gln
145 150 155 160

Ala Gly Gly Gln Ala Trp Gly Ile Ser Val Leu Asn Pro Asn Ser Thr
165 170 175

Lys Pro Trp Gly Asp Cys Asp Gly Ala Arg Pro His Leu Leu Leu Ser
180 185 190

Phe Pro Phe Gly Gln Leu Ser Phe Gly Phe Thr Gln Glu Pro Gln Gln
195 200 205

Gly Ser Val Tyr Leu Asp Tyr Leu Ala Leu Gln Tyr Asn Val Ser Phe
210 215 220

Pro Gln Ala Ala Gln Trp Thr Phe Ser Gly Gln Asn Ala Ser Leu Arg
225 230 235 240

Ala Leu Gln Ala Pro Leu Gly Gln Ser Phe Ser Cys Arg Asn Ala Ser
245 250 255

Ile Leu Leu Thr Pro Ala Leu Arg Leu Asp Leu Leu His Leu Lys Leu
260 265 270

Gln Ala Ala Gln Leu Pro Pro Ser Gly Ala Phe Gly Pro Ser Phe Ser
275 280 285

Cys Pro Ser Glu His Phe Asn Leu Leu Pro Leu Ile Val Gly Val Ile
290 295 300

Ser Leu Gly Leu Leu Ala Leu Ala Leu Val Thr Phe Cys Ile Ile Arg
305 310 315 320

Arg Arg Pro Pro Thr Tyr Gln Pro Leu
325

<210> 87

<211> 322

<212> PRT

<213> Equus caballus

<400> 87

Met Arg Leu Ala Val Leu Phe Ser Gly Ala Leu Leu Gly Leu Leu Ala
1 5 10 15

ITI-08-PCT_Sequence_Listing_ST25.txt

Ala	Gln	Glu	Thr	Gly	Asn	Asp	Cys	Pro	His	Lys	Lys	Ser	Ala	Thr	Leu	20	25	30
Leu	Pro	Ser	Phe	Thr	Val	Thr	Pro	Thr	Ala	Thr	Glu	Ser	Thr	Ala	Ser	35	40	45
Pro	Gly	Thr	Thr	Ser	His	Gln	Thr	Thr	Gln	Ser	His	Arg	Thr	Thr	Thr	50	55	60
Thr	Gly	Thr	Thr	Ser	Asp	His	Pro	Thr	Thr	Ala	Thr	His	Asn	Pro	Thr	65	70	75
Thr	Thr	Ser	His	Gly	Asn	Thr	Thr	Val	His	Pro	Thr	Thr	Ser	Asn	Ser	85	90	95
Thr	Val	Thr	Ser	Pro	Gly	Ser	Ala	Ser	Ser	Ser	Pro	His	Pro	Arg	Pro	100	105	110
Pro	Pro	Pro	Ser	Pro	Ser	Pro	Ser	Pro	Gly	Ser	Lys	Glu	Ala	Ile	Gly	115	120	125
Asp	Tyr	Ile	Trp	Thr	Asn	Gly	Ser	Gln	Pro	Cys	Val	Arg	Leu	Gln	Ala	130	135	140
Gln	Ile	Gln	Ile	Arg	Val	Leu	Tyr	Pro	Thr	Leu	Gly	Gly	Gly	Lys	Ala	145	150	155
Trp	Gly	Ile	Ser	Val	Leu	Asn	Pro	Asn	Lys	Thr	Lys	Ala	Gln	Gly	Gly	165	170	175
Cys	Ala	His	Pro	His	Leu	Leu	Leu	Ser	Phe	Pro	Tyr	Gly	Gln	Leu	Ser	180	185	190
Phe	Gly	Phe	Lys	Gln	Glu	Pro	Leu	Gln	Ser	Thr	Val	Tyr	Leu	Asn	Tyr	195	200	205
Ile	Ala	Val	Glu	Tyr	Asn	Val	Ser	Phe	Pro	Gln	Ala	Ala	Gln	Trp	Thr	210	215	220
Phe	Leu	Val	Gln	Asn	Ser	Ser	Leu	Arg	Asp	Leu	Gln	Ala	Pro	Leu	Gly	225	230	235
Gln	Arg	Phe	Ser	Cys	Arg	Asn	Ala	Ser	Ile	Ala	Leu	Ser	Pro	Ala	Phe	245	250	255
His	Leu	Asp	Leu	Leu	Ser	Leu	Lys	Leu	Gln	Ala	Ala	Gln	Leu	Thr	Pro	260	265	270
Thr	Gly	Ala	Phe	Gly	Pro	Ser	Phe	Ser	Cys	Pro	Ser	Asp	Gln	Ser	Ile	275	280	285

ITI-08-PCT_Sequence_Listing_ST25.txt

Leu Leu Pro Leu Ile Ile Gly Leu Ile Leu Leu Gly Leu Phe Ala Leu
290 295 300

Val Leu Ile Thr Phe Cys Val Ile Arg Arg Arg Pro Pro Thr Tyr Gln
305 310 315 320

Ala Leu

<210> 88

<211> 305

<212> PRT

<213> Oryctolagus cuniculus

<400> 88

Met Arg Leu Pro Val Leu Phe Leu Ala Leu Leu Gly Leu His Ala Ala
1 5 10 15

Ser Ser Gly Thr Thr Ser His Arg Thr Thr Lys Asn Pro His Thr Thr
20 25 30

Ser His Ser Thr Ala Thr Pro Gly Thr Thr Ser His Arg Pro Thr Thr
35 40 45

Ala Thr Pro Thr Thr Gly His Gly Asn Val Thr Val His Pro Thr Thr
50 55 60

Ser Asn Thr Thr Ser Asn Thr Thr Thr Thr Thr Gly Thr Ser Pro Gly
65 70 75 80

Phe Ser Thr Ser Thr Pro His Pro Gly Pro Pro Pro Pro Pro Pro Ser
85 90 95

Pro Ser Pro Gly Ser Arg Glu Ala Val Gly Asn Tyr Thr Trp Thr Asn
100 105 110

Gly Ser Gln Pro Cys Val Gln Leu Gln Ala Gln Ile Gln Ile Arg Val
115 120 125

Leu Tyr Pro Thr Gln Gly Gly Gly Gln Ala Trp Gly Met Ser Val Leu
130 135 140

Asn Pro Asn Arg Thr Lys Ala Gln Gly Gly Cys Glu Gly Pro Arg Pro
145 150 155 160

His Leu Leu Leu Ser Phe Pro Tyr Gly Gln Leu Ser Phe Gly Phe Lys
165 170 175

Gln Asp Pro Gly Gln Gly Gln Ser Ala Val Tyr Leu Ser Tyr Leu Ala
180 185 190

Val Glu Tyr Asn Val Ser Phe Pro Gln Ala Ala Arg Trp Thr Phe Ser

ITI-08-PCT_Sequence_Listing_ST25.txt

195

200

205

Ala Gln Asn Ala Ser Leu Arg Asp Leu Gln Ala Pro Leu Gly Gln Ser
210 215 220

Phe Ser Cys Arg Asn Ala Ser Ile Ala Val Ser Pro Ala Leu His Leu
225 230 235 240

Asp Leu Leu Ser Leu Arg Val Gln Ala Ala Gln Leu Pro Arg Thr Gly
245 250 255

Ile Phe Gly Pro Ser Phe Ser Cys Pro Ala Asp His Pro Ser Ile Leu
260 265 270

Val Pro Leu Ile Ile Gly Leu Ile Leu Val Gly Leu Leu Ala Leu Val
275 280 285

Leu Val Ala Phe Cys Ile Ala Arg Arg Arg Pro Ser Ala Tyr Gln Ala
290 295 300

Leu
305

<210> 89

<211> 291

<212> PRT

<213> Sus scrofa

<400> 89

Met Thr Leu Ala Val Leu Phe Leu Gly Ala Leu Leu Gly Leu Leu Ala
1 5 10 15

Glu Ser Thr Thr Ser His Arg Thr Thr Thr Pro Arg Thr Thr Thr Thr
20 25 30

Gly Thr Thr Ser His Gly Pro Thr Thr Val Thr His Asn Pro Ala Thr
35 40 45

Thr Thr Ser His Gly Asn Ala Thr Val His Pro Thr Ser Ser Ser Thr
50 55 60

Ala Thr Ser Pro Gly Ser Ser Thr Arg Pro Pro His Pro Gly Pro Pro
65 70 75 80

Pro Pro Ser Pro Ser Pro Ser Pro Gly Ser Gln Glu Ala Ile Gly Asp
85 90 95

Tyr Thr Trp Thr Asn Gly Ser Gln Pro Cys Val Gln Leu Gln Ala Gln
100 105 110

Ile Gln Ile Arg Val Leu Tyr Pro Thr Gln Gly Gly Gly Glu Ala Trp

ITI-08-PCT_Sequence_Listing_ST25.txt

```

115              120              125
Gly Ile Ser Val Leu Asn Pro Asn Lys Thr Lys Ala Leu Gly Gly Cys
130              135              140
Glu Gly Ala His Pro His Val Arg Leu Ser Phe Pro Tyr Gly Gln Leu
145              150              155              160
Thr Phe Gly Phe Lys Gln Gln Pro Gln Glu Ser Thr Val Tyr Leu Asn
165              170              175
Tyr Met Ala Val Glu Tyr Asn Val Ser Phe Pro Arg Ala Ala Gln Trp
180              185              190
Thr Phe Ser Val Gln Asn Ser Ser Leu Arg Asp Leu Gln Thr Pro Val
195              200              205
Gly Arg Ser Tyr Ser Cys Arg Asn Ala Ser Ile Ile Leu Ser Thr Ala
210              215              220
Phe His Leu Asp Leu Leu Ser Leu Lys Leu Gln Ala Ala Gln Leu Pro
225              230              235              240
Pro Thr Gly Asn Phe Gly Pro Ser Phe Ser Cys Pro Ser Asp Gln Thr
245              250              255
Ile Leu Leu Pro Leu Ile Ile Gly Leu Ile Phe Leu Gly Leu Leu Ile
260              265              270
Leu Val Leu Val Thr Phe Cys Ile Ile Arg Arg Arg Pro Pro Ala Tyr
275              280              285
Gln Pro Leu
290

```

```

<210> 90
<211> 354
<212> PRT
<213> Papio anubis

```

```

<400> 90

```

```

Met Arg Leu Ala Val Leu Phe Ser Gly Ala Leu Leu Gly Leu Leu Ala
1      5      10      15
Ala Gln Gly Thr Gly Asn Asp Cys Pro His Lys Lys Ser Ala Thr Leu
20     25     30
Leu Pro Ser Phe Thr Val Thr Pro Thr Ala Thr Glu Ser Thr Gly Thr
35     40     45
Thr Ser His Arg Thr Thr Lys Ser His Lys Thr Thr Thr His Arg Thr

```

50					55					60				
Thr	Thr	Gly	Thr	Thr	Ser	His	Arg	Pro	Thr	Thr	Ala	Thr	His	Asn
				70					75					
Asn	Thr	Thr	Ser	His	Arg	Asn	Ala	Thr	Val	His	Pro	Thr	Ser	Asn
				85					90					
Thr	Ala	Thr	Ser	Gln	Gly	Pro	Ser	Thr	Ala	Thr	His	Arg	Pro	Ala
				100					105					
Thr	Ser	His	Gly	Asn	Ala	Thr	Val	His	Pro	Thr	Ser	Asn	Ser	Thr
				115					120					
Thr	Ser	Pro	Gly	Leu	Thr	Ser	Ser	Ala	His	Pro	Gly	Pro	Pro	Pro
				130					135					
Ser	Pro	Ser	Pro	Ser	Pro	Ala	Ser	Lys	Glu	Thr	Ile	Gly	Asp	Tyr
				150					155					
Trp	Thr	Asn	Gly	Ser	Gln	Pro	Cys	Val	His	Leu	Gln	Ala	Gln	Ile
				165					170					
Ile	Arg	Val	Met	Tyr	Thr	Thr	Gln	Gly	Gly	Gly	Glu	Ala	Trp	Gly
				180					185					
Ser	Val	Leu	Asn	Pro	Asn	Lys	Thr	Lys	Val	Gln	Gly	Ser	Cys	Glu
				195					200					
Ala	His	Pro	His	Leu	Leu	Leu	Ser	Phe	Pro	Tyr	Gly	His	Leu	Ser
				210					215					
Gly	Phe	Met	Gln	Asp	Leu	Gln	Gln	Arg	Val	Val	Tyr	Leu	Ser	Tyr
				230					235					
Ala	Val	Glu	Tyr	Asn	Val	Ser	Phe	Pro	His	Ala	Ala	Gln	Trp	Thr
				245					250					
Ser	Ala	Gln	Asn	Ala	Ser	Leu	Arg	Asp	Leu	Gln	Ala	Pro	Leu	Gly
				260					265					
Ser	Phe	Ser	Cys	Ser	Asn	Ser	Ser	Ile	Ile	Leu	Ser	Pro	Ala	Val
				275					280					
Leu	Asp	Leu	Leu	Ser	Leu	Arg	Leu	Gln	Ala	Ala	Gln	Leu	Pro	His
				290					295					
Gly	Val	Phe	Gly	Gln	Ser	Phe	Ser	Cys	Pro	Ser	Asp	Arg	Ser	Ile
				310					315					
Leu	Pro	Leu	Ile	Ile	Gly	Leu	Val	Leu	Leu	Gly	Leu	Leu	Ala	Leu
				325					330					

ITI-08-PCT_Sequence_Listing_ST25.txt

Val Leu Ile Ala Phe Cys Ile Val Arg Arg Arg Pro Ser Ala Tyr Gln
340 345 350

Ala Leu

<210> 91

<211> 323

<212> PRT

<213> Monodelphis domestica

<400> 91

Met Arg Leu Ser Leu Leu Leu Ser Gly Ile Leu Leu Gly Leu Leu Ala
1 5 10 15

Glu Gln Gly Ala Gly Asp Lys Cys Pro Gln Glu Lys Ser Val Thr Leu
20 25 30

Val Pro Ser Phe Thr Val Thr Thr Ile Ala Thr Glu Arg Ser Thr Thr
35 40 45

Ser Pro Glu Thr Thr Thr Ser Ser Gly Ser Thr Ala Thr Thr Tyr Arg
50 55 60

Thr Ser Thr Ala Ala Thr Thr Pro His Ser Asn Ser Thr Ala Thr Ser
65 70 75 80

Tyr Ser Thr Thr Ser Glu Gly Thr Ala Val Thr His Gly Thr Thr Thr
85 90 95

Ser Pro Arg Asn Thr Ser Thr Thr Ser Thr Ser Gln Ser Val Pro Val
100 105 110

Pro Pro Ser Pro Gln Pro Thr Ser Ser Pro Ser Gly Ala Val Gly Asp
115 120 125

Tyr Ile Gly Ala Asn Gly Ser Gln Leu Cys Val His Leu Arg Ala Gln
130 135 140

Ile Gln Met Arg Val Leu Tyr Gln Ala Ser Gly Gly Gly Lys Leu Trp
145 150 155 160

Gly Ile Phe Val Leu Asn Pro Asn Arg Thr Met Ala Gln Gly Asn Cys
165 170 175

Glu Ala Asn His Ser Ser Leu Ile Leu Ser Phe Pro Asn Gly Lys Leu
180 185 190

Ile Phe Gly Phe Lys Gln Asp Ser Ile Lys Lys Ile Val Tyr Leu Ser
195 200 205

ITI-08-PCT_Sequence_Listing_ST25.txt

His Leu Ala Thr Glu Phe Asn Val Ser Phe Pro Ser Ala Thr Arg Trp
210 215 220

Ile Phe Ser Val Glu Asn Ser Ser Leu Gln Asp Leu Gln Thr Pro Leu
225 230 235 240

Gly His Ser Phe Ser Cys Arg Asn Arg Ser Ile Ala Leu Ser Pro Asp
245 250 255

Ile His Leu Asp Leu Leu Ser Leu Gln Leu Gln Ala Ala Gln Leu Ser
260 265 270

Ser Ser Gly Ala Phe Gly Ala Ala Phe Ser Cys Ser Ala Asp Leu Asn
275 280 285

Ile Leu Val Pro Leu Val Val Gly Leu Val Leu Leu Thr Leu Leu Ile
290 295 300

Leu Val Leu Ser Ala Phe Cys Ile Ser Arg Arg Arg Pro Pro Ala Tyr
305 310 315 320

Gln Pro Leu

<210> 92

<211> 263

<212> PRT

<213> Ornithorhynchus anatinus

<400> 92

Met Gly Leu Thr Leu Pro Leu Pro Ala Gln Gly Ser Gln Cys Arg Ala
1 5 10 15

Asn Cys Pro His Lys Lys Ser Ala Thr Leu Val Pro Ser Phe Thr Val
20 25 30

Thr Pro Thr Ala Thr Ser Gly Pro Thr Thr Thr Ala His Gln Thr Thr
35 40 45

Thr Asp His Gly Thr Thr Thr Ser His Glu Thr Thr Thr Ser Gln Gly
50 55 60

Thr Ser Thr His Gly Thr Ser Thr Pro His Thr Thr Thr Thr Gly His
65 70 75 80

Gly Thr Thr Thr Gly His Gln Asn Thr Ser His Ser Thr Thr Thr Ser
85 90 95

His Gly Thr Ser Thr Pro His Lys Thr Thr Thr Arg His Pro Thr Thr
100 105 110

Ser His Gly Thr Thr Thr Ser His Gly Thr Ser Thr Gly His Trp Thr

ITI-08-PCT_Sequence_Listing_ST25.txt

```

115              120              125
Ala Arg Pro Thr Ile Arg Pro Gly Pro Pro Pro Pro Pro Pro Ser Pro
130              135              140
Gly Lys Ala Val Gly Asn Tyr Thr Val Phe Asn Gly Ser Gln Pro Cys
145              150              155              160
Leu Arg Leu Arg Ala Glu Ile Arg Leu Trp Val Leu Tyr Gln Ala Gln
165              170              175
Glu Glu Gly Glu Ala Pro Pro Val Ser Gly Ala Ala Ser Phe Pro Pro
180              185              190
Pro Arg Pro Arg Pro Val Ala Gly Glu Gly Asp Gly Glu Arg Ser Arg
195              200              205
Val Thr Pro Val Ala Ser Ala Met Thr Val Glu Gly Gly Ser Arg Ala
210              215              220
Gly Phe Ala Met Leu Gly Ala Glu Val Arg Ser Arg Ala Pro Ser Leu
225              230              235              240
Gly Arg Ala Gly Lys Thr Arg Leu Arg Ile His Gln Pro Val Val Val
245              250              255
Leu Gln His Thr Tyr Tyr Val
260

```

<210> 93
 <211> 280
 <212> PRT
 <213> Homo sapiens

<400> 93

```

Met Asp Leu Gln Gly Arg Gly Val Pro Ser Ile Asp Arg Leu Arg Val
1              5              10              15
Leu Leu Met Leu Phe His Thr Met Ala Gln Ile Met Ala Glu Gln Glu
20              25              30
Val Glu Asn Leu Ser Gly Leu Ser Thr Asn Pro Glu Lys Asp Ile Phe
35              40              45
Val Val Arg Glu Asn Gly Thr Thr Cys Leu Met Ala Glu Phe Ala Ala
50              55              60
Lys Phe Ile Val Pro Tyr Asp Val Trp Ala Ser Asn Tyr Val Asp Leu
65              70              75              80
Ile Thr Glu Gln Ala Asp Ile Ala Leu Thr Arg Gly Ala Glu Val Lys

```

ITI-08-PCT_Sequence_Listing_ST25.txt

85 90 95

Gly Arg Cys Gly His Ser Gln Ser Glu Leu Gln Val Phe Trp Val Asp
100 105 110

Arg Ala Tyr Ala Leu Lys Met Leu Phe Val Lys Glu Ser His Asn Met
115 120 125

Ser Lys Gly Pro Glu Ala Thr Trp Arg Leu Ser Lys Val Gln Phe Val
130 135 140

Tyr Asp Ser Ser Glu Lys Thr His Phe Lys Asp Ala Val Ser Ala Gly
145 150 155 160

Lys His Thr Ala Asn Ser His His Leu Ser Ala Leu Val Thr Pro Ala
165 170 175

Gly Lys Ser Tyr Glu Cys Gln Ala Gln Gln Thr Ile Ser Leu Ala Ser
180 185 190

Ser Asp Pro Gln Lys Thr Val Thr Met Ile Leu Ser Ala Val His Ile
195 200 205

Gln Pro Phe Asp Ile Ile Ser Asp Phe Val Phe Ser Glu Glu His Lys
210 215 220

Cys Pro Val Asp Glu Arg Glu Gln Leu Glu Glu Thr Leu Pro Leu Ile
225 230 235 240

Leu Gly Leu Ile Leu Gly Leu Val Ile Met Val Thr Leu Ala Ile Tyr
245 250 255

His Val His His Lys Met Thr Ala Asn Gln Val Gln Ile Pro Arg Asp
260 265 270

Arg Ser Gln Tyr Lys His Met Gly
275 280

<210> 94

<211> 280

<212> PRT

<213> Pan troglodytes

<400> 94

Met Asp Leu Arg Gly Arg Ala Val Pro Ser Ile Asp Arg Leu Arg Val
1 5 10 15

Leu Leu Met Leu Phe His Thr Met Ala Gln Ile Met Ala Glu Gln Glu
20 25 30

Val Glu Asn Leu Ser Gly Leu Ser Thr Asn Pro Glu Lys Asp Ile Phe

ITI-08-PCT_Sequence_Listing_ST25.txt

```

35          40          45
Val Val Arg Glu Asn Gly Thr Thr Cys Leu Met Ala Glu Phe Ala Ala
50          55          60

Lys Phe Ile Val Pro Tyr Asp Val Trp Ala Ser Asn Tyr Val Asp Leu
65          70          75          80

Ile Thr Glu Gln Ala Asp Ile Ala Leu Thr Arg Gly Ala Glu Val Lys
85          90          95

Gly Arg Cys Gly His Ser Glu Ser Glu Leu Gln Val Phe Trp Val Asp
100         105         110

Arg Ala Tyr Ala Leu Lys Met Leu Phe Val Lys Glu Ser His Asn Met
115         120         125

Ser Lys Gly Pro Glu Ala Thr Trp Arg Leu Ser Lys Val Gln Phe Val
130         135         140

Tyr Asp Ser Ser Glu Lys Thr His Phe Lys Asp Ala Val Ser Ala Gly
145         150         155         160

Lys His Thr Ala Asn Ser His His Leu Ser Ala Leu Val Thr Pro Ala
165         170         175

Gly Lys Ser Tyr Glu Cys Gln Ala Gln Gln Thr Ile Ser Leu Ala Ser
180         185         190

Ser Asp Leu Gln Lys Thr Val Thr Met Ile Leu Ser Ala Val His Ile
195         200         205

Gln Pro Phe Asp Ile Ile Ser Asp Phe Val Phe Ser Glu Glu His Lys
210         215         220

Cys Pro Val Asp Glu Arg Glu Gln Leu Glu Glu Thr Leu Pro Leu Ile
225         230         235         240

Leu Gly Leu Ile Leu Gly Leu Val Ile Met Val Thr Leu Ala Ile Tyr
245         250         255

His Val His His Lys Met Thr Ala Asn Gln Val Gln Ile Pro Arg Asp
260         265         270

Arg Ser Gln Tyr Lys His Met Gly
275         280

<210> 95
<211> 280
<212> PRT
<213> Macaca mulatta

```

ITI-08-PCT_Sequence_Listing_ST25.txt

<400> 95

```

Met Asp Leu Gln Gly Arg Ala Val Pro Ser Val Asp Arg Leu Arg Val
1      5      10      15

Leu Leu Met Leu Phe His Thr Met Ala Gln Ile Met Ala Glu Gln Glu
20      25      30

Val Glu Asn Leu Ser Gly Leu Ser Thr Asn Pro Glu Lys Asp Ile Phe
35      40      45

Val Val Arg Glu Asn Gly Thr Thr Cys Leu Met Ala Glu Phe Ala Ala
50      55      60

Lys Phe Ile Val Pro Tyr Asp Val Trp Ala Ser Asn Tyr Val Asp Leu
65      70      75      80

Ile Thr Glu Gln Ala Asp Ile Ala Leu Thr Arg Gly Ala Glu Val Lys
85      90      95

Gly Arg Cys Gly His Ser Glu Ser Glu Leu Gln Val Phe Trp Val Asp
100     105     110

Arg Ala Tyr Ala Leu Lys Met Leu Phe Val Lys Glu Ser His Asn Thr
115     120     125

Ser Lys Gly Pro Glu Ala Thr Trp Arg Leu Ser Lys Val Gln Phe Val
130     135     140

Tyr Asp Ser Ser Glu Lys Thr His Phe Lys Asp Ala Val Ser Ala Gly
145     150     155     160

Lys His Thr Ala Asn Ser His His Leu Ser Ala Leu Val Thr Pro Ala
165     170     175

Gly Lys Ser Tyr Glu Cys Gln Ala Gln Gln Thr Ile Ser Leu Ala Ser
180     185     190

Ser Asp Pro Gln Lys Met Val Thr Met Ile Leu Ser Ala Val His Ile
195     200     205

Gln Pro Phe Asp Ile Ile Ser Asp Phe Val Phe Ser Glu Glu His Lys
210     215     220

Cys Pro Val Asp Glu Arg Glu Gln Leu Glu Glu Thr Leu Pro Leu Ile
225     230     235     240

Leu Gly Leu Ile Leu Gly Leu Val Ile Val Val Thr Leu Thr Ile Tyr
245     250     255

His Val His His Lys Met Thr Ala Asn Gln Val Gln Ile Pro Arg Asp
260     265     270

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Arg Ser Gln Tyr Lys His Met Gly
275 280

<210> 96

<211> 280

<212> PRT

<213> Canis lupus familiaris

<400> 96

Met Asp Leu Arg Gly Arg Ala Phe Pro Ser Val Tyr Arg Leu Arg Val
1 5 10 15

Leu Leu Met Leu Phe Tyr Thr Met Ala Arg Ile Thr Ala Glu Gln Glu
20 25 30

Val Glu Asn Leu Ser Gly Leu Ser Thr Asn Pro Glu Lys Asp Ile Phe
35 40 45

Val Val Arg Glu Asn Gly Thr Thr Cys Leu Met Ala Glu Phe Ala Ala
50 55 60

Lys Phe Ile Val Pro Tyr Asp Val Trp Ala Ser Asn Tyr Val Asp Leu
65 70 75 80

Ile Thr Glu Gln Ala Asp Ile Ser Leu Thr Arg Gly Ala Glu Val Lys
85 90 95

Gly His Cys Gly His Asn Glu Ser Glu Leu Gln Val Phe Trp Val Asp
100 105 110

Arg Ala Tyr Ala Leu Lys Met Leu Phe Val Lys Glu Ser Arg Asn Ala
115 120 125

Ser Lys Gly Pro Glu Ala Thr Trp Arg Leu Ser Lys Val Gln Phe Val
130 135 140

Tyr Asp Ser Ser Glu Lys Thr His Phe Lys Asp Ala Val Ser Ala Gly
145 150 155 160

Lys His Thr Ala Asn Ser His Arg Leu Ser Ala Leu Val Thr Pro Ala
165 170 175

Gly Lys Ser Tyr Glu Cys Gln Ala Gln Gln Ser Ile Ser Leu Ala Ser
180 185 190

Ser Asp Pro Gln Lys Thr Val Thr Met Ile Leu Ser Ala Val His Ile
195 200 205

Gln Pro Phe Asp Ile Ile Ser Asp Phe Val Phe Ser Glu Glu His Lys
210 215 220

ITI-08-PCT_Sequence_Listing_ST25.txt

Cys Pro Val Asp Glu Arg Glu Gln Leu Glu Glu Thr Leu Pro Leu Ile
225 230 235 240

Leu Gly Leu Ile Leu Gly Leu Val Ile Val Val Thr Leu Ala Ile Tyr
245 250 255

His Ile His His Lys Met Thr Ala Asn Gln Val Gln Ile Pro Arg Asp
260 265 270

Arg Ser Gln Tyr Lys His Met Gly
275 280

<210> 97

<211> 280

<212> PRT

<213> Bos taurus

<400> 97

Met Asp Leu Arg Arg Arg Ala Leu Leu Gly Val Asp Gly Leu Arg Val
1 5 10 15

Leu Leu Met Leu Phe His Thr Val Thr Arg Ile Met Ala Glu Gln Glu
20 25 30

Val Glu Asn Leu Ser Gly Leu Ser Thr Asn Pro Glu Lys Asp Ile Phe
35 40 45

Val Val Arg Glu Asn Gly Thr Thr Cys Leu Met Ala Glu Phe Ala Ala
50 55 60

Lys Phe Ile Val Pro Tyr Asp Val Trp Ala Ser Asn Tyr Val Asp Leu
65 70 75 80

Ile Thr Glu Gln Ala Asp Ile Ser Leu Thr Arg Gly Ala Glu Val Lys
85 90 95

Gly His Cys Gly His Asp Glu Ser Glu Leu Gln Val Phe Trp Val Asp
100 105 110

Arg Ala Tyr Ala Leu Lys Met Leu Phe Leu Lys Glu Ser His Asn Thr
115 120 125

Pro Lys Gly Pro Glu Ala Thr Trp Lys Leu Ser Lys Val Gln Phe Val
130 135 140

Tyr Asp Ser Ser Glu Lys Thr His Phe Lys Asp Ala Val Ser Ala Gly
145 150 155 160

Lys His Thr Ala Asn Ser His His Leu Ser Ala Leu Val Thr Pro Ala
165 170 175

ITI-08-PCT_Sequence_Listing_ST25.txt

Gly Lys Ser Tyr Glu Cys Gln Ala Gln Gln Thr Ile Ser Leu Ala Ser
180 185 190

Ser Asp Pro Gln Lys Thr Val Thr Met Ile Leu Ser Ala Val His Ile
195 200 205

Gln Pro Phe Asp Ile Ile Ser Asp Phe Val Phe Ser Glu Glu His Lys
210 215 220

Cys Pro Val Asp Glu Arg Glu Gln Leu Glu Glu Thr Leu Pro Leu Ile
225 230 235 240

Leu Gly Leu Ile Leu Gly Leu Val Ile Val Val Thr Leu Val Ile Tyr
245 250 255

His Ile His His Lys Met Thr Ala Asn Gln Val Gln Ile Pro Arg Asp
260 265 270

Arg Ser Gln Tyr Lys His Met Gly
275 280

<210> 98
<211> 280
<212> PRT
<213> Mus musculus

<400> 98

Met Asp Leu Arg Val Arg Thr Leu Leu Gly Gly Asp Arg Leu Arg Ile
1 5 10 15

Leu Leu Met Phe Phe His Val Met Val Gln Thr Val Ala Glu Gln Glu
20 25 30

Val Glu Asn Leu Ser Gly Leu Ser Thr Asn Pro Glu Lys Asp Ile Phe
35 40 45

Val Val Arg Glu Asn Gly Thr Thr Cys Leu Met Ala Glu Phe Ala Ala
50 55 60

Lys Phe Ile Val Pro Tyr Asp Val Trp Ala Ser Asn Tyr Val Asp Leu
65 70 75 80

Ile Thr Glu Gln Ala Glu Ile Ser Leu Thr Arg Gly Ala Glu Val Lys
85 90 95

Gly His Cys Gly His Asn Glu Ser Glu Leu Glu Val Phe Trp Val Asp
100 105 110

His Ala Tyr Thr Leu Arg Met Leu Phe Val Lys Glu Ser His Asn Thr
115 120 125

ITI-08-PCT_Sequence_Listing_ST25.txt

Ser Lys Gly Pro Glu Ala Thr Trp Asn Leu Asn Lys Val His Phe Val
130 135 140

Tyr Asp Ser Ser Glu Lys Thr His Phe Lys Ala Pro Val Lys Val Asn
145 150 155 160

Lys Tyr Ile Ala Ser Ser His His Leu Ser Ala Leu Val Thr Pro Ala
165 170 175

Gly Met Ser Tyr Glu Cys Gln Ala Gln Gln Thr Ile Ser Leu Ala Ser
180 185 190

Ser Asp Pro Gln Lys Thr Val Thr Met Ile Leu Ser Ala Val His Ile
195 200 205

Gln Pro Phe Asp Ile Ile Ser Asp Phe Val Phe Ser Glu Glu His Lys
210 215 220

Cys Pro Val Asp Glu Gln Glu Gln Leu Glu Glu Thr Leu Pro Leu Ile
225 230 235 240

Leu Gly Leu Ile Leu Gly Leu Val Ile Val Ile Thr Leu Val Ile Tyr
245 250 255

His Ile His His Lys Met Thr Ala Asn Gln Val Gln Ile Pro Arg Asp
260 265 270

Arg Ser Gln Tyr Lys His Met Gly
275 280

<210> 99

<211> 280

<212> PRT

<213> Rattus norvegicus

<400> 99

Met Asp Leu Arg Gly Arg Ala Leu Leu Gly Gly Asp Arg Leu Arg Ile
1 5 10 15

Leu Leu Met Phe Phe His Ala Met Ala Gln Thr Val Ala Glu Gln Glu
20 25 30

Val Glu Asn Leu Ser Gly Leu Ser Thr Asn Pro Glu Lys Asp Ile Phe
35 40 45

Val Val Arg Glu Asn Gly Thr Thr Cys Leu Met Ala Glu Phe Ala Ala
50 55 60

Lys Phe Ile Val Pro Tyr Asp Val Trp Ala Ser Asn Tyr Val Asp Leu
65 70 75 80

ITI-08-PCT_Sequence_Listing_ST25.txt

Ile Thr Glu Gln Ala Glu Ile Ser Leu Thr Arg Gly Ala Glu Val Lys
85 90 95

Gly Arg Cys Gly His Asn Glu Ser Glu Leu Gln Val Phe Trp Val Asp
100 105 110

Arg Ala Tyr Thr Leu Lys Met Leu Phe Val Lys Glu Ser His Asn Thr
115 120 125

Ser Lys Gly Leu Glu Ala Thr Trp Lys Leu Ser Lys Val Gln Phe Val
130 135 140

Tyr Asp Ser Ser Glu Lys Thr His Phe Lys Asp Ala Val Ser Ala Gly
145 150 155 160

Lys His Thr Ala Asn Ser His His Leu Ser Ala Leu Val Thr Pro Ala
165 170 175

Gly Met Ser Tyr Glu Cys Gln Ala Gln Gln Thr Ile Ser Leu Ala Ser
180 185 190

Ser Asp Pro Gln Lys Thr Val Thr Met Ile Leu Ser Ala Val His Ile
195 200 205

Gln Pro Phe Asp Ile Ile Ser Asp Phe Val Phe Ser Glu Glu His Lys
210 215 220

Cys Pro Val Asp Glu Arg Glu Gln Leu Glu Glu Thr Leu Pro Leu Ile
225 230 235 240

Leu Gly Leu Ile Leu Gly Leu Val Ile Val Ile Thr Leu Val Ile Tyr
245 250 255

His Ile His His Lys Met Thr Ala Asn Gln Val Gln Ile Pro Arg Asp
260 265 270

Arg Ser Gln Tyr Lys His Met Gly
275 280

<210> 100
<211> 299
<212> PRT
<213> Gallus gallus

<400> 100

Met Ala Ala Gly Arg Leu Pro Gly Leu Leu Phe Leu Leu His Ala Ala
1 5 10 15

Ala Arg Leu Ala Ala Glu Gln Glu Val Glu Asn Leu Ser Gly Leu Ser
20 25 30

ITI-08-PCT_Sequence_Listing_ST25.txt

Pro	Asn	Pro	Glu	Lys	Asp	Ile	Phe	Val	Val	Arg	Glu	Asn	Arg	Thr	Thr	35	40	45	
Cys	Leu	Met	Ala	Glu	Phe	Ala	Ala	Lys	Phe	Val	Val	Pro	Tyr	Asp	Val	50	55	60	
Trp	Ala	Ser	Asn	Tyr	Val	Asp	Leu	Ile	Thr	Glu	Gln	Ala	Asp	Ile	Pro	65	70	75	80
Leu	Ser	Arg	Gly	Ala	Glu	Met	Lys	Gly	Lys	Cys	Gly	Thr	Asn	Glu	Ser	85	90	95	
Glu	Leu	Glu	Ile	Ser	Trp	Leu	Glu	Arg	Ala	Tyr	Thr	Leu	Lys	Leu	Phe	100	105	110	
Phe	Leu	Lys	Val	Arg	Gly	Cys	Pro	Arg	Arg	Leu	Gly	Arg	Gly	Arg	Cys	115	120	125	
Ala	Ala	Ala	Leu	Arg	Gly	Pro	Asp	Gln	Pro	Cys	Pro	Pro	Gln	Glu	Gly	130	135	140	
His	Asn	Thr	Ser	Arg	Gly	Pro	Glu	Ala	Phe	Trp	Arg	Leu	Ser	Arg	Ile	145	150	155	160
Gln	Phe	Ser	Tyr	Asp	Thr	Ser	Glu	Arg	Thr	Tyr	Phe	Lys	Asp	Ala	Val	165	170	175	
Ser	Pro	Gly	Lys	His	Thr	Ala	Ser	Ser	His	Arg	Leu	Ser	Ala	Leu	Val	180	185	190	
Thr	Pro	Ala	Gly	Lys	Ser	Tyr	Glu	Cys	Gln	Ala	Gln	Gln	Thr	Ile	Ser	195	200	205	
Leu	Ile	Ser	Ser	Asp	His	Gln	Lys	Ser	Val	Gln	Leu	Leu	Leu	Ser	Glu	210	215	220	
Val	Arg	Ile	Gln	Pro	Phe	Asp	Ile	Thr	Ala	Asp	Phe	Val	Phe	Ser	Glu	225	230	235	240
Glu	His	Lys	Cys	Pro	Val	Asp	Gln	Arg	Glu	Gln	Leu	Glu	Glu	Thr	Leu	245	250	255	
Pro	Leu	Ile	Leu	Gly	Leu	Ile	Leu	Gly	Leu	Val	Ile	Val	Ile	Thr	Leu	260	265	270	
Cys	Val	Tyr	His	Ile	His	His	Lys	Leu	Thr	Ala	Asn	Gln	Val	Gln	Ile	275	280	285	
Pro	Arg	Asp	Arg	Ser	Gln	Tyr	Lys	His	Met	Gly						290	295		

ITI-08-PCT_Sequence_Listing_ST25.txt

<210> 101
 <211> 276
 <212> PRT
 <213> *Xenopus tropicalis*

<400> 101

```

Met Asp Tyr Arg Ala Cys Thr Ser Ala Leu Arg Met Pro Val Leu Leu
1          5          10          15

Leu Leu Leu Cys Thr Phe Ser Cys Asn Leu Ala Glu Gln Glu Val Glu
          20          25          30

Asn Leu Ser Gly Leu Ser Ser Asn Pro Asp Lys Asn Ile Phe Ala Ile
          35          40          45

Arg Glu Asn Gly Thr Thr Cys Leu Met Ala Glu Phe Ser Ala Arg Ile
          50          55          60

Leu Val Pro Tyr Glu Val Pro Ser Ser Asn Glu Val Asp Trp Asp Leu
65          70          75          80

Glu Glu Ala Ser Ile Gln Leu Pro Arg Asp Thr Glu Ile Arg Gly Lys
          85          90          95

Cys Trp Asn Asn Glu Ser Glu Leu His Leu Ser Trp Leu Asp Lys Ala
          100          105          110

Tyr Thr Leu Lys Leu Phe Phe Ser Lys Glu Gly Gln Asp Ala Ser Lys
          115          120          125

Ser Arg Ser Trp Lys Met Ser Lys Ile Gln Phe Leu Tyr Asp Pro Ser
          130          135          140

Glu His Thr Ile Phe Lys Ser Gly Ala Arg Pro Gly Arg His Thr Ala
145          150          155          160

Asn Ser His His Leu Ser Leu Met Val Thr Pro Ala Gly Met Ser Tyr
          165          170          175

Glu Cys Glu Ala Thr Gln Arg Ile Ser Leu Thr Ser Thr Asp His Gln
          180          185          190

Lys Ile Val Val Leu Tyr Leu Ser Glu Val His Leu Gln Pro Phe Asp
          195          200          205

Ile Lys Ser Asp Phe Val Tyr Ser Glu Glu Tyr Lys Cys Pro Thr Asp
          210          215          220

Gln Arg Lys Gln Leu Glu Glu Thr Leu Pro Leu Ile Leu Gly Leu Thr
225          230          235          240
    
```

ITI-08-PCT_Sequence_Listing_ST25.txt

Leu Gly Val Ala Ile Leu Ile Ile Val Ala Val Tyr His Ile His His
245 250 255

Lys Met Thr Ala Asn Gln Val Gln Ile Pro Arg Asp Arg Ser Leu Tyr
260 265 270

Lys His Met Gly
275

<210> 102
<211> 338
<212> PRT
<213> Rattus norvegicus

<400> 102

Met Val Gly Arg Val Gln Pro Asp Arg Lys Gln Leu Pro Leu Val Leu
1 5 10 15

Leu Arg Leu Leu Cys Leu Leu Pro Thr Gly Leu Pro Val Arg Ser Val
20 25 30

Asp Phe Asn Arg Gly Thr Asp Asn Ile Thr Val Arg Gln Gly Asp Thr
35 40 45

Ala Ile Leu Arg Cys Val Val Glu Asp Lys Asn Ser Lys Val Ala Trp
50 55 60

Leu Asn Arg Ser Gly Ile Ile Phe Ala Gly His Asp Lys Trp Ser Leu
65 70 75 80

Asp Pro Arg Val Glu Leu Glu Lys Arg His Ala Leu Glu Tyr Ser Leu
85 90 95

Arg Ile Gln Lys Val Asp Val Tyr Asp Glu Gly Ser Tyr Thr Cys Ser
100 105 110

Val Gln Thr Gln His Glu Pro Lys Thr Ser Gln Val Tyr Leu Ile Val
115 120 125

Gln Val Pro Pro Lys Ile Ser Asn Ile Ser Ser Asp Val Thr Val Asn
130 135 140

Glu Gly Ser Asn Val Thr Leu Val Cys Met Ala Asn Gly Arg Pro Glu
145 150 155 160

Pro Val Ile Thr Trp Arg His Leu Thr Pro Leu Gly Arg Glu Phe Glu
165 170 175

Gly Glu Glu Glu Tyr Leu Glu Ile Leu Gly Ile Thr Arg Glu Gln Ser
180 185 190

ITI-08-PCT_Sequence_Listing_ST25.txt

Gly Lys Tyr Glu Cys Lys Ala Ala Asn Glu Val Ser Ser Ala Asp Val
195 200 205

Lys Gln Val Lys Val Thr Val Asn Tyr Pro Pro Thr Ile Thr Glu Ser
210 215 220

Lys Ser Asn Glu Ala Thr Thr Gly Arg Gln Ala Ser Leu Lys Cys Glu
225 230 235 240

Ala Ser Ala Val Pro Ala Pro Asp Phe Glu Trp Tyr Arg Asp Asp Thr
245 250 255

Arg Ile Asn Ser Ala Asn Gly Leu Glu Ile Lys Ser Thr Glu Gly Gln
260 265 270

Ser Ser Leu Thr Val Thr Asn Val Thr Glu Glu His Tyr Gly Asn Tyr
275 280 285

Thr Cys Val Ala Ala Asn Lys Leu Gly Val Thr Asn Ala Ser Leu Val
290 295 300

Leu Phe Arg Pro Gly Ser Val Arg Gly Ile Asn Gly Ser Ile Ser Leu
305 310 315 320

Ala Val Pro Leu Trp Leu Leu Ala Ala Ser Leu Phe Cys Leu Leu Ser
325 330 335

Lys Cys

<210> 103

<211> 338

<212> PRT

<213> Equus caballus

<400> 103

Met Val Gly Arg Val Gln Pro Asp Arg Lys Gln Leu Pro Leu Val Leu
1 5 10 15

Leu Arg Leu Leu Cys Leu Leu Pro Thr Gly Leu Pro Val Arg Ser Val
20 25 30

Asp Phe Asn Arg Gly Thr Asp Asn Ile Thr Val Arg Gln Gly Asp Thr
35 40 45

Ala Ile Leu Arg Cys Val Val Glu Asp Lys Asn Ser Lys Val Ala Trp
50 55 60

Leu Asn Arg Ser Gly Ile Ile Phe Ala Gly His Asp Lys Trp Ser Leu
65 70 75 80

Asp Pro Arg Val Glu Leu Glu Lys Arg His Ser Leu Glu Tyr Ser Leu

ITI-08-PCT_Sequence_Listing_ST25.txt

85 90 95

Arg Ile Gln Lys Val Asp Val Tyr Asp Glu Gly Ser Tyr Thr Cys Ser
100 105 110

Val Gln Thr Gln His Glu Pro Lys Thr Ser Gln Val Tyr Leu Ile Val
115 120 125

Gln Val Pro Pro Lys Ile Ser Asn Ile Ser Ser Asp Val Thr Val Asn
130 135 140

Glu Gly Ser Asn Val Thr Leu Val Cys Met Ala Asn Gly Arg Pro Glu
145 150 155 160

Pro Val Ile Thr Trp Arg His Leu Thr Pro Thr Gly Arg Glu Phe Glu
165 170 175

Gly Glu Glu Glu Tyr Leu Glu Ile Leu Gly Ile Thr Arg Glu Gln Ser
180 185 190

Gly Lys Tyr Glu Cys Lys Ala Ala Asn Glu Val Ser Ser Ala Asp Val
195 200 205

Lys Gln Val Lys Val Thr Val Asn Tyr Pro Pro Thr Ile Thr Glu Ser
210 215 220

Lys Ser Asn Glu Ala Thr Thr Gly Arg Gln Ala Ser Leu Lys Cys Glu
225 230 235 240

Ala Ser Ala Val Pro Ala Pro Asp Phe Glu Trp Tyr Arg Asp Asp Thr
245 250 255

Arg Ile Thr Ser Ala Asn Gly Leu Glu Ile Lys Ser Thr Glu Gly Gln
260 265 270

Ser Ser Leu Thr Val Ala Asn Val Thr Glu Glu His Tyr Gly Asn Tyr
275 280 285

Thr Cys Val Ala Ala Asn Asn Leu Gly Val Thr Asn Ala Ser Leu Val
290 295 300

Leu Phe Arg Pro Gly Ser Val Arg Gly Ile Asn Gly Ser Ile Ser Leu
305 310 315 320

Ala Val Pro Leu Trp Leu Leu Ala Ala Ser Leu Leu Cys Leu Leu Ser
325 330 335

Lys Cys

<210> 104

<211> 338

<212> PRT

ITI-08-PCT_Sequence_Listing_ST25.txt

<213> Sus scrofa

<400> 104

```

Met Val Ala Arg Val Gln Pro Asp Arg Lys Gln Leu Pro Leu Val Leu
1          5          10          15

Leu Arg Leu Leu Cys Leu Leu Pro Thr Gly Leu Pro Val Arg Ser Val
          20          25          30

Asp Phe Asn Arg Gly Thr Asp Asn Ile Thr Val Arg Gln Gly Asp Thr
          35          40          45

Ala Ile Leu Arg Cys Val Val Glu Asp Lys Asn Ser Lys Val Ala Trp
          50          55          60

Leu Asn Arg Ser Gly Ile Ile Phe Ala Gly His Asp Lys Trp Ser Leu
65          70          75          80

Asp Pro Arg Val Glu Leu Glu Lys Arg His Ser Leu Glu Tyr Ser Leu
          85          90          95

Arg Ile Gln Lys Val Asp Val Tyr Asp Glu Gly Ser Tyr Thr Cys Ser
          100          105          110

Val Gln Thr Gln His Glu Pro Lys Thr Ser Gln Val Tyr Leu Ile Val
          115          120          125

Gln Val Pro Pro Lys Ile Ser Asn Ile Ser Ser Asp Val Thr Val Asn
          130          135          140

Glu Gly Ser Asn Val Thr Leu Val Cys Met Ala Asn Gly Arg Pro Glu
145          150          155          160

Pro Val Ile Thr Trp Arg His Leu Thr Pro Thr Gly Arg Glu Leu Glu
          165          170          175

Gly Glu Glu Glu Tyr Leu Glu Ile Leu Gly Ile Thr Arg Glu Gln Ser
          180          185          190

Gly Lys Tyr Glu Cys Lys Ala Ala Asn Glu Val Ser Ser Ala Asp Val
          195          200          205

Lys Gln Val Lys Val Thr Val Asn Tyr Pro Pro Thr Ile Thr Glu Ser
          210          215          220

Lys Ser Asn Glu Ala Thr Thr Gly Arg Lys Ala Ser Leu Lys Cys Glu
225          230          235          240

Ala Ser Ala Val Pro Ala Pro Asp Phe Glu Trp Tyr Arg Asp Asp Thr
          245          250          255

```


ITI-08-PCT_Sequence_Listing_ST25.txt

Arg Ile Asn Ser Ala Asn Gly Leu Glu Ile Lys Ser Thr Glu Gly Gln
260 265 270

Ser Ser Leu Thr Val Thr Asn Val Thr Glu Glu His Tyr Gly Asn Tyr
275 280 285

Thr Cys Val Ala Ala Asn Asn Leu Gly Val Thr Asn Ala Ser Leu Val
290 295 300

Leu Phe Arg Pro Gly Ser Val Arg Gly Ile Asn Gly Ser Ile Ser Leu
305 310 315 320

Ala Val Pro Leu Trp Leu Leu Ala Ala Ser Leu Leu Cys Leu Leu Ser
325 330 335

Lys Cys

<210> 105

<211> 338

<212> PRT

<213> Bos taurus

<400> 105

Met Val Ala Arg Val Gln Pro Asp Arg Lys Gln Leu Pro Leu Val Leu
1 5 10 15

Leu Arg Leu Leu Cys Leu Leu Pro Thr Gly Leu Pro Val Arg Ser Val
20 25 30

Asp Phe Asn Arg Gly Thr Asp Asn Ile Thr Val Arg Gln Gly Asp Thr
35 40 45

Ala Ile Leu Arg Cys Val Val Glu Asp Lys Asn Ser Lys Val Ala Trp
50 55 60

Leu Asn Arg Ser Gly Ile Ile Phe Ala Gly His Asp Lys Trp Ser Leu
65 70 75 80

Asp Pro Arg Val Glu Leu Glu Lys Arg His Ser Leu Glu Tyr Ser Leu
85 90 95

Arg Ile Gln Lys Val Asp Val Tyr Asp Glu Gly Ser Tyr Thr Cys Ser
100 105 110

Val Gln Thr Gln His Glu Pro Lys Thr Ser Gln Val Tyr Leu Ile Val
115 120 125

Gln Val Pro Pro Lys Ile Ser Asn Ile Ser Ser Asp Val Thr Val Asn
130 135 140

Glu Gly Ser Asn Val Thr Leu Val Cys Met Ala Asn Gly Arg Pro Glu

ITI-08-PCT_Sequence_Listing_ST25.txt

```

145                150                155                160
Pro Val Ile Thr Trp Arg His Leu Thr Pro Thr Gly Arg Glu Phe Glu
                165                170                175

Gly Glu Glu Glu Tyr Leu Glu Ile Leu Gly Ile Thr Arg Glu Gln Ser
                180                185                190

Gly Lys Tyr Glu Cys Lys Ala Ala Asn Glu Val Ser Ser Ala Asp Val
                195                200                205

Lys Gln Val Lys Val Thr Val Asn Tyr Pro Pro Thr Ile Thr Glu Ser
                210                215                220

Lys Ser Asn Glu Ala Thr Thr Gly Arg Lys Ala Ser Leu Lys Cys Glu
225                230                235                240

Ala Ser Ala Val Pro Ala Pro Asp Phe Glu Trp Tyr Arg Asp Asp Thr
                245                250                255

Arg Ile Asn Ser Ala Asn Gly Leu Glu Ile Lys Ser Thr Glu Gly Gln
                260                265                270

Ser Ser Leu Thr Val Thr Asn Val Thr Glu Glu His Tyr Gly Asn Tyr
                275                280                285

Thr Cys Val Ala Ala Asn Asn Leu Gly Met Thr Asn Ala Ser Leu Val
                290                295                300

Leu Phe Arg Pro Gly Ser Val Arg Gly Ile Asn Gly Ser Ile Ser Leu
305                310                315                320

Ala Val Pro Leu Trp Leu Leu Ala Ala Ser Leu Leu Cys Leu Leu Ser
                325                330                335

```

Lys Cys

```

<210> 106
<211> 417
<212> PRT
<213> Anopheles gambiae str. PEST

```

<400> 106

```

Met Ser Phe Ala Gly Glu Ala Ala Ser Gln Ile Leu Asn Lys Ala Glu
1                5                10                15

Pro Leu Phe Ile Ser Arg Ser Glu Ala Phe Lys Phe Ala Val Gly Asp
                20                25                30

Thr Ile Thr Leu Pro Cys Glu Val Ala Ser Pro Gly Thr Tyr Val Leu
                35                40                45

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Ala	Trp	Lys	Arg	Gly	Ile	Ala	Ile	Leu	Thr	Ala	Gly	Ser	Val	Lys	Val	50	55	60	
Thr	Pro	Asp	Pro	Arg	Val	Arg	Leu	Val	Asn	Gly	Tyr	Ser	Leu	Gln	Ile	65	70	75	80
Arg	Asp	Ala	Val	Pro	Gln	Asp	Ala	Gly	Asp	Tyr	Ile	Cys	Gln	Ile	Ala	85	90	95	
Met	Leu	Asp	Pro	Arg	Glu	Ile	Thr	His	Ser	Val	Glu	Ile	Leu	Val	Pro	100	105	110	
Pro	Lys	Ile	Thr	His	Val	Thr	Ser	Gly	Gly	His	Leu	Gln	Val	Arg	Lys	115	120	125	
Gly	Ser	Pro	Val	Arg	Leu	Glu	Cys	Ser	Ala	Thr	Gly	Asn	Pro	Met	Pro	130	135	140	
Asn	Ile	Thr	Trp	Thr	Arg	Lys	Asn	Asn	Leu	Leu	Pro	Asn	Gly	Glu	Glu	145	150	155	160
Gln	Phe	Thr	Asn	Pro	Val	Tyr	Val	Ile	Glu	Asn	Met	Asp	Arg	His	Lys	165	170	175	
Gly	Gly	Thr	Tyr	Ile	Cys	Thr	Ala	Asn	Asn	Gly	Val	Gly	Gln	Val	Ala	180	185	190	
Thr	Ser	Gln	Ile	Ile	Leu	His	Val	Leu	Tyr	Pro	Pro	Glu	Ile	Ser	Val	195	200	205	
Glu	Asn	Pro	Thr	Val	Tyr	Ser	Gly	Glu	Gly	Gln	Glu	Ala	Met	Leu	Val	210	215	220	
Cys	Ile	Val	His	Gly	Glu	Ser	Gln	Pro	Glu	Val	Leu	Trp	His	Lys	Asp	225	230	235	240
Thr	Met	Gln	Ile	Asp	Gln	Thr	Glu	Arg	His	Val	Ile	Glu	Asn	Arg	Gly	245	250	255	
Ala	Arg	His	Thr	Leu	Ile	Ile	Arg	Lys	Val	His	Pro	Gln	Asp	Phe	Gly	260	265	270	
Asn	Tyr	Ser	Cys	Ile	Ala	Asp	Asn	Gln	Leu	Gly	Lys	Thr	Arg	Lys	Thr	275	280	285	
Val	Thr	Leu	Thr	Gly	Lys	Pro	Lys	Thr	Ala	Val	Phe	Arg	Ser	Val	Pro	290	295	300	
Asn	Ser	Gln	Trp	Lys	Asp	Lys	Tyr	Asn	Ile	Ser	Trp	Ile	Val	Asp	Ser	305	310	315	320

ITI-08-PCT_Sequence_Listing_ST25.txt

His Ser Pro Ile Glu Glu Phe Lys Leu Tyr Tyr Arg Gln Met Thr Phe
325 330 335

Ser Ile Gly Gln Leu Gln Pro Leu Gln Thr Asp Trp Arg Asp Ile Val
340 345 350

Leu Pro Ala Phe Pro Tyr Ser His His Tyr Thr Gln Gly Met Ser Tyr
355 360 365

Leu Ile Arg Gly Leu Glu Pro Asp Gln Gln Tyr Glu Ala Arg Val Gln
370 375 380

Ser Arg Asn Arg Tyr Gly Trp Ser Asp Phe Ser Glu Ser Phe Leu Phe
385 390 395 400

Thr Thr Ser Asn Thr Gly Lys Trp Met Gly Gln Cys Cys Thr Asn Pro
405 410 415

Gly

<210> 107

<211> 334

<212> PRT

<213> *Xenopus tropicalis*

<400> 107

Met Arg Pro Cys Leu Leu His Ser Ile Trp Met Leu Gly Phe Val Leu
1 5 10 15

Cys Leu Leu Ser Leu Gln Gly Leu Pro Val Arg Ser Gly Asp Phe Asn
20 25 30

Arg Ser Thr Asp Asn Ile Thr Val Arg Gln Gly Asp Thr Ala Ile Leu
35 40 45

Arg Cys Phe Val Glu Asp Arg Ser Ser Arg Val Ala Trp Leu Asn Arg
50 55 60

Ser Gly Ile Ile Phe Ala Gly Asp Asp Lys Trp Ser Leu Asp Pro Arg
65 70 75 80

Val Glu Leu Glu Lys Arg Ser Leu Leu Glu Tyr Ser Leu Arg Ile Gln
85 90 95

Lys Val Asp Val Ser Asp Glu Gly Pro Tyr Thr Cys Ser Val Gln Thr
100 105 110

Lys Gln His Thr Lys Thr Thr Gln Val Tyr Leu Ile Val Gln Val Pro
115 120 125

Pro Lys Ile Ser Asn Ile Ser Ala Asp Ile Thr Val Asn Glu Gly Ser

ITI-08-PCT_Sequence_Listing_ST25.txt

130

135

140

Asn Val Thr Leu Met Cys Ile Ala Tyr Gly Arg Pro Glu Pro Met Ile
145 150 155 160

Thr Trp Arg His Leu Thr Pro Thr Ala Arg Asp Phe Glu Gly Glu Glu
165 170 175

Glu Phe Leu Glu Ile Gln Gly Ile Thr Arg Glu Gln Ser Gly Arg Tyr
180 185 190

Glu Cys Lys Ala Ala Asn Glu Val Ala Ser Ala Asp Val Lys Gln Val
195 200 205

Arg Val Thr Val Asn Tyr Pro Pro Ile Ile Thr Glu Ser Lys Ser Asn
210 215 220

Glu Ala Thr Thr Gly Lys Gln Ala Ile Leu Arg Cys Glu Ala Ser Ala
225 230 235 240

Val Pro Ala Pro Asp Phe Glu Trp Tyr Lys Asp Asp Thr Arg Ile Asn
245 250 255

Ser Ala Gln Gly Leu Glu Ile Arg Asn Thr Gly Ser Arg Ser Val Leu
260 265 270

Met Val Ala Asn Val Thr Glu Glu His Tyr Gly Asn Tyr Thr Cys Val
275 280 285

Ala Ala Asn Lys Leu Gly Ile Thr Asn Thr Ser Leu Tyr Leu Tyr Ile
290 295 300

Gly Pro Gly Thr Pro Ile Asp Ser Ala Thr Ser Leu Ala Ala Ser Leu
305 310 315 320

Trp Leu Met Ala Asn Leu Leu Phe Cys Leu Phe Cys Thr Cys
325 330

<210> 108

<211> 338

<212> PRT

<213> Canis lupus familiaris

<400> 108

Met Leu Gly Ala Arg Arg Pro Pro Arg Ser Gln Leu Pro Leu Val Leu
1 5 10 15

Leu Arg Leu Leu Cys Leu Leu Pro Thr Gly Leu Pro Val Arg Ser Val
20 25 30

Asp Phe Asn Arg Gly Thr Asp Asn Ile Thr Val Arg Gln Gly Asp Thr

ITI-08-PCT_Sequence_Listing_ST25.txt

35						40						45					
Ala	Ile	Leu	Arg	Cys	Val	Val	Glu	Asp	Lys	Asn	Ser	Lys	Val	Ala	Trp		
50						55					60						
Leu	Asn	Arg	Ser	Gly	Ile	Ile	Phe	Ala	Gly	His	Asp	Lys	Trp	Ser	Leu		
65					70					75					80		
Asp	Pro	Arg	Val	Glu	Leu	Glu	Lys	Arg	His	Ser	Leu	Glu	Tyr	Ser	Leu		
				85					90					95			
Arg	Ile	Gln	Lys	Val	Asp	Val	Tyr	Asp	Glu	Gly	Ser	Tyr	Thr	Cys	Ser		
			100					105					110				
Val	Gln	Thr	Gln	His	Glu	Pro	Lys	Thr	Ser	Gln	Val	Tyr	Leu	Ile	Val		
			115				120					125					
Gln	Val	Pro	Pro	Lys	Ile	Ser	Asn	Ile	Ser	Ser	Asp	Val	Thr	Val	Asn		
						135					140						
Glu	Gly	Ser	Asn	Val	Thr	Leu	Val	Cys	Met	Ala	Asn	Gly	Arg	Pro	Glu		
145					150					155					160		
Pro	Val	Ile	Thr	Trp	Arg	His	Leu	Thr	Pro	Thr	Gly	Arg	Glu	Phe	Glu		
				165					170					175			
Gly	Glu	Glu	Glu	Tyr	Leu	Glu	Ile	Leu	Gly	Ile	Thr	Arg	Glu	Gln	Ser		
			180					185					190				
Gly	Lys	Tyr	Glu	Cys	Lys	Ala	Ala	Asn	Glu	Val	Ser	Ser	Ala	Asp	Val		
		195					200					205					
Arg	Gln	Val	Lys	Val	Thr	Val	Asn	Tyr	Pro	Pro	Thr	Ile	Thr	Glu	Ser		
	210					215					220						
Lys	Ser	Asn	Glu	Ala	Thr	Thr	Gly	Arg	Lys	Ala	Ser	Leu	Lys	Cys	Glu		
225					230					235					240		
Ala	Ser	Ala	Val	Pro	Ala	Pro	Asp	Phe	Glu	Trp	Tyr	Arg	Asp	Asp	Thr		
				245					250					255			
Arg	Ile	Asn	Ser	Ala	Asn	Gly	Leu	Glu	Ile	Lys	Ser	Thr	Glu	Gly	Gln		
			260					265					270				
Ser	Ser	Leu	Thr	Val	Thr	Asn	Val	Thr	Glu	Glu	His	Tyr	Gly	Asn	Tyr		
		275					280					285					
Thr	Cys	Val	Ala	Ala	Asn	Asn	Leu	Gly	Val	Thr	Asn	Ala	Ser	Leu	Val		
		290				295					300						
Leu	Phe	Arg	Pro	Gly	Ser	Val	Arg	Gly	Ile	Asn	Gly	Ser	Ile	Ser	Leu		
305					310					315					320		

ITI-08-PCT_Sequence_Listing_ST25.txt

Ala Val Pro Leu Trp Leu Leu Ala Ala Ser Leu Leu Cys Leu Leu Ser
325 330 335

Lys Cys

<210> 109
<211> 338
<212> PRT
<213> Monodelphis domestica

<400> 109

Met Val Gly Arg Val His Pro Asp Arg Lys Gln Leu Pro Leu Val Leu
1 5 10 15

Leu Arg Leu Leu Cys Leu Leu Pro Thr Gly Leu Pro Val Arg Gly Val
20 25 30

Asp Phe Thr Arg Gly Thr Asp Asn Ile Thr Val Arg Gln Gly Asp Thr
35 40 45

Ala Ile Leu Arg Cys Tyr Val Glu Asp Lys Ser Ser Lys Val Ala Trp
50 55 60

Leu Asn Arg Ser Gly Ile Ile Phe Ala Gly His Asp Lys Trp Ser Leu
65 70 75 80

Asp Pro Arg Val Glu Leu Glu Lys Arg Thr Ala Leu Glu Tyr Ser Leu
85 90 95

Arg Ile Gln Lys Val Asp Val Tyr Asp Glu Gly Ser Tyr Thr Cys Ser
100 105 110

Val Gln Thr Gln His Gln Pro Lys Thr Ser Gln Val Tyr Leu Ile Val
115 120 125

Gln Val Pro Pro Lys Ile Ser Asn Ile Ser Ser Asp Val Thr Val Asn
130 135 140

Glu Gly Ser Asn Val Thr Leu Val Cys Met Ala Asn Gly Arg Pro Glu
145 150 155 160

Pro Val Ile Thr Trp Arg His Leu Thr Pro Thr Gly Arg Glu Phe Glu
165 170 175

Gly Glu Glu Glu Tyr Leu Glu Ile Leu Gly Ile Thr Arg Glu Gln Ser
180 185 190

Gly Lys Tyr Glu Cys Lys Ala Ala Asn Glu Val Ser Ser Ala Asp Val
195 200 205

ITI-08-PCT_Sequence_Listing_ST25.txt

Lys Gln Val Lys Val Thr Val Asn Tyr Pro Pro Thr Ile Thr Glu Ser
210 215 220

Lys Ser Asn Glu Ala Thr Thr Gly Arg Gln Ala Ser Leu Lys Cys Glu
225 230 235 240

Ala Ser Ala Val Pro Ala Pro Asp Phe Glu Trp Tyr Arg Asp Asp Thr
245 250 255

Arg Ile Asn Ser Ala Asn Gly Leu Glu Ile Lys Ser Ile Glu Gly Gln
260 265 270

Ser Leu Leu Met Val Thr Asn Val Thr Glu Glu His Tyr Gly Asn Tyr
275 280 285

Thr Cys Val Ala Ala Asn Lys Leu Gly Val Thr Asn Ala Ser Leu Ile
290 295 300

Leu Phe Arg Pro Gly Ser Val Arg Gly Ile Asn Gly Ser Ile Ser Leu
305 310 315 320

Ala Val Pro Leu Trp Leu Leu Ala Ala Ser Leu Phe Cys Leu Leu Ser
325 330 335

Lys Cys

<210> 110
<211> 338
<212> PRT
<213> Gallus gallus

<400> 110

Met Val Ala Arg Ala Gln Pro Asp Arg Lys Gln Leu Pro Leu Val Leu
1 5 10 15

Leu Arg Leu Leu Cys Leu Leu Pro Thr Gly Leu Pro Val Arg Ser Val
20 25 30

Asp Phe Thr Arg Gly Thr Asp Asn Ile Thr Val Arg Gln Gly Asp Thr
35 40 45

Ala Ile Leu Arg Cys Phe Val Glu Asp Arg Ser Ser Lys Val Ala Trp
50 55 60

Leu Asn Arg Ser Gly Ile Ile Phe Ala Gly Glu Asp Lys Trp Ser Leu
65 70 75 80

Asp Pro Arg Val Glu Leu Glu Lys Arg Ser Pro Leu Glu Tyr Ser Leu
85 90 95

Arg Ile Gln Lys Val Asp Val Tyr Asp Glu Gly Ser Tyr Thr Cys Ser

ITI-08-PCT_Sequence_Listing_ST25.txt

100

105

110

Val Gln Thr Gln His His Pro Lys Thr Ser Gln Val Tyr Leu Ile Val
115 120 125

Gln Val Pro Pro Lys Ile Ser Asn Ile Ser Ser Asp Ile Thr Val Asn
130 135 140

Glu Gly Ser Asn Val Thr Leu Val Cys Met Ala Asn Gly Arg Pro Glu
145 150 155 160

Pro Val Ile Thr Trp Arg His Leu Thr Pro Thr Gly Lys Glu Phe Glu
165 170 175

Gly Glu Glu Glu Tyr Leu Glu Ile Leu Gly Ile Thr Arg Glu Gln Ser
180 185 190

Gly Lys Tyr Glu Cys Lys Ala Ala Asn Glu Val Ala Ser Ala Asp Val
195 200 205

Lys Gln Val Arg Val Thr Val Asn Tyr Pro Pro Thr Ile Thr Glu Ser
210 215 220

Lys Ser Asn Glu Ala Ala Thr Gly Arg Gln Ala Leu Leu Arg Cys Glu
225 230 235 240

Ala Ser Ala Val Pro Thr Pro Asp Phe Glu Trp Tyr Arg Asp Asp Thr
245 250 255

Arg Ile Asn Ser Ala Asn Gly Leu Glu Ile Lys Ser Thr Gly Ser Gln
260 265 270

Ser Leu Leu Met Val Ala Asn Val Thr Glu Glu His Tyr Gly Asn Tyr
275 280 285

Thr Cys Val Ala Ala Asn Lys Leu Gly Val Thr Asn Ala Ser Leu Tyr
290 295 300

Leu Tyr Arg Pro Gly Thr Gly Arg Val Asp Asn Gly Ser Val Ser Leu
305 310 315 320

Ala Val Pro Leu Trp Leu Leu Ala Ala Ser Leu Leu Cys Leu Leu Ser
325 330 335

Lys Cys

<210> 111

<211> 335

<212> PRT

<213> Taeniopygia guttata

<400> 111

ITI-08-PCT_Sequence_Listing_ST25.txt

Met	Arg	Thr	Tyr	Trp	Leu	His	Ser	Ile	Trp	Val	Leu	Gly	Phe	Phe	Leu	1	5	10	15
Ser	Leu	Phe	Ser	Leu	Gln	Gly	Leu	Pro	Val	Arg	Ser	Val	Asp	Phe	Thr	20	25	30	
Arg	Gly	Thr	Asp	Asn	Ile	Thr	Val	Arg	Gln	Gly	Asp	Thr	Ala	Ile	Leu	35	40	45	
Arg	Cys	Tyr	Val	Glu	Asp	Arg	Ser	Ser	Lys	Val	Ala	Trp	Leu	Asn	Arg	50	55	60	
Ser	Gly	Ile	Ile	Phe	Ala	Gly	Glu	Asp	Lys	Trp	Ser	Leu	Asp	Pro	Arg	65	70	75	
Val	Glu	Leu	Glu	Lys	Arg	Asn	Pro	Leu	Glu	Tyr	Ser	Leu	Arg	Ile	Gln	85	90	95	
Lys	Val	Asp	Val	Tyr	Asp	Glu	Gly	Ser	Tyr	Thr	Cys	Ser	Val	Gln	Thr	100	105	110	
Gln	His	His	Pro	Lys	Thr	Ser	Gln	Val	Tyr	Leu	Ile	Val	Gln	Val	Pro	115	120	125	
Pro	Lys	Ile	Ser	Asn	Ile	Ser	Ser	Asp	Ile	Thr	Val	Asn	Glu	Gly	Ser	130	135	140	
Asn	Val	Thr	Leu	Val	Cys	Met	Ala	Asn	Gly	Arg	Pro	Glu	Pro	Val	Ile	145	150	155	
Thr	Trp	Arg	His	Leu	Thr	Pro	Thr	Gly	Lys	Glu	Phe	Glu	Gly	Glu	Glu	165	170	175	
Glu	Tyr	Leu	Glu	Ile	Leu	Gly	Ile	Thr	Arg	Glu	Gln	Ser	Gly	Lys	Tyr	180	185	190	
Glu	Cys	Lys	Ala	Ala	Asn	Glu	Val	Ala	Ser	Ala	Asp	Val	Lys	Gln	Val	195	200	205	
Arg	Val	Thr	Val	Asn	Tyr	Pro	Pro	Thr	Ile	Thr	Glu	Ser	Lys	Ser	Asn	210	215	220	
Glu	Ala	Ala	Thr	Gly	Arg	Gln	Ala	Leu	Leu	Arg	Cys	Glu	Ala	Ser	Ala	225	230	235	
Val	Pro	Thr	Pro	Asp	Phe	Glu	Trp	Tyr	Arg	Asp	Asp	Thr	Arg	Ile	Asn	245	250	255	
Ser	Ala	Asn	Gly	Leu	Glu	Ile	Lys	Ser	Thr	Gly	Ser	Gln	Ser	Leu	Leu	260	265	270	

ITI-08-PCT_Sequence_Listing_ST25.txt

Met Val Ala Asn Val Thr Glu Glu His Tyr Gly Asn Tyr Thr Cys Val
275 280 285

Ala Ala Asn Lys Leu Gly Val Thr Asn Ala Ser Leu Tyr Leu Tyr Arg
290 295 300

Pro Gly Thr Gly Arg Val Asp Asn Gly Ser Met Ser Leu Ala Val Pro
305 310 315 320

Leu Trp Leu Leu Ala Ala Ser Leu Leu Cys Leu Leu Ser Lys Cys
325 330 335

<210> 112

<211> 334

<212> PRT

<213> Xenopus tropicalis

<400> 112

Met Arg Pro Cys Leu Leu His Ser Ile Trp Met Leu Gly Phe Val Leu
1 5 10 15

Cys Leu Leu Ser Leu Gln Gly Leu Pro Val Arg Ser Gly Asp Phe Asn
20 25 30

Arg Ser Thr Asp Asn Ile Thr Val Arg Gln Gly Asp Thr Ala Ile Leu
35 40 45

Arg Cys Phe Val Glu Asp Arg Ser Ser Arg Val Ala Trp Leu Asn Arg
50 55 60

Ser Gly Ile Ile Phe Ala Gly Asp Asp Lys Trp Ser Leu Asp Pro Arg
65 70 75 80

Val Glu Leu Glu Lys Arg Ser Leu Leu Glu Tyr Ser Leu Arg Ile Gln
85 90 95

Lys Val Asp Val Ser Asp Glu Gly Pro Tyr Thr Cys Ser Val Gln Thr
100 105 110

Lys Gln His Thr Lys Thr Thr Gln Val Tyr Leu Ile Val Gln Val Pro
115 120 125

Pro Lys Ile Ser Asn Ile Ser Ala Asp Ile Thr Val Asn Glu Gly Ser
130 135 140

Asn Val Thr Leu Met Cys Ile Ala Tyr Gly Arg Pro Glu Pro Met Ile
145 150 155 160

Thr Trp Arg His Leu Thr Pro Thr Ala Arg Asp Phe Glu Gly Glu Glu
165 170 175

ITI-08-PCT_Sequence_Listing_ST25.txt

Glu Phe Leu Glu Ile Gln Gly Ile Thr Arg Glu Gln Ser Gly Arg Tyr
180 185 190

Glu Cys Lys Ala Ala Asn Glu Val Ala Ser Ala Asp Val Lys Gln Val
195 200 205

Arg Val Thr Val Asn Tyr Pro Pro Ile Ile Thr Glu Ser Lys Ser Asn
210 215 220

Glu Ala Thr Thr Gly Lys Gln Ala Ile Leu Arg Cys Glu Ala Ser Ala
225 230 235 240

Val Pro Ala Pro Asp Phe Glu Trp Tyr Lys Asp Asp Thr Arg Ile Asn
245 250 255

Ser Ala Gln Gly Leu Glu Ile Arg Asn Thr Gly Ser Arg Ser Val Leu
260 265 270

Met Val Ala Asn Val Thr Glu Glu His Tyr Gly Asn Tyr Thr Cys Val
275 280 285

Ala Ala Asn Lys Leu Gly Ile Thr Asn Thr Ser Leu Tyr Leu Tyr Ile
290 295 300

Gly Pro Gly Thr Pro Ile Asp Ser Ala Thr Ser Leu Ala Ala Ser Leu
305 310 315 320

Trp Leu Met Ala Asn Leu Leu Phe Cys Leu Phe Cys Thr Cys
325 330

<210> 113

<211> 337

<212> PRT

<213> Oreochromis niloticus

<400> 113

Met Gln Val Gly Arg Lys Ser Cys Trp Arg Gln Leu Gln Ala Ser Phe
1 5 10 15

Phe Arg Leu Leu Cys Leu Ile Pro Thr Gly Phe Pro Val Arg Ser Val
20 25 30

Asp Met Gln Arg Ala Thr Asp Asn Ile Thr Ile Arg Gln Gly Asp Thr
35 40 45

Ala Ile Ile Arg Cys Tyr Val Asp Asp Lys Val Ser Lys Val Ala Trp
50 55 60

Leu Asn Arg Ser Asn Ile Ile Phe Ala Gly Gln Asp Lys Trp Ser Leu
65 70 75 80

ITI-08-PCT_Sequence_Listing_ST25.txt

```

Asp Pro Arg Val Asp Leu Val Thr Lys Gly Gln Leu Glu Tyr Ser Leu
      85                      90                      95

Arg Ile Gln Lys Val Asp Val Tyr Asp Glu Gly Ser Tyr Thr Cys Ser
      100                      105                      110

Ile Gln Thr Lys Gln Gln Pro Lys Thr Ser Gln Val Tyr Leu Ile Val
      115                      120                      125

Gln Val Pro Ala Ser Ile Tyr Gln Val Ser Asn Asp Ile Thr Val Asn
      130                      135                      140

Glu Gly Ser Asn Val Thr Leu Ser Cys Leu Ala Asn Gly Arg Pro Asp
145                      150                      155                      160

Pro Ala Ile Thr Trp Arg Leu Leu Asn Pro Ser Ala Glu Pro Leu Asp
      165                      170                      175

Gly Glu Glu Tyr Leu Asp Ile Ile Gly Ile Met Arg Thr Gln Ala Gly
      180                      185                      190

Arg Tyr Glu Cys Lys Ala Ser Asn Asp Val Ala Thr Pro Asp Val Lys
      195                      200                      205

Tyr Val Asn Val Ile Val Asn Tyr Pro Pro Thr Ile Lys Lys Thr Gln
      210                      215                      220

Ser Ser Glu Thr Pro Val Gly Arg Asn Gly Thr Leu Arg Cys Glu Val
225                      230                      235                      240

Thr Ala Val Pro Thr Pro Glu Phe Glu Trp Tyr Arg Asp Asp Lys Arg
      245                      250                      255

Leu Ala Asn Thr Gln Ser Ile Thr Ile Gln Thr Ser Gly Thr Thr Thr
      260                      265                      270

Ser Leu Thr Ile Ala Asn Ile Thr Glu Glu Asp Tyr Gly Asn Tyr Thr
      275                      280                      285

Cys Val Ala Ser Asn Arg Leu Gly Val Gln Asn Ala Ser Leu Phe Leu
      290                      295                      300

Tyr Arg Pro Gly Thr Gly Arg Asp Ile Asn Gly Ser Ala Cys Val Ser
305                      310                      315                      320

Gln Ser Leu Trp Leu Leu Leu Ala Ser Phe Ala Cys Leu Phe Leu Lys
      325                      330                      335

```

Cys

<210> 114

<211> 561

ITI-08-PCT_Sequence_Listing_ST25.txt

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 114

Met Glu Ser Arg Gly Arg Arg Cys Pro Glu Met Ile Ser Val Leu Gly
1 5 10 15

Pro Ile Ser Gly His Val Leu Lys Ala Val Phe Ser Arg Gly Asp Thr
20 25 30

Pro Val Leu Pro His Glu Thr Arg Leu Leu Gln Thr Gly Ile His Val
35 40 45

Arg Val Ser Gln Pro Ser Leu Ile Leu Val Ser Gln Tyr Thr Pro Asp
50 55 60

Ser Thr Pro Cys His Arg Gly Asp Asn Gln Leu Gln Val Gln His Thr
65 70 75 80

Tyr Phe Thr Gly Ser Glu Val Glu Asn Val Ser Val Asn Val His Asn
85 90 95

Pro Thr Gly Arg Ser Ile Cys Pro Ser Gln Glu Pro Met Ser Ile Tyr
100 105 110

Val Tyr Ala Leu Pro Leu Lys Met Leu Asn Ile Pro Ser Ile Asn Val
115 120 125

His His Tyr Pro Ser Ala Ala Glu Arg Lys His Arg His Leu Pro Val
130 135 140

Ala Asp Ala Val Ile His Ala Ser Gly Lys Gln Met Trp Gln Ala Arg
145 150 155 160

Leu Thr Val Ser Gly Leu Ala Trp Thr Arg Gln Gln Asn Gln Trp Lys
165 170 175

Glu Pro Asp Val Tyr Tyr Thr Ser Ala Phe Val Phe Pro Thr Lys Asp
180 185 190

Val Ala Leu Arg His Val Val Cys Ala His Glu Leu Val Cys Ser Met
195 200 205

Glu Asn Thr Arg Ala Thr Lys Met Gln Val Ile Gly Asp Gln Tyr Val
210 215 220

Lys Val Tyr Leu Glu Ser Phe Cys Glu Asp Val Pro Ser Gly Lys Leu
225 230 235 240

ITI-08-PCT_Sequence_Listing_ST25.txt

Phe	Met	His	Val	Thr	Leu	Gly	Ser	Asp	Val	Glu	Glu	Asp	Leu	Thr	Met	245	250	255
Thr	Arg	Asn	Pro	Gln	Pro	Phe	Met	Arg	Pro	His	Glu	Arg	Asn	Gly	Phe	260	265	270
Thr	Val	Leu	Cys	Pro	Lys	Asn	Met	Ile	Ile	Lys	Pro	Gly	Lys	Ile	Ser	275	280	285
His	Ile	Met	Leu	Asp	Val	Ala	Phe	Thr	Ser	His	Glu	His	Phe	Gly	Leu	290	295	300
Leu	Cys	Pro	Lys	Ser	Ile	Pro	Gly	Leu	Ser	Ile	Ser	Gly	Asn	Leu	Leu	305	310	315
Met	Asn	Gly	Gln	Gln	Ile	Phe	Leu	Glu	Val	Gln	Ala	Ile	Arg	Glu	Thr	325	330	335
Val	Glu	Leu	Arg	Gln	Tyr	Asp	Pro	Val	Ala	Ala	Leu	Phe	Phe	Phe	Asp	340	345	350
Ile	Asp	Leu	Leu	Leu	Gln	Arg	Gly	Pro	Gln	Tyr	Ser	Glu	His	Pro	Thr	355	360	365
Phe	Thr	Ser	Gln	Tyr	Arg	Ile	Gln	Gly	Lys	Leu	Glu	Tyr	Arg	His	Thr	370	375	380
Trp	Asp	Arg	His	Asp	Glu	Gly	Ala	Ala	Gln	Gly	Asp	Asp	Asp	Val	Trp	385	390	395
Thr	Ser	Gly	Ser	Asp	Ser	Asp	Glu	Glu	Leu	Val	Thr	Thr	Glu	Arg	Lys	405	410	415
Thr	Pro	Arg	Val	Thr	Gly	Gly	Gly	Ala	Met	Ala	Gly	Ala	Ser	Thr	Ser	420	425	430
Ala	Gly	Arg	Lys	Arg	Lys	Ser	Ala	Ser	Ser	Ala	Thr	Ala	Cys	Thr	Ser	435	440	445
Gly	Val	Met	Thr	Arg	Gly	Arg	Leu	Lys	Ala	Glu	Ser	Thr	Val	Ala	Pro	450	455	460
Glu	Glu	Asp	Thr	Asp	Glu	Asp	Ser	Asp	Asn	Glu	Ile	His	Asn	Pro	Ala	465	470	475
Val	Phe	Thr	Trp	Pro	Pro	Trp	Gln	Ala	Gly	Ile	Leu	Ala	Arg	Asn	Leu	485	490	495
Val	Pro	Met	Val	Ala	Thr	Val	Gln	Gly	Gln	Asn	Leu	Lys	Tyr	Gln	Glu	500	505	510

ITI-08-PCT_Sequence_Listing_ST25.txt

Phe Phe Trp Asp Ala Asn Asp Ile Tyr Arg Ile Phe Ala Glu Leu Glu
515 520 525

Gly Val Trp Gln Pro Ala Ala Gln Pro Lys Arg Arg Arg His Arg Gln
530 535 540

Asp Ala Leu Pro Gly Pro Cys Ile Ala Ser Thr Pro Lys Lys His Arg
545 550 555 560

Gly

<210> 115

<211> 146

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 115

Leu Leu Gln Thr Gly Ile His Val Arg Val Ser Gln Pro Ser Leu Gly
1 5 10 15

Pro Gly Pro Gly Ala Leu Pro Leu Lys Met Leu Asn Ile Pro Ser Ile
20 25 30

Asn Val His Gly Pro Gly Pro Gly Asp Gln Tyr Val Lys Val Tyr Leu
35 40 45

Glu Ser Phe Cys Glu Asp Val Gly Pro Gly Pro Gly Ile Ile Lys Pro
50 55 60

Gly Lys Ile Ser His Ile Met Leu Asp Val Ala Phe Thr Ser His Gly
65 70 75 80

Pro Gly Pro Gly Pro Gln Tyr Ser Glu His Pro Thr Phe Thr Ser Gln
85 90 95

Tyr Arg Ile Gln Gly Lys Leu Gly Pro Gly Pro Gly Pro Pro Trp Gln
100 105 110

Ala Gly Ile Leu Ala Arg Asn Leu Val Pro Met Val Gly Pro Gly Pro
115 120 125

Gly Lys Tyr Gln Glu Phe Phe Trp Asp Ala Asn Asp Ile Tyr Arg Ile
130 135 140

Phe Ala
145

<210> 116

ITI-08-PCT_Sequence_Listing_ST25.txt

<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 116

Leu Leu Gln Thr Gly Ile His Val Arg Val Ser Gln Pro Ser Leu Pro
1 5 10 15

Met Gly Leu Pro Ala Leu Pro Leu Lys Met Leu Asn Ile Pro Ser Ile
20 25 30

Asn Val His Pro Met Gly Leu Pro Asp Gln Tyr Val Lys Val Tyr Leu
35 40 45

Glu Ser Phe Cys Glu Asp Val Pro Met Gly Leu Pro Ile Ile Lys Pro
50 55 60

Gly Lys Ile Ser His Ile Met Leu Asp Val Ala Phe Thr Ser His Pro
65 70 75 80

Met Gly Leu Pro Pro Gln Tyr Ser Glu His Pro Thr Phe Thr Ser Gln
85 90 95

Tyr Arg Ile Gln Gly Lys Leu Pro Met Gly Leu Pro Pro Pro Trp Gln
100 105 110

Ala Gly Ile Leu Ala Arg Asn Leu Val Pro Met Val Pro Met Gly Leu
115 120 125

Pro Lys Tyr Gln Glu Phe Phe Trp Asp Ala Asn Asp Ile Tyr Arg Ile
130 135 140

Phe Ala
145

<210> 117
<211> 906
<212> PRT
<213> Human herpesvirus 5

<220>
<223> Strain AD169

<400> 117

Met Glu Ser Arg Ile Trp Cys Leu Val Val Cys Val Asn Leu Cys Ile
1 5 10 15

ITI-08-PCT_Sequence_Listing_ST25.txt

Val	Cys	Leu	Gly	Ala	Ala	Val	Ser	Ser	Ser	Ser	Thr	Ser	His	Ala	Thr	20	25	30
Ser	Ser	Thr	His	Asn	Gly	Ser	His	Thr	Ser	Arg	Thr	Thr	Ser	Ala	Gln	35	40	45
Thr	Arg	Ser	Val	Tyr	Ser	Gln	His	Val	Thr	Ser	Ser	Glu	Ala	Val	Ser	50	55	60
His	Arg	Ala	Asn	Glu	Thr	Ile	Tyr	Asn	Thr	Thr	Leu	Lys	Tyr	Gly	Asp	65	70	75
Val	Val	Gly	Val	Asn	Thr	Thr	Lys	Tyr	Pro	Tyr	Arg	Val	Cys	Ser	Met	85	90	95
Ala	Gln	Gly	Thr	Asp	Leu	Ile	Arg	Phe	Glu	Arg	Asn	Ile	Ile	Cys	Thr	100	105	110
Ser	Met	Lys	Pro	Ile	Asn	Glu	Asp	Leu	Asp	Glu	Gly	Ile	Met	Val	Val	115	120	125
Tyr	Lys	Arg	Asn	Ile	Val	Ala	His	Thr	Phe	Lys	Val	Arg	Val	Tyr	Gln	130	135	140
Lys	Val	Leu	Thr	Phe	Arg	Arg	Ser	Tyr	Ala	Tyr	Ile	Tyr	Thr	Thr	Tyr	145	150	155
Leu	Leu	Gly	Ser	Asn	Thr	Glu	Tyr	Val	Ala	Pro	Pro	Met	Trp	Glu	Ile	165	170	175
His	His	Ile	Asn	Lys	Phe	Ala	Gln	Cys	Tyr	Ser	Ser	Tyr	Ser	Arg	Val	180	185	190
Ile	Gly	Gly	Thr	Val	Phe	Val	Ala	Tyr	His	Arg	Asp	Ser	Tyr	Glu	Asn	195	200	205
Lys	Thr	Met	Gln	Leu	Ile	Pro	Asp	Asp	Tyr	Ser	Asn	Thr	His	Ser	Thr	210	215	220
Arg	Tyr	Val	Thr	Val	Lys	Asp	Gln	Trp	His	Ser	Arg	Gly	Ser	Thr	Trp	225	230	235
Leu	Tyr	Arg	Glu	Thr	Cys	Asn	Leu	Asn	Cys	Met	Leu	Thr	Ile	Thr	Thr	245	250	255
Ala	Arg	Ser	Lys	Tyr	Pro	Tyr	His	Phe	Phe	Ala	Thr	Ser	Thr	Gly	Asp	260	265	270
Val	Val	Tyr	Ile	Ser	Pro	Phe	Tyr	Asn	Gly	Thr	Asn	Arg	Asn	Ala	Ser	275	280	285
Tyr	Phe	Gly	Glu	Asn	Ala	Asp	Lys	Phe	Phe	Ile	Phe	Pro	Asn	Tyr	Thr			

ITI-08-PCT_Sequence_Listing_ST25.txt

290

295

300

Ile Val Ser Asp Phe Gly Arg Pro Asn Ala Ala Pro Glu Thr His Arg
 305 310 315 320

Leu Val Ala Phe Leu Glu Arg Ala Asp Ser Val Ile Ser Trp Asp Ile
 325 330 335

Gln Asp Glu Lys Asn Val Thr Cys Gln Leu Thr Phe Trp Glu Ala Ser
 340 345 350

Glu Arg Thr Ile Arg Ser Glu Ala Glu Asp Ser Tyr His Phe Ser Ser
 355 360 365

Ala Lys Met Thr Ala Thr Phe Leu Ser Lys Lys Gln Glu Val Asn Met
 370 375 380

Ser Asp Ser Ala Leu Asp Cys Val Arg Asp Glu Ala Ile Asn Lys Leu
 385 390 395 400

Gln Gln Ile Phe Asn Thr Ser Tyr Asn Gln Thr Tyr Glu Lys Tyr Gly
 405 410 415

Asn Val Ser Val Phe Glu Thr Ser Gly Gly Leu Val Val Phe Trp Gln
 420 425 430

Gly Ile Lys Gln Lys Ser Leu Val Glu Leu Glu Arg Leu Ala Asn Arg
 435 440 445

Ser Ser Leu Asn Ile Thr His Arg Thr Arg Arg Ser Thr Ser Asp Asn
 450 455 460

Asn Thr Thr His Leu Ser Ser Met Glu Ser Val His Asn Leu Val Tyr
 465 470 475 480

Ala Gln Leu Gln Phe Thr Tyr Asp Thr Leu Arg Gly Tyr Ile Asn Arg
 485 490 495

Ala Leu Ala Gln Ile Ala Glu Ala Trp Cys Val Asp Gln Arg Arg Thr
 500 505 510

Leu Glu Val Phe Lys Glu Leu Ser Lys Ile Asn Pro Ser Ala Ile Leu
 515 520 525

Ser Ala Ile Tyr Asn Lys Pro Ile Ala Ala Arg Phe Met Gly Asp Val
 530 535 540

Leu Gly Leu Ala Ser Cys Val Thr Ile Asn Gln Thr Ser Val Lys Val
 545 550 555 560

Leu Arg Asp Met Asn Val Lys Glu Ser Pro Gly Arg Cys Tyr Ser Arg
 565 570 575

ITI-08-PCT_Sequence_Listing_ST25.txt

Pro	Val	Val	Ile	Phe	Asn	Phe	Ala	Asn	Ser	Ser	Tyr	Val	Gln	Tyr	Gly	580	585	590
Gln	Leu	Gly	Glu	Asp	Asn	Glu	Ile	Leu	Leu	Gly	Asn	His	Arg	Thr	Glu	595	600	605
Glu	Cys	Gln	Leu	Pro	Ser	Leu	Lys	Ile	Phe	Ile	Ala	Gly	Asn	Ser	Ala	610	615	620
Tyr	Glu	Tyr	Val	Asp	Tyr	Leu	Phe	Lys	Arg	Met	Ile	Asp	Leu	Ser	Ser	625	630	635
Ile	Ser	Thr	Val	Asp	Ser	Met	Ile	Ala	Leu	Asp	Ile	Asp	Pro	Leu	Glu	645	650	655
Asn	Thr	Asp	Phe	Arg	Val	Leu	Glu	Leu	Tyr	Ser	Gln	Lys	Glu	Leu	Arg	660	665	670
Ser	Ser	Asn	Val	Phe	Asp	Leu	Glu	Glu	Ile	Met	Arg	Glu	Phe	Asn	Ser	675	680	685
Tyr	Lys	Gln	Arg	Val	Lys	Tyr	Val	Glu	Asp	Lys	Val	Val	Asp	Pro	Leu	690	695	700
Pro	Pro	Tyr	Leu	Lys	Gly	Leu	Asp	Asp	Leu	Met	Ser	Gly	Leu	Gly	Ala	705	710	715
Ala	Gly	Lys	Ala	Val	Gly	Val	Ala	Ile	Gly	Ala	Val	Gly	Gly	Ala	Val	725	730	735
Ala	Ser	Val	Val	Glu	Gly	Val	Ala	Thr	Phe	Leu	Lys	Asn	Pro	Phe	Gly	740	745	750
Ala	Phe	Thr	Ile	Ile	Leu	Val	Ala	Ile	Ala	Val	Val	Ile	Ile	Thr	Tyr	755	760	765
Leu	Ile	Tyr	Thr	Arg	Gln	Arg	Arg	Leu	Cys	Thr	Gln	Pro	Leu	Gln	Asn	770	775	780
Leu	Phe	Pro	Tyr	Leu	Val	Ser	Ala	Asp	Gly	Thr	Thr	Val	Thr	Ser	Gly	785	790	795
Ser	Thr	Lys	Asp	Thr	Ser	Leu	Gln	Ala	Pro	Pro	Ser	Tyr	Glu	Glu	Ser	805	810	815
Val	Tyr	Asn	Ser	Gly	Arg	Lys	Gly	Pro	Gly	Pro	Pro	Ser	Ser	Asp	Ala	820	825	830
Ser	Thr	Ala	Ala	Pro	Pro	Tyr	Thr	Asn	Glu	Gln	Ala	Tyr	Gln	Met	Leu	835	840	845

ITI-08-PCT_Sequence_Listing_ST25.txt

Leu Ala Leu Ala Arg Leu Asp Ala Glu Gln Arg Ala Gln Gln Asn Gly
850 855 860

Thr Asp Ser Leu Asp Gly Gln Thr Gly Thr Gln Asp Lys Gly Gln Lys
865 870 875 880

Pro Asn Leu Leu Asp Arg Leu Arg His Arg Lys Asn Gly Tyr Arg His
885 890 895

Leu Lys Asp Ser Asp Glu Glu Glu Asn Val
900 905

<210> 118
<211> 863
<212> PRT
<213> Human herpesvirus 5

<220>
<223> Strain AD169

<400> 118

Val Ser Ser Ser Ser Thr Ser His Ala Thr Ser Ser Thr His Asn Gly
1 5 10 15

Ser His Thr Ser Arg Thr Thr Ser Ala Gln Thr Arg Ser Val Tyr Ser
20 25 30

Gln His Val Thr Ser Ser Glu Ala Val Ser His Arg Ala Asn Glu Thr
35 40 45

Ile Tyr Asn Thr Thr Leu Lys Tyr Gly Asp Val Val Gly Val Asn Thr
50 55 60

Thr Lys Tyr Pro Tyr Arg Val Cys Ser Met Ala Gln Gly Thr Asp Leu
65 70 75 80

Ile Arg Phe Glu Arg Asn Ile Ile Cys Thr Ser Met Lys Pro Ile Asn
85 90 95

Glu Asp Leu Asp Glu Gly Ile Met Val Val Tyr Lys Arg Asn Ile Val
100 105 110

Ala His Thr Phe Lys Val Arg Val Tyr Gln Lys Val Leu Thr Phe Arg
115 120 125

Arg Ser Tyr Ala Tyr Ile Tyr Thr Thr Tyr Leu Leu Gly Ser Asn Thr
130 135 140

Glu Tyr Val Ala Pro Pro Met Trp Glu Ile His His Ile Asn Lys Phe
145 150 155 160

ITI-08-PCT_Sequence_Listing_ST25.txt

Ala	Gln	Cys	Tyr	Ser	Ser	Tyr	Ser	Arg	Val	Ile	Gly	Gly	Thr	Val	Phe	
				165					170					175		
Val	Ala	Tyr	His	Arg	Asp	Ser	Tyr	Glu	Asn	Lys	Thr	Met	Gln	Leu	Ile	
			180					185					190			
Pro	Asp	Asp	Tyr	Ser	Asn	Thr	His	Ser	Thr	Arg	Tyr	Val	Thr	Val	Lys	
		195					200					205				
Asp	Gln	Trp	His	Ser	Arg	Gly	Ser	Thr	Trp	Leu	Tyr	Arg	Glu	Thr	Cys	
	210					215					220					
Asn	Leu	Asn	Cys	Met	Leu	Thr	Ile	Thr	Thr	Ala	Arg	Ser	Lys	Tyr	Pro	
225					230					235					240	
Tyr	His	Phe	Phe	Ala	Thr	Ser	Thr	Gly	Asp	Val	Val	Tyr	Ile	Ser	Pro	
				245					250					255		
Phe	Tyr	Asn	Gly	Thr	Asn	Arg	Asn	Ala	Ser	Tyr	Phe	Gly	Glu	Asn	Ala	
			260					265					270			
Asp	Lys	Phe	Phe	Ile	Phe	Pro	Asn	Tyr	Thr	Ile	Val	Ser	Asp	Phe	Gly	
		275					280					285				
Arg	Pro	Asn	Ala	Ala	Pro	Glu	Thr	His	Arg	Leu	Val	Ala	Phe	Leu	Glu	
	290					295					300					
Arg	Ala	Asp	Ser	Val	Ile	Ser	Trp	Asp	Ile	Gln	Asp	Glu	Lys	Asn	Val	
305					310					315					320	
Thr	Cys	Gln	Leu	Thr	Phe	Trp	Glu	Ala	Ser	Glu	Arg	Thr	Ile	Arg	Ser	
				325					330					335		
Glu	Ala	Glu	Asp	Ser	Tyr	His	Phe	Ser	Ser	Ala	Lys	Met	Thr	Ala	Thr	
			340					345					350			
Phe	Leu	Ser	Lys	Lys	Gln	Glu	Val	Asn	Met	Ser	Asp	Ser	Ala	Leu	Asp	
		355					360					365				
Cys	Val	Arg	Asp	Glu	Ala	Ile	Asn	Lys	Leu	Gln	Gln	Ile	Phe	Asn	Thr	
	370					375					380					
Ser	Tyr	Asn	Gln	Thr	Tyr	Glu	Lys	Tyr	Gly	Asn	Val	Ser	Val	Phe	Glu	
385					390					395					400	
Thr	Ser	Gly	Gly	Leu	Val	Val	Phe	Trp	Gln	Gly	Ile	Lys	Gln	Lys	Ser	
				405					410					415		
Leu	Val	Glu	Leu	Glu	Arg	Leu	Ala	Asn	Arg	Ser	Ser	Leu	Asn	Ile	Thr	
			420					425					430			
His	Arg	Thr	Arg	Arg	Ser	Thr	Ser	Asp	Asn	Asn	Thr	Thr	His	Leu	Ser	

ITI-08-PCT_Sequence_Listing_ST25.txt

```

435                               440                               445
Ser Met Glu Ser Val His Asn Leu Val Tyr Ala Gln Leu Gln Phe Thr
450                               455                               460

Tyr Asp Thr Leu Arg Gly Tyr Ile Asn Arg Ala Leu Ala Gln Ile Ala
465                               470                               475                               480

Glu Ala Trp Cys Val Asp Gln Arg Arg Thr Leu Glu Val Phe Lys Glu
485                               490                               495

Leu Ser Lys Ile Asn Pro Ser Ala Ile Leu Ser Ala Ile Tyr Asn Lys
500                               505                               510

Pro Ile Ala Ala Arg Phe Met Gly Asp Val Leu Gly Leu Ala Ser Cys
515                               520                               525

Val Thr Ile Asn Gln Thr Ser Val Lys Val Leu Arg Asp Met Asn Val
530                               535                               540

Lys Glu Ser Pro Gly Arg Cys Tyr Ser Arg Pro Val Val Ile Phe Asn
545                               550                               555                               560

Phe Ala Asn Ser Ser Tyr Val Gln Tyr Gly Gln Leu Gly Glu Asp Asn
565                               570                               575

Glu Ile Leu Leu Gly Asn His Arg Thr Glu Glu Cys Gln Leu Pro Ser
580                               585                               590

Leu Lys Ile Phe Ile Ala Gly Asn Ser Ala Tyr Glu Tyr Val Asp Tyr
595                               600                               605

Leu Phe Lys Arg Met Ile Asp Leu Ser Ser Ile Ser Thr Val Asp Ser
610                               615                               620

Met Ile Ala Leu Asp Ile Asp Pro Leu Glu Asn Thr Asp Phe Arg Val
625                               630                               635                               640

Leu Glu Leu Tyr Ser Gln Lys Glu Leu Arg Ser Ser Asn Val Phe Asp
645                               650                               655

Leu Glu Glu Ile Met Arg Glu Phe Asn Ser Tyr Lys Gln Arg Val Lys
660                               665                               670

Tyr Val Glu Asp Lys Val Val Asp Pro Leu Pro Pro Tyr Leu Lys Gly
675                               680                               685

Leu Asp Asp Leu Met Ser Gly Leu Gly Ala Ala Gly Lys Ala Val Gly
690                               695                               700

Val Ala Ile Gly Ala Val Gly Gly Ala Val Ala Ser Val Val Glu Gly
705                               710                               715                               720

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Val Ala Thr Phe Leu Lys Asn Pro Thr Arg Gln Arg Arg Leu Cys Thr
725 730 735

Gln Pro Leu Gln Asn Leu Phe Pro Tyr Leu Val Ser Ala Asp Gly Thr
740 745 750

Thr Val Thr Ser Gly Ser Thr Lys Asp Thr Ser Leu Gln Ala Pro Pro
755 760 765

Ser Tyr Glu Glu Ser Val Tyr Asn Ser Gly Arg Lys Gly Pro Gly Pro
770 775 780

Pro Ser Ser Asp Ala Ser Thr Ala Ala Pro Pro Tyr Thr Asn Glu Gln
785 790 795 800

Ala Tyr Gln Met Leu Leu Ala Leu Ala Arg Leu Asp Ala Glu Gln Arg
805 810 815

Ala Gln Gln Asn Gly Thr Asp Ser Leu Asp Gly Gln Thr Gly Thr Gln
820 825 830

Asp Lys Gly Gln Lys Pro Asn Leu Leu Asp Arg Leu Arg His Arg Lys
835 840 845

Asn Gly Tyr Arg His Leu Lys Asp Ser Asp Glu Glu Glu Asn Val
850 855 860

<210> 119

<211> 79

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 119

Thr Thr Ser Ala Gln Thr Arg Ser Val Tyr Ser Gln His Val Thr Gly
1 5 10 15

Pro Gly Pro Gly Gln Leu Ile Pro Asp Asp Tyr Ser Asn Thr His Ser
20 25 30

Thr Arg Tyr Val Gly Pro Gly Pro Gly Val Ser Val Phe Glu Thr Ser
35 40 45

Gly Gly Leu Val Val Phe Trp Gln Gly Pro Gly Pro Gly Asn Ser Ala
50 55 60

Tyr Glu Tyr Val Asp Tyr Leu Phe Lys Arg Met Ile Asp Leu Ser
65 70 75

ITI-08-PCT_Sequence_Listing_ST25.txt

<210> 120
 <211> 79
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 120

Thr Thr Ser Ala Gln Thr Arg Ser Val Tyr Ser Gln His Val Thr Pro
 1 5 10 15

Met Gly Leu Pro Gln Leu Ile Pro Asp Asp Tyr Ser Asn Thr His Ser
 20 25 30

Thr Arg Tyr Val Pro Met Gly Leu Pro Val Ser Val Phe Glu Thr Ser
 35 40 45

Gly Gly Leu Val Val Phe Trp Gln Pro Met Gly Leu Pro Asn Ser Ala
 50 55 60

Tyr Glu Tyr Val Asp Tyr Leu Phe Lys Arg Met Ile Asp Leu Ser
 65 70 75

<210> 121
 <211> 491
 <212> PRT
 <213> Human herpesvirus 5

<220>
 <223> Strain AD169

<400> 121

Met Glu Ser Ser Ala Lys Arg Lys Met Asp Pro Asp Asn Pro Asp Glu
 1 5 10 15

Gly Pro Ser Ser Lys Val Pro Arg Pro Glu Thr Pro Val Thr Lys Ala
 20 25 30

Thr Thr Phe Leu Gln Thr Met Leu Arg Lys Glu Val Asn Ser Gln Leu
 35 40 45

Ser Leu Gly Asp Pro Leu Phe Pro Glu Leu Ala Glu Glu Ser Leu Lys
 50 55 60

Thr Phe Glu Gln Val Thr Glu Asp Cys Asn Glu Asn Pro Glu Lys Asp
 65 70 75 80

Val Leu Ala Glu Leu Val Lys Gln Ile Lys Val Arg Val Asp Met Val

ITI-08-PCT_Sequence_Listing_ST25.txt

85

90

95

Arg His Arg Ile Lys Glu His Met Leu Lys Lys Tyr Thr Gln Thr Glu
 100 105 110

Glu Lys Phe Thr Gly Ala Phe Asn Met Met Gly Gly Cys Leu Gln Asn
 115 120 125

Ala Leu Asp Ile Leu Asp Lys Val His Glu Pro Phe Glu Glu Met Lys
 130 135 140

Cys Ile Gly Leu Thr Met Gln Ser Met Tyr Glu Asn Tyr Ile Val Pro
 145 150 155 160

Glu Asp Lys Arg Glu Met Trp Met Ala Cys Ile Lys Glu Leu His Asp
 165 170 175

Val Ser Lys Gly Ala Ala Asn Lys Leu Gly Gly Ala Leu Gln Ala Lys
 180 185 190

Ala Arg Ala Lys Lys Asp Glu Leu Arg Arg Lys Met Met Tyr Met Cys
 195 200 205

Tyr Arg Asn Ile Glu Phe Phe Thr Lys Asn Ser Ala Phe Pro Lys Thr
 210 215 220

Thr Asn Gly Cys Ser Gln Ala Met Ala Ala Leu Gln Asn Leu Pro Gln
 225 230 235 240

Cys Ser Pro Asp Glu Ile Met Ala Tyr Ala Gln Lys Ile Phe Lys Ile
 245 250 255

Leu Asp Glu Glu Arg Asp Lys Val Leu Thr His Ile Asp His Ile Phe
 260 265 270

Met Asp Ile Leu Thr Thr Cys Val Glu Thr Met Cys Asn Glu Tyr Lys
 275 280 285

Val Thr Ser Asp Ala Cys Met Met Thr Met Tyr Gly Gly Ile Ser Leu
 290 295 300

Leu Ser Glu Phe Cys Arg Val Leu Cys Cys Tyr Val Leu Glu Glu Thr
 305 310 315 320

Ser Val Met Leu Ala Lys Arg Pro Leu Ile Thr Lys Pro Glu Val Ile
 325 330 335

Ser Val Met Lys Arg Arg Ile Glu Glu Ile Cys Met Lys Val Phe Ala
 340 345 350

Gln Tyr Ile Leu Gly Ala Asp Pro Leu Arg Val Cys Ser Pro Ser Val
 355 360 365

ITI-08-PCT_Sequence_Listing_ST25.txt

Asp Asp Leu Arg Ala Ile Ala Glu Glu Ser Asp Glu Glu Glu Ala Ile
370 375 380

Val Ala Tyr Thr Leu Ala Thr Ala Gly Val Ser Ser Ser Asp Ser Leu
385 390 395 400

Val Ser Pro Pro Glu Ser Pro Val Pro Ala Thr Ile Pro Leu Ser Ser
405 410 415

Val Ile Val Ala Glu Asn Ser Asp Gln Glu Glu Ser Glu Gln Ser Asp
420 425 430

Glu Glu Glu Glu Glu Gly Ala Gln Glu Glu Arg Glu Asp Thr Val Ser
435 440 445

Val Lys Ser Glu Pro Val Ser Glu Ile Glu Glu Val Ala Pro Glu Glu
450 455 460

Glu Glu Asp Gly Ala Glu Glu Pro Thr Ala Ser Gly Gly Lys Ser Thr
465 470 475 480

His Pro Met Val Thr Arg Ser Lys Ala Asp Gln
485 490

<210> 122
<211> 156
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 122

Val Leu Ala Glu Leu Val Lys Gln Ile Lys Val Arg Val Asp Met Val
1 5 10 15

Arg His Arg Ile Lys Glu His Met Leu Lys Lys Tyr Thr Gln Gly Pro
20 25 30

Gly Pro Gly Ile Val Pro Glu Asp Lys Arg Glu Met Trp Met Ala Cys
35 40 45

Ile Lys Glu Leu His Gly Pro Gly Pro Gly Lys Asp Glu Leu Arg Arg
50 55 60

Lys Met Met Tyr Met Cys Tyr Arg Asn Ile Glu Phe Phe Thr Lys Asn
65 70 75 80

Ser Ala Phe Pro Lys Thr Thr Gly Pro Gly Pro Gly Ser Val Met Lys
85 90 95

ITI-08-PCT_Sequence_Listing_ST25.txt

Arg Arg Ile Glu Glu Ile Cys Met Lys Val Phe Ala Gln Tyr Ile Gly
100 105 110

Pro Gly Pro Gly Ala Ile Ala Glu Glu Ser Asp Glu Glu Glu Ala Ile
115 120 125

Val Ala Tyr Gly Pro Gly Pro Gly Val Lys Ser Glu Pro Val Ser Glu
130 135 140

Ile Glu Glu Val Ala Pro Glu Glu Glu Glu Asp Gly
145 150 155

<210> 123

<211> 156

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 123

Val Leu Ala Glu Leu Val Lys Gln Ile Lys Val Arg Val Asp Met Val
1 5 10 15

Arg His Arg Ile Lys Glu His Met Leu Lys Lys Tyr Thr Gln Pro Met
20 25 30

Gly Leu Pro Ile Val Pro Glu Asp Lys Arg Glu Met Trp Met Ala Cys
35 40 45

Ile Lys Glu Leu His Pro Met Gly Leu Pro Lys Asp Glu Leu Arg Arg
50 55 60

Lys Met Met Tyr Met Cys Tyr Arg Asn Ile Glu Phe Phe Thr Lys Asn
65 70 75 80

Ser Ala Phe Pro Lys Thr Thr Pro Met Gly Leu Pro Ser Val Met Lys
85 90 95

Arg Arg Ile Glu Glu Ile Cys Met Lys Val Phe Ala Gln Tyr Ile Pro
100 105 110

Met Gly Leu Pro Ala Ile Ala Glu Glu Ser Asp Glu Glu Glu Ala Ile
115 120 125

Val Ala Tyr Pro Met Gly Leu Pro Val Lys Ser Glu Pro Val Ser Glu
130 135 140

Ile Glu Glu Val Ala Pro Glu Glu Glu Glu Asp Gly
145 150 155

ITI-08-PCT_Sequence_Listing_ST25.txt

<210> 124
 <211> 79
 <212> PRT
 <213> Human betaherpesvirus 5

<400> 124

Met Leu Ser Val Met Val Ser Ser Ser Leu Val Leu Ile Val Phe Phe
 1 5 10 15

Leu Gly Ala Ser Glu Glu Ala Lys Pro Ala Thr Thr Thr Thr Ile Lys
 20 25 30

Asn Thr Lys Pro Gln Cys Arg Pro Glu Asp Tyr Ala Thr Arg Leu Gln
 35 40 45

Asp Leu Arg Val Thr Phe His Arg Val Lys Pro Thr Leu Val Gly His
 50 55 60

Val Gly Thr Val Tyr Cys Asp Gly Leu Ser Phe Pro Arg Val Gly
 65 70 75

<210> 125
 <211> 54
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 125

Ala Thr Thr Thr Thr Ile Lys Asn Thr Lys Pro Gln Cys Arg Pro Glu
 1 5 10 15

Asp Tyr Ala Thr Arg Leu Gln Asp Leu Arg Val Thr Phe His Arg Val
 20 25 30

Lys Pro Thr Leu Val Gly His Val Gly Thr Val Tyr Cys Asp Gly Leu
 35 40 45

Ser Phe Pro Arg Val Gly
 50

<210> 126
 <211> 354
 <212> PRT
 <213> Human betaherpesvirus 5

<400> 126

ITI-08-PCT_Sequence_Listing_ST25.txt

Met	Thr	Pro	Thr	Thr	Thr	Thr	Ala	Glu	Leu	Thr	Thr	Glu	Phe	Asp	Tyr	1	5	10	15
Asp	Glu	Asp	Ala	Thr	Pro	Cys	Val	Phe	Thr	Asp	Val	Leu	Asn	Gln	Ser	20	25	30	
Lys	Pro	Val	Thr	Leu	Phe	Leu	Tyr	Gly	Val	Val	Phe	Leu	Phe	Gly	Ser	35	40	45	
Ile	Gly	Asn	Phe	Leu	Val	Ile	Phe	Thr	Ile	Thr	Trp	Arg	Arg	Arg	Ile	50	55	60	
Gln	Cys	Ser	Gly	Asp	Val	Tyr	Phe	Ile	Asn	Leu	Ala	Ala	Ala	Asp	Leu	65	70	75	80
Leu	Phe	Val	Cys	Thr	Leu	Pro	Leu	Trp	Met	Gln	Tyr	Leu	Leu	Asp	His	85	90	95	
Asn	Ser	Leu	Ala	Ser	Val	Pro	Cys	Thr	Leu	Leu	Thr	Ala	Cys	Phe	Tyr	100	105	110	
Val	Ala	Met	Phe	Ala	Ser	Leu	Cys	Phe	Ile	Thr	Glu	Ile	Ala	Leu	Asp	115	120	125	
Arg	Tyr	Tyr	Ala	Ile	Val	Tyr	Met	Arg	Tyr	Arg	Pro	Val	Lys	Gln	Ala	130	135	140	
Cys	Leu	Phe	Ser	Ile	Phe	Trp	Trp	Ile	Phe	Ala	Val	Ile	Ile	Ala	Ile	145	150	155	160
Pro	His	Phe	Met	Val	Val	Thr	Lys	Lys	Asp	Asn	Gln	Cys	Met	Thr	Asp	165	170	175	
Tyr	Asp	Tyr	Leu	Glu	Val	Ser	Tyr	Pro	Ile	Ile	Leu	Asn	Val	Glu	Leu	180	185	190	
Met	Leu	Gly	Ala	Phe	Val	Ile	Pro	Leu	Ser	Val	Ile	Ser	Tyr	Cys	Tyr	195	200	205	
Tyr	Arg	Ile	Ser	Arg	Ile	Val	Ala	Val	Ser	Gln	Ser	Arg	His	Lys	Gly	210	215	220	
Arg	Ile	Val	Arg	Val	Leu	Ile	Ala	Val	Val	Leu	Val	Phe	Ile	Ile	Phe	225	230	235	240
Trp	Leu	Pro	Tyr	His	Leu	Thr	Leu	Phe	Val	Asp	Thr	Leu	Lys	Leu	Leu	245	250	255	
Lys	Trp	Ile	Ser	Ser	Ser	Cys	Glu	Phe	Glu	Arg	Ser	Leu	Lys	Arg	Ala	260	265	270	
Leu	Ile	Leu	Thr	Glu	Ser	Leu	Ala	Phe	Cys	His	Cys	Cys	Leu	Asn	Pro				

ITI-08-PCT_Sequence_Listing_ST25.txt

275

280

285

Leu Leu Tyr Val Phe Val Gly Thr Lys Phe Arg Gln Glu Leu His Cys
290 295 300

Leu Leu Ala Glu Phe Arg Gln Arg Leu Phe Ser Arg Asp Val Ser Trp
305 310 315 320

Tyr His Ser Met Ser Phe Ser Arg Arg Ser Ser Pro Ser Arg Arg Glu
325 330 335

Thr Ser Ser Asp Thr Leu Ser Asp Glu Val Cys Arg Val Ser Gln Ile
340 345 350

Ile Pro

<210> 127

<211> 191

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 127

Met Thr Pro Thr Thr Thr Thr Ala Glu Leu Thr Thr Glu Phe Asp Tyr
1 5 10 15

Asp Glu Asp Ala Thr Pro Cys Val Phe Thr Asp Val Leu Asn Gln Ser
20 25 30

Lys Pro Val Thr Thr Trp Arg Arg Arg Ile Gln Cys Ser Gly Asp Asp
35 40 45

His Asn Ser Leu Glu Ile Ala Leu Asp Arg Tyr Tyr Ala Ile Val Tyr
50 55 60

Met Arg Tyr Arg Pro Val Lys Gln Thr Lys Lys Asp Asn Gln Cys Met
65 70 75 80

Thr Asp Tyr Asp Tyr Leu Glu Val Ser Tyr Pro Arg Ile Ser Arg Ile
85 90 95

Val Ala Val Ser Gln Ser Arg His Lys Gly Arg Ile Val Arg Asp Thr
100 105 110

Leu Lys Leu Leu Lys Trp Ile Ser Ser Ser Cys Glu Phe Glu Arg Ser
115 120 125

Leu Lys Arg Gly Thr Lys Phe Arg Gln Glu Leu His Cys Leu Leu Ala
130 135 140

ITI-08-PCT_Sequence_Listing_ST25.txt

Glu Phe Arg Gln Arg Leu Phe Ser Arg Asp Val Ser Trp Tyr His Ser
145 150 155 160

Met Ser Phe Ser Arg Arg Ser Ser Pro Ser Arg Arg Glu Thr Ser Ser
165 170 175

Asp Thr Leu Ser Asp Glu Val Cys Arg Val Ser Gln Ile Ile Pro
180 185 190

<210> 128
<211> 327
<212> PRT
<213> Homo sapiens

<400> 128

Met Leu Pro Arg Val Gly Cys Pro Ala Leu Pro Leu Pro Pro Pro Pro
1 5 10 15

Leu Leu Pro Leu Leu Pro Leu Leu Leu Leu Leu Gly Ala Ser Gly
20 25 30

Gly Gly Gly Gly Ala Arg Ala Glu Val Leu Phe Arg Cys Pro Pro Cys
35 40 45

Thr Pro Glu Arg Leu Ala Ala Cys Gly Pro Pro Pro Val Ala Pro Pro
50 55 60

Ala Ala Val Ala Ala Val Ala Gly Gly Ala Arg Met Pro Cys Ala Glu
65 70 75 80

Leu Val Arg Glu Pro Gly Cys Gly Cys Cys Ser Val Cys Ala Arg Leu
85 90 95

Glu Gly Glu Ala Cys Gly Val Tyr Thr Pro Arg Cys Gly Gln Gly Leu
100 105 110

Arg Cys Tyr Pro His Pro Gly Ser Glu Leu Pro Leu Gln Ala Leu Val
115 120 125

Met Gly Glu Gly Thr Cys Glu Lys Arg Arg Asp Ala Glu Tyr Gly Ala
130 135 140

Ser Pro Glu Gln Val Ala Asp Asn Gly Asp Asp His Ser Glu Gly Gly
145 150 155 160

Leu Val Glu Asn His Val Asp Ser Thr Met Asn Met Leu Gly Gly Gly
165 170 175

Gly Ser Ala Gly Arg Lys Pro Leu Lys Ser Gly Met Lys Glu Leu Ala
180 185 190

ITI-08-PCT_Sequence_Listing_ST25.txt

Val Phe Arg Glu Lys Val Thr Glu Gln His Arg Gln Met Gly Lys Gly
195 200 205

Gly Lys His His Leu Gly Leu Glu Glu Pro Lys Lys Leu Arg Pro Pro
210 215 220

Pro Ala Arg Thr Pro Cys Gln Gln Glu Leu Asp Gln Val Leu Glu Arg
225 230 235 240

Ile Ser Thr Met Arg Leu Pro Asp Glu Arg Gly Pro Leu Glu His Leu
245 250 255

Tyr Ser Leu His Ile Pro Asn Cys Asp Lys His Gly Leu Tyr Asn Leu
260 265 270

Lys Gln Cys Lys Met Ser Leu Asn Gln Arg Gly Glu Cys Trp Cys Val
275 280 285

Asn Pro Asn Thr Gly Lys Leu Ile Gln Gly Ala Pro Thr Ile Arg Gly
290 295 300

Asp Pro Glu Cys His Leu Phe Tyr Asn Glu Gln Gln Glu Ala Arg Gly
305 310 315 320

Val His Thr Gln Arg Met Gln
325

<210> 129
<211> 175
<212> PRT
<213> Human cytomegalovirus

<220>
<223> Strain AD169

<400> 129

Met Leu Ser Val Met Val Ser Ser Ser Leu Val Leu Ile Val Phe Phe
1 5 10 15

Leu Gly Ala Ser Glu Glu Ala Lys Pro Ala Thr Thr Thr Ile Lys Asn
20 25 30

Thr Lys Pro Gln Cys Arg Pro Glu Asp Tyr Ala Thr Arg Leu Gln Asp
35 40 45

Leu Arg Val Thr Phe His Arg Val Lys Pro Thr Leu Gln Arg Glu Asp
50 55 60

Asp Tyr Ser Val Trp Leu Asp Gly Thr Val Val Lys Gly Cys Trp Gly
65 70 75 80

ITI-08-PCT_Sequence_Listing_ST25.txt

Cys Ser Val Met Asp Trp Leu Leu Arg Arg Tyr Leu Glu Ile Val Phe
85 90 95

Pro Ala Gly Asp His Val Tyr Pro Gly Leu Lys Thr Glu Leu His Ser
100 105 110

Met Arg Ser Thr Leu Glu Ser Ile Tyr Lys Asp Met Arg Gln Cys Pro
115 120 125

Leu Leu Gly Cys Gly Asp Lys Ser Val Ile Ser Arg Leu Ser Gln Glu
130 135 140

Ala Glu Arg Lys Ser Asp Asn Gly Thr Arg Lys Gly Leu Ser Glu Leu
145 150 155 160

Asp Thr Leu Phe Ser Arg Leu Glu Glu Tyr Leu His Ser Arg Lys
165 170 175

<210> 130

<211> 150

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 130

Ala Thr Thr Thr Ile Lys Asn Thr Lys Pro Gln Cys Arg Pro Glu Asp
1 5 10 15

Tyr Ala Thr Arg Leu Gln Asp Leu Arg Val Thr Phe His Arg Val Lys
20 25 30

Pro Thr Leu Gln Arg Glu Asp Asp Tyr Ser Val Trp Leu Asp Gly Thr
35 40 45

Val Val Lys Gly Cys Trp Gly Cys Ser Val Met Asp Trp Leu Leu Arg
50 55 60

Arg Tyr Leu Glu Ile Val Phe Pro Ala Gly Asp His Val Tyr Pro Gly
65 70 75 80

Leu Lys Thr Glu Leu His Ser Met Arg Ser Thr Leu Glu Ser Ile Tyr
85 90 95

Lys Asp Met Arg Gln Cys Pro Leu Leu Gly Cys Gly Asp Lys Ser Val
100 105 110

Ile Ser Arg Leu Ser Gln Glu Ala Glu Arg Lys Ser Asp Asn Gly Thr
115 120 125

ITI-08-PCT_Sequence_Listing_ST25.txt

Arg Lys Gly Leu Ser Glu Leu Asp Thr Leu Phe Ser Arg Leu Glu Glu
130 135 140

Tyr Leu His Ser Arg Lys
145 150

<210> 131
<211> 176
<212> PRT
<213> Human cytomegalovirus

<220>
<223> Strain Merlin

<400> 131

Met Lys Pro Leu Val Met Leu Ile Cys Phe Gly Val Ile Leu Leu Glu
1 5 10 15

Leu Gly Val Thr Lys Val Cys Gln His Asn Glu Val Gln Leu Gly Asn
20 25 30

Glu Cys Cys Pro Pro Cys Gly Leu Gly Gln Arg Val Thr Lys Val Cys
35 40 45

Thr Glu Arg Thr Ser Val Thr Cys Thr Pro Cys Pro Asn Gly Thr Tyr
50 55 60

Val Ser Gly Leu Tyr Asn Cys Thr Asp Cys Thr Gln Cys Asn Val Thr
65 70 75 80

Gln Val Met Ile Arg Asn Cys Thr Ser Thr Asn Asn Thr Val Cys Ala
85 90 95

Pro Lys Asn His Thr Tyr Phe Ser Thr Pro Gly Val Gln His His Lys
100 105 110

Gln Arg Gln Gln Asn His Thr Ala His Ile Thr Val Lys Gln Gly Lys
115 120 125

Ser Gly Arg His Thr Leu Ala Trp Leu Ser Leu Phe Ile Phe Leu Val
130 135 140

Gly Ile Ile Leu Leu Ile Leu Tyr Leu Ile Ala Ala Tyr Arg Ser Glu
145 150 155 160

Arg Cys Gln Gln Cys Cys Ser Ile Gly Lys Ile Phe Tyr Arg Thr Leu
165 170 175

<210> 132
<211> 135

ITI-08-PCT_Sequence_Listing_ST25.txt

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 132

Lys Val Cys Gln His Asn Glu Val Gln Leu Gly Asn Glu Cys Cys Pro
1 5 10 15

Pro Cys Gly Leu Gly Gln Arg Val Thr Lys Val Cys Thr Glu Arg Thr
20 25 30

Ser Val Thr Cys Thr Pro Cys Pro Asn Gly Thr Tyr Val Ser Gly Leu
35 40 45

Tyr Asn Cys Thr Asp Cys Thr Gln Cys Asn Val Thr Gln Val Met Ile
50 55 60

Arg Asn Cys Thr Ser Thr Asn Asn Thr Val Cys Ala Pro Lys Asn His
65 70 75 80

Thr Tyr Phe Ser Thr Pro Gly Val Gln His His Lys Gln Arg Gln Gln
85 90 95

Asn His Thr Ala His Ile Thr Val Lys Gln Gly Lys Ser Gly Arg His
100 105 110

Thr Ala Ala Tyr Arg Ser Glu Arg Cys Gln Gln Cys Cys Ser Ile Gly
115 120 125

Lys Ile Phe Tyr Arg Thr Leu
130 135

<210> 133
<211> 338
<212> PRT
<213> Human cytomegalovirus

<220>
<223> Strain Merlin

<400> 133

Met Cys Arg Arg Glu Ser Leu Arg Thr Leu Pro Trp Leu Phe Trp Val
1 5 10 15

Leu Leu Ser Cys Pro Arg Leu Leu Glu Tyr Ser Ser Ser Ser Phe Pro
20 25 30

Phe Ala Thr Ala Asp Ile Ala Glu Lys Met Trp Ala Glu Asn Tyr Glu

35 40 45

Page 194

ITI-08-PCT_Sequence_Listing_ST25.txt

Tyr Arg Arg Leu Pro Thr Tyr Asp Ser Tyr Pro Gly Val Lys Lys Met
325 330 335

Lys Arg

<210> 134
<211> 281
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 134

Asp Ile Ala Glu Lys Met Trp Ala Glu Asn Tyr Glu Thr Thr Ser Pro
1 5 10 15

Ala Pro Val Leu Val Ala Glu Gly Glu Gln Val Thr Ile Pro Cys Thr
20 25 30

Val Met Thr His Ser Trp Pro Met Val Ser Ile Arg Ala Arg Phe Cys
35 40 45

Arg Ser His Asp Gly Ser Asp Glu Leu Ile Leu Asp Ala Val Lys Gly
50 55 60

His Arg Leu Met Asn Gly Leu Gln Tyr Arg Leu Pro Tyr Ala Thr Trp
65 70 75 80

Asn Phe Ser Gln Leu His Leu Gly Gln Ile Phe Ser Leu Thr Phe Asn
85 90 95

Val Ser Thr Asp Thr Ala Gly Met Tyr Glu Cys Val Leu Arg Asn Tyr
100 105 110

Ser His Gly Leu Ile Met Gln Arg Phe Val Ile Leu Thr Gln Leu Glu
115 120 125

Thr Leu Ser Arg Pro Asp Glu Pro Cys Cys Thr Pro Ala Leu Gly Arg
130 135 140

Tyr Ser Leu Gly Asp Gln Ile Trp Ser Pro Thr Pro Trp Arg Leu Arg
145 150 155 160

Asn His Asp Cys Gly Met Tyr Arg Gly Phe Gln Arg Asn Tyr Phe Tyr
165 170 175

Ile Gly Arg Ala Asp Ala Glu Asp Cys Trp Lys Pro Ala Cys Pro Asp
180 185 190

ITI-08-PCT_Sequence_Listing_ST25.txt

Glu Glu Pro Asp Arg Cys Trp Thr Val Ile Gln Arg Tyr Arg Leu Pro
195 200 205

Gly Asp Cys Tyr Arg Ser Gln Pro His Pro Pro Lys Phe Leu Pro Val
210 215 220

Thr Pro Ala Pro Pro Ala Asp Ile Asp Thr Gly Met Ser Pro Trp Ala
225 230 235 240

Thr Arg Tyr Leu Gln Cys Cys Gly Arg Trp Cys Pro Thr Pro Gly Arg
245 250 255

Gly Arg Arg Gly Gly Glu Gly Tyr Arg Arg Leu Pro Thr Tyr Asp Ser
260 265 270

Tyr Pro Gly Val Lys Lys Met Lys Arg
275 280

<210> 135
<211> 215
<212> PRT
<213> Human cytomegalovirus

<220>
<223> Strain AD169

<400> 135

Met Asn Leu Val Met Leu Ile Leu Ala Leu Trp Ala Pro Val Ala Gly
1 5 10 15

Ser Met Pro Glu Leu Ser Leu Thr Leu Phe Asp Glu Pro Pro Pro Leu
20 25 30

Val Glu Thr Glu Pro Leu Pro Pro Leu Ser Asp Val Ser Glu Tyr Arg
35 40 45

Val Glu Tyr Ser Glu Ala Arg Cys Val Leu Arg Ser Gly Gly Arg Leu
50 55 60

Glu Ala Leu Trp Thr Leu Arg Gly Asn Leu Ser Val Pro Thr Pro Thr
65 70 75 80

Pro Arg Val Tyr Tyr Gln Thr Leu Glu Gly Tyr Ala Asp Arg Val Pro
85 90 95

Thr Pro Val Glu Asp Val Ser Glu Ser Leu Val Ala Lys Arg Tyr Trp
100 105 110

Leu Arg Asp Tyr Arg Val Pro Gln Arg Thr Lys Leu Val Leu Phe Tyr
115 120 125

ITI-08-PCT_Sequence_Listing_ST25.txt

Phe Ser Pro Cys His Gln Cys Gln Thr Tyr Tyr Val Glu Cys Glu Pro
130 135 140

Arg Cys Leu Val Pro Trp Val Pro Leu Trp Ser Ser Leu Glu Asp Ile
145 150 155 160

Glu Arg Leu Leu Phe Glu Asp Arg Arg Leu Met Ala Tyr Tyr Ala Leu
165 170 175

Thr Ile Lys Ser Ala Gln Tyr Thr Leu Met Met Val Ala Val Ile Gln
180 185 190

Val Phe Trp Gly Leu Tyr Val Lys Gly Trp Leu His Arg His Phe Pro
195 200 205

Trp Met Phe Ser Asp Gln Trp
210 215

<210> 136
<211> 178
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 136

Met Pro Glu Leu Ser Leu Thr Leu Phe Asp Glu Pro Pro Pro Leu Val
1 5 10 15

Glu Thr Glu Pro Leu Pro Pro Leu Ser Asp Val Ser Glu Tyr Arg Val
20 25 30

Glu Tyr Ser Glu Ala Arg Cys Val Leu Arg Ser Gly Gly Arg Leu Glu
35 40 45

Ala Leu Trp Thr Leu Arg Gly Asn Leu Ser Val Pro Thr Pro Thr Pro
50 55 60

Arg Val Tyr Tyr Gln Thr Leu Glu Gly Tyr Ala Asp Arg Val Pro Thr
65 70 75 80

Pro Val Glu Asp Val Ser Glu Ser Leu Val Ala Lys Arg Tyr Trp Leu
85 90 95

Arg Asp Tyr Arg Val Pro Gln Arg Thr Lys Leu Val Leu Phe Tyr Phe
100 105 110

Ser Pro Cys His Gln Cys Gln Thr Tyr Tyr Val Glu Cys Glu Pro Arg
115 120 125

ITI-08-PCT_Sequence_Listing_ST25.txt

Cys Leu Val Pro Trp Val Pro Leu Trp Ser Ser Leu Glu Asp Ile Glu
130 135 140

Arg Leu Leu Phe Glu Asp Arg Arg Leu Met Ala Tyr Tyr Ala Leu Thr
145 150 155 160

Ile Lys Ser Ala Gln Tyr His Arg His Phe Pro Trp Met Phe Ser Asp
165 170 175

Gln Trp

<210> 137

<211> 742

<212> PRT

<213> Human cytomegalovirus

<400> 137

Met Arg Pro Gly Leu Pro Ser Tyr Leu Ile Val Leu Ala Val Cys Leu
1 5 10 15

Leu Ser His Leu Leu Ser Pro Arg Tyr Gly Ala Glu Ala Val Ser Glu
20 25 30

Pro Leu Asp Lys Ala Phe His Leu Leu Leu Asn Thr Tyr Gly Arg Pro
35 40 45

Ile Arg Phe Leu Arg Glu Asn Ala Thr Gln Cys Thr Tyr Asn Ser Ser
50 55 60

Leu Arg Asn Ser Thr Val Val Arg Glu Asn Ala Ile Ser Phe Asn Phe
65 70 75 80

Phe Gln Ser Tyr Asn Gln Tyr Tyr Val Phe His Met Pro Arg Cys Leu
85 90 95

Phe Ala Gly Pro Leu Ala Glu Gln Phe Leu Asn Gln Val Asp Leu Thr
100 105 110

Glu Thr Leu Glu Arg Tyr Gln Gln Arg Leu Asn Thr Tyr Ala Leu Val
115 120 125

Ser Lys Asp Leu Ala Ser Tyr Arg Ser Phe Ser Gln Gln Leu Lys Ala
130 135 140

Gln Asp Ser Leu Gly Glu Gln Pro Thr Thr Val Pro Pro Pro Ile Asp
145 150 155 160

Leu Ser Ile Pro His Val Trp Met Pro Pro Gln Thr Thr Pro His Gly
165 170 175

Trp Thr Glu Ser His Thr Thr Ser Gly Leu His Arg Pro His Phe Asn

180 185 190

Page 199

ITI-08-PCT_Sequence_Listing_ST25.txt

Gln	Glu	Leu	Tyr	Leu	Met	Gly	Ser	Leu	Val	His	Ser	Met	Leu	Val	His
465					470					475					480
Thr	Thr	Glu	Arg	Arg	Glu	Ile	Phe	Ile	Val	Glu	Thr	Gly	Leu	Cys	Ser
				485					490					495	
Leu	Ala	Glu	Leu	Ser	His	Phe	Thr	Gln	Leu	Leu	Ala	His	Pro	His	His
			500					505					510		
Glu	Tyr	Leu	Ser	Asp	Leu	Tyr	Thr	Pro	Cys	Ser	Ser	Ser	Gly	Arg	Arg
		515					520					525			
Asp	His	Ser	Leu	Glu	Arg	Leu	Thr	Arg	Leu	Phe	Pro	Asp	Ala	Thr	Val
	530					535					540				
Pro	Thr	Thr	Val	Pro	Thr	Ala	Leu	Ser	Ile	Leu	Ser	Thr	Met	Gln	Pro
545					550					555					560
Ser	Thr	Leu	Glu	Thr	Phe	Pro	Asp	Leu	Phe	Cys	Leu	Pro	Leu	Gly	Glu
				565					570					575	
Ser	Phe	Ser	Ala	Leu	Thr	Val	Ser	Glu	His	Val	Ser	Tyr	Val	Val	Thr
			580					585					590		
Asn	Gln	Tyr	Leu	Ile	Lys	Gly	Ile	Ser	Tyr	Pro	Val	Ser	Thr	Thr	Val
		595				600						605			
Val	Gly	Gln	Ser	Leu	Ile	Ile	Thr	Gln	Thr	Asp	Ser	Gln	Ser	Lys	Cys
	610					615					620				
Glu	Leu	Thr	Arg	Asn	Met	His	Thr	Thr	His	Ser	Ile	Thr	Ala	Ala	Leu
625					630					635					640
Asn	Ile	Ser	Leu	Glu	Asn	Cys	Ala	Phe	Cys	Gln	Ser	Ala	Leu	Leu	Glu
				645					650					655	
Tyr	Asp	Asp	Thr	Gln	Gly	Val	Ile	Asn	Ile	Met	Tyr	Met	His	Asp	Ser
			660					665					670		
Asp	Asp	Val	Leu	Phe	Ala	Leu	Asp	Pro	Tyr	Asn	Glu	Val	Val	Val	Ser
		675					680					685			
Ser	Pro	Arg	Thr	His	Tyr	Leu	Met	Leu	Leu	Lys	Asn	Gly	Thr	Val	Leu
	690					695					700				
Glu	Val	Thr	Asp	Val	Val	Val	Asp	Ala	Thr	Asp	Ser	Arg	Leu	Leu	Met
705					710					715					720
Met	Ser	Val	Tyr	Ala	Leu	Ser	Ala	Ile	Ile	Gly	Ile	Tyr	Leu	Leu	Tyr
				725					730					735	

ITI-08-PCT_Sequence_Listing_ST25.txt

Arg Met Leu Lys Thr Cys
740

<210> 138
<211> 694
<212> PRT
<213> Human cytomegalovirus

<400> 138

Val Ser Glu Pro Leu Asp Lys Ala Phe His Leu Leu Leu Asn Thr Tyr
1 5 10 15

Gly Arg Pro Ile Arg Phe Leu Arg Glu Asn Ala Thr Gln Cys Thr Tyr
20 25 30

Asn Ser Ser Leu Arg Asn Ser Thr Val Val Arg Glu Asn Ala Ile Ser
35 40 45

Phe Asn Phe Phe Gln Ser Tyr Asn Gln Tyr Tyr Val Phe His Met Pro
50 55 60

Arg Cys Leu Phe Ala Gly Pro Leu Ala Glu Gln Phe Leu Asn Gln Val
65 70 75 80

Asp Leu Thr Glu Thr Leu Glu Arg Tyr Gln Gln Arg Leu Asn Thr Tyr
85 90 95

Ala Leu Val Ser Lys Asp Leu Ala Ser Tyr Arg Ser Phe Ser Gln Gln
100 105 110

Leu Lys Ala Gln Asp Ser Leu Gly Glu Gln Pro Thr Thr Val Pro Pro
115 120 125

Pro Ile Asp Leu Ser Ile Pro His Val Trp Met Pro Pro Gln Thr Thr
130 135 140

Pro His Gly Trp Thr Glu Ser His Thr Thr Ser Gly Leu His Arg Pro
145 150 155 160

His Phe Asn Gln Thr Cys Ile Leu Phe Asp Gly His Asp Leu Leu Phe
165 170 175

Ser Thr Val Thr Pro Cys Leu His Gln Gly Phe Tyr Leu Ile Asp Glu
180 185 190

Leu Arg Tyr Val Lys Ile Thr Leu Thr Glu Asp Phe Phe Val Val Thr
195 200 205

Val Ser Ile Asp Asp Asp Thr Pro Met Leu Leu Ile Phe Gly His Leu
210 215 220

ITI-08-PCT_Sequence_Listing_ST25.txt

```

Pro Arg Val Leu Phe Lys Ala Pro Tyr Gln Arg Asp Asn Phe Ile Leu
225                230                235                240

Arg Gln Thr Glu Lys His Glu Leu Leu Val Leu Val Lys Lys Asp Gln
                245                250                255

Leu Asn Arg His Ser Tyr Leu Lys Asp Pro Asp Phe Leu Asp Ala Ala
                260                265                270

Leu Asp Phe Asn Tyr Leu Asp Leu Ser Ala Leu Leu Arg Asn Ser Phe
                275                280                285

His Arg Tyr Ala Val Asp Val Leu Lys Ser Gly Arg Cys Gln Met Leu
                290                295                300

Asp Arg Arg Thr Val Glu Met Ala Phe Ala Tyr Ala Leu Ala Leu Phe
305                310                315                320

Ala Ala Ala Arg Gln Glu Glu Ala Gly Ala Gln Val Ser Val Pro Arg
                325                330                335

Ala Leu Asp Arg Gln Ala Ala Leu Leu Gln Ile Gln Glu Phe Met Ile
                340                345                350

Thr Cys Leu Ser Gln Thr Pro Pro Arg Thr Thr Leu Leu Leu Tyr Pro
                355                360                365

Thr Ala Val Asp Leu Ala Lys Arg Ala Leu Trp Thr Pro Asn Gln Ile
                370                375                380

Thr Asp Ile Thr Ser Leu Val Arg Leu Val Tyr Ile Leu Ser Lys Gln
385                390                395                400

Asn Gln Gln His Leu Ile Pro Gln Trp Ala Leu Arg Gln Ile Ala Asp
                405                410                415

Phe Ala Leu Lys Leu His Lys Thr His Leu Ala Ser Phe Leu Ser Ala
                420                425                430

Phe Ala Arg Gln Glu Leu Tyr Leu Met Gly Ser Leu Val His Ser Met
                435                440                445

Leu Val His Thr Thr Glu Arg Arg Glu Ile Phe Ile Val Glu Thr Gly
                450                455                460

Leu Cys Ser Leu Ala Glu Leu Ser His Phe Thr Gln Leu Leu Ala His
465                470                475                480

Pro His His Glu Tyr Leu Ser Asp Leu Tyr Thr Pro Cys Ser Ser Ser
                485                490                495

Gly Arg Arg Asp His Ser Leu Glu Arg Leu Thr Arg Leu Phe Pro Asp

```

ITI-08-PCT_Sequence_Listing_ST25.txt

500

505

510

Ala Thr Val Pro Thr Thr Val Pro Thr Ala Leu Ser Ile Leu Ser Thr
515 520 525

Met Gln Pro Ser Thr Leu Glu Thr Phe Pro Asp Leu Phe Cys Leu Pro
530 535 540

Leu Gly Glu Ser Phe Ser Ala Leu Thr Val Ser Glu His Val Ser Tyr
545 550 555 560

Val Val Thr Asn Gln Tyr Leu Ile Lys Gly Ile Ser Tyr Pro Val Ser
565 570 575

Thr Thr Val Val Gly Gln Ser Leu Ile Ile Thr Gln Thr Asp Ser Gln
580 585 590

Ser Lys Cys Glu Leu Thr Arg Asn Met His Thr Thr His Ser Ile Thr
595 600 605

Ala Ala Leu Asn Ile Ser Leu Glu Asn Cys Ala Phe Cys Gln Ser Ala
610 615 620

Leu Leu Glu Tyr Asp Asp Thr Gln Gly Val Ile Asn Ile Met Tyr Met
625 630 635 640

His Asp Ser Asp Asp Val Leu Phe Ala Leu Asp Pro Tyr Asn Glu Val
645 650 655

Val Val Ser Ser Pro Arg Thr His Tyr Leu Met Leu Leu Lys Asn Gly
660 665 670

Thr Val Leu Glu Val Thr Asp Val Val Val Asp Ala Thr Asp Ser Arg
675 680 685

Arg Met Leu Lys Thr Cys
690

<210> 139
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 139

Thr Tyr Asn Ser Ser Leu Arg Asn Ser Thr Val Val Arg Glu Asn Ala
1 5 10 15

Ile Ser Phe Asn Phe Phe Gln Ser Tyr Asn Gln Tyr Tyr Val Phe His

ITI-08-PCT_Sequence_Listing_ST25.txt

20

25

30

Met Pro Arg Gly Pro Gly Pro Gly Asp Leu Thr Glu Thr Leu Glu Arg
35 40 45

Tyr Gln Gln Arg Leu Asn Thr Tyr Ala Leu Val Ser Lys Asp Leu Ala
50 55 60

Ser Tyr Arg Ser Phe Ser Gly Pro Gly Pro Gly Ser His Thr Thr Ser
65 70 75 80

Gly Leu His Arg Pro His Phe Asn Gln Thr Cys Ile Leu Phe Asp Gly
85 90 95

Pro Gly Pro Gly Gln Leu Asn Arg His Ser Tyr Leu Lys Asp Pro Asp
100 105 110

Phe Leu Asp Ala Ala Leu Asp Phe
115 120

<210> 140

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 140

Thr Tyr Asn Ser Ser Leu Arg Asn Ser Thr Val Val Arg Glu Asn Ala
1 5 10 15

Ile Ser Phe Asn Phe Phe Gln Ser Tyr Asn Gln Tyr Tyr Val Phe His
20 25 30

Met Pro Arg Pro Met Gly Leu Pro Asp Leu Thr Glu Thr Leu Glu Arg
35 40 45

Tyr Gln Gln Arg Leu Asn Thr Tyr Ala Leu Val Ser Lys Asp Leu Ala
50 55 60

Ser Tyr Arg Ser Phe Ser Pro Met Gly Leu Pro Ser His Thr Thr Ser
65 70 75 80

Gly Leu His Arg Pro His Phe Asn Gln Thr Cys Ile Leu Phe Asp Pro
85 90 95

Met Gly Leu Pro Gln Leu Asn Arg His Ser Tyr Leu Lys Asp Pro Asp
100 105 110

Phe Leu Asp Ala Ala Leu Asp Phe

ITI-08-PCT_Sequence_Listing_ST25.txt

115

120

<210> 141
 <211> 579
 <212> PRT
 <213> Human cytomegalovirus

<220>
 <223> Strain Towne

<400> 141

Met	Glu	Ser	Ser	Ala	Lys	Arg	Lys	Met	Asp	Pro	Asp	Asn	Pro	Asp	Glu
1				5					10					15	
Gly	Pro	Ser	Ser	Lys	Val	Pro	Arg	Pro	Glu	Thr	Pro	Val	Thr	Lys	Ala
			20					25					30		
Thr	Thr	Phe	Leu	Gln	Thr	Met	Leu	Arg	Lys	Glu	Val	Asn	Ser	Gln	Leu
		35					40					45			
Ser	Leu	Gly	Asp	Pro	Leu	Phe	Pro	Glu	Leu	Ala	Glu	Glu	Ser	Leu	Lys
	50					55					60				
Thr	Phe	Glu	Arg	Val	Thr	Glu	Asp	Cys	Asn	Glu	Asn	Pro	Glu	Lys	Asp
65					70					75					80
Val	Leu	Ala	Glu	Leu	Gly	Asp	Ile	Leu	Ala	Gln	Ala	Val	Asn	His	Ala
				85					90					95	
Gly	Ile	Asp	Ser	Ser	Ser	Thr	Gly	Pro	Thr	Leu	Thr	Thr	His	Ser	Cys
			100					105					110		
Ser	Val	Ser	Ser	Ala	Pro	Leu	Asn	Lys	Pro	Thr	Pro	Thr	Ser	Val	Ala
		115					120					125			
Val	Thr	Asn	Thr	Pro	Leu	Pro	Gly	Ala	Ser	Ala	Thr	Pro	Glu	Leu	Ser
	130					135					140				
Pro	Arg	Lys	Lys	Pro	Arg	Lys	Thr	Thr	Arg	Pro	Phe	Lys	Val	Ile	Ile
145					150					155					160
Lys	Pro	Pro	Val	Pro	Pro	Ala	Pro	Ile	Met	Leu	Pro	Leu	Ile	Lys	Gln
				165					170					175	
Glu	Asp	Ile	Lys	Pro	Glu	Pro	Asp	Phe	Thr	Ile	Gln	Tyr	Arg	Asn	Lys
			180					185					190		
Ile	Ile	Asp	Thr	Ala	Gly	Cys	Ile	Val	Ile	Ser	Asp	Ser	Glu	Glu	Glu
		195					200					205			
Gln	Gly	Glu	Glu	Val	Glu	Thr	Arg	Gly	Ala	Thr	Ala	Ser	Ser	Pro	Ser

210				215				220				225			
Gly	Ser	Gly	Thr	Pro	Arg	Val	Thr	Ser	Pro	Thr	His	Pro	Leu	Ser	
				230					235					240	
Met	Asn	His	Pro	Pro	Leu	Pro	Asp	Pro	Leu	Gly	Arg	Pro	Asp	Glu	
				245					250					255	
Ser	Ser	Ser	Ser	Ser	Ser	Ser	Cys	Ser	Ser	Ala	Ser	Asp	Ser	Glu	
				260					265					270	
Glu	Ser	Glu	Glu	Met	Lys	Cys	Ser	Ser	Gly	Gly	Gly	Ala	Ser	Val	
				275					280					285	
Ser	Ser	His	His	Gly	Arg	Gly	Gly	Phe	Gly	Gly	Ala	Ala	Ser	Ser	
				290					295					300	
Leu	Leu	Ser	Cys	Gly	His	Gln	Ser	Ser	Gly	Gly	Ala	Ser	Thr	Gly	
				310					315					320	
Arg	Lys	Lys	Lys	Ser	Lys	Arg	Ile	Ser	Glu	Leu	Asp	Asn	Glu	Lys	
				325					330					335	
Arg	Asn	Ile	Met	Lys	Asp	Lys	Asn	Thr	Pro	Phe	Cys	Thr	Pro	Asn	
				340					345					350	
Gln	Thr	Arg	Arg	Gly	Arg	Val	Lys	Ile	Asp	Glu	Val	Ser	Arg	Met	
				355					360					365	
Arg	Asn	Thr	Asn	Arg	Ser	Leu	Glu	Tyr	Lys	Asn	Leu	Pro	Phe	Thr	
				370					375					380	
Pro	Ser	Met	His	Gln	Val	Leu	Asp	Glu	Ala	Ile	Lys	Ala	Cys	Lys	
				390					395					400	
Met	Gln	Val	Asn	Asn	Lys	Gly	Ile	Gln	Ile	Ile	Tyr	Thr	Arg	Asn	
				405					410					415	
Glu	Val	Lys	Ser	Glu	Val	Asp	Ala	Val	Arg	Cys	Arg	Leu	Gly	Thr	
				420					425					430	
Cys	Asn	Leu	Ala	Leu	Ser	Thr	Pro	Phe	Leu	Met	Glu	His	Thr	Met	
				435					440					445	
Val	Thr	His	Pro	Pro	Glu	Val	Ala	Gln	Arg	Thr	Ala	Asp	Ala	Cys	
				450					455					460	
Glu	Gly	Val	Lys	Ala	Ala	Trp	Ser	Leu	Lys	Glu	Leu	His	Thr	His	
				470					475					480	
Leu	Cys	Pro	Arg	Ser	Ser	Asp	Tyr	Arg	Asn	Met	Ile	Ile	His	Ala	
				485					490					495	

ITI-08-PCT_Sequence_Listing_ST25.txt

Ala Thr Pro Val Asp Leu Leu Gly Ala Leu Asn Leu Cys Leu Pro Leu
500 505 510

Met Gln Lys Phe Pro Lys Gln Val Met Val Arg Ile Phe Ser Thr Asn
515 520 525

Gln Gly Gly Phe Met Leu Pro Ile Tyr Glu Thr Ala Ala Lys Ala Tyr
530 535 540

Ala Val Gly Gln Phe Glu Gln Pro Thr Glu Thr Pro Pro Glu Asp Leu
545 550 555 560

Asp Thr Leu Ser Leu Ala Ile Glu Ala Ala Ile Gln Asp Leu Arg Asn
565 570 575

Lys Ser Gln

<210> 142
<211> 60
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 142

Arg Arg Gly Arg Val Lys Ile Asp Glu Val Ser Arg Met Phe Arg Gly
1 5 10 15

Pro Gly Pro Gly Gly Ile Gln Ile Ile Tyr Thr Arg Asn His Glu Val
20 25 30

Lys Ser Glu Gly Pro Gly Pro Gly Leu Ser Thr Pro Phe Leu Met Glu
35 40 45

His Thr Met Pro Val Thr His Pro Pro Glu Val Ala
50 55 60

<210> 143
<211> 60
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 143

Arg Arg Gly Arg Val Lys Ile Asp Glu Val Ser Arg Met Phe Arg Pro
1 5 10 15

ITI-08-PCT_Sequence_Listing_ST25.txt

Met Gly Leu Pro Gly Ile Gln Ile Ile Tyr Thr Arg Asn His Glu Val
20 25 30

Lys Ser Glu Pro Met Gly Leu Pro Leu Ser Thr Pro Phe Leu Met Glu
35 40 45

His Thr Met Pro Val Thr His Pro Pro Glu Val Ala
50 55 60

<210> 144
<211> 1132
<212> PRT
<213> Homo sapiens

<400> 144

Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
1 5 10 15

His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
20 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu
65 70 75 80

Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val
85 90 95

Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro
100 105 110

Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr
115 120 125

Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val
130 135 140

Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val
145 150 155 160

Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr
165 170 175

Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly
180 185 190

ITI-08-PCT_Sequence_Listing_ST25.txt

Pro	Arg	Arg	Arg	Leu	Gly	Cys	Glu	Arg	Ala	Trp	Asn	His	Ser	Val	Arg	195	200	205
Glu	Ala	Gly	Val	Pro	Leu	Gly	Leu	Pro	Ala	Pro	Gly	Ala	Arg	Arg	Arg	210	215	220
Gly	Gly	Ser	Ala	Ser	Arg	Ser	Leu	Pro	Leu	Pro	Lys	Arg	Pro	Arg	Arg	225	230	235
Gly	Ala	Ala	Pro	Glu	Pro	Glu	Arg	Thr	Pro	Val	Gly	Gln	Gly	Ser	Trp	245	250	255
Ala	His	Pro	Gly	Arg	Thr	Arg	Gly	Pro	Ser	Asp	Arg	Gly	Phe	Cys	Val	260	265	270
Val	Ser	Pro	Ala	Arg	Pro	Ala	Glu	Glu	Ala	Thr	Ser	Leu	Glu	Gly	Ala	275	280	285
Leu	Ser	Gly	Thr	Arg	His	Ser	His	Pro	Ser	Val	Gly	Arg	Gln	His	His	290	295	300
Ala	Gly	Pro	Pro	Ser	Thr	Ser	Arg	Pro	Pro	Arg	Pro	Trp	Asp	Thr	Pro	305	310	315
Cys	Pro	Pro	Val	Tyr	Ala	Glu	Thr	Lys	His	Phe	Leu	Tyr	Ser	Ser	Gly	325	330	335
Asp	Lys	Glu	Gln	Leu	Arg	Pro	Ser	Phe	Leu	Leu	Ser	Ser	Leu	Arg	Pro	340	345	350
Ser	Leu	Thr	Gly	Ala	Arg	Arg	Leu	Val	Glu	Thr	Ile	Phe	Leu	Gly	Ser	355	360	365
Arg	Pro	Trp	Met	Pro	Gly	Thr	Pro	Arg	Arg	Leu	Pro	Arg	Leu	Pro	Gln	370	375	380
Arg	Tyr	Trp	Gln	Met	Arg	Pro	Leu	Phe	Leu	Glu	Leu	Leu	Gly	Asn	His	385	390	395
Ala	Gln	Cys	Pro	Tyr	Gly	Val	Leu	Leu	Lys	Thr	His	Cys	Pro	Leu	Arg	405	410	415
Ala	Ala	Val	Thr	Pro	Ala	Ala	Gly	Val	Cys	Ala	Arg	Glu	Lys	Pro	Gln	420	425	430
Gly	Ser	Val	Ala	Ala	Pro	Glu	Glu	Glu	Asp	Thr	Asp	Pro	Arg	Arg	Leu	435	440	445
Val	Gln	Leu	Leu	Arg	Gln	His	Ser	Ser	Pro	Trp	Gln	Val	Tyr	Gly	Phe	450	455	460

ITI-08-PCT_Sequence_Listing_ST25.txt

Val	Arg	Ala	Cys	Leu	Arg	Arg	Leu	Val	Pro	Pro	Gly	Leu	Trp	Gly	Ser	465	470	475	480
Arg	His	Asn	Glu	Arg	Arg	Phe	Leu	Arg	Asn	Thr	Lys	Lys	Phe	Ile	Ser	485	490		495
Leu	Gly	Lys	His	Ala	Lys	Leu	Ser	Leu	Gln	Glu	Leu	Thr	Trp	Lys	Met	500	505	510	
Ser	Val	Arg	Asp	Cys	Ala	Trp	Leu	Arg	Arg	Ser	Pro	Gly	Val	Gly	Cys	515	520	525	
Val	Pro	Ala	Ala	Glu	His	Arg	Leu	Arg	Glu	Glu	Ile	Leu	Ala	Lys	Phe	530	535	540	
Leu	His	Trp	Leu	Met	Ser	Val	Tyr	Val	Val	Glu	Leu	Leu	Arg	Ser	Phe	545	550	555	560
Phe	Tyr	Val	Thr	Glu	Thr	Thr	Phe	Gln	Lys	Asn	Arg	Leu	Phe	Phe	Tyr	565	570	575	
Arg	Lys	Ser	Val	Trp	Ser	Lys	Leu	Gln	Ser	Ile	Gly	Ile	Arg	Gln	His	580	585	590	
Leu	Lys	Arg	Val	Gln	Leu	Arg	Glu	Leu	Ser	Glu	Ala	Glu	Val	Arg	Gln	595	600	605	
His	Arg	Glu	Ala	Arg	Pro	Ala	Leu	Leu	Thr	Ser	Arg	Leu	Arg	Phe	Ile	610	615	620	
Pro	Lys	Pro	Asp	Gly	Leu	Arg	Pro	Ile	Val	Asn	Met	Asp	Tyr	Val	Val	625	630	635	640
Gly	Ala	Arg	Thr	Phe	Arg	Arg	Glu	Lys	Arg	Ala	Glu	Arg	Leu	Thr	Ser	645	650	655	
Arg	Val	Lys	Ala	Leu	Phe	Ser	Val	Leu	Asn	Tyr	Glu	Arg	Ala	Arg	Arg	660	665	670	
Pro	Gly	Leu	Leu	Gly	Ala	Ser	Val	Leu	Gly	Leu	Asp	Asp	Ile	His	Arg	675	680	685	
Ala	Trp	Arg	Thr	Phe	Val	Leu	Arg	Val	Arg	Ala	Gln	Asp	Pro	Pro	Pro	690	695	700	
Glu	Leu	Tyr	Phe	Val	Lys	Val	Asp	Val	Thr	Gly	Ala	Tyr	Asp	Thr	Ile	705	710	715	720
Pro	Gln	Asp	Arg	Leu	Thr	Glu	Val	Ile	Ala	Ser	Ile	Ile	Lys	Pro	Gln	725	730	735	
Asn	Thr	Tyr	Cys	Val	Arg	Arg	Tyr	Ala	Val	Val	Gln	Lys	Ala	Ala	His				

ITI-08-PCT_Sequence_Listing_ST25.txt

```

740                               745                               750
Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp
755                               760                               765
Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser
770                               775                               780
Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu
785                               790                               795                               800
Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His
805                               810                               815
Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro
820                               825                               830
Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp
835                               840                               845
Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu
850                               855                               860
Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala
865                               870                               875                               880
Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys
885                               890                               895
Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu
900                               905                               910
Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe
915                               920                               925
Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser
930                               935                               940
Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe
945                               950                               955                               960
Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly
965                               970                               975
Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn
980                               985                               990
Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln
995                               1000                               1005
Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln
1010                               1015                               1020

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp
 1025 1030 1035

Thr Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly
 1040 1045 1050

Met Ser Leu Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu
 1055 1060 1065

Ala Val Gln Trp Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr
 1070 1075 1080

Arg His Arg Val Thr Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr
 1085 1090 1095

Ala Gln Thr Gln Leu Ser Arg Lys Leu Pro Gly Thr Thr Leu Thr
 1100 1105 1110

Ala Leu Glu Ala Ala Ala Asn Pro Ala Leu Pro Ser Asp Phe Lys
 1115 1120 1125

Thr Ile Leu Asp
 1130

<210> 145
 <211> 965
 <212> PRT
 <213> Homo sapiens

<400> 145

Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly Ala Ala Thr Gln
 1 5 10 15

Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg Arg Leu Gly Cys
 20 25 30

Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly Val Pro Leu Gly
 35 40 45

Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly Gly Ser Ala Ser Arg Ser
 50 55 60

Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala Pro Glu Pro Glu
 65 70 75 80

Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro Gly Arg Thr Arg
 85 90 95

Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro Ala Arg Pro Ala
 100 105 110

ITI-08-PCT_Sequence_Listing_ST25.txt

Glu	Glu	Ala	Thr	Ser	Leu	Glu	Gly	Ala	Leu	Ser	Gly	Thr	Arg	His	Ser		
		115					120					125					
His	Pro	Ser	Val	Gly	Arg	Gln	His	His	Ala	Gly	Pro	Pro	Ser	Thr	Ser		
	130					135					140						
Arg	Pro	Pro	Arg	Pro	Trp	Asp	Thr	Pro	Cys	Pro	Pro	Val	Tyr	Ala	Glu		
145					150					155					160		
Thr	Lys	His	Phe	Leu	Tyr	Ser	Ser	Gly	Asp	Lys	Glu	Gln	Leu	Arg	Pro		
				165					170					175			
Ser	Phe	Leu	Leu	Ser	Ser	Leu	Arg	Pro	Ser	Leu	Thr	Gly	Ala	Arg	Arg		
			180					185					190				
Leu	Val	Glu	Thr	Ile	Phe	Leu	Gly	Ser	Arg	Pro	Trp	Met	Pro	Gly	Thr		
		195					200					205					
Pro	Arg	Arg	Leu	Pro	Arg	Leu	Pro	Gln	Arg	Tyr	Trp	Gln	Met	Arg	Pro		
	210					215					220						
Leu	Phe	Leu	Glu	Leu	Leu	Gly	Asn	His	Ala	Gln	Cys	Pro	Tyr	Gly	Val		
225					230					235					240		
Leu	Leu	Lys	Thr	His	Cys	Pro	Leu	Arg	Ala	Ala	Val	Thr	Pro	Ala	Ala		
				245					250					255			
Gly	Val	Cys	Ala	Arg	Glu	Lys	Pro	Gln	Gly	Ser	Val	Ala	Ala	Pro	Glu		
			260					265					270				
Glu	Glu	Asp	Thr	Asp	Pro	Arg	Arg	Leu	Val	Gln	Leu	Leu	Arg	Gln	His		
		275					280					285					
Ser	Ser	Pro	Trp	Gln	Val	Tyr	Gly	Phe	Val	Arg	Ala	Cys	Leu	Arg	Arg		
	290					295					300						
Leu	Val	Pro	Pro	Gly	Leu	Trp	Gly	Ser	Arg	His	Asn	Glu	Arg	Arg	Phe		
305					310					315					320		
Leu	Arg	Asn	Thr	Lys	Lys	Phe	Ile	Ser	Leu	Gly	Lys	His	Ala	Lys	Leu		
				325					330					335			
Ser	Leu	Gln	Glu	Leu	Thr	Trp	Lys	Met	Ser	Val	Arg	Asp	Cys	Ala	Trp		
			340					345					350				
Leu	Arg	Arg	Ser	Pro	Gly	Val	Gly	Cys	Val	Pro	Ala	Ala	Glu	His	Arg		
		355					360					365					
Leu	Arg	Glu	Glu	Ile	Leu	Ala	Lys	Phe	Leu	His	Trp	Leu	Met	Ser	Val		
		370				375					380						

ITI-08-PCT_Sequence_Listing_ST25.txt

Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val Thr Glu Thr Thr
 385 390 395 400
 Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser Val Trp Ser Lys
 405 410 415
 Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg Val Gln Leu Arg
 420 425 430
 Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu Ala Arg Pro Ala
 435 440 445
 Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro Asp Gly Leu Arg
 450 455 460
 Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg Thr Phe Arg Arg
 465 470 475 480
 Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg Val Lys Ala Leu Phe Ser
 485 490 495
 Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu Leu Gly Ala Ser
 500 505 510
 Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg Thr Phe Val Leu
 515 520 525
 Arg Val Arg Ala Gln Asp Pro Pro Pro Glu Leu Tyr Phe Val Lys Val
 530 535 540
 Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro Gln Asp Arg Leu Thr Glu
 545 550 555 560
 Val Ile Ala Ser Ile Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg
 565 570 575
 Tyr Ala Val Val Gln Lys Ala Ala His Gly His Val Arg Lys Ala Phe
 580 585 590
 Lys Ser His Val Ser Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln
 595 600 605
 Phe Val Ala His Leu Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val
 610 615 620
 Ile Glu Gln Ser Ser Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp
 625 630 635 640
 Val Phe Leu Arg Phe Met Cys His His Ala Val Arg Ile Arg Gly Lys
 645 650 655
 Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr

ITI-08-PCT_Sequence_Listing_ST25.txt

```

660
Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala
675
665
670
Gly Ile Arg Arg Asp Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu
690
695
700
Leu Val Thr Pro His Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu
705
710
715
720
Val Arg Gly Val Pro Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr
725
730
735
Val Val Asn Phe Pro Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe
740
745
750
Val Gln Met Pro Ala His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu
755
760
765
Asp Thr Arg Thr Leu Glu Val Gln Ser Asp Tyr Ser Ser Tyr Ala Arg
770
775
780
Thr Ser Ile Arg Ala Ser Leu Thr Phe Asn Arg Gly Phe Lys Ala Gly
785
790
795
800
Arg Asn Met Arg Arg Lys Leu Phe Gly Val Leu Arg Leu Lys Cys His
805
810
815
Ser Leu Phe Leu Asp Leu Gln Val Asn Ser Leu Gln Thr Val Cys Thr
820
825
830
Asn Ile Tyr Lys Ile Leu Leu Leu Gln Ala Tyr Arg Phe His Ala Cys
835
840
845
Val Leu Gln Leu Pro Phe His Gln Gln Val Trp Lys Asn Pro Thr Phe
850
855
860
Phe Leu Arg Val Ile Ser Asp Thr Ala Ser Leu Cys Tyr Ser Ile Leu
865
870
875
880
Lys Ala Lys Asn Ala Gly Met Ser Leu Gly Ala Lys Gly Ala Ala Gly
885
890
895
Pro Leu Pro Ser Glu Ala Val Gln Trp Leu Cys His Gln Ala Phe Leu
900
905
910
Leu Lys Leu Thr Arg His Arg Val Thr Tyr Val Pro Leu Leu Gly Ser
915
920
925
Leu Arg Thr Ala Gln Thr Gln Leu Ser Arg Lys Leu Pro Gly Thr Thr
930
935
940

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Leu Thr Ala Leu Glu Ala Ala Ala Asn Pro Ala Leu Pro Ser Asp Phe
945 950 955 960

Lys Thr Ile Leu Asp
965

<210> 146
<211> 1065
<212> PRT
<213> Homo sapiens

<400> 146

Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
1 5 10 15

His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
20 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu
65 70 75 80

Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val
85 90 95

Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro
100 105 110

Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr
115 120 125

Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val
130 135 140

Gly Asp Asp Gly Pro Pro Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala
145 150 155 160

Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu
165 170 175

Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly Val Pro Leu Gly Leu
180 185 190

Pro Ala Pro Gly Ala Arg Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu
195 200 205

ITI-08-PCT_Sequence_Listing_ST25.txt

Pro	Leu	Pro	Lys	Arg	Pro	Arg	Arg	Gly	Ala	Ala	Pro	Glu	Pro	Glu	Arg	210	215	220	
Thr	Pro	Val	Gly	Gln	Gly	Ser	Trp	Ala	His	Pro	Gly	Arg	Thr	Arg	Gly	225	230	235	240
Pro	Ser	Asp	Arg	Gly	Phe	Cys	Val	Val	Ser	Pro	Ala	Arg	Pro	Ala	Glu	245	250	255	
Glu	Ala	Thr	Ser	Leu	Glu	Gly	Ala	Leu	Ser	Gly	Thr	Arg	His	Ser	His	260	265	270	
Pro	Ser	Val	Gly	Arg	Gln	His	His	Ala	Gly	Pro	Pro	Ser	Thr	Ser	Arg	275	280	285	
Pro	Pro	Arg	Pro	Trp	Asp	Thr	Pro	Cys	Pro	Pro	Val	Tyr	Ala	Glu	Thr	290	295	300	
Lys	His	Phe	Leu	Tyr	Ser	Ser	Gly	Asp	Lys	Glu	Gln	Leu	Arg	Pro	Ser	305	310	315	320
Phe	Leu	Leu	Ser	Ser	Leu	Arg	Pro	Ser	Leu	Thr	Gly	Ala	Arg	Arg	Leu	325	330	335	
Val	Glu	Thr	Ile	Phe	Leu	Gly	Ser	Arg	Pro	Trp	Met	Pro	Gly	Thr	Pro	340	345	350	
Arg	Arg	Leu	Pro	Arg	Leu	Pro	Gln	Arg	Tyr	Trp	Gln	Met	Arg	Pro	Leu	355	360	365	
Phe	Leu	Glu	Leu	Leu	Gly	Asn	His	Ala	Gln	Cys	Pro	Tyr	Gly	Val	Leu	370	375	380	
Leu	Lys	Thr	His	Cys	Pro	Leu	Arg	Ala	Ala	Val	Thr	Pro	Ala	Ala	Gly	385	390	395	400
Val	Cys	Ala	Arg	Glu	Lys	Pro	Gln	Gly	Ser	Val	Ala	Ala	Pro	Glu	Glu	405	410	415	
Glu	Asp	Thr	Asp	Pro	Arg	Arg	Leu	Val	Gln	Leu	Leu	Arg	Gln	His	Ser	420	425	430	
Ser	Pro	Trp	Gln	Val	Tyr	Gly	Phe	Val	Arg	Ala	Cys	Leu	Arg	Arg	Leu	435	440	445	
Val	Pro	Pro	Gly	Leu	Trp	Gly	Ser	Arg	His	Asn	Glu	Arg	Arg	Phe	Leu	450	455	460	
Arg	Asn	Thr	Lys	Lys	Phe	Ile	Ser	Leu	Gly	Lys	His	Ala	Lys	Leu	Ser	465	470	475	480

ITI-08-PCT_Sequence_Listing_ST25.txt

Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg Asp Cys Ala Trp Leu
485 490 495

Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala Ala Glu His Arg Leu
500 505 510

Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp Leu Met Ser Val Tyr
515 520 525

Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe
530 535 540

Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu
545 550 555 560

Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg Val Gln Leu Arg Glu
565 570 575

Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu Ala Arg Pro Ala Leu
580 585 590

Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro
595 600 605

Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg Thr Phe Arg Arg Glu
610 615 620

Lys Arg Ala Glu Arg Leu Thr Ser Arg Val Lys Ala Leu Phe Ser Val
625 630 635 640

Leu Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu Leu Gly Ala Ser Val
645 650 655

Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg Thr Phe Val Leu Arg
660 665 670

Val Arg Ala Gln Asp Pro Pro Pro Glu Leu Tyr Phe Val Lys Val Ala
675 680 685

Ile Thr Gly Ala Tyr Asp Thr Ile Pro Gln Asp Arg Leu Thr Glu Val
690 695 700

Ile Ala Ser Ile Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr
705 710 715 720

Ala Val Val Gln Lys Ala Ala His Gly His Val Arg Lys Ala Phe Lys
725 730 735

Ser His Val Ser Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe
740 745 750

Val Ala His Leu Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile

ITI-08-PCT_Sequence_Listing_ST25.txt

```

755                               760                               765
Glu Gln Ser Ser Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val
770                               775                               780
Phe Leu Arg Phe Met Cys His His Ala Val Arg Ile Arg Gly Lys Ser
785                               790                               795                               800
Tyr Val Gln Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu
805                               810                               815
Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr
820                               825                               830
His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr
835                               840                               845
Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu
850                               855                               860
Asp Glu Ala Leu Asp Thr Arg Thr Leu Glu Val Gln Ser Asp Tyr Ser
865                               870                               875                               880
Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe Asn Arg Gly
885                               890                               895
Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly Val Leu Arg
900                               905                               910
Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn Ser Leu Gln
915                               920                               925
Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln Ala Tyr Arg
930                               935                               940
Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln Val Trp Lys
945                               950                               955                               960
Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala Ser Leu Cys
965                               970                               975
Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser Leu Gly Ala Lys
980                               985                               990
Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln Trp Leu Cys His
995                               1000                               1005
Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val Thr Tyr Val
1010                               1015                               1020
Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu Ser Arg
1025                               1030                               1035

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala Asn
1040 1045 1050

Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp
1055 1060 1065

<210> 147
<211> 142
<212> PRT
<213> Pongo abelii

<400> 147

Met Gly Ala Pro Thr Leu Pro Pro Ala Trp Gln Pro Phe Leu Lys Asp
1 5 10 15

His Arg Ile Ser Thr Phe Lys Asn Trp Pro Phe Leu Glu Gly Cys Ala
20 25 30

Cys Thr Pro Glu Arg Met Ala Glu Ala Gly Phe Ile His Cys Pro Thr
35 40 45

Glu Asn Glu Pro Asp Leu Ala Gln Cys Phe Phe Cys Phe Lys Glu Leu
50 55 60

Glu Gly Trp Glu Pro Asp Asp Asp Pro Ile Glu Glu His Lys Lys His
65 70 75 80

Ser Ser Gly Cys Ala Phe Leu Ser Val Lys Lys Gln Phe Glu Glu Leu
85 90 95

Thr Leu Gly Glu Phe Leu Lys Leu Asp Arg Glu Arg Ala Lys Asn Lys
100 105 110

Ile Ala Lys Glu Thr Asn Asn Lys Lys Lys Glu Phe Glu Glu Thr Ala
115 120 125

Lys Lys Val Arg Arg Ala Ile Glu Gln Leu Ala Ala Met Asp
130 135 140

<210> 148
<211> 452
<212> PRT
<213> Clostridium tetani

<400> 148

Met Lys Asn Leu Asp Cys Trp Val Asp Asn Glu Glu Asp Ile Asp Val
1 5 10 15

Ile Leu Lys Lys Ser Thr Ile Leu Asn Leu Asp Ile Asn Asn Asp Ile

ITI-08-PCT_Sequence_Listing_ST25.txt

20	25	30													
Ile	Ser	Asp	Ile	Ser	Gly	Phe	Asn	Ser	Ser	Val	Ile	Thr	Tyr	Pro	Asp
	35						40					45			
Ala	Gln	Leu	Val	Pro	Gly	Ile	Asn	Gly	Lys	Ala	Ile	His	Leu	Val	Asn
	50					55					60				
Asn	Glu	Ser	Ser	Glu	Val	Ile	Val	His	Lys	Ala	Met	Asp	Ile	Glu	Tyr
65					70					75				80	
Asn	Asp	Met	Phe	Asn	Asn	Phe	Thr	Val	Ser	Phe	Trp	Leu	Arg	Val	Pro
				85					90					95	
Lys	Val	Ser	Ala	Ser	His	Leu	Glu	Gln	Tyr	Gly	Thr	Asn	Glu	Tyr	Ser
			100					105					110		
Ile	Ile	Ser	Ser	Met	Lys	Lys	His	Ser	Leu	Ser	Ile	Gly	Ser	Gly	Trp
		115					120					125			
Ser	Val	Ser	Leu	Lys	Gly	Asn	Asn	Leu	Ile	Trp	Thr	Leu	Lys	Asp	Ser
	130					135					140				
Ala	Gly	Glu	Val	Arg	Gln	Ile	Thr	Phe	Arg	Asp	Leu	Pro	Asp	Lys	Phe
145					150					155					160
Asn	Ala	Tyr	Leu	Ala	Asn	Lys	Trp	Val	Phe	Ile	Thr	Ile	Thr	Asn	Asp
				165					170					175	
Arg	Leu	Ser	Ser	Ala	Asn	Leu	Tyr	Ile	Asn	Gly	Val	Leu	Met	Gly	Ser
			180					185					190		
Ala	Glu	Ile	Thr	Gly	Leu	Gly	Ala	Ile	Arg	Glu	Asp	Asn	Asn	Ile	Thr
		195					200					205			
Leu	Lys	Leu	Asp	Arg	Cys	Asn	Asn	Asn	Asn	Gln	Tyr	Val	Ser	Ile	Asp
	210					215					220				
Lys	Phe	Arg	Ile	Phe	Cys	Lys	Ala	Leu	Asn	Pro	Lys	Glu	Ile	Glu	Lys
225					230					235					240
Leu	Tyr	Thr	Ser	Tyr	Leu	Ser	Ile	Thr	Phe	Leu	Arg	Asp	Phe	Trp	Gly
				245					250					255	
Asn	Pro	Leu	Arg	Tyr	Asp	Thr	Glu	Tyr	Tyr	Leu	Ile	Pro	Val	Ala	Ser
			260					265					270		
Ser	Ser	Lys	Asp	Val	Gln	Leu	Lys	Asn	Ile	Thr	Asp	Tyr	Met	Tyr	Leu
		275					280					285			
Thr	Asn	Ala	Pro	Ser	Tyr	Thr	Asn	Gly	Lys	Leu	Asn	Ile	Tyr	Tyr	Arg
	290					295					300				

ITI-08-PCT_Sequence_Listing_ST25.txt

Arg Leu Tyr Asn Gly Leu Lys Phe Ile Ile Lys Arg Tyr Thr Pro Asn
305 310 315 320

Asn Glu Ile Asp Ser Phe Val Lys Ser Gly Asp Phe Ile Lys Leu Tyr
325 330 335

Val Ser Tyr Asn Asn Asn Glu His Ile Val Gly Tyr Pro Lys Asp Gly
340 345 350

Asn Ala Phe Asn Asn Leu Asp Arg Ile Leu Arg Val Gly Tyr Asn Ala
355 360 365

Pro Gly Ile Pro Leu Tyr Lys Lys Met Glu Ala Val Lys Leu Arg Asp
370 375 380

Leu Lys Thr Tyr Ser Val Gln Leu Lys Leu Tyr Asp Asp Lys Asn Ala
385 390 395 400

Ser Leu Gly Leu Val Gly Thr His Asn Gly Gln Ile Gly Asn Asp Pro
405 410 415

Asn Arg Asp Ile Leu Ile Ala Ser Asn Trp Tyr Phe Asn His Leu Lys
420 425 430

Asp Lys Ile Leu Gly Cys Asp Trp Tyr Phe Val Pro Thr Asp Glu Gly
435 440 445

Trp Thr Asn Asp
450

<210> 149
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 149

Pro Gly Ile Asn Gly Lys Ala Ile His Leu Val Asn Asn Glu Ser Ser
1 5 10 15

Glu Gly Pro Gly Pro Gly Phe Asn Asn Phe Thr Val Ser Phe Trp Leu
20 25 30

Arg Val Pro Lys Val Ser Ala Ser His Leu Glu Gln Tyr Gly Thr Gly
35 40 45

Pro Gly Pro Gly Tyr Val Ser Ile Asp Lys Phe Arg Ile Phe Cys Lys
50 55 60

ITI-08-PCT_Sequence_Listing_ST25.txt

Ala Leu Asn Pro Lys Glu Ile Glu Lys Leu Tyr Thr Ser Tyr Leu Ser
65 70 75 80

Gly Pro Gly Pro Gly Ile Leu Arg Val Gly Tyr Asn Ala Pro Gly Ile
85 90 95

Pro Leu Tyr Lys Lys Met Glu Ala Val Lys Leu Arg Asp Leu Lys
100 105 110

<210> 150
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 150

Pro Gly Ile Asn Gly Lys Ala Ile His Leu Val Asn Asn Glu Ser Ser
1 5 10 15

Glu Pro Met Gly Leu Pro Phe Asn Asn Phe Thr Val Ser Phe Trp Leu
20 25 30

Arg Val Pro Lys Val Ser Ala Ser His Leu Glu Gln Tyr Gly Thr Pro
35 40 45

Met Gly Leu Pro Tyr Val Ser Ile Asp Lys Phe Arg Ile Phe Cys Lys
50 55 60

Ala Leu Asn Pro Lys Glu Ile Glu Lys Leu Tyr Thr Ser Tyr Leu Ser
65 70 75 80

Pro Met Gly Leu Pro Ile Leu Arg Val Gly Tyr Asn Ala Pro Gly Ile
85 90 95

Pro Leu Tyr Lys Lys Met Glu Ala Val Lys Leu Arg Asp Leu Lys
100 105 110

<210> 151
<211> 180
<212> PRT
<213> Homo sapiens

<400> 151

Met Gln Ala Glu Gly Arg Gly Thr Gly Gly Ser Thr Gly Asp Ala Asp
1 5 10 15

Gly Pro Gly Gly Pro Gly Ile Pro Asp Gly Pro Gly Gly Asn Ala Gly

ITI-08-PCT_Sequence_Listing_ST25.txt

20

25

30

Gly Pro Gly Glu Ala Gly Ala Thr Gly Gly Arg Gly Pro Arg Gly Ala
35 40 45

Gly Ala Ala Arg Ala Ser Gly Pro Gly Gly Gly Ala Pro Arg Gly Pro
50 55 60

His Gly Gly Ala Ala Ser Gly Leu Asn Gly Cys Cys Arg Cys Gly Ala
65 70 75 80

Arg Gly Pro Glu Ser Arg Leu Leu Glu Phe Tyr Leu Ala Met Pro Phe
85 90 95

Ala Thr Pro Met Glu Ala Glu Leu Ala Arg Arg Ser Leu Ala Gln Asp
100 105 110

Ala Pro Pro Leu Pro Val Pro Gly Val Leu Leu Lys Glu Phe Thr Val
115 120 125

Ser Gly Asn Ile Leu Thr Ile Arg Leu Thr Ala Ala Asp His Arg Gln
130 135 140

Leu Gln Leu Ser Ile Ser Ser Cys Leu Gln Gln Leu Ser Leu Leu Met
145 150 155 160

Trp Ile Thr Gln Cys Phe Leu Pro Val Phe Leu Ala Gln Pro Pro Ser
165 170 175

Gly Gln Arg Arg
180

<210> 152

<211> 1255

<212> PRT

<213> Homo sapiens

<400> 152

Met Glu Leu Ala Ala Leu Cys Arg Trp Gly Leu Leu Leu Ala Leu Leu
1 5 10 15

Pro Pro Gly Ala Ala Ser Thr Gln Val Cys Thr Gly Thr Asp Met Lys
20 25 30

Leu Arg Leu Pro Ala Ser Pro Glu Thr His Leu Asp Met Leu Arg His
35 40 45

Leu Tyr Gln Gly Cys Gln Val Val Gln Gly Asn Leu Glu Leu Thr Tyr
50 55 60

Leu Pro Thr Asn Ala Ser Leu Ser Phe Leu Gln Asp Ile Gln Glu Val

ITI-08-PCT_Sequence_Listing_ST25.txt

```

65          70          75          80
Gln Gly Tyr Val Leu Ile Ala His Asn Gln Val Arg Gln Val Pro Leu
      85          90          95
Gln Arg Leu Arg Ile Val Arg Gly Thr Gln Leu Phe Glu Asp Asn Tyr
      100        105        110
Ala Leu Ala Val Leu Asp Asn Gly Asp Pro Leu Asn Asn Thr Thr Pro
      115        120        125
Val Thr Gly Ala Ser Pro Gly Gly Leu Arg Glu Leu Gln Leu Arg Ser
      130        135        140
Leu Thr Glu Ile Leu Lys Gly Gly Val Leu Ile Gln Arg Asn Pro Gln
      145        150        155        160
Leu Cys Tyr Gln Asp Thr Ile Leu Trp Lys Asp Ile Phe His Lys Asn
      165        170        175
Asn Gln Leu Ala Leu Thr Leu Ile Asp Thr Asn Arg Ser Arg Ala Cys
      180        185        190
His Pro Cys Ser Pro Met Cys Lys Gly Ser Arg Cys Trp Gly Glu Ser
      195        200        205
Ser Glu Asp Cys Gln Ser Leu Thr Arg Thr Val Cys Ala Gly Gly Cys
      210        215        220
Ala Arg Cys Lys Gly Pro Leu Pro Thr Asp Cys Cys His Glu Gln Cys
      225        230        235        240
Ala Ala Gly Cys Thr Gly Pro Lys His Ser Asp Cys Leu Ala Cys Leu
      245        250        255
His Phe Asn His Ser Gly Ile Cys Glu Leu His Cys Pro Ala Leu Val
      260        265        270
Thr Tyr Asn Thr Asp Thr Phe Glu Ser Met Pro Asn Pro Glu Gly Arg
      275        280        285
Tyr Thr Phe Gly Ala Ser Cys Val Thr Ala Cys Pro Tyr Asn Tyr Leu
      290        295        300
Ser Thr Asp Val Gly Ser Cys Thr Leu Val Cys Pro Leu His Asn Gln
      305        310        315        320
Glu Val Thr Ala Glu Asp Gly Thr Gln Arg Cys Glu Lys Cys Ser Lys
      325        330        335
Pro Cys Ala Arg Val Cys Tyr Gly Leu Gly Met Glu His Leu Arg Glu
      340        345        350

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Val	Arg	Ala	Val	Thr	Ser	Ala	Asn	Ile	Gln	Glu	Phe	Ala	Gly	Cys	Lys	355	360	365	
Lys	Ile	Phe	Gly	Ser	Leu	Ala	Phe	Leu	Pro	Glu	Ser	Phe	Asp	Gly	Asp	370	375	380	
Pro	Ala	Ser	Asn	Thr	Ala	Pro	Leu	Gln	Pro	Glu	Gln	Leu	Gln	Val	Phe	385	390	395	400
Glu	Thr	Leu	Glu	Glu	Ile	Thr	Gly	Tyr	Leu	Tyr	Ile	Ser	Ala	Trp	Pro	405	410	415	
Asp	Ser	Leu	Pro	Asp	Leu	Ser	Val	Phe	Gln	Asn	Leu	Gln	Val	Ile	Arg	420	425	430	
Gly	Arg	Ile	Leu	His	Asn	Gly	Ala	Tyr	Ser	Leu	Thr	Leu	Gln	Gly	Leu	435	440	445	
Gly	Ile	Ser	Trp	Leu	Gly	Leu	Arg	Ser	Leu	Arg	Glu	Leu	Gly	Ser	Gly	450	455	460	
Leu	Ala	Leu	Ile	His	His	Asn	Thr	His	Leu	Cys	Phe	Val	His	Thr	Val	465	470	475	480
Pro	Trp	Asp	Gln	Leu	Phe	Arg	Asn	Pro	His	Gln	Ala	Leu	Leu	His	Thr	485	490	495	
Ala	Asn	Arg	Pro	Glu	Asp	Glu	Cys	Val	Gly	Glu	Gly	Leu	Ala	Cys	His	500	505	510	
Gln	Leu	Cys	Ala	Arg	Gly	His	Cys	Trp	Gly	Pro	Gly	Pro	Thr	Gln	Cys	515	520	525	
Val	Asn	Cys	Ser	Gln	Phe	Leu	Arg	Gly	Gln	Glu	Cys	Val	Glu	Glu	Cys	530	535	540	
Arg	Val	Leu	Gln	Gly	Leu	Pro	Arg	Glu	Tyr	Val	Asn	Ala	Arg	His	Cys	545	550	555	560
Leu	Pro	Cys	His	Pro	Glu	Cys	Gln	Pro	Gln	Asn	Gly	Ser	Val	Thr	Cys	565	570	575	
Phe	Gly	Pro	Glu	Ala	Asp	Gln	Cys	Val	Ala	Cys	Ala	His	Tyr	Lys	Asp	580	585	590	
Pro	Pro	Phe	Cys	Val	Ala	Arg	Cys	Pro	Ser	Gly	Val	Lys	Pro	Asp	Leu	595	600	605	
Ser	Tyr	Met	Pro	Ile	Trp	Lys	Phe	Pro	Asp	Glu	Glu	Gly	Ala	Cys	Gln	610	615	620	

ITI-08-PCT_Sequence_Listing_ST25.txt

Pro	Cys	Pro	Ile	Asn	Cys	Thr	His	Ser	Cys	Val	Asp	Leu	Asp	Asp	Lys	625	630	635	640
Gly	Cys	Pro	Ala	Glu	Gln	Arg	Ala	Ser	Pro	Leu	Thr	Ser	Ile	Val	Ser	645	650	655	
Ala	Val	Val	Gly	Ile	Leu	Leu	Val	Val	Val	Leu	Gly	Val	Val	Phe	Gly	660	665	670	
Ile	Leu	Ile	Lys	Arg	Arg	Gln	Gln	Lys	Ile	Arg	Lys	Tyr	Thr	Met	Arg	675	680	685	
Arg	Leu	Leu	Gln	Glu	Thr	Glu	Leu	Val	Glu	Pro	Leu	Thr	Pro	Ser	Gly	690	695	700	
Ala	Met	Pro	Asn	Gln	Ala	Gln	Met	Arg	Ile	Leu	Lys	Glu	Thr	Glu	Leu	705	710	715	720
Arg	Lys	Val	Lys	Val	Leu	Gly	Ser	Gly	Ala	Phe	Gly	Thr	Val	Tyr	Lys	725	730	735	
Gly	Ile	Trp	Ile	Pro	Asp	Gly	Glu	Asn	Val	Lys	Ile	Pro	Val	Ala	Ile	740	745	750	
Lys	Val	Leu	Arg	Glu	Asn	Thr	Ser	Pro	Lys	Ala	Asn	Lys	Glu	Ile	Leu	755	760	765	
Asp	Glu	Ala	Tyr	Val	Met	Ala	Gly	Val	Gly	Ser	Pro	Tyr	Val	Ser	Arg	770	775	780	
Leu	Leu	Gly	Ile	Cys	Leu	Thr	Ser	Thr	Val	Gln	Leu	Val	Thr	Gln	Leu	785	790	795	800
Met	Pro	Tyr	Gly	Cys	Leu	Leu	Asp	His	Val	Arg	Glu	Asn	Arg	Gly	Arg	805	810	815	
Leu	Gly	Ser	Gln	Asp	Leu	Leu	Asn	Trp	Cys	Met	Gln	Ile	Ala	Lys	Gly	820	825	830	
Met	Ser	Tyr	Leu	Glu	Asp	Val	Arg	Leu	Val	His	Arg	Asp	Leu	Ala	Ala	835	840	845	
Arg	Asn	Val	Leu	Val	Lys	Ser	Pro	Asn	His	Val	Lys	Ile	Thr	Asp	Phe	850	855	860	
Gly	Leu	Ala	Arg	Leu	Leu	Asp	Ile	Asp	Glu	Thr	Glu	Tyr	His	Ala	Asp	865	870	875	880
Gly	Gly	Lys	Val	Pro	Ile	Lys	Trp	Met	Ala	Leu	Glu	Ser	Ile	Leu	Arg	885	890	895	
Arg	Arg	Phe	Thr	His	Gln	Ser	Asp	Val	Trp	Ser	Tyr	Gly	Val	Thr	Val				

ITI-08-PCT_Sequence_Listing_ST25.txt

```

          900                      905                      910
Trp Glu Leu Met Thr Phe Gly Ala Lys Pro Tyr Asp Gly Ile Pro Ala
    915                      920                      925

Arg Glu Ile Pro Asp Leu Leu Glu Lys Gly Glu Arg Leu Pro Gln Pro
    930                      935                      940

Pro Ile Cys Thr Ile Asp Val Tyr Met Ile Met Val Lys Cys Trp Met
    945                      950                      955                      960

Ile Asp Ser Glu Cys Arg Pro Arg Phe Arg Glu Leu Val Ser Glu Phe
    965                      970                      975

Ser Arg Met Ala Arg Asp Pro Gln Arg Phe Val Val Ile Gln Asn Glu
    980                      985                      990

Asp Leu Gly Pro Ala Ser Pro Leu Asp Ser Thr Phe Tyr Arg Ser Leu
    995                      1000                      1005

Leu Glu Asp Asp Asp Met Gly Asp Leu Val Asp Ala Glu Glu Tyr
    1010                      1015                      1020

Leu Val Pro Gln Gln Gly Phe Phe Cys Pro Asp Pro Ala Pro Gly
    1025                      1030                      1035

Ala Gly Gly Met Val His His Arg His Arg Ser Ser Ser Thr Arg
    1040                      1045                      1050

Ser Gly Gly Gly Asp Leu Thr Leu Gly Leu Glu Pro Ser Glu Glu
    1055                      1060                      1065

Glu Ala Pro Arg Ser Pro Leu Ala Pro Ser Glu Gly Ala Gly Ser
    1070                      1075                      1080

Asp Val Phe Asp Gly Asp Leu Gly Met Gly Ala Ala Lys Gly Leu
    1085                      1090                      1095

Gln Ser Leu Pro Thr His Asp Pro Ser Pro Leu Gln Arg Tyr Ser
    1100                      1105                      1110

Glu Asp Pro Thr Val Pro Leu Pro Ser Glu Thr Asp Gly Tyr Val
    1115                      1120                      1125

Ala Pro Leu Thr Cys Ser Pro Gln Pro Glu Tyr Val Asn Gln Pro
    1130                      1135                      1140

Asp Val Arg Pro Gln Pro Pro Ser Pro Arg Glu Gly Pro Leu Pro
    1145                      1150                      1155

Ala Ala Arg Pro Ala Gly Ala Thr Leu Glu Arg Ala Lys Thr Leu
    1160                      1165                      1170

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Ser Pro Gly Lys Asn Gly Val Val Lys Asp Val Phe Ala Phe Gly
 1175 1180 1185

Gly Ala Val Glu Asn Pro Glu Tyr Leu Thr Pro Gln Gly Gly Ala
 1190 1195 1200

Ala Pro Gln Pro His Pro Pro Pro Ala Phe Ser Pro Ala Phe Asp
 1205 1210 1215

Asn Leu Tyr Tyr Trp Asp Gln Asp Pro Pro Glu Arg Gly Ala Pro
 1220 1225 1230

Pro Ser Thr Phe Lys Gly Thr Pro Thr Ala Glu Asn Pro Glu Tyr
 1235 1240 1245

Leu Gly Leu Asp Val Pro Val
 1250 1255

<210> 153
 <211> 1196
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 153

Thr Gln Val Cys Thr Gly Thr Asp Met Lys Leu Arg Leu Pro Ala Ser
 1 5 10 15

Pro Glu Thr His Leu Asp Met Leu Arg His Leu Tyr Gln Gly Cys Gln
 20 25 30

Val Val Gln Gly Asn Leu Glu Leu Thr Tyr Leu Pro Thr Asn Ala Ser
 35 40 45

Leu Ser Phe Leu Gln Asp Ile Gln Glu Val Gln Gly Tyr Val Leu Ile
 50 55 60

Ala His Asn Gln Val Arg Gln Val Pro Leu Gln Arg Leu Arg Ile Val
 65 70 75 80

Arg Gly Thr Gln Leu Phe Glu Asp Asn Tyr Ala Leu Ala Val Leu Asp
 85 90 95

Asn Gly Asp Pro Leu Asn Asn Thr Thr Pro Val Thr Gly Ala Ser Pro
 100 105 110

Gly Gly Leu Arg Glu Leu Gln Leu Arg Ser Leu Thr Glu Ile Leu Lys
 115 120 125

ITI-08-PCT_Sequence_Listing_ST25.txt

Gly	Gly	Val	Leu	Ile	Gln	Arg	Asn	Pro	Gln	Leu	Cys	Tyr	Gln	Asp	Thr	130	135	140	
Ile	Leu	Trp	Lys	Asp	Ile	Phe	His	Lys	Asn	Asn	Gln	Leu	Ala	Leu	Thr	145	150	155	160
Leu	Ile	Asp	Thr	Asn	Arg	Ser	Arg	Ala	Cys	His	Pro	Cys	Ser	Pro	Met	165	170	175	
Cys	Lys	Gly	Ser	Arg	Cys	Trp	Gly	Glu	Ser	Ser	Glu	Asp	Cys	Gln	Ser	180	185	190	
Leu	Thr	Arg	Thr	Val	Cys	Ala	Gly	Gly	Cys	Ala	Arg	Cys	Lys	Gly	Pro	195	200	205	
Leu	Pro	Thr	Asp	Cys	Cys	His	Glu	Gln	Cys	Ala	Ala	Gly	Cys	Thr	Gly	210	215	220	
Pro	Lys	His	Ser	Asp	Cys	Leu	Ala	Cys	Leu	His	Phe	Asn	His	Ser	Gly	225	230	235	240
Ile	Cys	Glu	Leu	His	Cys	Pro	Ala	Leu	Val	Thr	Tyr	Asn	Thr	Asp	Thr	245	250	255	
Phe	Glu	Ser	Met	Pro	Asn	Pro	Glu	Gly	Arg	Tyr	Thr	Phe	Gly	Ala	Ser	260	265	270	
Cys	Val	Thr	Ala	Cys	Pro	Tyr	Asn	Tyr	Leu	Ser	Thr	Asp	Val	Gly	Ser	275	280	285	
Cys	Thr	Leu	Val	Cys	Pro	Leu	His	Asn	Gln	Glu	Val	Thr	Ala	Glu	Asp	290	295	300	
Gly	Thr	Gln	Arg	Cys	Glu	Lys	Cys	Ser	Lys	Pro	Cys	Ala	Arg	Val	Cys	305	310	315	320
Tyr	Gly	Leu	Gly	Met	Glu	His	Leu	Arg	Glu	Val	Arg	Ala	Val	Thr	Ser	325	330	335	
Ala	Asn	Ile	Gln	Glu	Phe	Ala	Gly	Cys	Lys	Lys	Ile	Phe	Gly	Ser	Leu	340	345	350	
Ala	Phe	Leu	Pro	Glu	Ser	Phe	Asp	Gly	Asp	Pro	Ala	Ser	Asn	Thr	Ala	355	360	365	
Pro	Leu	Gln	Pro	Glu	Gln	Leu	Gln	Val	Phe	Glu	Thr	Leu	Glu	Glu	Ile	370	375	380	
Thr	Gly	Tyr	Leu	Tyr	Ile	Ser	Ala	Trp	Pro	Asp	Ser	Leu	Pro	Asp	Leu	385	390	395	400

ITI-08-PCT_Sequence_Listing_ST25.txt

Ser Val Phe Gln Asn Leu Gln Val Ile Arg Gly Arg Ile Leu His Asn
405 410 415

Gly Ala Tyr Ser Leu Thr Leu Gln Gly Leu Gly Ile Ser Trp Leu Gly
420 425 430

Leu Arg Ser Leu Arg Glu Leu Gly Ser Gly Leu Ala Leu Ile His His
435 440 445

Asn Thr His Leu Cys Phe Val His Thr Val Pro Trp Asp Gln Leu Phe
450 455 460

Arg Asn Pro His Gln Ala Leu Leu His Thr Ala Asn Arg Pro Glu Asp
465 470 475 480

Glu Cys Val Gly Glu Gly Leu Ala Cys His Gln Leu Cys Ala Arg Gly
485 490 495

His Cys Trp Gly Pro Gly Pro Thr Gln Cys Val Asn Cys Ser Gln Phe
500 505 510

Leu Arg Gly Gln Glu Cys Val Glu Glu Cys Arg Val Leu Gln Gly Leu
515 520 525

Pro Arg Glu Tyr Val Asn Ala Arg His Cys Leu Pro Cys His Pro Glu
530 535 540

Cys Gln Pro Gln Asn Gly Ser Val Thr Cys Phe Gly Pro Glu Ala Asp
545 550 555 560

Gln Cys Val Ala Cys Ala His Tyr Lys Asp Pro Pro Phe Cys Val Ala
565 570 575

Arg Cys Pro Ser Gly Val Lys Pro Asp Leu Ser Tyr Met Pro Ile Trp
580 585 590

Lys Phe Pro Asp Glu Glu Gly Ala Cys Gln Pro Cys Pro Ile Asn Cys
595 600 605

Thr His Ser Cys Val Asp Leu Asp Asp Lys Gly Cys Pro Ala Glu Gln
610 615 620

Arg Ala Ser Pro Leu Thr Leu Leu Gln Glu Thr Glu Leu Val Glu Pro
625 630 635 640

Leu Thr Pro Ser Gly Ala Met Pro Asn Gln Ala Gln Met Arg Ile Leu
645 650 655

Lys Glu Thr Glu Leu Arg Lys Val Lys Val Leu Gly Ser Gly Ala Phe
660 665 670

Gly Thr Val Tyr Lys Gly Ile Trp Ile Pro Asp Gly Glu Asn Val Lys

ITI-08-PCT_Sequence_Listing_ST25.txt

```

        675                680                685
Ile Pro Val Ala Ile Ala Val Leu Arg Glu Asn Thr Ser Pro Lys Ala
690                695                700

Asn Lys Glu Ile Leu Asp Glu Ala Tyr Val Met Ala Gly Val Gly Ser
705                710                715                720

Pro Tyr Val Ser Arg Leu Leu Gly Ile Cys Leu Thr Ser Thr Val Gln
725                730                735

Leu Val Thr Gln Leu Met Pro Tyr Gly Cys Leu Leu Asp His Val Arg
740                745                750

Glu Asn Arg Gly Arg Leu Gly Ser Gln Asp Leu Leu Asn Trp Cys Met
755                760                765

Gln Ile Ala Lys Gly Met Ser Tyr Leu Glu Asp Val Arg Leu Val His
770                775                780

Arg Asp Leu Ala Ala Arg Asn Val Leu Val Lys Ser Pro Asn His Val
785                790                795                800

Lys Ile Thr Asp Phe Gly Leu Ala Arg Leu Leu Asp Ile Asp Glu Thr
805                810                815

Glu Tyr His Ala Asp Gly Gly Lys Val Pro Ile Lys Trp Met Ala Leu
820                825                830

Glu Ser Ile Leu Arg Arg Arg Phe Thr His Gln Ser Asp Val Trp Ser
835                840                845

Tyr Gly Val Thr Val Trp Glu Leu Met Thr Phe Gly Ala Lys Pro Tyr
850                855                860

Asp Gly Ile Pro Ala Arg Glu Ile Pro Asp Leu Leu Glu Lys Gly Glu
865                870                875                880

Arg Leu Pro Gln Pro Pro Ile Cys Thr Ile Asp Val Tyr Met Ile Met
885                890                895

Val Lys Cys Trp Met Ile Asp Ser Glu Cys Arg Pro Arg Phe Arg Glu
900                905                910

Leu Val Ser Glu Phe Ser Arg Met Ala Arg Asp Pro Gln Arg Phe Val
915                920                925

Val Ile Gln Asn Glu Asp Leu Gly Pro Ala Ser Pro Leu Asp Ser Thr
930                935                940

Phe Tyr Arg Ser Leu Leu Glu Asp Asp Asp Met Gly Asp Leu Val Asp
945                950                955                960

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Ala Glu Glu Tyr Leu Val Pro Gln Gln Gly Phe Phe Cys Pro Asp Pro
965 970 975

Ala Pro Gly Ala Gly Gly Met Val His His Arg His Arg Ser Ser Ser
980 985 990

Thr Arg Ser Gly Gly Gly Asp Leu Thr Leu Gly Leu Glu Pro Ser Glu
995 1000 1005

Glu Glu Ala Pro Arg Ser Pro Leu Ala Pro Ser Glu Gly Ala Gly
1010 1015 1020

Ser Asp Val Phe Asp Gly Asp Leu Gly Met Gly Ala Ala Lys Gly
1025 1030 1035

Leu Gln Ser Leu Pro Thr His Asp Pro Ser Pro Leu Gln Arg Tyr
1040 1045 1050

Ser Glu Asp Pro Thr Val Pro Leu Pro Ser Glu Thr Asp Gly Tyr
1055 1060 1065

Val Ala Pro Leu Thr Cys Ser Pro Gln Pro Glu Tyr Val Asn Gln
1070 1075 1080

Pro Asp Val Arg Pro Gln Pro Pro Ser Pro Arg Glu Gly Pro Leu
1085 1090 1095

Pro Ala Ala Arg Pro Ala Gly Ala Thr Leu Glu Arg Ala Lys Thr
1100 1105 1110

Leu Ser Pro Gly Lys Asn Gly Val Val Lys Asp Val Phe Ala Phe
1115 1120 1125

Gly Gly Ala Val Glu Asn Pro Glu Tyr Leu Thr Pro Gln Gly Gly
1130 1135 1140

Ala Ala Pro Gln Pro His Pro Pro Pro Ala Phe Ser Pro Ala Phe
1145 1150 1155

Asp Asn Leu Tyr Tyr Trp Asp Gln Asp Pro Pro Glu Arg Gly Ala
1160 1165 1170

Pro Pro Ser Thr Phe Lys Gly Thr Pro Thr Ala Glu Asn Pro Glu
1175 1180 1185

Tyr Leu Gly Leu Asp Val Pro Val
1190 1195

<210> 154

<211> 610

<212> PRT

<223> Synthetic Construct

Pro Lys His Ser Asp Cys Leu Ala Cys Leu His Phe Asn His Ser Gly
225 230 235 240

ITI-08-PCT_Sequence_Listing_ST25.txt

Ile	Cys	Glu	Leu	His	Cys	Pro	Ala	Leu	Val	Thr	Tyr	Asn	Thr	Asp	Thr	245	250	255
Phe	Glu	Ser	Met	Pro	Asn	Pro	Glu	Gly	Arg	Tyr	Thr	Phe	Gly	Ala	Ser	260	265	270
Cys	Val	Thr	Ala	Cys	Pro	Tyr	Asn	Tyr	Leu	Ser	Thr	Asp	Val	Gly	Ser	275	280	285
Cys	Thr	Leu	Val	Cys	Pro	Leu	His	Asn	Gln	Glu	Val	Thr	Ala	Glu	Asp	290	295	300
Gly	Thr	Gln	Arg	Cys	Glu	Lys	Cys	Ser	Lys	Pro	Cys	Ala	Arg	Val	Cys	305	310	315
Tyr	Gly	Leu	Gly	Met	Glu	His	Leu	Arg	Glu	Val	Arg	Ala	Val	Thr	Ser	325	330	335
Ala	Asn	Ile	Gln	Glu	Phe	Ala	Gly	Cys	Lys	Lys	Ile	Phe	Gly	Ser	Leu	340	345	350
Ala	Phe	Leu	Pro	Glu	Ser	Phe	Asp	Gly	Asp	Pro	Ala	Ser	Asn	Thr	Ala	355	360	365
Pro	Leu	Gln	Pro	Glu	Gln	Leu	Gln	Val	Phe	Glu	Thr	Leu	Glu	Glu	Ile	370	375	380
Thr	Gly	Tyr	Leu	Tyr	Ile	Ser	Ala	Trp	Pro	Asp	Ser	Leu	Pro	Asp	Leu	385	390	395
Ser	Val	Phe	Gln	Asn	Leu	Gln	Val	Ile	Arg	Gly	Arg	Ile	Leu	His	Asn	405	410	415
Gly	Ala	Tyr	Ser	Leu	Thr	Leu	Gln	Gly	Leu	Gly	Ile	Ser	Trp	Leu	Gly	420	425	430
Leu	Arg	Ser	Leu	Arg	Glu	Leu	Gly	Ser	Gly	Leu	Ala	Leu	Ile	His	His	435	440	445
Asn	Thr	His	Leu	Cys	Phe	Val	His	Thr	Val	Pro	Trp	Asp	Gln	Leu	Phe	450	455	460
Arg	Asn	Pro	His	Gln	Ala	Leu	Leu	His	Thr	Ala	Asn	Arg	Pro	Glu	Asp	465	470	475
Glu	Cys	Val	Gly	Glu	Gly	Leu	Ala	Cys	His	Gln	Leu	Cys	Ala	Arg	Gly	485	490	495
His	Cys	Trp	Gly	Pro	Gly	Pro	Thr	Gln	Cys	Val	Asn	Cys	Ser	Gln	Phe	500	505	510
Leu	Arg	Gly	Gln	Glu	Cys	Val	Glu	Glu	Cys	Arg	Val	Leu	Gln	Gly	Leu			

ITI-08-PCT_Sequence_Listing_ST25.txt

515

520

525

Pro Arg Glu Tyr Val Asn Ala Arg His Cys Leu Pro Cys His Pro Glu
530 535 540

Cys Gln Pro Gln Asn Gly Ser Val Thr Cys Phe Gly Pro Glu Ala Asp
545 550 555 560

Gln Cys Val Ala Cys Ala His Tyr Lys Asp Pro Pro Phe Cys Val Ala
565 570 575

Arg Cys Pro Ser Gly Val Lys Pro Asp Leu Ser Tyr Met Pro Ile Trp
580 585 590

Lys Phe Pro Asp Glu Glu Gly Ala Cys Gln Pro Cys Pro Ile Asn Cys
595 600 605

Thr His
610

<210> 155
<211> 1342
<212> PRT
<213> Homo sapiens

<400> 155

Met Arg Ala Asn Asp Ala Leu Gln Val Leu Gly Leu Leu Phe Ser Leu
1 5 10 15

Ala Arg Gly Ser Glu Val Gly Asn Ser Gln Ala Val Cys Pro Gly Thr
20 25 30

Leu Asn Gly Leu Ser Val Thr Gly Asp Ala Glu Asn Gln Tyr Gln Thr
35 40 45

Leu Tyr Lys Leu Tyr Glu Arg Cys Glu Val Val Met Gly Asn Leu Glu
50 55 60

Ile Val Leu Thr Gly His Asn Ala Asp Leu Ser Phe Leu Gln Trp Ile
65 70 75 80

Arg Glu Val Thr Gly Tyr Val Leu Val Ala Met Asn Glu Phe Ser Thr
85 90 95

Leu Pro Leu Pro Asn Leu Arg Val Val Arg Gly Thr Gln Val Tyr Asp
100 105 110

Gly Lys Phe Ala Ile Phe Val Met Leu Asn Tyr Asn Thr Asn Ser Ser
115 120 125

His Ala Leu Arg Gln Leu Arg Leu Thr Gln Leu Thr Glu Ile Leu Ser

ITI-08-PCT_Sequence_Listing_ST25.txt

```

130          135          140
Gly Gly Val Tyr Ile Glu Lys Asn Asp Lys Leu Cys His Met Asp Thr
145          150          155          160
Ile Asp Trp Arg Asp Ile Val Arg Asp Arg Asp Ala Glu Ile Val Val
165          170          175
Lys Asp Asn Gly Arg Ser Cys Pro Pro Cys His Glu Val Cys Lys Gly
180          185          190
Arg Cys Trp Gly Pro Gly Ser Glu Asp Cys Gln Thr Leu Thr Lys Thr
195          200          205
Ile Cys Ala Pro Gln Cys Asn Gly His Cys Phe Gly Pro Asn Pro Asn
210          215          220
Gln Cys Cys His Asp Glu Cys Ala Gly Gly Cys Ser Gly Pro Gln Asp
225          230          235          240
Thr Asp Cys Phe Ala Cys Arg His Phe Asn Asp Ser Gly Ala Cys Val
245          250          255
Pro Arg Cys Pro Gln Pro Leu Val Tyr Asn Lys Leu Thr Phe Gln Leu
260          265          270
Glu Pro Asn Pro His Thr Lys Tyr Gln Tyr Gly Gly Val Cys Val Ala
275          280          285
Ser Cys Pro His Asn Phe Val Val Asp Gln Thr Ser Cys Val Arg Ala
290          295          300
Cys Pro Pro Asp Lys Met Glu Val Asp Lys Asn Gly Leu Lys Met Cys
305          310          315          320
Glu Pro Cys Gly Gly Leu Cys Pro Lys Ala Cys Glu Gly Thr Gly Ser
325          330          335
Gly Ser Arg Phe Gln Thr Val Asp Ser Ser Asn Ile Asp Gly Phe Val
340          345          350
Asn Cys Thr Lys Ile Leu Gly Asn Leu Asp Phe Leu Ile Thr Gly Leu
355          360          365
Asn Gly Asp Pro Trp His Lys Ile Pro Ala Leu Asp Pro Glu Lys Leu
370          375          380
Asn Val Phe Arg Thr Val Arg Glu Ile Thr Gly Tyr Leu Asn Ile Gln
385          390          395          400
Ser Trp Pro Pro His Met His Asn Phe Ser Val Phe Ser Asn Leu Thr
405          410          415

```


ITI-08-PCT_Sequence_Listing_ST25.txt

Thr	Ile	Gly	Gly	Arg	Ser	Leu	Tyr	Asn	Arg	Gly	Phe	Ser	Leu	Leu	Ile	420	425	430
Met	Lys	Asn	Leu	Asn	Val	Thr	Ser	Leu	Gly	Phe	Arg	Ser	Leu	Lys	Glu	435	440	445
Ile	Ser	Ala	Gly	Arg	Ile	Tyr	Ile	Ser	Ala	Asn	Arg	Gln	Leu	Cys	Tyr	450	455	460
His	His	Ser	Leu	Asn	Trp	Thr	Lys	Val	Leu	Arg	Gly	Pro	Thr	Glu	Glu	465	470	475
Arg	Leu	Asp	Ile	Lys	His	Asn	Arg	Pro	Arg	Arg	Asp	Cys	Val	Ala	Glu	485	490	495
Gly	Lys	Val	Cys	Asp	Pro	Leu	Cys	Ser	Ser	Gly	Gly	Cys	Trp	Gly	Pro	500	505	510
Gly	Pro	Gly	Gln	Cys	Leu	Ser	Cys	Arg	Asn	Tyr	Ser	Arg	Gly	Gly	Val	515	520	525
Cys	Val	Thr	His	Cys	Asn	Phe	Leu	Asn	Gly	Glu	Pro	Arg	Glu	Phe	Ala	530	535	540
His	Glu	Ala	Glu	Cys	Phe	Ser	Cys	His	Pro	Glu	Cys	Gln	Pro	Met	Glu	545	550	555
Gly	Thr	Ala	Thr	Cys	Asn	Gly	Ser	Gly	Ser	Asp	Thr	Cys	Ala	Gln	Cys	565	570	575
Ala	His	Phe	Arg	Asp	Gly	Pro	His	Cys	Val	Ser	Ser	Cys	Pro	His	Gly	580	585	590
Val	Leu	Gly	Ala	Lys	Gly	Pro	Ile	Tyr	Lys	Tyr	Pro	Asp	Val	Gln	Asn	595	600	605
Glu	Cys	Arg	Pro	Cys	His	Glu	Asn	Cys	Thr	Gln	Gly	Cys	Lys	Gly	Pro	610	615	620
Glu	Leu	Gln	Asp	Cys	Leu	Gly	Gln	Thr	Leu	Val	Leu	Ile	Gly	Lys	Thr	625	630	635
His	Leu	Thr	Met	Ala	Leu	Thr	Val	Ile	Ala	Gly	Leu	Val	Val	Ile	Phe	645	650	655
Met	Met	Leu	Gly	Gly	Thr	Phe	Leu	Tyr	Trp	Arg	Gly	Arg	Arg	Ile	Gln	660	665	670
Asn	Lys	Arg	Ala	Met	Arg	Arg	Tyr	Leu	Glu	Arg	Gly	Glu	Ser	Ile	Glu	675	680	685

ITI-08-PCT_Sequence_Listing_ST25.txt

```

Pro Leu Asp Pro Ser Glu Lys Ala Asn Lys Val Leu Ala Arg Ile Phe
690                      695                      700

Lys Glu Thr Glu Leu Arg Lys Leu Lys Val Leu Gly Ser Gly Val Phe
705                      710                      715                      720

Gly Thr Val His Lys Gly Val Trp Ile Pro Glu Gly Glu Ser Ile Lys
725                      730                      735

Ile Pro Val Cys Ile Lys Val Ile Glu Asp Lys Ser Gly Arg Gln Ser
740                      745                      750

Phe Gln Ala Val Thr Asp His Met Leu Ala Ile Gly Ser Leu Asp His
755                      760                      765

Ala His Ile Val Arg Leu Leu Gly Leu Cys Pro Gly Ser Ser Leu Gln
770                      775                      780

Leu Val Thr Gln Tyr Leu Pro Leu Gly Ser Leu Leu Asp His Val Arg
785                      790                      795                      800

Gln His Arg Gly Ala Leu Gly Pro Gln Leu Leu Leu Asn Trp Gly Val
805                      810                      815

Gln Ile Ala Lys Gly Met Tyr Tyr Leu Glu Glu His Gly Met Val His
820                      825                      830

Arg Asn Leu Ala Ala Arg Asn Val Leu Leu Lys Ser Pro Ser Gln Val
835                      840                      845

Gln Val Ala Asp Phe Gly Val Ala Asp Leu Leu Pro Pro Asp Asp Lys
850                      855                      860

Gln Leu Leu Tyr Ser Glu Ala Lys Thr Pro Ile Lys Trp Met Ala Leu
865                      870                      875                      880

Glu Ser Ile His Phe Gly Lys Tyr Thr His Gln Ser Asp Val Trp Ser
885                      890                      895

Tyr Gly Val Thr Val Trp Glu Leu Met Thr Phe Gly Ala Glu Pro Tyr
900                      905                      910

Ala Gly Leu Arg Leu Ala Glu Val Pro Asp Leu Leu Glu Lys Gly Glu
915                      920                      925

Arg Leu Ala Gln Pro Gln Ile Cys Thr Ile Asp Val Tyr Met Val Met
930                      935                      940

Val Lys Cys Trp Met Ile Asp Glu Asn Ile Arg Pro Thr Phe Lys Glu
945                      950                      955                      960

Leu Ala Asn Glu Phe Thr Arg Met Ala Arg Asp Pro Pro Arg Tyr Leu

```

ITI-08-PCT_Sequence_Listing_ST25.txt

965

970

975

Val Ile Lys Arg Glu Ser Gly Pro Gly Ile Ala Pro Gly Pro Glu Pro
 980 985 990

His Gly Leu Thr Asn Lys Lys Leu Glu Glu Val Glu Leu Glu Pro Glu
 995 1000 1005

Leu Asp Leu Asp Leu Asp Leu Glu Ala Glu Glu Asp Asn Leu Ala
 1010 1015 1020

Thr Thr Thr Leu Gly Ser Ala Leu Ser Leu Pro Val Gly Thr Leu
 1025 1030 1035

Asn Arg Pro Arg Gly Ser Gln Ser Leu Leu Ser Pro Ser Ser Gly
 1040 1045 1050

Tyr Met Pro Met Asn Gln Gly Asn Leu Gly Glu Ser Cys Gln Glu
 1055 1060 1065

Ser Ala Val Ser Gly Ser Ser Glu Arg Cys Pro Arg Pro Val Ser
 1070 1075 1080

Leu His Pro Met Pro Arg Gly Cys Leu Ala Ser Glu Ser Ser Glu
 1085 1090 1095

Gly His Val Thr Gly Ser Glu Ala Glu Leu Gln Glu Lys Val Ser
 1100 1105 1110

Met Cys Arg Ser Arg Ser Arg Ser Arg Ser Pro Arg Pro Arg Gly
 1115 1120 1125

Asp Ser Ala Tyr His Ser Gln Arg His Ser Leu Leu Thr Pro Val
 1130 1135 1140

Thr Pro Leu Ser Pro Pro Gly Leu Glu Glu Glu Asp Val Asn Gly
 1145 1150 1155

Tyr Val Met Pro Asp Thr His Leu Lys Gly Thr Pro Ser Ser Arg
 1160 1165 1170

Glu Gly Thr Leu Ser Ser Val Gly Leu Ser Ser Val Leu Gly Thr
 1175 1180 1185

Glu Glu Glu Asp Glu Asp Glu Glu Tyr Glu Tyr Met Asn Arg Arg
 1190 1195 1200

Arg Arg His Ser Pro Pro His Pro Pro Arg Pro Ser Ser Leu Glu
 1205 1210 1215

Glu Leu Gly Tyr Glu Tyr Met Asp Val Gly Ser Asp Leu Ser Ala
 1220 1225 1230

ITI-08-PCT_Sequence_Listing_ST25.txt

Ser Leu Gly Ser Thr Gln Ser Cys Pro Leu His Pro Val Pro Ile
1235 1240 1245

Met Pro Thr Ala Gly Thr Thr Pro Asp Glu Asp Tyr Glu Tyr Met
1250 1255 1260

Asn Arg Gln Arg Asp Gly Gly Gly Pro Gly Gly Asp Tyr Ala Ala
1265 1270 1275

Met Gly Ala Cys Pro Ala Ser Glu Gln Gly Tyr Glu Glu Met Arg
1280 1285 1290

Ala Phe Gln Gly Pro Gly His Gln Ala Pro His Val His Tyr Ala
1295 1300 1305

Arg Leu Lys Thr Leu Arg Ser Leu Glu Ala Thr Asp Ser Ala Phe
1310 1315 1320

Asp Asn Pro Asp Tyr Trp His Ser Arg Leu Phe Pro Lys Ala Asn
1325 1330 1335

Ala Gln Arg Thr
1340

<210> 156
<211> 1295
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 156

Ser Glu Val Gly Asn Ser Gln Ala Val Cys Pro Gly Thr Leu Asn Gly
1 5 10 15

Leu Ser Val Thr Gly Asp Ala Glu Asn Gln Tyr Gln Thr Leu Tyr Lys
20 25 30

Leu Tyr Glu Arg Cys Glu Val Val Met Gly Asn Leu Glu Ile Val Leu
35 40 45

Thr Gly His Asn Ala Asp Leu Ser Phe Leu Gln Trp Ile Arg Glu Val
50 55 60

Thr Gly Tyr Val Leu Val Ala Met Asn Glu Phe Ser Thr Leu Pro Leu
65 70 75 80

Pro Asn Leu Arg Val Val Arg Gly Thr Gln Val Tyr Asp Gly Lys Phe
85 90 95

ITI-08-PCT_Sequence_Listing_ST25.txt

Ala	Ile	Phe	Val	Met	Leu	Asn	Tyr	Asn	Thr	Asn	Ser	Ser	His	Ala	Leu	100	105	110
Arg	Gln	Leu	Arg	Leu	Thr	Gln	Leu	Thr	Glu	Ile	Leu	Ser	Gly	Gly	Val	115	120	125
Tyr	Ile	Glu	Lys	Asn	Asp	Lys	Leu	Cys	His	Met	Asp	Thr	Ile	Asp	Trp	130	135	140
Arg	Asp	Ile	Val	Arg	Asp	Arg	Asp	Ala	Glu	Ile	Val	Val	Lys	Asp	Asn	145	150	155
Gly	Arg	Ser	Cys	Pro	Pro	Cys	His	Glu	Val	Cys	Lys	Gly	Arg	Cys	Trp	165	170	175
Gly	Pro	Gly	Ser	Glu	Asp	Cys	Gln	Thr	Leu	Thr	Lys	Thr	Ile	Cys	Ala	180	185	190
Pro	Gln	Cys	Asn	Gly	His	Cys	Phe	Gly	Pro	Asn	Pro	Asn	Gln	Cys	Cys	195	200	205
His	Asp	Glu	Cys	Ala	Gly	Gly	Cys	Ser	Gly	Pro	Gln	Asp	Thr	Asp	Cys	210	215	220
Phe	Ala	Cys	Arg	His	Phe	Asn	Asp	Ser	Gly	Ala	Cys	Val	Pro	Arg	Cys	225	230	235
Pro	Gln	Pro	Leu	Val	Tyr	Asn	Lys	Leu	Thr	Phe	Gln	Leu	Glu	Pro	Asn	245	250	255
Pro	His	Thr	Lys	Tyr	Gln	Tyr	Gly	Gly	Val	Cys	Val	Ala	Ser	Cys	Pro	260	265	270
His	Asn	Phe	Val	Val	Asp	Gln	Thr	Ser	Cys	Val	Arg	Ala	Cys	Pro	Pro	275	280	285
Asp	Lys	Met	Glu	Val	Asp	Lys	Asn	Gly	Leu	Lys	Met	Cys	Glu	Pro	Cys	290	295	300
Gly	Gly	Leu	Cys	Pro	Lys	Ala	Cys	Glu	Gly	Thr	Gly	Ser	Gly	Ser	Arg	305	310	315
Phe	Gln	Thr	Val	Asp	Ser	Ser	Asn	Ile	Asp	Gly	Phe	Val	Asn	Cys	Thr	325	330	335
Lys	Ile	Leu	Gly	Asn	Leu	Asp	Phe	Leu	Ile	Thr	Gly	Leu	Asn	Gly	Asp	340	345	350
Pro	Trp	His	Lys	Ile	Pro	Ala	Leu	Asp	Pro	Glu	Lys	Leu	Asn	Val	Phe	355	360	365

ITI-08-PCT_Sequence_Listing_ST25.txt

Arg	Thr	Val	Arg	Glu	Ile	Thr	Gly	Tyr	Leu	Asn	Ile	Gln	Ser	Trp	Pro	370	375	380	
Pro	His	Met	His	Asn	Phe	Ser	Val	Phe	Ser	Asn	Leu	Thr	Thr	Ile	Gly	385	390	395	400
Gly	Arg	Ser	Leu	Tyr	Asn	Arg	Gly	Phe	Ser	Leu	Leu	Ile	Met	Lys	Asn	405	410	415	
Leu	Asn	Val	Thr	Ser	Leu	Gly	Phe	Arg	Ser	Leu	Lys	Glu	Ile	Ser	Ala	420	425	430	
Gly	Arg	Ile	Tyr	Ile	Ser	Ala	Asn	Arg	Gln	Leu	Cys	Tyr	His	His	Ser	435	440	445	
Leu	Asn	Trp	Thr	Lys	Val	Leu	Arg	Gly	Pro	Thr	Glu	Glu	Arg	Leu	Asp	450	455	460	
Ile	Lys	His	Asn	Arg	Pro	Arg	Arg	Asp	Cys	Val	Ala	Glu	Gly	Lys	Val	465	470	475	480
Cys	Asp	Pro	Leu	Cys	Ser	Ser	Gly	Gly	Cys	Trp	Gly	Pro	Gly	Pro	Gly	485	490	495	
Gln	Cys	Leu	Ser	Cys	Arg	Asn	Tyr	Ser	Arg	Gly	Gly	Val	Cys	Val	Thr	500	505	510	
His	Cys	Asn	Phe	Leu	Asn	Gly	Glu	Pro	Arg	Glu	Phe	Ala	His	Glu	Ala	515	520	525	
Glu	Cys	Phe	Ser	Cys	His	Pro	Glu	Cys	Gln	Pro	Met	Glu	Gly	Thr	Ala	530	535	540	
Thr	Cys	Asn	Gly	Ser	Gly	Ser	Asp	Thr	Cys	Ala	Gln	Cys	Ala	His	Phe	545	550	555	560
Arg	Asp	Gly	Pro	His	Cys	Val	Ser	Ser	Cys	Pro	His	Gly	Val	Leu	Gly	565	570	575	
Ala	Lys	Gly	Pro	Ile	Tyr	Lys	Tyr	Pro	Asp	Val	Gln	Asn	Glu	Cys	Arg	580	585	590	
Pro	Cys	His	Glu	Asn	Cys	Thr	Gln	Gly	Cys	Lys	Gly	Pro	Glu	Leu	Gln	595	600	605	
Asp	Cys	Leu	Gly	Gln	Thr	Leu	Val	Leu	Ile	Gly	Lys	Thr	His	Leu	Thr	610	615	620	
Tyr	Trp	Arg	Gly	Arg	Arg	Ile	Gln	Asn	Lys	Arg	Ala	Met	Arg	Arg	Tyr	625	630	635	640
Leu	Glu	Arg	Gly	Glu	Ser	Ile	Glu	Pro	Leu	Asp	Pro	Ser	Glu	Lys	Ala				

ITI-08-PCT_Sequence_Listing_ST25.txt

645 650 655

Asn Lys Val Leu Ala Arg Ile Phe Lys Glu Thr Glu Leu Arg Lys Leu
660 665 670

Lys Val Leu Gly Ser Gly Val Phe Gly Thr Val His Lys Gly Val Trp
675 680 685

Ile Pro Glu Gly Glu Ser Ile Lys Ile Pro Val Cys Ile Lys Val Ile
690 695 700

Glu Asp Lys Ser Gly Arg Gln Ser Phe Gln Ala Val Thr Asp His Met
705 710 715 720

Leu Ala Ile Gly Ser Leu Asp His Ala His Ile Val Arg Leu Leu Gly
725 730 735

Leu Cys Pro Gly Ser Ser Leu Gln Leu Val Thr Gln Tyr Leu Pro Leu
740 745 750

Gly Ser Leu Leu Asp His Val Arg Gln His Arg Gly Ala Leu Gly Pro
755 760 765

Gln Leu Leu Leu Asn Trp Gly Val Gln Ile Ala Lys Gly Met Tyr Tyr
770 775 780

Leu Glu Glu His Gly Met Val His Arg Asn Leu Ala Ala Arg Asn Val
785 790 795 800

Leu Leu Lys Ser Pro Ser Gln Val Gln Val Ala Asp Phe Gly Val Ala
805 810 815

Asp Leu Leu Pro Pro Asp Asp Lys Gln Leu Leu Glu Ser Glu Ala Lys
820 825 830

Thr Pro Ile Lys Trp Met Ala Leu Glu Ser Ile His Phe Gly Lys Tyr
835 840 845

Thr His Gln Ser Asp Val Trp Ser Tyr Gly Val Thr Val Trp Glu Leu
850 855 860

Met Thr Phe Gly Ala Glu Pro Tyr Ala Gly Leu Arg Leu Ala Glu Val
865 870 875 880

Pro Asp Leu Leu Glu Lys Gly Glu Arg Leu Ala Gln Pro Gln Ile Cys
885 890 895

Thr Ile Asp Val Tyr Met Val Met Val Lys Cys Trp Met Ile Asp Glu
900 905 910

Asn Ile Arg Pro Thr Phe Lys Glu Leu Ala Asn Glu Phe Thr Arg Met
915 920 925

ITI-08-PCT_Sequence_Listing_ST25.txt

Ala	Arg	Asp	Pro	Pro	Arg	Tyr	Leu	Val	Ile	Lys	Arg	Glu	Ser	Gly	Pro	930	935	940	
Gly	Ile	Ala	Pro	Gly	Pro	Glu	Pro	His	Gly	Leu	Thr	Asn	Lys	Lys	Leu	945	950	955	960
Glu	Glu	Val	Glu	Leu	Glu	Pro	Glu	Leu	Asp	Leu	Asp	Leu	Asp	Leu	Glu	965	970	975	
Ala	Glu	Glu	Asp	Asn	Leu	Ala	Thr	Thr	Thr	Leu	Gly	Ser	Ala	Leu	Ser	980	985	990	
Leu	Pro	Val	Gly	Thr	Leu	Asn	Arg	Pro	Arg	Gly	Ser	Gln	Ser	Leu	Leu	995	1000	1005	
Ser	Pro	Ser	Ser	Gly	Tyr	Met	Pro	Met	Asn	Gln	Gly	Asn	Leu	Gly		1010	1015	1020	
Glu	Ser	Cys	Gln	Glu	Ser	Ala	Val	Ser	Gly	Ser	Ser	Glu	Arg	Cys		1025	1030	1035	
Pro	Arg	Pro	Val	Ser	Leu	His	Pro	Met	Pro	Arg	Gly	Cys	Leu	Ala		1040	1045	1050	
Ser	Glu	Ser	Ser	Glu	Gly	His	Val	Thr	Gly	Ser	Glu	Ala	Glu	Leu		1055	1060	1065	
Gln	Glu	Lys	Val	Ser	Met	Cys	Arg	Ser	Arg	Ser	Arg	Ser	Arg	Ser		1070	1075	1080	
Pro	Arg	Pro	Arg	Gly	Asp	Ser	Ala	Tyr	His	Ser	Gln	Arg	His	Ser		1085	1090	1095	
Leu	Leu	Thr	Pro	Val	Thr	Pro	Leu	Ser	Pro	Pro	Gly	Leu	Glu	Glu		1100	1105	1110	
Glu	Asp	Val	Asn	Gly	Tyr	Val	Met	Pro	Asp	Thr	His	Leu	Lys	Gly		1115	1120	1125	
Thr	Pro	Ser	Ser	Arg	Glu	Gly	Thr	Leu	Ser	Ser	Val	Gly	Leu	Ser		1130	1135	1140	
Ser	Val	Leu	Gly	Thr	Glu	Glu	Glu	Asp	Glu	Asp	Glu	Glu	Tyr	Glu		1145	1150	1155	
Tyr	Met	Asn	Pro	His	Pro	Pro	Arg	Pro	Ser	Ser	Leu	Glu	Glu	Leu		1160	1165	1170	
Gly	Tyr	Glu	Tyr	Met	Asp	Val	Gly	Ser	Asp	Leu	Ser	Ala	Ser	Leu		1175	1180	1185	

ITI-08-PCT_Sequence_Listing_ST25.txt

Gly Ser Thr Gln Ser Cys Pro Leu His Pro Val Pro Ile Met Pro
 1190 1195 1200

Thr Ala Gly Thr Thr Pro Asp Glu Asp Tyr Glu Tyr Met Asn Arg
 1205 1210 1215

Gln Arg Asp Gly Gly Gly Pro Gly Gly Asp Tyr Ala Ala Met Gly
 1220 1225 1230

Ala Cys Pro Ala Ser Glu Gln Gly Tyr Glu Glu Met Arg Ala Phe
 1235 1240 1245

Gln Gly Pro Gly His Gln Ala Pro His Val His Tyr Ala Arg Leu
 1250 1255 1260

Lys Thr Leu Arg Ser Leu Glu Ala Thr Asp Ser Ala Phe Asp Asn
 1265 1270 1275

Pro Asp Tyr Trp His Ser Arg Leu Phe Pro Lys Ala Asn Ala Gln
 1280 1285 1290

Arg Thr
 1295

<210> 157
 <211> 624
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 157

Ser Glu Val Gly Asn Ser Gln Ala Val Cys Pro Gly Thr Leu Asn Gly
 1 5 10 15

Leu Ser Val Thr Gly Asp Ala Glu Asn Gln Tyr Gln Thr Leu Tyr Lys
 20 25 30

Leu Tyr Glu Arg Cys Glu Val Val Met Gly Asn Leu Glu Ile Val Leu
 35 40 45

Thr Gly His Asn Ala Asp Leu Ser Phe Leu Gln Trp Ile Arg Glu Val
 50 55 60

Thr Gly Tyr Val Leu Val Ala Met Asn Glu Phe Ser Thr Leu Pro Leu
 65 70 75 80

Pro Asn Leu Arg Val Val Arg Gly Thr Gln Val Tyr Asp Gly Lys Phe
 85 90 95

ITI-08-PCT_Sequence_Listing_ST25.txt

Ala	Ile	Phe	Val	Met	Leu	Asn	Tyr	Asn	Thr	Asn	Ser	Ser	His	Ala	Leu	100	105	110
Arg	Gln	Leu	Arg	Leu	Thr	Gln	Leu	Thr	Glu	Ile	Leu	Ser	Gly	Gly	Val	115	120	125
Tyr	Ile	Glu	Lys	Asn	Asp	Lys	Leu	Cys	His	Met	Asp	Thr	Ile	Asp	Trp	130	135	140
Arg	Asp	Ile	Val	Arg	Asp	Arg	Asp	Ala	Glu	Ile	Val	Val	Lys	Asp	Asn	145	150	155
Gly	Arg	Ser	Cys	Pro	Pro	Cys	His	Glu	Val	Cys	Lys	Gly	Arg	Cys	Trp	165	170	175
Gly	Pro	Gly	Ser	Glu	Asp	Cys	Gln	Thr	Leu	Thr	Lys	Thr	Ile	Cys	Ala	180	185	190
Pro	Gln	Cys	Asn	Gly	His	Cys	Phe	Gly	Pro	Asn	Pro	Asn	Gln	Cys	Cys	195	200	205
His	Asp	Glu	Cys	Ala	Gly	Gly	Cys	Ser	Gly	Pro	Gln	Asp	Thr	Asp	Cys	210	215	220
Phe	Ala	Cys	Arg	His	Phe	Asn	Asp	Ser	Gly	Ala	Cys	Val	Pro	Arg	Cys	225	230	235
Pro	Gln	Pro	Leu	Val	Tyr	Asn	Lys	Leu	Thr	Phe	Gln	Leu	Glu	Pro	Asn	245	250	255
Pro	His	Thr	Lys	Tyr	Gln	Tyr	Gly	Gly	Val	Cys	Val	Ala	Ser	Cys	Pro	260	265	270
His	Asn	Phe	Val	Val	Asp	Gln	Thr	Ser	Cys	Val	Arg	Ala	Cys	Pro	Pro	275	280	285
Asp	Lys	Met	Glu	Val	Asp	Lys	Asn	Gly	Leu	Lys	Met	Cys	Glu	Pro	Cys	290	295	300
Gly	Gly	Leu	Cys	Pro	Lys	Ala	Cys	Glu	Gly	Thr	Gly	Ser	Gly	Ser	Arg	305	310	315
Phe	Gln	Thr	Val	Asp	Ser	Ser	Asn	Ile	Asp	Gly	Phe	Val	Asn	Cys	Thr	325	330	335
Lys	Ile	Leu	Gly	Asn	Leu	Asp	Phe	Leu	Ile	Thr	Gly	Leu	Asn	Gly	Asp	340	345	350
Pro	Trp	His	Lys	Ile	Pro	Ala	Leu	Asp	Pro	Glu	Lys	Leu	Asn	Val	Phe	355	360	365
Arg	Thr	Val	Arg	Glu	Ile	Thr	Gly	Tyr	Leu	Asn	Ile	Gln	Ser	Trp	Pro			

ITI-08-PCT_Sequence_Listing_ST25.txt

370

375

380

Pro His Met His Asn Phe Ser Val Phe Ser Asn Leu Thr Thr Ile Gly
385 390 395 400

Gly Arg Ser Leu Tyr Asn Arg Gly Phe Ser Leu Leu Ile Met Lys Asn
405 410 415

Leu Asn Val Thr Ser Leu Gly Phe Arg Ser Leu Lys Glu Ile Ser Ala
420 425 430

Gly Arg Ile Tyr Ile Ser Ala Asn Arg Gln Leu Cys Tyr His His Ser
435 440 445

Leu Asn Trp Thr Lys Val Leu Arg Gly Pro Thr Glu Glu Arg Leu Asp
450 455 460

Ile Lys His Asn Arg Pro Arg Arg Asp Cys Val Ala Glu Gly Lys Val
465 470 475 480

Cys Asp Pro Leu Cys Ser Ser Gly Gly Cys Trp Gly Pro Gly Pro Gly
485 490 495

Gln Cys Leu Ser Cys Arg Asn Tyr Ser Arg Gly Gly Val Cys Val Thr
500 505 510

His Cys Asn Phe Leu Asn Gly Glu Pro Arg Glu Phe Ala His Glu Ala
515 520 525

Glu Cys Phe Ser Cys His Pro Glu Cys Gln Pro Met Glu Gly Thr Ala
530 535 540

Thr Cys Asn Gly Ser Gly Ser Asp Thr Cys Ala Gln Cys Ala His Phe
545 550 555 560

Arg Asp Gly Pro His Cys Val Ser Ser Cys Pro His Gly Val Leu Gly
565 570 575

Ala Lys Gly Pro Ile Tyr Lys Tyr Pro Asp Val Gln Asn Glu Cys Arg
580 585 590

Pro Cys His Glu Asn Cys Thr Gln Gly Cys Lys Gly Pro Glu Leu Gln
595 600 605

Asp Cys Leu Gly Gln Thr Leu Val Leu Ile Gly Lys Thr His Leu Thr
610 615 620

<210> 158
<211> 283
<212> PRT
<213> Homo sapiens

ITI-08-PCT_Sequence_Listing_ST25.txt

<400> 158

```

Met Glu Pro Pro Gly Asp Trp Gly Pro Pro Pro Trp Arg Ser Thr Pro
1      5      10
Lys Thr Asp Val Leu Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala
      20      25      30
Pro Cys Tyr Ala Pro Ala Leu Pro Ser Cys Lys Glu Asp Glu Tyr Pro
      35      40      45
Val Gly Ser Glu Cys Cys Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys
      50      55      60
Glu Ala Cys Gly Glu Leu Thr Gly Thr Val Cys Glu Pro Cys Pro Pro
65      70      75      80
Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys
      85      90      95
Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg Asn Cys Ser
      100      105      110
Arg Thr Glu Asn Ala Val Cys Gly Cys Ser Pro Gly His Phe Cys Ile
      115      120      125
Val Gln Asp Gly Asp His Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser
      130      135      140
Ser Pro Gly Gln Arg Val Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr
145      150      155      160
Leu Cys Gln Asn Cys Pro Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu
      165      170      175
Glu Glu Cys Gln His Gln Thr Lys Cys Ser Trp Leu Val Thr Lys Ala
      180      185      190
Gly Ala Gly Thr Ser Ser Ser His Trp Val Trp Trp Phe Leu Ser Gly
      195      200      205
Ser Leu Val Ile Val Ile Val Cys Ser Thr Val Gly Leu Ile Ile Cys
      210      215      220
Val Lys Arg Arg Lys Pro Arg Gly Asp Val Val Lys Val Ile Val Ser
225      230      235      240
Val Gln Arg Lys Arg Gln Glu Ala Glu Gly Glu Ala Thr Val Ile Glu
      245      250      255
Ala Leu Gln Ala Pro Pro Asp Val Thr Thr Val Ala Val Glu Glu Thr
      260      265      270

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Ile Pro Ser Phe Thr Gly Arg Ser Pro Asn His
275 280

<210> 159
<211> 164
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 159

Leu Pro Ser Cys Lys Glu Asp Glu Tyr Pro Val Gly Ser Glu Cys Cys
1 5 10 15

Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys Glu Ala Cys Gly Glu Leu
20 25 30

Thr Gly Thr Val Cys Glu Pro Cys Pro Pro Gly Thr Tyr Ile Ala His
35 40 45

Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys Gln Met Cys Asp Pro Ala
50 55 60

Met Gly Leu Arg Ala Ser Arg Asn Cys Ser Arg Thr Glu Asn Ala Val
65 70 75 80

Cys Gly Cys Ser Pro Gly His Phe Cys Ile Val Gln Asp Gly Asp His
85 90 95

Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser Ser Pro Gly Gln Arg Val
100 105 110

Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr Leu Cys Gln Asn Cys Pro
115 120 125

Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu Glu Glu Cys Gln His Gln
130 135 140

Thr Lys Cys Ser Trp Leu Val Thr Lys Ala Gly Ala Gly Thr Ser Ser
145 150 155 160

Ser His Trp Val

<210> 160
<211> 150
<212> PRT
<213> Human papillomavirus type 16

<400> 160

ITI-08-PCT_Sequence_Listing_ST25.txt

Met His Gln Lys Arg Thr Ala Met Phe Gln Asp Pro Gln Glu Ser Gly
1 5 10 15

Arg Lys Leu Pro Gln Leu Cys Thr Glu Leu Gln Thr Thr Ile His Asp
20 25 30

Ile Ile Leu Glu Cys Val Tyr Cys Lys Gln Gln Leu Leu Arg Arg Glu
35 40 45

Val Tyr Asp Arg Asp Leu Cys Ile Val Tyr Arg Asp Gly Asn Pro Tyr
50 55 60

Ala Val Cys Asp Lys Cys Leu Lys Phe Tyr Ser Lys Ile Ser Glu Tyr
65 70 75 80

Arg His Tyr Cys Tyr Ser Leu Tyr Gly Thr Thr Leu Glu Gln Gln Tyr
85 90 95

Asn Lys Pro Leu Cys Asp Leu Leu Ile Arg Cys Ile Asn Cys Gln Lys
100 105 110

Pro Leu Gln Arg His Leu Asp Lys Lys Gln Arg Phe His Asn Ile Arg
115 120 125

Gly Arg Trp Thr Gly Arg Cys Met Ser Cys Cys Arg Ser Ser Arg Thr
130 135 140

Arg Arg Glu Thr Gln Leu
145 150

<210> 161
<211> 150
<212> PRT
<213> Human papillomavirus type 18

<400> 161

Met Ala Arg Phe Glu Asp Pro Thr Arg Ser Gly Tyr Lys Leu Pro Asp
1 5 10 15

Leu Cys Thr Glu Leu Asn Thr Ser Leu Gln Asp Ile Glu Ile Thr Cys
20 25 30

Val Tyr Cys Lys Thr Val Leu Glu Leu Thr Glu Val Phe Glu Lys Asp
35 40 45

Leu Phe Val Val Tyr Arg Asp Ser Ile Pro His Ala Ala Cys His Lys
50 55 60

Cys Ile Asp Phe Tyr Ser Arg Ile Arg Glu Leu Arg His Tyr Ser Asp
65 70 75 80

ITI-08-PCT_Sequence_Listing_ST25.txt

Ser Val Tyr Gly Asp Thr Leu Glu Lys Leu Thr Asn Thr Gly Leu Tyr
85 90 95

Asn Leu Leu Ile Arg Cys Leu Arg Cys Gln Lys Pro Leu Leu Arg His
100 105 110

Leu Asn Glu Lys Arg Arg Phe His Asn Ile Ala Gly His Tyr Arg Gly
115 120 125

Gln Cys His Ser Cys Cys Asn Arg Ala Arg Gln Glu Arg Leu Gln Arg
130 135 140

Arg Arg Glu Thr Gln Val
145 150

<210> 162
<211> 98
<212> PRT
<213> Human papillomavirus type 16

<400> 162

Met His Gly Asp Thr Pro Thr Leu His Glu Tyr Met Leu Asp Leu Gln
1 5 10 15

Pro Glu Thr Thr Asp Leu Tyr Gly Tyr Gly Gln Leu Asn Asp Ser Ser
20 25 30

Glu Glu Glu Asp Glu Ile Asp Gly Pro Ala Gly Gln Ala Glu Pro Asp
35 40 45

Arg Ala His Tyr Asn Ile Val Thr Phe Cys Cys Lys Cys Asp Ser Thr
50 55 60

Leu Arg Leu Cys Val Gln Ser Thr His Val Asp Ile Arg Thr Leu Glu
65 70 75 80

Asp Leu Leu Met Gly Thr Leu Gly Ile Val Cys Pro Ile Cys Ser Gln
85 90 95

Lys Pro

<210> 163
<211> 105
<212> PRT
<213> Human papillomavirus type 18

<400> 163

Met His Gly Pro Lys Ala Thr Leu Gln Asp Ile Val Leu His Leu Glu
1 5 10 15

ITI-08-PCT_Sequence_Listing_ST25.txt

Pro Gln Asn Glu Ile Pro Val Asp Leu Leu Gly His Gly Gln Leu Ser
20 25 30

Asp Ser Glu Glu Glu Asn Asp Glu Ile Asp Gly Val Asn His Gln His
35 40 45

Leu Pro Ala Arg Arg Ala Glu Pro Gln Arg His Thr Met Leu Cys Met
50 55 60

Cys Cys Lys Cys Glu Ala Arg Ile Glu Leu Val Val Glu Ser Ser Ala
65 70 75 80

Asp Asp Leu Arg Ala Phe Gln Gln Leu Phe Leu Asn Thr Leu Ser Phe
85 90 95

Val Cys Pro Trp Cys Ala Ser Gln Gln
100 105

<210> 164
<211> 253
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 164

Met His Gln Lys Arg Thr Ala Met Phe Gln Asp Pro Gln Glu Ser Gly
1 5 10 15

Arg Lys Leu Pro Gln Leu Cys Thr Glu Leu Gln Thr Thr Ile His Asp
20 25 30

Ile Ile Leu Glu Cys Val Tyr Cys Lys Gln Gln Leu Leu Arg Arg Glu
35 40 45

Val Tyr Asp Arg Asp Leu Cys Ile Val Tyr Arg Asp Gly Asn Pro Tyr
50 55 60

Ala Val Cys Asp Lys Cys Leu Lys Phe Tyr Ser Lys Ile Ser Glu Tyr
65 70 75 80

Arg His Tyr Cys Tyr Ser Leu Tyr Gly Thr Thr Leu Glu Gln Gln Tyr
85 90 95

Asn Lys Pro Leu Cys Asp Leu Leu Ile Arg Cys Ile Asn Cys Gln Lys
100 105 110

Pro Leu Gln Arg His Leu Asp Lys Lys Gln Arg Phe His Asn Ile Arg
115 120 125

ITI-08-PCT_Sequence_Listing_ST25.txt

Gly Arg Trp Thr Gly Arg Cys Met Ser Cys Cys Arg Ser Ser Arg Thr
130 135 140

Arg Arg Glu Thr Gln Leu Gly Pro Gly Pro Gly Met His Gly Asp Thr
145 150 155 160

Pro Thr Leu His Glu Tyr Met Leu Asp Leu Gln Pro Glu Thr Thr Asp
165 170 175

Leu Tyr Gly Tyr Gly Gln Leu Asn Asp Ser Ser Glu Glu Glu Asp Glu
180 185 190

Ile Asp Gly Pro Ala Gly Gln Ala Glu Pro Asp Arg Ala His Tyr Asn
195 200 205

Ile Val Thr Phe Cys Cys Lys Cys Asp Ser Thr Leu Arg Leu Cys Val
210 215 220

Gln Ser Thr His Val Asp Ile Arg Thr Leu Glu Asp Leu Leu Met Gly
225 230 235 240

Thr Leu Gly Ile Val Cys Pro Ile Cys Ser Gln Lys Pro
245 250

<210> 165

<211> 260

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 165

Met Ala Arg Phe Glu Asp Pro Thr Arg Ser Gly Tyr Lys Leu Pro Asp
1 5 10 15

Leu Cys Thr Glu Leu Asn Thr Ser Leu Gln Asp Ile Glu Ile Thr Cys
20 25 30

Val Tyr Cys Lys Thr Val Leu Glu Leu Thr Glu Val Phe Glu Lys Asp
35 40 45

Leu Phe Val Val Tyr Arg Asp Ser Ile Pro His Ala Ala Cys His Lys
50 55 60

Cys Ile Asp Phe Tyr Ser Arg Ile Arg Glu Leu Arg His Tyr Ser Asp
65 70 75 80

Ser Val Tyr Gly Asp Thr Leu Glu Lys Leu Thr Asn Thr Gly Leu Tyr
85 90 95

ITI-08-PCT_Sequence_Listing_ST25.txt

Asn Leu Leu Ile Arg Cys Leu Arg Cys Gln Lys Pro Leu Leu Arg His
100 105 110

Leu Asn Glu Lys Arg Arg Phe His Asn Ile Ala Gly His Tyr Arg Gly
115 120 125

Gln Cys His Ser Cys Cys Asn Arg Ala Arg Gln Glu Arg Leu Gln Arg
130 135 140

Arg Arg Glu Thr Gln Val Gly Pro Gly Pro Gly Met His Gly Pro Lys
145 150 155 160

Ala Thr Leu Gln Asp Ile Val Leu His Leu Glu Pro Gln Asn Glu Ile
165 170 175

Pro Val Asp Leu Leu Gly His Gly Gln Leu Ser Asp Ser Glu Glu Glu
180 185 190

Asn Asp Glu Ile Asp Gly Val Asn His Gln His Leu Pro Ala Arg Arg
195 200 205

Ala Glu Pro Gln Arg His Thr Met Leu Cys Met Cys Cys Lys Cys Glu
210 215 220

Ala Arg Ile Glu Leu Val Val Glu Ser Ser Ala Asp Asp Leu Arg Ala
225 230 235 240

Phe Gln Gln Leu Phe Leu Asn Thr Leu Ser Phe Val Cys Pro Trp Cys
245 250 255

Ala Ser Gln Gln
260

<210> 166
<211> 518
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 166

Met His Gln Lys Arg Thr Ala Met Phe Gln Asp Pro Gln Glu Ser Gly
1 5 10 15

Arg Lys Leu Pro Gln Leu Cys Thr Glu Leu Gln Thr Thr Ile His Asp
20 25 30

Ile Ile Leu Glu Cys Val Tyr Cys Lys Gln Gln Leu Leu Arg Arg Glu
35 40 45

ITI-08-PCT_Sequence_Listing_ST25.txt

Val	Tyr	Asp	Arg	Asp	Leu	Cys	Ile	Val	Tyr	Arg	Asp	Gly	Asn	Pro	Tyr	50	55	60	
Ala	Val	Cys	Asp	Lys	Cys	Leu	Lys	Phe	Tyr	Ser	Lys	Ile	Ser	Glu	Tyr	65	70	75	80
Arg	His	Tyr	Cys	Tyr	Ser	Leu	Tyr	Gly	Thr	Thr	Leu	Glu	Gln	Gln	Tyr	85	90	95	
Asn	Lys	Pro	Leu	Cys	Asp	Leu	Leu	Ile	Arg	Cys	Ile	Asn	Cys	Gln	Lys	100	105	110	
Pro	Leu	Gln	Arg	His	Leu	Asp	Lys	Lys	Gln	Arg	Phe	His	Asn	Ile	Arg	115	120	125	
Gly	Arg	Trp	Thr	Gly	Arg	Cys	Met	Ser	Cys	Cys	Arg	Ser	Ser	Arg	Thr	130	135	140	
Arg	Arg	Glu	Thr	Gln	Leu	Gly	Pro	Gly	Pro	Gly	Met	Ala	Arg	Phe	Glu	145	150	155	160
Asp	Pro	Thr	Arg	Ser	Gly	Tyr	Lys	Leu	Pro	Asp	Leu	Cys	Thr	Glu	Leu	165	170	175	
Asn	Thr	Ser	Leu	Gln	Asp	Ile	Glu	Ile	Thr	Cys	Val	Tyr	Cys	Lys	Thr	180	185	190	
Val	Leu	Glu	Leu	Thr	Glu	Val	Phe	Glu	Lys	Asp	Leu	Phe	Val	Val	Tyr	195	200	205	
Arg	Asp	Ser	Ile	Pro	His	Ala	Ala	Cys	His	Lys	Cys	Ile	Asp	Phe	Tyr	210	215	220	
Ser	Arg	Ile	Arg	Glu	Leu	Arg	His	Tyr	Ser	Asp	Ser	Val	Tyr	Gly	Asp	225	230	235	240
Thr	Leu	Glu	Lys	Leu	Thr	Asn	Thr	Gly	Leu	Tyr	Asn	Leu	Leu	Ile	Arg	245	250	255	
Cys	Leu	Arg	Cys	Gln	Lys	Pro	Leu	Leu	Arg	His	Leu	Asn	Glu	Lys	Arg	260	265	270	
Arg	Phe	His	Asn	Ile	Ala	Gly	His	Tyr	Arg	Gly	Gln	Cys	His	Ser	Cys	275	280	285	
Cys	Asn	Arg	Ala	Arg	Gln	Glu	Arg	Leu	Gln	Arg	Arg	Arg	Glu	Thr	Gln	290	295	300	
Val	Gly	Pro	Gly	Pro	Gly	Met	His	Gly	Asp	Thr	Pro	Thr	Leu	His	Glu	305	310	315	320

ITI-08-PCT_Sequence_Listing_ST25.txt

Tyr Met Leu Asp Leu Gln Pro Glu Thr Thr Asp Leu Tyr Gly Tyr Gly
325 330 335

Gln Leu Asn Asp Ser Ser Glu Glu Glu Asp Glu Ile Asp Gly Pro Ala
340 345 350

Gly Gln Ala Glu Pro Asp Arg Ala His Tyr Asn Ile Val Thr Phe Cys
355 360 365

Cys Lys Cys Asp Ser Thr Leu Arg Leu Cys Val Gln Ser Thr His Val
370 375 380

Asp Ile Arg Thr Leu Glu Asp Leu Leu Met Gly Thr Leu Gly Ile Val
385 390 395 400

Cys Pro Ile Cys Ser Gln Lys Pro Gly Pro Gly Pro Gly Met His Gly
405 410 415

Pro Lys Ala Thr Leu Gln Asp Ile Val Leu His Leu Glu Pro Gln Asn
420 425 430

Glu Ile Pro Val Asp Leu Leu Gly His Gly Gln Leu Ser Asp Ser Glu
435 440 445

Glu Glu Asn Asp Glu Ile Asp Gly Val Asn His Gln His Leu Pro Ala
450 455 460

Arg Arg Ala Glu Pro Gln Arg His Thr Met Leu Cys Met Cys Cys Lys
465 470 475 480

Cys Glu Ala Arg Ile Glu Leu Val Val Glu Ser Ser Ala Asp Asp Leu
485 490 495

Arg Ala Phe Gln Gln Leu Phe Leu Asn Thr Leu Ser Phe Val Cys Pro
500 505 510

Trp Cys Ala Ser Gln Gln
515

<210> 167
<211> 158
<212> PRT
<213> Homo sapiens

<400> 167

Met Gln Ala Glu Gly Arg Gly Thr Gly Gly Ser Thr Gly Asp Ala Asp
1 5 10 15

Gly Pro Gly Gly Pro Gly Ile Pro Asp Gly Pro Gly Gly Asn Ala Gly
20 25 30

ITI-08-PCT_Sequence_Listing_ST25.txt

Gly Pro Gly Glu Ala Gly Ala Thr Gly Gly Arg Gly Pro Arg Gly Ala
35 40 45

Gly Ala Ala Arg Ala Ser Gly Pro Gly Gly Gly Ala Pro Arg Gly Pro
50 55 60

His Gly Gly Ala Ala Ser Gly Leu Asn Gly Cys Cys Arg Cys Gly Ala
65 70 75 80

Arg Gly Pro Glu Ser Arg Leu Leu Glu Phe Tyr Leu Ala Met Pro Phe
85 90 95

Ala Thr Pro Met Glu Ala Glu Leu Ala Arg Arg Ser Leu Ala Gln Asp
100 105 110

Ala Pro Pro Leu Pro Val Pro Gly Val Leu Leu Lys Glu Phe Thr Val
115 120 125

Ser Gly Asn Ile Leu Thr Ile Arg Leu Thr Ala Ala Asp His Arg Gln
130 135 140

Leu Gln Leu Ser Ile Ser Ser Cys Leu Gln Gln Gln Arg Arg
145 150 155

<210> 168
<211> 79
<212> PRT
<213> Homo sapiens

<400> 168

Ala Arg Gly Pro Glu Ser Arg Leu Leu Glu Phe Tyr Leu Ala Met Pro
1 5 10 15

Phe Ala Thr Pro Met Glu Ala Glu Leu Ala Arg Arg Ser Leu Ala Gln
20 25 30

Asp Ala Pro Pro Leu Pro Val Pro Gly Val Leu Leu Lys Glu Phe Thr
35 40 45

Val Ser Gly Asn Ile Leu Thr Ile Arg Leu Thr Ala Ala Asp His Arg
50 55 60

Gln Leu Gln Leu Ser Ile Ser Ser Cys Leu Gln Gln Gln Arg Arg
65 70 75

<210> 169
<211> 641
<212> PRT
<213> Human gammaherpesvirus 4

<400> 169

ITI-08-PCT_Sequence_Listing_ST25.txt

```

Met Ser Asp Glu Gly Pro Gly Thr Gly Pro Gly Asn Gly Leu Gly Glu
1      5      10      15

Lys Gly Asp Thr Ser Gly Pro Glu Gly Ser Gly Gly Ser Gly Pro Gln
      20      25      30

Arg Arg Gly Gly Asp Asn His Gly Arg Gly Arg Gly Arg Gly Arg Gly
      35      40      45

Arg Gly Gly Gly Arg Pro Gly Ala Pro Gly Gly Ser Gly Ser Gly Pro
      50      55      60

Arg His Arg Asp Gly Val Arg Arg Pro Gln Lys Arg Pro Ser Cys Ile
65      70      75      80

Gly Cys Lys Gly Thr His Gly Gly Thr Gly Ala Gly Ala Gly Ala Gly
      85      90      95

Gly Ala Gly Ala Gly Gly Ala Gly Ala Gly Gly Gly Gly Ala Gly Ala Gly
      100      105      110

Gly Gly Ala Gly Gly Ala Gly Gly Ala Gly Gly Ala Gly Ala Gly Gly
      115      120      125

Gly Ala Gly Ala Gly Gly Gly Ala Gly Gly Ala Gly Gly Ala Gly Ala
      130      135      140

Gly Gly Gly Ala Gly Ala Gly Gly Gly Ala Gly Gly Ala Gly Ala Gly
145      150      155      160

Gly Gly Ala Gly Gly Ala Gly Gly Ala Gly Ala Gly Gly Gly Ala Gly
      165      170      175

Ala Gly Gly Gly Ala Gly Gly Ala Gly Ala Gly Gly Gly Gly Ala Gly Gly
      180      185      190

Ala Gly Gly Ala Gly Ala Gly Gly Gly Ala Gly Ala Gly Gly Ala Gly
      195      200      205

Gly Ala Gly Gly Ala Gly Ala Gly Gly Ala Gly Ala Gly Gly Gly Ala
      210      215      220

Gly Gly Ala Gly Gly Ala Gly Ala Gly Gly Ala Gly Ala Gly Ala Gly Ala
225      230      235      240

Gly Ala Gly Gly Ala Gly Ala Gly Gly Ala Gly Gly Ala Gly Ala Gly Ala
      245      250      255

Gly Ala Gly Gly Ala Gly Ala Gly Gly Ala Gly Gly Ala Gly Ala Gly Ala
      260      265      270

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Gly Gly Ala Gly Gly Ala Gly Ala Gly Gly Gly Ala Gly Gly Ala Gly
275 280 285

Ala Gly Gly Ala Gly Gly Ala Gly Ala Gly Gly Ala Gly Gly Ala Gly
290 295 300

Ala Gly Gly Ala Gly Gly Ala Gly Ala Gly Gly Ala Gly Ala Gly
305 310 315 320

Gly Ala Gly Ala Gly Gly Gly Gly Arg Gly Arg Gly Gly Ser Gly Gly
325 330 335

Arg Gly Arg Gly Gly Ser Gly Gly Arg Gly Arg Gly Gly Ser Gly Gly
340 345 350

Arg Arg Gly Arg Gly Arg Glu Arg Ala Arg Gly Gly Ser Arg Glu Arg
355 360 365

Ala Arg Gly Arg Gly Arg Gly Arg Gly Glu Lys Arg Pro Arg Ser Pro
370 375 380

Ser Ser Gln Ser Ser Ser Ser Gly Ser Pro Pro Arg Arg Pro Pro Pro
385 390 395 400

Gly Arg Arg Pro Phe Phe His Pro Val Gly Glu Ala Asp Tyr Phe Glu
405 410 415

Tyr His Gln Glu Gly Gly Pro Asp Gly Glu Pro Asp Val Pro Pro Gly
420 425 430

Ala Ile Glu Gln Gly Pro Ala Asp Asp Pro Gly Glu Gly Pro Ser Thr
435 440 445

Gly Pro Arg Gly Gln Gly Asp Gly Gly Arg Arg Lys Lys Gly Gly Trp
450 455 460

Phe Gly Lys His Arg Gly Gln Gly Gly Ser Asn Pro Lys Phe Glu Asn
465 470 475 480

Ile Ala Glu Gly Leu Arg Ala Leu Leu Ala Arg Ser His Val Glu Arg
485 490 495

Thr Thr Asp Glu Gly Thr Trp Val Ala Gly Val Phe Val Tyr Gly Gly
500 505 510

Ser Lys Thr Ser Leu Tyr Asn Leu Arg Arg Gly Thr Ala Leu Ala Ile
515 520 525

Pro Gln Cys Arg Leu Thr Pro Leu Ser Arg Leu Pro Phe Gly Met Ala
530 535 540

Pro Gly Pro Gly Pro Gln Pro Gly Pro Leu Arg Glu Ser Ile Val Cys

ITI-08-PCT_Sequence_Listing_ST25.txt

```

545                550                555                560
Tyr Phe Met Val Phe Leu Gln Thr His Ile Phe Ala Glu Val Leu Lys
                    565                570                575
Asp Ala Ile Lys Asp Leu Val Met Thr Lys Pro Ala Pro Thr Cys Asn
                    580                585                590
Ile Arg Val Thr Val Cys Ser Phe Asp Asp Gly Val Asp Leu Pro Pro
                    595                600                605
Trp Phe Pro Pro Met Val Glu Gly Ala Ala Ala Glu Gly Asp Asp Gly
                    610                615                620
Asp Asp Gly Asp Glu Gly Gly Asp Gly Asp Glu Gly Glu Glu Gly Gln
625                630                635                640
Glu
<210> 170
<211> 391
<212> PRT
<213> Human gammaherpesvirus 4
<400> 170
Met Ser Asp Glu Gly Pro Gly Thr Gly Pro Gly Asn Gly Leu Gly Glu
1                5                10                15
Lys Gly Asp Thr Ser Gly Pro Glu Gly Ser Gly Gly Ser Gly Pro Gln
                20                25                30
Arg Arg Gly Gly Asp Asn His Gly Arg Gly Arg Gly Arg Gly Arg Gly
                35                40                45
Arg Gly Gly Gly Arg Pro Gly Ala Pro Gly Gly Ser Gly Ser Gly Pro
                50                55                60
Arg His Arg Asp Gly Val Arg Arg Pro Gln Lys Arg Pro Ser Cys Ile
65                70                75                80
Gly Cys Lys Gly Thr His Arg Gly Arg Gly Gly Ser Gly Gly Arg Gly
                85                90                95
Arg Gly Gly Ser Gly Gly Arg Arg Gly Arg Gly Arg Glu Arg Ala Arg
                100                105                110
Gly Gly Ser Arg Glu Arg Ala Arg Gly Arg Gly Arg Gly Arg Gly Glu
                115                120                125
Lys Arg Pro Arg Ser Pro Ser Ser Gln Ser Ser Ser Ser Gly Ser Pro
                130                135                140

```


ITI-08-PCT_Sequence_Listing_ST25.txt

```

Pro Arg Arg Pro Pro Pro Gly Arg Arg Pro Phe Phe His Pro Val Gly
145                      150                      155                      160

Glu Ala Asp Tyr Phe Glu Tyr His Gln Glu Gly Gly Pro Asp Gly Glu
                      165                      170                      175

Pro Asp Val Pro Pro Gly Ala Ile Glu Gln Gly Pro Ala Asp Asp Pro
                      180                      185                      190

Gly Glu Gly Pro Ser Thr Gly Pro Arg Gly Gln Gly Asp Gly Gly Arg
195                      200                      205

Arg Lys Lys Gly Gly Trp Phe Gly Lys His Arg Gly Gln Gly Gly Ser
210                      215                      220

Asn Pro Lys Phe Glu Asn Ile Ala Glu Gly Leu Arg Ala Leu Leu Ala
225                      230                      235

Arg Ser His Val Glu Arg Thr Thr Asp Glu Gly Thr Trp Val Ala Gly
245                      250                      255

Val Phe Val Tyr Gly Gly Ser Lys Thr Ser Leu Tyr Asn Leu Arg Arg
260                      265                      270

Gly Thr Ala Leu Ala Ile Pro Gln Cys Arg Leu Thr Pro Leu Ser Arg
275                      280                      285

Leu Pro Phe Gly Met Ala Pro Gly Pro Gly Pro Gln Pro Gly Pro Leu
290                      295                      300

Arg Glu Ser Ile Val Cys Tyr Phe Met Val Phe Leu Gln Thr His Ile
305                      310                      315

Phe Ala Glu Val Leu Lys Asp Ala Ile Lys Asp Leu Val Met Thr Lys
325                      330                      335

Pro Ala Pro Thr Cys Asn Ile Arg Val Thr Val Cys Ser Phe Asp Asp
340                      345                      350

Gly Val Asp Leu Pro Pro Trp Phe Pro Pro Met Val Glu Gly Ala Ala
355                      360                      365

Ala Glu Gly Asp Asp Gly Asp Asp Gly Asp Glu Gly Gly Asp Gly Asp
370                      375                      380

Glu Gly Glu Glu Gly Gln Glu
385                      390

```

<210> 171

<211> 860

<212> PRT

ITI-08-PCT_Sequence_Listing_ST25.txt

<213> Human gammaherpesvirus 4

<400> 171

```

Met Glu Ala Ala Leu Leu Val Cys Gln Tyr Thr Ile Gln Ser Leu Ile
1          5          10          15

His Leu Thr Gly Glu Asp Pro Gly Phe Phe Asn Val Glu Ile Pro Glu
          20          25          30

Phe Pro Phe Tyr Pro Thr Cys Asn Val Cys Thr Ala Asp Val Asn Val
          35          40          45

Thr Ile Asn Phe Asp Val Gly Gly Lys Lys His Gln Leu Asp Leu Asp
          50          55          60

Phe Gly Gln Leu Thr Pro His Thr Lys Ala Val Tyr Gln Pro Arg Gly
65          70          75          80

Ala Phe Gly Gly Ser Glu Asn Ala Thr Asn Leu Phe Leu Leu Glu Leu
          85          90          95

Leu Gly Ala Gly Glu Leu Ala Leu Thr Met Arg Ser Lys Lys Leu Pro
          100          105          110

Ile Asn Val Thr Thr Gly Glu Glu Gln Gln Val Ser Leu Glu Ser Val
          115          120          125

Asp Val Tyr Phe Gln Asp Val Phe Gly Thr Met Trp Cys His His Ala
          130          135          140

Glu Met Gln Asn Pro Val Tyr Leu Ile Pro Glu Thr Val Pro Tyr Ile
145          150          155          160

Lys Trp Asp Asn Cys Asn Ser Thr Asn Ile Thr Ala Val Val Arg Ala
          165          170          175

Gln Gly Leu Asp Val Thr Leu Pro Leu Ser Leu Pro Thr Ser Ala Gln
          180          185          190

Asp Ser Asn Phe Ser Val Lys Thr Glu Met Leu Gly Asn Glu Ile Asp
          195          200          205

Ile Glu Cys Ile Met Glu Asp Gly Glu Ile Ser Gln Val Leu Pro Gly
          210          215          220

Asp Asn Lys Phe Asn Ile Thr Cys Ser Gly Tyr Glu Ser His Val Pro
225          230          235          240

Ser Gly Gly Ile Leu Thr Ser Thr Ser Pro Val Ala Thr Pro Ile Pro
          245          250          255

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Gly Thr Gly Tyr Ala Tyr Ser Leu Arg Leu Thr Pro Arg Pro Val Ser
260 265 270

Arg Phe Leu Gly Asn Asn Ser Ile Leu Tyr Val Phe Tyr Ser Gly Asn
275 280 285

Gly Pro Lys Ala Ser Gly Gly Asp Tyr Cys Ile Gln Ser Asn Ile Val
290 295 300

Phe Ser Asp Glu Ile Pro Ala Ser Gln Asp Met Pro Thr Asn Thr Thr
305 310 315 320

Asp Ile Thr Tyr Val Gly Asp Asn Ala Thr Tyr Ser Val Pro Met Val
325 330 335

Thr Ser Glu Asp Ala Asn Ser Pro Asn Val Thr Val Thr Ala Phe Trp
340 345 350

Ala Trp Pro Asn Asn Thr Glu Thr Asp Phe Lys Cys Lys Trp Thr Leu
355 360 365

Thr Ser Gly Thr Pro Ser Gly Cys Glu Asn Ile Ser Gly Ala Phe Ala
370 375 380

Ser Asn Arg Thr Phe Asp Ile Thr Val Ser Gly Leu Gly Thr Ala Pro
385 390 395 400

Lys Thr Leu Ile Ile Thr Arg Thr Ala Thr Asn Ala Thr Thr Thr Thr
405 410 415

His Lys Val Ile Phe Ser Lys Ala Pro Glu Ser Thr Thr Thr Ser Pro
420 425 430

Thr Leu Asn Thr Thr Gly Phe Ala Asp Pro Asn Thr Thr Thr Gly Leu
435 440 445

Pro Ser Ser Thr His Val Pro Thr Asn Leu Thr Ala Pro Ala Ser Thr
450 455 460

Gly Pro Thr Val Ser Thr Ala Asp Val Thr Ser Pro Thr Pro Ala Gly
465 470 475 480

Thr Thr Ser Gly Ala Ser Pro Val Thr Pro Ser Pro Ser Pro Trp Asp
485 490 495

Asn Gly Thr Glu Ser Lys Ala Pro Asp Met Thr Ser Ser Thr Ser Pro
500 505 510

Val Thr Thr Pro Thr Pro Asn Ala Thr Ser Pro Thr Pro Ala Val Thr
515 520 525

Thr Pro Thr Pro Asn Ala Thr Ser Pro Thr Pro Ala Val Thr Thr Pro

ITI-08-PCT_Sequence_Listing_ST25.txt

```

530          535          540
Thr Pro Asn Ala Thr Ser Pro Thr Leu Gly Lys Thr Ser Pro Thr Ser
545          550          555          560
Ala Val Thr Thr Pro Thr Pro Asn Ala Thr Ser Pro Thr Leu Gly Lys
565          570          575
Thr Ser Pro Thr Ser Ala Val Thr Thr Pro Thr Pro Asn Ala Thr Ser
580          585          590
Pro Thr Leu Gly Lys Thr Ser Pro Thr Ser Ala Val Thr Thr Pro Thr
595          600          605
Pro Asn Ala Thr Gly Pro Thr Val Gly Glu Thr Ser Pro Gln Ala Asn
610          615          620
Ala Thr Asn His Thr Leu Gly Gly Thr Ser Pro Thr Pro Val Val Thr
625          630          635          640
Ser Gln Pro Lys Asn Ala Thr Ser Ala Val Thr Thr Gly Gln His Asn
645          650          655
Ile Thr Ser Ser Ser Thr Ser Ser Met Ser Leu Arg Pro Ser Ser Asn
660          665          670
Pro Glu Thr Leu Ser Pro Ser Thr Ser Asp Asn Ser Thr Ser His Met
675          680          685
Pro Leu Leu Thr Ser Ala His Pro Thr Gly Gly Glu Asn Ile Thr Gln
690          695          700
Val Thr Pro Ala Ser Ile Ser Thr His His Val Ser Thr Ser Ser Pro
705          710          715          720
Ala Pro Arg Pro Gly Thr Thr Ser Gln Ala Ser Gly Pro Gly Asn Ser
725          730          735
Ser Thr Ser Thr Lys Pro Gly Glu Val Asn Val Thr Lys Gly Thr Pro
740          745          750
Pro Gln Asn Ala Thr Ser Pro Gln Ala Pro Ser Gly Gln Lys Thr Ala
755          760          765
Val Pro Thr Val Thr Ser Thr Gly Gly Lys Ala Asn Ser Thr Thr Gly
770          775          780
Gly Lys His Thr Thr Gly His Gly Ala Arg Thr Ser Thr Glu Pro Thr
785          790          795          800
Thr Asp Tyr Gly Gly Asp Ser Thr Thr Pro Arg Pro Arg Tyr Asn Ala
805          810          815

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Thr Thr Tyr Leu Pro Pro Ser Thr Ser Ser Lys Leu Arg Pro Arg Trp
820 825 830

Thr Phe Thr Ser Pro Pro Val Thr Thr Ala Gln Ala Thr Val Pro Val
835 840 845

Pro Pro Thr Ser Gln Pro Arg Phe Ser Asn Leu Ser
850 855 860

<210> 172
<211> 497
<212> PRT
<213> Human gammaherpesvirus 4

<400> 172

Met Gly Ser Leu Glu Met Val Pro Met Gly Ala Gly Pro Pro Ser Pro
1 5 10 15

Gly Gly Asp Pro Asp Gly Tyr Asp Gly Gly Asn Asn Ser Gln Tyr Pro
20 25 30

Ser Ala Ser Gly Ser Ser Gly Asn Thr Pro Thr Pro Pro Asn Asp Glu
35 40 45

Glu Arg Glu Ser Asn Glu Glu Pro Pro Pro Pro Tyr Glu Asp Pro Tyr
50 55 60

Trp Gly Asn Gly Asp Arg His Ser Asp Tyr Gln Pro Leu Gly Thr Gln
65 70 75 80

Asp Gln Ser Leu Tyr Leu Gly Leu Gln His Asp Gly Asn Asp Gly Leu
85 90 95

Pro Pro Pro Pro Tyr Ser Pro Arg Asp Asp Ser Ser Gln His Ile Tyr
100 105 110

Glu Glu Ala Gly Arg Gly Ser Met Asn Pro Val Cys Leu Pro Val Ile
115 120 125

Val Ala Pro Tyr Leu Phe Trp Leu Ala Ala Ile Ala Ala Ser Cys Phe
130 135 140

Thr Ala Ser Val Ser Thr Val Val Thr Ala Thr Gly Leu Ala Leu Ser
145 150 155 160

Leu Leu Leu Leu Ala Ala Val Ala Ser Ser Tyr Ala Ala Ala Gln Arg
165 170 175

Lys Leu Leu Thr Pro Val Thr Val Leu Thr Ala Val Val Thr Phe Phe
180 185 190

ITI-08-PCT_Sequence_Listing_ST25.txt

Ala	Ile	Cys	Leu	Thr	Trp	Arg	Ile	Glu	Asp	Pro	Pro	Phe	Asn	Ser	Leu	195	200	205
Leu	Phe	Ala	Leu	Leu	Ala	Ala	Ala	Gly	Gly	Leu	Gln	Gly	Ile	Tyr	Val	210	215	220
Leu	Val	Met	Leu	Val	Leu	Leu	Ile	Leu	Ala	Tyr	Arg	Arg	Arg	Trp	Arg	225	230	235
Arg	Leu	Thr	Val	Cys	Gly	Gly	Ile	Met	Phe	Leu	Ala	Cys	Val	Leu	Val	245	250	255
Leu	Ile	Val	Asp	Ala	Val	Leu	Gln	Leu	Ser	Pro	Leu	Leu	Gly	Ala	Val	260	265	270
Thr	Val	Val	Ser	Met	Thr	Leu	Leu	Leu	Leu	Ala	Phe	Val	Leu	Trp	Leu	275	280	285
Ser	Ser	Pro	Gly	Gly	Leu	Gly	Thr	Leu	Gly	Ala	Ala	Leu	Leu	Thr	Leu	290	295	300
Ala	Ala	Ala	Leu	Ala	Leu	Leu	Ala	Ser	Leu	Ile	Leu	Gly	Thr	Leu	Asn	305	310	315
Leu	Thr	Thr	Met	Phe	Leu	Leu	Met	Leu	Leu	Trp	Thr	Leu	Val	Val	Leu	325	330	335
Leu	Ile	Cys	Ser	Ser	Cys	Ser	Ser	Cys	Pro	Leu	Ser	Lys	Ile	Leu	Leu	340	345	350
Ala	Arg	Leu	Phe	Leu	Tyr	Ala	Leu	Ala	Leu	Leu	Leu	Leu	Ala	Ser	Ala	355	360	365
Leu	Ile	Ala	Gly	Gly	Ser	Ile	Leu	Gln	Thr	Asn	Phe	Lys	Ser	Leu	Ser	370	375	380
Ser	Thr	Glu	Phe	Ile	Pro	Asn	Leu	Phe	Cys	Met	Leu	Leu	Leu	Ile	Val	385	390	395
Ala	Gly	Ile	Leu	Phe	Ile	Leu	Ala	Ile	Leu	Thr	Glu	Trp	Gly	Ser	Gly	405	410	415
Asn	Arg	Thr	Tyr	Gly	Pro	Val	Phe	Met	Cys	Leu	Gly	Gly	Leu	Leu	Thr	420	425	430
Met	Val	Ala	Gly	Ala	Val	Trp	Leu	Thr	Val	Met	Ser	Asn	Thr	Leu	Leu	435	440	445
Ser	Ala	Trp	Ile	Leu	Thr	Ala	Gly	Phe	Leu	Ile	Phe	Leu	Ile	Gly	Phe	450	455	460

ITI-08-PCT_Sequence_Listing_ST25.txt

Ala Leu Phe Gly Val Ile Arg Cys Cys Arg Tyr Cys Cys Tyr Tyr Cys
465 470 475 480

Leu Thr Leu Glu Ser Glu Glu Arg Pro Pro Thr Pro Tyr Arg Asn Thr
485 490 495

Val

<210> 173
<211> 540
<212> PRT
<213> Homo sapiens

<400> 173

Ala Gln Pro Pro Pro Pro Pro Pro Asp Ala Thr Cys His Gln Val Arg
1 5 10 15

Ser Phe Phe Gln Arg Leu Gln Pro Gly Leu Lys Trp Val Pro Glu Thr
20 25 30

Pro Val Pro Gly Ser Asp Leu Gln Val Cys Leu Pro Lys Gly Pro Thr
35 40 45

Cys Cys Ser Arg Lys Met Glu Glu Lys Tyr Gln Leu Thr Ala Arg Leu
50 55 60

Asn Met Glu Gln Leu Leu Gln Ser Ala Ser Met Glu Leu Lys Phe Leu
65 70 75 80

Ile Ile Gln Asn Ala Ala Val Phe Gln Glu Ala Phe Glu Ile Val Val
85 90 95

Arg His Ala Lys Asn Tyr Thr Asn Ala Met Phe Lys Asn Asn Tyr Pro
100 105 110

Ser Leu Thr Pro Gln Ala Phe Glu Phe Val Gly Glu Phe Phe Thr Asp
115 120 125

Val Ser Leu Tyr Ile Leu Gly Ser Asp Ile Asn Val Asp Asp Met Val
130 135 140

Asn Glu Leu Phe Asp Ser Leu Phe Pro Val Ile Tyr Thr Gln Leu Met
145 150 155 160

Asn Pro Gly Leu Pro Asp Ser Ala Leu Asp Ile Asn Glu Cys Leu Arg
165 170 175

Gly Ala Arg Arg Asp Leu Lys Val Phe Gly Asn Phe Pro Lys Leu Ile
180 185 190

Met Thr Gln Val Ser Lys Ser Leu Gln Val Thr Arg Ile Phe Leu Gln

195 200 205

Page 269

ITI-08-PCT_Sequence_Listing_ST25.txt

Glu Cys Ile Gly Gly Ser Gly Asp Gly Met Ile Lys Val Lys Asn Gln
485 490 495

Leu Arg Phe Leu Ala Glu Leu Ala Tyr Asp Leu Asp Val Asp Asp Ala
500 505 510

Pro Gly Asn Ser Gln Gln Ala Thr Pro Lys Asp Asn Glu Ile Ser Thr
515 520 525

Phe His Asn Leu Gly Asn Val His Ser Pro Leu Lys
530 535 540

<210> 174
<211> 192
<212> PRT
<213> Hepatitis B virus

<220>
<221> SITE
<222> (192)..(192)
<223> Xaa can be any naturally occurring amino acid

<400> 174

Met Gln Trp Asn Ser Thr Thr Phe His Gln Thr Leu Gln Asp Pro Arg
1 5 10 15

Val Arg Gly Leu Tyr Phe Pro Ala Gly Gly Ser Ser Ser Gly Thr Val
20 25 30

Asn Pro Val Leu Thr Thr Ala Ser Pro Leu Ser Ser Ile Phe Ser Arg
35 40 45

Ile Gly Asp Pro Ala Leu Asn Met Glu Asn Ile Thr Ser Gly Thr Ile
50 55 60

Pro Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly
65 70 75 80

Thr Thr Val Cys Leu Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His
85 90 95

Ser Pro Thr Ser Cys Pro Pro Thr Cys Pro Gly Tyr Arg Trp Met Cys
100 105 110

Leu Arg Arg Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Ile Pro
115 120 125

Gly Ser Ser Thr Thr Ser Thr Gly Pro Cys Arg Thr Cys Met Thr Thr
130 135 140

ITI-08-PCT_Sequence_Listing_ST25.txt

Ala Gln Gly Thr Ser Met Tyr Pro Ser Cys Cys Cys Thr Lys Pro Ser
145 150 155 160

Asp Gly Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Gly
165 170 175

Lys Phe Leu Trp Glu Trp Ala Ser Ala Arg Tyr Trp Gly Pro Ser Xaa
180 185 190

<210> 175

<211> 120

<212> PRT

<213> Hepatitis B virus

<400> 175

Met Ala Ala Arg Leu Cys Cys Gln Leu Asp Pro Ala Arg Asp Val Leu
1 5 10 15

Cys Leu Arg Pro Val Gly Ala Glu Ser Arg Gly Arg Pro Leu Ser Gly
20 25 30

Pro Leu Gly Ala Leu Pro Ser Pro Ser Pro Ser Ala Val Pro Ala Asp
35 40 45

His Gly Ala His Leu Ser Leu Arg Gly Leu Pro Val Cys Ala Phe Ser
50 55 60

Ser Ala Gly Pro Cys Ala Leu Arg Phe Thr Ser Ala Arg Arg Met Glu
65 70 75 80

Thr Thr Val Asn Ala His Gln Ile Leu Pro Lys Val Leu His Lys Arg
85 90 95

Thr Phe Gly Leu Ser Ala Met Ser Thr Thr Asp Leu Glu Ala Tyr Phe
100 105 110

Lys Asp Cys Val Phe Lys Asp Trp
115 120

<210> 176

<211> 120

<212> PRT

<213> Homo sapiens

<400> 176

Met Met Thr Gly Thr Ile Glu Thr Thr Gly Asn Ile Ser Ala Glu Lys
1 5 10 15

Gly Gly Ser Ile Ile Leu Gln Cys His Leu Ser Ser Thr Thr Ala Gln
20 25 30

ITI-08-PCT_Sequence_Listing_ST25.txt

Val Thr Gln Val Asn Trp Glu Gln Gln Asp Gln Leu Leu Ala Ile Cys
35 40 45

Asn Ala Asp Leu Gly Trp His Ile Ser Pro Ser Phe Lys Asp Arg Val
50 55 60

Ala Pro Gly Pro Gly Leu Gly Leu Thr Leu Gln Ser Leu Thr Val Asn
65 70 75 80

Asp Thr Gly Glu Tyr Phe Cys Ile Tyr His Thr Tyr Pro Asp Gly Thr
85 90 95

Tyr Thr Gly Arg Ile Phe Leu Glu Val Leu Glu Ser Ser Val Ala Glu
100 105 110

His Gly Ala Arg Phe Gln Ile Pro
115 120

<210> 177

<211> 289

<212> PRT

<213> Homo sapiens

<400> 177

Glu Asp Gly Gly Pro Ala Cys Tyr Gly Gly Phe Asp Leu Tyr Phe Ile
1 5 10 15

Leu Asp Lys Ser Gly Ser Val Leu His His Trp Asn Glu Ile Tyr Tyr
20 25 30

Phe Val Glu Gln Leu Ala His Lys Phe Ile Ser Pro Gln Leu Arg Met
35 40 45

Ser Phe Ile Val Phe Ser Thr Arg Gly Thr Thr Leu Met Lys Leu Thr
50 55 60

Glu Asp Arg Glu Gln Ile Arg Gln Gly Leu Glu Glu Leu Gln Lys Val
65 70 75 80

Leu Pro Gly Gly Asp Thr Tyr Met His Glu Gly Phe Glu Arg Ala Ser
85 90 95

Glu Gln Ile Tyr Tyr Glu Asn Arg Gln Gly Tyr Arg Thr Ala Ser Val
100 105 110

Ile Ile Ala Leu Thr Asp Gly Glu Leu His Glu Asp Leu Phe Phe Tyr
115 120 125

Ser Glu Arg Glu Ala Asn Arg Ser Arg Asp Leu Gly Ala Ile Val Tyr
130 135 140

ITI-08-PCT_Sequence_Listing_ST25.txt

Cys Val Gly Val Lys Asp Phe Asn Glu Thr Gln Leu Ala Arg Ile Ala
145 150 155 160

Asp Ser Lys Asp His Val Phe Pro Val Asn Asp Gly Phe Gln Ala Leu
165 170 175

Gln Gly Ile Ile His Ser Ile Leu Lys Lys Ser Cys Ile Glu Ile Leu
180 185 190

Ala Ala Glu Pro Ser Thr Ile Cys Ala Gly Glu Ser Phe Gln Val Val
195 200 205

Val Arg Gly Asn Gly Phe Arg His Ala Arg Asn Val Asp Arg Val Leu
210 215 220

Cys Ser Phe Lys Ile Asn Asp Ser Val Thr Leu Asn Glu Lys Pro Phe
225 230 235 240

Ser Val Glu Asp Thr Tyr Leu Leu Cys Pro Ala Pro Ile Leu Lys Glu
245 250 255

Val Gly Met Lys Ala Ala Leu Gln Val Ser Met Asn Asp Gly Leu Ser
260 265 270

Phe Ile Ser Ser Ser Val Ile Ile Thr Thr Thr His Cys Ser Asp Gly
275 280 285

Ser

<210> 178
<211> 719
<212> PRT
<213> Homo sapiens

<400> 178

Gln Asp Pro Trp Ala Ala Glu Pro Arg Ala Ala Cys Gly Pro Ser Ser
1 5 10 15

Cys Tyr Ala Leu Phe Pro Arg Arg Arg Thr Phe Leu Glu Ala Trp Arg
20 25 30

Ala Cys Arg Glu Leu Gly Gly Asp Leu Ala Thr Pro Arg Thr Pro Glu
35 40 45

Glu Ala Gln Arg Val Asp Ser Leu Val Gly Ala Gly Pro Ala Ser Arg
50 55 60

Leu Leu Trp Ile Gly Leu Gln Arg Gln Ala Arg Gln Cys Gln Leu Gln
65 70 75 80

ITI-08-PCT_Sequence_Listing_ST25.txt

Arg	Pro	Leu	Arg	Gly	Phe	Thr	Trp	Thr	Thr	Gly	Asp	Gln	Asp	Thr	Ala	
				85					90					95		
Phe	Thr	Asn	Trp	Ala	Gln	Pro	Ala	Ser	Gly	Gly	Pro	Cys	Pro	Ala	Gln	
			100					105					110			
Arg	Cys	Val	Ala	Leu	Glu	Ala	Ser	Gly	Glu	His	Arg	Trp	Leu	Glu	Gly	
		115					120					125				
Ser	Cys	Thr	Leu	Ala	Val	Asp	Gly	Tyr	Leu	Cys	Gln	Phe	Gly	Phe	Glu	
	130					135					140					
Gly	Ala	Cys	Pro	Ala	Leu	Gln	Asp	Glu	Ala	Gly	Gln	Ala	Gly	Pro	Ala	
145					150					155					160	
Val	Tyr	Thr	Thr	Pro	Phe	His	Leu	Val	Ser	Thr	Glu	Phe	Glu	Trp	Leu	
				165					170					175		
Pro	Phe	Gly	Ser	Val	Ala	Ala	Val	Gln	Cys	Gln	Ala	Gly	Arg	Gly	Ala	
			180					185					190			
Ser	Leu	Leu	Cys	Val	Lys	Gln	Pro	Glu	Gly	Gly	Val	Gly	Trp	Ser	Arg	
	195						200					205				
Ala	Gly	Pro	Leu	Cys	Leu	Gly	Thr	Gly	Cys	Ser	Pro	Asp	Asn	Gly	Gly	
	210					215					220					
Cys	Glu	His	Glu	Cys	Val	Glu	Glu	Val	Asp	Gly	His	Val	Ser	Cys	Arg	
225					230					235					240	
Cys	Thr	Glu	Gly	Phe	Arg	Leu	Ala	Ala	Asp	Gly	Arg	Ser	Cys	Glu	Asp	
				245					250					255		
Pro	Cys	Ala	Gln	Ala	Pro	Cys	Glu	Gln	Gln	Cys	Glu	Pro	Gly	Gly	Pro	
			260					265					270			
Gln	Gly	Tyr	Ser	Cys	His	Cys	Arg	Leu	Gly	Phe	Arg	Pro	Ala	Glu	Asp	
		275					280					285				
Asp	Pro	His	Arg	Cys	Val	Asp	Thr	Asp	Glu	Cys	Gln	Ile	Ala	Gly	Val	
	290					295					300					
Cys	Gln	Gln	Met	Cys	Val	Asn	Tyr	Val	Gly	Gly	Phe	Glu	Cys	Tyr	Cys	
305					310					315					320	
Ser	Glu	Gly	His	Glu	Leu	Glu	Ala	Asp	Gly	Ile	Ser	Cys	Ser	Pro	Ala	
				325					330					335		
Gly	Ala	Met	Gly	Ala	Gln	Ala	Ser	Gln	Asp	Leu	Gly	Asp	Glu	Leu	Leu	
			340					345					350			
Asp	Asp	Gly	Glu	Asp	Glu	Glu	Asp	Glu	Asp	Glu	Ala	Trp	Lys	Ala	Phe	

ITI-08-PCT_Sequence_Listing_ST25.txt

```

355                               360                               365
Asn Gly Gly Trp Thr Glu Met Pro Gly Ile Leu Trp Met Glu Pro Thr
370                               375                               380

Gln Pro Pro Asp Phe Ala Leu Ala Tyr Arg Pro Ser Phe Pro Glu Asp
385                               390                               395                               400

Arg Glu Pro Gln Ile Pro Tyr Pro Glu Pro Thr Trp Pro Pro Pro Leu
405                               410                               415

Ser Ala Pro Arg Val Pro Tyr His Ser Ser Val Leu Ser Val Thr Arg
420                               425                               430

Pro Val Val Val Ser Ala Thr His Pro Thr Leu Pro Ser Ala His Gln
435                               440                               445

Pro Pro Val Ile Pro Ala Thr His Pro Ala Leu Ser Arg Asp His Gln
450                               455                               460

Ile Pro Val Ile Ala Ala Asn Tyr Pro Asp Leu Pro Ser Ala Tyr Gln
465                               470                               475                               480

Pro Gly Ile Leu Ser Val Ser His Ser Ala Gln Pro Pro Ala His Gln
485                               490                               495

Pro Pro Met Ile Ser Thr Lys Tyr Pro Glu Leu Phe Pro Ala His Gln
500                               505                               510

Ser Pro Met Phe Pro Asp Thr Arg Val Ala Gly Thr Gln Thr Thr Thr
515                               520                               525

His Leu Pro Gly Ile Pro Pro Asn His Ala Pro Leu Val Thr Thr Leu
530                               535                               540

Gly Ala Gln Leu Pro Pro Gln Ala Pro Asp Ala Leu Val Leu Arg Thr
545                               550                               555                               560

Gln Ala Thr Gln Leu Pro Ile Ile Pro Thr Ala Gln Pro Ser Leu Thr
565                               570                               575

Thr Thr Ser Arg Ser Pro Val Ser Pro Ala His Gln Ile Ser Val Pro
580                               585                               590

Ala Ala Thr Gln Pro Ala Ala Leu Pro Thr Leu Leu Pro Ser Gln Ser
595                               600                               605

Pro Thr Asn Gln Thr Ser Pro Ile Ser Pro Thr His Pro His Ser Lys
610                               615                               620

Ala Pro Gln Ile Pro Arg Glu Asp Gly Pro Ser Pro Lys Leu Ala Leu
625                               630                               635                               640

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Trp Leu Pro Ser Pro Ala Pro Thr Ala Ala Pro Thr Ala Leu Gly Glu
645 650 655

Ala Gly Leu Ala Glu His Ser Gln Arg Asp Asp Arg Trp Leu Tyr Cys
660 665 670

Thr Arg Cys Gly Pro His Ala Pro Asn Lys Arg Ile Thr Asp Cys Tyr
675 680 685

Arg Trp Val Ile His Ala Gly Ser Lys Ser Pro Thr Glu Pro Met Pro
690 695 700

Pro Arg Gly Ser Leu Thr Gly Val Gln Thr Cys Arg Thr Ser Val
705 710 715

<210> 179

<211> 653

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 179

Thr Gln Val Cys Thr Gly Thr Asp Met Lys Leu Arg Leu Pro Ala Ser
1 5 10 15

Pro Glu Thr His Leu Asp Met Leu Arg His Leu Tyr Gln Gly Cys Gln
20 25 30

Val Val Gln Gly Asn Leu Glu Leu Thr Tyr Leu Pro Thr Asn Ala Ser
35 40 45

Leu Ser Phe Leu Gln Asp Ile Gln Glu Val Gln Gly Tyr Val Leu Ile
50 55 60

Ala His Asn Gln Val Arg Gln Val Pro Leu Gln Arg Leu Arg Ile Val
65 70 75 80

Arg Gly Thr Gln Leu Phe Glu Asp Asn Tyr Ala Leu Ala Val Leu Asp
85 90 95

Asn Gly Asp Pro Leu Asn Asn Thr Thr Pro Val Thr Gly Ala Ser Pro
100 105 110

Gly Gly Leu Arg Glu Leu Gln Leu Arg Ser Leu Thr Glu Ile Leu Lys
115 120 125

Gly Gly Val Leu Ile Gln Arg Asn Pro Gln Leu Cys Tyr Gln Asp Thr
130 135 140

ITI-08-PCT_Sequence_Listing_ST25.txt

Ile	Leu	Trp	Lys	Asp	Ile	Phe	His	Lys	Asn	Asn	Gln	Leu	Ala	Leu	Thr	145	150	155	160
Leu	Ile	Asp	Thr	Asn	Arg	Ser	Arg	Ala	Cys	His	Pro	Cys	Ser	Pro	Met	165	170	175	
Cys	Lys	Gly	Ser	Arg	Cys	Trp	Gly	Glu	Ser	Ser	Glu	Asp	Cys	Gln	Ser	180	185	190	
Leu	Thr	Arg	Thr	Val	Cys	Ala	Gly	Gly	Cys	Ala	Arg	Cys	Lys	Gly	Pro	195	200	205	
Leu	Pro	Thr	Asp	Cys	Cys	His	Glu	Gln	Cys	Ala	Ala	Gly	Cys	Thr	Gly	210	215	220	
Pro	Lys	His	Ser	Asp	Cys	Leu	Ala	Cys	Leu	His	Phe	Asn	His	Ser	Gly	225	230	235	240
Ile	Cys	Glu	Leu	His	Cys	Pro	Ala	Leu	Val	Thr	Tyr	Asn	Thr	Asp	Thr	245	250	255	
Phe	Glu	Ser	Met	Pro	Asn	Pro	Glu	Gly	Arg	Tyr	Thr	Phe	Gly	Ala	Ser	260	265	270	
Cys	Val	Thr	Ala	Cys	Pro	Tyr	Asn	Tyr	Leu	Ser	Thr	Asp	Val	Gly	Ser	275	280	285	
Cys	Thr	Leu	Val	Cys	Pro	Leu	His	Asn	Gln	Glu	Val	Thr	Ala	Glu	Asp	290	295	300	
Gly	Thr	Gln	Arg	Cys	Glu	Lys	Cys	Ser	Lys	Pro	Cys	Ala	Arg	Val	Cys	305	310	315	320
Tyr	Gly	Leu	Gly	Met	Glu	His	Leu	Arg	Glu	Val	Arg	Ala	Val	Thr	Ser	325	330	335	
Ala	Asn	Ile	Gln	Glu	Phe	Ala	Gly	Cys	Lys	Lys	Ile	Phe	Gly	Ser	Leu	340	345	350	
Ala	Phe	Leu	Pro	Glu	Ser	Phe	Asp	Gly	Asp	Pro	Ala	Ser	Asn	Thr	Ala	355	360	365	
Pro	Leu	Gln	Pro	Glu	Gln	Leu	Gln	Val	Phe	Glu	Thr	Leu	Glu	Glu	Ile	370	375	380	
Thr	Gly	Tyr	Leu	Tyr	Ile	Ser	Ala	Trp	Pro	Asp	Ser	Leu	Pro	Asp	Leu	385	390	395	400
Ser	Val	Phe	Gln	Asn	Leu	Gln	Val	Ile	Arg	Gly	Arg	Ile	Leu	His	Asn	405	410	415	

ITI-08-PCT_Sequence_Listing_ST25.txt

Gly Ala Tyr Ser Leu Thr Leu Gln Gly Leu Gly Ile Ser Trp Leu Gly
420 425 430

Leu Arg Ser Leu Arg Glu Leu Gly Ser Gly Leu Ala Leu Ile His His
435 440 445

Asn Thr His Leu Cys Phe Val His Thr Val Pro Trp Asp Gln Leu Phe
450 455 460

Arg Asn Pro His Gln Ala Leu Leu His Thr Ala Asn Arg Pro Glu Asp
465 470 475 480

Glu Cys Val Gly Glu Gly Leu Ala Cys His Gln Leu Cys Ala Arg Gly
485 490 495

His Cys Trp Gly Pro Gly Pro Thr Gln Cys Val Asn Cys Ser Gln Phe
500 505 510

Leu Arg Gly Gln Glu Cys Val Glu Glu Cys Arg Val Leu Gln Gly Leu
515 520 525

Pro Arg Glu Tyr Val Asn Ala Arg His Cys Leu Pro Cys His Pro Glu
530 535 540

Cys Gln Pro Gln Asn Gly Ser Val Thr Cys Phe Gly Pro Glu Ala Asp
545 550 555 560

Gln Cys Val Ala Cys Ala His Tyr Lys Asp Pro Pro Phe Cys Val Ala
565 570 575

Arg Cys Pro Ser Gly Val Lys Pro Asp Leu Ser Tyr Met Pro Ile Trp
580 585 590

Lys Phe Pro Asp Glu Glu Gly Ala Cys Gln Pro Cys Pro Ile Asn Cys
595 600 605

Thr His Ser Cys Val Asp Leu Asp Asp Lys Gly Cys Pro Ala Glu Gln
610 615 620

Arg Ala Ser Pro Leu Thr Ser Ile Val Ser Ala Val Val Gly Ile Leu
625 630 635 640

Leu Val Val Val Leu Gly Val Val Phe Gly Ile Leu Ile
645 650

<210> 180
<211> 651
<212> PRT
<213> Homo sapiens

<400> 180

ITI-08-PCT_Sequence_Listing_ST25.txt

Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val Ala Glu Gly Lys Glu
 1 5 10 15
 Val Leu Leu Leu Val His Asn Leu Pro Gln His Leu Phe Gly Tyr Ser
 20 25 30
 Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Ile Gly Tyr
 35 40 45
 Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Tyr Ser Gly Arg
 50 55 60
 Glu Ile Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Ile Ile Gln
 65 70 75 80
 Asn Asp Thr Gly Phe Tyr Thr Leu His Val Ile Lys Ser Asp Leu Val
 85 90 95
 Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu Pro Lys
 100 105 110
 Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro Val Glu Asp Lys Asp Ala
 115 120 125
 Val Ala Phe Thr Cys Glu Pro Glu Thr Gln Asp Ala Thr Tyr Leu Trp
 130 135 140
 Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Gln Leu Ser
 145 150 155 160
 Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn Val Thr Arg Asn Asp Thr
 165 170 175
 Ala Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Ala Arg Arg Ser
 180 185 190
 Asp Ser Val Ile Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro Thr Ile
 195 200 205
 Ser Pro Leu Asn Thr Ser Tyr Arg Ser Gly Glu Asn Leu Asn Leu Ser
 210 215 220
 Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Phe Val Asn
 225 230 235 240
 Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn Ile Thr
 245 250 255
 Val Asn Asn Ser Gly Ser Tyr Thr Cys Gln Ala His Asn Ser Asp Thr
 260 265 270
 Gly Leu Asn Arg Thr Thr Val Thr Thr Ile Thr Val Tyr Ala Glu Pro

ITI-08-PCT_Sequence_Listing_ST25.txt

```

275                280                285
Pro  Lys  Pro  Phe  Ile  Thr  Ser  Asn  Asn  Ser  Asn  Pro  Val  Glu  Asp  Glu
290                295                300

Asp  Ala  Val  Ala  Leu  Thr  Cys  Glu  Pro  Glu  Ile  Gln  Asn  Thr  Thr  Tyr
305                310                315                320

Leu  Trp  Trp  Val  Asn  Asn  Gln  Ser  Leu  Pro  Val  Ser  Pro  Arg  Leu  Gln
325                330                335

Leu  Ser  Asn  Asp  Asn  Arg  Thr  Leu  Thr  Leu  Leu  Ser  Val  Thr  Arg  Asn
340                345                350

Asp  Val  Gly  Pro  Tyr  Glu  Cys  Gly  Ile  Gln  Asn  Lys  Leu  Ser  Val  Asp
355                360                365

His  Ser  Asp  Pro  Val  Ile  Leu  Asn  Val  Leu  Tyr  Gly  Pro  Asp  Asp  Pro
370                375                380

Thr  Ile  Ser  Pro  Ser  Tyr  Thr  Tyr  Tyr  Arg  Pro  Gly  Val  Asn  Leu  Ser
385                390                395                400

Leu  Ser  Cys  His  Ala  Ala  Ser  Asn  Pro  Pro  Ala  Gln  Tyr  Ser  Trp  Leu
405                410                415

Ile  Asp  Gly  Asn  Ile  Gln  Gln  His  Thr  Gln  Glu  Leu  Phe  Ile  Ser  Asn
420                425                430

Ile  Thr  Glu  Lys  Asn  Ser  Gly  Leu  Tyr  Thr  Cys  Gln  Ala  Asn  Asn  Ser
435                440                445

Ala  Ser  Gly  His  Ser  Arg  Thr  Thr  Val  Lys  Thr  Ile  Thr  Val  Ser  Ala
450                455                460

Glu  Leu  Pro  Lys  Pro  Ser  Ile  Ser  Ser  Asn  Asn  Ser  Lys  Pro  Val  Glu
465                470                475                480

Asp  Lys  Asp  Ala  Val  Ala  Phe  Thr  Cys  Glu  Pro  Glu  Ala  Gln  Asn  Thr
485                490                495

Thr  Tyr  Leu  Trp  Trp  Val  Asn  Gly  Gln  Ser  Leu  Pro  Val  Ser  Pro  Arg
500                505                510

Leu  Gln  Leu  Ser  Asn  Gly  Asn  Arg  Thr  Leu  Thr  Leu  Phe  Asn  Val  Thr
515                520                525

Arg  Asn  Asp  Ala  Arg  Ala  Tyr  Val  Cys  Gly  Ile  Gln  Asn  Ser  Val  Ser
530                535                540

Ala  Asn  Arg  Ser  Asp  Pro  Val  Thr  Leu  Asp  Val  Leu  Tyr  Gly  Pro  Asp
545                550                555                560

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Thr Pro Ile Ile Ser Pro Pro Asp Ser Ser Tyr Leu Ser Gly Ala Asn
565 570 575

Leu Asn Leu Ser Cys His Ser Ala Ser Asn Pro Ser Pro Gln Tyr Ser
580 585 590

Trp Arg Ile Asn Gly Ile Pro Gln Gln His Thr Gln Val Leu Phe Ile
595 600 605

Ala Lys Ile Thr Pro Asn Asn Asn Gly Thr Tyr Ala Cys Phe Val Ser
610 615 620

Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Ser Ile Thr Val
625 630 635 640

Ser Ala Ser Gly Thr Ser Pro Gly Leu Ser Ala
645 650

<210> 181
<211> 76
<212> PRT
<213> Homo sapiens

<400> 181

Met Lys Thr Asn Asp Thr Tyr Met Lys Phe Ser Trp Leu Thr Val Pro
1 5 10 15

Glu Lys Ser Leu Asp Lys Glu His Arg Cys Ile Val Arg His Glu Asn
20 25 30

Asn Lys Asn Gly Val Asp Gln Glu Ile Ile Phe Pro Pro Ile Lys Thr
35 40 45

Asp Val Ile Thr Met Asp Pro Lys Asp Asn Cys Ser Lys Asp Ala Asn
50 55 60

Asp Thr Leu Leu Leu Gln Leu Thr Asn Thr Ser Ala
65 70 75

<210> 182
<211> 324
<212> PRT
<213> Homo sapiens

<400> 182

Met Val Gln Arg Leu Trp Val Ser Arg Leu Leu Arg His Arg Lys Ala
1 5 10 15

Gln Leu Pro Pro Leu Leu Leu Glu Val Gly Val Glu Glu Lys Ser Ala

ITI-08-PCT_Sequence_Listing_ST25.txt

20

25

30

Ser Asp His Trp Arg Gly Arg Tyr Gly Arg Arg Arg Pro Leu Ala Gly
 35 40 45

Leu Leu Cys Pro Asp Pro Arg Pro Thr Pro Leu Glu Ala Leu Leu Ser
 50 55 60

Asp Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala Asp Trp Asp Thr
 65 70 75 80

Ser Ala Leu Ala Pro Tyr Leu Gly Thr Gln Glu Glu Cys Glu Glu Ala
 85 90 95

Ala Leu Gly Pro Thr Glu Pro Ala Glu Gly Leu Ser Ala Pro Ser Leu
 100 105 110

Ser Pro His Cys Cys Pro Cys Arg Ala Arg Leu Ala Phe Arg Asn Leu
 115 120 125

Gly Ala Leu Leu Pro Arg Leu His Gln Leu Cys Cys Arg Met Pro Arg
 130 135 140

Thr Leu Arg Arg Leu Val Gly Glu Gly Leu Tyr Gln Gly Val Pro Arg
 145 150 155 160

Ala Glu Pro Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly Val Arg
 165 170 175

Arg Leu Val Gln Arg Phe Gly Thr Arg Ala Ser Val Ala Val Val Thr
 180 185 190

Ala Ser Tyr His Arg Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly
 195 200 205

Asp Thr Gly Gly Ala Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu
 210 215 220

Pro Gly Pro Lys Pro Gly Ala Pro Phe Pro Asn Gly His Val Gly Ala
 225 230 235 240

Gly Gly Ser Gly Leu Leu Pro Pro Pro Pro Ala Leu Cys Gly Ala Ser
 245 250 255

Ala Cys Asp Val Ser Val Arg Val Val Val Gly Glu Pro Thr Glu Ala
 260 265 270

Arg Val Val Pro Gly Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp
 275 280 285

Ser Ala Phe Leu Leu Ser Gln Val Ala Pro Ser Leu Phe Met Gly Ser
 290 295 300

ITI-08-PCT_Sequence_Listing_ST25.txt

Ile Val Gln Leu Ser Gln Ser Val Thr Phe Asp Lys Ser Asp Leu Ala
305 310 315 320

Lys Tyr Ser Ala

<210> 183
<211> 729
<212> PRT
<213> Homo sapiens

<400> 183

Met Trp Asn Leu Leu His Glu Thr Asp Ser Ala Val Ala Thr Ala Arg
1 5 10 15

Arg Pro Arg Trp Leu Cys Lys Ser Ser Asn Glu Ala Thr Asn Ile Thr
20 25 30

Pro Lys His Asn Met Lys Ala Phe Leu Asp Glu Leu Lys Ala Glu Asn
35 40 45

Ile Lys Lys Phe Leu Tyr Asn Phe Thr Gln Ile Pro His Leu Ala Gly
50 55 60

Thr Glu Gln Asn Phe Gln Leu Ala Lys Gln Ile Gln Ser Gln Trp Lys
65 70 75 80

Glu Phe Gly Leu Asp Ser Val Glu Leu Ala His Tyr Asp Val Leu Leu
85 90 95

Ser Tyr Pro Asn Lys Thr His Pro Asn Tyr Ile Ser Ile Ile Asn Glu
100 105 110

Asp Gly Asn Glu Ile Phe Asn Thr Ser Leu Phe Glu Pro Pro Pro Pro
115 120 125

Gly Tyr Glu Asn Val Ser Asp Ile Val Pro Pro Phe Ser Ala Phe Ser
130 135 140

Pro Gln Gly Met Pro Glu Gly Asp Leu Val Tyr Val Asn Tyr Ala Arg
145 150 155 160

Thr Glu Asp Phe Phe Lys Leu Glu Arg Asp Met Lys Ile Asn Cys Ser
165 170 175

Gly Lys Ile Val Ile Ala Arg Tyr Gly Lys Val Phe Arg Gly Asn Lys
180 185 190

Val Lys Asn Ala Gln Leu Ala Gly Ala Lys Gly Val Ile Leu Tyr Ser
195 200 205

ITI-08-PCT_Sequence_Listing_ST25.txt

```

Asp Pro Ala Asp Tyr Phe Ala Pro Gly Val Lys Ser Tyr Pro Asp Gly
210                215                220

Trp Asn Leu Pro Gly Gly Gly Val Gln Arg Gly Asn Ile Leu Asn Leu
225                230                235                240

Asn Gly Ala Gly Asp Pro Leu Thr Pro Gly Tyr Pro Ala Asn Glu Tyr
                245                250                255

Ala Tyr Arg Arg Gly Ile Ala Glu Ala Val Gly Leu Pro Ser Ile Pro
                260                265                270

Val His Pro Ile Gly Tyr Tyr Asp Ala Gln Lys Leu Leu Glu Lys Met
                275                280                285

Gly Gly Ser Ala Pro Pro Asp Ser Ser Trp Arg Gly Ser Leu Lys Val
290                295                300

Pro Tyr Asn Val Gly Pro Gly Phe Thr Gly Asn Phe Ser Thr Gln Lys
305                310                315                320

Val Lys Met His Ile His Ser Thr Asn Glu Val Thr Arg Ile Tyr Asn
                325                330                335

Val Ile Gly Thr Leu Arg Gly Ala Val Glu Pro Asp Arg Tyr Val Ile
                340                345                350

Leu Gly Gly His Arg Asp Ser Trp Val Phe Gly Gly Ile Asp Pro Gln
355                360                365

Ser Gly Ala Ala Val Val His Glu Ile Val Arg Ser Phe Gly Thr Leu
370                375                380

Lys Lys Glu Gly Trp Arg Pro Arg Arg Thr Ile Leu Phe Ala Ser Trp
385                390                395                400

Asp Ala Glu Glu Phe Gly Leu Leu Gly Ser Thr Glu Trp Ala Glu Glu
                405                410                415

Asn Ser Arg Leu Leu Gln Glu Arg Gly Val Ala Tyr Ile Asn Ala Asp
420                425                430

Ser Ser Ile Glu Gly Asn Tyr Thr Leu Arg Val Asp Cys Thr Pro Leu
435                440                445

Met Tyr Ser Leu Val His Asn Leu Thr Lys Glu Leu Lys Ser Pro Asp
450                455                460

Glu Gly Phe Glu Gly Lys Ser Leu Tyr Glu Ser Trp Thr Lys Lys Ser
465                470                475                480

Pro Ser Pro Glu Phe Ser Gly Met Pro Arg Ile Ser Lys Leu Gly Ser

```

ITI-08-PCT_Sequence_Listing_ST25.txt

485 490 495

Gly Asn Asp Phe Glu Val Phe Phe Gln Arg Leu Gly Ile Ala Ser Gly
500 505 510

Arg Ala Arg Tyr Thr Lys Asn Trp Glu Thr Asn Lys Phe Ser Gly Tyr
515 520 525

Pro Leu Tyr His Ser Val Tyr Glu Thr Tyr Glu Leu Val Glu Lys Phe
530 535 540

Tyr Asp Pro Met Phe Lys Tyr His Leu Thr Val Ala Gln Val Arg Gly
545 550 555 560

Gly Met Val Phe Glu Leu Ala Asn Ser Ile Val Leu Pro Phe Asp Cys
565 570 575

Arg Asp Tyr Ala Val Val Leu Arg Lys Tyr Ala Asp Lys Ile Tyr Ser
580 585 590

Ile Ser Met Lys His Pro Gln Glu Met Lys Thr Tyr Ser Val Ser Phe
595 600 605

Asp Ser Leu Phe Ser Ala Val Lys Asn Phe Thr Glu Ile Ala Ser Lys
610 615 620

Phe Ser Glu Arg Leu Gln Asp Phe Asp Lys Ser Asn Pro Ile Val Leu
625 630 635 640

Arg Met Met Asn Asp Gln Leu Met Phe Leu Glu Arg Ala Phe Ile Asp
645 650 655

Pro Leu Gly Leu Pro Asp Arg Pro Phe Tyr Arg His Val Ile Tyr Ala
660 665 670

Pro Ser Ser His Asn Lys Tyr Ala Gly Glu Ser Phe Pro Gly Ile Tyr
675 680 685

Asp Ala Leu Phe Asp Ile Glu Ser Lys Val Asp Pro Ser Lys Ala Trp
690 695 700

Gly Glu Val Lys Arg Gln Ile Tyr Val Ala Ala Phe Thr Val Gln Ala
705 710 715 720

Ala Ala Glu Thr Leu Ser Glu Val Ala
725

<210> 184
<211> 165
<212> PRT
<213> Homo sapiens

ITI-08-PCT_Sequence_Listing_ST25.txt

<400> 184

```

Met Gly Ala Pro Thr Leu Pro Pro Ala Trp Gln Pro Phe Leu Lys Asp
1          5          10          15

His Arg Ile Ser Thr Phe Lys Asn Trp Pro Phe Leu Glu Gly Cys Ala
          20          25          30

Cys Thr Pro Glu Arg Met Ala Glu Ala Gly Phe Ile His Cys Pro Thr
          35          40          45

Glu Asn Glu Pro Asp Leu Ala Gln Cys Phe Phe Cys Phe Lys Glu Leu
          50          55          60

Glu Gly Trp Glu Pro Asp Asp Asp Pro Ile Gly Pro Gly Thr Val Ala
65          70          75          80

Tyr Ala Cys Asn Thr Ser Thr Leu Gly Gly Arg Gly Gly Arg Ile Thr
          85          90          95

Arg Glu Glu His Lys Lys His Ser Ser Gly Cys Ala Phe Leu Ser Val
          100          105          110

Lys Lys Gln Phe Glu Glu Leu Thr Leu Gly Glu Phe Leu Lys Leu Asp
          115          120          125

Arg Glu Arg Ala Lys Asn Lys Ile Ala Lys Glu Thr Asn Asn Lys Lys
          130          135          140

Lys Glu Phe Glu Glu Thr Ala Lys Lys Val Arg Arg Ala Ile Glu Gln
145          150          155          160

Leu Ala Ala Met Asp
          165

```

<210> 185

<211> 1137

<212> PRT

<213> Homo sapiens

<400> 185

```

Thr Gly Ser Gly His Ala Ser Ser Thr Pro Gly Gly Glu Lys Glu Thr
1          5          10          15

Ser Ala Thr Gln Arg Ser Ser Val Pro Ser Ser Thr Glu Lys Asn Ala
          20          25          30

Val Ser Met Thr Ser Ser Val Leu Ser Ser His Ser Pro Gly Ser Gly
          35          40          45

Ser Ser Thr Thr Gln Gly Gln Asp Val Thr Leu Ala Pro Ala Thr Glu

```

ITI-08-PCT_Sequence_Listing_ST25.txt

50

55

60

Pro Ala Ser Gly Ser Ala Ala Thr Trp Gly Gln Asp Val Thr Ser Val
65 70 75 80

Pro Val Thr Arg Pro Ala Leu Gly Ser Thr Thr Pro Pro Ala His Asp
85 90 95

Val Thr Ser Ala Pro Asp Asn Lys Pro Ala Pro Gly Ser Thr Ala Pro
100 105 110

Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro Gly
115 120 125

Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr Arg
130 135 140

Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala
145 150 155 160

Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His Gly
165 170 175

Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala Pro
180 185 190

Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro Gly
195 200 205

Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr Arg
210 215 220

Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala
225 230 235 240

Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His Gly
245 250 255

Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala Pro
260 265 270

Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro Gly
275 280 285

Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr Arg
290 295 300

Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala
305 310 315 320

Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His Gly
325 330 335

ITI-08-PCT_Sequence_Listing_ST25.txt

Val	Thr	Ser	Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala	Pro	340	345	350	
Pro	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro	Gly	355	360	365	
Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr	Arg	370	375	380	
Pro	Ala	Pro	Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala	385	390	395	400
Pro	Asp	Thr	Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	405	410	415	
Val	Thr	Ser	Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala	Pro	420	425	430	
Pro	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro	Gly	435	440	445	
Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr	Arg	450	455	460	
Pro	Ala	Pro	Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala	465	470	475	480
Pro	Asp	Thr	Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	485	490	495	
Val	Thr	Ser	Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala	Pro	500	505	510	
Pro	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro	Gly	515	520	525	
Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr	Arg	530	535	540	
Pro	Ala	Pro	Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala	545	550	555	560
Pro	Asp	Thr	Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	565	570	575	
Val	Thr	Ser	Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala	Pro	580	585	590	
Pro	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro	Gly	595	600	605	

ITI-08-PCT_Sequence_Listing_ST25.txt

Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr	Arg	610	615	620
Pro	Ala	Pro	Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala	625	630	635
Pro	Asp	Thr	Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	645	650	655
Val	Thr	Ser	Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala	Pro	660	665	670
Pro	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro	Gly	675	680	685
Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr	Arg	690	695	700
Pro	Ala	Pro	Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala	705	710	715
Pro	Asp	Thr	Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	725	730	735
Val	Thr	Ser	Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala	Pro	740	745	750
Pro	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro	Gly	755	760	765
Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr	Arg	770	775	780
Pro	Ala	Pro	Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala	785	790	795
Pro	Asp	Thr	Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	805	810	815
Val	Thr	Ser	Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala	Pro	820	825	830
Pro	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro	Gly	835	840	845
Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr	Arg	850	855	860
Pro	Ala	Pro	Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala	865	870	875
Pro	Asp	Thr	Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	880	885	890

ITI-08-PCT_Sequence_Listing_ST25.txt

885

890

895

Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala Pro
 900 905 910

Pro Ala His Gly Val Thr Ser Ala Pro Asp Asn Arg Pro Ala Leu Gly
 915 920 925

Ser Thr Ala Pro Pro Val His Asn Val Thr Ser Ala Ser Gly Ser Ala
 930 935 940

Ser Gly Ser Ala Ser Thr Leu Val His Asn Gly Thr Ser Ala Arg Ala
 945 950 955 960

Thr Thr Thr Pro Ala Ser Lys Ser Thr Pro Phe Ser Ile Pro Ser His
 965 970 975

His Ser Asp Thr Pro Thr Thr Leu Ala Ser His Ser Thr Lys Thr Asp
 980 985 990

Ala Ser Ser Thr His His Ser Ser Val Pro Pro Leu Thr Ser Ser Asn
 995 1000 1005

His Ser Thr Ser Pro Gln Leu Ser Thr Gly Val Ser Phe Phe Phe
 1010 1015 1020

Leu Ser Phe His Ile Ser Asn Leu Gln Phe Asn Ser Ser Leu Glu
 1025 1030 1035

Asp Pro Ser Thr Asp Tyr Tyr Gln Glu Leu Gln Arg Asp Ile Ser
 1040 1045 1050

Glu Met Phe Leu Gln Ile Tyr Lys Gln Gly Gly Phe Leu Gly Leu
 1055 1060 1065

Ser Asn Ile Lys Phe Arg Pro Gly Ser Val Val Val Gln Leu Thr
 1070 1075 1080

Leu Ala Phe Arg Glu Gly Thr Ile Asn Val His Asp Val Glu Thr
 1085 1090 1095

Gln Phe Asn Gln Tyr Lys Thr Glu Ala Ala Ser Arg Tyr Asn Leu
 1100 1105 1110

Thr Ile Ser Asp Val Ser Val Ser Asp Val Pro Phe Pro Phe Ser
 1115 1120 1125

Ala Gln Ser Gly Ala Gly Val Pro Gly
 1130 1135

<210> 186

<211> 252

ITI-08-PCT_Sequence_Listing_ST25.txt

<212> PRT

<213> Homo sapiens

<400> 186

Thr Gly Ser Gly His Ala Ser Ser Thr Pro Gly Gly Glu Lys Glu Thr
1 5 10 15

Ser Ala Thr Gln Arg Ser Ser Val Pro Ser Ser Thr Glu Lys Asn Ala
20 25 30

Leu Ser Thr Gly Val Ser Phe Phe Phe Leu Ser Phe His Ile Ser Asn
35 40 45

Leu Gln Phe Asn Ser Ser Leu Glu Asp Pro Ser Thr Asp Tyr Tyr Gln
50 55 60

Glu Leu Gln Arg Asp Ile Ser Glu Met Phe Leu Gln Ile Tyr Lys Gln
65 70 75 80

Gly Gly Phe Leu Gly Leu Ser Asn Ile Lys Phe Arg Pro Gly Ser Val
85 90 95

Val Val Gln Leu Thr Leu Ala Phe Arg Glu Gly Thr Ile Asn Val His
100 105 110

Asp Val Glu Thr Gln Phe Asn Gln Tyr Lys Thr Glu Ala Ala Ser Arg
115 120 125

Tyr Asn Leu Thr Ile Ser Asp Val Ser Val Ser Asp Val Pro Phe Pro
130 135 140

Phe Ser Ala Gln Ser Gly Ala Gly Val Pro Gly Trp Gly Ile Ala Leu
145 150 155 160

Leu Val Leu Val Cys Val Leu Val Ala Leu Ala Ile Val Tyr Leu Ile
165 170 175

Ala Leu Ala Val Cys Gln Cys Arg Arg Lys Asn Tyr Gly Gln Leu Asp
180 185 190

Ile Phe Pro Ala Arg Asp Thr Tyr His Pro Met Ser Glu Tyr Pro Thr
195 200 205

Tyr His Thr His Gly Arg Tyr Val Pro Pro Ser Ser Thr Asp Arg Ser
210 215 220

Pro Tyr Glu Lys Val Ser Ala Gly Asn Gly Gly Ser Ser Leu Ser Tyr
225 230 235 240

Thr Asn Pro Ala Val Ala Ala Thr Ser Ala Asn Leu
245 250

ITI-08-PCT_Sequence_Listing_ST25.txt

<210> 187
 <211> 241
 <212> PRT
 <213> Homo sapiens

<400> 187

```

Met  Lys  Ile  Phe  Met  Tyr  Leu  Leu  Thr  Val  Phe  Leu  Ile  Thr  Gln  Met
1      5      10      15

Ile  Gly  Ser  Ala  Leu  Phe  Ala  Val  Tyr  Leu  His  Arg  Arg  Leu  Asp  Lys
      20      25      30

Ile  Glu  Asp  Glu  Arg  Asn  Leu  His  Glu  Asp  Phe  Val  Phe  Met  Lys  Thr
      35      40      45

Ile  Gln  Arg  Cys  Asn  Thr  Gly  Glu  Arg  Ser  Leu  Ser  Leu  Leu  Asn  Cys
      50      55      60

Glu  Glu  Ile  Lys  Ser  Gln  Phe  Glu  Gly  Phe  Val  Lys  Asp  Ile  Met  Leu
65      70      75      80

Asn  Lys  Glu  Glu  Thr  Lys  Lys  Glu  Asn  Ser  Phe  Glu  Met  Gln  Lys  Gly
      85      90      95

Asp  Gln  Asn  Pro  Gln  Ile  Ala  Ala  His  Val  Ile  Ser  Glu  Ala  Ser  Ser
      100     105     110

Lys  Thr  Thr  Ser  Val  Leu  Gln  Trp  Ala  Glu  Lys  Gly  Tyr  Tyr  Thr  Met
      115     120     125

Ser  Asn  Asn  Leu  Val  Thr  Leu  Glu  Asn  Gly  Lys  Gln  Leu  Thr  Val  Lys
      130     135     140

Arg  Gln  Gly  Leu  Tyr  Tyr  Ile  Tyr  Ala  Gln  Val  Thr  Phe  Cys  Ser  Asn
145     150     155     160

Arg  Glu  Ala  Ser  Ser  Gln  Ala  Pro  Phe  Ile  Ala  Ser  Leu  Cys  Leu  Lys
      165     170     175

Ser  Pro  Gly  Arg  Phe  Glu  Arg  Ile  Leu  Leu  Arg  Ala  Ala  Asn  Thr  His
      180     185     190

Ser  Ser  Ala  Lys  Pro  Cys  Gly  Gln  Gln  Ser  Ile  His  Leu  Gly  Gly  Val
      195     200     205

Phe  Glu  Leu  Gln  Pro  Gly  Ala  Ser  Val  Phe  Val  Asn  Val  Thr  Asp  Pro
      210     215     220

Ser  Gln  Val  Ser  His  Gly  Thr  Gly  Phe  Thr  Ser  Phe  Gly  Leu  Leu  Lys
225     230     235     240
    
```

ITI-08-PCT_Sequence_Listing_ST25.txt

Leu

<210> 188
 <211> 449
 <212> PRT
 <213> Homo sapiens

<400> 188

Met	Gly	Ser	Asp	Val	Arg	Asp	Leu	Asn	Ala	Leu	Leu	Pro	Ala	Val	Pro
1				5					10					15	
Ser	Leu	Gly	Gly	Gly	Gly	Gly	Cys	Ala	Leu	Pro	Val	Ser	Gly	Ala	Ala
			20					25					30		
Gln	Trp	Ala	Pro	Val	Leu	Asp	Phe	Ala	Pro	Pro	Gly	Ala	Ser	Ala	Tyr
		35					40					45			
Gly	Ser	Leu	Gly	Gly	Pro	Ala	Pro	Pro	Pro	Ala	Pro	Pro	Pro	Pro	Pro
	50					55					60				
Pro	Pro	Pro	Pro	His	Ser	Phe	Ile	Lys	Gln	Glu	Pro	Ser	Trp	Gly	Gly
65					70					75					80
Ala	Glu	Pro	His	Glu	Glu	Gln	Cys	Leu	Ser	Ala	Phe	Thr	Val	His	Phe
				85					90					95	
Ser	Gly	Gln	Phe	Thr	Gly	Thr	Ala	Gly	Ala	Cys	Arg	Tyr	Gly	Pro	Phe
			100					105					110		
Gly	Pro	Pro	Pro	Pro	Ser	Gln	Ala	Ser	Ser	Gly	Gln	Ala	Arg	Met	Phe
		115					120					125			
Pro	Asn	Ala	Pro	Tyr	Leu	Pro	Ser	Cys	Leu	Glu	Ser	Gln	Pro	Ala	Ile
	130					135					140				
Arg	Asn	Gln	Gly	Tyr	Ser	Thr	Val	Thr	Phe	Asp	Gly	Thr	Pro	Ser	Tyr
145					150					155					160
Gly	His	Thr	Pro	Ser	His	His	Ala	Ala	Gln	Phe	Pro	Asn	His	Ser	Phe
				165					170					175	
Lys	His	Glu	Asp	Pro	Met	Gly	Gln	Gln	Gly	Ser	Leu	Gly	Glu	Gln	Gln
			180					185					190		
Tyr	Ser	Val	Pro	Pro	Pro	Val	Tyr	Gly	Cys	His	Thr	Pro	Thr	Asp	Ser
		195					200					205			
Cys	Thr	Gly	Ser	Gln	Ala	Leu	Leu	Leu	Arg	Thr	Pro	Tyr	Ser	Ser	Asp
	210					215					220				

ITI-08-PCT_Sequence_Listing_ST25.txt

Asn Leu Tyr Gln Met Thr Ser Gln Leu Glu Cys Met Thr Trp Asn Gln
225 230 235 240

Met Asn Leu Gly Ala Thr Leu Lys Gly Val Ala Ala Gly Ser Ser Ser
245 250 255

Ser Val Lys Trp Thr Glu Gly Gln Ser Asn His Ser Thr Gly Tyr Glu
260 265 270

Ser Asp Asn His Thr Thr Pro Ile Leu Cys Gly Ala Gln Tyr Arg Ile
275 280 285

His Thr His Gly Val Phe Arg Gly Ile Gln Asp Val Arg Arg Val Pro
290 295 300

Gly Val Ala Pro Thr Leu Val Arg Ser Ala Ser Glu Thr Ser Glu Lys
305 310 315 320

Arg Pro Phe Met Cys Ala Tyr Pro Gly Cys Asn Lys Arg Tyr Phe Lys
325 330 335

Leu Ser His Leu Gln Met His Ser Arg Lys His Thr Gly Glu Lys Pro
340 345 350

Tyr Gln Cys Asp Phe Lys Asp Cys Glu Arg Arg Phe Ser Arg Ser Asp
355 360 365

Gln Leu Lys Arg His Gln Arg Arg His Thr Gly Val Lys Pro Phe Gln
370 375 380

Cys Lys Thr Cys Gln Arg Lys Phe Ser Arg Ser Asp His Leu Lys Thr
385 390 395 400

His Thr Arg Thr His Thr Gly Lys Thr Ser Glu Lys Pro Phe Ser Cys
405 410 415

Arg Trp Pro Ser Cys Gln Lys Lys Phe Ala Arg Ser Asp Glu Leu Val
420 425 430

Arg His His Asn Met His Gln Arg Asn Met Thr Lys Leu Gln Leu Ala
435 440 445

Leu

<210> 189

<211> 322

<212> PRT

<213> Homo sapiens

<400> 189

Met Gly Ser Asp Val Arg Asp Leu Asn Ala Leu Leu Pro Ala Val Pro

ITI-08-PCT_Sequence_Listing_ST25.txt

```

1           5           10           15
Ser Leu Gly Gly Gly Gly Gly Cys Ala Leu Pro Val Ser Gly Ala Ala
      20           25           30
Gln Trp Ala Pro Val Leu Asp Phe Ala Pro Pro Gly Ala Ser Ala Tyr
      35           40           45
Gly Ser Leu Gly Gly Pro Ala Pro Pro Pro Ala Pro Pro Pro Pro
      50           55           60
Pro Pro Pro Pro His Ser Phe Ile Lys Gln Glu Pro Ser Trp Gly Gly
65           70           75           80
Ala Glu Pro His Glu Glu Gln Cys Leu Ser Ala Phe Thr Val His Phe
      85           90           95
Ser Gly Gln Phe Thr Gly Thr Ala Gly Ala Cys Arg Tyr Gly Pro Phe
      100          105          110
Gly Pro Pro Pro Pro Ser Gln Ala Ser Ser Gly Gln Ala Arg Met Phe
      115          120          125
Pro Asn Ala Pro Tyr Leu Pro Ser Cys Leu Glu Ser Gln Pro Ala Ile
      130          135          140
Arg Asn Gln Gly Tyr Ser Thr Val Thr Phe Asp Gly Thr Pro Ser Tyr
145          150          155          160
Gly His Thr Pro Ser His His Ala Ala Gln Phe Pro Asn His Ser Phe
      165          170          175
Lys His Glu Asp Pro Met Gly Gln Gln Gly Ser Leu Gly Glu Gln Gln
      180          185          190
Tyr Ser Val Pro Pro Pro Val Tyr Gly Cys His Thr Pro Thr Asp Ser
      195          200          205
Cys Thr Gly Ser Gln Ala Leu Leu Leu Arg Thr Pro Tyr Ser Ser Asp
      210          215          220
Asn Leu Tyr Gln Met Thr Ser Gln Leu Glu Cys Met Thr Trp Asn Gln
225          230          235          240
Met Asn Leu Gly Ala Thr Leu Lys Gly Val Ala Ala Gly Ser Ser Ser
      245          250          255
Ser Val Lys Trp Thr Glu Gly Gln Ser Asn His Ser Thr Gly Tyr Glu
      260          265          270
Ser Asp Asn His Thr Thr Pro Ile Leu Cys Gly Ala Gln Tyr Arg Ile
      275          280          285

```

ITI-08-PCT_Sequence_Listing_ST25.txt

His Thr His Gly Val Phe Arg Gly Ile Gln Asp Val Arg Arg Val Pro
290 295 300

Gly Val Ala Pro Thr Leu Val Arg Ser Ala Ser Glu Thr Ser Glu Lys
305 310 315 320

Arg Pro

<210> 190

<211> 509

<212> PRT

<213> Homo sapiens

<400> 190

Met Glu Arg Arg Arg Leu Trp Gly Ser Ile Gln Ser Arg Tyr Ile Ser
1 5 10 15

Met Ser Val Trp Thr Ser Pro Arg Arg Leu Val Glu Leu Ala Gly Gln
20 25 30

Ser Leu Leu Lys Asp Glu Ala Leu Ala Ile Ala Ala Leu Glu Leu Leu
35 40 45

Pro Arg Glu Leu Phe Pro Pro Leu Phe Met Ala Ala Phe Asp Gly Arg
50 55 60

His Ser Gln Thr Leu Lys Ala Met Val Gln Ala Trp Pro Phe Thr Cys
65 70 75 80

Leu Pro Leu Gly Val Leu Met Lys Gly Gln His Leu His Leu Glu Thr
85 90 95

Phe Lys Ala Val Leu Asp Gly Leu Asp Val Leu Leu Ala Gln Glu Val
100 105 110

Arg Pro Arg Arg Trp Lys Leu Gln Val Leu Asp Leu Arg Lys Asn Ser
115 120 125

His Gln Asp Phe Trp Thr Val Trp Ser Gly Asn Arg Ala Ser Leu Tyr
130 135 140

Ser Phe Pro Glu Pro Glu Ala Ala Gln Pro Met Thr Lys Lys Arg Lys
145 150 155 160

Val Asp Gly Leu Ser Thr Glu Ala Glu Gln Pro Phe Ile Pro Val Glu
165 170 175

Val Leu Val Asp Leu Phe Leu Lys Glu Gly Ala Cys Asp Glu Leu Phe
180 185 190

ITI-08-PCT_Sequence_Listing_ST25.txt

Ser Tyr Leu Ile Glu Lys Val Lys Arg Lys Lys Asn Val Leu Arg Leu
195 200 205

Cys Cys Lys Lys Leu Lys Ile Phe Ala Met Pro Met Gln Asp Ile Lys
210 215 220

Met Ile Leu Lys Met Val Gln Leu Asp Ser Ile Glu Asp Leu Glu Val
225 230 235 240

Thr Cys Thr Trp Lys Leu Pro Thr Leu Ala Lys Phe Ser Pro Tyr Leu
245 250 255

Gly Gln Met Ile Asn Leu Arg Arg Leu Leu Leu Ser His Ile His Ala
260 265 270

Ser Ser Tyr Ile Ser Pro Glu Lys Glu Glu Gln Tyr Ile Ala Gln Phe
275 280 285

Thr Ser Gln Phe Leu Ser Leu Gln Cys Leu Gln Ala Leu Tyr Val Asp
290 295 300

Ser Leu Phe Phe Leu Arg Gly Arg Leu Asp Gln Leu Leu Arg His Val
305 310 315 320

Met Asn Pro Leu Glu Thr Leu Ser Ile Thr Asn Cys Arg Leu Ser Glu
325 330 335

Gly Asp Val Met His Leu Ser Gln Ser Pro Ser Val Ser Gln Leu Ser
340 345 350

Val Leu Ser Leu Ser Gly Val Met Leu Thr Asp Val Ser Pro Glu Pro
355 360 365

Leu Gln Ala Leu Leu Glu Arg Ala Ser Ala Thr Leu Gln Asp Leu Val
370 375 380

Phe Asp Glu Cys Gly Ile Thr Asp Asp Gln Leu Leu Ala Leu Leu Pro
385 390 395 400

Ser Leu Ser His Cys Ser Gln Leu Thr Thr Leu Ser Phe Tyr Gly Asn
405 410 415

Ser Ile Ser Ile Ser Ala Leu Gln Ser Leu Leu Gln His Leu Ile Gly
420 425 430

Leu Ser Asn Leu Thr His Val Leu Tyr Pro Val Pro Leu Glu Ser Tyr
435 440 445

Glu Asp Ile His Gly Thr Leu His Leu Glu Arg Leu Ala Tyr Leu His
450 455 460

Ala Arg Leu Arg Glu Leu Leu Cys Glu Leu Gly Arg Pro Ser Met Val

ITI-08-PCT Sequence Listing ST25.txt

465 470 475 480

Trp Leu Ser Ala Asn Pro Cys Pro His Cys Gly Asp Arg Thr Phe Tyr
485 490 495

Asp Pro Glu Pro Ile Leu Cys Pro Cys Phe Met Pro Asn
500 505

<210>	191
<211>	210
<212>	PRT
<213>	Homo sapiens

<400> 191

Met Gln Ala Glu Gly Gln Gly Thr Gly Gly Ser Thr Gly Asp Ala Asp
1 5 10 15

Gly Pro Gly Gly Pro Gly Ile Pro Asp Gly Pro Gly Gly Asn Ala Gly
20 25 30

Gly Pro Gly Glu Ala Gly Ala Thr Gly Gly Arg Gly Pro Arg Gly Ala
35 40 45

Gly Ala Ala Arg Ala Ser Gly Pro Arg Gly Gly Ala Pro Arg Gly Pro
50 55 60

His Gly Gly Ala Ala Ser Ala Gln Asp Gly Arg Cys Pro Cys Gly Ala
65 70 75 80

Arg Arg Pro Asp Ser Arg Leu Leu Gln Leu His Ile Thr Met Pro Phe
85 90 95

Ser Ser Pro Met Glu Ala Glu Leu Val Arg Arg Ile Leu Ser Arg Asp
100 105 110

Ala Ala Pro Leu Pro Arg Pro Gly Ala Val Leu Lys Asp Phe Thr Val
115 120 125

Ser Gly Asn Leu Leu Phe Met Ser Val Arg Asp Gln Asp Arg Glu Gly
130 135 140

Ala Gly Arg Met Arg Val Val Gly Trp Gly Leu Gly Ser Ala Ser Pro
145 150 155 160

Glu Gly Gln Lys Ala Arg Asp Leu Arg Thr Pro Lys His Lys Val Ser
165 170 175

Glu Gln Arg Pro Gly Thr Pro Gly Pro Pro Pro Pro Glu Gly Ala Gln
180 185 190

Gly Asp Gly Cys Arg Gly Val Ala Phe Asn Val Met Phe Ser Ala Pro

ITI-08-PCT_Sequence_Listing_ST25.txt

195

200

205

His Ile
210

<210> 192
<211> 314
<212> PRT
<213> Homo sapiens

<400> 192

Met Pro Leu Glu Gln Arg Ser Gln His Cys Lys Pro Glu Glu Gly Leu
1 5 10 15

Glu Ala Arg Gly Glu Ala Leu Gly Leu Val Gly Ala Gln Ala Pro Ala
20 25 30

Thr Glu Glu Gln Glu Ala Ala Ser Ser Ser Ser Thr Leu Val Glu Val
35 40 45

Thr Leu Gly Glu Val Pro Ala Ala Glu Ser Pro Asp Pro Pro Gln Ser
50 55 60

Pro Gln Gly Ala Ser Ser Leu Pro Thr Thr Met Asn Tyr Pro Leu Trp
65 70 75 80

Ser Gln Ser Tyr Glu Asp Ser Ser Asn Gln Glu Glu Glu Gly Pro Ser
85 90 95

Thr Phe Pro Asp Leu Glu Ser Glu Phe Gln Ala Ala Leu Ser Arg Lys
100 105 110

Val Ala Glu Leu Val His Phe Leu Leu Leu Lys Tyr Arg Ala Arg Glu
115 120 125

Pro Val Thr Lys Ala Glu Met Leu Gly Ser Val Val Gly Asn Trp Gln
130 135 140

Tyr Phe Phe Pro Val Ile Phe Ser Lys Ala Ser Ser Ser Leu Gln Leu
145 150 155 160

Val Phe Gly Ile Glu Leu Met Glu Val Asp Pro Ile Gly His Leu Tyr
165 170 175

Ile Phe Ala Thr Cys Leu Gly Leu Ser Tyr Asp Gly Leu Leu Gly Asp
180 185 190

Asn Gln Ile Met Pro Lys Ala Gly Leu Leu Ile Ile Val Leu Ala Ile
195 200 205

Ile Ala Arg Glu Gly Asp Cys Ala Pro Glu Glu Lys Ile Trp Glu Glu

ITI-08-PCT_Sequence_Listing_ST25.txt

210

215

220

Leu Ser Val Leu Glu Val Phe Glu Gly Arg Glu Asp Ser Ile Leu Gly
225 230 235 240

Asp Pro Lys Lys Leu Leu Thr Gln His Phe Val Gln Glu Asn Tyr Leu
245 250 255

Glu Tyr Arg Gln Val Pro Gly Ser Asp Pro Ala Cys Tyr Glu Phe Leu
260 265 270

Trp Gly Pro Arg Ala Leu Val Glu Thr Ser Tyr Val Lys Val Leu His
275 280 285

His Met Val Lys Ile Ser Gly Gly Pro His Ile Ser Tyr Pro Pro Leu
290 295 300

His Glu Trp Val Leu Arg Glu Gly Glu Glu
305 310

<210> 193

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 193

Met Ala Pro Arg Ser Ala Arg Arg Pro Leu Leu Leu Leu Leu Leu Leu
1 5 10 15

Leu Leu Leu Gly Leu Met His Cys Ala Ser Ala Ala Met Phe Met Val
20 25 30

Lys Asn Gly Asn Gly Thr Ala Cys Ile Met Ala Asn Phe Ser Ala Ala
35 40 45

Phe Ser Val Asn Tyr Asp Thr Lys Ser Gly Pro Lys Asn Met Thr Leu
50 55 60

Asp Leu Pro Ser Asp Ala Thr Val Val Leu Asn Arg Ser Ser Cys Gly
65 70 75 80

Lys Glu Asn Thr Ser Asp Pro Ser Leu Val Ile Ala Phe Gly Arg Gly
85 90 95

His Thr Leu Thr Leu Asn Phe Thr Arg Asn Ala Thr Arg Tyr Ser Val
100 105 110

Gln Leu Met Ser Phe Val Tyr Asn Leu Ser Asp Thr His Leu Phe Pro

115				120				125					
Ser	Ser	Lys	Glu	Ile	Lys	Thr	Val	Glu	Ser	Ile	Thr	Asp	Ile
135				140				145					
Asp	Ile	Asp	Lys	Lys	Tyr	Arg	Cys	Val	Ser	Gly	Thr	Gln	Val
150				155				160					
Asn	Asn	Val	Thr	Val	Thr	Leu	His	Asp	Ala	Thr	Ile	Gln	Ala
165				170				175					
Ser	Asn	Ser	Ser	Phe	Ser	Arg	Gly	Glu	Thr	Arg	Cys	Glu	Gln
180				185				190					
Pro	Ser	Pro	Thr	Thr	Ala	Pro	Pro	Ala	Pro	Pro	Ser	Pro	Ser
195				200				205					
Pro	Val	Pro	Lys	Ser	Pro	Ser	Val	Asp	Lys	Tyr	Asn	Val	Ser
210				215				220					
Asn	Gly	Thr	Cys	Leu	Leu	Ala	Ser	Met	Gly	Leu	Gln	Leu	Asn
225				230				235					
Tyr	Glu	Arg	Lys	Asp	Asn	Thr	Thr	Val	Thr	Arg	Leu	Leu	Asn
240				245				250					
Pro	Asn	Lys	Thr	Ser	Ala	Ser	Gly	Ser	Cys	Gly	Ala	His	Leu
255				260				265					
Leu	Glu	Leu	His	Ser	Glu	Gly	Thr	Thr	Val	Leu	Leu	Phe	Gln
270				275				280					
Met	Asn	Ala	Ser	Ser	Ser	Arg	Phe	Phe	Leu	Gln	Gly	Ile	Gln
285				290				295					
Thr	Ile	Leu	Pro	Asp	Ala	Arg	Asp	Pro	Ala	Phe	Lys	Ala	Ala
300				305				310					
Ser	Leu	Arg	Ala	Leu	Gln	Ala	Thr	Val	Gly	Asn	Ser	Tyr	Lys
315				320				325					
Ala	Glu	Glu	His	Val	Arg	Val	Thr	Lys	Ala	Phe	Ser	Val	Asn
330				335				340					
Lys	Val	Trp	Val	Gln	Ala	Phe	Lys	Val	Glu	Gly	Gly	Gln	Phe
345				350				355					
Val	Glu	Glu	Cys	Leu	Leu	Asp	Glu	Asn	Ser	Leu	Glu	Met	Gly
360				365				370					
Thr	Leu	Pro	Pro	Ala	Trp	Gln	Pro	Phe	Leu	Lys	Asp	His	Arg
375				380				385					
390				395				400					

ITI-08-PCT_Sequence_Listing_ST25.txt

```

Ile Ser Thr Phe Lys Asn Trp Pro Phe Leu Glu Gly Cys Ala Cys Thr
              405                      410                      415

Pro Glu Arg Met Ala Glu Ala Gly Phe Ile His Cys Pro Thr Glu Asn
              420                      425                      430

Glu Pro Asp Leu Ala Gln Cys Phe Phe Cys Phe Lys Glu Leu Glu Gly
              435                      440                      445

Trp Glu Pro Asp Asp Asp Pro Ile Glu Glu His Lys Lys His Ser Ser
              450                      455                      460

Gly Cys Ala Phe Leu Ser Val Lys Lys Gln Phe Glu Glu Leu Thr Leu
465                      470                      475                      480

Gly Glu Phe Leu Lys Leu Asp Arg Glu Arg Ala Lys Asn Lys Ile Ala
              485                      490                      495

Lys Glu Thr Asn Asn Lys Lys Lys Glu Phe Glu Glu Thr Ala Lys Lys
              500                      505                      510

Val Arg Arg Ala Ile Glu Gln Leu Ala Ala Met Asp Glu Phe Thr Leu
              515                      520                      525

Ile Pro Ile Ala Val Gly Gly Ala Leu Ala Gly Leu Val Leu Ile Val
              530                      535                      540

Leu Ile Ala Tyr Leu Val Gly Arg Lys Arg Ser His Ala Gly Tyr Gln
545                      550                      555                      560

```

Thr Ile

```

<210> 194
<211> 558
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Synthetic Construct

```

```

<400> 194

```

```

Met Ala Pro Arg Ser Ala Arg Arg Pro Leu Leu Leu Leu Leu Leu
1              5              10              15

Leu Leu Leu Gly Leu Met His Cys Ala Ser Ala Met Gly Ala Pro Thr
              20              25              30

Leu Pro Pro Ala Trp Gln Pro Phe Leu Lys Asp His Arg Ile Ser Thr
              35              40              45

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Phe	Lys	Asn	Trp	Pro	Phe	Leu	Glu	Gly	Cys	Ala	Cys	Thr	Pro	Glu	Arg
50						55					60				
Met	Ala	Glu	Ala	Gly	Phe	Ile	His	Cys	Pro	Thr	Glu	Asn	Glu	Pro	Asp
65					70					75					80
Leu	Ala	Gln	Cys	Phe	Phe	Cys	Phe	Lys	Glu	Leu	Glu	Gly	Trp	Glu	Pro
				85					90					95	
Asp	Asp	Asp	Pro	Ile	Glu	Glu	His	Lys	Lys	His	Ser	Ser	Gly	Cys	Ala
			100					105					110		
Phe	Leu	Ser	Val	Lys	Lys	Gln	Phe	Glu	Glu	Leu	Thr	Leu	Gly	Glu	Phe
		115					120					125			
Leu	Lys	Leu	Asp	Arg	Glu	Arg	Ala	Lys	Asn	Lys	Ile	Ala	Lys	Glu	Thr
	130						135				140				
Asn	Asn	Lys	Lys	Lys	Glu	Phe	Glu	Glu	Thr	Ala	Lys	Lys	Val	Arg	Arg
145					150					155					160
Ala	Ile	Glu	Gln	Leu	Ala	Ala	Met	Asp	Ala	Met	Phe	Met	Val	Lys	Asn
				165					170					175	
Gly	Asn	Gly	Thr	Ala	Cys	Ile	Met	Ala	Asn	Phe	Ser	Ala	Ala	Phe	Ser
			180					185					190		
Val	Asn	Tyr	Asp	Thr	Lys	Ser	Gly	Pro	Lys	Asn	Met	Thr	Leu	Asp	Leu
		195					200					205			
Pro	Ser	Asp	Ala	Thr	Val	Val	Leu	Asn	Arg	Ser	Ser	Cys	Gly	Lys	Glu
	210					215					220				
Asn	Thr	Ser	Asp	Pro	Ser	Leu	Val	Ile	Ala	Phe	Gly	Arg	Gly	His	Thr
225					230					235					240
Leu	Thr	Leu	Asn	Phe	Thr	Arg	Asn	Ala	Thr	Arg	Tyr	Ser	Val	Gln	Leu
				245					250					255	
Met	Ser	Phe	Val	Tyr	Asn	Leu	Ser	Asp	Thr	His	Leu	Phe	Pro	Asn	Ala
			260					265					270		
Ser	Ser	Lys	Glu	Ile	Lys	Thr	Val	Glu	Ser	Ile	Thr	Asp	Ile	Arg	Ala
		275					280					285			
Asp	Ile	Asp	Lys	Lys	Tyr	Arg	Cys	Val	Ser	Gly	Thr	Gln	Val	His	Met
	290					295					300				
Asn	Asn	Val	Thr	Val	Thr	Leu	His	Asp	Ala	Thr	Ile	Gln	Ala	Tyr	Leu
305					310					315					320
Ser	Asn	Ser	Ser	Phe	Ser	Arg	Gly	Glu	Thr	Arg	Cys	Glu	Gln	Asp	Arg

ITI-08-PCT_Sequence_Listing_ST25.txt

325 330 335

Pro Ser Pro Thr Thr Ala Pro Pro Ala Pro Pro Ser Pro Ser Pro Ser
340 345 350

Pro Val Pro Lys Ser Pro Ser Val Asp Lys Tyr Asn Val Ser Gly Thr
355 360 365

Asn Gly Thr Cys Leu Leu Ala Ser Met Gly Leu Gln Leu Asn Leu Thr
370 375 380

Tyr Glu Arg Lys Asp Asn Thr Thr Val Thr Arg Leu Leu Asn Ile Asn
385 390 395 400

Pro Asn Lys Thr Ser Ala Ser Gly Ser Cys Gly Ala His Leu Val Thr
405 410 415

Leu Glu Leu His Ser Glu Gly Thr Thr Val Leu Leu Phe Gln Phe Gly
420 425 430

Met Asn Ala Ser Ser Ser Arg Phe Phe Leu Gln Gly Ile Gln Leu Asn
435 440 445

Thr Ile Leu Pro Asp Ala Arg Asp Pro Ala Phe Lys Ala Ala Asn Gly
450 455 460

Ser Leu Arg Ala Leu Gln Ala Thr Val Gly Asn Ser Tyr Lys Cys Asn
465 470 475 480

Ala Glu Glu His Val Arg Val Thr Lys Ala Phe Ser Val Asn Ile Phe
485 490 495

Lys Val Trp Val Gln Ala Phe Lys Val Glu Gly Gly Gln Phe Gly Ser
500 505 510

Val Glu Glu Cys Leu Leu Asp Glu Asn Ser Met Leu Ile Pro Ile Ala
515 520 525

Val Gly Gly Ala Leu Ala Gly Leu Val Leu Ile Val Leu Ile Ala Tyr
530 535 540

Leu Val Gly Arg Lys Arg Ser His Ala Gly Tyr Gln Thr Ile
545 550 555

<210> 195
<211> 370
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

ITI-08-PCT_Sequence_Listing_ST25.txt

<400> 195

```

Met Ala Pro Arg Ser Ala Arg Arg Pro Leu Leu Leu Leu Leu Leu Leu
1          5          10          15

Leu Leu Leu Gly Leu Met His Cys Ala Ser Ala Met Gly Ala Pro Thr
20          25          30

Leu Pro Pro Ala Trp Gln Pro Phe Leu Lys Asp His Arg Ile Ser Thr
35          40          45

Phe Lys Asn Trp Pro Phe Leu Glu Gly Cys Ala Cys Thr Pro Glu Arg
50          55          60

Met Ala Glu Ala Gly Phe Ile His Cys Pro Thr Glu Asn Glu Pro Asp
65          70          75          80

Leu Ala Gln Cys Phe Phe Cys Phe Lys Glu Leu Glu Gly Trp Glu Pro
85          90          95

Asp Asp Asp Pro Ile Glu Glu His Lys Lys His Ser Ser Gly Cys Ala
100         105         110

Phe Leu Ser Val Lys Lys Gln Phe Glu Glu Leu Thr Leu Gly Glu Phe
115         120         125

Leu Lys Leu Asp Arg Glu Arg Ala Lys Asn Lys Ile Ala Lys Glu Thr
130         135         140

Asn Asn Lys Lys Lys Glu Phe Glu Glu Thr Ala Lys Lys Val Arg Arg
145         150         155         160

Ala Ile Glu Gln Leu Ala Ala Met Asp Ala Met Phe Met Val Lys Asn
165         170         175

Gly Asn Gly Thr Ala Cys Ile Met Ala Asn Phe Ser Ala Ala Phe Ser
180         185         190

Val Asn Tyr Asp Thr Lys Ser Gly Pro Lys Asn Met Thr Leu Asp Leu
195         200         205

Pro Ser Asp Ala Thr Val Val Leu Asn Arg Ser Ser Cys Gly Lys Glu
210         215         220

Asn Thr Ser Asp Pro Ser Leu Val Ile Ala Phe Gly Arg Gly His Thr
225         230         235         240

Leu Thr Leu Asn Phe Thr Arg Asn Ala Thr Arg Tyr Ser Val Gln Leu
245         250         255

Met Ser Phe Val Tyr Asn Leu Ser Asp Thr His Leu Phe Pro Asn Ala
260         265         270

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Ser Ser Lys Glu Ile Lys Thr Val Glu Ser Ile Thr Asp Ile Arg Ala
275 280 285

Asp Ile Asp Lys Lys Tyr Arg Cys Val Ser Gly Thr Gln Val His Met
290 295 300

Asn Asn Val Thr Val Thr Leu His Asp Ala Thr Ile Gln Ala Tyr Leu
305 310 315 320

Ser Asn Ser Ser Phe Ser Arg Gly Glu Thr Arg Cys Glu Gln Asp Leu
325 330 335

Ile Pro Ile Ala Val Gly Gly Ala Leu Ala Gly Leu Val Leu Ile Val
340 345 350

Leu Ile Ala Tyr Leu Val Gly Arg Lys Arg Ser His Ala Gly Tyr Gln
355 360 365

Thr Ile
370

<210> 196
<211> 375
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 196

Met Ala Pro Arg Ser Ala Arg Arg Pro Leu Leu Leu Leu Leu Leu Leu
1 5 10 15

Leu Leu Leu Gly Leu Met His Cys Ala Ser Ala Ala Met Phe Met Val
20 25 30

Lys Asn Gly Asn Gly Thr Ala Cys Ile Met Ala Asn Phe Ser Ala Ala
35 40 45

Phe Ser Val Asn Tyr Asp Thr Lys Ser Gly Pro Lys Asn Met Thr Leu
50 55 60

Asp Leu Pro Ser Asp Ala Thr Val Val Leu Asn Arg Ser Ser Cys Gly
65 70 75 80

Lys Glu Asn Thr Ser Asp Pro Ser Leu Val Ile Ala Phe Gly Arg Gly
85 90 95

His Thr Leu Thr Leu Asn Phe Thr Arg Asn Ala Thr Arg Tyr Ser Val
100 105 110

ITI-08-PCT_Sequence_Listing_ST25.txt

Gln	Leu	Met	Ser	Phe	Val	Tyr	Asn	Leu	Ser	Asp	Thr	His	Leu	Phe	Pro	115	120	125
Asn	Ala	Ser	Ser	Lys	Glu	Ile	Lys	Thr	Val	Glu	Ser	Ile	Thr	Asp	Ile	130	135	140
Arg	Ala	Asp	Ile	Asp	Lys	Lys	Tyr	Arg	Cys	Val	Ser	Gly	Thr	Gln	Val	145	150	155
His	Met	Asn	Asn	Val	Thr	Val	Thr	Leu	His	Asp	Ala	Thr	Ile	Gln	Ala	165	170	175
Tyr	Leu	Ser	Asn	Ser	Ser	Phe	Ser	Arg	Gly	Glu	Thr	Arg	Cys	Glu	Gln	180	185	190
Asp	Leu	Glu	Met	Gly	Ala	Pro	Thr	Leu	Pro	Pro	Ala	Trp	Gln	Pro	Phe	195	200	205
Leu	Lys	Asp	His	Arg	Ile	Ser	Thr	Phe	Lys	Asn	Trp	Pro	Phe	Leu	Glu	210	215	220
Gly	Cys	Ala	Cys	Thr	Pro	Glu	Arg	Met	Ala	Glu	Ala	Gly	Phe	Ile	His	225	230	235
Cys	Pro	Thr	Glu	Asn	Glu	Pro	Asp	Leu	Ala	Gln	Cys	Phe	Phe	Cys	Phe	245	250	255
Lys	Glu	Leu	Glu	Gly	Trp	Glu	Pro	Asp	Asp	Asp	Pro	Ile	Glu	Glu	His	260	265	270
Lys	Lys	His	Ser	Ser	Gly	Cys	Ala	Phe	Leu	Ser	Val	Lys	Lys	Gln	Phe	275	280	285
Glu	Glu	Leu	Thr	Leu	Gly	Glu	Phe	Leu	Lys	Leu	Asp	Arg	Glu	Arg	Ala	290	295	300
Lys	Asn	Lys	Ile	Ala	Lys	Glu	Thr	Asn	Asn	Lys	Lys	Lys	Glu	Phe	Glu	305	310	315
Glu	Thr	Ala	Lys	Lys	Val	Arg	Arg	Ala	Ile	Glu	Gln	Leu	Ala	Ala	Met	325	330	335
Asp	Glu	Phe	Thr	Leu	Ile	Pro	Ile	Ala	Val	Gly	Gly	Ala	Leu	Ala	Gly	340	345	350
Leu	Val	Leu	Ile	Val	Leu	Ile	Ala	Tyr	Leu	Val	Gly	Arg	Lys	Arg	Ser	355	360	365
His	Ala	Gly	Tyr	Gln	Thr	Ile										370	375	

ITI-08-PCT_Sequence_Listing_ST25.txt

<210> 197
 <211> 527
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 197

```

Met Ala Pro Arg Ser Ala Arg Arg Pro Leu Leu Leu Leu Leu Leu
1          5          10          15

Leu Leu Leu Gly Leu Met His Cys Ala Ser Ala Ala Met Phe Met Val
20          25          30

Lys Asn Gly Asn Gly Thr Ala Cys Ile Met Ala Asn Phe Ser Ala Ala
35          40          45

Phe Ser Val Asn Tyr Asp Thr Lys Ser Gly Pro Lys Asn Met Thr Leu
50          55          60

Asp Leu Pro Ser Asp Ala Thr Val Val Leu Asn Arg Ser Ser Cys Gly
65          70          75          80

Lys Glu Asn Thr Ser Asp Pro Ser Leu Val Ile Ala Phe Gly Arg Gly
85          90          95

His Thr Leu Thr Leu Asn Phe Thr Arg Asn Ala Thr Arg Tyr Ser Val
100         105         110

Gln Leu Met Ser Phe Val Tyr Asn Leu Ser Asp Thr His Leu Phe Pro
115         120         125

Asn Ala Ser Ser Lys Glu Ile Lys Thr Val Glu Ser Ile Thr Asp Ile
130         135         140

Arg Ala Asp Ile Asp Lys Lys Tyr Arg Cys Val Ser Gly Thr Gln Val
145         150         155         160

His Met Asn Asn Val Thr Val Thr Leu His Asp Ala Thr Ile Gln Ala
165         170         175

Tyr Leu Ser Asn Ser Ser Phe Ser Arg Gly Glu Thr Arg Cys Glu Gln
180         185         190

Asp Leu Glu Met Gly Ala Pro Thr Leu Pro Pro Ala Trp Gln Pro Phe
195         200         205

Leu Lys Asp His Arg Ile Ser Thr Phe Lys Asn Trp Pro Phe Leu Glu
210         215         220
    
```

ITI-08-PCT_Sequence_Listing_ST25.txt

Gly	Cys	Ala	Cys	Thr	Pro	Glu	Arg	Met	Ala	Glu	Ala	Gly	Phe	Ile	His	225	230	235	240
Cys	Pro	Thr	Glu	Asn	Glu	Pro	Asp	Leu	Ala	Gln	Cys	Phe	Phe	Cys	Phe	245	250	255	
Lys	Glu	Leu	Glu	Gly	Trp	Glu	Pro	Asp	Asp	Asp	Pro	Ile	Glu	Glu	His	260	265	270	
Lys	Lys	His	Ser	Ser	Gly	Cys	Ala	Phe	Leu	Ser	Val	Lys	Lys	Gln	Phe	275	280	285	
Glu	Glu	Leu	Thr	Leu	Gly	Glu	Phe	Leu	Lys	Leu	Asp	Arg	Glu	Arg	Ala	290	295	300	
Lys	Asn	Lys	Ile	Ala	Lys	Glu	Thr	Asn	Asn	Lys	Lys	Lys	Glu	Phe	Glu	305	310	315	320
Glu	Thr	Ala	Lys	Lys	Val	Arg	Arg	Ala	Ile	Glu	Gln	Leu	Ala	Ala	Met	325	330	335	
Asp	Glu	Phe	Thr	Cys	Leu	Leu	Ala	Ser	Met	Gly	Leu	Gln	Leu	Asn	Leu	340	345	350	
Thr	Tyr	Glu	Arg	Lys	Asp	Asn	Thr	Thr	Val	Thr	Arg	Leu	Leu	Asn	Ile	355	360	365	
Asn	Pro	Asn	Lys	Thr	Ser	Ala	Ser	Gly	Ser	Cys	Gly	Ala	His	Leu	Val	370	375	380	
Thr	Leu	Glu	Leu	His	Ser	Glu	Gly	Thr	Thr	Val	Leu	Leu	Phe	Gln	Phe	385	390	395	400
Gly	Met	Asn	Ala	Ser	Ser	Ser	Arg	Phe	Phe	Leu	Gln	Gly	Ile	Gln	Leu	405	410	415	
Asn	Thr	Ile	Leu	Pro	Asp	Ala	Arg	Asp	Pro	Ala	Phe	Lys	Ala	Ala	Asn	420	425	430	
Gly	Ser	Leu	Arg	Ala	Leu	Gln	Ala	Thr	Val	Gly	Asn	Ser	Tyr	Lys	Cys	435	440	445	
Asn	Ala	Glu	Glu	His	Val	Arg	Val	Thr	Lys	Ala	Phe	Ser	Val	Asn	Ile	450	455	460	
Phe	Lys	Val	Trp	Val	Gln	Ala	Phe	Lys	Val	Glu	Gly	Gly	Gln	Phe	Gly	465	470	475	480
Ser	Val	Glu	Glu	Cys	Leu	Leu	Asp	Glu	Asn	Ser	Met	Leu	Ile	Pro	Ile	485	490	495	
Ala	Val	Gly	Gly	Ala	Leu	Ala	Gly	Leu	Val	Leu	Ile	Val	Leu	Ile	Ala				

ITI-08-PCT_Sequence_Listing_ST25.txt

500

505

510

Tyr Leu Val Gly Arg Lys Arg Ser His Ala Gly Tyr Gln Thr Ile
 515 520 525

<210> 198

<211> 365

<212> PRT

<213> Artificial Sequence

<220>

<223> 1A01_HLA-A/m__Homo_sapiens__P30443

<400> 198

Met Ala Val Met Ala Pro Arg Thr Leu Leu Leu Leu Leu Ser Gly Ala
 1 5 10 15

Leu Ala Leu Thr Gln Thr Trp Ala Gly Ser His Ser Met Arg Tyr Phe
 20 25 30

Phe Thr Ser Val Ser Arg Pro Gly Arg Gly Glu Pro Arg Phe Ile Ala
 35 40 45

Val Gly Tyr Val Asp Asp Thr Gln Phe Val Arg Phe Asp Ser Asp Ala
 50 55 60

Ala Ser Gln Lys Met Glu Pro Arg Ala Pro Trp Ile Glu Gln Glu Gly
 65 70 75 80

Pro Glu Tyr Trp Asp Gln Glu Thr Arg Asn Met Lys Ala His Ser Gln
 85 90 95

Thr Asp Arg Ala Asn Leu Gly Thr Leu Arg Gly Tyr Tyr Asn Gln Ser
 100 105 110

Glu Asp Gly Ser His Thr Ile Gln Ile Met Tyr Gly Cys Asp Val Gly
 115 120 125

Pro Asp Gly Arg Phe Leu Arg Gly Tyr Arg Gln Asp Ala Tyr Asp Gly
 130 135 140

Lys Asp Tyr Ile Ala Leu Asn Glu Asp Leu Arg Ser Trp Thr Ala Ala
 145 150 155 160

Asp Met Ala Ala Gln Ile Thr Lys Arg Lys Trp Glu Ala Val His Ala
 165 170 175

Ala Glu Gln Arg Arg Val Tyr Leu Glu Gly Arg Cys Val Asp Gly Leu
 180 185 190

Arg Arg Tyr Leu Glu Asn Gly Lys Glu Thr Leu Gln Arg Thr Asp Pro

ITI-08-PCT_Sequence_Listing_ST25.txt

```

195                200                205
Pro Lys Thr His Met Thr His His Pro Ile Ser Asp His Glu Ala Thr
 210                215                220
Leu Arg Cys Trp Ala Leu Gly Phe Tyr Pro Ala Glu Ile Thr Leu Thr
225                230                235                240
Trp Gln Arg Asp Gly Glu Asp Gln Thr Gln Asp Thr Glu Leu Val Glu
                245                250                255
Thr Arg Pro Ala Gly Asp Gly Thr Phe Gln Lys Trp Ala Ala Val Val
                260                265                270
Val Pro Ser Gly Glu Glu Gln Arg Tyr Thr Cys His Val Gln His Glu
                275                280                285
Gly Leu Pro Lys Pro Leu Thr Leu Arg Trp Glu Leu Ser Ser Gln Pro
 290                295                300
Thr Ile Pro Ile Val Gly Ile Ile Ala Gly Leu Val Leu Leu Gly Ala
305                310                315                320
Val Ile Thr Gly Ala Val Val Ala Ala Val Met Trp Arg Arg Lys Ser
                325                330                335
Ser Asp Arg Lys Gly Gly Ser Tyr Thr Gln Ala Ala Ser Ser Asp Ser
                340                345                350
Ala Gln Gly Ser Asp Val Ser Leu Thr Ala Cys Lys Val
                355                360                365

```

<210> 199
 <211> 365
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 1A02__Homo_sapiens__P01892

<400> 199

```

Met Ala Val Met Ala Pro Arg Thr Leu Val Leu Leu Leu Ser Gly Ala
1                5                10                15
Leu Ala Leu Thr Gln Thr Trp Ala Gly Ser His Ser Met Arg Tyr Phe
                20                25                30
Phe Thr Ser Val Ser Arg Pro Gly Arg Gly Glu Pro Arg Phe Ile Ala
                35                40                45
Val Gly Tyr Val Asp Asp Thr Gln Phe Val Arg Phe Asp Ser Asp Ala

```

ITI-08-PCT_Sequence_Listing_ST25.txt

50	55	60													
Ala	Ser	Gln	Arg	Met	Glu	Pro	Arg	Ala	Pro	Trp	Ile	Glu	Gln	Glu	Gly
65					70					75					80
Pro	Glu	Tyr	Trp	Asp	Gly	Glu	Thr	Arg	Lys	Val	Lys	Ala	His	Ser	Gln
				85					90					95	
Thr	His	Arg	Val	Asp	Leu	Gly	Thr	Leu	Arg	Gly	Tyr	Tyr	Asn	Gln	Ser
			100					105					110		
Glu	Ala	Gly	Ser	His	Thr	Val	Gln	Arg	Met	Tyr	Gly	Cys	Asp	Val	Gly
		115					120					125			
Ser	Asp	Trp	Arg	Phe	Leu	Arg	Gly	Tyr	His	Gln	Tyr	Ala	Tyr	Asp	Gly
	130					135					140				
Lys	Asp	Tyr	Ile	Ala	Leu	Lys	Glu	Asp	Leu	Arg	Ser	Trp	Thr	Ala	Ala
145					150					155					160
Asp	Met	Ala	Ala	Gln	Thr	Thr	Lys	His	Lys	Trp	Glu	Ala	Ala	His	Val
				165					170					175	
Ala	Glu	Gln	Leu	Arg	Ala	Tyr	Leu	Glu	Gly	Thr	Cys	Val	Glu	Trp	Leu
			180					185					190		
Arg	Arg	Tyr	Leu	Glu	Asn	Gly	Lys	Glu	Thr	Leu	Gln	Arg	Thr	Asp	Ala
		195					200					205			
Pro	Lys	Thr	His	Met	Thr	His	His	Ala	Val	Ser	Asp	His	Glu	Ala	Thr
	210					215					220				
Leu	Arg	Cys	Trp	Ala	Leu	Ser	Phe	Tyr	Pro	Ala	Glu	Ile	Thr	Leu	Thr
225					230					235					240
Trp	Gln	Arg	Asp	Gly	Glu	Asp	Gln	Thr	Gln	Asp	Thr	Glu	Leu	Val	Glu
				245					250					255	
Thr	Arg	Pro	Ala	Gly	Asp	Gly	Thr	Phe	Gln	Lys	Trp	Ala	Ala	Val	Val
			260					265					270		
Val	Pro	Ser	Gly	Gln	Glu	Gln	Arg	Tyr	Thr	Cys	His	Val	Gln	His	Glu
		275					280					285			
Gly	Leu	Pro	Lys	Pro	Leu	Thr	Leu	Arg	Trp	Glu	Pro	Ser	Ser	Gln	Pro
	290					295					300				
Thr	Ile	Pro	Ile	Val	Gly	Ile	Ile	Ala	Gly	Leu	Val	Leu	Phe	Gly	Ala
305					310					315					320
Val	Ile	Thr	Gly	Ala	Val	Val	Ala	Ala	Val	Met	Trp	Arg	Arg	Lys	Ser
				325					330					335	

ITI-08-PCT_Sequence_Listing_ST25.txt

Ser Asp Arg Lys Gly Gly Ser Tyr Ser Gln Ala Ala Ser Ser Asp Ser
340 345 350

Ala Gln Gly Ser Asp Val Ser Leu Thr Ala Cys Lys Val
355 360 365

<210> 200

<211> 420

<212> PRT

<213> Artificial Sequence

<220>

<223> 5T4__Homo_sapiens__Q13641

<400> 200

Met Pro Gly Gly Cys Ser Arg Gly Pro Ala Ala Gly Asp Gly Arg Leu
1 5 10 15

Arg Leu Ala Arg Leu Ala Leu Val Leu Leu Gly Trp Val Ser Ser Ser
20 25 30

Ser Pro Thr Ser Ser Ala Ser Ser Phe Ser Ser Ser Ala Pro Phe Leu
35 40 45

Ala Ser Ala Val Ser Ala Gln Pro Pro Leu Pro Asp Gln Cys Pro Ala
50 55 60

Leu Cys Glu Cys Ser Glu Ala Ala Arg Thr Val Lys Cys Val Asn Arg
65 70 75 80

Asn Leu Thr Glu Val Pro Thr Asp Leu Pro Ala Tyr Val Arg Asn Leu
85 90 95

Phe Leu Thr Gly Asn Gln Leu Ala Val Leu Pro Ala Gly Ala Phe Ala
100 105 110

Arg Arg Pro Pro Leu Ala Glu Leu Ala Ala Leu Asn Leu Ser Gly Ser
115 120 125

Arg Leu Asp Glu Val Arg Ala Gly Ala Phe Glu His Leu Pro Ser Leu
130 135 140

Arg Gln Leu Asp Leu Ser His Asn Pro Leu Ala Asp Leu Ser Pro Phe
145 150 155 160

Ala Phe Ser Gly Ser Asn Ala Ser Val Ser Ala Pro Ser Pro Leu Val
165 170 175

Glu Leu Ile Leu Asn His Ile Val Pro Pro Glu Asp Glu Arg Gln Asn
180 185 190

ITI-08-PCT_Sequence_Listing_ST25.txt

```

Arg Ser Phe Glu Gly Met Val Val Ala Ala Leu Leu Ala Gly Arg Ala
    195                200                205

Leu Gln Gly Leu Arg Arg Leu Glu Leu Ala Ser Asn His Phe Leu Tyr
    210                215                220

Leu Pro Arg Asp Val Leu Ala Gln Leu Pro Ser Leu Arg His Leu Asp
    225                230                235                240

Leu Ser Asn Asn Ser Leu Val Ser Leu Thr Tyr Val Ser Phe Arg Asn
    245                250                255

Leu Thr His Leu Glu Ser Leu His Leu Glu Asp Asn Ala Leu Lys Val
    260                265                270

Leu His Asn Gly Thr Leu Ala Glu Leu Gln Gly Leu Pro His Ile Arg
    275                280                285

Val Phe Leu Asp Asn Asn Pro Trp Val Cys Asp Cys His Met Ala Asp
    290                295                300

Met Val Thr Trp Leu Lys Glu Thr Glu Val Val Gln Gly Lys Asp Arg
    305                310                315                320

Leu Thr Cys Ala Tyr Pro Glu Lys Met Arg Asn Arg Val Leu Leu Glu
    325                330                335

Leu Asn Ser Ala Asp Leu Asp Cys Asp Pro Ile Leu Pro Pro Ser Leu
    340                345                350

Gln Thr Ser Tyr Val Phe Leu Gly Ile Val Leu Ala Leu Ile Gly Ala
    355                360                365

Ile Phe Leu Leu Val Leu Tyr Leu Asn Arg Lys Gly Ile Lys Lys Trp
    370                375                380

Met His Asn Ile Arg Asp Ala Cys Arg Asp His Met Glu Gly Tyr His
    385                390                395                400

Tyr Arg Tyr Glu Ile Asn Ala Asp Pro Arg Leu Thr Asn Leu Ser Ser
    405                410                415

Asn Ser Asp Val
    420

```

```

<210> 201
<211> 543
<212> PRT
<213> Artificial Sequence

```

```

<220>

```

ITI-08-PCT_Sequence_Listing_ST25.txt

<223> ACRBP__Homo_sapiens__Q8NEB7

<400> 201

Met	Arg	Lys	Pro	Ala	Ala	Gly	Phe	Leu	Pro	Ser	Leu	Leu	Lys	Val	Leu	1	5	10	15
Leu	Leu	Pro	Leu	Ala	Pro	Ala	Ala	Ala	Gln	Asp	Ser	Thr	Gln	Ala	Ser	20	25	30	
Thr	Pro	Gly	Ser	Pro	Leu	Ser	Pro	Thr	Glu	Tyr	Glu	Arg	Phe	Phe	Ala	35	40	45	
Leu	Leu	Thr	Pro	Thr	Trp	Lys	Ala	Glu	Thr	Thr	Cys	Arg	Leu	Arg	Ala	50	55	60	
Thr	His	Gly	Cys	Arg	Asn	Pro	Thr	Leu	Val	Gln	Leu	Asp	Gln	Tyr	Glu	65	70	75	80
Asn	His	Gly	Leu	Val	Pro	Asp	Gly	Ala	Val	Cys	Ser	Asn	Leu	Pro	Tyr	85	90	95	
Ala	Ser	Trp	Phe	Glu	Ser	Phe	Cys	Gln	Phe	Thr	His	Tyr	Arg	Cys	Ser	100	105	110	
Asn	His	Val	Tyr	Tyr	Ala	Lys	Arg	Val	Leu	Cys	Ser	Gln	Pro	Val	Ser	115	120	125	
Ile	Leu	Ser	Pro	Asn	Thr	Leu	Lys	Glu	Ile	Glu	Ala	Ser	Ala	Glu	Val	130	135	140	
Ser	Pro	Thr	Thr	Met	Thr	Ser	Pro	Ile	Ser	Pro	His	Phe	Thr	Val	Thr	145	150	155	160
Glu	Arg	Gln	Thr	Phe	Gln	Pro	Trp	Pro	Glu	Arg	Leu	Ser	Asn	Asn	Val	165	170	175	
Glu	Glu	Leu	Leu	Gln	Ser	Ser	Leu	Ser	Leu	Gly	Gly	Gln	Glu	Gln	Ala	180	185	190	
Pro	Glu	His	Lys	Gln	Glu	Gln	Gly	Val	Glu	His	Arg	Gln	Glu	Pro	Thr	195	200	205	
Gln	Glu	His	Lys	Gln	Glu	Glu	Gly	Gln	Lys	Gln	Glu	Glu	Gln	Glu	Glu	210	215	220	
Glu	Gln	Glu	Glu	Glu	Gly	Lys	Gln	Glu	Glu	Gly	Gln	Gly	Thr	Lys	Glu	225	230	235	240
Gly	Arg	Glu	Ala	Val	Ser	Gln	Leu	Gln	Thr	Asp	Ser	Glu	Pro	Lys	Phe	245	250	255	

ITI-08-PCT_Sequence_Listing_ST25.txt

His Ser Glu Ser Leu Ser Ser Asn Pro Ser Ser Phe Ala Pro Arg Val
260 265 270

Arg Glu Val Glu Ser Thr Pro Met Ile Met Glu Asn Ile Gln Glu Leu
275 280 285

Ile Arg Ser Ala Gln Glu Ile Asp Glu Met Asn Glu Ile Tyr Asp Glu
290 295 300

Asn Ser Tyr Trp Arg Asn Gln Asn Pro Gly Ser Leu Leu Gln Leu Pro
305 310 315 320

His Thr Glu Ala Leu Leu Val Leu Cys Tyr Ser Ile Val Glu Asn Thr
325 330 335

Cys Ile Ile Thr Pro Thr Ala Lys Ala Trp Lys Tyr Met Glu Glu Glu
340 345 350

Ile Leu Gly Phe Gly Lys Ser Val Cys Asp Ser Leu Gly Arg Arg His
355 360 365

Met Ser Thr Cys Ala Leu Cys Asp Phe Cys Ser Leu Lys Leu Glu Gln
370 375 380

Cys His Ser Glu Ala Ser Leu Gln Arg Gln Gln Cys Asp Thr Ser His
385 390 395 400

Lys Thr Pro Phe Val Ser Pro Leu Leu Ala Ser Gln Ser Leu Ser Ile
405 410 415

Gly Asn Gln Val Gly Ser Pro Glu Ser Gly Arg Phe Tyr Gly Leu Asp
420 425 430

Leu Tyr Gly Gly Leu His Met Asp Phe Trp Cys Ala Arg Leu Ala Thr
435 440 445

Lys Gly Cys Glu Asp Val Arg Val Ser Gly Trp Leu Gln Thr Glu Phe
450 455 460

Leu Ser Phe Gln Asp Gly Asp Phe Pro Thr Lys Ile Cys Asp Thr Asp
465 470 475 480

Tyr Ile Gln Tyr Pro Asn Tyr Cys Ser Phe Lys Ser Gln Gln Cys Leu
485 490 495

Met Arg Asn Arg Asn Arg Lys Val Ser Arg Met Arg Cys Leu Gln Asn
500 505 510

Glu Thr Tyr Ser Ala Leu Ser Pro Gly Lys Ser Glu Asp Val Val Leu
515 520 525

Arg Trp Ser Gln Glu Phe Ser Thr Leu Thr Leu Gly Gln Phe Gly

ITI-08-PCT_Sequence_Listing_ST25.txt

530

535

540

<210> 202

<211> 609

<212> PRT

<213> Artificial Sequence

<220>

<223> AFP__Homo_sapiens__P02771

<400> 202

Met Lys Trp Val Glu Ser Ile Phe Leu Ile Phe Leu Leu Asn Phe Thr
 1 5 10 15

Glu Ser Arg Thr Leu His Arg Asn Glu Tyr Gly Ile Ala Ser Ile Leu
 20 25 30

Asp Ser Tyr Gln Cys Thr Ala Glu Ile Ser Leu Ala Asp Leu Ala Thr
 35 40 45

Ile Phe Phe Ala Gln Phe Val Gln Glu Ala Thr Tyr Lys Glu Val Ser
 50 55 60

Lys Met Val Lys Asp Ala Leu Thr Ala Ile Glu Lys Pro Thr Gly Asp
 65 70 75 80

Glu Gln Ser Ser Gly Cys Leu Glu Asn Gln Leu Pro Ala Phe Leu Glu
 85 90 95

Glu Leu Cys His Glu Lys Glu Ile Leu Glu Lys Tyr Gly His Ser Asp
 100 105 110

Cys Cys Ser Gln Ser Glu Glu Gly Arg His Asn Cys Phe Leu Ala His
 115 120 125

Lys Lys Pro Thr Pro Ala Ser Ile Pro Leu Phe Gln Val Pro Glu Pro
 130 135 140

Val Thr Ser Cys Glu Ala Tyr Glu Glu Asp Arg Glu Thr Phe Met Asn
 145 150 155 160

Lys Phe Ile Tyr Glu Ile Ala Arg Arg His Pro Phe Leu Tyr Ala Pro
 165 170 175

Thr Ile Leu Leu Trp Ala Ala Arg Tyr Asp Lys Ile Ile Pro Ser Cys
 180 185 190

Cys Lys Ala Glu Asn Ala Val Glu Cys Phe Gln Thr Lys Ala Ala Thr
 195 200 205

Val Thr Lys Glu Leu Arg Glu Ser Ser Leu Leu Asn Gln His Ala Cys

ITI-08-PCT_Sequence_Listing_ST25.txt

210		215		220															
Ala	Val	Met	Lys	Asn	Phe	Gly	Thr	Arg	Thr	Phe	Gln	Ala	Ile	Thr	Val				
225					230					235					240				
Thr	Lys	Leu	Ser	Gln	Lys	Phe	Thr	Lys	Val	Asn	Phe	Thr	Glu	Ile	Gln				
				245					250					255					
Lys	Leu	Val	Leu	Asp	Val	Ala	His	Val	His	Glu	His	Cys	Cys	Arg	Gly				
			260					265					270						
Asp	Val	Leu	Asp	Cys	Leu	Gln	Asp	Gly	Glu	Lys	Ile	Met	Ser	Tyr	Ile				
		275					280					285							
Cys	Ser	Gln	Gln	Asp	Thr	Leu	Ser	Asn	Lys	Ile	Thr	Glu	Cys	Cys	Lys				
	290					295					300								
Leu	Thr	Thr	Leu	Glu	Arg	Gly	Gln	Cys	Ile	Ile	His	Ala	Glu	Asn	Asp				
305					310					315					320				
Glu	Lys	Pro	Glu	Gly	Leu	Ser	Pro	Asn	Leu	Asn	Arg	Phe	Leu	Gly	Asp				
				325					330					335					
Arg	Asp	Phe	Asn	Gln	Phe	Ser	Ser	Gly	Glu	Lys	Asn	Ile	Phe	Leu	Ala				
			340					345					350						
Ser	Phe	Val	His	Glu	Tyr	Ser	Arg	Arg	His	Pro	Gln	Leu	Ala	Val	Ser				
		355					360					365							
Val	Ile	Leu	Arg	Val	Ala	Lys	Gly	Tyr	Gln	Glu	Leu	Leu	Glu	Lys	Cys				
	370					375					380								
Phe	Gln	Thr	Glu	Asn	Pro	Leu	Glu	Cys	Gln	Asp	Lys	Gly	Glu	Glu	Glu				
385					390					395					400				
Leu	Gln	Lys	Tyr	Ile	Gln	Glu	Ser	Gln	Ala	Leu	Ala	Lys	Arg	Ser	Cys				
				405					410					415					
Gly	Leu	Phe	Gln	Lys	Leu	Gly	Glu	Tyr	Tyr	Leu	Gln	Asn	Ala	Phe	Leu				
			420					425					430						
Val	Ala	Tyr	Thr	Lys	Lys	Ala	Pro	Gln	Leu	Thr	Ser	Ser	Glu	Leu	Met				
		435					440					445							
Ala	Ile	Thr	Arg	Lys	Met	Ala	Ala	Thr	Ala	Ala	Thr	Cys	Cys	Gln	Leu				
	450					455					460								
Ser	Glu	Asp	Lys	Leu	Leu	Ala	Cys	Gly	Glu	Gly	Ala	Ala	Asp	Ile	Ile				
465					470					475					480				
Ile	Gly	His	Leu	Cys	Ile	Arg	His	Glu	Met	Thr	Pro	Val	Asn	Pro	Gly				
			485						490					495					

ITI-08-PCT_Sequence_Listing_ST25.txt

Val Gly Gln Cys Cys Thr Ser Ser Tyr Ala Asn Arg Arg Pro Cys Phe
500 505 510

Ser Ser Leu Val Val Asp Glu Thr Tyr Val Pro Pro Ala Phe Ser Asp
515 520 525

Asp Lys Phe Ile Phe His Lys Asp Leu Cys Gln Ala Gln Gly Val Ala
530 535 540

Leu Gln Thr Met Lys Gln Glu Phe Leu Ile Asn Leu Val Lys Gln Lys
545 550 555 560

Pro Gln Ile Thr Glu Glu Gln Leu Glu Ala Val Ile Ala Asp Phe Ser
565 570 575

Gly Leu Leu Glu Lys Cys Cys Gln Gly Gln Glu Gln Glu Val Cys Phe
580 585 590

Ala Glu Glu Gly Gln Lys Leu Ile Ser Lys Thr Arg Ala Ala Leu Gly
595 600 605

Val

<210> 203

<211> 854

<212> PRT

<213> Artificial Sequence

<220>

<223> AKAP4__Homo_sapiens__Q5JQC9

<400> 203

Met Met Ala Tyr Ser Asp Thr Thr Met Met Ser Asp Asp Ile Asp Trp
1 5 10 15

Leu Arg Ser His Arg Gly Val Cys Lys Val Asp Leu Tyr Asn Pro Glu
20 25 30

Gly Gln Gln Asp Gln Asp Arg Lys Val Ile Cys Phe Val Asp Val Ser
35 40 45

Thr Leu Asn Val Glu Asp Lys Asp Tyr Lys Asp Ala Ala Ser Ser Ser
50 55 60

Ser Glu Gly Asn Leu Asn Leu Gly Ser Leu Glu Glu Lys Glu Ile Ile
65 70 75 80

Val Ile Lys Asp Thr Glu Lys Lys Asp Gln Ser Lys Thr Glu Gly Ser
85 90 95

ITI-08-PCT_Sequence_Listing_ST25.txt

Val	Cys	Leu	Phe	Lys	Gln	Ala	Pro	Ser	Asp	Pro	Val	Ser	Val	Leu	Asn	
			100					105					110			
Trp	Leu	Leu	Ser	Asp	Leu	Gln	Lys	Tyr	Ala	Leu	Gly	Phe	Gln	His	Ala	
		115					120					125				
Leu	Ser	Pro	Ser	Thr	Ser	Thr	Cys	Lys	His	Lys	Val	Gly	Asp	Thr	Glu	
	130					135					140					
Gly	Glu	Tyr	His	Arg	Ala	Ser	Ser	Glu	Asn	Cys	Tyr	Ser	Val	Tyr	Ala	
145					150					155					160	
Asp	Gln	Val	Asn	Ile	Asp	Tyr	Leu	Met	Asn	Arg	Pro	Gln	Asn	Leu	Arg	
			165						170					175		
Leu	Glu	Met	Thr	Ala	Ala	Lys	Asn	Thr	Asn	Asn	Asn	Gln	Ser	Pro	Ser	
			180					185					190			
Ala	Pro	Pro	Ala	Lys	Pro	Pro	Ser	Thr	Gln	Arg	Ala	Val	Ile	Ser	Pro	
		195					200					205				
Asp	Gly	Glu	Cys	Ser	Ile	Asp	Asp	Leu	Ser	Phe	Tyr	Val	Asn	Arg	Leu	
	210					215					220					
Ser	Ser	Leu	Val	Ile	Gln	Met	Ala	His	Lys	Glu	Ile	Lys	Glu	Lys	Leu	
225					230					235					240	
Glu	Gly	Lys	Ser	Lys	Cys	Leu	His	His	Ser	Ile	Cys	Pro	Ser	Pro	Gly	
				245					250					255		
Asn	Lys	Glu	Arg	Ile	Ser	Pro	Arg	Thr	Pro	Ala	Ser	Lys	Ile	Ala	Ser	
			260					265					270			
Glu	Met	Ala	Tyr	Glu	Ala	Val	Glu	Leu	Thr	Ala	Ala	Glu	Met	Arg	Gly	
		275					280					285				
Thr	Gly	Glu	Glu	Ser	Arg	Glu	Gly	Gly	Gln	Lys	Ser	Phe	Leu	Tyr	Ser	
	290					295					300					
Glu	Leu	Ser	Asn	Lys	Ser	Lys	Ser	Gly	Asp	Lys	Gln	Met	Ser	Gln	Arg	
305					310					315					320	
Glu	Ser	Lys	Glu	Phe	Ala	Asp	Ser	Ile	Ser	Lys	Gly	Leu	Met	Val	Tyr	
				325					330					335		
Ala	Asn	Gln	Val	Ala	Ser	Asp	Met	Met	Val	Ser	Leu	Met	Lys	Thr	Leu	
			340					345					350			
Lys	Val	His	Ser	Ser	Gly	Lys	Pro	Ile	Pro	Ala	Ser	Val	Val	Leu	Lys	
		355					360					365				
Arg	Val	Leu	Leu	Arg	His	Thr	Lys	Glu	Ile	Val	Ser	Asp	Leu	Ile	Asp	

ITI-08-PCT_Sequence_Listing_ST25.txt

370

375

380

Ser Cys Met Lys Asn Leu His Asn Ile Thr Gly Val Leu Met Thr Asp
 385 390 395 400

Ser Asp Phe Val Ser Ala Val Lys Arg Asn Leu Phe Asn Gln Trp Lys
 405 410 415

Gln Asn Ala Thr Asp Ile Met Glu Ala Met Leu Lys Arg Leu Val Ser
 420 425 430

Ala Leu Ile Gly Glu Glu Lys Glu Thr Lys Ser Gln Ser Leu Ser Tyr
 435 440 445

Ala Ser Leu Lys Ala Gly Ser His Asp Pro Lys Cys Arg Asn Gln Ser
 450 455 460

Leu Glu Phe Ser Thr Met Lys Ala Glu Met Lys Glu Arg Asp Lys Gly
 465 470 475 480

Lys Met Lys Ser Asp Pro Cys Lys Ser Leu Thr Ser Ala Glu Lys Val
 485 490 495

Gly Glu His Ile Leu Lys Glu Gly Leu Thr Ile Trp Asn Gln Lys Gln
 500 505 510

Gly Asn Ser Cys Lys Val Ala Thr Lys Ala Cys Ser Asn Lys Asp Glu
 515 520 525

Lys Gly Glu Lys Ile Asn Ala Ser Thr Asp Ser Leu Ala Lys Asp Leu
 530 535 540

Ile Val Ser Ala Leu Lys Leu Ile Gln Tyr His Leu Thr Gln Gln Thr
 545 550 555 560

Lys Gly Lys Asp Thr Cys Glu Glu Asp Cys Pro Gly Ser Thr Met Gly
 565 570 575

Tyr Met Ala Gln Ser Thr Gln Tyr Glu Lys Cys Gly Gly Gly Gln Ser
 580 585 590

Ala Lys Ala Leu Ser Val Lys Gln Leu Glu Ser His Arg Ala Pro Gly
 595 600 605

Pro Ser Thr Cys Gln Lys Glu Asn Gln His Leu Asp Ser Gln Lys Met
 610 615 620

Asp Met Ser Asn Ile Val Leu Met Leu Ile Gln Lys Leu Leu Asn Glu
 625 630 635 640

Asn Pro Phe Lys Cys Glu Asp Pro Cys Glu Gly Glu Asn Lys Cys Ser
 645 650 655

ITI-08-PCT_Sequence_Listing_ST25.txt

Glu Pro Arg Ala Ser Lys Ala Ala Ser Met Ser Asn Arg Ser Asp Lys
660 665 670

Ala Glu Glu Gln Cys Gln Glu His Gln Glu Leu Asp Cys Thr Ser Gly
675 680 685

Met Lys Gln Ala Asn Gly Gln Phe Ile Asp Lys Leu Val Glu Ser Val
690 695 700

Met Lys Leu Cys Leu Ile Met Ala Lys Tyr Ser Asn Asp Gly Ala Ala
705 710 715 720

Leu Ala Glu Leu Glu Glu Gln Ala Ala Ser Ala Asn Lys Pro Asn Phe
725 730 735

Arg Gly Thr Arg Cys Ile His Ser Gly Ala Met Pro Gln Asn Tyr Gln
740 745 750

Asp Ser Leu Gly His Glu Val Ile Val Asn Asn Gln Cys Ser Thr Asn
755 760 765

Ser Leu Gln Lys Gln Leu Gln Ala Val Leu Gln Trp Ile Ala Ala Ser
770 775 780

Gln Phe Asn Val Pro Met Leu Tyr Phe Met Gly Asp Lys Asp Gly Gln
785 790 795 800

Leu Glu Lys Leu Pro Gln Val Ser Ala Lys Ala Ala Glu Lys Gly Tyr
805 810 815

Ser Val Gly Gly Leu Leu Gln Glu Val Met Lys Phe Ala Lys Glu Arg
820 825 830

Gln Pro Asp Glu Ala Val Gly Lys Val Ala Arg Lys Gln Leu Leu Asp
835 840 845

Trp Leu Leu Ala Asn Leu
850

<210> 204
<211> 416
<212> PRT
<213> Artificial Sequence

<220>
<223> alpha-actinin-_4/m__Homo_sapiens__B4DSX0

<400> 204

Met Val Asp Tyr His Ala Ala Asn Gln Ser Tyr Gln Tyr Gly Pro Ser
1 5 10 15

ITI-08-PCT_Sequence_Listing_ST25.txt

Ser	Ala	Gly	Asn	Gly	Ala	Gly	Gly	Gly	Gly	Ser	Met	Gly	Asp	Tyr	Met	20	25	30
Ala	Gln	Glu	Asp	Asp	Trp	Asp	Arg	Asp	Leu	Leu	Leu	Asp	Pro	Ala	Trp	35	40	45
Glu	Lys	Gln	Gln	Arg	Lys	Thr	Phe	Thr	Ala	Trp	Cys	Asn	Ser	His	Leu	50	55	60
Arg	Lys	Ala	Gly	Thr	Gln	Ile	Glu	Asn	Ile	Asp	Glu	Asp	Phe	Arg	Asp	65	70	75
Gly	Leu	Lys	Leu	Met	Leu	Leu	Leu	Glu	Val	Ile	Ser	Gly	Glu	Arg	Leu	85	90	95
Pro	Lys	Pro	Glu	Arg	Gly	Lys	Met	Arg	Val	His	Lys	Ile	Asn	Asn	Val	100	105	110
Asn	Lys	Ala	Leu	Asp	Phe	Ile	Ala	Ser	Lys	Gly	Val	Lys	Leu	Val	Ser	115	120	125
Ile	Gly	Ala	Glu	Glu	Ile	Val	Asp	Gly	Asn	Ala	Lys	Met	Thr	Leu	Gly	130	135	140
Met	Ile	Trp	Thr	Ile	Ile	Leu	Arg	Phe	Ala	Ile	Gln	Asp	Ile	Ser	Val	145	150	155
Glu	Glu	Thr	Ser	Ala	Lys	Glu	Gly	Leu	Leu	Leu	Trp	Cys	Gln	Arg	Lys	165	170	175
Thr	Ala	Pro	Tyr	Lys	Asn	Val	Asn	Val	Gln	Asn	Phe	His	Ile	Ser	Trp	180	185	190
Lys	Asp	Gly	Leu	Ala	Phe	Asn	Ala	Leu	Ile	His	Arg	His	Arg	Pro	Glu	195	200	205
Leu	Ile	Glu	Tyr	Asp	Lys	Leu	Arg	Lys	Asp	Asp	Pro	Val	Thr	Asn	Leu	210	215	220
Asn	Asn	Ala	Phe	Glu	Val	Ala	Glu	Lys	Tyr	Leu	Asp	Ile	Pro	Lys	Met	225	230	235
Leu	Asp	Ala	Glu	Asp	Ile	Val	Asn	Thr	Ala	Arg	Pro	Asp	Glu	Lys	Ala	245	250	255
Ile	Met	Thr	Tyr	Val	Ser	Ser	Phe	Tyr	His	Ala	Phe	Ser	Gly	Ala	Gln	260	265	270
Lys	Ala	Glu	Thr	Ala	Ala	Asn	Arg	Ile	Cys	Lys	Val	Leu	Ala	Val	Asn	275	280	285

ITI-08-PCT_Sequence_Listing_ST25.txt

Gln Glu Asn Glu His Leu Met Glu Asp Tyr Glu Lys Leu Ala Ser Asp
290 295 300

Leu Leu Glu Trp Ile Arg Arg Thr Ile Pro Trp Leu Glu Asp Arg Val
305 310 315 320

Pro Gln Lys Thr Ile Gln Glu Met Gln Gln Lys Leu Glu Asp Phe Arg
325 330 335

Asp Tyr Arg Arg Val His Lys Pro Pro Lys Val Gln Glu Lys Cys Gln
340 345 350

Leu Glu Ile Asn Phe Asn Thr Leu Gln Thr Lys Leu Arg Leu Ser Asn
355 360 365

Arg Pro Ala Phe Met Pro Ser Trp Arg Ser Arg Ala Ser Ser Ser Pro
370 375 380

Thr Ser Thr Cys Ala Ala Ser Ser Pro Ala Arg Pro Met Leu Trp Gly
385 390 395 400

Pro Gly Ser Arg Pro Arg Trp Arg Arg Ser Gly Ala Ser Pro Leu Arg
405 410 415

<210> 205

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> alpha-actinin-_4/m__Homo_sapiens__B4E337

<400> 205

Met Val Asp Tyr His Ala Ala Asn Gln Ser Tyr Gln Tyr Gly Pro Ser
1 5 10 15

Ser Ala Gly Asn Gly Ala Gly Gly Gly Gly Ser Met Gly Asp Tyr Met
20 25 30

Ala Gln Glu Asp Asp Trp Asp Arg Asp Leu Leu Leu Asp Pro Ala Trp
35 40 45

Glu Lys Gln Gln Arg Lys Thr Phe Thr Ala Trp Cys Asn Ser His Leu
50 55 60

Arg Lys Ala Gly Thr Gln Ile Glu Asn Ile Asp Glu Asp Phe Arg Asp
65 70 75 80

Gly Leu Lys Leu Met Leu Leu Leu Glu Val Ile Ser Gly Glu Arg Leu
85 90 95

ITI-08-PCT_Sequence_Listing_ST25.txt

```

Pro  Lys  Pro  Glu  Arg  Gly  Lys  Met  Arg  Val  His  Lys  Ile  Asn  Asn  Val
      100                      105                      110

Asn  Lys  Ala  Leu  Asp  Phe  Ile  Ala  Ser  Lys  Gly  Val  Lys  Leu  Val  Ser
      115                      120                      125

Ile  Gly  Ala  Glu  Glu  Ile  Val  Asp  Gly  Asn  Ala  Lys  Met  Thr  Leu  Gly
      130                      135                      140

Met  Ile  Trp  Thr  Ile  Ile  Leu  Arg  Phe  Ala  Ile  Gln  Asp  Ile  Ser  Val
145                      150                      155                      160

Glu  Glu  Thr  Ser  Ala  Lys  Glu  Gly  Leu  Leu  Leu  Trp  Cys  Gln  Arg  Lys
      165                      170                      175

Thr  Ala  Pro  Tyr  Lys  Asn  Val  Asn  Val  Gln  Asn  Phe  His  Ile  Ser  Trp
      180                      185                      190

Lys  Asp  Gly  Leu  Ala  Phe  Asn  Ala  Leu  Ile  His  Arg  His  Arg  Pro  Glu
      195                      200                      205

Leu  Ile  Glu  Tyr  Asp  Lys  Leu  Arg  Lys  Asp  Asp  Pro  Val  Thr  Asn  Leu
      210                      215                      220

Asn  Asn  Ala  Phe  Glu  Val  Ala  Glu  Lys  Tyr  Leu  Asp  Ile  Pro  Lys  Met
225                      230                      235                      240

Leu  Asp  Ala  Glu  Asp  Ile  Val  Asn  Thr  Ala  Arg  Pro  Asp  Glu  Lys  Ala
      245                      250                      255

Ile  Met  Thr  Tyr  Val  Ser  Ser  Phe  Tyr  His  Ala  Phe  Ser  Gly  Ala  Gln
      260                      265                      270

Lys  Ala  Glu  Thr  Ala  Ala  Asn  Arg  Ile  Cys  Lys  Val  Leu  Ala  Val  Asn
      275                      280                      285

Gln  Glu  Asn  Glu  His  Leu  Met  Glu  Asp  Tyr  Glu  Lys  Leu  Ala  Ser  Asp
      290                      295                      300

Leu  Leu  Glu  Trp  Ile  Gln  Arg  Thr  Ile  Pro  Trp  Leu  Glu  Asp  Arg  Val
305                      310                      315                      320

Pro  Gln  Lys  Ala  Ile  Gln  Glu  Met  Gln  Gln  Lys  Leu  Glu  Asp  Phe  Arg
      325                      330                      335

Asp  Tyr  Arg  Arg  Val  His  Lys  Pro  Pro  Lys  Val  Gln  Glu  Lys  Cys  Gln
      340                      345                      350

Leu  Glu  Ile  Asn  Phe  Asn  Thr  Leu  Gln  Thr  Lys  Leu  Arg  Leu  Ser  Asn
      355                      360                      365

Arg  Pro  Ala  Phe  Met  Pro  Ser  Glu  Gly  Lys  Met  Val  Ser  Asp  Ile  Asn

```


ITI-08-PCT_Sequence_Listing_ST25.txt

370

375

380

Asn Gly Trp Gln His Leu Glu Gln Ala Glu Lys Gly Tyr Glu Glu Trp
385 390 395 400

Leu Leu Asn Glu Ile Arg Arg Leu Glu Arg Leu Asp His Leu Ala Glu
405 410 415

Lys Phe Arg Gln Lys Ala Ser Ile His Glu Ala Trp Thr Asp Gly Lys
420 425 430

Glu Ala Met Leu Lys His Arg Asp Tyr Glu Thr Ala Thr Leu Ser Asp
435 440 445

Ile Lys Ala Leu Ile Arg Lys His Glu Ala Phe Glu Ser Asp Leu Ala
450 455 460

Ala His Gln Asp Arg Val Glu Gln Ile Ala Ala Ile Ala Gln Glu Leu
465 470 475 480

Asn Glu Leu Asp Tyr Tyr Asp Ser His Asn Val Asn Thr Pro Asp Gly
485 490 495

Leu Gln Glu Gly Pro Gly Gln Pro His Ser Pro Ile Pro Pro Leu Cys
500 505 510

Ile Tyr Ala Lys His Ser Leu Gln Ser Ser Gly Val Gly Gly Trp Ala
515 520 525

Gly Arg Gly Trp Gly Arg Leu Ser Pro Leu Ser Leu Cys Gly Leu Ala
530 535 540

Arg Arg Phe Pro Arg Pro Gly Trp Gly Asp Leu Gly Pro Ala Leu Leu
545 550 555 560

Val Trp

<210> 206

<211> 911

<212> PRT

<213> Artificial Sequence

<220>

<223> alpha-actinin-_4/m__Homo_sapiens__043707

<400> 206

Met Val Asp Tyr His Ala Ala Asn Gln Ser Tyr Gln Tyr Gly Pro Ser
1 5 10 15

Ser Ala Gly Asn Gly Ala Gly Gly Gly Gly Ser Met Gly Asp Tyr Met
20 25 30

ITI-08-PCT_Sequence_Listing_ST25.txt

Ala	Gln	Glu	Asp	Asp	Trp	Asp	Arg	Asp	Leu	Leu	Leu	Asp	Pro	Ala	Trp	35	40	45	
Glu	Lys	Gln	Gln	Arg	Lys	Thr	Phe	Thr	Ala	Trp	Cys	Asn	Ser	His	Leu	50	55	60	
Arg	Lys	Ala	Gly	Thr	Gln	Ile	Glu	Asn	Ile	Asp	Glu	Asp	Phe	Arg	Asp	65	70	75	80
Gly	Leu	Lys	Leu	Met	Leu	Leu	Leu	Glu	Val	Ile	Ser	Gly	Glu	Arg	Leu	85	90	95	
Pro	Lys	Pro	Glu	Arg	Gly	Lys	Met	Arg	Val	His	Lys	Ile	Asn	Asn	Val	100	105	110	
Asn	Lys	Ala	Leu	Asp	Phe	Ile	Ala	Ser	Lys	Gly	Val	Lys	Leu	Val	Ser	115	120	125	
Ile	Gly	Ala	Glu	Glu	Ile	Val	Asp	Gly	Asn	Ala	Lys	Met	Thr	Leu	Gly	130	135	140	
Met	Ile	Trp	Thr	Ile	Ile	Leu	Arg	Phe	Ala	Ile	Gln	Asp	Ile	Ser	Val	145	150	155	160
Glu	Glu	Thr	Ser	Ala	Lys	Glu	Gly	Leu	Leu	Leu	Trp	Cys	Gln	Arg	Lys	165	170	175	
Thr	Ala	Pro	Tyr	Lys	Asn	Val	Asn	Val	Gln	Asn	Phe	His	Ile	Ser	Trp	180	185	190	
Lys	Asp	Gly	Leu	Ala	Phe	Asn	Ala	Leu	Ile	His	Arg	His	Arg	Pro	Glu	195	200	205	
Leu	Ile	Glu	Tyr	Asp	Lys	Leu	Arg	Lys	Asp	Asp	Pro	Val	Thr	Asn	Leu	210	215	220	
Asn	Asn	Ala	Phe	Glu	Val	Ala	Glu	Lys	Tyr	Leu	Asp	Ile	Pro	Lys	Met	225	230	235	240
Leu	Asp	Ala	Glu	Asp	Ile	Val	Asn	Thr	Ala	Arg	Pro	Asp	Glu	Lys	Ala	245	250	255	
Ile	Met	Thr	Tyr	Val	Ser	Ser	Phe	Tyr	His	Ala	Phe	Ser	Gly	Ala	Gln	260	265	270	
Lys	Ala	Glu	Thr	Ala	Ala	Asn	Arg	Ile	Cys	Lys	Val	Leu	Ala	Val	Asn	275	280	285	
Gln	Glu	Asn	Glu	His	Leu	Met	Glu	Asp	Tyr	Glu	Lys	Leu	Ala	Ser	Asp	290	295	300	

ITI-08-PCT_Sequence_Listing_ST25.txt

Leu Leu Glu Trp Ile Arg Arg Thr Ile Pro Trp Leu Glu Asp Arg Val
 305 310 315 320
 Pro Gln Lys Thr Ile Gln Glu Met Gln Gln Lys Leu Glu Asp Phe Arg
 325 330 335
 Asp Tyr Arg Arg Val His Lys Pro Pro Lys Val Gln Glu Lys Cys Gln
 340 345 350
 Leu Glu Ile Asn Phe Asn Thr Leu Gln Thr Lys Leu Arg Leu Ser Asn
 355 360 365
 Arg Pro Ala Phe Met Pro Ser Glu Gly Lys Met Val Ser Asp Ile Asn
 370 375 380
 Asn Gly Trp Gln His Leu Glu Gln Ala Glu Lys Gly Tyr Glu Glu Trp
 385 390 395 400
 Leu Leu Asn Glu Ile Arg Arg Leu Glu Arg Leu Asp His Leu Ala Glu
 405 410 415
 Lys Phe Arg Gln Lys Ala Ser Ile His Glu Ala Trp Thr Asp Gly Lys
 420 425 430
 Glu Ala Met Leu Lys His Arg Asp Tyr Glu Thr Ala Thr Leu Ser Asp
 435 440 445
 Ile Lys Ala Leu Ile Arg Lys His Glu Ala Phe Glu Ser Asp Leu Ala
 450 455 460
 Ala His Gln Asp Arg Val Glu Gln Ile Ala Ala Ile Ala Gln Glu Leu
 465 470 475 480
 Asn Glu Leu Asp Tyr Tyr Asp Ser His Asn Val Asn Thr Arg Cys Gln
 485 490 495
 Lys Ile Cys Asp Gln Trp Asp Ala Leu Gly Ser Leu Thr His Ser Arg
 500 505 510
 Arg Glu Ala Leu Glu Lys Thr Glu Lys Gln Leu Glu Ala Ile Asp Gln
 515 520 525
 Leu His Leu Glu Tyr Ala Lys Arg Ala Ala Pro Phe Asn Asn Trp Met
 530 535 540
 Glu Ser Ala Met Glu Asp Leu Gln Asp Met Phe Ile Val His Thr Ile
 545 550 555 560
 Glu Glu Ile Glu Gly Leu Ile Ser Ala His Asp Gln Phe Lys Ser Thr
 565 570 575
 Leu Pro Asp Ala Asp Arg Glu Arg Glu Ala Ile Leu Ala Ile His Lys

ITI-08-PCT_Sequence_Listing_ST25.txt

580	585	590																	
Glu	Ala	Gln	Arg	Ile	Ala	Glu	Ser	Asn	His	Ile	Lys	Leu	Ser	Gly	Ser				
	595						600					605							
Asn	Pro	Tyr	Thr	Thr	Val	Thr	Pro	Gln	Ile	Ile	Asn	Ser	Lys	Trp	Glu				
	610					615					620								
Lys	Val	Gln	Gln	Leu	Val	Pro	Lys	Arg	Asp	His	Ala	Leu	Leu	Glu	Glu				
625				630					635					640					
Gln	Ser	Lys	Gln	Gln	Ser	Asn	Glu	His	Leu	Arg	Arg	Gln	Phe	Ala	Ser				
			645						650				655						
Gln	Ala	Asn	Val	Val	Gly	Pro	Trp	Ile	Gln	Thr	Lys	Met	Glu	Glu	Ile				
		660						665					670						
Gly	Arg	Ile	Ser	Ile	Glu	Met	Asn	Gly	Thr	Leu	Glu	Asp	Gln	Leu	Ser				
	675						680					685							
His	Leu	Lys	Gln	Tyr	Glu	Arg	Ser	Ile	Val	Asp	Tyr	Lys	Pro	Asn	Leu				
	690					695					700								
Asp	Leu	Leu	Glu	Gln	Gln	His	Gln	Leu	Ile	Gln	Glu	Ala	Leu	Ile	Phe				
705				710					715					720					
Asp	Asn	Lys	His	Thr	Asn	Tyr	Thr	Met	Glu	His	Ile	Arg	Val	Gly	Trp				
			725						730					735					
Glu	Gln	Leu	Leu	Thr	Thr	Ile	Ala	Arg	Thr	Ile	Asn	Glu	Val	Glu	Asn				
		740						745					750						
Gln	Ile	Leu	Thr	Arg	Asp	Ala	Lys	Gly	Ile	Ser	Gln	Glu	Gln	Met	Gln				
	755						760					765							
Glu	Phe	Arg	Ala	Ser	Phe	Asn	His	Phe	Asp	Lys	Asp	His	Gly	Gly	Ala				
	770					775					780								
Leu	Gly	Pro	Glu	Glu	Phe	Lys	Ala	Cys	Leu	Ile	Ser	Leu	Gly	Tyr	Asp				
785				790					795					800					
Val	Glu	Asn	Asp	Arg	Gln	Gly	Glu	Ala	Glu	Phe	Asn	Arg	Ile	Met	Ser				
			805						810					815					
Leu	Val	Asp	Pro	Asn	His	Ser	Gly	Leu	Val	Thr	Phe	Gln	Ala	Phe	Ile				
		820						825					830						
Asp	Phe	Met	Ser	Arg	Glu	Thr	Thr	Asp	Thr	Asp	Thr	Ala	Asp	Gln	Val				
	835						840					845							
Ile	Ala	Ser	Phe	Lys	Val	Leu	Ala	Gly	Asp	Lys	Asn	Phe	Ile	Thr	Ala				
	850					855					860								

ITI-08-PCT_Sequence_Listing_ST25.txt

Glu Glu Leu Arg Arg Glu Leu Pro Pro Asp Gln Ala Glu Tyr Cys Ile
865 870 875 880

Ala Arg Met Ala Pro Tyr Gln Gly Pro Asp Ala Val Pro Gly Ala Leu
885 890 895

Asp Tyr Lys Ser Phe Ser Thr Ala Leu Tyr Gly Glu Ser Asp Leu
900 905 910

<210> 207

<211> 198

<212> PRT

<213> Artificial Sequence

<220>

<223> alpha-methylacyl-coenzyme_A_racemase__Homo_sapiens__A0A024RE16

<400> 207

Met Ala Leu Gln Gly Ile Ser Val Met Glu Leu Ser Gly Leu Ala Pro
1 5 10 15

Gly Pro Phe Cys Ala Met Val Leu Ala Asp Phe Gly Ala Arg Val Val
20 25 30

Arg Val Asp Arg Pro Gly Ser Arg Tyr Asp Val Ser Arg Leu Gly Arg
35 40 45

Gly Lys Arg Ser Leu Val Leu Asp Leu Lys Gln Pro Arg Gly Ala Ala
50 55 60

Val Leu Arg Arg Leu Cys Lys Arg Ser Asp Val Leu Leu Glu Pro Phe
65 70 75 80

Arg Arg Gly Val Met Glu Lys Leu Gln Leu Gly Pro Glu Ile Leu Gln
85 90 95

Arg Glu Asn Pro Arg Leu Ile Tyr Ala Arg Leu Ser Gly Phe Gly Gln
100 105 110

Ser Gly Ser Phe Cys Arg Leu Ala Gly His Asp Ile Asn Tyr Leu Ala
115 120 125

Leu Ser Gly Gly Arg Asn Ser Ile Phe Lys Phe Phe Ser Val Glu Asn
130 135 140

Ser Glu Ile Glu Ser Val Gly Ser Thr Ser Arg Thr Glu His Val Gly
145 150 155 160

Trp Trp Ser Thr Phe Leu Tyr Asp Leu Gln Asp Ser Arg Trp Gly Ile
165 170 175

ITI-08-PCT_Sequence_Listing_ST25.txt

His Gly Cys Trp Ser Asn Arg Thr Pro Val Leu Arg Ala Ala Asp Gln
180 185 190

Arg Thr Trp Thr Lys Val
195

<210> 208

<211> 198

<212> PRT

<213> Artificial Sequence

<220>

<223> alpha-methylacyl-coenzyme_A_racemase__Homo_sapiens__A8KAC3

<400> 208

Met Ala Leu Gln Gly Ile Ser Val Val Glu Leu Ser Gly Leu Ala Pro
1 5 10 15

Gly Pro Phe Cys Ala Met Val Leu Ala Asp Phe Gly Ala Arg Val Val
20 25 30

Arg Val Asp Arg Pro Gly Ser Arg Tyr Asp Val Ser Arg Leu Gly Arg
35 40 45

Gly Lys Arg Ser Leu Val Leu Asp Leu Lys Gln Pro Arg Gly Ala Ala
50 55 60

Val Leu Arg Arg Leu Cys Lys Arg Ser Asp Val Leu Leu Glu Pro Phe
65 70 75 80

Arg Arg Gly Val Met Glu Lys Leu Gln Leu Gly Pro Glu Ile Leu Gln
85 90 95

Arg Glu Asn Pro Arg Leu Ile Tyr Ala Arg Leu Ser Gly Phe Gly Gln
100 105 110

Ser Gly Ser Phe Cys Arg Leu Ala Gly His Asp Ile Asn Tyr Leu Ala
115 120 125

Leu Ser Gly Gly Arg Asn Ser Ile Phe Lys Phe Phe Ser Val Glu Asn
130 135 140

Ser Glu Ile Glu Ser Val Gly Ser Thr Ser Arg Thr Glu His Val Gly
145 150 155 160

Trp Trp Ser Thr Phe Leu Tyr Asp Leu Gln Asp Ser Arg Trp Gly Ile
165 170 175

His Gly Cys Trp Ser Asn Arg Thr Pro Phe Leu Arg Ala Ala Asp Gln
180 185 190

ITI-08-PCT_Sequence_Listing_ST25.txt

Arg Thr Trp Thr Lys Val
195

<210> 209

<211> 920

<212> PRT

<213> Artificial Sequence

<220>

<223> ANDR__Homo_sapiens__P10275

<400> 209

Met Glu Val Gln Leu Gly Leu Gly Arg Val Tyr Pro Arg Pro Pro Ser
1 5 10 15

Lys Thr Tyr Arg Gly Ala Phe Gln Asn Leu Phe Gln Ser Val Arg Glu
20 25 30

Val Ile Gln Asn Pro Gly Pro Arg His Pro Glu Ala Ala Ser Ala Ala
35 40 45

Pro Pro Gly Ala Ser Leu Leu Leu Leu Gln Gln Gln Gln Gln Gln
50 55 60

Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
65 70 75 80

Glu Thr Ser Pro Arg Gln Gln Gln Gln Gln Gln Gly Glu Asp Gly Ser
85 90 95

Pro Gln Ala His Arg Arg Gly Pro Thr Gly Tyr Leu Val Leu Asp Glu
100 105 110

Glu Gln Gln Pro Ser Gln Pro Gln Ser Ala Leu Glu Cys His Pro Glu
115 120 125

Arg Gly Cys Val Pro Glu Pro Gly Ala Ala Val Ala Ala Ser Lys Gly
130 135 140

Leu Pro Gln Gln Leu Pro Ala Pro Pro Asp Glu Asp Asp Ser Ala Ala
145 150 155 160

Pro Ser Thr Leu Ser Leu Leu Gly Pro Thr Phe Pro Gly Leu Ser Ser
165 170 175

Cys Ser Ala Asp Leu Lys Asp Ile Leu Ser Glu Ala Ser Thr Met Gln
180 185 190

Leu Leu Gln Gln Gln Gln Gln Glu Ala Val Ser Glu Gly Ser Ser Ser
195 200 205

ITI-08-PCT_Sequence_Listing_ST25.txt

Gly	Arg	Ala	Arg	Glu	Ala	Ser	Gly	Ala	Pro	Thr	Ser	Ser	Lys	Asp	Asn	210	215	220
Tyr	Leu	Gly	Gly	Thr	Ser	Thr	Ile	Ser	Asp	Asn	Ala	Lys	Glu	Leu	Cys	225	230	235
Lys	Ala	Val	Ser	Val	Ser	Met	Gly	Leu	Gly	Val	Glu	Ala	Leu	Glu	His	245	250	255
Leu	Ser	Pro	Gly	Glu	Gln	Leu	Arg	Gly	Asp	Cys	Met	Tyr	Ala	Pro	Leu	260	265	270
Leu	Gly	Val	Pro	Pro	Ala	Val	Arg	Pro	Thr	Pro	Cys	Ala	Pro	Leu	Ala	275	280	285
Glu	Cys	Lys	Gly	Ser	Leu	Leu	Asp	Asp	Ser	Ala	Gly	Lys	Ser	Thr	Glu	290	295	300
Asp	Thr	Ala	Glu	Tyr	Ser	Pro	Phe	Lys	Gly	Gly	Tyr	Thr	Lys	Gly	Leu	305	310	315
Glu	Gly	Glu	Ser	Leu	Gly	Cys	Ser	Gly	Ser	Ala	Ala	Ala	Gly	Ser	Ser	325	330	335
Gly	Thr	Leu	Glu	Leu	Pro	Ser	Thr	Leu	Ser	Leu	Tyr	Lys	Ser	Gly	Ala	340	345	350
Leu	Asp	Glu	Ala	Ala	Ala	Tyr	Gln	Ser	Arg	Asp	Tyr	Tyr	Asn	Phe	Pro	355	360	365
Leu	Ala	Leu	Ala	Gly	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	His	Pro	His	370	375	380
Ala	Arg	Ile	Lys	Leu	Glu	Asn	Pro	Leu	Asp	Tyr	Gly	Ser	Ala	Trp	Ala	385	390	395
Ala	Ala	Ala	Ala	Gln	Cys	Arg	Tyr	Gly	Asp	Leu	Ala	Ser	Leu	His	Gly	405	410	415
Ala	Gly	Ala	Ala	Gly	Pro	Gly	Ser	Gly	Ser	Pro	Ser	Ala	Ala	Ala	Ser	420	425	430
Ser	Ser	Trp	His	Thr	Leu	Phe	Thr	Ala	Glu	Glu	Gly	Gln	Leu	Tyr	Gly	435	440	445
Pro	Cys	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	450	455	460
Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Glu	Ala	Gly	Ala	Val	Ala	Pro	465	470	475

ITI-08-PCT_Sequence_Listing_ST25.txt

Tyr	Gly	Tyr	Thr	Arg	Pro	Pro	Gln	Gly	Leu	Ala	Gly	Gln	Glu	Ser	Asp	
				485					490					495		
Phe	Thr	Ala	Pro	Asp	Val	Trp	Tyr	Pro	Gly	Gly	Met	Val	Ser	Arg	Val	
			500					505					510			
Pro	Tyr	Pro	Ser	Pro	Thr	Cys	Val	Lys	Ser	Glu	Met	Gly	Pro	Trp	Met	
		515					520					525				
Asp	Ser	Tyr	Ser	Gly	Pro	Tyr	Gly	Asp	Met	Arg	Leu	Glu	Thr	Ala	Arg	
	530					535					540					
Asp	His	Val	Leu	Pro	Ile	Asp	Tyr	Tyr	Phe	Pro	Pro	Gln	Lys	Thr	Cys	
545					550					555					560	
Leu	Ile	Cys	Gly	Asp	Glu	Ala	Ser	Gly	Cys	His	Tyr	Gly	Ala	Leu	Thr	
			565						570					575		
Cys	Gly	Ser	Cys	Lys	Val	Phe	Phe	Lys	Arg	Ala	Ala	Glu	Gly	Lys	Gln	
			580					585					590			
Lys	Tyr	Leu	Cys	Ala	Ser	Arg	Asn	Asp	Cys	Thr	Ile	Asp	Lys	Phe	Arg	
		595					600					605				
Arg	Lys	Asn	Cys	Pro	Ser	Cys	Arg	Leu	Arg	Lys	Cys	Tyr	Glu	Ala	Gly	
	610					615					620					
Met	Thr	Leu	Gly	Ala	Arg	Lys	Leu	Lys	Lys	Leu	Gly	Asn	Leu	Lys	Leu	
625					630					635					640	
Gln	Glu	Glu	Gly	Glu	Ala	Ser	Ser	Thr	Thr	Ser	Pro	Thr	Glu	Glu	Thr	
			645						650					655		
Thr	Gln	Lys	Leu	Thr	Val	Ser	His	Ile	Glu	Gly	Tyr	Glu	Cys	Gln	Pro	
			660					665					670			
Ile	Phe	Leu	Asn	Val	Leu	Glu	Ala	Ile	Glu	Pro	Gly	Val	Val	Cys	Ala	
		675					680					685				
Gly	His	Asp	Asn	Asn	Gln	Pro	Asp	Ser	Phe	Ala	Ala	Leu	Leu	Ser	Ser	
	690					695					700					
Leu	Asn	Glu	Leu	Gly	Glu	Arg	Gln	Leu	Val	His	Val	Val	Lys	Trp	Ala	
705					710					715					720	
Lys	Ala	Leu	Pro	Gly	Phe	Arg	Asn	Leu	His	Val	Asp	Asp	Gln	Met	Ala	
			725						730					735		
Val	Ile	Gln	Tyr	Ser	Trp	Met	Gly	Leu	Met	Val	Phe	Ala	Met	Gly	Trp	
			740					745					750			
Arg	Ser	Phe	Thr	Asn	Val	Asn	Ser	Arg	Met	Leu	Tyr	Phe	Ala	Pro	Asp	

ITI-08-PCT_Sequence_Listing_ST25.txt

755

760

765

Leu Val Phe Asn Glu Tyr Arg Met His Lys Ser Arg Met Tyr Ser Gln
770 775 780

Cys Val Arg Met Arg His Leu Ser Gln Glu Phe Gly Trp Leu Gln Ile
785 790 795 800

Thr Pro Gln Glu Phe Leu Cys Met Lys Ala Leu Leu Leu Phe Ser Ile
805 810 815

Ile Pro Val Asp Gly Leu Lys Asn Gln Lys Phe Phe Asp Glu Leu Arg
820 825 830

Met Asn Tyr Ile Lys Glu Leu Asp Arg Ile Ile Ala Cys Lys Arg Lys
835 840 845

Asn Pro Thr Ser Cys Ser Arg Arg Phe Tyr Gln Leu Thr Lys Leu Leu
850 855 860

Asp Ser Val Gln Pro Ile Ala Arg Glu Leu His Gln Phe Thr Phe Asp
865 870 875 880

Leu Leu Ile Lys Ser His Met Val Ser Val Asp Phe Pro Glu Met Met
885 890 895

Ala Glu Ile Ile Ser Val Gln Val Pro Lys Ile Leu Ser Gly Lys Val
900 905 910

Lys Pro Ile Tyr Phe His Thr Gln
915 920

<210> 210
<211> 412
<212> PRT
<213> Artificial Sequence

<220>
<223> ART-4__Homo_sapiens__Q9ULX3

<400> 210

Met Ala Pro Val Glu His Val Val Ala Asp Ala Gly Ala Phe Leu Arg
1 5 10 15

His Ala Ala Leu Gln Asp Ile Gly Lys Asn Ile Tyr Thr Ile Arg Glu
20 25 30

Val Val Thr Glu Ile Arg Asp Lys Ala Thr Arg Arg Arg Leu Ala Val
35 40 45

Leu Pro Tyr Glu Leu Arg Phe Lys Glu Pro Leu Pro Glu Tyr Val Arg

ITI-08-PCT_Sequence_Listing_ST25.txt

50	55	60														
Leu	Val	Thr	Glu	Phe	Ser	Lys	Lys	Thr	Gly	Asp	Tyr	Pro	Ser	Leu	Ser	
65					70					75					80	
Ala	Thr	Asp	Ile	Gln	Val	Leu	Ala	Leu	Thr	Tyr	Gln	Leu	Glu	Ala	Glu	
				85					90					95		
Phe	Val	Gly	Val	Ser	His	Leu	Lys	Gln	Glu	Pro	Gln	Lys	Val	Lys	Val	
			100					105					110			
Ser	Ser	Ser	Ile	Gln	His	Pro	Glu	Thr	Pro	Leu	His	Ile	Ser	Gly	Phe	
			115				120					125				
His	Leu	Pro	Tyr	Lys	Pro	Lys	Pro	Pro	Gln	Glu	Thr	Glu	Lys	Gly	His	
	130					135					140					
Ser	Ala	Cys	Glu	Pro	Glu	Asn	Leu	Glu	Phe	Ser	Ser	Phe	Met	Phe	Trp	
145					150					155					160	
Arg	Asn	Pro	Leu	Pro	Asn	Ile	Asp	His	Glu	Leu	Gln	Glu	Leu	Leu	Ile	
				165					170					175		
Asp	Arg	Gly	Glu	Asp	Val	Pro	Ser	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Asn	
			180					185					190			
Gly	Phe	Glu	Asp	Arg	Lys	Asp	Asp	Ser	Asp	Asp	Asp	Gly	Gly	Gly	Trp	
		195					200					205				
Ile	Thr	Pro	Ser	Asn	Ile	Lys	Gln	Ile	Gln	Gln	Glu	Leu	Glu	Gln	Cys	
	210					215					220					
Asp	Val	Pro	Glu	Asp	Val	Arg	Val	Gly	Cys	Leu	Thr	Thr	Asp	Phe	Ala	
225					230					235					240	
Met	Gln	Asn	Val	Leu	Leu	Gln	Met	Gly	Leu	His	Val	Leu	Ala	Val	Asn	
				245					250					255		
Gly	Met	Leu	Ile	Arg	Glu	Ala	Arg	Ser	Tyr	Ile	Leu	Arg	Cys	His	Gly	
			260					265					270			
Cys	Phe	Lys	Thr	Thr	Ser	Asp	Met	Ser	Arg	Val	Phe	Cys	Ser	His	Cys	
		275					280					285				
Gly	Asn	Lys	Thr	Leu	Lys	Lys	Val	Ser	Val	Thr	Val	Ser	Asp	Asp	Gly	
	290					295					300					
Thr	Leu	His	Met	His	Phe	Ser	Arg	Asn	Pro	Lys	Val	Leu	Asn	Pro	Arg	
305					310					315					320	
Gly	Leu	Arg	Tyr	Ser	Leu	Pro	Thr	Pro	Lys	Gly	Gly	Lys	Tyr	Ala	Ile	
				325					330					335		

ITI-08-PCT_Sequence_Listing_ST25.txt

Asn Pro His Leu Thr Glu Asp Gln Arg Phe Pro Gln Leu Arg Leu Ser
340 345 350

Gln Lys Ala Arg Gln Lys Thr Asn Val Phe Ala Pro Asp Tyr Ile Ala
355 360 365

Gly Val Ser Pro Phe Val Glu Asn Asp Ile Ser Ser Arg Ser Ala Thr
370 375 380

Leu Gln Val Arg Asp Ser Thr Leu Gly Ala Gly Arg Arg Arg Leu Asn
385 390 395 400

Pro Asn Ala Ser Arg Lys Lys Phe Val Lys Lys Arg
405 410

<210> 211

<211> 327

<212> PRT

<213> Artificial Sequence

<220>

<223> ARTC1/m__Homo_sapiens__P52961

<400> 211

Met Gln Met Pro Ala Met Met Ser Leu Leu Leu Val Ser Val Gly Leu
1 5 10 15

Met Glu Ala Leu Gln Ala Gln Ser His Pro Ile Thr Arg Arg Asp Leu
20 25 30

Phe Ser Gln Glu Ile Gln Leu Asp Met Ala Leu Ala Ser Phe Asp Asp
35 40 45

Gln Tyr Ala Gly Cys Ala Ala Ala Met Thr Ala Ala Leu Pro Asp Leu
50 55 60

Asn His Thr Glu Phe Gln Ala Asn Gln Val Tyr Ala Asp Ser Trp Thr
65 70 75 80

Leu Ala Ser Ser Gln Trp Gln Glu Arg Gln Ala Arg Trp Pro Glu Trp
85 90 95

Ser Leu Ser Pro Thr Arg Pro Ser Pro Pro Pro Leu Gly Phe Arg Asp
100 105 110

Glu His Gly Val Ala Leu Leu Ala Tyr Thr Ala Asn Ser Pro Leu His
115 120 125

Lys Glu Phe Asn Ala Ala Val Arg Glu Ala Gly Arg Ser Arg Ala His
130 135 140

ITI-08-PCT_Sequence_Listing_ST25.txt

Tyr Leu His His Phe Ser Phe Lys Thr Leu His Phe Leu Leu Thr Glu
 145 150 155 160
 Ala Leu Gln Leu Leu Gly Ser Gly Gln Arg Pro Pro Arg Cys His Gln
 165 170 175
 Val Phe Arg Gly Val His Gly Leu Arg Phe Arg Pro Ala Gly Pro Arg
 180 185 190
 Ala Thr Val Arg Leu Gly Gly Phe Ala Ser Ala Ser Leu Lys His Val
 195 200 205
 Ala Ala Gln Gln Phe Gly Glu Asp Thr Phe Phe Gly Ile Trp Thr Cys
 210 215 220
 Leu Gly Ala Pro Ile Lys Gly Tyr Ser Phe Phe Pro Gly Glu Glu Glu
 225 230 235 240
 Val Leu Ile Pro Pro Phe Glu Thr Phe Gln Val Ile Asn Ala Ser Arg
 245 250 255
 Leu Ala Gln Gly Pro Ala Arg Ile Tyr Leu Arg Ala Leu Gly Lys His
 260 265 270
 Ser Thr Tyr Asn Cys Glu Tyr Ile Lys Asp Lys Lys Cys Lys Ser Gly
 275 280 285
 Pro Cys His Leu Asp Asn Ser Ala Met Gly Gln Ser Pro Leu Ser Ala
 290 295 300
 Val Trp Ser Leu Leu Leu Leu Leu Trp Phe Leu Val Val Arg Ala Phe
 305 310 315 320
 Pro Asp Gly Pro Gly Leu Leu
 325

<210> 212
 <211> 344
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> AURKB__Homo_sapiens__Q96GD4

<400> 212

Met Ala Gln Lys Glu Asn Ser Tyr Pro Trp Pro Tyr Gly Arg Gln Thr
 1 5 10 15
 Ala Pro Ser Gly Leu Ser Thr Leu Pro Gln Arg Val Leu Arg Lys Glu
 20 25 30

ITI-08-PCT_Sequence_Listing_ST25.txt

Pro	Val	Thr	Pro	Ser	Ala	Leu	Val	Leu	Met	Ser	Arg	Ser	Asn	Val	Gln	35	40	45	
Pro	Thr	Ala	Ala	Pro	Gly	Gln	Lys	Val	Met	Glu	Asn	Ser	Ser	Gly	Thr	50	55	60	
Pro	Asp	Ile	Leu	Thr	Arg	His	Phe	Thr	Ile	Asp	Asp	Phe	Glu	Ile	Gly	65	70	75	80
Arg	Pro	Leu	Gly	Lys	Gly	Lys	Phe	Gly	Asn	Val	Tyr	Leu	Ala	Arg	Glu	85	90	95	
Lys	Lys	Ser	His	Phe	Ile	Val	Ala	Leu	Lys	Val	Leu	Phe	Lys	Ser	Gln	100	105	110	
Ile	Glu	Lys	Glu	Gly	Val	Glu	His	Gln	Leu	Arg	Arg	Glu	Ile	Glu	Ile	115	120	125	
Gln	Ala	His	Leu	His	His	Pro	Asn	Ile	Leu	Arg	Leu	Tyr	Asn	Tyr	Phe	130	135	140	
Tyr	Asp	Arg	Arg	Arg	Ile	Tyr	Leu	Ile	Leu	Glu	Tyr	Ala	Pro	Arg	Gly	145	150	155	160
Glu	Leu	Tyr	Lys	Glu	Leu	Gln	Lys	Ser	Cys	Thr	Phe	Asp	Glu	Gln	Arg	165	170	175	
Thr	Ala	Thr	Ile	Met	Glu	Glu	Leu	Ala	Asp	Ala	Leu	Met	Tyr	Cys	His	180	185	190	
Gly	Lys	Lys	Val	Ile	His	Arg	Asp	Ile	Lys	Pro	Glu	Asn	Leu	Leu	Leu	195	200	205	
Gly	Leu	Lys	Gly	Glu	Leu	Lys	Ile	Ala	Asp	Phe	Gly	Trp	Ser	Val	His	210	215	220	
Ala	Pro	Ser	Leu	Arg	Arg	Lys	Thr	Met	Cys	Gly	Thr	Leu	Asp	Tyr	Leu	225	230	235	240
Pro	Pro	Glu	Met	Ile	Glu	Gly	Arg	Met	His	Asn	Glu	Lys	Val	Asp	Leu	245	250	255	
Trp	Cys	Ile	Gly	Val	Leu	Cys	Tyr	Glu	Leu	Leu	Val	Gly	Asn	Pro	Pro	260	265	270	
Phe	Glu	Ser	Ala	Ser	His	Asn	Glu	Thr	Tyr	Arg	Arg	Ile	Val	Lys	Val	275	280	285	
Asp	Leu	Lys	Phe	Pro	Ala	Ser	Val	Pro	Met	Gly	Ala	Gln	Asp	Leu	Ile	290	295	300	

ITI-08-PCT_Sequence_Listing_ST25.txt

Ser Lys Leu Leu Arg His Asn Pro Ser Glu Arg Leu Pro Leu Ala Gln
305 310 315 320

Val Ser Ala His Pro Trp Val Arg Ala Asn Ser Arg Arg Val Leu Pro
325 330 335

Pro Ser Ala Leu Gln Ser Val Ala
340

<210> 213
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> B2MG__Homo_sapiens__P61769

<400> 213

Met Ser Arg Ser Val Ala Leu Ala Val Leu Ala Leu Leu Ser Leu Ser
1 5 10 15

Gly Leu Glu Ala Ile Gln Arg Thr Pro Lys Ile Gln Val Tyr Ser Arg
20 25 30

His Pro Ala Glu Asn Gly Lys Ser Asn Phe Leu Asn Cys Tyr Val Ser
35 40 45

Gly Phe His Pro Ser Asp Ile Glu Val Asp Leu Leu Lys Asn Gly Glu
50 55 60

Arg Ile Glu Lys Val Glu His Ser Asp Leu Ser Phe Ser Lys Asp Trp
65 70 75 80

Ser Phe Tyr Leu Leu Tyr Tyr Thr Glu Phe Thr Pro Thr Glu Lys Asp
85 90 95

Glu Tyr Ala Cys Arg Val Asn His Val Thr Leu Ser Gln Pro Lys Ile
100 105 110

Val Lys Trp Asp Arg Asp Met
115

<210> 214
<211> 378
<212> PRT
<213> Artificial Sequence

<220>
<223> B3GN5__Homo_sapiens__Q9BYG0

<400> 214

ITI-08-PCT_Sequence_Listing_ST25.txt

```

Met Arg Met Leu Val Ser Gly Arg Arg Val Lys Lys Trp Gln Leu Ile
1          5          10          15

Ile Gln Leu Phe Ala Thr Cys Phe Leu Ala Ser Leu Met Phe Phe Trp
          20          25          30

Glu Pro Ile Asp Asn His Ile Val Ser His Met Lys Ser Tyr Ser Tyr
          35          40          45

Arg Tyr Leu Ile Asn Ser Tyr Asp Phe Val Asn Asp Thr Leu Ser Leu
          50          55          60

Lys His Thr Ser Ala Gly Pro Arg Tyr Gln Tyr Leu Ile Asn His Lys
65          70          75          80

Glu Lys Cys Gln Ala Gln Asp Val Leu Leu Leu Leu Phe Val Lys Thr
          85          90          95

Ala Pro Glu Asn Tyr Asp Arg Arg Ser Gly Ile Arg Arg Thr Trp Gly
          100          105          110

Asn Glu Asn Tyr Val Arg Ser Gln Leu Asn Ala Asn Ile Lys Thr Leu
          115          120          125

Phe Ala Leu Gly Thr Pro Asn Pro Leu Glu Gly Glu Glu Leu Gln Arg
          130          135          140

Lys Leu Ala Trp Glu Asp Gln Arg Tyr Asn Asp Ile Ile Gln Gln Asp
145          150          155          160

Phe Val Asp Ser Phe Tyr Asn Leu Thr Leu Lys Leu Leu Met Gln Phe
          165          170          175

Ser Trp Ala Asn Thr Tyr Cys Pro His Ala Lys Phe Leu Met Thr Ala
          180          185          190

Asp Asp Asp Ile Phe Ile His Met Pro Asn Leu Ile Glu Tyr Leu Gln
          195          200          205

Ser Leu Glu Gln Ile Gly Val Gln Asp Phe Trp Ile Gly Arg Val His
          210          215          220

Arg Gly Ala Pro Pro Ile Arg Asp Lys Ser Ser Lys Tyr Tyr Val Ser
225          230          235          240

Tyr Glu Met Tyr Gln Trp Pro Ala Tyr Pro Asp Tyr Thr Ala Gly Ala
          245          250          255

Ala Tyr Val Ile Ser Gly Asp Val Ala Ala Lys Val Tyr Glu Ala Ser
          260          265          270

```


ITI-08-PCT_Sequence_Listing_ST25.txt

Gln Thr Leu Asn Ser Ser Leu Tyr Ile Asp Asp Val Phe Met Gly Leu
275 280 285

Cys Ala Asn Lys Ile Gly Ile Val Pro Gln Asp His Val Phe Phe Ser
290 295 300

Gly Glu Gly Lys Thr Pro Tyr His Pro Cys Ile Tyr Glu Lys Met Met
305 310 315 320

Thr Ser His Gly His Leu Glu Asp Leu Gln Asp Leu Trp Lys Asn Ala
325 330 335

Thr Asp Pro Lys Val Lys Thr Ile Ser Lys Gly Phe Phe Gly Gln Ile
340 345 350

Tyr Cys Arg Leu Met Lys Ile Ile Leu Leu Cys Lys Ile Ser Tyr Val
355 360 365

Asp Thr Tyr Pro Cys Arg Ala Ala Phe Ile
370 375

<210> 215

<211> 533

<212> PRT

<213> Artificial Sequence

<220>

<223> B4GN1__Homo_sapiens__Q00973

<400> 215

Met Trp Leu Gly Arg Arg Ala Leu Cys Ala Leu Val Leu Leu Ala
1 5 10 15

Cys Ala Ser Leu Gly Leu Leu Tyr Ala Ser Thr Arg Asp Ala Pro Gly
20 25 30

Leu Arg Leu Pro Leu Ala Pro Trp Ala Pro Pro Gln Ser Pro Arg Arg
35 40 45

Pro Glu Leu Pro Asp Leu Ala Pro Glu Pro Arg Tyr Ala His Ile Pro
50 55 60

Val Arg Ile Lys Glu Gln Val Val Gly Leu Leu Ala Trp Asn Asn Cys
65 70 75 80

Ser Cys Glu Ser Ser Gly Gly Gly Leu Pro Leu Pro Phe Gln Lys Gln
85 90 95

Val Arg Ala Ile Asp Leu Thr Lys Ala Phe Asp Pro Ala Glu Leu Arg
100 105 110

ITI-08-PCT_Sequence_Listing_ST25.txt

Ala	Ala	Ser	Ala	Thr	Arg	Glu	Gln	Glu	Phe	Gln	Ala	Phe	Leu	Ser	Arg	115	120	125	
Ser	Gln	Ser	Pro	Ala	Asp	Gln	Leu	Leu	Ile	Ala	Pro	Ala	Asn	Ser	Pro	130	135	140	
Leu	Gln	Tyr	Pro	Leu	Gln	Gly	Val	Glu	Val	Gln	Pro	Leu	Arg	Ser	Ile	145	150	155	160
Leu	Val	Pro	Gly	Leu	Ser	Leu	Gln	Ala	Ala	Ser	Gly	Gln	Glu	Val	Tyr	165	170	175	
Gln	Val	Asn	Leu	Thr	Ala	Ser	Leu	Gly	Thr	Trp	Asp	Val	Ala	Gly	Glu	180	185	190	
Val	Thr	Gly	Val	Thr	Leu	Thr	Gly	Glu	Gly	Gln	Ala	Asp	Leu	Thr	Leu	195	200	205	
Val	Ser	Pro	Gly	Leu	Asp	Gln	Leu	Asn	Arg	Gln	Leu	Gln	Leu	Val	Thr	210	215	220	
Tyr	Ser	Ser	Arg	Ser	Tyr	Gln	Thr	Asn	Thr	Ala	Asp	Thr	Val	Arg	Phe	225	230	235	240
Ser	Thr	Glu	Gly	His	Glu	Ala	Ala	Phe	Thr	Ile	Arg	Ile	Arg	His	Pro	245	250	255	
Pro	Asn	Pro	Arg	Leu	Tyr	Pro	Pro	Gly	Ser	Leu	Pro	Gln	Gly	Ala	Gln	260	265	270	
Tyr	Asn	Ile	Ser	Ala	Leu	Val	Thr	Ile	Ala	Thr	Lys	Thr	Phe	Leu	Arg	275	280	285	
Tyr	Asp	Arg	Leu	Arg	Ala	Leu	Ile	Thr	Ser	Ile	Arg	Arg	Phe	Tyr	Pro	290	295	300	
Thr	Val	Thr	Val	Val	Ile	Ala	Asp	Asp	Ser	Asp	Lys	Pro	Glu	Arg	Val	305	310	315	320
Ser	Gly	Pro	Tyr	Val	Glu	His	Tyr	Leu	Met	Pro	Phe	Gly	Lys	Gly	Trp	325	330	335	
Phe	Ala	Gly	Arg	Asn	Leu	Ala	Val	Ser	Gln	Val	Thr	Thr	Lys	Tyr	Val	340	345	350	
Leu	Trp	Val	Asp	Asp	Asp	Phe	Val	Phe	Thr	Ala	Arg	Thr	Arg	Leu	Glu	355	360	365	
Arg	Leu	Val	Asp	Val	Leu	Glu	Arg	Thr	Pro	Leu	Asp	Leu	Val	Gly	Gly	370	375	380	
Ala	Val	Arg	Glu	Ile	Ser	Gly	Phe	Ala	Thr	Thr	Tyr	Arg	Gln	Leu	Leu				

ITI-08-PCT_Sequence_Listing_ST25.txt

385 390 395 400

Ser Val Glu Pro Gly Ala Pro Gly Leu Gly Asn Cys Leu Arg Gln Arg
405 410 415

Arg Gly Phe His His Glu Leu Val Gly Phe Pro Gly Cys Val Val Thr
420 425 430

Asp Gly Val Val Asn Phe Phe Leu Ala Arg Thr Asp Lys Val Arg Glu
435 440 445

Val Gly Phe Asp Pro Arg Leu Ser Arg Val Ala His Leu Glu Phe Phe
450 455 460

Leu Asp Gly Leu Gly Ser Leu Arg Val Gly Ser Cys Ser Asp Val Val
465 470 475 480

Val Asp His Ala Ser Lys Leu Lys Leu Pro Trp Thr Ser Arg Asp Ala
485 490 495

Gly Ala Glu Thr Tyr Ala Arg Tyr Arg Tyr Pro Gly Ser Leu Asp Glu
500 505 510

Ser Gln Met Ala Lys His Arg Leu Leu Phe Phe Lys His Arg Leu Gln
515 520 525

Cys Met Thr Ser Gln
530

<210> 216
<211> 282
<212> PRT
<213> Artificial Sequence

<220>
<223> B7H4__Homo_sapiens__Q7Z7D3

<400> 216

Met Ala Ser Leu Gly Gln Ile Leu Phe Trp Ser Ile Ile Ser Ile Ile
1 5 10 15

Ile Ile Leu Ala Gly Ala Ile Ala Leu Ile Ile Gly Phe Gly Ile Ser
20 25 30

Gly Arg His Ser Ile Thr Val Thr Thr Val Ala Ser Ala Gly Asn Ile
35 40 45

Gly Glu Asp Gly Ile Leu Ser Cys Thr Phe Glu Pro Asp Ile Lys Leu
50 55 60

Ser Asp Ile Val Ile Gln Trp Leu Lys Glu Gly Val Leu Gly Leu Val

ITI-08-PCT_Sequence_Listing_ST25.txt

```

65              70              75              80
His Glu Phe Lys Glu Gly Lys Asp Glu Leu Ser Glu Gln Asp Glu Met
      85              90              95
Phe Arg Gly Arg Thr Ala Val Phe Ala Asp Gln Val Ile Val Gly Asn
      100             105             110
Ala Ser Leu Arg Leu Lys Asn Val Gln Leu Thr Asp Ala Gly Thr Tyr
      115             120             125
Lys Cys Tyr Ile Ile Thr Ser Lys Gly Lys Gly Asn Ala Asn Leu Glu
      130             135             140
Tyr Lys Thr Gly Ala Phe Ser Met Pro Glu Val Asn Val Asp Tyr Asn
145             150             155             160
Ala Ser Ser Glu Thr Leu Arg Cys Glu Ala Pro Arg Trp Phe Pro Gln
      165             170             175
Pro Thr Val Val Trp Ala Ser Gln Val Asp Gln Gly Ala Asn Phe Ser
      180             185             190
Glu Val Ser Asn Thr Ser Phe Glu Leu Asn Ser Glu Asn Val Thr Met
      195             200             205
Lys Val Val Ser Val Leu Tyr Asn Val Thr Ile Asn Asn Thr Tyr Ser
      210             215             220
Cys Met Ile Glu Asn Asp Ile Ala Lys Ala Thr Gly Asp Ile Lys Val
225             230             235             240
Thr Glu Ser Glu Ile Lys Arg Arg Ser His Leu Gln Leu Leu Asn Ser
      245             250             255
Lys Ala Ser Leu Cys Val Ser Ser Phe Phe Ala Ile Ser Trp Ala Leu
      260             265             270
Leu Pro Leu Ser Pro Tyr Leu Met Leu Lys
      275             280

```

<210> 217

<211> 43

<212> PRT

<213> Artificial Sequence

<220>

<223> BAGE-1__Homo_sapiens__Q13072

<400> 217

```

Met Ala Ala Arg Ala Val Phe Leu Ala Leu Ser Ala Gln Leu Leu Gln

```

ITI-08-PCT_Sequence_Listing_ST25.txt

```

1              5              10              15
Ala Arg Leu Met Lys Glu Glu Ser Pro Val Val Ser Trp Arg Leu Glu
      20              25              30

Pro Glu Asp Gly Thr Ala Leu Cys Phe Ile Phe
      35              40

<210> 218
<211> 385
<212> PRT
<213> Artificial Sequence

<220>
<223> BASI__Homo_sapiens__P35613

<400> 218

Met Ala Ala Ala Leu Phe Val Leu Leu Gly Phe Ala Leu Leu Gly Thr
1              5              10              15
His Gly Ala Ser Gly Ala Ala Gly Phe Val Gln Ala Pro Leu Ser Gln
      20              25              30
Gln Arg Trp Val Gly Gly Ser Val Glu Leu His Cys Glu Ala Val Gly
      35              40              45
Ser Pro Val Pro Glu Ile Gln Trp Trp Phe Glu Gly Gln Gly Pro Asn
      50              55              60
Asp Thr Cys Ser Gln Leu Trp Asp Gly Ala Arg Leu Asp Arg Val His
65              70              75              80
Ile His Ala Thr Tyr His Gln His Ala Ala Ser Thr Ile Ser Ile Asp
      85              90              95
Thr Leu Val Glu Glu Asp Thr Gly Thr Tyr Glu Cys Arg Ala Ser Asn
      100             105             110
Asp Pro Asp Arg Asn His Leu Thr Arg Ala Pro Arg Val Lys Trp Val
      115             120             125
Arg Ala Gln Ala Val Val Leu Val Leu Glu Pro Gly Thr Val Phe Thr
      130             135             140
Thr Val Glu Asp Leu Gly Ser Lys Ile Leu Leu Thr Cys Ser Leu Asn
145             150             155             160
Asp Ser Ala Thr Glu Val Thr Gly His Arg Trp Leu Lys Gly Gly Val
      165             170             175
Val Leu Lys Glu Asp Ala Leu Pro Gly Gln Lys Thr Glu Phe Lys Val

```

ITI-08-PCT_Sequence_Listing_ST25.txt

180

185

190

Asp Ser Asp Asp Gln Trp Gly Glu Tyr Ser Cys Val Phe Leu Pro Glu
195 200 205

Pro Met Gly Thr Ala Asn Ile Gln Leu His Gly Pro Pro Arg Val Lys
210 215 220

Ala Val Lys Ser Ser Glu His Ile Asn Glu Gly Glu Thr Ala Met Leu
225 230 235 240

Val Cys Lys Ser Glu Ser Val Pro Pro Val Thr Asp Trp Ala Trp Tyr
245 250 255

Lys Ile Thr Asp Ser Glu Asp Lys Ala Leu Met Asn Gly Ser Glu Ser
260 265 270

Arg Phe Phe Val Ser Ser Ser Gln Gly Arg Ser Glu Leu His Ile Glu
275 280 285

Asn Leu Asn Met Glu Ala Asp Pro Gly Gln Tyr Arg Cys Asn Gly Thr
290 295 300

Ser Ser Lys Gly Ser Asp Gln Ala Ile Ile Thr Leu Arg Val Arg Ser
305 310 315 320

His Leu Ala Ala Leu Trp Pro Phe Leu Gly Ile Val Ala Glu Val Leu
325 330 335

Val Leu Val Thr Ile Ile Phe Ile Tyr Glu Lys Arg Arg Lys Pro Glu
340 345 350

Asp Val Leu Asp Asp Asp Asp Ala Gly Ser Ala Pro Leu Lys Ser Ser
355 360 365

Gly Gln His Gln Asn Asp Lys Gly Lys Asn Val Arg Gln Arg Asn Ser
370 375 380

Ser
385

<210> 219

<211> 239

<212> PRT

<213> Artificial Sequence

<220>

<223> BCL-2__Homo_sapiens__A9QXG9

<400> 219

Met Ala His Ala Gly Arg Thr Gly Tyr Asp Asn Arg Glu Ile Val Met

ITI-08-PCT_Sequence_Listing_ST25.txt

```

1           5           10           15
Lys Tyr Ile His Tyr Lys Leu Ser Gln Arg Gly Tyr Glu Trp Asp Ala
      20           25           30
Gly Asp Val Gly Ala Ala Pro Pro Gly Ala Ala Pro Ala Pro Gly Ile
      35           40           45
Phe Ser Ser Gln Pro Gly His Thr Pro His Pro Ala Ala Ser Arg Asp
      50           55           60
Pro Val Ala Arg Thr Ser Pro Leu Gln Thr Pro Ala Ala Pro Gly Ala
      65           70           75           80
Ala Ala Gly Pro Ala Leu Ser Pro Val Pro Pro Val Val His Leu Thr
      85           90           95
Leu Arg Gln Ala Gly Asp Asp Phe Ser Arg Arg Tyr Arg Arg Asp Phe
      100           105           110
Ala Glu Met Ser Ser Gln Leu His Leu Thr Pro Phe Thr Ala Arg Gly
      115           120           125
Arg Phe Ala Thr Val Val Glu Glu Leu Phe Arg Asp Gly Val Asn Trp
      130           135           140
Gly Arg Ile Val Ala Phe Phe Glu Phe Gly Gly Val Met Cys Val Glu
      145           150           155           160
Ser Val Asn Arg Glu Met Ser Pro Leu Val Asp Asn Ile Ala Leu Trp
      165           170           175
Met Thr Glu Tyr Leu Asn Arg His Leu His Thr Trp Ile Gln Asp Asn
      180           185           190
Gly Gly Trp Asp Ala Phe Val Glu Leu Tyr Gly Pro Ser Met Arg Pro
      195           200           205
Leu Phe Asp Phe Ser Trp Leu Ser Leu Lys Thr Leu Leu Ser Leu Ala
      210           215           220
Leu Val Gly Ala Cys Ile Thr Leu Gly Ala Tyr Leu Ser His Lys
      225           230           235
<210> 220
<211> 429
<212> PRT
<213> Artificial Sequence

<220>
<223> bcr/abl__Homo_sapiens__A9UEZ4

```

ITI-08-PCT_Sequence_Listing_ST25.txt

<400> 220

```

Met Val Asp Pro Val Gly Phe Ala Glu Ala Trp Lys Ala Gln Phe Pro
1           5           10           15

Asp Ser Glu Pro Pro Arg Met Glu Leu Arg Ser Val Gly Asp Ile Glu
          20           25           30

Gln Glu Leu Glu Arg Cys Lys Ala Ser Ile Arg Arg Leu Glu Gln Glu
          35           40           45

Val Asn Gln Glu Arg Phe Arg Met Ile Tyr Leu Gln Thr Leu Leu Ala
50           55           60

Lys Glu Lys Lys Ser Tyr Asp Arg Gln Arg Trp Gly Phe Arg Arg Ala
65           70           75           80

Ala Gln Ala Pro Asp Gly Ala Ser Glu Pro Arg Ala Ser Ala Ser Arg
          85           90           95

Pro Gln Pro Ala Pro Ala Asp Gly Ala Asp Pro Pro Pro Ala Glu Glu
          100          105          110

Pro Glu Ala Arg Pro Asp Gly Glu Gly Ser Pro Gly Lys Ala Arg Pro
          115          120          125

Gly Thr Ala Arg Arg Pro Gly Ala Ala Ala Ser Gly Glu Arg Asp Asp
          130          135          140

Arg Gly Pro Pro Ala Ser Val Ala Ala Leu Arg Ser Asn Phe Glu Arg
145           150           155           160

Ile Arg Lys Gly His Gly Gln Pro Gly Ala Asp Ala Glu Lys Pro Phe
          165          170          175

Tyr Val Asn Val Glu Phe His His Glu Arg Gly Leu Val Lys Val Asn
          180          185          190

Asp Lys Glu Val Ser Asp Arg Ile Ser Ser Leu Gly Ser Gln Ala Met
          195          200          205

Gln Met Glu Arg Lys Lys Ser Gln His Gly Ala Gly Ser Ser Val Gly
          210          215          220

Asp Ala Ser Arg Pro Pro Tyr Arg Gly Arg Ser Ser Glu Ser Ser Cys
225           230           235           240

Gly Val Asp Gly Asp Tyr Glu Asp Ala Glu Leu Asn Pro Arg Phe Leu
          245          250          255

Lys Asp Asn Leu Ile Asp Ala Asn Gly Gly Ser Arg Pro Pro Trp Pro
          260          265          270

```


ITI-08-PCT_Sequence_Listing_ST25.txt

Pro Leu Glu Tyr Gln Pro Tyr Gln Ser Ile Tyr Val Gly Gly Met Met
275 280 285

Glu Gly Glu Gly Lys Gly Pro Leu Leu Arg Ser Gln Ser Thr Ser Glu
290 295 300

Gln Glu Lys Arg Leu Thr Trp Pro Arg Arg Ser Tyr Ser Pro Arg Ser
305 310 315 320

Phe Glu Asp Cys Gly Gly Gly Tyr Thr Pro Asp Cys Ser Ser Asn Glu
325 330 335

Asn Leu Thr Ser Ser Glu Glu Asp Phe Ser Ser Gly Gln Ser Ser Arg
340 345 350

Val Ser Pro Ser Pro Thr Thr Tyr Arg Met Phe Arg Asp Lys Ser Arg
355 360 365

Ser Pro Ser Gln Asn Ser Gln Gln Ser Phe Asp Ser Ser Ser Pro Pro
370 375 380

Thr Pro Gln Cys His Lys Arg His Arg His Cys Pro Val Val Val Ser
385 390 395 400

Glu Ala Thr Ile Val Gly Val Arg Lys Thr Gly Gln Ile Trp Pro Asn
405 410 415

Asp Gly Glu Gly Ala Phe His Gly Asp Ala Asp Gly Gly
420 425

<210> 221

<211> 554

<212> PRT

<213> Artificial Sequence

<220>

<223> bcr/abl__Homo_sapiens__A9UEZ7

<400> 221

Met Val Asp Pro Val Gly Phe Ala Glu Ala Trp Lys Ala Gln Phe Pro
1 5 10 15

Asp Ser Glu Pro Pro Arg Met Glu Leu Arg Ser Val Gly Asp Ile Glu
20 25 30

Gln Glu Leu Glu Arg Cys Lys Ala Ser Ile Arg Arg Leu Glu Gln Glu
35 40 45

Val Asn Gln Glu Arg Phe Arg Met Ile Tyr Leu Gln Thr Leu Leu Ala
50 55 60

ITI-08-PCT_Sequence_Listing_ST25.txt

Lys	Glu	Lys	Lys	Ser	Tyr	Asp	Arg	Gln	Arg	Trp	Gly	Phe	Arg	Arg	Ala	65	70	75	80
Ala	Gln	Ala	Pro	Asp	Gly	Ala	Ser	Glu	Pro	Arg	Ala	Ser	Ala	Ser	Arg	85	90	95	
Pro	Gln	Pro	Ala	Pro	Ala	Asp	Gly	Ala	Asp	Pro	Pro	Pro	Ala	Glu	Glu	100	105	110	
Pro	Glu	Ala	Arg	Pro	Asp	Gly	Glu	Gly	Ser	Pro	Gly	Lys	Ala	Arg	Pro	115	120	125	
Gly	Thr	Ala	Arg	Arg	Pro	Gly	Ala	Ala	Ala	Ser	Gly	Glu	Arg	Asp	Asp	130	135	140	
Arg	Gly	Pro	Pro	Ala	Ser	Val	Ala	Ala	Leu	Arg	Ser	Asn	Phe	Glu	Arg	145	150	155	160
Ile	Arg	Lys	Gly	His	Gly	Gln	Pro	Gly	Ala	Asp	Ala	Glu	Lys	Pro	Phe	165	170	175	
Tyr	Val	Asn	Val	Glu	Phe	His	His	Glu	Arg	Gly	Leu	Val	Lys	Val	Asn	180	185	190	
Asp	Lys	Glu	Val	Ser	Asp	Arg	Ile	Ser	Ser	Leu	Gly	Ser	Gln	Ala	Met	195	200	205	
Gln	Met	Glu	Arg	Lys	Lys	Ser	Gln	His	Gly	Ala	Gly	Ser	Ser	Val	Gly	210	215	220	
Asp	Ala	Ser	Arg	Pro	Pro	Tyr	Arg	Gly	Arg	Ser	Ser	Glu	Ser	Ser	Cys	225	230	235	240
Gly	Val	Asp	Gly	Asp	Tyr	Glu	Asp	Ala	Glu	Leu	Asn	Pro	Arg	Phe	Leu	245	250	255	
Lys	Asp	Asn	Leu	Ile	Asp	Ala	Asn	Gly	Gly	Ser	Arg	Pro	Pro	Trp	Pro	260	265	270	
Pro	Leu	Glu	Tyr	Gln	Pro	Tyr	Gln	Ser	Ile	Tyr	Val	Gly	Gly	Met	Met	275	280	285	
Glu	Gly	Glu	Gly	Lys	Gly	Pro	Leu	Leu	Arg	Ser	Gln	Ser	Thr	Ser	Glu	290	295	300	
Gln	Glu	Lys	Arg	Leu	Thr	Trp	Pro	Arg	Arg	Ser	Tyr	Ser	Pro	Arg	Ser	305	310	315	320
Phe	Glu	Asp	Cys	Gly	Gly	Gly	Tyr	Thr	Pro	Asp	Cys	Ser	Ser	Asn	Glu	325	330	335	

ITI-08-PCT_Sequence_Listing_ST25.txt

Asn Leu Thr Ser Ser Glu Glu Asp Phe Ser Ser Gly Gln Ser Ser Arg
340 345 350

Val Ser Pro Ser Pro Thr Thr Tyr Arg Met Phe Arg Asp Lys Ser Arg
355 360 365

Ser Pro Ser Gln Asn Ser Gln Gln Ser Phe Asp Ser Ser Ser Pro Pro
370 375 380

Thr Pro Gln Cys His Lys Arg His Arg His Cys Pro Val Val Val Ser
385 390 395 400

Glu Ala Thr Ile Val Gly Val Arg Lys Thr Gly Gln Ile Trp Pro Asn
405 410 415

Asp Gly Glu Gly Ala Phe His Gly Asp Ala Asp Gly Ser Phe Gly Thr
420 425 430

Pro Pro Gly Tyr Gly Cys Ala Ala Asp Arg Ala Glu Glu Gln Arg Arg
435 440 445

His Gln Asp Gly Leu Pro Tyr Ile Asp Asp Ser Pro Ser Ser Ser Pro
450 455 460

His Leu Ser Ser Lys Gly Arg Gly Ser Arg Asp Ala Leu Val Ser Gly
465 470 475 480

Ala Leu Glu Ser Thr Lys Ala Ser Glu Leu Asp Leu Glu Lys Gly Leu
485 490 495

Glu Met Arg Lys Trp Val Leu Ser Gly Ile Leu Ala Ser Glu Glu Thr
500 505 510

Tyr Leu Ser His Leu Glu Ala Leu Leu Leu Pro Met Lys Pro Leu Lys
515 520 525

Ala Ala Ala Thr Thr Ser Gln Pro Val Leu Thr Ser Gln Gln Ile Glu
530 535 540

Thr Ile Phe Phe Lys Val Pro Asp Leu Leu
545 550

<210> 222
<211> 514
<212> PRT
<213> Artificial Sequence

<220>
<223> bcr/abl__Homo_sapiens__A9UEZ8

<400> 222

ITI-08-PCT_Sequence_Listing_ST25.txt

```

Met Val Asp Pro Val Gly Phe Ala Glu Ala Trp Lys Ala Gln Phe Pro
1          5          10          15

Asp Ser Glu Pro Pro Arg Met Glu Leu Arg Ser Val Gly Asp Ile Glu
          20          25          30

Gln Glu Leu Glu Arg Cys Lys Ala Ser Ile Arg Arg Leu Glu Gln Glu
          35          40          45

Val Asn Gln Glu Arg Phe Arg Met Ile Tyr Leu Gln Thr Leu Leu Ala
          50          55          60

Lys Glu Lys Lys Ser Tyr Asp Arg Gln Arg Trp Gly Phe Arg Arg Ala
65          70          75          80

Ala Gln Ala Pro Asp Gly Ala Ser Glu Pro Arg Ala Ser Ala Ser Arg
          85          90          95

Pro Gln Pro Ala Pro Ala Asp Gly Ala Asp Pro Pro Pro Ala Glu Glu
          100          105          110

Pro Glu Ala Arg Pro Asp Gly Glu Gly Ser Pro Gly Lys Ala Arg Pro
          115          120          125

Gly Thr Ala Arg Arg Pro Gly Ala Ala Ala Ser Gly Glu Arg Asp Asp
          130          135          140

Arg Gly Pro Pro Ala Ser Val Ala Ala Leu Arg Ser Asn Phe Glu Arg
145          150          155          160

Ile Arg Lys Gly His Gly Gln Pro Gly Ala Asp Ala Glu Lys Pro Phe
          165          170          175

Tyr Val Asn Val Glu Phe His His Glu Arg Gly Leu Val Lys Val Asn
          180          185          190

Asp Lys Glu Val Ser Asp Arg Ile Ser Ser Leu Gly Ser Gln Ala Met
          195          200          205

Gln Met Glu Arg Lys Lys Ser Gln His Gly Ala Gly Ser Ser Val Gly
          210          215          220

Asp Ala Ser Arg Pro Pro Tyr Arg Gly Arg Ser Ser Glu Ser Ser Cys
225          230          235          240

Gly Val Asp Gly Asp Tyr Glu Asp Ala Glu Leu Asn Pro Arg Phe Leu
          245          250          255

Lys Asp Asn Leu Ile Asp Ala Asn Gly Gly Ser Arg Pro Pro Trp Pro
          260          265          270

Pro Leu Glu Tyr Gln Pro Tyr Gln Ser Ile Tyr Val Gly Gly Met Met

```

ITI-08-PCT_Sequence_Listing_ST25.txt

```

275                280                285
Glu Gly Glu Gly Lys Gly Pro Leu Leu Arg Ser Gln Ser Thr Ser Glu
290                295                300
Gln Glu Lys Arg Leu Thr Trp Pro Arg Arg Ser Tyr Ser Pro Arg Ser
305                310                315                320
Phe Glu Asp Cys Gly Gly Gly Tyr Thr Pro Asp Cys Ser Ser Asn Glu
325                330                335
Asn Leu Thr Ser Ser Glu Glu Asp Phe Ser Ser Gly Gln Ser Ser Arg
340                345                350
Val Ser Pro Ser Pro Thr Thr Tyr Arg Met Phe Arg Asp Lys Ser Arg
355                360                365
Ser Pro Ser Gln Asn Ser Gln Gln Ser Phe Asp Ser Ser Ser Pro Pro
370                375                380
Thr Pro Gln Cys His Lys Arg His Arg His Cys Pro Val Val Val Ser
385                390                395                400
Glu Ala Thr Ile Val Gly Val Arg Lys Thr Gly Gln Ile Trp Pro Asn
405                410                415
Asp Gly Glu Gly Ala Phe His Gly Asp Ala Asp Gly Ser Phe Gly Thr
420                425                430
Pro Pro Gly Tyr Gly Cys Ala Ala Asp Arg Ala Glu Glu Gln Arg Arg
435                440                445
His Gln Asp Gly Leu Pro Tyr Ile Asp Asp Ser Pro Ser Ser Ser Pro
450                455                460
His Leu Ser Ser Lys Gly Arg Gly Ser Arg Asp Ala Leu Val Ser Gly
465                470                475                480
Ala Leu Glu Ser Thr Lys Ala Ser Glu Leu Asp Leu Glu Lys Gly Leu
485                490                495
Glu Met Arg Lys Trp Val Leu Ser Gly Ile Leu Ala Ser Glu Glu Ile
500                505                510

```

Thr Leu

<210> 223
 <211> 441
 <212> PRT
 <213> Artificial Sequence

<220>

ITI-08-PCT_Sequence_Listing_ST25.txt

<223> bcr/abl__Homo_sapiens__A9UEZ9

<400> 223

```

Met Val Asp Pro Val Gly Phe Ala Glu Ala Trp Lys Ala Gln Phe Pro
1          5          10          15

Asp Ser Glu Pro Pro Arg Met Glu Leu Arg Ser Val Gly Asp Ile Glu
          20          25          30

Gln Glu Leu Glu Arg Cys Lys Ala Ser Ile Arg Arg Leu Glu Gln Glu
          35          40          45

Val Asn Gln Glu Arg Phe Arg Met Ile Tyr Leu Gln Thr Leu Leu Ala
          50          55          60

Lys Glu Lys Lys Ser Tyr Asp Arg Gln Arg Trp Gly Phe Arg Arg Ala
65          70          75          80

Ala Gln Ala Pro Asp Gly Ala Ser Glu Pro Arg Ala Ser Ala Ser Arg
          85          90          95

Pro Gln Pro Ala Pro Ala Asp Gly Ala Asp Pro Pro Pro Ala Glu Glu
          100          105          110

Pro Glu Ala Arg Pro Asp Gly Glu Gly Ser Pro Gly Lys Ala Arg Pro
          115          120          125

Gly Thr Ala Arg Arg Pro Gly Ala Ala Ala Ser Gly Glu Arg Asp Asp
          130          135          140

Arg Gly Pro Pro Ala Ser Val Ala Ala Leu Arg Ser Asn Phe Glu Arg
145          150          155          160

Ile Arg Lys Gly His Gly Gln Pro Gly Ala Asp Ala Glu Lys Pro Phe
          165          170          175

Tyr Val Asn Val Glu Phe His His Glu Arg Gly Leu Val Lys Val Asn
          180          185          190

Asp Lys Glu Val Ser Asp Arg Ile Ser Ser Leu Gly Ser Gln Ala Met
          195          200          205

Gln Met Glu Arg Lys Lys Ser Gln His Gly Ala Gly Ser Ser Val Gly
          210          215          220

Asp Ala Ser Arg Pro Pro Tyr Arg Gly Arg Ser Ser Glu Ser Ser Cys
225          230          235          240

Gly Val Asp Gly Asp Tyr Glu Asp Ala Glu Leu Asn Pro Arg Phe Leu
          245          250          255

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Lys Asp Asn Leu Ile Asp Ala Asn Gly Gly Ser Arg Pro Pro Trp Pro
260 265 270

Pro Leu Glu Tyr Gln Pro Tyr Gln Ser Ile Tyr Val Gly Gly Met Met
275 280 285

Glu Gly Glu Gly Lys Gly Pro Leu Leu Arg Ser Gln Ser Thr Ser Glu
290 295 300

Gln Glu Lys Arg Leu Thr Trp Pro Arg Arg Ser Tyr Ser Pro Arg Ser
305 310 315 320

Phe Glu Asp Cys Gly Gly Gly Tyr Thr Pro Asp Cys Ser Ser Asn Glu
325 330 335

Asn Leu Thr Ser Ser Glu Glu Asp Phe Ser Ser Gly Gln Ser Ser Arg
340 345 350

Val Ser Pro Ser Pro Thr Thr Tyr Arg Met Phe Arg Asp Lys Ser Arg
355 360 365

Ser Pro Ser Gln Asn Ser Gln Gln Ser Phe Asp Ser Ser Ser Pro Pro
370 375 380

Thr Pro Gln Cys His Lys Arg His Arg His Cys Pro Val Val Val Ser
385 390 395 400

Glu Ala Thr Ile Val Gly Val Arg Lys Thr Gly Gln Ile Trp Pro Asn
405 410 415

Asp Gly Glu Gly Ala Phe His Gly Asp Ala Asp Gly Ser Leu Glu Leu
420 425 430

Gln Gly Lys Pro Ser Arg Trp Thr Gln
435 440

<210> 224

<211> 524

<212> PRT

<213> Artificial Sequence

<220>

<223> bcr/abl__Homo_sapiens__A9UF00

<400> 224

Met Val Asp Pro Val Gly Phe Ala Glu Ala Trp Lys Ala Gln Phe Pro
1 5 10 15

Asp Ser Glu Pro Pro Arg Met Glu Leu Arg Ser Val Gly Asp Ile Glu
20 25 30

ITI-08-PCT_Sequence_Listing_ST25.txt

Gln Glu Leu Glu Arg Cys Lys Ala Ser Ile Arg Arg Leu Glu Gln Glu
35 40 45

Val Asn Gln Glu Arg Phe Arg Met Ile Tyr Leu Gln Thr Leu Leu Ala
50 55 60

Lys Glu Lys Lys Ser Tyr Asp Arg Gln Arg Trp Gly Phe Arg Arg Ala
65 70 75 80

Ala Gln Ala Pro Asp Gly Ala Ser Glu Pro Arg Ala Ser Ala Ser Arg
85 90 95

Pro Gln Pro Ala Pro Ala Asp Gly Ala Asp Pro Pro Pro Ala Glu Glu
100 105 110

Pro Glu Ala Arg Pro Asp Gly Glu Gly Ser Pro Gly Lys Ala Arg Pro
115 120 125

Gly Thr Ala Arg Arg Pro Gly Ala Ala Ala Ser Gly Glu Arg Asp Asp
130 135 140

Arg Gly Pro Pro Ala Ser Val Ala Ala Leu Arg Ser Asn Phe Glu Arg
145 150 155 160

Ile Arg Lys Gly His Gly Gln Pro Gly Ala Asp Ala Glu Lys Pro Phe
165 170 175

Tyr Val Asn Val Glu Phe His His Glu Arg Gly Leu Val Lys Val Asn
180 185 190

Asp Lys Glu Val Ser Asp Arg Ile Ser Ser Leu Gly Ser Gln Ala Met
195 200 205

Gln Met Glu Arg Lys Lys Ser Gln His Gly Ala Gly Ser Ser Val Gly
210 215 220

Asp Ala Ser Arg Pro Pro Tyr Arg Gly Arg Ser Ser Glu Ser Ser Cys
225 230 235 240

Gly Val Asp Gly Asp Tyr Glu Asp Ala Glu Leu Asn Pro Arg Phe Leu
245 250 255

Lys Asp Asn Leu Ile Asp Ala Asn Gly Gly Ser Arg Pro Pro Trp Pro
260 265 270

Pro Leu Glu Tyr Gln Pro Tyr Gln Ser Ile Tyr Val Gly Gly Met Met
275 280 285

Glu Gly Glu Gly Lys Gly Pro Leu Leu Arg Ser Gln Ser Thr Ser Glu
290 295 300

Gln Glu Lys Arg Leu Thr Trp Pro Arg Arg Ser Tyr Ser Pro Arg Ser

ITI-08-PCT_Sequence_Listing_ST25.txt

```

305          310          315          320
Phe Glu Asp Cys Gly Gly Gly Tyr Thr Pro Asp Cys Ser Ser Asn Glu
          325          330          335
Asn Leu Thr Ser Ser Glu Glu Asp Phe Ser Ser Gly Gln Ser Ser Arg
          340          345          350
Val Ser Pro Ser Pro Thr Thr Tyr Arg Met Phe Arg Asp Lys Ser Arg
          355          360          365
Ser Pro Ser Gln Asn Ser Gln Gln Ser Phe Asp Ser Ser Ser Pro Pro
          370          375          380
Thr Pro Gln Cys His Lys Arg His Arg His Cys Pro Val Val Val Ser
385          390          395          400
Glu Ala Thr Ile Val Gly Val Arg Lys Thr Gly Gln Ile Trp Pro Asn
          405          410          415
Asp Gly Glu Gly Ala Phe His Gly Asp Ala Asp Gly Ser Phe Gly Thr
          420          425          430
Pro Pro Gly Tyr Gly Cys Ala Ala Asp Arg Ala Glu Glu Gln Arg Arg
          435          440          445
His Gln Asp Gly Leu Pro Tyr Ile Asp Asp Ser Pro Ser Ser Ser Pro
          450          455          460
His Leu Ser Ser Lys Gly Arg Gly Ser Arg Asp Ala Leu Val Ser Gly
465          470          475          480
Ala Leu Glu Ser Thr Lys Ala Ser Glu Leu Asp Leu Glu Lys Gly Leu
          485          490          495
Glu Met Arg Lys Trp Asp Pro Val Lys Met Thr Pro Thr Phe Ser Leu
          500          505          510
His Cys Met Ile Leu Trp Pro Val Glu Ile Thr Leu
          515          520

<210> 225
<211> 465
<212> PRT
<213> Artificial Sequence

<220>
<223> bcr/abl__Homo_sapiens__A9UF01

<400> 225
Met Val Asp Pro Val Gly Phe Ala Glu Ala Trp Lys Ala Gln Phe Pro

```

ITI-08-PCT_Sequence_Listing_ST25.txt

1		5		10		15											
Asp	Ser	Glu	Pro	Pro	Arg	Met	Glu	Leu	Arg	Ser	Val	Gly	Asp	Ile	Glu		
			20					25					30				
Gln	Glu	Leu	Glu	Arg	Cys	Lys	Ala	Ser	Ile	Arg	Arg	Leu	Glu	Gln	Glu		
		35					40					45					
Val	Asn	Gln	Glu	Arg	Phe	Arg	Met	Ile	Tyr	Leu	Gln	Thr	Leu	Leu	Ala		
	50					55					60						
Lys	Glu	Lys	Lys	Ser	Tyr	Asp	Arg	Gln	Arg	Trp	Gly	Phe	Arg	Arg	Ala		
65					70					75					80		
Ala	Gln	Ala	Pro	Asp	Gly	Ala	Ser	Glu	Pro	Arg	Ala	Ser	Ala	Ser	Arg		
				85					90					95			
Pro	Gln	Pro	Ala	Pro	Ala	Asp	Gly	Ala	Asp	Pro	Pro	Pro	Ala	Glu	Glu		
			100					105					110				
Pro	Glu	Ala	Arg	Pro	Asp	Gly	Glu	Gly	Ser	Pro	Gly	Lys	Ala	Arg	Pro		
		115					120					125					
Gly	Thr	Ala	Arg	Arg	Pro	Gly	Ala	Ala	Ala	Ser	Gly	Glu	Arg	Asp	Asp		
	130					135					140						
Arg	Gly	Pro	Pro	Ala	Ser	Val	Ala	Ala	Leu	Arg	Ser	Asn	Phe	Glu	Arg		
145					150					155					160		
Ile	Arg	Lys	Gly	His	Gly	Gln	Pro	Gly	Ala	Asp	Ala	Glu	Lys	Pro	Phe		
				165				170						175			
Tyr	Val	Asn	Val	Glu	Phe	His	His	Glu	Arg	Gly	Leu	Val	Lys	Val	Asn		
			180					185					190				
Asp	Lys	Glu	Val	Ser	Asp	Arg	Ile	Ser	Ser	Leu	Gly	Ser	Gln	Ala	Met		
		195					200					205					
Gln	Met	Glu	Arg	Lys	Lys	Ser	Gln	His	Gly	Ala	Gly	Ser	Ser	Val	Gly		
	210					215					220						
Asp	Ala	Ser	Arg	Pro	Pro	Tyr	Arg	Gly	Arg	Ser	Ser	Glu	Ser	Ser	Cys		
225					230					235					240		
Gly	Val	Asp	Gly	Asp	Tyr	Glu	Asp	Ala	Glu	Leu	Asn	Pro	Arg	Phe	Leu		
				245					250					255			
Lys	Asp	Asn	Leu	Ile	Asp	Ala	Asn	Gly	Gly	Ser	Arg	Pro	Pro	Trp	Pro		
			260					265					270				
Pro	Leu	Glu	Tyr	Gln	Pro	Tyr	Gln	Ser	Ile	Tyr	Val	Gly	Gly	Met	Met		
		275					280					285					

ITI-08-PCT_Sequence_Listing_ST25.txt

Glu Gly Glu Gly Lys Gly Pro Leu Leu Arg Ser Gln Ser Thr Ser Glu
290 295 300

Gln Glu Lys Arg Leu Thr Trp Pro Arg Arg Ser Tyr Ser Pro Arg Ser
305 310 315 320

Phe Glu Asp Cys Gly Gly Gly Tyr Thr Pro Asp Cys Ser Ser Asn Glu
325 330 335

Asn Leu Thr Ser Ser Glu Glu Asp Phe Ser Ser Gly Gln Ser Ser Arg
340 345 350

Val Ser Pro Ser Pro Thr Thr Tyr Arg Met Phe Arg Asp Lys Ser Arg
355 360 365

Ser Pro Ser Gln Asn Ser Gln Gln Ser Phe Asp Ser Ser Ser Pro Pro
370 375 380

Thr Pro Gln Cys His Lys Arg His Arg His Cys Pro Val Val Val Ser
385 390 395 400

Glu Ala Thr Ile Val Gly Val Arg Lys Thr Gly Gln Ile Trp Pro Asn
405 410 415

Asp Gly Glu Gly Ala Phe His Gly Glu His Pro Gly Ala Ala Glu Glu
420 425 430

Val Phe Gln Lys Leu Leu Pro Asp Ile Arg Gly Ala Ala Asp Ala Asp
435 440 445

Gln Leu Val Cys Glu Thr Pro Asp Cys Pro Gln His Ser Ala Asp His
450 455 460

Gln
465

<210> 226
<211> 458
<212> PRT
<213> Artificial Sequence

<220>
<223> bcr/abl__Homo_sapiens__A9UF03

<400> 226

Met Val Asp Pro Val Gly Phe Ala Glu Ala Trp Lys Ala Gln Phe Pro
1 5 10 15

Asp Ser Glu Pro Pro Arg Met Glu Leu Arg Ser Val Gly Asp Ile Glu
20 25 30

ITI-08-PCT_Sequence_Listing_ST25.txt

Gln Glu Leu Glu Arg Cys Lys Ala Ser Ile Arg Arg Leu Glu Gln Glu
35 40 45

Val Asn Gln Glu Arg Phe Arg Met Ile Tyr Leu Gln Thr Leu Leu Ala
50 55 60

Lys Glu Lys Lys Ser Tyr Asp Arg Gln Arg Trp Gly Phe Arg Arg Ala
65 70 75 80

Ala Gln Ala Pro Asp Gly Ala Ser Glu Pro Arg Ala Ser Ala Ser Arg
85 90 95

Pro Gln Pro Ala Pro Ala Asp Gly Ala Asp Pro Pro Pro Ala Glu Glu
100 105 110

Pro Glu Ala Arg Pro Asp Gly Glu Gly Ser Pro Gly Lys Ala Arg Pro
115 120 125

Gly Thr Ala Arg Arg Pro Gly Ala Ala Ala Ser Gly Glu Arg Asp Asp
130 135 140

Arg Gly Pro Pro Ala Ser Val Ala Ala Leu Arg Ser Asn Phe Glu Arg
145 150 155 160

Ile Arg Lys Gly His Gly Gln Pro Gly Ala Asp Ala Glu Lys Pro Phe
165 170 175

Tyr Val Asn Val Glu Phe His His Glu Arg Gly Leu Val Lys Val Asn
180 185 190

Asp Lys Glu Val Ser Asp Arg Ile Ser Ser Leu Gly Ser Gln Ala Met
195 200 205

Gln Met Glu Arg Lys Lys Ser Gln His Gly Ala Gly Ser Ser Val Gly
210 215 220

Asp Ala Ser Arg Pro Pro Tyr Arg Gly Arg Ser Ser Glu Ser Ser Cys
225 230 235 240

Gly Val Asp Gly Asp Tyr Glu Asp Ala Glu Leu Asn Pro Arg Phe Leu
245 250 255

Lys Asp Asn Leu Ile Asp Ala Asn Gly Gly Ser Arg Pro Pro Trp Pro
260 265 270

Pro Leu Glu Tyr Gln Pro Tyr Gln Ser Ile Tyr Val Gly Gly Met Met
275 280 285

Glu Gly Glu Gly Lys Gly Pro Leu Leu Arg Ser Gln Ser Thr Ser Glu
290 295 300

ITI-08-PCT_Sequence_Listing_ST25.txt

Gln Glu Lys Arg Leu Thr Trp Pro Arg Arg Ser Tyr Ser Pro Arg Ser
305 310 315 320

Phe Glu Asp Cys Gly Gly Gly Tyr Thr Pro Asp Cys Ser Ser Asn Glu
325 330 335

Asn Leu Thr Ser Ser Glu Glu Asp Phe Ser Ser Gly Gln Ser Ser Arg
340 345 350

Val Ser Pro Ser Pro Thr Thr Tyr Arg Met Phe Arg Asp Lys Ser Arg
355 360 365

Ser Pro Ser Gln Asn Ser Gln Gln Ser Phe Asp Ser Ser Ser Pro Pro
370 375 380

Thr Pro Gln Cys His Lys Arg His Arg His Cys Pro Val Val Val Ser
385 390 395 400

Glu Ala Thr Ile Val Gly Val Arg Lys Thr Gly Gln Ile Trp Pro Asn
405 410 415

Asp Gly Glu Gly Ala Phe His Gly Asp Ala Asp Gly Ser Phe Gly Thr
420 425 430

Pro Pro Gly Tyr Cys Cys Leu Cys Leu Pro Ala Trp Pro Ser Gly Cys
435 440 445

Thr Ala Ala Thr Ala Arg Val Thr Arg Ser
450 455

<210> 227

<211> 454

<212> PRT

<213> Artificial Sequence

<220>

<223> bcr/abl__Homo_sapiens__A9UF04

<400> 227

Met Val Asp Pro Val Gly Phe Ala Glu Ala Trp Lys Ala Gln Phe Pro
1 5 10 15

Asp Ser Glu Pro Pro Arg Met Glu Leu Arg Ser Val Gly Asp Ile Glu
20 25 30

Gln Glu Leu Glu Arg Cys Lys Ala Ser Ile Arg Arg Leu Glu Gln Glu
35 40 45

Val Asn Gln Glu Arg Phe Arg Met Ile Tyr Leu Gln Thr Leu Leu Ala
50 55 60

ITI-08-PCT_Sequence_Listing_ST25.txt

Lys Glu Lys Lys Ser Tyr Asp Arg Gln Arg Trp Gly Phe Arg Arg Ala
 65 70 75 80
 Ala Gln Ala Pro Asp Gly Ala Ser Glu Pro Arg Ala Ser Ala Ser Arg
 85 90 95
 Pro Gln Pro Ala Pro Ala Asp Gly Ala Asp Pro Pro Pro Ala Glu Glu
 100 105 110
 Pro Glu Ala Arg Pro Asp Gly Glu Gly Ser Pro Gly Lys Ala Arg Pro
 115 120 125
 Gly Thr Ala Arg Arg Pro Gly Ala Ala Ala Ser Gly Glu Arg Asp Asp
 130 135 140
 Arg Gly Pro Pro Ala Ser Val Ala Ala Leu Arg Ser Asn Phe Glu Arg
 145 150 155 160
 Ile Arg Lys Gly His Gly Gln Pro Gly Ala Asp Ala Glu Lys Pro Phe
 165 170 175
 Tyr Val Asn Val Glu Phe His His Glu Arg Gly Leu Val Lys Val Asn
 180 185 190
 Asp Lys Glu Val Ser Asp Arg Ile Ser Ser Leu Gly Ser Gln Ala Met
 195 200 205
 Gln Met Glu Arg Lys Lys Ser Gln His Gly Ala Gly Ser Ser Val Gly
 210 215 220
 Asp Ala Ser Arg Pro Pro Tyr Arg Gly Arg Ser Ser Glu Ser Ser Cys
 225 230 235 240
 Gly Val Asp Gly Asp Tyr Glu Asp Ala Glu Leu Asn Pro Arg Phe Leu
 245 250 255
 Lys Asp Asn Leu Ile Asp Ala Asn Gly Gly Ser Arg Pro Pro Trp Pro
 260 265 270
 Pro Leu Glu Tyr Gln Pro Tyr Gln Ser Ile Tyr Val Gly Gly Met Met
 275 280 285
 Glu Gly Glu Gly Lys Gly Pro Leu Leu Arg Ser Gln Ser Thr Ser Glu
 290 295 300
 Gln Glu Lys Arg Leu Thr Trp Pro Arg Arg Ser Tyr Ser Pro Arg Ser
 305 310 315 320
 Phe Glu Asp Cys Gly Gly Gly Tyr Thr Pro Asp Cys Ser Ser Asn Glu
 325 330 335
 Asn Leu Thr Ser Ser Glu Glu Asp Phe Ser Ser Gly Gln Ser Ser Arg

ITI-08-PCT_Sequence_Listing_ST25.txt

340

345

350

Val Ser Pro Ser Pro Thr Thr Tyr Arg Met Phe Arg Asp Lys Ser Arg
355 360 365

Ser Pro Ser Gln Asn Ser Gln Gln Ser Phe Asp Ser Ser Ser Pro Pro
370 375 380

Thr Pro Gln Cys His Lys Arg His Arg His Cys Pro Val Val Val Ser
385 390 395 400

Glu Ala Thr Ile Val Gly Val Arg Lys Thr Gly Gln Ile Trp Pro Asn
405 410 415

Asp Gly Glu Gly Ala Phe His Gly Asp Ala Asp Gly Ser Phe Gly Thr
420 425 430

Pro Pro Gly Tyr Gly Cys Ala Ala Gly Arg Pro Pro His Leu Thr Glu
435 440 445

Leu Pro Val Gln His Gln
450

<210> 228

<211> 467

<212> PRT

<213> Artificial Sequence

<220>

<223> bcr/abl__Homo_sapiens__A9UF05

<400> 228

Met Val Asp Pro Val Gly Phe Ala Glu Ala Trp Lys Ala Gln Phe Pro
1 5 10 15

Asp Ser Glu Pro Pro Arg Met Glu Leu Arg Ser Val Gly Asp Ile Glu
20 25 30

Gln Glu Leu Glu Arg Cys Lys Ala Ser Ile Arg Arg Leu Glu Gln Glu
35 40 45

Val Asn Gln Glu Arg Phe Arg Met Ile Tyr Leu Gln Thr Leu Leu Ala
50 55 60

Lys Glu Lys Lys Ser Tyr Asp Arg Gln Arg Trp Gly Phe Arg Arg Ala
65 70 75 80

Ala Gln Ala Pro Asp Gly Ala Ser Glu Pro Arg Ala Ser Ala Ser Arg
85 90 95

Pro Gln Pro Ala Pro Ala Asp Gly Ala Asp Pro Pro Pro Ala Glu Glu

ITI-08-PCT_Sequence_Listing_ST25.txt

100	105	110															
Pro	Glu	Ala	Arg	Pro	Asp	Gly	Glu	Gly	Ser	Pro	Gly	Lys	Ala	Arg	Pro		
	115						120					125					
Gly	Thr	Ala	Arg	Arg	Pro	Gly	Ala	Ala	Ala	Ser	Gly	Glu	Arg	Asp	Asp		
	130					135					140						
Arg	Gly	Pro	Pro	Ala	Ser	Val	Ala	Ala	Leu	Arg	Ser	Asn	Phe	Glu	Arg		
145					150					155					160		
Ile	Arg	Lys	Gly	His	Gly	Gln	Pro	Gly	Ala	Asp	Ala	Glu	Lys	Pro	Phe		
				165					170					175			
Tyr	Val	Asn	Val	Glu	Phe	His	His	Glu	Arg	Gly	Leu	Val	Lys	Val	Asn		
		180						185					190				
Asp	Lys	Glu	Val	Ser	Asp	Arg	Ile	Ser	Ser	Leu	Gly	Ser	Gln	Ala	Met		
	195						200					205					
Gln	Met	Glu	Arg	Lys	Lys	Ser	Gln	His	Gly	Ala	Gly	Ser	Ser	Val	Gly		
	210					215					220						
Asp	Ala	Ser	Arg	Pro	Pro	Tyr	Arg	Gly	Arg	Ser	Ser	Glu	Ser	Ser	Cys		
225					230					235					240		
Gly	Val	Asp	Gly	Asp	Tyr	Glu	Asp	Ala	Glu	Leu	Asn	Pro	Arg	Phe	Leu		
				245					250					255			
Lys	Asp	Asn	Leu	Ile	Asp	Ala	Asn	Gly	Gly	Ser	Arg	Pro	Pro	Trp	Pro		
			260					265						270			
Pro	Leu	Glu	Tyr	Gln	Pro	Tyr	Gln	Ser	Ile	Tyr	Val	Gly	Gly	Met	Met		
	275						280					285					
Glu	Gly	Glu	Gly	Lys	Gly	Pro	Leu	Leu	Arg	Ser	Gln	Ser	Thr	Ser	Glu		
	290					295					300						
Gln	Glu	Lys	Arg	Leu	Thr	Trp	Pro	Arg	Arg	Ser	Tyr	Ser	Pro	Arg	Ser		
305					310					315					320		
Phe	Glu	Asp	Cys	Gly	Gly	Gly	Tyr	Thr	Pro	Asp	Cys	Ser	Ser	Asn	Glu		
				325					330					335			
Asn	Leu	Thr	Ser	Ser	Glu	Glu	Asp	Phe	Ser	Ser	Gly	Gln	Ser	Ser	Arg		
			340					345					350				
Val	Ser	Pro	Ser	Pro	Thr	Thr	Tyr	Arg	Met	Phe	Arg	Asp	Lys	Ser	Arg		
	355						360					365					
Ser	Pro	Ser	Gln	Asn	Ser	Gln	Gln	Ser	Phe	Asp	Ser	Ser	Ser	Pro	Pro		
	370					375					380						

ITI-08-PCT_Sequence_Listing_ST25.txt

Thr Pro Gln Cys His Lys Arg His Arg His Cys Pro Val Val Val Ser
385 390 395 400

Glu Ala Thr Ile Val Gly Val Arg Lys Thr Gly Gln Ile Trp Pro Asn
405 410 415

Asp Gly Glu Gly Ala Phe His Gly Asp Ala Val Leu Lys Thr Glu Val
420 425 430

Pro His Gln Gly Val Arg Arg Ala Arg Leu Ser Leu Glu Ala Leu Gly
435 440 445

Glu Asp Pro Ser Phe Leu Phe Pro Ala Ser Asp Gly Pro Arg His Ser
450 455 460

Ser Thr Trp
465

<210> 229
<211> 513
<212> PRT
<213> Artificial Sequence

<220>
<223> bcr/abl__Homo_sapiens__A9UF06

<400> 229

Met Val Asp Pro Val Gly Phe Ala Glu Ala Trp Lys Ala Gln Phe Pro
1 5 10 15

Asp Ser Glu Pro Pro Arg Met Glu Leu Arg Ser Val Gly Asp Ile Glu
20 25 30

Gln Glu Leu Glu Arg Cys Lys Ala Ser Ile Arg Arg Leu Glu Gln Glu
35 40 45

Val Asn Gln Glu Arg Phe Arg Met Ile Tyr Leu Gln Thr Leu Leu Ala
50 55 60

Lys Glu Lys Lys Ser Tyr Asp Arg Gln Arg Trp Gly Phe Arg Arg Ala
65 70 75 80

Ala Gln Ala Pro Asp Gly Ala Ser Glu Pro Arg Ala Ser Ala Ser Arg
85 90 95

Pro Gln Pro Ala Pro Ala Asp Gly Ala Asp Pro Pro Pro Ala Glu Glu
100 105 110

Pro Glu Ala Arg Pro Asp Gly Glu Gly Ser Pro Gly Lys Ala Arg Pro
115 120 125

ITI-08-PCT_Sequence_Listing_ST25.txt

Gly	Thr	Ala	Arg	Arg	Pro	Gly	Ala	Ala	Ala	Ser	Gly	Glu	Arg	Asp	Asp	130	135	140	
Arg	Gly	Pro	Pro	Ala	Ser	Val	Ala	Ala	Leu	Arg	Ser	Asn	Phe	Glu	Arg	145	150	155	160
Ile	Arg	Lys	Gly	His	Gly	Gln	Pro	Gly	Ala	Asp	Ala	Glu	Lys	Pro	Phe	165	170	175	
Tyr	Val	Asn	Val	Glu	Phe	His	His	Glu	Arg	Gly	Leu	Val	Lys	Val	Asn	180	185	190	
Asp	Lys	Glu	Val	Ser	Asp	Arg	Ile	Ser	Ser	Leu	Gly	Ser	Gln	Ala	Met	195	200	205	
Gln	Met	Glu	Arg	Lys	Lys	Ser	Gln	His	Gly	Ala	Gly	Ser	Ser	Val	Gly	210	215	220	
Asp	Ala	Ser	Arg	Pro	Pro	Tyr	Arg	Gly	Arg	Ser	Ser	Glu	Ser	Ser	Cys	225	230	235	240
Gly	Val	Asp	Gly	Asp	Tyr	Glu	Asp	Ala	Glu	Leu	Asn	Pro	Arg	Phe	Leu	245	250	255	
Lys	Asp	Asn	Leu	Ile	Asp	Ala	Asn	Gly	Gly	Ser	Arg	Pro	Pro	Trp	Pro	260	265	270	
Pro	Leu	Glu	Tyr	Gln	Pro	Tyr	Gln	Ser	Ile	Tyr	Val	Gly	Gly	Met	Met	275	280	285	
Glu	Gly	Glu	Gly	Lys	Gly	Pro	Leu	Leu	Arg	Ser	Gln	Ser	Thr	Ser	Glu	290	295	300	
Gln	Glu	Lys	Arg	Leu	Thr	Trp	Pro	Arg	Arg	Ser	Tyr	Ser	Pro	Arg	Ser	305	310	315	320
Phe	Glu	Asp	Cys	Gly	Gly	Gly	Tyr	Thr	Pro	Asp	Cys	Ser	Ser	Asn	Glu	325	330	335	
Asn	Leu	Thr	Ser	Ser	Glu	Glu	Asp	Phe	Ser	Ser	Gly	Gln	Ser	Ser	Arg	340	345	350	
Val	Ser	Pro	Ser	Pro	Thr	Thr	Tyr	Arg	Met	Phe	Arg	Asp	Lys	Ser	Arg	355	360	365	
Ser	Pro	Ser	Gln	Asn	Ser	Gln	Gln	Ser	Phe	Asp	Ser	Ser	Ser	Pro	Pro	370	375	380	
Thr	Pro	Gln	Cys	His	Lys	Arg	His	Arg	His	Cys	Pro	Val	Val	Val	Ser	385	390	395	400

ITI-08-PCT_Sequence_Listing_ST25.txt

Glu Ala Thr Ile Val Gly Val Arg Lys Thr Gly Gln Ile Trp Pro Asn
405 410 415

Asp Gly Glu Gly Ala Phe His Gly Asp Ala Asp Gly Ser Phe Gly Thr
420 425 430

Pro Pro Gly Tyr Gly Cys Ala Ala Asp Arg Ala Glu Glu Gln Arg Arg
435 440 445

His Gln Asp Gly Leu Pro Tyr Ile Asp Asp Ser Pro Ser Ser Ser Pro
450 455 460

His Leu Ser Ser Lys Gly Arg Gly Ser Arg Asp Ala Leu Val Ser Gly
465 470 475 480

Ala Leu Glu Ser Thr Lys Ala Ser Glu Leu Asp Pro Val Lys Met Thr
485 490 495

Pro Thr Phe Ser Leu His Cys Met Ile Leu Trp Pro Val Glu Ile Thr
500 505 510

Leu

<210> 230

<211> 406

<212> PRT

<213> Artificial Sequence

<220>

<223> bcr/abl__Homo_sapiens__A9UF08

<400> 230

Met Val Asp Pro Val Gly Phe Ala Glu Ala Trp Lys Ala Gln Phe Pro
1 5 10 15

Asp Ser Glu Pro Pro Arg Met Glu Leu Arg Ser Val Gly Asp Ile Glu
20 25 30

Gln Glu Leu Glu Arg Cys Lys Ala Ser Ile Arg Arg Leu Glu Gln Glu
35 40 45

Val Asn Gln Glu Arg Phe Arg Met Ile Tyr Leu Gln Thr Leu Leu Ala
50 55 60

Lys Glu Lys Lys Ser Tyr Asp Arg Gln Arg Trp Gly Phe Arg Arg Ala
65 70 75 80

Ala Gln Ala Pro Asp Gly Ala Ser Glu Pro Arg Ala Ser Ala Ser Arg
85 90 95

Pro Gln Pro Ala Pro Ala Asp Gly Ala Asp Pro Pro Pro Ala Glu Glu

ITI-08-PCT_Sequence_Listing_ST25.txt

```

100          105          110
Pro Glu Ala Arg Pro Asp Gly Glu Gly Ser Pro Gly Lys Ala Arg Pro
115          120          125

Gly Thr Ala Arg Arg Pro Gly Ala Ala Ala Ser Gly Glu Arg Asp Asp
130          135          140

Arg Gly Pro Pro Ala Ser Val Ala Ala Leu Arg Ser Asn Phe Glu Arg
145          150          155          160

Ile Arg Lys Gly His Gly Gln Pro Gly Ala Asp Ala Glu Lys Pro Phe
165          170          175

Tyr Val Asn Val Glu Phe His His Glu Arg Gly Leu Val Lys Val Asn
180          185          190

Asp Lys Glu Val Ser Asp Arg Ile Ser Ser Leu Gly Ser Gln Ala Met
195          200          205

Gln Met Glu Arg Lys Lys Ser Gln His Gly Ala Gly Ser Ser Val Gly
210          215          220

Asp Ala Ser Arg Pro Pro Tyr Arg Gly Arg Ser Ser Glu Ser Ser Cys
225          230          235          240

Gly Val Asp Gly Asp Tyr Glu Asp Ala Glu Leu Asn Pro Arg Phe Leu
245          250          255

Lys Asp Asn Leu Ile Asp Ala Asn Gly Gly Ser Arg Pro Pro Trp Pro
260          265          270

Pro Leu Glu Tyr Gln Pro Tyr Gln Ser Ile Tyr Val Gly Gly Met Met
275          280          285

Glu Gly Glu Gly Lys Gly Pro Leu Leu Arg Ser Gln Ser Thr Ser Glu
290          295          300

Gln Glu Lys Arg Leu Thr Trp Pro Arg Arg Ser Tyr Ser Pro Arg Ser
305          310          315          320

Phe Glu Asp Cys Gly Gly Gly Tyr Thr Pro Asp Cys Ser Ser Asn Glu
325          330          335

Asn Leu Thr Ser Ser Glu Glu Asp Phe Ser Ser Gly Gln Ser Ser Arg
340          345          350

Val Ser Pro Ser Pro Thr Thr Tyr Arg Met Phe Arg Asp Lys Ser Arg
355          360          365

Ser Pro Ser Gln Asn Ser Gln Gln Ser Phe Asp Ser Ser Ser Pro Pro
370          375          380

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Thr Pro Gln Cys His Lys Arg His Arg His Cys Pro Val Val Val Ser
385 390 395 400

Glu Ala Thr Ser Gly Gln
405

<210> 231

<211> 781

<212> PRT

<213> Artificial Sequence

<220>

<223> beta-catenin/m__Homo_sapiens__P35222

<400> 231

Met Ala Thr Gln Ala Asp Leu Met Glu Leu Asp Met Ala Met Glu Pro
1 5 10 15

Asp Arg Lys Ala Ala Val Ser His Trp Gln Gln Gln Ser Tyr Leu Asp
20 25 30

Ser Gly Ile His Ser Gly Ala Thr Thr Thr Ala Pro Ser Leu Ser Gly
35 40 45

Lys Gly Asn Pro Glu Glu Glu Asp Val Asp Thr Ser Gln Val Leu Tyr
50 55 60

Glu Trp Glu Gln Gly Phe Ser Gln Ser Phe Thr Gln Glu Gln Val Ala
65 70 75 80

Asp Ile Asp Gly Gln Tyr Ala Met Thr Arg Ala Gln Arg Val Arg Ala
85 90 95

Ala Met Phe Pro Glu Thr Leu Asp Glu Gly Met Gln Ile Pro Ser Thr
100 105 110

Gln Phe Asp Ala Ala His Pro Thr Asn Val Gln Arg Leu Ala Glu Pro
115 120 125

Ser Gln Met Leu Lys His Ala Val Val Asn Leu Ile Asn Tyr Gln Asp
130 135 140

Asp Ala Glu Leu Ala Thr Arg Ala Ile Pro Glu Leu Thr Lys Leu Leu
145 150 155 160

Asn Asp Glu Asp Gln Val Val Val Asn Lys Ala Ala Val Met Val His
165 170 175

Gln Leu Ser Lys Lys Glu Ala Ser Arg His Ala Ile Met Arg Ser Pro
180 185 190

ITI-08-PCT_Sequence_Listing_ST25.txt

Gln	Met	Val	Ser	Ala	Ile	Val	Arg	Thr	Met	Gln	Asn	Thr	Asn	Asp	Val	195	200	205
Glu	Thr	Ala	Arg	Cys	Thr	Ala	Gly	Thr	Leu	His	Asn	Leu	Ser	His	His	210	215	220
Arg	Glu	Gly	Leu	Leu	Ala	Ile	Phe	Lys	Ser	Gly	Gly	Ile	Pro	Ala	Leu	225	230	235
Val	Lys	Met	Leu	Gly	Ser	Pro	Val	Asp	Ser	Val	Leu	Phe	Tyr	Ala	Ile	245	250	255
Thr	Thr	Leu	His	Asn	Leu	Leu	Leu	His	Gln	Glu	Gly	Ala	Lys	Met	Ala	260	265	270
Val	Arg	Leu	Ala	Gly	Gly	Leu	Gln	Lys	Met	Val	Ala	Leu	Leu	Asn	Lys	275	280	285
Thr	Asn	Val	Lys	Phe	Leu	Ala	Ile	Thr	Thr	Asp	Cys	Leu	Gln	Ile	Leu	290	295	300
Ala	Tyr	Gly	Asn	Gln	Glu	Ser	Lys	Leu	Ile	Ile	Leu	Ala	Ser	Gly	Gly	305	310	315
Pro	Gln	Ala	Leu	Val	Asn	Ile	Met	Arg	Thr	Tyr	Thr	Tyr	Glu	Lys	Leu	325	330	335
Leu	Trp	Thr	Thr	Ser	Arg	Val	Leu	Lys	Val	Leu	Ser	Val	Cys	Ser	Ser	340	345	350
Asn	Lys	Pro	Ala	Ile	Val	Glu	Ala	Gly	Gly	Met	Gln	Ala	Leu	Gly	Leu	355	360	365
His	Leu	Thr	Asp	Pro	Ser	Gln	Arg	Leu	Val	Gln	Asn	Cys	Leu	Trp	Thr	370	375	380
Leu	Arg	Asn	Leu	Ser	Asp	Ala	Ala	Thr	Lys	Gln	Glu	Gly	Met	Glu	Gly	385	390	395
Leu	Leu	Gly	Thr	Leu	Val	Gln	Leu	Leu	Gly	Ser	Asp	Asp	Ile	Asn	Val	405	410	415
Val	Thr	Cys	Ala	Ala	Gly	Ile	Leu	Ser	Asn	Leu	Thr	Cys	Asn	Asn	Tyr	420	425	430
Lys	Asn	Lys	Met	Met	Val	Cys	Gln	Val	Gly	Gly	Ile	Glu	Ala	Leu	Val	435	440	445
Arg	Thr	Val	Leu	Arg	Ala	Gly	Asp	Arg	Glu	Asp	Ile	Thr	Glu	Pro	Ala	450	455	460

ITI-08-PCT_Sequence_Listing_ST25.txt

Ile	Cys	Ala	Leu	Arg	His	Leu	Thr	Ser	Arg	His	Gln	Glu	Ala	Glu	Met	465	470	475	480
Ala	Gln	Asn	Ala	Val	Arg	Leu	His	Tyr	Gly	Leu	Pro	Val	Val	Val	Lys		485	490	495
Leu	Leu	His	Pro	Pro	Ser	His	Trp	Pro	Leu	Ile	Lys	Ala	Thr	Val	Gly	500		505	510
Leu	Ile	Arg	Asn	Leu	Ala	Leu	Cys	Pro	Ala	Asn	His	Ala	Pro	Leu	Arg	515	520		525
Glu	Gln	Gly	Ala	Ile	Pro	Arg	Leu	Val	Gln	Leu	Leu	Val	Arg	Ala	His	530	535	540	
Gln	Asp	Thr	Gln	Arg	Arg	Thr	Ser	Met	Gly	Gly	Thr	Gln	Gln	Gln	Phe	545	550	555	560
Val	Glu	Gly	Val	Arg	Met	Glu	Glu	Ile	Val	Glu	Gly	Cys	Thr	Gly	Ala		565	570	575
Leu	His	Ile	Leu	Ala	Arg	Asp	Val	His	Asn	Arg	Ile	Val	Ile	Arg	Gly	580	585		590
Leu	Asn	Thr	Ile	Pro	Leu	Phe	Val	Gln	Leu	Leu	Tyr	Ser	Pro	Ile	Glu	595	600		605
Asn	Ile	Gln	Arg	Val	Ala	Ala	Gly	Val	Leu	Cys	Glu	Leu	Ala	Gln	Asp	610	615	620	
Lys	Glu	Ala	Ala	Glu	Ala	Ile	Glu	Ala	Glu	Gly	Ala	Thr	Ala	Pro	Leu	625	630	635	640
Thr	Glu	Leu	Leu	His	Ser	Arg	Asn	Glu	Gly	Val	Ala	Thr	Tyr	Ala	Ala		645	650	655
Ala	Val	Leu	Phe	Arg	Met	Ser	Glu	Asp	Lys	Pro	Gln	Asp	Tyr	Lys	Lys	660	665		670
Arg	Leu	Ser	Val	Glu	Leu	Thr	Ser	Ser	Leu	Phe	Arg	Thr	Glu	Pro	Met	675	680		685
Ala	Trp	Asn	Glu	Thr	Ala	Asp	Leu	Gly	Leu	Asp	Ile	Gly	Ala	Gln	Gly	690	695	700	
Glu	Pro	Leu	Gly	Tyr	Arg	Gln	Asp	Asp	Pro	Ser	Tyr	Arg	Ser	Phe	His	705	710	715	720
Ser	Gly	Gly	Tyr	Gly	Gln	Asp	Ala	Leu	Gly	Met	Asp	Pro	Met	Met	Glu		725	730	735
His	Glu	Met	Gly	Gly	His	His	Pro	Gly	Ala	Asp	Tyr	Pro	Val	Asp	Gly				

ITI-08-PCT_Sequence_Listing_ST25.txt

740

745

750

Leu Pro Asp Leu Gly His Ala Gln Asp Leu Met Asp Gly Leu Pro Pro
755 760 765

Gly Asp Ser Asn Gln Leu Ala Trp Phe Asp Thr Asp Leu
770 775 780

<210> 232

<211> 563

<212> PRT

<213> Artificial Sequence

<220>

<223> beta-catenin/m__Homo_sapiens__Q8WYA6

<400> 232

Met Asp Val Gly Glu Leu Leu Ser Tyr Gln Pro Asn Arg Gly Thr Lys
1 5 10 15

Arg Pro Arg Asp Asp Glu Glu Glu Glu Gln Lys Met Arg Arg Lys Gln
20 25 30

Thr Gly Thr Arg Glu Arg Gly Arg Tyr Arg Glu Glu Glu Met Thr Val
35 40 45

Val Glu Glu Ala Asp Asp Asp Lys Lys Arg Leu Leu Gln Ile Ile Asp
50 55 60

Arg Asp Gly Glu Glu Glu Glu Glu Glu Glu Glu Pro Leu Asp Glu Ser
65 70 75 80

Ser Val Lys Lys Met Ile Leu Thr Phe Glu Lys Arg Ser Tyr Lys Asn
85 90 95

Gln Glu Leu Arg Ile Lys Phe Pro Asp Asn Pro Glu Lys Phe Met Glu
100 105 110

Ser Glu Leu Asp Leu Asn Asp Ile Ile Gln Glu Met His Val Val Ala
115 120 125

Thr Met Pro Asp Leu Tyr His Leu Leu Val Glu Leu Asn Ala Val Gln
130 135 140

Ser Leu Leu Gly Leu Leu Gly His Asp Asn Thr Asp Val Ser Ile Ala
145 150 155 160

Val Val Asp Leu Leu Gln Glu Leu Thr Asp Ile Asp Thr Leu His Glu
165 170 175

Ser Glu Glu Gly Ala Glu Val Leu Ile Asp Ala Leu Val Asp Gly Gln

ITI-08-PCT_Sequence_Listing_ST25.txt

180	185	190																	
Val	Val	Ala	Leu	Leu	Val	Gln	Asn	Leu	Glu	Arg	Leu	Asp	Glu	Ser	Val				
	195						200					205							
Lys	Glu	Glu	Ala	Asp	Gly	Val	His	Asn	Thr	Leu	Ala	Ile	Val	Glu	Asn				
	210					215					220								
Met	Ala	Glu	Phe	Arg	Pro	Glu	Met	Cys	Thr	Glu	Gly	Ala	Gln	Gln	Gly				
225					230					235					240				
Leu	Leu	Gln	Trp	Leu	Leu	Lys	Arg	Leu	Lys	Ala	Lys	Met	Pro	Phe	Asp				
				245					250					255					
Ala	Asn	Lys	Leu	Tyr	Cys	Ser	Glu	Val	Leu	Ala	Ile	Leu	Leu	Gln	Asp				
			260					265					270						
Asn	Asp	Glu	Asn	Arg	Glu	Leu	Leu	Gly	Glu	Leu	Asp	Gly	Ile	Asp	Val				
	275						280					285							
Leu	Leu	Gln	Gln	Leu	Ser	Val	Phe	Lys	Arg	His	Asn	Pro	Ser	Thr	Ala				
	290					295					300								
Glu	Glu	Gln	Glu	Met	Met	Glu	Asn	Leu	Phe	Asp	Ser	Leu	Cys	Ser	Cys				
305					310					315					320				
Leu	Met	Leu	Ser	Ser	Asn	Arg	Glu	Arg	Phe	Leu	Lys	Gly	Glu	Gly	Leu				
				325					330					335					
Gln	Leu	Met	Asn	Leu	Met	Leu	Arg	Glu	Lys	Lys	Ile	Ser	Arg	Ser	Ser				
			340					345					350						
Ala	Leu	Lys	Val	Leu	Asp	His	Ala	Met	Ile	Gly	Pro	Glu	Gly	Thr	Asp				
	355						360					365							
Asn	Cys	His	Lys	Phe	Val	Asp	Ile	Leu	Gly	Leu	Arg	Thr	Ile	Phe	Pro				
	370					375					380								
Leu	Phe	Met	Lys	Ser	Pro	Arg	Lys	Ile	Lys	Lys	Val	Gly	Thr	Thr	Glu				
385					390					395					400				
Lys	Glu	His	Glu	Glu	His	Val	Cys	Ser	Ile	Leu	Ala	Ser	Leu	Leu	Arg				
			405						410					415					
Asn	Leu	Arg	Gly	Gln	Gln	Arg	Thr	Arg	Leu	Leu	Asn	Lys	Phe	Thr	Glu				
			420					425					430						
Asn	Asp	Ser	Glu	Lys	Val	Asp	Arg	Leu	Met	Glu	Leu	His	Phe	Lys	Tyr				
	435						440					445							
Leu	Gly	Ala	Met	Gln	Val	Ala	Asp	Lys	Lys	Ile	Glu	Gly	Glu	Lys	His				
	450					455					460								

ITI-08-PCT_Sequence_Listing_ST25.txt

Asp Met Val Arg Arg Gly Glu Ile Ile Asp Asn Asp Thr Glu Glu Glu
465 470 475 480

Phe Tyr Leu Arg Arg Leu Asp Ala Gly Leu Phe Val Leu Gln His Ile
485 490 495

Cys Tyr Ile Met Ala Glu Ile Cys Asn Ala Asn Val Pro Gln Ile Arg
500 505 510

Gln Arg Val His Gln Ile Leu Asn Met Arg Gly Ser Ser Ile Lys Ile
515 520 525

Val Arg His Ile Ile Lys Glu Tyr Ala Glu Asn Ile Gly Asp Gly Arg
530 535 540

Ser Pro Glu Phe Arg Glu Asn Glu Gln Lys Arg Ile Leu Gly Leu Leu
545 550 555 560

Glu Asn Phe

<210> 233

<211> 610

<212> PRT

<213> Artificial Sequence

<220>

<223> BING-4__Homo_sapiens__015213

<400> 233

Met Glu Thr Ala Pro Lys Pro Gly Lys Asp Val Pro Pro Lys Lys Asp
1 5 10 15

Lys Leu Gln Thr Lys Arg Lys Lys Pro Arg Arg Tyr Trp Glu Glu Glu
20 25 30

Thr Val Pro Thr Thr Ala Gly Ala Ser Pro Gly Pro Pro Arg Asn Lys
35 40 45

Lys Asn Arg Glu Leu Arg Pro Gln Arg Pro Lys Asn Ala Tyr Ile Leu
50 55 60

Lys Lys Ser Arg Ile Ser Lys Lys Pro Gln Val Pro Lys Lys Pro Arg
65 70 75 80

Glu Trp Lys Asn Pro Glu Ser Gln Arg Gly Leu Ser Gly Thr Gln Asp
85 90 95

Pro Phe Pro Gly Pro Ala Pro Val Pro Val Glu Val Val Gln Lys Phe
100 105 110

ITI-08-PCT_Sequence_Listing_ST25.txt

Cys Arg Ile Asp Lys Ser Arg Lys Leu Pro His Ser Lys Ala Lys Thr
 115 120 125
 Arg Ser Arg Leu Glu Val Ala Glu Ala Glu Glu Glu Glu Thr Ser Ile
 130 135 140
 Lys Ala Ala Arg Ser Glu Leu Leu Leu Ala Glu Glu Pro Gly Phe Leu
 145 150 155 160
 Glu Gly Glu Asp Gly Glu Asp Thr Ala Lys Ile Cys Gln Ala Asp Ile
 165 170 175
 Val Glu Ala Val Asp Ile Ala Ser Ala Ala Lys His Phe Asp Leu Asn
 180 185 190
 Leu Arg Gln Phe Gly Pro Tyr Arg Leu Asn Tyr Ser Arg Thr Gly Arg
 195 200 205
 His Leu Ala Phe Gly Gly Arg Arg Gly His Val Ala Ala Leu Asp Trp
 210 215 220
 Val Thr Lys Lys Leu Met Cys Glu Ile Asn Val Met Glu Ala Val Arg
 225 230 235 240
 Asp Ile Arg Phe Leu His Ser Glu Ala Leu Leu Ala Val Ala Gln Asn
 245 250 255
 Arg Trp Leu His Ile Tyr Asp Asn Gln Gly Ile Glu Leu His Cys Ile
 260 265 270
 Arg Arg Cys Asp Arg Val Thr Arg Leu Glu Phe Leu Pro Phe His Phe
 275 280 285
 Leu Leu Ala Thr Ala Ser Glu Thr Gly Phe Leu Thr Tyr Leu Asp Val
 290 295 300
 Ser Val Gly Lys Ile Val Ala Ala Leu Asn Ala Arg Ala Gly Arg Leu
 305 310 315 320
 Asp Val Met Ser Gln Asn Pro Tyr Asn Ala Val Ile His Leu Gly His
 325 330 335
 Ser Asn Gly Thr Val Ser Leu Trp Ser Pro Ala Met Lys Glu Pro Leu
 340 345 350
 Ala Lys Ile Leu Cys His Arg Gly Gly Val Arg Ala Val Ala Val Asp
 355 360 365
 Ser Thr Gly Thr Tyr Met Ala Thr Ser Gly Leu Asp His Gln Leu Lys
 370 375 380
 Ile Phe Asp Leu Arg Gly Thr Tyr Gln Pro Leu Ser Thr Arg Thr Leu

ITI-08-PCT_Sequence_Listing_ST25.txt

```

385          390          395          400
Pro His Gly Ala Gly His Leu Ala Phe Ser Gln Arg Gly Leu Leu Val
          405          410          415
Ala Gly Met Gly Asp Val Val Asn Ile Trp Ala Gly Gln Gly Lys Ala
          420          425          430
Ser Pro Pro Ser Leu Glu Gln Pro Tyr Leu Thr His Arg Leu Ser Gly
          435          440          445
Pro Val His Gly Leu Gln Phe Cys Pro Phe Glu Asp Val Leu Gly Val
          450          455          460
Gly His Thr Gly Gly Ile Thr Ser Met Leu Val Pro Gly Ala Gly Glu
465          470          475          480
Pro Asn Phe Asp Gly Leu Glu Ser Asn Pro Tyr Arg Ser Arg Lys Gln
          485          490          495
Arg Gln Glu Trp Glu Val Lys Ala Leu Leu Glu Lys Val Pro Ala Glu
          500          505          510
Leu Ile Cys Leu Asp Pro Arg Ala Leu Ala Glu Val Asp Val Ile Ser
          515          520          525
Leu Glu Gln Gly Lys Lys Glu Gln Ile Glu Arg Leu Gly Tyr Asp Pro
          530          535          540
Gln Ala Lys Ala Pro Phe Gln Pro Lys Pro Lys Gln Lys Gly Arg Ser
545          550          555          560
Ser Thr Ala Ser Leu Val Lys Arg Lys Arg Lys Val Met Asp Glu Glu
          565          570          575
His Arg Asp Lys Val Arg Gln Ser Leu Gln Gln Gln His His Lys Glu
          580          585          590
Ala Lys Ala Lys Pro Thr Gly Ala Arg Pro Ser Ala Leu Asp Arg Phe
          595          600          605
Val Arg
          610

```

```

<210> 234
<211> 298
<212> PRT
<213> Artificial Sequence

<220>
<223> BIRC7__Homo_sapiens__Q96CA5

```

ITI-08-PCT_Sequence_Listing_ST25.txt

<400> 234

Met	Gly	Pro	Lys	Asp	Ser	Ala	Lys	Cys	Leu	His	Arg	Gly	Pro	Gln	Pro	1	5	10	15
Ser	His	Trp	Ala	Ala	Gly	Asp	Gly	Pro	Thr	Gln	Glu	Arg	Cys	Gly	Pro	20	25	30	
Arg	Ser	Leu	Gly	Ser	Pro	Val	Leu	Gly	Leu	Asp	Thr	Cys	Arg	Ala	Trp	35	40	45	
Asp	His	Val	Asp	Gly	Gln	Ile	Leu	Gly	Gln	Leu	Arg	Pro	Leu	Thr	Glu	50	55	60	
Glu	Glu	Glu	Glu	Glu	Gly	Ala	Gly	Ala	Thr	Leu	Ser	Arg	Gly	Pro	Ala	65	70	75	80
Phe	Pro	Gly	Met	Gly	Ser	Glu	Glu	Leu	Arg	Leu	Ala	Ser	Phe	Tyr	Asp	85	90	95	
Trp	Pro	Leu	Thr	Ala	Glu	Val	Pro	Pro	Glu	Leu	Leu	Ala	Ala	Ala	Gly	100	105	110	
Phe	Phe	His	Thr	Gly	His	Gln	Asp	Lys	Val	Arg	Cys	Phe	Phe	Cys	Tyr	115	120	125	
Gly	Gly	Leu	Gln	Ser	Trp	Lys	Arg	Gly	Asp	Asp	Pro	Trp	Thr	Glu	His	130	135	140	
Ala	Lys	Trp	Phe	Pro	Ser	Cys	Gln	Phe	Leu	Leu	Arg	Ser	Lys	Gly	Arg	145	150	155	160
Asp	Phe	Val	His	Ser	Val	Gln	Glu	Thr	His	Ser	Gln	Leu	Leu	Gly	Ser	165	170	175	
Trp	Asp	Pro	Trp	Glu	Glu	Pro	Glu	Asp	Ala	Ala	Pro	Val	Ala	Pro	Ser	180	185	190	
Val	Pro	Ala	Ser	Gly	Tyr	Pro	Glu	Leu	Pro	Thr	Pro	Arg	Arg	Glu	Val	195	200	205	
Gln	Ser	Glu	Ser	Ala	Gln	Glu	Pro	Gly	Gly	Val	Ser	Pro	Ala	Glu	Ala	210	215	220	
Gln	Arg	Ala	Trp	Trp	Val	Leu	Glu	Pro	Pro	Gly	Ala	Arg	Asp	Val	Glu	225	230	235	240
Ala	Gln	Leu	Arg	Arg	Leu	Gln	Glu	Glu	Arg	Thr	Cys	Lys	Val	Cys	Leu	245	250	255	
Asp	Arg	Ala	Val	Ser	Ile	Val	Phe	Val	Pro	Cys	Gly	His	Leu	Val	Cys	260	265	270	

ITI-08-PCT_Sequence_Listing_ST25.txt

Ala Glu Cys Ala Pro Gly Leu Gln Leu Cys Pro Ile Cys Arg Ala Pro
275 280 285

Val Arg Ser Arg Val Arg Thr Phe Leu Ser
290 295

<210> 235

<211> 759

<212> PRT

<213> Artificial Sequence

<220>

<223> BRCA1/m__Homo_sapiens__A0A024R1V0

<400> 235

Met Asp Leu Ser Ala Leu Arg Val Glu Glu Val Gln Asn Val Ile Asn
1 5 10 15

Ala Met Gln Lys Ile Leu Glu Cys Pro Ile Cys Leu Glu Leu Ile Lys
20 25 30

Glu Pro Val Ser Thr Lys Cys Asp His Ile Phe Cys Lys Phe Cys Met
35 40 45

Leu Lys Leu Leu Asn Gln Lys Lys Gly Pro Ser Gln Cys Pro Leu Cys
50 55 60

Lys Asn Asp Ile Thr Lys Arg Ser Leu Gln Glu Ser Thr Arg Phe Ser
65 70 75 80

Gln Leu Val Glu Glu Leu Leu Lys Ile Ile Cys Ala Phe Gln Leu Asp
85 90 95

Thr Gly Leu Glu Tyr Ala Asn Ser Tyr Asn Phe Ala Lys Lys Glu Asn
100 105 110

Asn Ser Pro Glu His Leu Lys Asp Glu Val Ser Ile Ile Gln Ser Met
115 120 125

Gly Tyr Arg Asn Arg Ala Lys Arg Leu Leu Gln Ser Glu Pro Glu Asn
130 135 140

Pro Ser Leu Gln Glu Thr Ser Leu Ser Val Gln Leu Ser Asn Leu Gly
145 150 155 160

Thr Val Arg Thr Leu Arg Thr Lys Gln Arg Ile Gln Pro Gln Lys Thr
165 170 175

Ser Val Tyr Ile Glu Leu Gly Ser Asp Ser Ser Glu Asp Thr Val Asn
180 185 190

ITI-08-PCT_Sequence_Listing_ST25.txt

Lys Ala Thr Tyr Cys Ser Val Gly Asp Gln Glu Leu Leu Gln Ile Thr
 195 200 205
 Pro Gln Gly Thr Arg Asp Glu Ile Ser Leu Asp Ser Ala Lys Lys Ala
 210 215 220
 Ala Cys Glu Phe Ser Glu Thr Asp Val Thr Asn Thr Glu His His Gln
 225 230 235 240
 Pro Ser Asn Asn Asp Leu Asn Thr Thr Glu Lys Arg Ala Ala Glu Arg
 245 250 255
 His Pro Glu Lys Tyr Gln Gly Glu Ala Ala Ser Gly Cys Glu Ser Glu
 260 265 270
 Thr Ser Val Ser Glu Asp Cys Ser Gly Leu Ser Ser Gln Ser Asp Ile
 275 280 285
 Leu Thr Thr Gln Gln Arg Asp Thr Met Gln His Asn Leu Ile Lys Leu
 290 295 300
 Gln Gln Glu Met Ala Glu Leu Glu Ala Val Leu Glu Gln His Gly Ser
 305 310 315 320
 Gln Pro Ser Asn Ser Tyr Pro Ser Ile Ile Ser Asp Ser Ser Ala Leu
 325 330 335
 Glu Asp Leu Arg Asn Pro Glu Gln Ser Thr Ser Glu Lys Val Leu Thr
 340 345 350
 Ser Gln Lys Ser Ser Glu Tyr Pro Ile Ser Gln Asn Pro Glu Gly Leu
 355 360 365
 Ser Ala Asp Lys Phe Glu Val Ser Ala Asp Ser Ser Thr Ser Lys Asn
 370 375 380
 Lys Glu Pro Gly Val Glu Arg Ser Ser Pro Ser Lys Cys Pro Ser Leu
 385 390 395 400
 Asp Asp Arg Trp Tyr Met His Ser Cys Ser Gly Ser Leu Gln Asn Arg
 405 410 415
 Asn Tyr Pro Ser Gln Glu Glu Leu Ile Lys Val Val Asp Val Glu Glu
 420 425 430
 Gln Gln Leu Glu Glu Ser Gly Pro His Asp Leu Thr Glu Thr Ser Tyr
 435 440 445
 Leu Pro Arg Gln Asp Leu Glu Gly Thr Pro Tyr Leu Glu Ser Gly Ile
 450 455 460

ITI-08-PCT_Sequence_Listing_ST25.txt

Ser	Leu	Phe	Ser	Asp	Asp	Pro	Glu	Ser	Asp	Pro	Ser	Glu	Asp	Arg	Ala	465	470	475	480
Pro	Glu	Ser	Ala	Arg	Val	Gly	Asn	Ile	Pro	Ser	Ser	Thr	Ser	Ala	Leu		485	490	495
Lys	Val	Pro	Gln	Leu	Lys	Val	Ala	Glu	Ser	Ala	Gln	Ser	Pro	Ala	Ala		500	505	510
Ala	His	Thr	Thr	Asp	Thr	Ala	Gly	Tyr	Asn	Ala	Met	Glu	Glu	Ser	Val		515	520	525
Ser	Arg	Glu	Lys	Pro	Glu	Leu	Thr	Ala	Ser	Thr	Glu	Arg	Val	Asn	Lys		530	535	540
Arg	Met	Ser	Met	Val	Val	Ser	Gly	Leu	Thr	Pro	Glu	Glu	Phe	Met	Leu		545	550	555
Val	Tyr	Lys	Phe	Ala	Arg	Lys	His	His	Ile	Thr	Leu	Thr	Asn	Leu	Ile		565	570	575
Thr	Glu	Glu	Thr	Thr	His	Val	Val	Met	Lys	Thr	Asp	Ala	Glu	Phe	Val		580	585	590
Cys	Glu	Arg	Thr	Leu	Lys	Tyr	Phe	Leu	Gly	Ile	Ala	Gly	Gly	Lys	Trp		595	600	605
Val	Val	Ser	Tyr	Phe	Trp	Val	Thr	Gln	Ser	Ile	Lys	Glu	Arg	Lys	Met		610	615	620
Leu	Asn	Glu	His	Asp	Phe	Glu	Val	Arg	Gly	Asp	Val	Val	Asn	Gly	Arg		625	630	635
Asn	His	Gln	Gly	Pro	Lys	Arg	Ala	Arg	Glu	Ser	Gln	Asp	Arg	Lys	Ile		645	650	655
Phe	Arg	Gly	Leu	Glu	Ile	Cys	Cys	Tyr	Gly	Pro	Phe	Thr	Asn	Met	Pro		660	665	670
Thr	Asp	Gln	Leu	Glu	Trp	Met	Val	Gln	Leu	Cys	Gly	Ala	Ser	Val	Val		675	680	685
Lys	Glu	Leu	Ser	Ser	Phe	Thr	Leu	Gly	Thr	Gly	Val	His	Pro	Ile	Val		690	695	700
Val	Val	Gln	Pro	Asp	Ala	Trp	Thr	Glu	Asp	Asn	Gly	Phe	His	Ala	Ile		705	710	715
Gly	Gln	Met	Cys	Glu	Ala	Pro	Val	Val	Thr	Arg	Glu	Trp	Val	Leu	Asp		725	730	735
Ser	Val	Ala	Leu	Tyr	Gln	Cys	Gln	Glu	Leu	Asp	Thr	Tyr	Leu	Ile	Pro				

ITI-08-PCT_Sequence_Listing_ST25.txt

740

745

750

Gln Ile Pro His Ser His Tyr
755

<210> 236

<211> 719

<212> PRT

<213> Artificial Sequence

<220>

<223> BRCA1/m__Homo_sapiens__A0A024R1V7

<400> 236

Met Asp Leu Ser Ala Leu Arg Val Glu Glu Val Gln Asn Val Ile Asn
1 5 10 15

Ala Met Gln Lys Ile Leu Glu Cys Pro Ile Cys Leu Glu Leu Ile Lys
20 25 30

Glu Pro Val Ser Thr Lys Cys Asp His Ile Phe Cys Lys Phe Cys Met
35 40 45

Leu Lys Leu Leu Asn Gln Lys Lys Gly Pro Ser Gln Cys Pro Leu Cys
50 55 60

Lys Asn Asp Ile Thr Lys Arg Ser Leu Gln Glu Ser Thr Arg Phe Ser
65 70 75 80

Gln Leu Val Glu Glu Leu Leu Lys Ile Ile Cys Ala Phe Gln Leu Asp
85 90 95

Thr Gly Leu Glu Tyr Ala Asn Ser Tyr Asn Phe Ala Lys Lys Glu Asn
100 105 110

Asn Ser Pro Glu His Leu Lys Asp Glu Val Ser Ile Ile Gln Ser Met
115 120 125

Gly Tyr Arg Asn Arg Ala Lys Arg Leu Leu Gln Ser Glu Pro Glu Asn
130 135 140

Pro Ser Leu Gln Glu Thr Ser Leu Ser Val Gln Leu Ser Asn Leu Gly
145 150 155 160

Thr Val Arg Thr Leu Arg Thr Lys Gln Arg Ile Gln Pro Gln Lys Thr
165 170 175

Ser Val Tyr Ile Glu Leu Ala Ala Cys Glu Phe Ser Glu Thr Asp Val
180 185 190

Thr Asn Thr Glu His His Gln Pro Ser Asn Asn Asp Leu Asn Thr Thr

ITI-08-PCT_Sequence_Listing_ST25.txt

```

195                200                205
Glu Lys Arg Ala Ala Glu Arg His Pro Glu Lys Tyr Gln Gly Glu Ala
210                215                220
Ala Ser Gly Cys Glu Ser Glu Thr Ser Val Ser Glu Asp Cys Ser Gly
225                230                235                240
Leu Ser Ser Gln Ser Asp Ile Leu Thr Thr Gln Gln Arg Asp Thr Met
245                250                255
Gln His Asn Leu Ile Lys Leu Gln Gln Glu Met Ala Glu Leu Glu Ala
260                265                270
Val Leu Glu Gln His Gly Ser Gln Pro Ser Asn Ser Tyr Pro Ser Ile
275                280                285
Ile Ser Asp Ser Ser Ala Leu Glu Asp Leu Arg Asn Pro Glu Gln Ser
290                295                300
Thr Ser Glu Lys Ala Val Leu Thr Ser Gln Lys Ser Ser Glu Tyr Pro
305                310                315                320
Ile Ser Gln Asn Pro Glu Gly Leu Ser Ala Asp Lys Phe Glu Val Ser
325                330                335
Ala Asp Ser Ser Thr Ser Lys Asn Lys Glu Pro Gly Val Glu Arg Ser
340                345                350
Ser Pro Ser Lys Cys Pro Ser Leu Asp Asp Arg Trp Tyr Met His Ser
355                360                365
Cys Ser Gly Ser Leu Gln Asn Arg Asn Tyr Pro Ser Gln Glu Glu Leu
370                375                380
Ile Lys Val Val Asp Val Glu Glu Gln Gln Leu Glu Glu Ser Gly Pro
385                390                395                400
His Asp Leu Thr Glu Thr Ser Tyr Leu Pro Arg Gln Asp Leu Glu Gly
405                410                415
Thr Pro Tyr Leu Glu Ser Gly Ile Ser Leu Phe Ser Asp Asp Pro Glu
420                425                430
Ser Asp Pro Ser Glu Asp Arg Ala Pro Glu Ser Ala Arg Val Gly Asn
435                440                445
Ile Pro Ser Ser Thr Ser Ala Leu Lys Val Pro Gln Leu Lys Val Ala
450                455                460
Glu Ser Ala Gln Ser Pro Ala Ala Ala His Thr Thr Asp Thr Ala Gly
465                470                475                480

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Tyr	Asn	Ala	Met	Glu	Glu	Ser	Val	Ser	Arg	Glu	Lys	Pro	Glu	Leu	Thr	
				485					490					495		
Ala	Ser	Thr	Glu	Arg	Val	Asn	Lys	Arg	Met	Ser	Met	Val	Val	Ser	Gly	
			500					505					510			
Leu	Thr	Pro	Glu	Glu	Phe	Met	Leu	Val	Tyr	Lys	Phe	Ala	Arg	Lys	His	
		515					520					525				
His	Ile	Thr	Leu	Thr	Asn	Leu	Ile	Thr	Glu	Glu	Thr	Thr	His	Val	Val	
	530					535					540					
Met	Lys	Thr	Asp	Ala	Glu	Phe	Val	Cys	Glu	Arg	Thr	Leu	Lys	Tyr	Phe	
545					550				555						560	
Leu	Gly	Ile	Ala	Gly	Gly	Lys	Trp	Val	Val	Ser	Tyr	Phe	Trp	Val	Thr	
				565					570					575		
Gln	Ser	Ile	Lys	Glu	Arg	Lys	Met	Leu	Asn	Glu	His	Asp	Phe	Glu	Val	
			580					585					590			
Arg	Gly	Asp	Val	Val	Asn	Gly	Arg	Asn	His	Gln	Gly	Pro	Lys	Arg	Ala	
		595					600					605				
Arg	Glu	Ser	Gln	Asp	Arg	Lys	Ile	Phe	Arg	Gly	Leu	Glu	Ile	Cys	Cys	
	610					615					620					
Tyr	Gly	Pro	Phe	Thr	Asn	Met	Pro	Thr	Asp	Gln	Leu	Glu	Trp	Met	Val	
625					630					635					640	
Gln	Leu	Cys	Gly	Ala	Ser	Val	Val	Lys	Glu	Leu	Ser	Ser	Phe	Thr	Leu	
				645					650					655		
Gly	Thr	Gly	Val	His	Pro	Ile	Val	Val	Val	Gln	Pro	Asp	Ala	Trp	Thr	
			660					665					670			
Glu	Asp	Asn	Gly	Phe	His	Ala	Ile	Gly	Gln	Met	Cys	Glu	Ala	Pro	Val	
		675					680					685				
Val	Thr	Arg	Glu	Trp	Val	Leu	Asp	Ser	Val	Ala	Leu	Tyr	Gln	Cys	Gln	
	690					695					700					
Glu	Leu	Asp	Thr	Tyr	Leu	Ile	Pro	Gln	Ile	Pro	His	Ser	His	Tyr		
705					710				715							

<210> 237
 <211> 721
 <212> PRT
 <213> Artificial Sequence

<220>

ITI-08-PCT_Sequence_Listing_ST25.txt

<223> BRCA1/m__Homo_sapiens__A0A024R1Z8

<400> 237

Met	Asp	Leu	Ser	Ala	Leu	Arg	Val	Glu	Glu	Val	Gln	Asn	Val	Ile	Asn	1	5	10	15
Ala	Met	Gln	Lys	Ile	Leu	Glu	Cys	Pro	Ile	Cys	Leu	Glu	Leu	Ile	Lys	20	25	30	
Glu	Pro	Val	Ser	Thr	Lys	Cys	Asp	His	Ile	Phe	Cys	Lys	Phe	Cys	Met	35	40	45	
Leu	Lys	Leu	Leu	Asn	Gln	Lys	Lys	Gly	Pro	Ser	Gln	Cys	Pro	Leu	Cys	50	55	60	
Lys	Asn	Asp	Ile	Thr	Lys	Arg	Ser	Leu	Gln	Glu	Ser	Thr	Arg	Phe	Ser	65	70	75	80
Gln	Leu	Val	Glu	Glu	Leu	Leu	Lys	Ile	Ile	Cys	Ala	Phe	Gln	Leu	Asp	85	90	95	
Thr	Gly	Leu	Glu	Tyr	Ala	Asn	Ser	Tyr	Asn	Phe	Ala	Lys	Lys	Glu	Asn	100	105	110	
Asn	Ser	Pro	Glu	His	Leu	Lys	Asp	Glu	Val	Ser	Ile	Ile	Gln	Ser	Met	115	120	125	
Gly	Tyr	Arg	Asn	Arg	Ala	Lys	Arg	Leu	Leu	Gln	Ser	Glu	Pro	Glu	Asn	130	135	140	
Pro	Ser	Leu	Gln	Glu	Thr	Ser	Leu	Ser	Val	Gln	Leu	Ser	Asn	Leu	Gly	145	150	155	160
Thr	Val	Arg	Thr	Leu	Arg	Thr	Lys	Gln	Arg	Ile	Gln	Pro	Gln	Lys	Thr	165	170	175	
Ser	Val	Tyr	Ile	Glu	Leu	Gly	Ser	Asp	Ser	Ser	Glu	Asp	Thr	Val	Asn	180	185	190	
Lys	Ala	Thr	Tyr	Cys	Ser	Val	Gly	Asp	Gln	Glu	Leu	Leu	Gln	Ile	Thr	195	200	205	
Pro	Gln	Gly	Thr	Arg	Asp	Glu	Ile	Ser	Leu	Asp	Ser	Ala	Lys	Lys	Gly	210	215	220	
Glu	Ala	Ala	Ser	Gly	Cys	Glu	Ser	Glu	Thr	Ser	Val	Ser	Glu	Asp	Cys	225	230	235	240
Ser	Gly	Leu	Ser	Ser	Gln	Ser	Asp	Ile	Leu	Thr	Thr	Gln	Gln	Arg	Asp	245	250	255	

Thr	Met	Gln	His	Asn	Leu	Ile	Lys	Leu	Gln	Gln	Glu	Met	Ala	Glu	Leu
			260									270			
Glu	Ala	Val	Leu	Glu	Gln	His	Gly	Ser	Gln	Pro	Ser	Asn	Ser	Tyr	Pro
			275									285			
Ser	Ile	Ile	Ser	Asp	Ser	Ser	Ala	Leu	Glu	Asp	Leu	Arg	Asn	Pro	Glu
			290									300			
Gln	Ser	Thr	Ser	Glu	Lys	Ala	Val	Leu	Thr	Ser	Gln	Lys	Ser	Ser	Glu
			305									315			
Tyr	Pro	Ile	Ser	Gln	Asn	Pro	Glu	Gly	Leu	Ser	Ala	Asp	Lys	Phe	Glu
			325									335			
Val	Ser	Ala	Asp	Ser	Ser	Thr	Ser	Lys	Asn	Lys	Glu	Pro	Gly	Val	Glu
			340									350			
Arg	Ser	Ser	Pro	Ser	Lys	Cys	Pro	Ser	Leu	Asp	Asp	Arg	Trp	Tyr	Met
			355									365			
His	Ser	Cys	Ser	Gly	Ser	Leu	Gln	Asn	Arg	Asn	Tyr	Pro	Ser	Gln	Glu
			370									380			
Glu	Leu	Ile	Lys	Val	Val	Asp	Val	Glu	Glu	Gln	Gln	Leu	Glu	Glu	Ser
			385									395			
Gly	Pro	His	Asp	Leu	Thr	Glu	Thr	Ser	Tyr	Leu	Pro	Arg	Gln	Asp	Leu
			405									415			
Glu	Gly	Thr	Pro	Tyr	Leu	Glu	Ser	Gly	Ile	Ser	Leu	Phe	Ser	Asp	Asp
			420									430			
Pro	Glu	Ser	Asp	Pro	Ser	Glu	Asp	Arg	Ala	Pro	Glu	Ser	Ala	Arg	Val
			435									445			
Gly	Asn	Ile	Pro	Ser	Ser	Thr	Ser	Ala	Leu	Lys	Val	Pro	Gln	Leu	Lys
			450									460			
Val	Ala	Glu	Ser	Ala	Gln	Ser	Pro	Ala	Ala	Ala	His	Thr	Thr	Asp	Thr
			465									475			
Ala	Gly	Tyr	Asn	Ala	Met	Glu	Glu	Ser	Val	Ser	Arg	Glu	Lys	Pro	Glu
			485									495			
Leu	Thr	Ala	Ser	Thr	Glu	Arg	Val	Asn	Lys	Arg	Met	Ser	Met	Val	Val
			500									510			
Ser	Gly	Leu	Thr	Pro	Glu	Glu	Phe	Met	Leu	Val	Tyr	Lys	Phe	Ala	Arg
			515									525			
Lys	His	His	Ile	Thr	Leu	Thr	Asn	Leu	Ile	Thr	Glu	Glu	Thr	Thr	His

ITI-08-PCT_Sequence_Listing_ST25.txt

530

535

540

Val Val Met Lys Thr Asp Ala Glu Phe Val Cys Glu Arg Thr Leu Lys
545 550 555 560

Tyr Phe Leu Gly Ile Ala Gly Gly Lys Trp Val Val Ser Tyr Phe Trp
565 570 575

Val Thr Gln Ser Ile Lys Glu Arg Lys Met Leu Asn Glu His Asp Phe
580 585 590

Glu Val Arg Gly Asp Val Val Asn Gly Arg Asn His Gln Gly Pro Lys
595 600 605

Arg Ala Arg Glu Ser Gln Asp Arg Lys Ile Phe Arg Gly Leu Glu Ile
610 615 620

Cys Cys Tyr Gly Pro Phe Thr Asn Met Pro Thr Asp Gln Leu Glu Trp
625 630 635 640

Met Val Gln Leu Cys Gly Ala Ser Val Val Lys Glu Leu Ser Ser Phe
645 650 655

Thr Leu Gly Thr Gly Val His Pro Ile Val Val Val Gln Pro Asp Ala
660 665 670

Trp Thr Glu Asp Asn Gly Phe His Ala Ile Gly Gln Met Cys Glu Ala
675 680 685

Pro Val Val Thr Arg Glu Trp Val Leu Asp Ser Val Ala Leu Tyr Gln
690 695 700

Cys Gln Glu Leu Asp Thr Tyr Leu Ile Pro Gln Ile Pro His Ser His
705 710 715 720

Tyr

<210> 238

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> BRCA1/m__Homo_sapiens__A0A068BFX7

<400> 238

Met Asp Leu Ser Ala Leu Arg Val Glu Glu Val
1 5 10

<210> 239

<211> 173

ITI-08-PCT_Sequence_Listing_ST25.txt

<212> PRT

<213> Artificial Sequence

<220>

<223> BRCA1/m__Homo_sapiens__C6YB45

<400> 239

Met Asp Ala Glu Phe Val Cys Glu Arg Thr Leu Lys Tyr Phe Leu Gly
1 5 10 15

Ile Ala Gly Gly Lys Trp Val Val Ser Tyr Phe Trp Val Thr Gln Ser
20 25 30

Ile Lys Glu Arg Lys Met Leu Asn Glu His Asp Phe Glu Val Arg Gly
35 40 45

Asp Val Val Asn Gly Arg Asn His Gln Gly Pro Lys Arg Ala Arg Glu
50 55 60

Ser Gln Asp Arg Lys Ile Phe Arg Gly Leu Glu Ile Cys Cys Tyr Gly
65 70 75 80

Pro Phe Thr Asn Met Pro Thr Asp Gln Leu Glu Trp Met Val Gln Leu
85 90 95

Cys Gly Ala Ser Val Val Lys Glu Leu Ser Ser Phe Thr Leu Gly Thr
100 105 110

Gly Val His Pro Ile Val Val Val Gln Pro Asp Ala Trp Thr Glu Asp
115 120 125

Asn Gly Phe His Ala Ile Gly Gln Met Cys Glu Ala Pro Val Val Thr
130 135 140

Arg Glu Trp Val Leu Asp Ser Val Ala Leu Tyr Gln Cys Gln Glu Leu
145 150 155 160

Asp Thr Tyr Leu Ile Pro Gln Ile Pro His Ser His Tyr
165 170

<210> 240

<211> 354

<212> PRT

<213> Artificial Sequence

<220>

<223> BRCA1/m__Homo_sapiens__C6YB47

<400> 240

Met His Ser Cys Ser Gly Ser Leu Gln Asn Arg Asn Tyr Pro Ser Gln

ITI-08-PCT_Sequence_Listing_ST25.txt

1		5		10		15											
Glu	Glu	Leu	Ile	Lys	Val	Val	Asp	Val	Glu	Glu	Gln	Gln	Leu	Glu	Glu		
		20					25						30				
Ser	Gly	Pro	His	Asp	Leu	Thr	Glu	Thr	Ser	Tyr	Leu	Pro	Arg	Gln	Asp		
		35					40					45					
Leu	Glu	Gly	Thr	Pro	Tyr	Leu	Glu	Ser	Gly	Ile	Ser	Leu	Phe	Ser	Asp		
	50					55					60						
Asp	Pro	Glu	Ser	Asp	Pro	Ser	Glu	Asp	Arg	Ala	Pro	Glu	Ser	Ala	Arg		
65					70				75						80		
Val	Gly	Asn	Ile	Pro	Ser	Ser	Thr	Ser	Ala	Leu	Lys	Val	Pro	Gln	Leu		
				85					90					95			
Lys	Val	Ala	Glu	Ser	Ala	Gln	Gly	Pro	Ala	Ala	Ala	His	Thr	Thr	Asp		
		100					105						110				
Thr	Ala	Gly	Tyr	Asn	Ala	Met	Glu	Glu	Ser	Val	Ser	Arg	Glu	Lys	Pro		
		115					120					125					
Glu	Leu	Thr	Ala	Ser	Thr	Glu	Arg	Val	Asn	Lys	Arg	Met	Ser	Met	Val		
	130					135					140						
Val	Ser	Gly	Leu	Thr	Pro	Glu	Glu	Phe	Met	Leu	Val	Tyr	Lys	Phe	Ala		
145					150					155					160		
Arg	Lys	His	His	Ile	Thr	Leu	Thr	Asn	Leu	Ile	Thr	Glu	Glu	Thr	Thr		
				165					170					175			
His	Val	Val	Met	Lys	Thr	Asp	Ala	Glu	Phe	Val	Cys	Glu	Arg	Thr	Leu		
			180					185					190				
Lys	Tyr	Phe	Leu	Gly	Ile	Ala	Gly	Gly	Lys	Trp	Val	Val	Ser	Tyr	Phe		
		195					200					205					
Trp	Val	Thr	Gln	Ser	Ile	Lys	Glu	Arg	Lys	Met	Leu	Asn	Glu	His	Asp		
	210					215					220						
Phe	Glu	Val	Arg	Gly	Asp	Val	Val	Asn	Gly	Arg	Asn	His	Gln	Gly	Pro		
225					230					235					240		
Lys	Arg	Ala	Arg	Glu	Ser	Gln	Asp	Arg	Lys	Ile	Phe	Arg	Gly	Leu	Glu		
				245					250					255			
Ile	Cys	Cys	Tyr	Gly	Pro	Phe	Thr	Asn	Met	Pro	Thr	Asp	Gln	Leu	Glu		
			260					265					270				
Trp	Met	Val	Gln	Leu	Cys	Gly	Ala	Ser	Val	Val	Lys	Glu	Leu	Ser	Ser		
		275					280					285					

ITI-08-PCT_Sequence_Listing_ST25.txt

Phe Thr Leu Gly Thr Gly Val His Pro Ile Val Val Val Gln Pro Asp
290 295 300

Ala Trp Thr Glu Asp Asn Gly Phe His Ala Ile Gly Gln Met Cys Glu
305 310 315 320

Thr Pro Val Val Thr Arg Glu Trp Val Leu Asp Ser Val Ala Leu Tyr
325 330 335

Gln Cys Gln Glu Leu Asp Thr Tyr Leu Ile Pro Gln Ile Pro His Ser
340 345 350

His Tyr

<210> 241

<211> 680

<212> PRT

<213> Artificial Sequence

<220>

<223> BRCA1/m__Homo_sapiens__G3XAC3

<400> 241

Met Asp Leu Ser Ala Leu Arg Val Glu Glu Val Gln Asn Val Ile Asn
1 5 10 15

Ala Met Gln Lys Ile Leu Glu Cys Pro Ile Cys Leu Glu Leu Ile Lys
20 25 30

Glu Pro Val Ser Thr Lys Cys Asp His Ile Phe Cys Lys Phe Cys Met
35 40 45

Leu Lys Leu Leu Asn Gln Lys Lys Gly Pro Ser Gln Cys Pro Leu Cys
50 55 60

Lys Asn Asp Ile Thr Lys Arg Ser Leu Gln Glu Ser Thr Arg Phe Ser
65 70 75 80

Gln Leu Val Glu Glu Leu Leu Lys Ile Ile Cys Ala Phe Gln Leu Asp
85 90 95

Thr Gly Leu Glu Tyr Ala Asn Ser Tyr Asn Phe Ala Lys Lys Glu Asn
100 105 110

Asn Ser Pro Glu His Leu Lys Asp Glu Val Ser Ile Ile Gln Ser Met
115 120 125

Gly Tyr Arg Asn Arg Ala Lys Arg Leu Leu Gln Ser Glu Pro Glu Asn
130 135 140

ITI-08-PCT_Sequence_Listing_ST25.txt

Pro	Ser	Leu	Gln	Glu	Thr	Ser	Leu	Ser	Val	Gln	Leu	Ser	Asn	Leu	Gly
145					150					155					160
Thr	Val	Arg	Thr	Leu	Arg	Thr	Lys	Gln	Arg	Ile	Gln	Pro	Gln	Lys	Thr
				165					170					175	
Ser	Val	Tyr	Ile	Glu	Leu	Gly	Glu	Ala	Ala	Ser	Gly	Cys	Glu	Ser	Glu
			180					185					190		
Thr	Ser	Val	Ser	Glu	Asp	Cys	Ser	Gly	Leu	Ser	Ser	Gln	Ser	Asp	Ile
		195					200					205			
Leu	Thr	Thr	Gln	Gln	Arg	Asp	Thr	Met	Gln	His	Asn	Leu	Ile	Lys	Leu
	210					215					220				
Gln	Gln	Glu	Met	Ala	Glu	Leu	Glu	Ala	Val	Leu	Glu	Gln	His	Gly	Ser
225					230					235					240
Gln	Pro	Ser	Asn	Ser	Tyr	Pro	Ser	Ile	Ile	Ser	Asp	Ser	Ser	Ala	Leu
				245					250					255	
Glu	Asp	Leu	Arg	Asn	Pro	Glu	Gln	Ser	Thr	Ser	Glu	Lys	Ala	Val	Leu
			260					265					270		
Thr	Ser	Gln	Lys	Ser	Ser	Glu	Tyr	Pro	Ile	Ser	Gln	Asn	Pro	Glu	Gly
		275					280					285			
Leu	Ser	Ala	Asp	Lys	Phe	Glu	Val	Ser	Ala	Asp	Ser	Ser	Thr	Ser	Lys
	290					295					300				
Asn	Lys	Glu	Pro	Gly	Val	Glu	Arg	Ser	Ser	Pro	Ser	Lys	Cys	Pro	Ser
305					310					315					320
Leu	Asp	Asp	Arg	Trp	Tyr	Met	His	Ser	Cys	Ser	Gly	Ser	Leu	Gln	Asn
				325					330					335	
Arg	Asn	Tyr	Pro	Ser	Gln	Glu	Glu	Leu	Ile	Lys	Val	Val	Asp	Val	Glu
			340					345					350		
Glu	Gln	Gln	Leu	Glu	Glu	Ser	Gly	Pro	His	Asp	Leu	Thr	Glu	Thr	Ser
		355					360					365			
Tyr	Leu	Pro	Arg	Gln	Asp	Leu	Glu	Gly	Thr	Pro	Tyr	Leu	Glu	Ser	Gly
	370					375					380				
Ile	Ser	Leu	Phe	Ser	Asp	Asp	Pro	Glu	Ser	Asp	Pro	Ser	Glu	Asp	Arg
385					390					395					400
Ala	Pro	Glu	Ser	Ala	Arg	Val	Gly	Asn	Ile	Pro	Ser	Ser	Thr	Ser	Ala
				405				410						415	
Leu	Lys	Val	Pro	Gln	Leu	Lys	Val	Ala	Glu	Ser	Ala	Gln	Ser	Pro	Ala

ITI-08-PCT_Sequence_Listing_ST25.txt

420

425

430

Ala Ala His Thr Thr Asp Thr Ala Gly Tyr Asn Ala Met Glu Glu Ser
 435 440 445

Val Ser Arg Glu Lys Pro Glu Leu Thr Ala Ser Thr Glu Arg Val Asn
 450 455 460

Lys Arg Met Ser Met Val Val Ser Gly Leu Thr Pro Glu Glu Phe Met
 465 470 475 480

Leu Val Tyr Lys Phe Ala Arg Lys His His Ile Thr Leu Thr Asn Leu
 485 490 495

Ile Thr Glu Glu Thr Thr His Val Val Met Lys Thr Asp Ala Glu Phe
 500 505 510

Val Cys Glu Arg Thr Leu Lys Tyr Phe Leu Gly Ile Ala Gly Gly Lys
 515 520 525

Trp Val Val Ser Tyr Phe Trp Val Thr Gln Ser Ile Lys Glu Arg Lys
 530 535 540

Met Leu Asn Glu His Asp Phe Glu Val Arg Gly Asp Val Val Asn Gly
 545 550 555 560

Arg Asn His Gln Gly Pro Lys Arg Ala Arg Glu Ser Gln Asp Arg Lys
 565 570 575

Ile Phe Arg Gly Leu Glu Ile Cys Cys Tyr Gly Pro Phe Thr Asn Met
 580 585 590

Pro Thr Asp Gln Leu Glu Trp Met Val Gln Leu Cys Gly Ala Ser Val
 595 600 605

Val Lys Glu Leu Ser Ser Phe Thr Leu Gly Thr Gly Val His Pro Ile
 610 615 620

Val Val Val Gln Pro Asp Ala Trp Thr Glu Asp Asn Gly Phe His Ala
 625 630 635 640

Ile Gly Gln Met Cys Glu Ala Pro Val Val Thr Arg Glu Trp Val Leu
 645 650 655

Asp Ser Val Ala Leu Tyr Gln Cys Gln Glu Leu Asp Thr Tyr Leu Ile
 660 665 670

Pro Gln Ile Pro His Ser His Tyr
 675 680

<210> 242

<211> 181

ITI-08-PCT_Sequence_Listing_ST25.txt

<212> PRT

<213> Artificial Sequence

<220>

<223> BY55__Homo_sapiens__095971

<400> 242

Met Leu Leu Glu Pro Gly Arg Gly Cys Cys Ala Leu Ala Ile Leu Leu
1 5 10 15

Ala Ile Val Asp Ile Gln Ser Gly Gly Cys Ile Asn Ile Thr Ser Ser
20 25 30

Ala Ser Gln Glu Gly Thr Arg Leu Asn Leu Ile Cys Thr Val Trp His
35 40 45

Lys Lys Glu Glu Ala Glu Gly Phe Val Val Phe Leu Cys Lys Asp Arg
50 55 60

Ser Gly Asp Cys Ser Pro Glu Thr Ser Leu Lys Gln Leu Arg Leu Lys
65 70 75 80

Arg Asp Pro Gly Ile Asp Gly Val Gly Glu Ile Ser Ser Gln Leu Met
85 90 95

Phe Thr Ile Ser Gln Val Thr Pro Leu His Ser Gly Thr Tyr Gln Cys
100 105 110

Cys Ala Arg Ser Gln Lys Ser Gly Ile Arg Leu Gln Gly His Phe Phe
115 120 125

Ser Ile Leu Phe Thr Glu Thr Gly Asn Tyr Thr Val Thr Gly Leu Lys
130 135 140

Gln Arg Gln His Leu Glu Phe Ser His Asn Glu Gly Thr Leu Ser Ser
145 150 155 160

Gly Phe Leu Gln Glu Lys Val Trp Val Met Leu Val Thr Ser Leu Val
165 170 175

Ala Leu Gln Ala Leu
180

<210> 243

<211> 109

<212> PRT

<213> Artificial Sequence

<220>

<223> CAMEL__Homo_sapiens__095987

ITI-08-PCT_Sequence_Listing_ST25.txt

<400> 243

Met Leu Met Ala Gln Glu Ala Leu Ala Phe Leu Met Ala Gln Gly Ala
1 5 10 15

Met Leu Ala Ala Gln Glu Arg Arg Val Pro Arg Ala Ala Glu Val Pro
20 25 30

Gly Ala Gln Gly Gln Gln Gly Pro Arg Gly Arg Glu Glu Ala Pro Arg
35 40 45

Gly Val Arg Met Ala Val Pro Leu Leu Arg Arg Met Glu Gly Ala Pro
50 55 60

Ala Gly Pro Gly Gly Arg Thr Ala Ala Cys Phe Ser Cys Thr Ser Arg
65 70 75 80

Cys Leu Ser Arg Arg Pro Trp Lys Arg Ser Trp Ser Ala Gly Ser Cys
85 90 95

Pro Gly Met Pro His Leu Ser Pro Asp Gln Gly Arg Phe
100 105

<210> 244

<211> 522

<212> PRT

<213> Artificial Sequence

<220>

<223> CASPA__Homo_sapiens__Q92851-4

<400> 244

Met Lys Ser Gln Gly Gln His Trp Tyr Ser Ser Ser Asp Lys Asn Cys
1 5 10 15

Lys Val Ser Phe Arg Glu Lys Leu Leu Ile Ile Asp Ser Asn Leu Gly
20 25 30

Val Gln Asp Val Glu Asn Leu Lys Phe Leu Cys Ile Gly Leu Val Pro
35 40 45

Asn Lys Lys Leu Glu Lys Ser Ser Ser Ala Ser Asp Val Phe Glu His
50 55 60

Leu Leu Ala Glu Asp Leu Leu Ser Glu Glu Asp Pro Phe Phe Leu Ala
65 70 75 80

Glu Leu Leu Tyr Ile Ile Arg Gln Lys Lys Leu Leu Gln His Leu Asn
85 90 95

Cys Thr Lys Glu Glu Val Glu Arg Leu Leu Pro Thr Arg Gln Arg Val

ITI-08-PCT_Sequence_Listing_ST25.txt

100	105	110															
Ser	Leu	Phe	Arg	Asn	Leu	Leu	Tyr	Glu	Leu	Ser	Glu	Gly	Ile	Asp	Ser		
	115						120					125					
Glu	Asn	Leu	Lys	Asp	Met	Ile	Phe	Leu	Leu	Lys	Asp	Ser	Leu	Pro	Lys		
	130					135					140						
Thr	Glu	Met	Thr	Ser	Leu	Ser	Phe	Leu	Ala	Phe	Leu	Glu	Lys	Gln	Gly		
145					150					155					160		
Lys	Ile	Asp	Glu	Asp	Asn	Leu	Thr	Cys	Leu	Glu	Asp	Leu	Cys	Lys	Thr		
				165					170					175			
Val	Val	Pro	Lys	Leu	Leu	Arg	Asn	Ile	Glu	Lys	Tyr	Lys	Arg	Glu	Lys		
			180					185					190				
Ala	Ile	Gln	Ile	Val	Thr	Pro	Pro	Val	Asp	Lys	Glu	Ala	Glu	Ser	Tyr		
		195					200					205					
Gln	Gly	Glu	Glu	Glu	Leu	Val	Ser	Gln	Thr	Asp	Val	Lys	Thr	Phe	Leu		
	210					215					220						
Glu	Ala	Leu	Pro	Gln	Glu	Ser	Trp	Gln	Asn	Lys	His	Ala	Gly	Ser	Asn		
225					230					235					240		
Gly	Asn	Arg	Ala	Thr	Asn	Gly	Ala	Pro	Ser	Leu	Val	Ser	Arg	Gly	Met		
				245					250					255			
Gln	Gly	Ala	Ser	Ala	Asn	Thr	Leu	Asn	Ser	Glu	Thr	Ser	Thr	Lys	Arg		
			260					265						270			
Ala	Ala	Val	Tyr	Arg	Met	Asn	Arg	Asn	His	Arg	Gly	Leu	Cys	Val	Ile		
		275					280					285					
Val	Asn	Asn	His	Ser	Phe	Thr	Ser	Leu	Lys	Asp	Arg	Gln	Gly	Thr	His		
	290					295					300						
Lys	Asp	Ala	Glu	Ile	Leu	Ser	His	Val	Phe	Gln	Trp	Leu	Gly	Phe	Thr		
305					310					315					320		
Val	His	Ile	His	Asn	Asn	Val	Thr	Lys	Val	Glu	Met	Glu	Met	Val	Leu		
				325					330					335			
Gln	Lys	Gln	Lys	Cys	Asn	Pro	Ala	His	Ala	Asp	Gly	Asp	Cys	Phe	Val		
			340					345					350				
Phe	Cys	Ile	Leu	Thr	His	Gly	Arg	Phe	Gly	Ala	Val	Tyr	Ser	Ser	Asp		
		355					360					365					
Glu	Ala	Leu	Ile	Pro	Ile	Arg	Glu	Ile	Met	Ser	His	Phe	Thr	Ala	Leu		
	370					375					380						

ITI-08-PCT_Sequence_Listing_ST25.txt

Gln Cys Pro Arg Leu Ala Glu Lys Pro Lys Leu Phe Phe Ile Gln Ala
385 390 395 400

Cys Gln Gly Glu Glu Ile Gln Pro Ser Val Ser Ile Glu Ala Asp Ala
405 410 415

Leu Asn Pro Glu Gln Ala Pro Thr Ser Leu Gln Asp Ser Ile Pro Ala
420 425 430

Glu Ala Asp Phe Leu Leu Gly Leu Ala Thr Val Pro Gly Tyr Val Ser
435 440 445

Phe Arg His Val Glu Glu Gly Ser Trp Tyr Ile Gln Ser Leu Cys Asn
450 455 460

His Leu Lys Lys Leu Val Pro Arg His Glu Asp Ile Leu Ser Ile Leu
465 470 475 480

Thr Ala Val Asn Asp Asp Val Ser Arg Arg Val Asp Lys Gln Gly Thr
485 490 495

Lys Lys Gln Met Pro Gln Pro Ala Phe Thr Leu Arg Lys Lys Leu Val
500 505 510

Phe Pro Val Pro Leu Asp Ala Leu Ser Leu
515 520

<210> 245
<211> 339
<212> PRT
<213> Artificial Sequence

<220>
<223> cathepsin_B__Homo_sapiens__A0A024R374

<400> 245

Met Trp Gln Leu Trp Ala Ser Leu Cys Cys Leu Leu Val Leu Ala Asn
1 5 10 15

Ala Arg Ser Arg Pro Ser Phe His Pro Leu Ser Asp Glu Leu Val Asn
20 25 30

Tyr Val Asn Lys Arg Asn Thr Thr Trp Gln Ala Gly His Asn Phe Tyr
35 40 45

Asn Val Asp Met Ser Tyr Leu Lys Arg Leu Cys Gly Thr Phe Leu Gly
50 55 60

Gly Pro Lys Pro Pro Gln Arg Val Met Phe Thr Glu Asp Leu Lys Leu
65 70 75 80

ITI-08-PCT_Sequence_Listing_ST25.txt

```

Pro  Ala  Ser  Phe  Asp  Ala  Arg  Glu  Gln  Trp  Pro  Gln  Cys  Pro  Thr  Ile
      85                      90                      95

Lys  Glu  Ile  Arg  Asp  Gln  Gly  Ser  Cys  Gly  Ser  Cys  Trp  Ala  Phe  Gly
      100                      105                      110

Ala  Val  Glu  Ala  Ile  Ser  Asp  Arg  Ile  Cys  Ile  His  Thr  Asn  Ala  His
      115                      120                      125

Val  Ser  Val  Glu  Val  Ser  Ala  Glu  Asp  Leu  Leu  Thr  Cys  Cys  Gly  Ser
      130                      135                      140

Met  Cys  Gly  Asp  Gly  Cys  Asn  Gly  Gly  Tyr  Pro  Ala  Glu  Ala  Trp  Asn
145                      150                      155                      160

Phe  Trp  Thr  Arg  Lys  Gly  Leu  Val  Ser  Gly  Gly  Leu  Tyr  Glu  Ser  His
      165                      170                      175

Val  Gly  Cys  Arg  Pro  Tyr  Ser  Ile  Pro  Pro  Cys  Glu  His  His  Val  Asn
      180                      185                      190

Gly  Ser  Arg  Pro  Pro  Cys  Thr  Gly  Glu  Gly  Asp  Thr  Pro  Lys  Cys  Ser
      195                      200                      205

Lys  Ile  Cys  Glu  Pro  Gly  Tyr  Ser  Pro  Thr  Tyr  Lys  Gln  Asp  Lys  His
      210                      215                      220

Tyr  Gly  Tyr  Asn  Ser  Tyr  Ser  Val  Ser  Asn  Ser  Glu  Lys  Asp  Ile  Met
225                      230                      235                      240

Ala  Glu  Ile  Tyr  Lys  Asn  Gly  Pro  Val  Glu  Gly  Ala  Phe  Ser  Val  Tyr
      245                      250                      255

Ser  Asp  Phe  Leu  Leu  Tyr  Lys  Ser  Gly  Val  Tyr  Gln  His  Val  Thr  Gly
      260                      265                      270

Glu  Met  Met  Gly  Gly  His  Ala  Ile  Arg  Ile  Leu  Gly  Trp  Gly  Val  Glu
      275                      280                      285

Asn  Gly  Thr  Pro  Tyr  Trp  Leu  Val  Ala  Asn  Ser  Trp  Asn  Thr  Asp  Trp
      290                      295                      300

Gly  Asp  Asn  Gly  Phe  Phe  Lys  Ile  Leu  Arg  Gly  Gln  Asp  His  Cys  Gly
305                      310                      315                      320

Ile  Glu  Ser  Glu  Val  Val  Ala  Gly  Ile  Pro  Arg  Thr  Asp  Gln  Tyr  Trp
      325                      330                      335

Glu  Lys  Ile

```

<210> 246

ITI-08-PCT_Sequence_Listing_ST25.txt

<211> 339
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> cathepsin_B__Homo_sapiens__P07858

<400> 246

Met Trp Gln Leu Trp Ala Ser Leu Cys Cys Leu Leu Val Leu Ala Asn
 1 5 10 15

Ala Arg Ser Arg Pro Ser Phe His Pro Leu Ser Asp Glu Leu Val Asn
 20 25 30

Tyr Val Asn Lys Arg Asn Thr Thr Trp Gln Ala Gly His Asn Phe Tyr
 35 40 45

Asn Val Asp Met Ser Tyr Leu Lys Arg Leu Cys Gly Thr Phe Leu Gly
 50 55 60

Gly Pro Lys Pro Pro Gln Arg Val Met Phe Thr Glu Asp Leu Lys Leu
 65 70 75 80

Pro Ala Ser Phe Asp Ala Arg Glu Gln Trp Pro Gln Cys Pro Thr Ile
 85 90 95

Lys Glu Ile Arg Asp Gln Gly Ser Cys Gly Ser Cys Trp Ala Phe Gly
 100 105 110

Ala Val Glu Ala Ile Ser Asp Arg Ile Cys Ile His Thr Asn Ala His
 115 120 125

Val Ser Val Glu Val Ser Ala Glu Asp Leu Leu Thr Cys Cys Gly Ser
 130 135 140

Met Cys Gly Asp Gly Cys Asn Gly Gly Tyr Pro Ala Glu Ala Trp Asn
 145 150 155 160

Phe Trp Thr Arg Lys Gly Leu Val Ser Gly Gly Leu Tyr Glu Ser His
 165 170 175

Val Gly Cys Arg Pro Tyr Ser Ile Pro Pro Cys Glu His His Val Asn
 180 185 190

Gly Ser Arg Pro Pro Cys Thr Gly Glu Gly Asp Thr Pro Lys Cys Ser
 195 200 205

Lys Ile Cys Glu Pro Gly Tyr Ser Pro Thr Tyr Lys Gln Asp Lys His
 210 215 220

Tyr Gly Tyr Asn Ser Tyr Ser Val Ser Asn Ser Glu Lys Asp Ile Met

ITI-08-PCT_Sequence_Listing_ST25.txt

```

225                230                235                240
Ala Glu Ile Tyr Lys Asn Gly Pro Val Glu Gly Ala Phe Ser Val Tyr
                245                250                255

Ser Asp Phe Leu Leu Tyr Lys Ser Gly Val Tyr Gln His Val Thr Gly
                260                265                270

Glu Met Met Gly Gly His Ala Ile Arg Ile Leu Gly Trp Gly Val Glu
                275                280                285

Asn Gly Thr Pro Tyr Trp Leu Val Ala Asn Ser Trp Asn Thr Asp Trp
                290                295                300

Gly Asp Asn Gly Phe Phe Lys Ile Leu Arg Gly Gln Asp His Cys Gly
305                310                315                320

Ile Glu Ser Glu Val Val Ala Gly Ile Pro Arg Thr Asp Gln Tyr Trp
                325                330                335

```

Glu Lys Ile

```

<210> 247
<211> 333
<212> PRT
<213> Artificial Sequence

<220>
<223> cathepsin_L__Homo_sapiens__A0A024R276

<400> 247

```

```

Met Asn Pro Thr Leu Ile Leu Ala Ala Phe Cys Leu Gly Ile Ala Ser
1                5                10                15

Ala Thr Leu Thr Phe Asp His Ser Leu Glu Ala Gln Trp Thr Lys Trp
                20                25                30

Lys Ala Met His Asn Arg Leu Tyr Gly Met Asn Glu Glu Gly Trp Arg
                35                40                45

Arg Ala Val Trp Glu Lys Asn Met Lys Met Ile Glu Leu His Asn Gln
                50                55                60

Glu Tyr Arg Glu Gly Lys His Ser Phe Thr Met Ala Met Asn Ala Phe
65                70                75                80

Gly Asp Met Thr Ser Glu Glu Phe Arg Gln Val Met Asn Gly Phe Gln
                85                90                95

Asn Arg Lys Pro Arg Lys Gly Lys Val Phe Gln Glu Pro Leu Phe Tyr
                100                105                110

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Glu Ala Pro Arg Ser Val Asp Trp Arg Glu Lys Gly Tyr Val Thr Pro
115 120 125

Val Lys Asn Gln Gly Gln Cys Gly Ser Cys Trp Ala Phe Ser Ala Thr
130 135 140

Gly Ala Leu Glu Gly Gln Met Phe Arg Lys Thr Gly Arg Leu Ile Ser
145 150 155 160

Leu Ser Glu Gln Asn Leu Val Asp Cys Ser Gly Pro Gln Gly Asn Glu
165 170 175

Gly Cys Asn Gly Gly Leu Met Asp Tyr Ala Phe Gln Tyr Val Gln Asp
180 185 190

Asn Gly Gly Leu Asp Ser Glu Glu Ser Tyr Pro Tyr Glu Ala Thr Glu
195 200 205

Glu Ser Cys Lys Tyr Asn Pro Lys Tyr Ser Val Ala Asn Asp Thr Gly
210 215 220

Phe Val Asp Ile Pro Lys Gln Glu Lys Ala Leu Met Lys Ala Val Ala
225 230 235 240

Thr Val Gly Pro Ile Ser Val Ala Ile Asp Ala Gly His Glu Ser Phe
245 250 255

Leu Phe Tyr Lys Glu Gly Ile Tyr Phe Glu Pro Asp Cys Ser Ser Glu
260 265 270

Asp Met Asp His Gly Val Leu Val Val Gly Tyr Gly Phe Glu Ser Thr
275 280 285

Glu Ser Asp Asn Asn Lys Tyr Trp Leu Val Lys Asn Ser Trp Gly Glu
290 295 300

Glu Trp Gly Met Gly Gly Tyr Val Lys Met Ala Lys Asp Arg Arg Asn
305 310 315 320

His Cys Gly Ile Ala Ser Ala Ala Ser Tyr Pro Thr Val
325 330

<210> 248

<211> 333

<212> PRT

<213> Artificial Sequence

<220>

<223> cathepsin_L__Homo_sapiens__P07711

<400> 248

ITI-08-PCT_Sequence_Listing_ST25.txt

```

Met Asn Pro Thr Leu Ile Leu Ala Ala Phe Cys Leu Gly Ile Ala Ser
1          5          10          15

Ala Thr Leu Thr Phe Asp His Ser Leu Glu Ala Gln Trp Thr Lys Trp
          20          25          30

Lys Ala Met His Asn Arg Leu Tyr Gly Met Asn Glu Glu Gly Trp Arg
          35          40          45

Arg Ala Val Trp Glu Lys Asn Met Lys Met Ile Glu Leu His Asn Gln
          50          55          60

Glu Tyr Arg Glu Gly Lys His Ser Phe Thr Met Ala Met Asn Ala Phe
65          70          75          80

Gly Asp Met Thr Ser Glu Glu Phe Arg Gln Val Met Asn Gly Phe Gln
          85          90          95

Asn Arg Lys Pro Arg Lys Gly Lys Val Phe Gln Glu Pro Leu Phe Tyr
          100          105          110

Glu Ala Pro Arg Ser Val Asp Trp Arg Glu Lys Gly Tyr Val Thr Pro
          115          120          125

Val Lys Asn Gln Gly Gln Cys Gly Ser Cys Trp Ala Phe Ser Ala Thr
          130          135          140

Gly Ala Leu Glu Gly Gln Met Phe Arg Lys Thr Gly Arg Leu Ile Ser
145          150          155          160

Leu Ser Glu Gln Asn Leu Val Asp Cys Ser Gly Pro Gln Gly Asn Glu
          165          170          175

Gly Cys Asn Gly Gly Leu Met Asp Tyr Ala Phe Gln Tyr Val Gln Asp
          180          185          190

Asn Gly Gly Leu Asp Ser Glu Glu Ser Tyr Pro Tyr Glu Ala Thr Glu
          195          200          205

Glu Ser Cys Lys Tyr Asn Pro Lys Tyr Ser Val Ala Asn Asp Thr Gly
          210          215          220

Phe Val Asp Ile Pro Lys Gln Glu Lys Ala Leu Met Lys Ala Val Ala
225          230          235          240

Thr Val Gly Pro Ile Ser Val Ala Ile Asp Ala Gly His Glu Ser Phe
          245          250          255

Leu Phe Tyr Lys Glu Gly Ile Tyr Phe Glu Pro Asp Cys Ser Ser Glu
          260          265          270

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Asp Met Asp His Gly Val Leu Val Val Gly Tyr Gly Phe Glu Ser Thr
275 280 285

Glu Ser Asp Asn Asn Lys Tyr Trp Leu Val Lys Asn Ser Trp Gly Glu
290 295 300

Glu Trp Gly Met Gly Gly Tyr Val Lys Met Ala Lys Asp Arg Arg Asn
305 310 315 320

His Cys Gly Ile Ala Ser Ala Ala Ser Tyr Pro Thr Val
325 330

<210> 249

<211> 151

<212> PRT

<213> Artificial Sequence

<220>

<223> cathepsin_L__Homo_sapiens__Q9HBQ7

<400> 249

Met Asp Tyr Ala Phe Gln Tyr Val Gln Asp Asn Gly Gly Leu Asp Ser
1 5 10 15

Glu Glu Ser Tyr Pro Tyr Glu Ala Thr Glu Glu Ser Cys Lys Tyr Asn
20 25 30

Pro Lys Tyr Ser Val Ala Asn Asp Thr Gly Phe Val Asp Ile Pro Lys
35 40 45

Gln Glu Lys Ala Leu Met Lys Ala Val Ala Thr Val Gly Pro Ile Ser
50 55 60

Val Ala Ile Asp Ala Gly His Glu Ser Phe Leu Phe Tyr Lys Glu Gly
65 70 75 80

Ile Tyr Phe Glu Pro Asp Cys Ser Ser Glu Asp Met Asp His Gly Val
85 90 95

Leu Val Val Gly Tyr Gly Phe Glu Ser Thr Glu Ser Asp Asn Asn Lys
100 105 110

Tyr Trp Leu Val Lys Asn Ser Trp Gly Glu Glu Trp Gly Met Gly Gly
115 120 125

Tyr Val Lys Met Ala Lys Asp Arg Arg Asn His Cys Gly Ile Ala Ser
130 135 140

Ala Ala Ser Tyr Pro Thr Val
145 150

ITI-08-PCT_Sequence_Listing_ST25.txt

<210> 250

<211> 327

<212> PRT

<213> Artificial Sequence

<220>

<223> CD1A__Homo_sapiens__P06126

<400> 250

Met Leu Phe Leu Leu Leu Pro Leu Leu Ala Val Leu Pro Gly Asp Gly
1 5 10 15

Asn Ala Asp Gly Leu Lys Glu Pro Leu Ser Phe His Val Thr Trp Ile
20 25 30

Ala Ser Phe Tyr Asn His Ser Trp Lys Gln Asn Leu Val Ser Gly Trp
35 40 45

Leu Ser Asp Leu Gln Thr His Thr Trp Asp Ser Asn Ser Ser Thr Ile
50 55 60

Val Phe Leu Cys Pro Trp Ser Arg Gly Asn Phe Ser Asn Glu Glu Trp
65 70 75 80

Lys Glu Leu Glu Thr Leu Phe Arg Ile Arg Thr Ile Arg Ser Phe Glu
85 90 95

Gly Ile Arg Arg Tyr Ala His Glu Leu Gln Phe Glu Tyr Pro Phe Glu
100 105 110

Ile Gln Val Thr Gly Gly Cys Glu Leu His Ser Gly Lys Val Ser Gly
115 120 125

Ser Phe Leu Gln Leu Ala Tyr Gln Gly Ser Asp Phe Val Ser Phe Gln
130 135 140

Asn Asn Ser Trp Leu Pro Tyr Pro Val Ala Gly Asn Met Ala Lys His
145 150 155 160

Phe Cys Lys Val Leu Asn Gln Asn Gln His Glu Asn Asp Ile Thr His
165 170 175

Asn Leu Leu Ser Asp Thr Cys Pro Arg Phe Ile Leu Gly Leu Leu Asp
180 185 190

Ala Gly Lys Ala His Leu Gln Arg Gln Val Lys Pro Glu Ala Trp Leu
195 200 205

Ser His Gly Pro Ser Pro Gly Pro Gly His Leu Gln Leu Val Cys His
210 215 220

ITI-08-PCT_Sequence_Listing_ST25.txt

Val Ser Gly Phe Tyr Pro Lys Pro Val Trp Val Met Trp Met Arg Gly
225 230 235 240

Glu Gln Glu Gln Gln Gly Thr Gln Arg Gly Asp Ile Leu Pro Ser Ala
245 250 255

Asp Gly Thr Trp Tyr Leu Arg Ala Thr Leu Glu Val Ala Ala Gly Glu
260 265 270

Ala Ala Asp Leu Ser Cys Arg Val Lys His Ser Ser Leu Glu Gly Gln
275 280 285

Asp Ile Val Leu Tyr Trp Glu His His Ser Ser Val Gly Phe Ile Ile
290 295 300

Leu Ala Val Ile Val Pro Leu Leu Leu Leu Ile Gly Leu Ala Leu Trp
305 310 315 320

Phe Arg Lys Arg Cys Phe Cys
325

<210> 251

<211> 333

<212> PRT

<213> Artificial Sequence

<220>

<223> CD1B__Homo_sapiens__P29016

<400> 251

Met Leu Leu Leu Pro Phe Gln Leu Leu Ala Val Leu Phe Pro Gly Gly
1 5 10 15

Asn Ser Glu His Ala Phe Gln Gly Pro Thr Ser Phe His Val Ile Gln
20 25 30

Thr Ser Ser Phe Thr Asn Ser Thr Trp Ala Gln Thr Gln Gly Ser Gly
35 40 45

Trp Leu Asp Asp Leu Gln Ile His Gly Trp Asp Ser Asp Ser Gly Thr
50 55 60

Ala Ile Phe Leu Lys Pro Trp Ser Lys Gly Asn Phe Ser Asp Lys Glu
65 70 75 80

Val Ala Glu Leu Glu Glu Ile Phe Arg Val Tyr Ile Phe Gly Phe Ala
85 90 95

Arg Glu Val Gln Asp Phe Ala Gly Asp Phe Gln Met Lys Tyr Pro Phe
100 105 110

ITI-08-PCT_Sequence_Listing_ST25.txt

Glu Ile Gln Gly Ile Ala Gly Cys Glu Leu His Ser Gly Gly Ala Ile
115 120 125

Val Ser Phe Leu Arg Gly Ala Leu Gly Gly Leu Asp Phe Leu Ser Val
130 135 140

Lys Asn Ala Ser Cys Val Pro Ser Pro Glu Gly Gly Ser Arg Ala Gln
145 150 155 160

Lys Phe Cys Ala Leu Ile Ile Gln Tyr Gln Gly Ile Met Glu Thr Val
165 170 175

Arg Ile Leu Leu Tyr Glu Thr Cys Pro Arg Tyr Leu Leu Gly Val Leu
180 185 190

Asn Ala Gly Lys Ala Asp Leu Gln Arg Gln Val Lys Pro Glu Ala Trp
195 200 205

Leu Ser Ser Gly Pro Ser Pro Gly Pro Gly Arg Leu Gln Leu Val Cys
210 215 220

His Val Ser Gly Phe Tyr Pro Lys Pro Val Trp Val Met Trp Met Arg
225 230 235 240

Gly Glu Gln Glu Gln Gln Gly Thr Gln Leu Gly Asp Ile Leu Pro Asn
245 250 255

Ala Asn Trp Thr Trp Tyr Leu Arg Ala Thr Leu Asp Val Ala Asp Gly
260 265 270

Glu Ala Ala Gly Leu Ser Cys Arg Val Lys His Ser Ser Leu Glu Gly
275 280 285

Gln Asp Ile Ile Leu Tyr Trp Arg Asn Pro Thr Ser Ile Gly Ser Ile
290 295 300

Val Leu Ala Ile Ile Val Pro Ser Leu Leu Leu Leu Leu Cys Leu Ala
305 310 315 320

Leu Trp Tyr Met Arg Arg Arg Ser Tyr Gln Asn Ile Pro
325 330

<210> 252

<211> 333

<212> PRT

<213> Artificial Sequence

<220>

<223> CD1C__Homo_sapiens__P29017

<400> 252

ITI-08-PCT_Sequence_Listing_ST25.txt

```

Met Leu Phe Leu Gln Phe Leu Leu Leu Ala Leu Leu Leu Pro Gly Gly
1      5      10      15

Asp Asn Ala Asp Ala Ser Gln Glu His Val Ser Phe His Val Ile Gln
20      25      30

Ile Phe Ser Phe Val Asn Gln Ser Trp Ala Arg Gly Gln Gly Ser Gly
35      40      45

Trp Leu Asp Glu Leu Gln Thr His Gly Trp Asp Ser Glu Ser Gly Thr
50      55      60

Ile Ile Phe Leu His Asn Trp Ser Lys Gly Asn Phe Ser Asn Glu Glu
65      70      75      80

Leu Ser Asp Leu Glu Leu Leu Phe Arg Phe Tyr Leu Phe Gly Leu Thr
85      90      95

Arg Glu Ile Gln Asp His Ala Ser Gln Asp Tyr Ser Lys Tyr Pro Phe
100     105     110

Glu Val Gln Val Lys Ala Gly Cys Glu Leu His Ser Gly Lys Ser Pro
115     120     125

Glu Gly Phe Phe Gln Val Ala Phe Asn Gly Leu Asp Leu Leu Ser Phe
130     135     140

Gln Asn Thr Thr Trp Val Pro Ser Pro Gly Cys Gly Ser Leu Ala Gln
145     150     155     160

Ser Val Cys His Leu Leu Asn His Gln Tyr Glu Gly Val Thr Glu Thr
165     170     175

Val Tyr Asn Leu Ile Arg Ser Thr Cys Pro Arg Phe Leu Leu Gly Leu
180     185     190

Leu Asp Ala Gly Lys Met Tyr Val His Arg Gln Val Arg Pro Glu Ala
195     200     205

Trp Leu Ser Ser Arg Pro Ser Leu Gly Ser Gly Gln Leu Leu Leu Val
210     215     220

Cys His Ala Ser Gly Phe Tyr Pro Lys Pro Val Trp Val Thr Trp Met
225     230     235     240

Arg Asn Glu Gln Glu Gln Leu Gly Thr Lys His Gly Asp Ile Leu Pro
245     250     255

Asn Ala Asp Gly Thr Trp Tyr Leu Gln Val Ile Leu Glu Val Ala Ser
260     265     270

Glu Glu Pro Ala Gly Leu Ser Cys Arg Val Arg His Ser Ser Leu Gly

```

ITI-08-PCT_Sequence_Listing_ST25.txt

275

280

285

Gly Gln Asp Ile Ile Leu Tyr Trp Gly His His Phe Ser Met Asn Trp
290 295 300

Ile Ala Leu Val Val Ile Val Pro Leu Val Ile Leu Ile Val Leu Val
305 310 315 320

Leu Trp Phe Lys Lys His Cys Ser Tyr Gln Asp Ile Leu
325 330

<210> 253

<211> 335

<212> PRT

<213> Artificial Sequence

<220>

<223> CD1D__Homo_sapiens__P15813

<400> 253

Met Gly Cys Leu Leu Phe Leu Leu Leu Trp Ala Leu Leu Gln Ala Trp
1 5 10 15

Gly Ser Ala Glu Val Pro Gln Arg Leu Phe Pro Leu Arg Cys Leu Gln
20 25 30

Ile Ser Ser Phe Ala Asn Ser Ser Trp Thr Arg Thr Asp Gly Leu Ala
35 40 45

Trp Leu Gly Glu Leu Gln Thr His Ser Trp Ser Asn Asp Ser Asp Thr
50 55 60

Val Arg Ser Leu Lys Pro Trp Ser Gln Gly Thr Phe Ser Asp Gln Gln
65 70 75 80

Trp Glu Thr Leu Gln His Ile Phe Arg Val Tyr Arg Ser Ser Phe Thr
85 90 95

Arg Asp Val Lys Glu Phe Ala Lys Met Leu Arg Leu Ser Tyr Pro Leu
100 105 110

Glu Leu Gln Val Ser Ala Gly Cys Glu Val His Pro Gly Asn Ala Ser
115 120 125

Asn Asn Phe Phe His Val Ala Phe Gln Gly Lys Asp Ile Leu Ser Phe
130 135 140

Gln Gly Thr Ser Trp Glu Pro Thr Gln Glu Ala Pro Leu Trp Val Asn
145 150 155 160

Leu Ala Ile Gln Val Leu Asn Gln Asp Lys Trp Thr Arg Glu Thr Val

ITI-08-PCT_Sequence_Listing_ST25.txt

165 170 175

Gln Trp Leu Leu Asn Gly Thr Cys Pro Gln Phe Val Ser Gly Leu Leu
180 185 190

Glu Ser Gly Lys Ser Glu Leu Lys Lys Gln Val Lys Pro Lys Ala Trp
195 200 205

Leu Ser Arg Gly Pro Ser Pro Gly Pro Gly Arg Leu Leu Leu Val Cys
210 215 220

His Val Ser Gly Phe Tyr Pro Lys Pro Val Trp Val Lys Trp Met Arg
225 230 235 240

Gly Glu Gln Glu Gln Gln Gly Thr Gln Pro Gly Asp Ile Leu Pro Asn
245 250 255

Ala Asp Glu Thr Trp Tyr Leu Arg Ala Thr Leu Asp Val Val Ala Gly
260 265 270

Glu Ala Ala Gly Leu Ser Cys Arg Val Lys His Ser Ser Leu Glu Gly
275 280 285

Gln Asp Ile Val Leu Tyr Trp Gly Gly Ser Tyr Thr Ser Met Gly Leu
290 295 300

Ile Ala Leu Ala Val Leu Ala Cys Leu Leu Phe Leu Leu Ile Val Gly
305 310 315 320

Phe Thr Ser Arg Phe Lys Arg Gln Thr Ser Tyr Gln Gly Val Leu
325 330 335

<210> 254
<211> 388
<212> PRT
<213> Artificial Sequence

<220>
<223> CD1E__Homo_sapiens__P15812

<400> 254

Met Leu Leu Leu Phe Leu Leu Phe Glu Gly Leu Cys Cys Pro Gly Glu
1 5 10 15

Asn Thr Ala Ala Pro Gln Ala Leu Gln Ser Tyr His Leu Ala Ala Glu
20 25 30

Glu Gln Leu Ser Phe Arg Met Leu Gln Thr Ser Ser Phe Ala Asn His
35 40 45

Ser Trp Ala His Ser Glu Gly Ser Gly Trp Leu Gly Asp Leu Gln Thr

ITI-08-PCT_Sequence_Listing_ST25.txt

50	55	60													
His	Gly	Trp	Asp	Thr	Val	Leu	Gly	Thr	Ile	Arg	Phe	Leu	Lys	Pro	Trp
65					70					75					80
Ser	His	Gly	Asn	Phe	Ser	Lys	Gln	Glu	Leu	Lys	Asn	Leu	Gln	Ser	Leu
				85					90					95	
Phe	Gln	Leu	Tyr	Phe	His	Ser	Phe	Ile	Gln	Ile	Val	Gln	Ala	Ser	Ala
			100					105					110		
Gly	Gln	Phe	Gln	Leu	Glu	Tyr	Pro	Phe	Glu	Ile	Gln	Ile	Leu	Ala	Gly
		115					120					125			
Cys	Arg	Met	Asn	Ala	Pro	Gln	Ile	Phe	Leu	Asn	Met	Ala	Tyr	Gln	Gly
	130					135					140				
Ser	Asp	Phe	Leu	Ser	Phe	Gln	Gly	Ile	Ser	Trp	Glu	Pro	Ser	Pro	Gly
145					150					155					160
Ala	Gly	Ile	Arg	Ala	Gln	Asn	Ile	Cys	Lys	Val	Leu	Asn	Arg	Tyr	Leu
				165					170					175	
Asp	Ile	Lys	Glu	Ile	Leu	Gln	Ser	Leu	Leu	Gly	His	Thr	Cys	Pro	Arg
			180					185					190		
Phe	Leu	Ala	Gly	Leu	Met	Glu	Ala	Gly	Glu	Ser	Glu	Leu	Lys	Arg	Lys
		195					200					205			
Val	Lys	Pro	Glu	Ala	Trp	Leu	Ser	Cys	Gly	Pro	Ser	Pro	Gly	Pro	Gly
	210					215					220				
Arg	Leu	Gln	Leu	Val	Cys	His	Val	Ser	Gly	Phe	Tyr	Pro	Lys	Pro	Val
225					230					235					240
Trp	Val	Met	Trp	Met	Arg	Gly	Glu	Gln	Glu	Gln	Arg	Gly	Thr	Gln	Arg
				245					250					255	
Gly	Asp	Val	Leu	Pro	Asn	Ala	Asp	Glu	Thr	Trp	Tyr	Leu	Arg	Ala	Thr
			260					265					270		
Leu	Asp	Val	Ala	Ala	Gly	Glu	Ala	Ala	Gly	Leu	Ser	Cys	Arg	Val	Lys
		275					280					285			
His	Ser	Ser	Leu	Gly	Gly	His	Asp	Leu	Ile	Ile	His	Trp	Gly	Gly	Tyr
	290					295					300				
Ser	Ile	Phe	Leu	Ile	Leu	Ile	Cys	Leu	Thr	Val	Ile	Val	Thr	Leu	Val
305					310					315					320
Ile	Leu	Val	Val	Val	Asp	Ser	Arg	Leu	Lys	Lys	Gln	Ser	Ser	Asn	Lys
				325					330					335	

ITI-08-PCT_Sequence_Listing_ST25.txt

Asn Ile Leu Ser Pro His Thr Pro Ser Pro Val Phe Leu Met Gly Ala
340 345 350

Asn Thr Gln Asp Thr Lys Asn Ser Arg His Gln Phe Cys Leu Ala Gln
355 360 365

Val Ser Trp Ile Lys Asn Arg Val Leu Lys Lys Trp Lys Thr Arg Leu
370 375 380

Asn Gln Leu Trp
385

<210> 255

<211> 297

<212> PRT

<213> Artificial Sequence

<220>

<223> CD20__Homo_sapiens__P11836

<400> 255

Met Thr Thr Pro Arg Asn Ser Val Asn Gly Thr Phe Pro Ala Glu Pro
1 5 10 15

Met Lys Gly Pro Ile Ala Met Gln Ser Gly Pro Lys Pro Leu Phe Arg
20 25 30

Arg Met Ser Ser Leu Val Gly Pro Thr Gln Ser Phe Phe Met Arg Glu
35 40 45

Ser Lys Thr Leu Gly Ala Val Gln Ile Met Asn Gly Leu Phe His Ile
50 55 60

Ala Leu Gly Gly Leu Leu Met Ile Pro Ala Gly Ile Tyr Ala Pro Ile
65 70 75 80

Cys Val Thr Val Trp Tyr Pro Leu Trp Gly Gly Ile Met Tyr Ile Ile
85 90 95

Ser Gly Ser Leu Leu Ala Ala Thr Glu Lys Asn Ser Arg Lys Cys Leu
100 105 110

Val Lys Gly Lys Met Ile Met Asn Ser Leu Ser Leu Phe Ala Ala Ile
115 120 125

Ser Gly Met Ile Leu Ser Ile Met Asp Ile Leu Asn Ile Lys Ile Ser
130 135 140

His Phe Leu Lys Met Glu Ser Leu Asn Phe Ile Arg Ala His Thr Pro
145 150 155 160

ITI-08-PCT_Sequence_Listing_ST25.txt

Tyr Ile Asn Ile Tyr Asn Cys Glu Pro Ala Asn Pro Ser Glu Lys Asn
165 170 175

Ser Pro Ser Thr Gln Tyr Cys Tyr Ser Ile Gln Ser Leu Phe Leu Gly
180 185 190

Ile Leu Ser Val Met Leu Ile Phe Ala Phe Phe Gln Glu Leu Val Ile
195 200 205

Ala Gly Ile Val Glu Asn Glu Trp Lys Arg Thr Cys Ser Arg Pro Lys
210 215 220

Ser Asn Ile Val Leu Leu Ser Ala Glu Glu Lys Lys Glu Gln Thr Ile
225 230 235 240

Glu Ile Lys Glu Glu Val Val Gly Leu Thr Glu Thr Ser Ser Gln Pro
245 250 255

Lys Asn Glu Glu Asp Ile Glu Ile Ile Pro Ile Gln Glu Glu Glu Glu
260 265 270

Glu Glu Thr Glu Thr Asn Phe Pro Glu Pro Pro Gln Asp Gln Glu Ser
275 280 285

Ser Pro Ile Glu Asn Asp Ser Ser Pro
290 295

<210> 256
<211> 662
<212> PRT
<213> Artificial Sequence

<220>
<223> CD22__Homo_sapiens__060926

<400> 256

Met Glu Ser Lys Thr Glu Lys Trp Met Glu Arg Ile His Leu Asn Val
1 5 10 15

Ser Glu Arg Pro Phe Pro Pro His Ile Gln Leu Pro Pro Glu Ile Gln
20 25 30

Glu Ser Gln Glu Val Thr Leu Thr Cys Leu Leu Asn Phe Ser Cys Tyr
35 40 45

Gly Tyr Pro Ile Gln Leu Gln Trp Leu Leu Glu Gly Val Pro Met Arg
50 55 60

Gln Ala Ala Val Thr Ser Thr Ser Leu Thr Ile Lys Ser Val Phe Thr
65 70 75 80

ITI-08-PCT_Sequence_Listing_ST25.txt

Arg	Ser	Glu	Leu	Lys	Phe	Ser	Pro	Gln	Trp	Ser	His	His	Gly	Lys	Ile	85	90	95
Val	Thr	Cys	Gln	Leu	Gln	Asp	Ala	Asp	Gly	Lys	Phe	Leu	Ser	Asn	Asp	100	105	110
Thr	Val	Gln	Leu	Asn	Val	Lys	His	Thr	Pro	Lys	Leu	Glu	Ile	Lys	Val	115	120	125
Thr	Pro	Ser	Asp	Ala	Ile	Val	Arg	Glu	Gly	Asp	Ser	Val	Thr	Met	Thr	130	135	140
Cys	Glu	Val	Ser	Ser	Thr	Asn	Pro	Glu	Tyr	Thr	Thr	Val	Ser	Trp	Leu	145	150	155
Lys	Asp	Gly	Thr	Ser	Leu	Lys	Lys	Gln	Asn	Thr	Phe	Thr	Leu	Asn	Leu	165	170	175
Arg	Glu	Val	Thr	Lys	Asp	Gln	Ser	Gly	Lys	Tyr	Cys	Cys	Gln	Val	Ser	180	185	190
Asn	Asp	Val	Gly	Pro	Gly	Arg	Ser	Glu	Glu	Val	Phe	Leu	Gln	Val	Gln	195	200	205
Tyr	Ala	Pro	Glu	Pro	Ser	Thr	Val	Gln	Ile	Leu	His	Ser	Pro	Ala	Val	210	215	220
Glu	Gly	Ser	Gln	Val	Glu	Phe	Leu	Cys	Met	Ser	Leu	Ala	Asn	Pro	Leu	225	230	235
Pro	Thr	Asn	Tyr	Thr	Trp	Tyr	His	Asn	Gly	Lys	Glu	Met	Gln	Gly	Arg	245	250	255
Thr	Glu	Glu	Lys	Val	His	Ile	Pro	Lys	Ile	Leu	Pro	Trp	His	Ala	Gly	260	265	270
Thr	Tyr	Ser	Cys	Val	Ala	Glu	Asn	Ile	Leu	Gly	Thr	Gly	Gln	Arg	Gly	275	280	285
Pro	Gly	Ala	Glu	Leu	Asp	Val	Gln	Tyr	Pro	Pro	Lys	Lys	Val	Thr	Thr	290	295	300
Val	Ile	Gln	Asn	Pro	Met	Pro	Ile	Arg	Glu	Gly	Asp	Thr	Val	Thr	Leu	305	310	315
Ser	Cys	Asn	Tyr	Asn	Ser	Ser	Asn	Pro	Ser	Val	Thr	Arg	Tyr	Glu	Trp	325	330	335
Lys	Pro	His	Gly	Ala	Trp	Glu	Glu	Pro	Ser	Leu	Gly	Val	Leu	Lys	Ile	340	345	350

ITI-08-PCT_Sequence_Listing_ST25.txt

Gln Lys Val Gly Trp Asp Asn Thr Thr Ile Ala Cys Ala Arg Cys Asn
355 360 365

Ser Trp Cys Ser Trp Ala Ser Pro Val Ala Leu Asn Val Gln Tyr Ala
370 375 380

Pro Arg Asp Val Arg Val Arg Lys Ile Lys Pro Leu Ser Glu Ile His
385 390 395 400

Ser Gly Asn Ser Val Ser Leu Gln Cys Asp Phe Ser Ser Ser His Pro
405 410 415

Lys Glu Val Gln Phe Phe Trp Glu Lys Asn Gly Arg Leu Leu Gly Lys
420 425 430

Glu Ser Gln Leu Asn Phe Asp Ser Ile Ser Pro Glu Asp Ala Gly Ser
435 440 445

Tyr Ser Cys Trp Val Asn Asn Ser Ile Gly Gln Thr Ala Ser Lys Ala
450 455 460

Trp Thr Leu Glu Val Leu Tyr Ala Pro Arg Arg Leu Arg Val Ser Met
465 470 475 480

Ser Pro Gly Asp Gln Val Met Glu Gly Lys Ser Ala Thr Leu Arg Cys
485 490 495

Glu Ser Asp Ala Asn Pro Pro Val Ser His Tyr Thr Trp Phe Asp Trp
500 505 510

Asn Asn Gln Ser Leu Pro Tyr His Ser Gln Lys Leu Arg Leu Glu Pro
515 520 525

Val Lys Val Gln His Ser Gly Ala Tyr Trp Cys Gln Gly Thr Asn Ser
530 535 540

Val Gly Lys Gly Arg Ser Pro Leu Ser Thr Leu Thr Val Tyr Tyr Ser
545 550 555 560

Pro Glu Thr Ile Gly Arg Arg Val Ala Val Gly Leu Gly Ser Cys Leu
565 570 575

Ala Ile Leu Ile Leu Ala Ile Cys Gly Leu Lys Leu Gln Arg Arg Asp
580 585 590

Ala Glu Ser Ser Glu Met Gln Arg Pro Pro Arg Thr Cys Asp Asp Thr
595 600 605

Val Thr Tyr Ser Ala Leu His Lys Arg Gln Val Gly Asp Tyr Glu Asn
610 615 620

Val Ile Pro Asp Phe Pro Glu Asp Glu Gly Ile His Tyr Ser Glu Leu

ITI-08-PCT_Sequence_Listing_ST25.txt

625 630 635 640

Ile Gln Phe Gly Val Gly Glu Arg Pro Gln Ala Gln Glu Asn Val Asp
645 650 655

Tyr Val Ile Leu Lys His
660

<210> 257
<211> 847
<212> PRT
<213> Artificial Sequence

<220>
<223> CD22__Homo_sapiens__P20273

<400> 257

Met His Leu Leu Gly Pro Trp Leu Leu Leu Leu Val Leu Glu Tyr Leu
1 5 10 15

Ala Phe Ser Asp Ser Ser Lys Trp Val Phe Glu His Pro Glu Thr Leu
20 25 30

Tyr Ala Trp Glu Gly Ala Cys Val Trp Ile Pro Cys Thr Tyr Arg Ala
35 40 45

Leu Asp Gly Asp Leu Glu Ser Phe Ile Leu Phe His Asn Pro Glu Tyr
50 55 60

Asn Lys Asn Thr Ser Lys Phe Asp Gly Thr Arg Leu Tyr Glu Ser Thr
65 70 75 80

Lys Asp Gly Lys Val Pro Ser Glu Gln Lys Arg Val Gln Phe Leu Gly
85 90 95

Asp Lys Asn Lys Asn Cys Thr Leu Ser Ile His Pro Val His Leu Asn
100 105 110

Asp Ser Gly Gln Leu Gly Leu Arg Met Glu Ser Lys Thr Glu Lys Trp
115 120 125

Met Glu Arg Ile His Leu Asn Val Ser Glu Arg Pro Phe Pro Pro His
130 135 140

Ile Gln Leu Pro Pro Glu Ile Gln Glu Ser Gln Glu Val Thr Leu Thr
145 150 155 160

Cys Leu Leu Asn Phe Ser Cys Tyr Gly Tyr Pro Ile Gln Leu Gln Trp
165 170 175

Leu Leu Glu Gly Val Pro Met Arg Gln Ala Ala Val Thr Ser Thr Ser

ITI-08-PCT_Sequence_Listing_ST25.txt

180	185	190													
Leu Thr Ile Lys Ser Val Phe Thr Arg Ser Glu Leu Lys Phe Ser Pro															
195	200	205													
Gln Trp Ser His His Gly Lys Ile Val Thr Cys Gln Leu Gln Asp Ala															
210	215	220													
Asp Gly Lys Phe Leu Ser Asn Asp Thr Val Gln Leu Asn Val Lys His															
225	230	235													
Thr Pro Lys Leu Glu Ile Lys Val Thr Pro Ser Asp Ala Ile Val Arg															
245	250	255													
Glu Gly Asp Ser Val Thr Met Thr Cys Glu Val Ser Ser Ser Asn Pro															
260	265	270													
Glu Tyr Thr Thr Val Ser Trp Leu Lys Asp Gly Thr Ser Leu Lys Lys															
275	280	285													
Gln Asn Thr Phe Thr Leu Asn Leu Arg Glu Val Thr Lys Asp Gln Ser															
290	295	300													
Gly Lys Tyr Cys Cys Gln Val Ser Asn Asp Val Gly Pro Gly Arg Ser															
305	310	315													
Glu Glu Val Phe Leu Gln Val Gln Tyr Ala Pro Glu Pro Ser Thr Val															
325	330	335													
Gln Ile Leu His Ser Pro Ala Val Glu Gly Ser Gln Val Glu Phe Leu															
340	345	350													
Cys Met Ser Leu Ala Asn Pro Leu Pro Thr Asn Tyr Thr Trp Tyr His															
355	360	365													
Asn Gly Lys Glu Met Gln Gly Arg Thr Glu Glu Lys Val His Ile Pro															
370	375	380													
Lys Ile Leu Pro Trp His Ala Gly Thr Tyr Ser Cys Val Ala Glu Asn															
385	390	395													
Ile Leu Gly Thr Gly Gln Arg Gly Pro Gly Ala Glu Leu Asp Val Gln															
405	410	415													
Tyr Pro Pro Lys Lys Val Thr Thr Val Ile Gln Asn Pro Met Pro Ile															
420	425	430													
Arg Glu Gly Asp Thr Val Thr Leu Ser Cys Asn Tyr Asn Ser Ser Asn															
435	440	445													
Pro Ser Val Thr Arg Tyr Glu Trp Lys Pro His Gly Ala Trp Glu Glu															
450	455	460													

ITI-08-PCT_Sequence_Listing_ST25.txt

Pro	Ser	Leu	Gly	Val	Leu	Lys	Ile	Gln	Asn	Val	Gly	Trp	Asp	Asn	Thr	465	470	475	480
Thr	Ile	Ala	Cys	Ala	Ala	Cys	Asn	Ser	Trp	Cys	Ser	Trp	Ala	Ser	Pro		485	490	495
Val	Ala	Leu	Asn	Val	Gln	Tyr	Ala	Pro	Arg	Asp	Val	Arg	Val	Arg	Lys		500	505	510
Ile	Lys	Pro	Leu	Ser	Glu	Ile	His	Ser	Gly	Asn	Ser	Val	Ser	Leu	Gln		515	520	525
Cys	Asp	Phe	Ser	Ser	Ser	His	Pro	Lys	Glu	Val	Gln	Phe	Phe	Trp	Glu		530	535	540
Lys	Asn	Gly	Arg	Leu	Leu	Gly	Lys	Glu	Ser	Gln	Leu	Asn	Phe	Asp	Ser		545	550	555
Ile	Ser	Pro	Glu	Asp	Ala	Gly	Ser	Tyr	Ser	Cys	Trp	Val	Asn	Asn	Ser		565	570	575
Ile	Gly	Gln	Thr	Ala	Ser	Lys	Ala	Trp	Thr	Leu	Glu	Val	Leu	Tyr	Ala		580	585	590
Pro	Arg	Arg	Leu	Arg	Val	Ser	Met	Ser	Pro	Gly	Asp	Gln	Val	Met	Glu		595	600	605
Gly	Lys	Ser	Ala	Thr	Leu	Thr	Cys	Glu	Ser	Asp	Ala	Asn	Pro	Pro	Val		610	615	620
Ser	His	Tyr	Thr	Trp	Phe	Asp	Trp	Asn	Asn	Gln	Ser	Leu	Pro	Tyr	His		625	630	635
Ser	Gln	Lys	Leu	Arg	Leu	Glu	Pro	Val	Lys	Val	Gln	His	Ser	Gly	Ala		645	650	655
Tyr	Trp	Cys	Gln	Gly	Thr	Asn	Ser	Val	Gly	Lys	Gly	Arg	Ser	Pro	Leu		660	665	670
Ser	Thr	Leu	Thr	Val	Tyr	Tyr	Ser	Pro	Glu	Thr	Ile	Gly	Arg	Arg	Val		675	680	685
Ala	Val	Gly	Leu	Gly	Ser	Cys	Leu	Ala	Ile	Leu	Ile	Leu	Ala	Ile	Cys		690	695	700
Gly	Leu	Lys	Leu	Gln	Arg	Arg	Trp	Lys	Arg	Thr	Gln	Ser	Gln	Gln	Gly		705	710	715
Leu	Gln	Glu	Asn	Ser	Ser	Gly	Gln	Ser	Phe	Phe	Val	Arg	Asn	Lys	Lys		725	730	735

ITI-08-PCT_Sequence_Listing_ST25.txt

Val Arg Arg Ala Pro Leu Ser Glu Gly Pro His Ser Leu Gly Cys Tyr
740 745 750

Asn Pro Met Met Glu Asp Gly Ile Ser Tyr Thr Thr Leu Arg Phe Pro
755 760 765

Glu Met Asn Ile Pro Arg Thr Gly Asp Ala Glu Ser Ser Glu Met Gln
770 775 780

Arg Pro Pro Pro Asp Cys Asp Asp Thr Val Thr Tyr Ser Ala Leu His
785 790 795 800

Lys Arg Gln Val Gly Asp Tyr Glu Asn Val Ile Pro Asp Phe Pro Glu
805 810 815

Asp Glu Gly Ile His Tyr Ser Glu Leu Ile Gln Phe Gly Val Gly Glu
820 825 830

Arg Pro Gln Ala Gln Glu Asn Val Asp Tyr Val Ile Leu Lys His
835 840 845

<210> 258

<211> 847

<212> PRT

<213> Artificial Sequence

<220>

<223> CD22__Homo_sapiens__Q0EAF5

<400> 258

Met His Leu Leu Gly Pro Trp Leu Leu Leu Leu Val Leu Glu Tyr Leu
1 5 10 15

Ala Phe Ser Asp Ser Ser Lys Trp Val Phe Glu His Pro Glu Thr Leu
20 25 30

Tyr Ala Trp Glu Gly Ala Cys Val Trp Ile Pro Cys Thr Tyr Arg Ala
35 40 45

Leu Asp Gly Asp Leu Glu Ser Phe Ile Leu Phe His Asn Pro Glu Tyr
50 55 60

Asn Lys Asn Thr Ser Lys Phe Asp Gly Thr Arg Leu Tyr Glu Ser Thr
65 70 75 80

Lys Asp Gly Lys Val Pro Ser Glu Gln Lys Arg Val Gln Phe Leu Gly
85 90 95

Asp Lys Asn Lys Asn Cys Thr Leu Ser Ile His Pro Val His Leu Asn
100 105 110

ITI-08-PCT_Sequence_Listing_ST25.txt

Asp	Ser	Gly	Gln	Leu	Gly	Leu	Arg	Met	Glu	Ser	Lys	Thr	Glu	Lys	Trp	115	120	125	
Met	Glu	Arg	Ile	His	Leu	Asn	Val	Ser	Glu	Arg	Pro	Phe	Pro	Pro	His	130	135	140	
Ile	Gln	Leu	Pro	Pro	Glu	Ile	Gln	Glu	Ser	Gln	Glu	Val	Thr	Leu	Thr	145	150	155	160
Cys	Leu	Leu	Asn	Phe	Ser	Cys	Tyr	Gly	Tyr	Pro	Ile	Gln	Leu	Gln	Trp	165	170	175	
Leu	Leu	Glu	Gly	Val	Pro	Met	Arg	Gln	Ala	Ala	Val	Thr	Ser	Thr	Ser	180	185	190	
Leu	Thr	Ile	Lys	Ser	Val	Phe	Thr	Arg	Ser	Glu	Leu	Lys	Phe	Ser	Pro	195	200	205	
Gln	Trp	Ser	His	His	Gly	Lys	Ile	Val	Thr	Cys	Gln	Leu	Gln	Asp	Ala	210	215	220	
Asp	Gly	Lys	Phe	Leu	Ser	Asn	Asp	Thr	Val	Gln	Leu	Asn	Val	Lys	His	225	230	235	240
Thr	Pro	Lys	Leu	Glu	Ile	Lys	Val	Thr	Pro	Ser	Asp	Ala	Ile	Val	Arg	245	250	255	
Glu	Gly	Asp	Ser	Val	Thr	Met	Thr	Cys	Glu	Val	Ser	Ser	Ser	Asn	Pro	260	265	270	
Glu	Tyr	Thr	Thr	Val	Ser	Trp	Leu	Lys	Asp	Gly	Thr	Ser	Leu	Lys	Lys	275	280	285	
Gln	Asn	Thr	Phe	Thr	Leu	Asn	Leu	Arg	Glu	Val	Thr	Lys	Asp	Gln	Ser	290	295	300	
Gly	Lys	Tyr	Cys	Cys	Gln	Val	Ser	Asn	Asp	Val	Gly	Pro	Gly	Arg	Ser	305	310	315	320
Glu	Glu	Val	Phe	Leu	Gln	Val	Gln	Tyr	Ala	Pro	Glu	Pro	Ser	Thr	Val	325	330	335	
Gln	Ile	Leu	His	Ser	Pro	Ala	Val	Glu	Gly	Ser	Gln	Val	Glu	Phe	Leu	340	345	350	
Cys	Met	Ser	Leu	Ala	Asn	Pro	Leu	Pro	Thr	Asn	Tyr	Thr	Trp	Tyr	His	355	360	365	
Asn	Gly	Lys	Glu	Met	Gln	Gly	Arg	Thr	Glu	Glu	Lys	Val	His	Ile	Pro	370	375	380	
Lys	Ile	Leu	Pro	Trp	His	Ala	Gly	Thr	Tyr	Ser	Cys	Val	Ala	Glu	Asn				

ITI-08-PCT_Sequence_Listing_ST25.txt

```

385          390          395          400
Ile Leu Gly Thr Gly Gln Arg Gly Pro Gly Ala Glu Leu Asp Val Gln
          405          410          415
Tyr Pro Pro Lys Lys Val Thr Thr Val Ile Gln Asn Pro Met Pro Ile
          420          425          430
Arg Glu Gly Asp Thr Val Thr Leu Ser Cys Asn Tyr Asn Ser Ser Asn
          435          440          445
Pro Ser Val Thr Arg Tyr Glu Trp Lys Pro His Gly Ala Trp Glu Glu
          450          455          460
Pro Ser Leu Gly Val Leu Lys Ile Gln Asn Val Gly Trp Asp Asn Thr
465          470          475          480
Thr Ile Ala Cys Ala Ala Cys Asn Ser Trp Cys Ser Trp Ala Ser Pro
          485          490          495
Val Ala Leu Asn Val Gln Tyr Ala Pro Arg Asp Val Arg Val Arg Lys
          500          505          510
Ile Lys Pro Leu Ser Glu Ile His Ser Gly Asn Ser Val Ser Leu Gln
          515          520          525
Cys Asp Phe Ser Ser Ser His Pro Lys Glu Val Gln Phe Phe Trp Glu
          530          535          540
Lys Asn Gly Arg Leu Leu Gly Lys Glu Ser Gln Leu Asn Phe Asp Ser
545          550          555          560
Ile Ser Pro Glu Asp Ala Gly Ser Tyr Ser Cys Trp Val Asn Asn Ser
          565          570          575
Ile Gly Gln Thr Ala Ser Lys Ala Trp Thr Leu Glu Val Leu Tyr Ala
          580          585          590
Pro Arg Arg Leu Arg Val Ser Met Ser Pro Gly Asp Gln Val Met Glu
          595          600          605
Gly Lys Ser Ala Thr Leu Thr Cys Glu Ser Asp Ala Asn Pro Pro Val
          610          615          620
Ser His Tyr Thr Trp Phe Asp Trp Asn Asn Gln Ser Leu Pro Tyr His
625          630          635          640
Ser Gln Lys Leu Arg Leu Glu Pro Val Lys Val Gln His Ser Gly Ala
          645          650          655
Tyr Trp Cys Gln Gly Thr Asn Ser Val Gly Lys Gly Arg Ser Pro Leu
          660          665          670

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Ser Thr Leu Thr Val Tyr Tyr Ser Pro Glu Thr Ile Gly Arg Arg Val
675 680 685

Ala Val Gly Leu Gly Ser Cys Leu Ala Ile Leu Ile Leu Ala Ile Cys
690 695 700

Gly Leu Lys Leu Gln Arg Arg Trp Lys Arg Thr Gln Ser Gln Gln Gly
705 710 715 720

Leu Gln Glu Asn Ser Ser Gly Gln Ser Phe Phe Val Arg Asn Lys Lys
725 730 735

Val Arg Arg Ala Pro Leu Ser Glu Gly Pro His Ser Leu Gly Cys Tyr
740 745 750

Asn Pro Met Met Glu Asp Gly Ile Ser Tyr Thr Thr Leu Arg Phe Pro
755 760 765

Glu Met Asn Ile Pro Arg Thr Gly Asp Ala Glu Ser Ser Glu Met Gln
770 775 780

Arg Pro Pro Pro Asp Cys Asp Asp Thr Val Thr Tyr Ser Ala Leu His
785 790 795 800

Lys Arg Gln Val Gly Asp Tyr Glu Asn Val Ile Pro Asp Phe Pro Glu
805 810 815

Asp Glu Gly Ile His Tyr Ser Glu Leu Ile Gln Phe Gly Val Gly Glu
820 825 830

Arg Pro Gln Ala Gln Glu Asn Val Asp Tyr Val Ile Leu Lys His
835 840 845

<210> 259

<211> 534

<212> PRT

<213> Artificial Sequence

<220>

<223> CD276__Homo_sapiens__Q5ZPR3

<400> 259

Met Leu Arg Arg Arg Gly Ser Pro Gly Met Gly Val His Val Gly Ala
1 5 10 15

Ala Leu Gly Ala Leu Trp Phe Cys Leu Thr Gly Ala Leu Glu Val Gln
20 25 30

Val Pro Glu Asp Pro Val Val Ala Leu Val Gly Thr Asp Ala Thr Leu
35 40 45

ITI-08-PCT_Sequence_Listing_ST25.txt

Cys	Cys	Ser	Phe	Ser	Pro	Glu	Pro	Gly	Phe	Ser	Leu	Ala	Gln	Leu	Asn	50	55	60
Leu	Ile	Trp	Gln	Leu	Thr	Asp	Thr	Lys	Gln	Leu	Val	His	Ser	Phe	Ala	65	70	75
Glu	Gly	Gln	Asp	Gln	Gly	Ser	Ala	Tyr	Ala	Asn	Arg	Thr	Ala	Leu	Phe	85	90	95
Pro	Asp	Leu	Leu	Ala	Gln	Gly	Asn	Ala	Ser	Leu	Arg	Leu	Gln	Arg	Val	100	105	110
Arg	Val	Ala	Asp	Glu	Gly	Ser	Phe	Thr	Cys	Phe	Val	Ser	Ile	Arg	Asp	115	120	125
Phe	Gly	Ser	Ala	Ala	Val	Ser	Leu	Gln	Val	Ala	Ala	Pro	Tyr	Ser	Lys	130	135	140
Pro	Ser	Met	Thr	Leu	Glu	Pro	Asn	Lys	Asp	Leu	Arg	Pro	Gly	Asp	Thr	145	150	155
Val	Thr	Ile	Thr	Cys	Ser	Ser	Tyr	Gln	Gly	Tyr	Pro	Glu	Ala	Glu	Val	165	170	175
Phe	Trp	Gln	Asp	Gly	Gln	Gly	Val	Pro	Leu	Thr	Gly	Asn	Val	Thr	Thr	180	185	190
Ser	Gln	Met	Ala	Asn	Glu	Gln	Gly	Leu	Phe	Asp	Val	His	Ser	Ile	Leu	195	200	205
Arg	Val	Val	Leu	Gly	Ala	Asn	Gly	Thr	Tyr	Ser	Cys	Leu	Val	Arg	Asn	210	215	220
Pro	Val	Leu	Gln	Gln	Asp	Ala	His	Ser	Ser	Val	Thr	Ile	Thr	Pro	Gln	225	230	235
Arg	Ser	Pro	Thr	Gly	Ala	Val	Glu	Val	Gln	Val	Pro	Glu	Asp	Pro	Val	245	250	255
Val	Ala	Leu	Val	Gly	Thr	Asp	Ala	Thr	Leu	Arg	Cys	Ser	Phe	Ser	Pro	260	265	270
Glu	Pro	Gly	Phe	Ser	Leu	Ala	Gln	Leu	Asn	Leu	Ile	Trp	Gln	Leu	Thr	275	280	285
Asp	Thr	Lys	Gln	Leu	Val	His	Ser	Phe	Thr	Glu	Gly	Arg	Asp	Gln	Gly	290	295	300
Ser	Ala	Tyr	Ala	Asn	Arg	Thr	Ala	Leu	Phe	Pro	Asp	Leu	Leu	Ala	Gln	305	310	315

ITI-08-PCT_Sequence_Listing_ST25.txt

Gly Asn Ala Ser Leu Arg Leu Gln Arg Val Arg Val Ala Asp Glu Gly
325 330 335

Ser Phe Thr Cys Phe Val Ser Ile Arg Asp Phe Gly Ser Ala Ala Val
340 345 350

Ser Leu Gln Val Ala Ala Pro Tyr Ser Lys Pro Ser Met Thr Leu Glu
355 360 365

Pro Asn Lys Asp Leu Arg Pro Gly Asp Thr Val Thr Ile Thr Cys Ser
370 375 380

Ser Tyr Arg Gly Tyr Pro Glu Ala Glu Val Phe Trp Gln Asp Gly Gln
385 390 395 400

Gly Val Pro Leu Thr Gly Asn Val Thr Thr Ser Gln Met Ala Asn Glu
405 410 415

Gln Gly Leu Phe Asp Val His Ser Val Leu Arg Val Val Leu Gly Ala
420 425 430

Asn Gly Thr Tyr Ser Cys Leu Val Arg Asn Pro Val Leu Gln Gln Asp
435 440 445

Ala His Gly Ser Val Thr Ile Thr Gly Gln Pro Met Thr Phe Pro Pro
450 455 460

Glu Ala Leu Trp Val Thr Val Gly Leu Ser Val Cys Leu Ile Ala Leu
465 470 475 480

Leu Val Ala Leu Ala Phe Val Cys Trp Arg Lys Ile Lys Gln Ser Cys
485 490 495

Glu Glu Glu Asn Ala Gly Ala Glu Asp Gln Asp Gly Glu Gly Glu Gly
500 505 510

Ser Lys Thr Ala Leu Gln Pro Leu Lys His Ser Asp Ser Lys Glu Asp
515 520 525

Asp Gly Gln Glu Ile Ala
530

<210> 260
<211> 212
<212> PRT
<213> Artificial Sequence

<220>
<223> CD33__Homo_sapiens__B4DF51

<400> 260

ITI-08-PCT_Sequence_Listing_ST25.txt

Met Pro Leu Leu Leu Leu Leu Pro Leu Leu Trp Ala Asp Leu Thr His
1 5 10 15

Arg Pro Lys Ile Leu Ile Pro Gly Thr Leu Glu Pro Gly His Ser Lys
20 25 30

Asn Leu Thr Cys Ser Val Ser Trp Ala Cys Glu Gln Gly Thr Pro Pro
35 40 45

Ile Phe Ser Trp Leu Ser Ala Ala Pro Thr Ser Leu Gly Pro Arg Thr
50 55 60

Thr His Ser Ser Val Leu Ile Ile Thr Pro Arg Pro Gln Asp His Gly
65 70 75 80

Thr Asn Leu Thr Cys Gln Val Lys Phe Ala Gly Ala Gly Val Thr Thr
85 90 95

Glu Arg Thr Ile Gln Leu Asn Val Thr Tyr Val Pro Gln Asn Pro Thr
100 105 110

Thr Gly Ile Phe Pro Gly Asp Gly Ser Gly Lys Gln Glu Thr Arg Ala
115 120 125

Gly Val Val His Gly Ala Ile Gly Gly Ala Gly Val Thr Ala Leu Leu
130 135 140

Ala Leu Cys Leu Cys Leu Ile Phe Phe Ile Val Lys Thr His Arg Arg
145 150 155 160

Lys Ala Ala Arg Thr Ala Val Gly Arg Asn Asp Thr His Pro Thr Thr
165 170 175

Gly Ser Ala Ser Pro Val Ser Asp Gly Ala Ser Trp His Pro Val Cys
180 185 190

Pro Ala Asp Thr Ser Ser Gln Cys Gly Pro Pro Ser Cys Pro Ile Gln
195 200 205

His Phe Gln Asn
210

<210> 261

<211> 364

<212> PRT

<213> Artificial Sequence

<220>

<223> CD33__Homo_sapiens__P20138

<400> 261

ITI-08-PCT_Sequence_Listing_ST25.txt

Met	Pro	Leu	Leu	Leu	Leu	Leu	Pro	Leu	Leu	Trp	Ala	Gly	Ala	Leu	Ala	1	5	10	15
Met	Asp	Pro	Asn	Phe	Trp	Leu	Gln	Val	Gln	Glu	Ser	Val	Thr	Val	Gln	20	25	30	
Glu	Gly	Leu	Cys	Val	Leu	Val	Pro	Cys	Thr	Phe	Phe	His	Pro	Ile	Pro	35	40	45	
Tyr	Tyr	Asp	Lys	Asn	Ser	Pro	Val	His	Gly	Tyr	Trp	Phe	Arg	Glu	Gly	50	55	60	
Ala	Ile	Ile	Ser	Arg	Asp	Ser	Pro	Val	Ala	Thr	Asn	Lys	Leu	Asp	Gln	65	70	75	80
Glu	Val	Gln	Glu	Glu	Thr	Gln	Gly	Arg	Phe	Arg	Leu	Leu	Gly	Asp	Pro	85	90	95	
Ser	Arg	Asn	Asn	Cys	Ser	Leu	Ser	Ile	Val	Asp	Ala	Arg	Arg	Arg	Asp	100	105	110	
Asn	Gly	Ser	Tyr	Phe	Phe	Arg	Met	Glu	Arg	Gly	Ser	Thr	Lys	Tyr	Ser	115	120	125	
Tyr	Lys	Ser	Pro	Gln	Leu	Ser	Val	His	Val	Thr	Asp	Leu	Thr	His	Arg	130	135	140	
Pro	Lys	Ile	Leu	Ile	Pro	Gly	Thr	Leu	Glu	Pro	Gly	His	Ser	Lys	Asn	145	150	155	160
Leu	Thr	Cys	Ser	Val	Ser	Trp	Ala	Cys	Glu	Gln	Gly	Thr	Pro	Pro	Ile	165	170	175	
Phe	Ser	Trp	Leu	Ser	Ala	Ala	Pro	Thr	Ser	Leu	Gly	Pro	Arg	Thr	Thr	180	185	190	
His	Ser	Ser	Val	Leu	Ile	Ile	Thr	Pro	Arg	Pro	Gln	Asp	His	Gly	Thr	195	200	205	
Asn	Leu	Thr	Cys	Gln	Val	Lys	Phe	Ala	Gly	Ala	Gly	Val	Thr	Thr	Glu	210	215	220	
Arg	Thr	Ile	Gln	Leu	Asn	Val	Thr	Tyr	Val	Pro	Gln	Asn	Pro	Thr	Thr	225	230	235	240
Gly	Ile	Phe	Pro	Gly	Asp	Gly	Ser	Gly	Lys	Gln	Glu	Thr	Arg	Ala	Gly	245	250	255	
Val	Val	His	Gly	Ala	Ile	Gly	Gly	Ala	Gly	Val	Thr	Ala	Leu	Leu	Ala	260	265	270	
Leu	Cys	Leu	Cys	Leu	Ile	Phe	Phe	Ile	Val	Lys	Thr	His	Arg	Arg	Lys				

ITI-08-PCT_Sequence_Listing_ST25.txt

275 280 285

Ala Ala Arg Thr Ala Val Gly Arg Asn Asp Thr His Pro Thr Thr Gly
290 295 300

Ser Ala Ser Pro Lys His Gln Lys Lys Ser Lys Leu His Gly Pro Thr
305 310 315 320

Glu Thr Ser Ser Cys Ser Gly Ala Ala Pro Thr Val Glu Met Asp Glu
325 330 335

Glu Leu His Tyr Ala Ser Leu Asn Phe His Gly Met Asn Pro Ser Lys
340 345 350

Asp Thr Ser Thr Glu Tyr Ser Glu Val Arg Thr Gln
355 360

<210> 262
<211> 364
<212> PRT
<213> Artificial Sequence

<220>
<223> CD33__Homo_sapiens__Q546G0

<400> 262

Met Pro Leu Leu Leu Leu Leu Pro Leu Leu Trp Ala Gly Ala Leu Ala
1 5 10 15

Met Asp Pro Asn Phe Trp Leu Gln Val Gln Glu Ser Val Thr Val Gln
20 25 30

Glu Gly Leu Cys Val Leu Val Pro Cys Thr Phe Phe His Pro Ile Pro
35 40 45

Tyr Tyr Asp Lys Asn Ser Pro Val His Gly Tyr Trp Phe Arg Glu Gly
50 55 60

Ala Ile Ile Ser Arg Asp Ser Pro Val Ala Thr Asn Lys Leu Asp Gln
65 70 75 80

Glu Val Gln Glu Glu Thr Gln Gly Arg Phe Arg Leu Leu Gly Asp Pro
85 90 95

Ser Arg Asn Asn Cys Ser Leu Ser Ile Val Asp Ala Arg Arg Arg Asp
100 105 110

Asn Gly Ser Tyr Phe Phe Arg Met Glu Arg Gly Ser Thr Lys Tyr Ser
115 120 125

Tyr Lys Ser Pro Gln Leu Ser Val His Val Thr Asp Leu Thr His Arg

ITI-08-PCT_Sequence_Listing_ST25.txt

130

135

140

Pro Lys Ile Leu Ile Pro Gly Thr Leu Glu Pro Gly His Ser Lys Asn
145 150 155 160

Leu Thr Cys Ser Val Ser Trp Ala Cys Glu Gln Gly Thr Pro Pro Ile
165 170 175

Phe Ser Trp Leu Ser Ala Ala Pro Thr Ser Leu Gly Pro Arg Thr Thr
180 185 190

His Ser Ser Val Leu Ile Ile Thr Pro Arg Pro Gln Asp His Gly Thr
195 200 205

Asn Leu Thr Cys Gln Val Lys Phe Ala Gly Ala Gly Val Thr Thr Glu
210 215 220

Arg Thr Ile Gln Leu Asn Val Thr Tyr Val Pro Gln Asn Pro Thr Thr
225 230 235 240

Gly Ile Phe Pro Gly Asp Gly Ser Gly Lys Gln Glu Thr Arg Ala Gly
245 250 255

Val Val His Gly Ala Ile Gly Gly Ala Gly Val Thr Ala Leu Leu Ala
260 265 270

Leu Cys Leu Cys Leu Ile Phe Phe Ile Val Lys Thr His Arg Arg Lys
275 280 285

Ala Ala Arg Thr Ala Val Gly Arg Asn Asp Thr His Pro Thr Thr Gly
290 295 300

Ser Ala Ser Pro Lys His Gln Lys Lys Ser Lys Leu His Gly Pro Thr
305 310 315 320

Glu Thr Ser Ser Cys Ser Gly Ala Ala Pro Thr Val Glu Met Asp Glu
325 330 335

Glu Leu His Tyr Ala Ser Leu Asn Phe His Gly Met Asn Pro Ser Lys
340 345 350

Asp Thr Ser Thr Glu Tyr Ser Glu Val Arg Thr Gln
355 360

<210> 263

<211> 207

<212> PRT

<213> Artificial Sequence

<220>

<223> CD3E__Homo_sapiens__P07766

ITI-08-PCT_Sequence_Listing_ST25.txt

<400> 263

```

Met Gln Ser Gly Thr His Trp Arg Val Leu Gly Leu Cys Leu Leu Ser
1          5          10          15

Val Gly Val Trp Gly Gln Asp Gly Asn Glu Glu Met Gly Gly Ile Thr
          20          25          30

Gln Thr Pro Tyr Lys Val Ser Ile Ser Gly Thr Thr Val Ile Leu Thr
          35          40          45

Cys Pro Gln Tyr Pro Gly Ser Glu Ile Leu Trp Gln His Asn Asp Lys
          50          55          60

Asn Ile Gly Gly Asp Glu Asp Asp Lys Asn Ile Gly Ser Asp Glu Asp
65          70          75          80

His Leu Ser Leu Lys Glu Phe Ser Glu Leu Glu Gln Ser Gly Tyr Tyr
          85          90          95

Val Cys Tyr Pro Arg Gly Ser Lys Pro Glu Asp Ala Asn Phe Tyr Leu
          100          105          110

Tyr Leu Arg Ala Arg Val Cys Glu Asn Cys Met Glu Met Asp Val Met
          115          120          125

Ser Val Ala Thr Ile Val Ile Val Asp Ile Cys Ile Thr Gly Gly Leu
          130          135          140

Leu Leu Leu Val Tyr Tyr Trp Ser Lys Asn Arg Lys Ala Lys Ala Lys
145          150          155          160

Pro Val Thr Arg Gly Ala Gly Ala Gly Gly Arg Gln Arg Gly Gln Asn
          165          170          175

Lys Glu Arg Pro Pro Pro Val Pro Asn Pro Asp Tyr Glu Pro Ile Arg
          180          185          190

Lys Gly Gln Arg Asp Leu Tyr Ser Gly Leu Asn Gln Arg Arg Ile
          195          200          205

```

<210> 264

<211> 164

<212> PRT

<213> Artificial Sequence

<220>

<223> CD3Z__Homo_sapiens__P20963

<400> 264

```

Met Lys Trp Lys Ala Leu Phe Thr Ala Ala Ile Leu Gln Ala Gln Leu

```

ITI-08-PCT_Sequence_Listing_ST25.txt

```

1           5           10           15
Pro Ile Thr Glu Ala Gln Ser Phe Gly Leu Leu Asp Pro Lys Leu Cys
      20           25           30

Tyr Leu Leu Asp Gly Ile Leu Phe Ile Tyr Gly Val Ile Leu Thr Ala
      35           40           45

Leu Phe Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr
      50           55           60

Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg
65           70           75           80

Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met
      85           90           95

Gly Gly Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn
      100          105          110

Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met
      115          120          125

Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly
      130          135          140

Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala
145          150          155          160

```

Leu Pro Pro Arg

```

<210> 265
<211> 742
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> CD44_Isoform_1__Homo_sapiens__P16070

```

<400> 265

```

Met Asp Lys Phe Trp Trp His Ala Ala Trp Gly Leu Cys Leu Val Pro
1           5           10           15

Leu Ser Leu Ala Gln Ile Asp Leu Asn Ile Thr Cys Arg Phe Ala Gly
      20           25           30

Val Phe His Val Glu Lys Asn Gly Arg Tyr Ser Ile Ser Arg Thr Glu
      35           40           45

Ala Ala Asp Leu Cys Lys Ala Phe Asn Ser Thr Leu Pro Thr Met Ala
      50           55           60

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Gln Met Glu Lys Ala Leu Ser Ile Gly Phe Glu Thr Cys Arg Tyr Gly
 65 70 75 80
 Phe Ile Glu Gly His Val Val Ile Pro Arg Ile His Pro Asn Ser Ile
 85 90 95
 Cys Ala Ala Asn Asn Thr Gly Val Tyr Ile Leu Thr Ser Asn Thr Ser
 100 105 110
 Gln Tyr Asp Thr Tyr Cys Phe Asn Ala Ser Ala Pro Pro Glu Glu Asp
 115 120 125
 Cys Thr Ser Val Thr Asp Leu Pro Asn Ala Phe Asp Gly Pro Ile Thr
 130 135 140
 Ile Thr Ile Val Asn Arg Asp Gly Thr Arg Tyr Val Gln Lys Gly Glu
 145 150 155 160
 Tyr Arg Thr Asn Pro Glu Asp Ile Tyr Pro Ser Asn Pro Thr Asp Asp
 165 170 175
 Asp Val Ser Ser Gly Ser Ser Ser Glu Arg Ser Ser Thr Ser Gly Gly
 180 185 190
 Tyr Ile Phe Tyr Thr Phe Ser Thr Val His Pro Ile Pro Asp Glu Asp
 195 200 205
 Ser Pro Trp Ile Thr Asp Ser Thr Asp Arg Ile Pro Ala Thr Thr Leu
 210 215 220
 Met Ser Thr Ser Ala Thr Ala Thr Glu Thr Ala Thr Lys Arg Gln Glu
 225 230 235 240
 Thr Trp Asp Trp Phe Ser Trp Leu Phe Leu Pro Ser Glu Ser Lys Asn
 245 250 255
 His Leu His Thr Thr Thr Gln Met Ala Gly Thr Ser Ser Asn Thr Ile
 260 265 270
 Ser Ala Gly Trp Glu Pro Asn Glu Glu Asn Glu Asp Glu Arg Asp Arg
 275 280 285
 His Leu Ser Phe Ser Gly Ser Gly Ile Asp Asp Asp Glu Asp Phe Ile
 290 295 300
 Ser Ser Thr Ile Ser Thr Thr Pro Arg Ala Phe Asp His Thr Lys Gln
 305 310 315 320
 Asn Gln Asp Trp Thr Gln Trp Asn Pro Ser His Ser Asn Pro Glu Val
 325 330 335

ITI-08-PCT_Sequence_Listing_ST25.txt

Leu Leu Gln Thr Thr Thr Arg Met Thr Asp Val Asp Arg Asn Gly Thr
 340 345 350
 Thr Ala Tyr Glu Gly Asn Trp Asn Pro Glu Ala His Pro Pro Leu Ile
 355 360 365
 His His Glu His His Glu Glu Glu Thr Pro His Ser Thr Ser Thr
 370 375 380
 Ile Gln Ala Thr Pro Ser Ser Thr Thr Glu Glu Thr Ala Thr Gln Lys
 385 390 395 400
 Glu Gln Trp Phe Gly Asn Arg Trp His Glu Gly Tyr Arg Gln Thr Pro
 405 410 415
 Lys Glu Asp Ser His Ser Thr Thr Gly Thr Ala Ala Ala Ser Ala His
 420 425 430
 Thr Ser His Pro Met Gln Gly Arg Thr Thr Pro Ser Pro Glu Asp Ser
 435 440 445
 Ser Trp Thr Asp Phe Phe Asn Pro Ile Ser His Pro Met Gly Arg Gly
 450 455 460
 His Gln Ala Gly Arg Arg Met Asp Met Asp Ser Ser His Ser Ile Thr
 465 470 475 480
 Leu Gln Pro Thr Ala Asn Pro Asn Thr Gly Leu Val Glu Asp Leu Asp
 485 490 495
 Arg Thr Gly Pro Leu Ser Met Thr Thr Gln Gln Ser Asn Ser Gln Ser
 500 505 510
 Phe Ser Thr Ser His Glu Gly Leu Glu Glu Asp Lys Asp His Pro Thr
 515 520 525
 Thr Ser Thr Leu Thr Ser Ser Asn Arg Asn Asp Val Thr Gly Gly Arg
 530 535 540
 Arg Asp Pro Asn His Ser Glu Gly Ser Thr Thr Leu Leu Glu Gly Tyr
 545 550 555 560
 Thr Ser His Tyr Pro His Thr Lys Glu Ser Arg Thr Phe Ile Pro Val
 565 570 575
 Thr Ser Ala Lys Thr Gly Ser Phe Gly Val Thr Ala Val Thr Val Gly
 580 585 590
 Asp Ser Asn Ser Asn Val Asn Arg Ser Leu Ser Gly Asp Gln Asp Thr
 595 600 605
 Phe His Pro Ser Gly Gly Ser His Thr Thr His Gly Ser Glu Ser Asp

ITI-08-PCT_Sequence_Listing_ST25.txt

610

615

620

Gly His Ser His Gly Ser Gln Glu Gly Gly Ala Asn Thr Thr Ser Gly
625 630 635 640

Pro Ile Arg Thr Pro Gln Ile Pro Glu Trp Leu Ile Ile Leu Ala Ser
645 650 655

Leu Leu Ala Leu Ala Leu Ile Leu Ala Val Cys Ile Ala Val Asn Ser
660 665 670

Arg Arg Arg Cys Gly Gln Lys Lys Lys Leu Val Ile Asn Ser Gly Asn
675 680 685

Gly Ala Val Glu Asp Arg Lys Pro Ser Gly Leu Asn Gly Glu Ala Ser
690 695 700

Lys Ser Gln Glu Met Val His Leu Val Asn Lys Glu Ser Ser Glu Thr
705 710 715 720

Pro Asp Gln Phe Met Thr Ala Asp Glu Thr Arg Asn Leu Gln Asn Val
725 730 735

Asp Met Lys Ile Gly Val
740

<210> 266

<211> 699

<212> PRT

<213> Artificial Sequence

<220>

<223> CD44_Isoform_6__Homo_sapiens__P16070-6

<400> 266

Met Asp Lys Phe Trp Trp His Ala Ala Trp Gly Leu Cys Leu Val Pro
1 5 10 15

Leu Ser Leu Ala Gln Ile Asp Leu Asn Ile Thr Cys Arg Phe Ala Gly
20 25 30

Val Phe His Val Glu Lys Asn Gly Arg Tyr Ser Ile Ser Arg Thr Glu
35 40 45

Ala Ala Asp Leu Cys Lys Ala Phe Asn Ser Thr Leu Pro Thr Met Ala
50 55 60

Gln Met Glu Lys Ala Leu Ser Ile Gly Phe Glu Thr Cys Arg Tyr Gly
65 70 75 80

Phe Ile Glu Gly His Val Val Ile Pro Arg Ile His Pro Asn Ser Ile

ITI-08-PCT_Sequence_Listing_ST25.txt

85

90

95

Cys Ala Ala Asn Asn Thr Gly Val Tyr Ile Leu Thr Ser Asn Thr Ser
 100 105 110

Gln Tyr Asp Thr Tyr Cys Phe Asn Ala Ser Ala Pro Pro Glu Glu Asp
 115 120 125

Cys Thr Ser Val Thr Asp Leu Pro Asn Ala Phe Asp Gly Pro Ile Thr
 130 135 140

Ile Thr Ile Val Asn Arg Asp Gly Thr Arg Tyr Val Gln Lys Gly Glu
 145 150 155 160

Tyr Arg Thr Asn Pro Glu Asp Ile Tyr Pro Ser Asn Pro Thr Asp Asp
 165 170 175

Asp Val Ser Ser Gly Ser Ser Ser Glu Arg Ser Ser Thr Ser Gly Gly
 180 185 190

Tyr Ile Phe Tyr Thr Phe Ser Thr Val His Pro Ile Pro Asp Glu Asp
 195 200 205

Ser Pro Trp Ile Thr Asp Ser Thr Asp Arg Ile Pro Ala Thr Thr Leu
 210 215 220

Met Ser Thr Ser Ala Thr Ala Thr Glu Thr Ala Thr Lys Arg Gln Glu
 225 230 235 240

Thr Trp Asp Trp Phe Ser Trp Leu Phe Leu Pro Ser Glu Ser Lys Asn
 245 250 255

His Leu His Thr Thr Thr Gln Met Ala Gly Thr Ser Ser Asn Thr Ile
 260 265 270

Ser Ala Gly Trp Glu Pro Asn Glu Glu Asn Glu Asp Glu Arg Asp Arg
 275 280 285

His Leu Ser Phe Ser Gly Ser Gly Ile Asp Asp Asp Glu Asp Phe Ile
 290 295 300

Ser Ser Thr Ile Ser Thr Thr Pro Arg Ala Phe Asp His Thr Lys Gln
 305 310 315 320

Asn Gln Asp Trp Thr Gln Trp Asn Pro Ser His Ser Asn Pro Glu Val
 325 330 335

Leu Leu Gln Thr Thr Thr Arg Met Thr Asp Val Asp Arg Asn Gly Thr
 340 345 350

Thr Ala Tyr Glu Gly Asn Trp Asn Pro Glu Ala His Pro Pro Leu Ile
 355 360 365

ITI-08-PCT_Sequence_Listing_ST25.txt

His	His	Glu	His	His	Glu	Glu	Glu	Glu	Thr	Pro	His	Ser	Thr	Ser	Thr	370	375	380	
Thr	Ala	Ser	Ala	His	Thr	Ser	His	Pro	Met	Gln	Gly	Arg	Thr	Thr	Pro	385	390	395	400
Ser	Pro	Glu	Asp	Ser	Ser	Trp	Thr	Asp	Phe	Phe	Asn	Pro	Ile	Ser	His	405	410	415	
Pro	Met	Gly	Arg	Gly	His	Gln	Ala	Gly	Arg	Arg	Met	Asp	Met	Asp	Ser	420	425	430	
Ser	His	Ser	Ile	Thr	Leu	Gln	Pro	Thr	Ala	Asn	Pro	Asn	Thr	Gly	Leu	435	440	445	
Val	Glu	Asp	Leu	Asp	Arg	Thr	Gly	Pro	Leu	Ser	Met	Thr	Thr	Gln	Gln	450	455	460	
Ser	Asn	Ser	Gln	Ser	Phe	Ser	Thr	Ser	His	Glu	Gly	Leu	Glu	Glu	Asp	465	470	475	480
Lys	Asp	His	Pro	Thr	Thr	Ser	Thr	Leu	Thr	Ser	Ser	Asn	Arg	Asn	Asp	485	490	495	
Val	Thr	Gly	Gly	Arg	Arg	Asp	Pro	Asn	His	Ser	Glu	Gly	Ser	Thr	Thr	500	505	510	
Leu	Leu	Glu	Gly	Tyr	Thr	Ser	His	Tyr	Pro	His	Thr	Lys	Glu	Ser	Arg	515	520	525	
Thr	Phe	Ile	Pro	Val	Thr	Ser	Ala	Lys	Thr	Gly	Ser	Phe	Gly	Val	Thr	530	535	540	
Ala	Val	Thr	Val	Gly	Asp	Ser	Asn	Ser	Asn	Val	Asn	Arg	Ser	Leu	Ser	545	550	555	560
Gly	Asp	Gln	Asp	Thr	Phe	His	Pro	Ser	Gly	Gly	Ser	His	Thr	Thr	His	565	570	575	
Gly	Ser	Glu	Ser	Asp	Gly	His	Ser	His	Gly	Ser	Gln	Glu	Gly	Gly	Ala	580	585	590	
Asn	Thr	Thr	Ser	Gly	Pro	Ile	Arg	Thr	Pro	Gln	Ile	Pro	Glu	Trp	Leu	595	600	605	
Ile	Ile	Leu	Ala	Ser	Leu	Leu	Ala	Leu	Ala	Leu	Ile	Leu	Ala	Val	Cys	610	615	620	
Ile	Ala	Val	Asn	Ser	Arg	Arg	Arg	Cys	Gly	Gln	Lys	Lys	Lys	Leu	Val	625	630	635	640

ITI-08-PCT_Sequence_Listing_ST25.txt

Ile Asn Ser Gly Asn Gly Ala Val Glu Asp Arg Lys Pro Ser Gly Leu
645 650 655

Asn Gly Glu Ala Ser Lys Ser Gln Glu Met Val His Leu Val Asn Lys
660 665 670

Glu Ser Ser Glu Thr Pro Asp Gln Phe Met Thr Ala Asp Glu Thr Arg
675 680 685

Asn Leu Gln Asn Val Asp Met Lys Ile Gly Val
690 695

<210> 267

<211> 458

<212> PRT

<213> Artificial Sequence

<220>

<223> CD4__Homo_sapiens__P01730

<400> 267

Met Asn Arg Gly Val Pro Phe Arg His Leu Leu Leu Val Leu Gln Leu
1 5 10 15

Ala Leu Leu Pro Ala Ala Thr Gln Gly Lys Lys Val Val Leu Gly Lys
20 25 30

Lys Gly Asp Thr Val Glu Leu Thr Cys Thr Ala Ser Gln Lys Lys Ser
35 40 45

Ile Gln Phe His Trp Lys Asn Ser Asn Gln Ile Lys Ile Leu Gly Asn
50 55 60

Gln Gly Ser Phe Leu Thr Lys Gly Pro Ser Lys Leu Asn Asp Arg Ala
65 70 75 80

Asp Ser Arg Arg Ser Leu Trp Asp Gln Gly Asn Phe Pro Leu Ile Ile
85 90 95

Lys Asn Leu Lys Ile Glu Asp Ser Asp Thr Tyr Ile Cys Glu Val Glu
100 105 110

Asp Gln Lys Glu Glu Val Gln Leu Leu Val Phe Gly Leu Thr Ala Asn
115 120 125

Ser Asp Thr His Leu Leu Gln Gly Gln Ser Leu Thr Leu Thr Leu Glu
130 135 140

Ser Pro Pro Gly Ser Ser Pro Ser Val Gln Cys Arg Ser Pro Arg Gly
145 150 155 160

ITI-08-PCT_Sequence_Listing_ST25.txt

Lys Asn Ile Gln Gly Gly Lys Thr Leu Ser Val Ser Gln Leu Glu Leu
 165 170 175
 Gln Asp Ser Gly Thr Trp Thr Cys Thr Val Leu Gln Asn Gln Lys Lys
 180 185 190
 Val Glu Phe Lys Ile Asp Ile Val Val Leu Ala Phe Gln Lys Ala Ser
 195 200 205
 Ser Ile Val Tyr Lys Lys Glu Gly Glu Gln Val Glu Phe Ser Phe Pro
 210 215 220
 Leu Ala Phe Thr Val Glu Lys Leu Thr Gly Ser Gly Glu Leu Trp Trp
 225 230 235 240
 Gln Ala Glu Arg Ala Ser Ser Ser Lys Ser Trp Ile Thr Phe Asp Leu
 245 250 255
 Lys Asn Lys Glu Val Ser Val Lys Arg Val Thr Gln Asp Pro Lys Leu
 260 265 270
 Gln Met Gly Lys Lys Leu Pro Leu His Leu Thr Leu Pro Gln Ala Leu
 275 280 285
 Pro Gln Tyr Ala Gly Ser Gly Asn Leu Thr Leu Ala Leu Glu Ala Lys
 290 295 300
 Thr Gly Lys Leu His Gln Glu Val Asn Leu Val Val Met Arg Ala Thr
 305 310 315 320
 Gln Leu Gln Lys Asn Leu Thr Cys Glu Val Trp Gly Pro Thr Ser Pro
 325 330 335
 Lys Leu Met Leu Ser Leu Lys Leu Glu Asn Lys Glu Ala Lys Val Ser
 340 345 350
 Lys Arg Glu Lys Ala Val Trp Val Leu Asn Pro Glu Ala Gly Met Trp
 355 360 365
 Gln Cys Leu Leu Ser Asp Ser Gly Gln Val Leu Leu Glu Ser Asn Ile
 370 375 380
 Lys Val Leu Pro Thr Trp Ser Thr Pro Val Gln Pro Met Ala Leu Ile
 385 390 395 400
 Val Leu Gly Gly Val Ala Gly Leu Leu Leu Phe Ile Gly Leu Gly Ile
 405 410 415
 Phe Phe Cys Val Arg Cys Arg His Arg Arg Arg Gln Ala Glu Arg Met
 420 425 430
 Ser Gln Ile Lys Arg Leu Leu Ser Glu Lys Lys Thr Cys Gln Cys Pro

ITI-08-PCT_Sequence_Listing_ST25.txt

435

440

445

His Arg Phe Gln Lys Thr Cys Ser Pro Ile
450 455

<210> 268
<211> 61
<212> PRT
<213> Artificial Sequence

<220>
<223> CD52__Homo_sapiens__P31358

<400> 268

Met Lys Arg Phe Leu Phe Leu Leu Leu Thr Ile Ser Leu Leu Val Met
1 5 10 15

Val Gln Ile Gln Thr Gly Leu Ser Gly Gln Asn Asp Thr Ser Gln Thr
20 25 30

Ser Ser Pro Ser Ala Ser Ser Asn Ile Ser Gly Gly Ile Phe Leu Phe
35 40 45

Phe Val Ala Asn Ala Ile Ile His Leu Phe Cys Phe Ser
50 55 60

<210> 269
<211> 61
<212> PRT
<213> Artificial Sequence

<220>
<223> CD52__Homo_sapiens__Q6IBD0

<400> 269

Met Lys Arg Phe Leu Phe Leu Leu Leu Thr Ile Ser Leu Leu Val Met
1 5 10 15

Val Gln Ile Gln Thr Gly Leu Ser Gly Gln Asn Asp Thr Ser Gln Thr
20 25 30

Ser Ser Pro Ser Ala Ser Ser Ser Met Ser Gly Gly Ile Phe Leu Phe
35 40 45

Phe Val Ala Asn Ala Ile Ile His Leu Phe Cys Phe Ser
50 55 60

<210> 270
<211> 61
<212> PRT

ITI-08-PCT_Sequence_Listing_ST25.txt

<213> Artificial Sequence

<220>

<223> CD52__Homo_sapiens__V9HWN9

<400> 270

Met Lys Arg Phe Leu Phe Leu Leu Leu Thr Ile Ser Leu Leu Val Met
1 5 10 15

Val Gln Ile Gln Thr Gly Leu Ser Gly Gln Asn Asp Thr Ser Gln Thr
20 25 30

Ser Ser Pro Ser Ala Ser Ser Asn Ile Ser Gly Gly Ile Phe Leu Phe
35 40 45

Phe Val Ala Asn Ala Ile Ile His Leu Phe Cys Phe Ser
50 55 60

<210> 271

<211> 317

<212> PRT

<213> Artificial Sequence

<220>

<223> CD55__Homo_sapiens__B1AP15

<400> 271

Met Thr Val Ala Arg Pro Ser Val Pro Ala Ala Leu Pro Leu Leu Gly
1 5 10 15

Glu Leu Pro Arg Leu Leu Leu Leu Val Leu Leu Cys Leu Pro Ala Val
20 25 30

Trp Gly Asp Cys Gly Leu Pro Pro Asp Val Pro Asn Ala Gln Pro Ala
35 40 45

Leu Glu Gly Arg Thr Ser Phe Pro Glu Asp Thr Val Ile Thr Tyr Lys
50 55 60

Cys Glu Glu Ser Phe Val Lys Ile Pro Gly Glu Lys Asp Ser Val Ile
65 70 75 80

Cys Leu Lys Gly Ser Gln Trp Ser Asp Ile Glu Glu Phe Cys Asn Gln
85 90 95

Lys Ser Cys Pro Asn Pro Gly Glu Ile Arg Asn Gly Gln Ile Asp Val
100 105 110

Pro Gly Gly Ile Leu Phe Gly Ala Thr Ile Ser Phe Ser Cys Asn Thr
115 120 125

ITI-08-PCT_Sequence_Listing_ST25.txt

Gly Tyr Lys Leu Phe Gly Ser Thr Ser Ser Phe Cys Leu Ile Ser Gly
130 135 140

Ser Ser Val Gln Trp Ser Asp Pro Leu Pro Glu Cys Arg Glu Ile Tyr
145 150 155 160

Cys Pro Ala Pro Pro Gln Ile Asp Asn Gly Ile Ile Gln Gly Glu Arg
165 170 175

Asp His Tyr Gly Tyr Arg Gln Ser Val Thr Tyr Ala Cys Asn Lys Gly
180 185 190

Phe Thr Met Ile Gly Glu His Ser Ile Tyr Cys Thr Val Asn Asn Asp
195 200 205

Glu Gly Glu Trp Ser Gly Pro Pro Pro Glu Cys Arg Gly Lys Ser Leu
210 215 220

Thr Ser Lys Val Pro Pro Thr Val Gln Lys Pro Thr Thr Val Asn Val
225 230 235 240

Pro Thr Thr Glu Val Ser Pro Thr Ser Gln Lys Thr Thr Thr Lys Thr
245 250 255

Thr Thr Pro Asn Ala Gln Ala Thr Arg Ser Thr Pro Val Ser Arg Thr
260 265 270

Thr Lys His Phe His Glu Thr Thr Pro Asn Lys Gly Ser Gly Thr Thr
275 280 285

Ser Gly Thr Thr Arg Leu Leu Ser Gly His Thr Cys Phe Thr Leu Thr
290 295 300

Gly Leu Leu Gly Thr Leu Val Thr Met Gly Leu Leu Thr
305 310 315

<210> 272

<211> 293

<212> PRT

<213> Artificial Sequence

<220>

<223> CD55__Homo_sapiens__D3DT85

<400> 272

Met Ile Gly Glu His Ser Ile Tyr Cys Thr Val Asn Asn Asp Glu Gly
1 5 10 15

Glu Trp Ser Gly Pro Pro Pro Glu Cys Arg Gly Lys Ser Leu Thr Ser
20 25 30

ITI-08-PCT_Sequence_Listing_ST25.txt

Lys	Val	Pro	Pro	Thr	Val	Gln	Lys	Pro	Thr	Thr	Val	Asn	Val	Pro	Thr				
		35					40					45							
Thr	Glu	Val	Ser	Pro	Thr	Ser	Gln	Lys	Thr	Thr	Thr	Lys	Thr	Thr	Thr				
	50					55					60								
Pro	Asn	Ala	Gln	Gly	Thr	Glu	Thr	Pro	Ser	Val	Leu	Gln	Lys	His	Thr				
65					70					75					80				
Thr	Glu	Asn	Val	Ser	Ala	Thr	Arg	Thr	Pro	Pro	Thr	Pro	Gln	Lys	Pro				
				85					90					95					
Thr	Thr	Val	Asn	Val	Pro	Ala	Thr	Ile	Val	Thr	Pro	Thr	Pro	Gln	Lys				
			100					105						110					
Pro	Thr	Thr	Ile	Asn	Val	Pro	Ala	Thr	Gly	Val	Ser	Ser	Thr	Pro	Gln				
		115					120					125							
Arg	His	Thr	Ile	Val	Asn	Val	Ser	Ala	Thr	Gly	Thr	Leu	Pro	Thr	Leu				
	130					135					140								
Gln	Lys	Pro	Thr	Arg	Ala	Asn	Asp	Ser	Ala	Thr	Lys	Ser	Pro	Ala	Ala				
145					150					155					160				
Ala	Gln	Thr	Ser	Phe	Ile	Ser	Lys	Thr	Leu	Ser	Thr	Lys	Thr	Pro	Ser				
				165					170					175					
Ala	Ala	Gln	Asn	Pro	Met	Met	Thr	Asn	Ala	Ser	Ala	Thr	Gln	Ala	Thr				
			180					185					190						
Leu	Thr	Ala	Gln	Lys	Phe	Thr	Thr	Ala	Lys	Val	Ala	Phe	Thr	Gln	Ser				
		195					200					205							
Pro	Ser	Ala	Ala	Arg	Lys	Ser	Thr	Asn	Val	His	Ser	Pro	Val	Thr	Asn				
	210					215					220								
Gly	Leu	Lys	Ser	Thr	Gln	Arg	Phe	Pro	Ser	Ala	His	Ile	Thr	Ala	Thr				
225					230					235					240				
Arg	Ser	Thr	Pro	Val	Ser	Arg	Thr	Thr	Lys	His	Phe	His	Glu	Thr	Thr				
				245					250					255					
Pro	Asn	Lys	Gly	Ser	Gly	Thr	Thr	Ser	Gly	Thr	Thr	Arg	Leu	Leu	Ser				
			260					265					270						
Gly	His	Thr	Cys	Phe	Thr	Leu	Thr	Gly	Leu	Leu	Gly	Thr	Leu	Val	Thr				
		275					280					285							
Met	Gly	Leu	Leu	Thr															
	290																		

ITI-08-PCT_Sequence_Listing_ST25.txt

<210> 273

<211> 267

<212> PRT

<213> Artificial Sequence

<220>

<223> CD55__Homo_sapiens__D3DT86

<400> 273

Met Ile Gly Glu His Ser Ile Tyr Cys Thr Val Asn Asn Asp Glu Gly
1 5 10 15

Glu Trp Ser Gly Pro Pro Pro Glu Cys Arg Gly Lys Ser Leu Thr Ser
20 25 30

Lys Val Pro Pro Thr Val Gln Lys Pro Thr Thr Val Asn Val Pro Thr
35 40 45

Thr Glu Val Ser Pro Thr Ser Gln Lys Thr Thr Thr Lys Thr Thr Thr
50 55 60

Pro Asn Ala Gln Gly Thr Glu Thr Pro Ser Val Leu Gln Lys His Thr
65 70 75 80

Thr Glu Asn Val Ser Ala Thr Arg Thr Pro Pro Thr Pro Gln Lys Pro
85 90 95

Thr Thr Val Asn Val Pro Ala Thr Ile Val Thr Pro Thr Pro Gln Lys
100 105 110

Pro Thr Thr Ile Asn Val Pro Ala Thr Gly Val Ser Ser Thr Pro Gln
115 120 125

Arg His Thr Ile Val Asn Val Ser Ala Thr Gly Thr Leu Pro Thr Leu
130 135 140

Gln Lys Pro Thr Arg Ala Asn Asp Ser Ala Thr Lys Ser Pro Ala Ala
145 150 155 160

Ala Gln Thr Ser Phe Ile Ser Lys Thr Leu Ser Thr Lys Thr Pro Ser
165 170 175

Ala Ala Gln Asn Pro Met Met Thr Asn Ala Ser Ala Thr Gln Ala Thr
180 185 190

Leu Thr Ala Gln Lys Phe Thr Thr Ala Lys Val Ala Phe Thr Gln Ser
195 200 205

Pro Ser Ala Ala Pro Thr Arg Ser Thr Pro Val Ser Arg Thr Thr Lys
210 215 220

ITI-08-PCT_Sequence_Listing_ST25.txt

His Phe His Glu Thr Thr Pro Asn Lys Gly Ser Gly Thr Thr Ser Gly
225 230 235 240

Thr Thr Arg Leu Leu Ser Gly His Thr Cys Phe Thr Leu Thr Gly Leu
245 250 255

Leu Gly Thr Leu Val Thr Met Gly Leu Leu Thr
260 265

<210> 274

<211> 381

<212> PRT

<213> Artificial Sequence

<220>

<223> CD55__Homo_sapiens__P08174

<400> 274

Met Thr Val Ala Arg Pro Ser Val Pro Ala Ala Leu Pro Leu Leu Gly
1 5 10 15

Glu Leu Pro Arg Leu Leu Leu Leu Val Leu Leu Cys Leu Pro Ala Val
20 25 30

Trp Gly Asp Cys Gly Leu Pro Pro Asp Val Pro Asn Ala Gln Pro Ala
35 40 45

Leu Glu Gly Arg Thr Ser Phe Pro Glu Asp Thr Val Ile Thr Tyr Lys
50 55 60

Cys Glu Glu Ser Phe Val Lys Ile Pro Gly Glu Lys Asp Ser Val Ile
65 70 75 80

Cys Leu Lys Gly Ser Gln Trp Ser Asp Ile Glu Glu Phe Cys Asn Arg
85 90 95

Ser Cys Glu Val Pro Thr Arg Leu Asn Ser Ala Ser Leu Lys Gln Pro
100 105 110

Tyr Ile Thr Gln Asn Tyr Phe Pro Val Gly Thr Val Val Glu Tyr Glu
115 120 125

Cys Arg Pro Gly Tyr Arg Arg Glu Pro Ser Leu Ser Pro Lys Leu Thr
130 135 140

Cys Leu Gln Asn Leu Lys Trp Ser Thr Ala Val Glu Phe Cys Lys Lys
145 150 155 160

Lys Ser Cys Pro Asn Pro Gly Glu Ile Arg Asn Gly Gln Ile Asp Val
165 170 175

ITI-08-PCT_Sequence_Listing_ST25.txt

Pro Gly Gly Ile Leu Phe Gly Ala Thr Ile Ser Phe Ser Cys Asn Thr
180 185 190

Gly Tyr Lys Leu Phe Gly Ser Thr Ser Ser Phe Cys Leu Ile Ser Gly
195 200 205

Ser Ser Val Gln Trp Ser Asp Pro Leu Pro Glu Cys Arg Glu Ile Tyr
210 215 220

Cys Pro Ala Pro Pro Gln Ile Asp Asn Gly Ile Ile Gln Gly Glu Arg
225 230 235 240

Asp His Tyr Gly Tyr Arg Gln Ser Val Thr Tyr Ala Cys Asn Lys Gly
245 250 255

Phe Thr Met Ile Gly Glu His Ser Ile Tyr Cys Thr Val Asn Asn Asp
260 265 270

Glu Gly Glu Trp Ser Gly Pro Pro Pro Glu Cys Arg Gly Lys Ser Leu
275 280 285

Thr Ser Lys Val Pro Pro Thr Val Gln Lys Pro Thr Thr Val Asn Val
290 295 300

Pro Thr Thr Glu Val Ser Pro Thr Ser Gln Lys Thr Thr Thr Lys Thr
305 310 315 320

Thr Thr Pro Asn Ala Gln Ala Thr Arg Ser Thr Pro Val Ser Arg Thr
325 330 335

Thr Lys His Phe His Glu Thr Thr Pro Asn Lys Gly Ser Gly Thr Thr
340 345 350

Ser Gly Thr Thr Arg Leu Leu Ser Gly His Thr Cys Phe Thr Leu Thr
355 360 365

Gly Leu Leu Gly Thr Leu Val Thr Met Gly Leu Leu Thr
370 375 380

<210> 275

<211> 858

<212> PRT

<213> Artificial Sequence

<220>

<223> CD56__Homo_sapiens__P13591

<400> 275

Met Leu Gln Thr Lys Asp Leu Ile Trp Thr Leu Phe Phe Leu Gly Thr
1 5 10 15

ITI-08-PCT_Sequence_Listing_ST25.txt

Ala Val Ser Leu Gln Val Asp Ile Val Pro Ser Gln Gly Glu Ile Ser
20 25 30

Val Gly Glu Ser Lys Phe Phe Leu Cys Gln Val Ala Gly Asp Ala Lys
35 40 45

Asp Lys Asp Ile Ser Trp Phe Ser Pro Asn Gly Glu Lys Leu Thr Pro
50 55 60

Asn Gln Gln Arg Ile Ser Val Val Trp Asn Asp Asp Ser Ser Ser Thr
65 70 75 80

Leu Thr Ile Tyr Asn Ala Asn Ile Asp Asp Ala Gly Ile Tyr Lys Cys
85 90 95

Val Val Thr Gly Glu Asp Gly Ser Glu Ser Glu Ala Thr Val Asn Val
100 105 110

Lys Ile Phe Gln Lys Leu Met Phe Lys Asn Ala Pro Thr Pro Gln Glu
115 120 125

Phe Arg Glu Gly Glu Asp Ala Val Ile Val Cys Asp Val Val Ser Ser
130 135 140

Leu Pro Pro Thr Ile Ile Trp Lys His Lys Gly Arg Asp Val Ile Leu
145 150 155 160

Lys Lys Asp Val Arg Phe Ile Val Leu Ser Asn Asn Tyr Leu Gln Ile
165 170 175

Arg Gly Ile Lys Lys Thr Asp Glu Gly Thr Tyr Arg Cys Glu Gly Arg
180 185 190

Ile Leu Ala Arg Gly Glu Ile Asn Phe Lys Asp Ile Gln Val Ile Val
195 200 205

Asn Val Pro Pro Thr Ile Gln Ala Arg Gln Asn Ile Val Asn Ala Thr
210 215 220

Ala Asn Leu Gly Gln Ser Val Thr Leu Val Cys Asp Ala Glu Gly Phe
225 230 235 240

Pro Glu Pro Thr Met Ser Trp Thr Lys Asp Gly Glu Gln Ile Glu Gln
245 250 255

Glu Glu Asp Asp Glu Lys Tyr Ile Phe Ser Asp Asp Ser Ser Gln Leu
260 265 270

Thr Ile Lys Lys Val Asp Lys Asn Asp Glu Ala Glu Tyr Ile Cys Ile
275 280 285

Ala Glu Asn Lys Ala Gly Glu Gln Asp Ala Thr Ile His Leu Lys Val

290 295 300

Page 444

ITI-08-PCT_Sequence_Listing_ST25.txt

Lys	Pro	Glu	Thr	Thr	Tyr	Ala	Val	Arg	Leu	Ala	Ala	Leu	Asn	Gly	Lys		
			580					585					590				
Gly	Leu	Gly	Glu	Ile	Ser	Ala	Ala	Ser	Glu	Phe	Lys	Thr	Gln	Pro	Val		
		595					600					605					
Gln	Gly	Glu	Pro	Ser	Ala	Pro	Lys	Leu	Glu	Gly	Gln	Met	Gly	Glu	Asp		
	610					615					620						
Gly	Asn	Ser	Ile	Lys	Val	Asn	Leu	Ile	Lys	Gln	Asp	Asp	Gly	Gly	Ser		
625					630					635					640		
Pro	Ile	Arg	His	Tyr	Leu	Val	Arg	Tyr	Arg	Ala	Leu	Ser	Ser	Glu	Trp		
				645					650					655			
Lys	Pro	Glu	Ile	Arg	Leu	Pro	Ser	Gly	Ser	Asp	His	Val	Met	Leu	Lys		
			660					665					670				
Ser	Leu	Asp	Trp	Asn	Ala	Glu	Tyr	Glu	Val	Tyr	Val	Val	Ala	Glu	Asn		
		675					680					685					
Gln	Gln	Gly	Lys	Ser	Lys	Ala	Ala	His	Phe	Val	Phe	Arg	Thr	Ser	Ala		
	690					695					700						
Gln	Pro	Thr	Ala	Ile	Pro	Ala	Asn	Gly	Ser	Pro	Thr	Ser	Gly	Leu	Ser		
705					710					715					720		
Thr	Gly	Ala	Ile	Val	Gly	Ile	Leu	Ile	Val	Ile	Phe	Val	Leu	Leu	Leu		
				725					730				735				
Val	Val	Val	Asp	Ile	Thr	Cys	Tyr	Phe	Leu	Asn	Lys	Cys	Gly	Leu	Phe		
			740					745					750				
Met	Cys	Ile	Ala	Val	Asn	Leu	Cys	Gly	Lys	Ala	Gly	Pro	Gly	Ala	Lys		
		755					760					765					
Gly	Lys	Asp	Met	Glu	Glu	Gly	Lys	Ala	Ala	Phe	Ser	Lys	Asp	Glu	Ser		
	770					775					780						
Lys	Glu	Pro	Ile	Val	Glu	Val	Arg	Thr	Glu	Glu	Glu	Arg	Thr	Pro	Asn		
785					790					795					800		
His	Asp	Gly	Gly	Lys	His	Thr	Glu	Pro	Asn	Glu	Thr	Thr	Pro	Leu	Thr		
				805					810					815			
Glu	Pro	Glu	Lys	Gly	Pro	Val	Glu	Ala	Lys	Pro	Glu	Cys	Gln	Glu	Thr		
			820					825					830				
Glu	Thr	Lys	Pro	Ala	Pro	Ala	Glu	Val	Lys	Thr	Val	Pro	Asn	Asp	Ala		
		835					840					845					

ITI-08-PCT_Sequence_Listing_ST25.txt

Thr Gln Thr Lys Glu Asn Glu Ser Lys Ala
850 855

<210> 276
<211> 288
<212> PRT
<213> Artificial Sequence

<220>
<223> CD80__Homo_sapiens__A0N0P2

<400> 276

Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro Ser Lys Cys Pro Tyr
1 5 10 15

Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly Leu Ser His Phe Cys
20 25 30

Ser Gly Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu
35 40 45

Ser Cys Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile
50 55 60

Tyr Trp Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp
65 70 75 80

Met Asn Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr
85 90 95

Asn Asn Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly
100 105 110

Thr Tyr Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg
115 120 125

Glu His Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr
130 135 140

Pro Ser Ile Ser Asp Phe Glu Ile Pro Thr Ser Asn Ile Arg Arg Ile
145 150 155 160

Ile Cys Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu
165 170 175

Glu Asn Gly Glu Glu Leu Asn Ala Ile Asn Thr Thr Val Ser Gln Asp
180 185 190

Pro Glu Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met
195 200 205

ITI-08-PCT_Sequence_Listing_ST25.txt

Thr Thr Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg
210 215 220

Val Asn Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro
225 230 235 240

Asp Asn Leu Leu Pro Ser Trp Ala Ile Thr Leu Ile Ser Val Asn Gly
245 250 255

Ile Phe Val Ile Cys Cys Leu Thr Tyr Cys Phe Ala Pro Arg Cys Arg
260 265 270

Glu Arg Arg Arg Asn Glu Arg Leu Arg Arg Glu Ser Val Arg Pro Val
275 280 285

<210> 277

<211> 288

<212> PRT

<213> Artificial Sequence

<220>

<223> CD80__Homo_sapiens__P33681

<400> 277

Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro Ser Lys Cys Pro Tyr
1 5 10 15

Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly Leu Ser His Phe Cys
20 25 30

Ser Gly Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu
35 40 45

Ser Cys Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile
50 55 60

Tyr Trp Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp
65 70 75 80

Met Asn Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr
85 90 95

Asn Asn Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly
100 105 110

Thr Tyr Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg
115 120 125

Glu His Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr
130 135 140

ITI-08-PCT_Sequence_Listing_ST25.txt

Pro Ser Ile Ser Asp Phe Glu Ile Pro Thr Ser Asn Ile Arg Arg Ile
145 150 155 160

Ile Cys Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu
165 170 175

Glu Asn Gly Glu Glu Leu Asn Ala Ile Asn Thr Thr Val Ser Gln Asp
180 185 190

Pro Glu Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met
195 200 205

Thr Thr Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg
210 215 220

Val Asn Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro
225 230 235 240

Asp Asn Leu Leu Pro Ser Trp Ala Ile Thr Leu Ile Ser Val Asn Gly
245 250 255

Ile Phe Val Ile Cys Cys Leu Thr Tyr Cys Phe Ala Pro Arg Cys Arg
260 265 270

Glu Arg Arg Arg Asn Glu Arg Leu Arg Arg Glu Ser Val Arg Pro Val
275 280 285

<210> 278

<211> 329

<212> PRT

<213> Artificial Sequence

<220>

<223> CD86__Homo_sapiens__P42081

<400> 278

Met Asp Pro Gln Cys Thr Met Gly Leu Ser Asn Ile Leu Phe Val Met
1 5 10 15

Ala Phe Leu Leu Ser Gly Ala Ala Pro Leu Lys Ile Gln Ala Tyr Phe
20 25 30

Asn Glu Thr Ala Asp Leu Pro Cys Gln Phe Ala Asn Ser Gln Asn Gln
35 40 45

Ser Leu Ser Glu Leu Val Val Phe Trp Gln Asp Gln Glu Asn Leu Val
50 55 60

Leu Asn Glu Val Tyr Leu Gly Lys Glu Lys Phe Asp Ser Val His Ser
65 70 75 80

ITI-08-PCT_Sequence_Listing_ST25.txt

Lys Tyr Met Gly Arg Thr Ser Phe Asp Ser Asp Ser Trp Thr Leu Arg
85 90 95

Leu His Asn Leu Gln Ile Lys Asp Lys Gly Leu Tyr Gln Cys Ile Ile
100 105 110

His His Lys Lys Pro Thr Gly Met Ile Arg Ile His Gln Met Asn Ser
115 120 125

Glu Leu Ser Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Val Pro Ile
130 135 140

Ser Asn Ile Thr Glu Asn Val Tyr Ile Asn Leu Thr Cys Ser Ser Ile
145 150 155 160

His Gly Tyr Pro Glu Pro Lys Lys Met Ser Val Leu Leu Arg Thr Lys
165 170 175

Asn Ser Thr Ile Glu Tyr Asp Gly Val Met Gln Lys Ser Gln Asp Asn
180 185 190

Val Thr Glu Leu Tyr Asp Val Ser Ile Ser Leu Ser Val Ser Phe Pro
195 200 205

Asp Val Thr Ser Asn Met Thr Ile Phe Cys Ile Leu Glu Thr Asp Lys
210 215 220

Thr Arg Leu Leu Ser Ser Pro Phe Ser Ile Glu Leu Glu Asp Pro Gln
225 230 235 240

Pro Pro Pro Asp His Ile Pro Trp Ile Thr Ala Val Leu Pro Thr Val
245 250 255

Ile Ile Cys Val Met Val Phe Cys Leu Ile Leu Trp Lys Trp Lys Lys
260 265 270

Lys Lys Arg Pro Arg Asn Ser Tyr Lys Cys Gly Thr Asn Thr Met Glu
275 280 285

Arg Glu Glu Ser Glu Gln Thr Lys Lys Arg Glu Lys Ile His Ile Pro
290 295 300

Glu Arg Ser Asp Glu Ala Gln Arg Val Phe Lys Ser Ser Lys Thr Ser
305 310 315 320

Ser Cys Asp Lys Ser Asp Thr Cys Phe
325

<210> 279
<211> 235
<212> PRT
<213> Artificial Sequence

ITI-08-PCT_Sequence_Listing_ST25.txt

<220>

<223> CD8A__Homo_sapiens__P01732

<400> 279

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 Gln Phe Arg Val Ser Pro Leu Asp Arg Thr
20 25 30

Trp Asn Leu Gly Glu Thr Val Glu Leu Lys Cys Gln Val Leu Leu Ser
35 40 45

Asn Pro Thr Ser Gly Cys Ser Trp Leu Phe Gln Pro Arg Gly Ala Ala
50 55 60

Ala Ser Pro Thr Phe Leu Leu Tyr Leu Ser Gln Asn Lys Pro Lys Ala
65 70 75 80

Ala Glu Gly Leu Asp Thr Gln Arg Phe Ser Gly Lys Arg Leu Gly Asp
85 90 95

Thr Phe Val Leu Thr Leu Ser Asp Phe Arg Arg Glu Asn Glu Gly Tyr
100 105 110

Tyr Phe Cys Ser Ala Leu Ser Asn Ser Ile Met Tyr Phe Ser His Phe
115 120 125

Val Pro Val Phe Leu Pro Ala Lys Pro Thr Thr Thr Pro Ala Pro Arg
130 135 140

Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg
145 150 155 160

Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly
165 170 175

Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr
180 185 190

Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Asn His
195 200 205

Arg Asn Arg Arg Arg Val Cys Lys Cys Pro Arg Pro Val Val Lys Ser
210 215 220

Gly Asp Lys Pro Ser Leu Ser Ala Arg Tyr Val
225 230 235

<210> 280

ITI-08-PCT_Sequence_Listing_ST25.txt

<211> 823

<212> PRT

<213> Artificial Sequence

<220>

<223> CDC27/m__Homo_sapiens__G5EA36

<400> 280

Met Thr Val Leu Gln Glu Pro Val Gln Ala Ala Ile Trp Gln Ala Leu
1 5 10 15

Asn His Tyr Ala Tyr Arg Asp Ala Val Phe Leu Ala Glu Arg Leu Tyr
20 25 30

Ala Glu Val His Ser Glu Glu Ala Leu Phe Leu Leu Ala Thr Cys Tyr
35 40 45

Tyr Arg Ser Gly Lys Ala Tyr Lys Ala Tyr Arg Leu Leu Lys Gly His
50 55 60

Ser Cys Thr Thr Pro Gln Cys Lys Tyr Leu Leu Ala Lys Cys Cys Val
65 70 75 80

Asp Leu Ser Lys Leu Ala Glu Gly Glu Gln Ile Leu Ser Gly Gly Val
85 90 95

Phe Asn Lys Gln Lys Ser His Asp Asp Ile Val Thr Glu Phe Gly Asp
100 105 110

Ser Ala Cys Phe Thr Leu Ser Leu Leu Gly His Val Tyr Cys Lys Thr
115 120 125

Asp Arg Leu Ala Lys Gly Ser Glu Cys Tyr Gln Lys Ser Leu Ser Leu
130 135 140

Asn Pro Phe Leu Trp Ser Pro Phe Glu Ser Leu Cys Glu Ile Gly Glu
145 150 155 160

Lys Pro Asp Pro Asp Gln Thr Phe Lys Phe Thr Ser Leu Gln Asn Phe
165 170 175

Ser Asn Cys Leu Pro Asn Ser Cys Thr Thr Gln Val Pro Asn His Ser
180 185 190

Leu Ser His Arg Gln Pro Glu Thr Val Leu Thr Glu Thr Pro Gln Asp
195 200 205

Thr Ile Glu Leu Asn Arg Leu Asn Leu Glu Ser Ser Asn Ser Lys Tyr
210 215 220

Ser Leu Asn Thr Asp Ser Ser Val Ser Tyr Ile Asp Ser Ala Val Ile

ITI-08-PCT_Sequence_Listing_ST25.txt

```

225                230                235                240
Ser Pro Asp Thr Val Pro Leu Gly Thr Gly Thr Ser Ile Leu Ser Lys
                245                250                255

Gln Val Gln Asn Lys Pro Lys Thr Gly Arg Ser Leu Leu Gly Gly Pro
                260                265                270

Ala Ala Leu Ser Pro Leu Thr Pro Ser Phe Gly Ile Leu Pro Leu Glu
                275                280                285

Thr Pro Ser Pro Gly Asp Gly Ser Tyr Leu Gln Asn Tyr Thr Asn Thr
                290                295                300

Pro Pro Val Ile Asp Val Pro Ser Thr Gly Ala Pro Ser Lys Lys Ser
305                310                315                320

Val Ala Arg Ile Gly Gln Thr Gly Thr Lys Ser Val Phe Ser Gln Ser
                325                330                335

Gly Asn Ser Arg Glu Val Thr Pro Ile Leu Ala Gln Thr Gln Ser Ser
                340                345                350

Gly Pro Gln Thr Ser Thr Thr Pro Gln Val Leu Ser Pro Thr Ile Thr
                355                360                365

Ser Pro Pro Asn Ala Leu Pro Arg Arg Ser Ser Arg Leu Phe Thr Ser
                370                375                380

Asp Ser Ser Thr Thr Lys Glu Asn Ser Lys Lys Leu Lys Met Lys Phe
385                390                395                400

Pro Pro Lys Ile Pro Asn Arg Lys Thr Lys Ser Lys Thr Asn Lys Gly
                405                410                415

Gly Ile Thr Gln Pro Asn Ile Asn Asp Ser Leu Glu Ile Thr Lys Leu
                420                425                430

Asp Ser Ser Ile Ile Ser Glu Gly Lys Ile Ser Thr Ile Thr Pro Gln
                435                440                445

Ile Gln Ala Phe Asn Leu Gln Lys Ala Ala Ala Gly Leu Met Ser Leu
                450                455                460

Leu Arg Glu Met Gly Lys Gly Tyr Leu Ala Leu Cys Ser Tyr Asn Cys
465                470                475                480

Lys Glu Ala Ile Asn Ile Leu Ser His Leu Pro Ser His His Tyr Asn
                485                490                495

Thr Gly Trp Val Leu Cys Gln Ile Gly Arg Ala Tyr Phe Glu Leu Ser
                500                505                510

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Glu	Tyr	Met	Gln	Ala	Glu	Arg	Ile	Phe	Ser	Glu	Val	Arg	Arg	Ile	Glu	515	520	525
Asn	Tyr	Arg	Val	Glu	Gly	Met	Glu	Ile	Tyr	Ser	Thr	Thr	Leu	Trp	His	530	535	540
Leu	Gln	Lys	Asp	Val	Ala	Leu	Ser	Val	Leu	Ser	Lys	Asp	Leu	Thr	Asp	545	550	555
Met	Asp	Lys	Asn	Ser	Pro	Glu	Ala	Trp	Cys	Ala	Ala	Gly	Asn	Cys	Phe	565	570	575
Ser	Leu	Gln	Arg	Glu	His	Asp	Ile	Ala	Ile	Lys	Phe	Phe	Gln	Arg	Ala	580	585	590
Ile	Gln	Val	Asp	Pro	Asn	Tyr	Ala	Tyr	Ala	Tyr	Thr	Leu	Leu	Gly	His	595	600	605
Glu	Phe	Val	Leu	Thr	Glu	Glu	Leu	Asp	Lys	Ala	Leu	Ala	Cys	Phe	Arg	610	615	620
Asn	Ala	Ile	Arg	Val	Asn	Pro	Arg	His	Tyr	Asn	Ala	Trp	Tyr	Gly	Leu	625	630	635
Gly	Met	Ile	Tyr	Tyr	Lys	Gln	Glu	Lys	Phe	Ser	Leu	Ala	Glu	Met	His	645	650	655
Phe	Gln	Lys	Ala	Leu	Asp	Ile	Asn	Pro	Gln	Ser	Ser	Val	Leu	Leu	Cys	660	665	670
His	Ile	Gly	Val	Val	Gln	His	Ala	Leu	Lys	Lys	Ser	Glu	Lys	Ala	Leu	675	680	685
Asp	Thr	Leu	Asn	Lys	Ala	Ile	Val	Ile	Asp	Pro	Lys	Asn	Pro	Leu	Cys	690	695	700
Lys	Phe	His	Arg	Ala	Ser	Val	Leu	Phe	Ala	Asn	Glu	Lys	Tyr	Lys	Ser	705	710	715
Ala	Leu	Gln	Glu	Leu	Glu	Glu	Leu	Lys	Gln	Ile	Val	Pro	Lys	Glu	Ser	725	730	735
Leu	Val	Tyr	Phe	Leu	Ile	Gly	Lys	Val	Tyr	Lys	Lys	Leu	Gly	Gln	Thr	740	745	750
His	Leu	Ala	Leu	Met	Asn	Phe	Ser	Trp	Ala	Met	Asp	Leu	Asp	Pro	Lys	755	760	765
Gly	Ala	Asn	Asn	Gln	Ile	Lys	Glu	Ala	Ile	Asp	Lys	Arg	Tyr	Leu	Pro	770	775	780

ITI-08-PCT_Sequence_Listing_ST25.txt

Asp Asp Glu Glu Pro Ile Thr Gln Glu Glu Gln Ile Met Gly Thr Asp
785 790 795 800

Glu Ser Gln Glu Ser Ser Met Thr Asp Ala Asp Asp Thr Gln Leu His
805 810 815

Ala Ala Glu Ser Asp Glu Phe
820

<210> 281

<211> 824

<212> PRT

<213> Artificial Sequence

<220>

<223> CDC27/m__Homo_sapiens__P30260

<400> 281

Met Thr Val Leu Gln Glu Pro Val Gln Ala Ala Ile Trp Gln Ala Leu
1 5 10 15

Asn His Tyr Ala Tyr Arg Asp Ala Val Phe Leu Ala Glu Arg Leu Tyr
20 25 30

Ala Glu Val His Ser Glu Glu Ala Leu Phe Leu Leu Ala Thr Cys Tyr
35 40 45

Tyr Arg Ser Gly Lys Ala Tyr Lys Ala Tyr Arg Leu Leu Lys Gly His
50 55 60

Ser Cys Thr Thr Pro Gln Cys Lys Tyr Leu Leu Ala Lys Cys Cys Val
65 70 75 80

Asp Leu Ser Lys Leu Ala Glu Gly Glu Gln Ile Leu Ser Gly Gly Val
85 90 95

Phe Asn Lys Gln Lys Ser His Asp Asp Ile Val Thr Glu Phe Gly Asp
100 105 110

Ser Ala Cys Phe Thr Leu Ser Leu Leu Gly His Val Tyr Cys Lys Thr
115 120 125

Asp Arg Leu Ala Lys Gly Ser Glu Cys Tyr Gln Lys Ser Leu Ser Leu
130 135 140

Asn Pro Phe Leu Trp Ser Pro Phe Glu Ser Leu Cys Glu Ile Gly Glu
145 150 155 160

Lys Pro Asp Pro Asp Gln Thr Phe Lys Phe Thr Ser Leu Gln Asn Phe
165 170 175

ITI-08-PCT_Sequence_Listing_ST25.txt

```

Ser Asn Cys Leu Pro Asn Ser Cys Thr Thr Gln Val Pro Asn His Ser
180                               185                               190

Leu Ser His Arg Gln Pro Glu Thr Val Leu Thr Glu Thr Pro Gln Asp
195                               200                               205

Thr Ile Glu Leu Asn Arg Leu Asn Leu Glu Ser Ser Asn Ser Lys Tyr
210                               215                               220

Ser Leu Asn Thr Asp Ser Ser Val Ser Tyr Ile Asp Ser Ala Val Ile
225                               230                               235                               240

Ser Pro Asp Thr Val Pro Leu Gly Thr Gly Thr Ser Ile Leu Ser Lys
245                               250                               255

Gln Val Gln Asn Lys Pro Lys Thr Gly Arg Ser Leu Leu Gly Gly Pro
260                               265                               270

Ala Ala Leu Ser Pro Leu Thr Pro Ser Phe Gly Ile Leu Pro Leu Glu
275                               280                               285

Thr Pro Ser Pro Gly Asp Gly Ser Tyr Leu Gln Asn Tyr Thr Asn Thr
290                               295                               300

Pro Pro Val Ile Asp Val Pro Ser Thr Gly Ala Pro Ser Lys Lys Ser
305                               310                               315                               320

Val Ala Arg Ile Gly Gln Thr Gly Thr Lys Ser Val Phe Ser Gln Ser
325                               330                               335

Gly Asn Ser Arg Glu Val Thr Pro Ile Leu Ala Gln Thr Gln Ser Ser
340                               345                               350

Gly Pro Gln Thr Ser Thr Thr Pro Gln Val Leu Ser Pro Thr Ile Thr
355                               360                               365

Ser Pro Pro Asn Ala Leu Pro Arg Arg Ser Ser Arg Leu Phe Thr Ser
370                               375                               380

Asp Ser Ser Thr Thr Lys Glu Asn Ser Lys Lys Leu Lys Met Lys Phe
385                               390                               395                               400

Pro Pro Lys Ile Pro Asn Arg Lys Thr Lys Ser Lys Thr Asn Lys Gly
405                               410                               415

Gly Ile Thr Gln Pro Asn Ile Asn Asp Ser Leu Glu Ile Thr Lys Leu
420                               425                               430

Asp Ser Ser Ile Ile Ser Glu Gly Lys Ile Ser Thr Ile Thr Pro Gln
435                               440                               445

Ile Gln Ala Phe Asn Leu Gln Lys Ala Ala Ala Glu Gly Leu Met Ser

```

ITI-08-PCT_Sequence_Listing_ST25.txt

```

450          455          460
Leu Leu Arg Glu Met Gly Lys Gly Tyr Leu Ala Leu Cys Ser Tyr Asn
465          470          475          480
Cys Lys Glu Ala Ile Asn Ile Leu Ser His Leu Pro Ser His His Tyr
          485          490          495
Asn Thr Gly Trp Val Leu Cys Gln Ile Gly Arg Ala Tyr Phe Glu Leu
          500          505          510
Ser Glu Tyr Met Gln Ala Glu Arg Ile Phe Ser Glu Val Arg Arg Ile
          515          520          525
Glu Asn Tyr Arg Val Glu Gly Met Glu Ile Tyr Ser Thr Thr Leu Trp
          530          535          540
His Leu Gln Lys Asp Val Ala Leu Ser Val Leu Ser Lys Asp Leu Thr
545          550          555          560
Asp Met Asp Lys Asn Ser Pro Glu Ala Trp Cys Ala Ala Gly Asn Cys
          565          570          575
Phe Ser Leu Gln Arg Glu His Asp Ile Ala Ile Lys Phe Phe Gln Arg
          580          585          590
Ala Ile Gln Val Asp Pro Asn Tyr Ala Tyr Ala Tyr Thr Leu Leu Gly
          595          600          605
His Glu Phe Val Leu Thr Glu Glu Leu Asp Lys Ala Leu Ala Cys Phe
          610          615          620
Arg Asn Ala Ile Arg Val Asn Pro Arg His Tyr Asn Ala Trp Tyr Gly
625          630          635          640
Leu Gly Met Ile Tyr Tyr Lys Gln Glu Lys Phe Ser Leu Ala Glu Met
          645          650          655
His Phe Gln Lys Ala Leu Asp Ile Asn Pro Gln Ser Ser Val Leu Leu
          660          665          670
Cys His Ile Gly Val Val Gln His Ala Leu Lys Lys Ser Glu Lys Ala
          675          680          685
Leu Asp Thr Leu Asn Lys Ala Ile Val Ile Asp Pro Lys Asn Pro Leu
          690          695          700
Cys Lys Phe His Arg Ala Ser Val Leu Phe Ala Asn Glu Lys Tyr Lys
705          710          715          720
Ser Ala Leu Gln Glu Leu Glu Glu Leu Lys Gln Ile Val Pro Lys Glu
          725          730          735

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Ser Leu Val Tyr Phe Leu Ile Gly Lys Val Tyr Lys Lys Leu Gly Gln
740 745 750

Thr His Leu Ala Leu Met Asn Phe Ser Trp Ala Met Asp Leu Asp Pro
755 760 765

Lys Gly Ala Asn Asn Gln Ile Lys Glu Ala Ile Asp Lys Arg Tyr Leu
770 775 780

Pro Asp Asp Glu Glu Pro Ile Thr Gln Glu Glu Gln Ile Met Gly Thr
785 790 795 800

Asp Glu Ser Gln Glu Ser Ser Met Thr Asp Ala Asp Asp Thr Gln Leu
805 810 815

His Ala Ala Glu Ser Asp Glu Phe
820

<210> 282
<211> 595
<212> PRT
<213> Artificial Sequence

<220>
<223> CDE30__Homo_sapiens__P28908

<400> 282

Met Arg Val Leu Leu Ala Ala Leu Gly Leu Leu Phe Leu Gly Ala Leu
1 5 10 15

Arg Ala Phe Pro Gln Asp Arg Pro Phe Glu Asp Thr Cys His Gly Asn
20 25 30

Pro Ser His Tyr Tyr Asp Lys Ala Val Arg Arg Cys Cys Tyr Arg Cys
35 40 45

Pro Met Gly Leu Phe Pro Thr Gln Gln Cys Pro Gln Arg Pro Thr Asp
50 55 60

Cys Arg Lys Gln Cys Glu Pro Asp Tyr Tyr Leu Asp Glu Ala Asp Arg
65 70 75 80

Cys Thr Ala Cys Val Thr Cys Ser Arg Asp Asp Leu Val Glu Lys Thr
85 90 95

Pro Cys Ala Trp Asn Ser Ser Arg Val Cys Glu Cys Arg Pro Gly Met
100 105 110

Phe Cys Ser Thr Ser Ala Val Asn Ser Cys Ala Arg Cys Phe Phe His
115 120 125

ITI-08-PCT_Sequence_Listing_ST25.txt

Ser	Val	Cys	Pro	Ala	Gly	Met	Ile	Val	Lys	Phe	Pro	Gly	Thr	Ala	Gln	130	135	140
Lys	Asn	Thr	Val	Cys	Glu	Pro	Ala	Ser	Pro	Gly	Val	Ser	Pro	Ala	Cys	145	150	155
Ala	Ser	Pro	Glu	Asn	Cys	Lys	Glu	Pro	Ser	Ser	Gly	Thr	Ile	Pro	Gln	165	170	175
Ala	Lys	Pro	Thr	Pro	Val	Ser	Pro	Ala	Thr	Ser	Ser	Ala	Ser	Thr	Met	180	185	190
Pro	Val	Arg	Gly	Gly	Thr	Arg	Leu	Ala	Gln	Glu	Ala	Ala	Ser	Lys	Leu	195	200	205
Thr	Arg	Ala	Pro	Asp	Ser	Pro	Ser	Ser	Val	Gly	Arg	Pro	Ser	Ser	Asp	210	215	220
Pro	Gly	Leu	Ser	Pro	Thr	Gln	Pro	Cys	Pro	Glu	Gly	Ser	Gly	Asp	Cys	225	230	235
Arg	Lys	Gln	Cys	Glu	Pro	Asp	Tyr	Tyr	Leu	Asp	Glu	Ala	Gly	Arg	Cys	245	250	255
Thr	Ala	Cys	Val	Ser	Cys	Ser	Arg	Asp	Asp	Leu	Val	Glu	Lys	Thr	Pro	260	265	270
Cys	Ala	Trp	Asn	Ser	Ser	Arg	Thr	Cys	Glu	Cys	Arg	Pro	Gly	Met	Ile	275	280	285
Cys	Ala	Thr	Ser	Ala	Thr	Asn	Ser	Cys	Ala	Arg	Cys	Val	Pro	Tyr	Pro	290	295	300
Ile	Cys	Ala	Ala	Glu	Thr	Val	Thr	Lys	Pro	Gln	Asp	Met	Ala	Glu	Lys	305	310	315
Asp	Thr	Thr	Phe	Glu	Ala	Pro	Pro	Leu	Gly	Thr	Gln	Pro	Asp	Cys	Asn	325	330	335
Pro	Thr	Pro	Glu	Asn	Gly	Glu	Ala	Pro	Ala	Ser	Thr	Ser	Pro	Thr	Gln	340	345	350
Ser	Leu	Leu	Val	Asp	Ser	Gln	Ala	Ser	Lys	Thr	Leu	Pro	Ile	Pro	Thr	355	360	365
Ser	Ala	Pro	Val	Ala	Leu	Ser	Ser	Thr	Gly	Lys	Pro	Val	Leu	Asp	Ala	370	375	380
Gly	Pro	Val	Leu	Phe	Trp	Val	Ile	Leu	Val	Leu	Val	Val	Val	Val	Gly	385	390	395

ITI-08-PCT_Sequence_Listing_ST25.txt

Ser Ser Ala Phe Leu Leu Cys His Arg Arg Ala Cys Arg Lys Arg Ile
405 410 415

Arg Gln Lys Leu His Leu Cys Tyr Pro Val Gln Thr Ser Gln Pro Lys
420 425 430

Leu Glu Leu Val Asp Ser Arg Pro Arg Arg Ser Ser Thr Gln Leu Arg
435 440 445

Ser Gly Ala Ser Val Thr Glu Pro Val Ala Glu Glu Arg Gly Leu Met
450 455 460

Ser Gln Pro Leu Met Glu Thr Cys His Ser Val Gly Ala Ala Tyr Leu
465 470 475 480

Glu Ser Leu Pro Leu Gln Asp Ala Ser Pro Ala Gly Gly Pro Ser Ser
485 490 495

Pro Arg Asp Leu Pro Glu Pro Arg Val Ser Thr Glu His Thr Asn Asn
500 505 510

Lys Ile Glu Lys Ile Tyr Ile Met Lys Ala Asp Thr Val Ile Val Gly
515 520 525

Thr Val Lys Ala Glu Leu Pro Glu Gly Arg Gly Leu Ala Gly Pro Ala
530 535 540

Glu Pro Glu Leu Glu Glu Glu Leu Glu Ala Asp His Thr Pro His Tyr
545 550 555 560

Pro Glu Gln Glu Thr Glu Pro Pro Leu Gly Ser Cys Ser Asp Val Met
565 570 575

Leu Ser Val Glu Glu Glu Gly Lys Glu Asp Pro Leu Pro Thr Ala Ala
580 585 590

Ser Gly Lys
595

<210> 283

<211> 303

<212> PRT

<213> Artificial Sequence

<220>

<223> CDK4/m__Homo_sapiens__A0A024RBB6

<400> 283

Met Ala Thr Ser Arg Tyr Glu Pro Val Ala Glu Ile Gly Val Gly Ala
1 5 10 15

ITI-08-PCT_Sequence_Listing_ST25.txt

Tyr Gly Thr Val Tyr Lys Ala Arg Asp Pro His Ser Gly His Phe Val
 20 25 30
 Ala Leu Lys Ser Val Arg Val Pro Asn Gly Gly Gly Gly Gly Gly Gly
 35 40 45
 Leu Pro Ile Ser Thr Val Arg Glu Val Ala Leu Leu Arg Arg Leu Glu
 50 55 60
 Ala Phe Glu His Pro Asn Val Val Arg Leu Met Asp Val Cys Ala Thr
 65 70 75 80
 Ser Arg Thr Asp Arg Glu Ile Lys Val Thr Leu Val Phe Glu His Val
 85 90 95
 Asp Gln Asp Leu Arg Thr Tyr Leu Asp Lys Ala Pro Pro Pro Gly Leu
 100 105 110
 Pro Ala Glu Thr Ile Lys Asp Leu Met Arg Gln Phe Leu Arg Gly Leu
 115 120 125
 Asp Phe Leu His Ala Asn Cys Ile Val His Arg Asp Leu Lys Pro Glu
 130 135 140
 Asn Ile Leu Val Thr Ser Gly Gly Thr Val Lys Leu Ala Asp Phe Gly
 145 150 155 160
 Leu Ala Arg Ile Tyr Ser Tyr Gln Met Ala Leu Thr Pro Val Val Val
 165 170 175
 Thr Leu Trp Tyr Arg Ala Pro Glu Val Leu Leu Gln Ser Thr Tyr Ala
 180 185 190
 Thr Pro Val Asp Met Trp Ser Val Gly Cys Ile Phe Ala Glu Met Phe
 195 200 205
 Arg Arg Lys Pro Leu Phe Cys Gly Asn Ser Glu Ala Asp Gln Leu Gly
 210 215 220
 Lys Ile Phe Asp Leu Ile Gly Leu Pro Pro Glu Asp Asp Trp Pro Arg
 225 230 235 240
 Asp Val Ser Leu Pro Arg Gly Ala Phe Pro Pro Arg Gly Pro Arg Pro
 245 250 255
 Val Gln Ser Val Val Pro Glu Met Glu Glu Ser Gly Ala Gln Leu Leu
 260 265 270
 Leu Glu Met Leu Thr Phe Asn Pro His Lys Arg Ile Ser Ala Phe Arg
 275 280 285
 Ala Leu Gln His Ser Tyr Leu His Lys Asp Glu Gly Asn Pro Glu

ITI-08-PCT_Sequence_Listing_ST25.txt

290

295

300

<210> 284

<211> 303

<212> PRT

<213> Artificial Sequence

<220>

<223> CDK4/m__Homo_sapiens__P11802

<400> 284

Met Ala Thr Ser Arg Tyr Glu Pro Val Ala Glu Ile Gly Val Gly Ala
1 5 10 15

Tyr Gly Thr Val Tyr Lys Ala Arg Asp Pro His Ser Gly His Phe Val
20 25 30

Ala Leu Lys Ser Val Arg Val Pro Asn Gly Gly Gly Gly Gly Gly Gly
35 40 45

Leu Pro Ile Ser Thr Val Arg Glu Val Ala Leu Leu Arg Arg Leu Glu
50 55 60

Ala Phe Glu His Pro Asn Val Val Arg Leu Met Asp Val Cys Ala Thr
65 70 75 80

Ser Arg Thr Asp Arg Glu Ile Lys Val Thr Leu Val Phe Glu His Val
85 90 95

Asp Gln Asp Leu Arg Thr Tyr Leu Asp Lys Ala Pro Pro Pro Gly Leu
100 105 110

Pro Ala Glu Thr Ile Lys Asp Leu Met Arg Gln Phe Leu Arg Gly Leu
115 120 125

Asp Phe Leu His Ala Asn Cys Ile Val His Arg Asp Leu Lys Pro Glu
130 135 140

Asn Ile Leu Val Thr Ser Gly Gly Thr Val Lys Leu Ala Asp Phe Gly
145 150 155 160

Leu Ala Arg Ile Tyr Ser Tyr Gln Met Ala Leu Thr Pro Val Val Val
165 170 175

Thr Leu Trp Tyr Arg Ala Pro Glu Val Leu Leu Gln Ser Thr Tyr Ala
180 185 190

Thr Pro Val Asp Met Trp Ser Val Gly Cys Ile Phe Ala Glu Met Phe
195 200 205

Arg Arg Lys Pro Leu Phe Cys Gly Asn Ser Glu Ala Asp Gln Leu Gly

ITI-08-PCT_Sequence_Listing_ST25.txt

210

215

220

Lys Ile Phe Asp Leu Ile Gly Leu Pro Pro Glu Asp Asp Trp Pro Arg
225 230 235 240

Asp Val Ser Leu Pro Arg Gly Ala Phe Pro Pro Arg Gly Pro Arg Pro
245 250 255

Val Gln Ser Val Val Pro Glu Met Glu Glu Ser Gly Ala Gln Leu Leu
260 265 270

Leu Glu Met Leu Thr Phe Asn Pro His Lys Arg Ile Ser Ala Phe Arg
275 280 285

Ala Leu Gln His Ser Tyr Leu His Lys Asp Glu Gly Asn Pro Glu
290 295 300

<210> 285

<211> 229

<212> PRT

<213> Artificial Sequence

<220>

<223> CDK4/m__Homo_sapiens__Q6LC83

<400> 285

Met Asp Val Cys Ala Thr Ser Arg Thr Asp Arg Glu Ile Lys Val Thr
1 5 10 15

Leu Val Phe Glu His Val Asp Gln Asp Leu Arg Thr Tyr Leu Asp Lys
20 25 30

Ala Pro Pro Pro Gly Leu Pro Ala Glu Thr Ile Lys Asp Leu Met Arg
35 40 45

Gln Phe Leu Arg Gly Leu Asp Phe Leu His Ala Asn Cys Ile Val His
50 55 60

Arg Asp Leu Lys Pro Glu Asn Ile Leu Val Thr Ser Gly Gly Thr Val
65 70 75 80

Lys Leu Ala Asp Phe Gly Leu Ala Arg Ile Tyr Ser Tyr Gln Met Ala
85 90 95

Leu Thr Pro Val Val Val Thr Leu Trp Tyr Arg Ala Pro Glu Val Leu
100 105 110

Leu Gln Ser Thr Tyr Ala Thr Pro Val Asp Met Trp Ser Val Gly Cys
115 120 125

Ile Phe Ala Glu Met Phe Arg Arg Lys Pro Leu Phe Cys Gly Asn Ser

ITI-08-PCT_Sequence_Listing_ST25.txt

130

135

140

Glu Ala Asp Gln Leu Gly Lys Ile Phe Asp Leu Ile Gly Leu Pro Pro
145 150 155 160

Glu Asp Asp Trp Pro Arg Asp Val Ser Leu Pro Arg Gly Ala Phe Pro
165 170 175

Pro Arg Gly Pro Arg Pro Val Gln Ser Val Val Pro Glu Met Glu Glu
180 185 190

Ser Gly Ala Gln Leu Leu Leu Glu Met Leu Thr Phe Asn Pro His Lys
195 200 205

Arg Ile Ser Ala Phe Arg Ala Leu Gln His Ser Tyr Leu His Lys Asp
210 215 220

Glu Gly Asn Pro Glu
225

<210> 286

<211> 111

<212> PRT

<213> Artificial Sequence

<220>

<223> CDK4/m__Homo_sapiens__Q96BE9

<400> 286

Met Ala Thr Ser Arg Tyr Glu Pro Val Ala Glu Ile Gly Val Gly Ala
1 5 10 15

Tyr Gly Thr Val Tyr Lys Ala Arg Asp Pro His Ser Gly His Phe Val
20 25 30

Ala Leu Lys Ser Val Arg Val Pro Asn Gly Gly Gly Gly Gly Gly Gly
35 40 45

Leu Pro Ile Ser Thr Val Arg Glu Val Ala Leu Leu Arg Arg Leu Glu
50 55 60

Ala Phe Glu His Pro Asn Val Val Arg Leu Met Asp Val Cys Ala Thr
65 70 75 80

Ser Arg Thr Asp Arg Glu Ile Lys Arg Cys Phe Val Glu Ser Leu Ser
85 90 95

Ser Val Glu Thr Leu Lys Pro Thr Ser Trp Ala Lys Ser Leu Thr
100 105 110

<210> 287

ITI-08-PCT_Sequence_Listing_ST25.txt

<211> 142
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CDKN2A/m__Homo_sapiens__D1LYX3

<400> 287

Met Glu Pro Ala Ala Gly Ser Ser Met Glu Pro Ser Ala Asp Trp Leu
 1 5 10 15

Ala Thr Ala Ala Ala Arg Gly Arg Val Glu Glu Val Arg Ala Leu Leu
 20 25 30

Glu Ala Gly Ala Leu Pro Asn Ala Pro Asn Ser Tyr Gly Arg Arg Pro
 35 40 45

Ile Gln Val Met Met Met Gly Ser Ala Arg Val Ala Glu Leu Leu Leu
 50 55 60

Leu His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala Thr Leu Thr Arg
 65 70 75 80

Pro Val His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val
 85 90 95

Leu His Arg Ala Gly Ala Pro Cys Ala Met Pro Gly Ala Val Cys Pro
 100 105 110

Trp Thr Trp Leu Arg Ser Trp Ala Ile Ala Met Ser His Gly Thr Cys
 115 120 125

Ala Arg Leu Arg Gly Ala Pro Glu Ala Val Thr Met Pro Ala
 130 135 140

<210> 288
 <211> 116
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CDKN2A/m__Homo_sapiens__G3XAG3

<400> 288

Met Glu Pro Ala Ala Gly Ser Ser Met Glu Pro Ser Ala Asp Trp Leu
 1 5 10 15

Ala Thr Ala Ala Ala Arg Gly Arg Val Glu Glu Val Arg Ala Leu Leu
 20 25 30

ITI-08-PCT_Sequence_Listing_ST25.txt

Glu Ala Gly Ala Leu Pro Asn Ala Pro Asn Ser Tyr Gly Arg Arg Pro
35 40 45

Ile Gln Val Gly Arg Gly Ser Ala Ala Gly Ala Gly Asp Gly Gly Arg
50 55 60

Leu Trp Arg Thr Lys Phe Ala Gly Glu Leu Glu Ser Gly Ser Ala Ser
65 70 75 80

Ile Leu Arg Lys Lys Gly Arg Leu Pro Gly Glu Phe Ser Glu Gly Val
85 90 95

Cys Asn His Arg Pro Pro Pro Gly Asp Ala Leu Gly Ala Trp Glu Ala
100 105 110

Lys Glu Glu Glu
115

<210> 289

<211> 156

<212> PRT

<213> Artificial Sequence

<220>

<223> CDKN2A/m__Homo_sapiens__K7PML8

<400> 289

Met Glu Pro Ala Ala Gly Ser Ser Met Glu Pro Ser Ala Asp Trp Leu
1 5 10 15

Ala Thr Ala Ala Ala Arg Gly Arg Val Glu Glu Val Arg Ala Leu Leu
20 25 30

Glu Ala Gly Ala Leu Pro Asn Ala Pro Asn Ser Tyr Gly Arg Arg Pro
35 40 45

Ile Gln Val Met Met Met Gly Ser Ala Arg Val Ala Glu Leu Leu Leu
50 55 60

Leu His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala Thr Leu Thr Arg
65 70 75 80

Pro Val His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val
85 90 95

Leu His Arg Ala Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly Arg
100 105 110

Leu Pro Val Asp Leu Ala Glu Glu Leu Gly His Arg Asp Val Ala Arg
115 120 125

ITI-08-PCT_Sequence_Listing_ST25.txt

Tyr Leu Arg Ala Ala Ala Gly Gly Thr Arg Gly Ser Asn His Ala Arg
130 135 140

Ile Asp Ala Ala Glu Gly Pro Ser Asp Ile Pro Asp
145 150 155

<210> 290
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> CDKN2A/m__Homo_sapiens__L8E941

<400> 290

Met Glu Val Met Met Met Gly Ser Ala Arg Val Ala Glu Leu Leu Leu
1 5 10 15

Leu His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala Thr Leu Thr Arg
20 25 30

Pro Val His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val
35 40 45

Leu His Arg Ala Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly Arg
50 55 60

Leu Pro Val Asp Leu Ala Glu Glu Leu Gly His Arg Asp Val Ala Arg
65 70 75 80

Tyr Leu Arg Ala Ala Ala Gly Gly Thr Arg Gly Ser Asn His Ala Arg
85 90 95

Ile Asp Ala Ala Glu Gly Pro Ser Asp Ile Pro Asp
100 105

<210> 291
<211> 132
<212> PRT
<213> Artificial Sequence

<220>
<223> CDKN2A/m__Homo_sapiens__Q8N726

<400> 291

Met Val Arg Arg Phe Leu Val Thr Leu Arg Ile Arg Arg Ala Cys Gly
1 5 10 15

Pro Pro Arg Val Arg Val Phe Val Val His Ile Pro Arg Leu Thr Gly
20 25 30

ITI-08-PCT_Sequence_Listing_ST25.txt

Glu Trp Ala Ala Pro Gly Ala Pro Ala Ala Val Ala Leu Val Leu Met
35 40 45

Leu Leu Arg Ser Gln Arg Leu Gly Gln Gln Pro Leu Pro Arg Arg Pro
50 55 60

Gly His Asp Asp Gly Gln Arg Pro Ser Gly Gly Ala Ala Ala Ala Pro
65 70 75 80

Arg Arg Gly Ala Gln Leu Arg Arg Pro Arg His Ser His Pro Thr Arg
85 90 95

Ala Arg Arg Cys Pro Gly Gly Leu Pro Gly His Ala Gly Gly Ala Ala
100 105 110

Pro Gly Arg Gly Ala Ala Gly Arg Ala Arg Cys Leu Gly Pro Ser Ala
115 120 125

Arg Gly Pro Gly
130

<210> 292
<211> 702
<212> PRT
<213> Artificial Sequence

<220>
<223> CEA__Homo_sapiens__NP_004354

<400> 292

Met Glu Ser Pro Ser Ala Pro Pro His Arg Trp Cys Ile Pro Trp Gln
1 5 10 15

Arg Leu Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn Pro Pro Thr
20 25 30

Thr Ala Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val Ala Glu Gly
35 40 45

Lys Glu Val Leu Leu Leu Val His Asn Leu Pro Gln His Leu Phe Gly
50 55 60

Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Ile
65 70 75 80

Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Tyr Ser
85 90 95

Gly Arg Glu Ile Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Ile
100 105 110

ITI-08-PCT_Sequence_Listing_ST25.txt

Ile	Gln	Asn	Asp	Thr	Gly	Phe	Tyr	Thr	Leu	His	Val	Ile	Lys	Ser	Asp	115	120	125
Leu	Val	Asn	Glu	Glu	Ala	Thr	Gly	Gln	Phe	Arg	Val	Tyr	Pro	Glu	Leu	130	135	140
Pro	Lys	Pro	Ser	Ile	Ser	Ser	Asn	Asn	Ser	Lys	Pro	Val	Glu	Asp	Lys	145	150	155
Asp	Ala	Val	Ala	Phe	Thr	Cys	Glu	Pro	Glu	Thr	Gln	Asp	Ala	Thr	Tyr	165	170	175
Leu	Trp	Trp	Val	Asn	Asn	Gln	Ser	Leu	Pro	Val	Ser	Pro	Arg	Leu	Gln	180	185	190
Leu	Ser	Asn	Gly	Asn	Arg	Thr	Leu	Thr	Leu	Phe	Asn	Val	Thr	Arg	Asn	195	200	205
Asp	Thr	Ala	Ser	Tyr	Lys	Cys	Glu	Thr	Gln	Asn	Pro	Val	Ser	Ala	Arg	210	215	220
Arg	Ser	Asp	Ser	Val	Ile	Leu	Asn	Val	Leu	Tyr	Gly	Pro	Asp	Ala	Pro	225	230	235
Thr	Ile	Ser	Pro	Leu	Asn	Thr	Ser	Tyr	Arg	Ser	Gly	Glu	Asn	Leu	Asn	245	250	255
Leu	Ser	Cys	His	Ala	Ala	Ser	Asn	Pro	Pro	Ala	Gln	Tyr	Ser	Trp	Phe	260	265	270
Val	Asn	Gly	Thr	Phe	Gln	Gln	Ser	Thr	Gln	Glu	Leu	Phe	Ile	Pro	Asn	275	280	285
Ile	Thr	Val	Asn	Asn	Ser	Gly	Ser	Tyr	Thr	Cys	Gln	Ala	His	Asn	Ser	290	295	300
Asp	Thr	Gly	Leu	Asn	Arg	Thr	Thr	Val	Thr	Thr	Ile	Thr	Val	Tyr	Ala	305	310	315
Glu	Pro	Pro	Lys	Pro	Phe	Ile	Thr	Ser	Asn	Asn	Ser	Asn	Pro	Val	Glu	325	330	335
Asp	Glu	Asp	Ala	Val	Ala	Leu	Thr	Cys	Glu	Pro	Glu	Ile	Gln	Asn	Thr	340	345	350
Thr	Tyr	Leu	Trp	Trp	Val	Asn	Asn	Gln	Ser	Leu	Pro	Val	Ser	Pro	Arg	355	360	365
Leu	Gln	Leu	Ser	Asn	Asp	Asn	Arg	Thr	Leu	Thr	Leu	Leu	Ser	Val	Thr	370	375	380

ITI-08-PCT_Sequence_Listing_ST25.txt

Arg	Asn	Asp	Val	Gly	Pro	Tyr	Glu	Cys	Gly	Ile	Gln	Asn	Glu	Leu	Ser	385	390	395	400
Val	Asp	His	Ser	Asp	Pro	Val	Ile	Leu	Asn	Val	Leu	Tyr	Gly	Pro	Asp	405	410	415	
Asp	Pro	Thr	Ile	Ser	Pro	Ser	Tyr	Thr	Tyr	Tyr	Arg	Pro	Gly	Val	Asn	420	425	430	
Leu	Ser	Leu	Ser	Cys	His	Ala	Ala	Ser	Asn	Pro	Pro	Ala	Gln	Tyr	Ser	435	440	445	
Trp	Leu	Ile	Asp	Gly	Asn	Ile	Gln	Gln	His	Thr	Gln	Glu	Leu	Phe	Ile	450	455	460	
Ser	Asn	Ile	Thr	Glu	Lys	Asn	Ser	Gly	Leu	Tyr	Thr	Cys	Gln	Ala	Asn	465	470	475	480
Asn	Ser	Ala	Ser	Gly	His	Ser	Arg	Thr	Thr	Val	Lys	Thr	Ile	Thr	Val	485	490	495	
Ser	Ala	Glu	Leu	Pro	Lys	Pro	Ser	Ile	Ser	Ser	Asn	Asn	Ser	Lys	Pro	500	505	510	
Val	Glu	Asp	Lys	Asp	Ala	Val	Ala	Phe	Thr	Cys	Glu	Pro	Glu	Ala	Gln	515	520	525	
Asn	Thr	Thr	Tyr	Leu	Trp	Trp	Val	Asn	Gly	Gln	Ser	Leu	Pro	Val	Ser	530	535	540	
Pro	Arg	Leu	Gln	Leu	Ser	Asn	Gly	Asn	Arg	Thr	Leu	Thr	Leu	Phe	Asn	545	550	555	560
Val	Thr	Arg	Asn	Asp	Ala	Arg	Ala	Tyr	Val	Cys	Gly	Ile	Gln	Asn	Ser	565	570	575	
Val	Ser	Ala	Asn	Arg	Ser	Asp	Pro	Val	Thr	Leu	Asp	Val	Leu	Tyr	Gly	580	585	590	
Pro	Asp	Thr	Pro	Ile	Ile	Ser	Pro	Pro	Asp	Ser	Ser	Tyr	Leu	Ser	Gly	595	600	605	
Ala	Asn	Leu	Asn	Leu	Ser	Cys	His	Ser	Ala	Ser	Asn	Pro	Ser	Pro	Gln	610	615	620	
Tyr	Ser	Trp	Arg	Ile	Asn	Gly	Ile	Pro	Gln	Gln	His	Thr	Gln	Val	Leu	625	630	635	640
Phe	Ile	Ala	Lys	Ile	Thr	Pro	Asn	Asn	Asn	Gly	Thr	Tyr	Ala	Cys	Phe	645	650	655	
Val	Ser	Asn	Leu	Ala	Thr	Gly	Arg	Asn	Asn	Ser	Ile	Val	Lys	Ser	Ile				

ITI-08-PCT_Sequence_Listing_ST25.txt

660

665

670

Thr Val Ser Ala Ser Gly Thr Ser Pro Gly Leu Ser Ala Gly Ala Thr
675 680 685

Val Gly Ile Met Ile Gly Val Leu Val Gly Val Ala Leu Ile
690 695 700

<210> 293

<211> 344

<212> PRT

<213> Artificial Sequence

<220>

<223> CEAM6__Homo_sapiens__P40199

<400> 293

Met Gly Pro Pro Ser Ala Pro Pro Cys Arg Leu His Val Pro Trp Lys
1 5 10 15

Glu Val Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn Pro Pro Thr
20 25 30

Thr Ala Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val Ala Glu Gly
35 40 45

Lys Glu Val Leu Leu Leu Ala His Asn Leu Pro Gln Asn Arg Ile Gly
50 55 60

Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Ser Leu Ile Val
65 70 75 80

Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Tyr Ser
85 90 95

Gly Arg Glu Thr Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Val
100 105 110

Thr Gln Asn Asp Thr Gly Phe Tyr Thr Leu Gln Val Ile Lys Ser Asp
115 120 125

Leu Val Asn Glu Glu Ala Thr Gly Gln Phe His Val Tyr Pro Glu Leu
130 135 140

Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Asn Pro Val Glu Asp Lys
145 150 155 160

Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Val Gln Asn Thr Thr Tyr
165 170 175

Leu Trp Trp Val Asn Gly Gln Ser Leu Pro Val Ser Pro Arg Leu Gln

ITI-08-PCT_Sequence_Listing_ST25.txt

180

185

190

Leu Ser Asn Gly Asn Met Thr Leu Thr Leu Leu Ser Val Lys Arg Asn
195 200 205

Asp Ala Gly Ser Tyr Glu Cys Glu Ile Gln Asn Pro Ala Ser Ala Asn
210 215 220

Arg Ser Asp Pro Val Thr Leu Asn Val Leu Tyr Gly Pro Asp Gly Pro
225 230 235 240

Thr Ile Ser Pro Ser Lys Ala Asn Tyr Arg Pro Gly Glu Asn Leu Asn
245 250 255

Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Phe
260 265 270

Ile Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn
275 280 285

Ile Thr Val Asn Asn Ser Gly Ser Tyr Met Cys Gln Ala His Asn Ser
290 295 300

Ala Thr Gly Leu Asn Arg Thr Thr Val Thr Met Ile Thr Val Ser Gly
305 310 315 320

Ser Ala Pro Val Leu Ser Ala Val Ala Thr Val Gly Ile Thr Ile Gly
325 330 335

Val Leu Ala Arg Val Ala Leu Ile
340

<210> 294
<211> 390
<212> PRT
<213> Artificial Sequence

<220>
<223> CH3L2__Homo_sapiens__Q15782

<400> 294

Met Gly Ala Thr Thr Met Asp Gln Lys Ser Leu Trp Ala Gly Val Val
1 5 10 15

Val Leu Leu Leu Leu Gln Gly Gly Ser Ala Tyr Lys Leu Val Cys Tyr
20 25 30

Phe Thr Asn Trp Ser Gln Asp Arg Gln Glu Pro Gly Lys Phe Thr Pro
35 40 45

Glu Asn Ile Asp Pro Phe Leu Cys Ser His Leu Ile Tyr Ser Phe Ala

ITI-08-PCT_Sequence_Listing_ST25.txt

50	55	60														
Ser	Ile	Glu	Asn	Asn	Lys	Val	Ile	Ile	Lys	Asp	Lys	Ser	Glu	Val	Met	
65					70					75					80	
Leu	Tyr	Gln	Thr	Ile	Asn	Ser	Leu	Lys	Thr	Lys	Asn	Pro	Lys	Leu	Lys	
				85					90					95		
Ile	Leu	Leu	Ser	Ile	Gly	Gly	Tyr	Leu	Phe	Gly	Ser	Lys	Gly	Phe	His	
			100					105					110			
Pro	Met	Val	Asp	Ser	Ser	Thr	Ser	Arg	Leu	Glu	Phe	Ile	Asn	Ser	Ile	
		115					120					125				
Ile	Leu	Phe	Leu	Arg	Asn	His	Asn	Phe	Asp	Gly	Leu	Asp	Val	Ser	Trp	
	130				135						140					
Ile	Tyr	Pro	Asp	Gln	Lys	Glu	Asn	Thr	His	Phe	Thr	Val	Leu	Ile	His	
145					150					155					160	
Glu	Leu	Ala	Glu	Ala	Phe	Gln	Lys	Asp	Phe	Thr	Lys	Ser	Thr	Lys	Glu	
				165					170					175		
Arg	Leu	Leu	Leu	Thr	Ala	Gly	Val	Ser	Ala	Gly	Arg	Gln	Met	Ile	Asp	
			180					185					190			
Asn	Ser	Tyr	Gln	Val	Glu	Lys	Leu	Ala	Lys	Asp	Leu	Asp	Phe	Ile	Asn	
		195					200					205				
Leu	Leu	Ser	Phe	Asp	Phe	His	Gly	Ser	Trp	Glu	Lys	Pro	Leu	Ile	Thr	
	210					215					220					
Gly	His	Asn	Ser	Pro	Leu	Ser	Lys	Gly	Trp	Gln	Asp	Arg	Gly	Pro	Ser	
225					230					235					240	
Ser	Tyr	Tyr	Asn	Val	Glu	Tyr	Ala	Val	Gly	Tyr	Trp	Ile	His	Lys	Gly	
			245						250					255		
Met	Pro	Ser	Glu	Lys	Val	Val	Met	Gly	Ile	Pro	Thr	Tyr	Gly	His	Ser	
			260					265					270			
Phe	Thr	Leu	Ala	Ser	Ala	Glu	Thr	Thr	Val	Gly	Ala	Pro	Ala	Ser	Gly	
		275					280					285				
Pro	Gly	Ala	Ala	Gly	Pro	Ile	Thr	Glu	Ser	Ser	Gly	Phe	Leu	Ala	Tyr	
	290					295					300					
Tyr	Glu	Ile	Cys	Gln	Phe	Leu	Lys	Gly	Ala	Lys	Ile	Thr	Arg	Leu	Gln	
305					310					315					320	
Asp	Gln	Gln	Val	Pro	Tyr	Ala	Val	Lys	Gly	Asn	Gln	Trp	Val	Gly	Tyr	
				325					330					335		

ITI-08-PCT_Sequence_Listing_ST25.txt

Asp Asp Val Lys Ser Met Glu Thr Lys Val Gln Phe Leu Lys Asn Leu
340 345 350

Asn Leu Gly Gly Ala Met Ile Trp Ser Ile Asp Met Asp Asp Phe Thr
355 360 365

Gly Lys Ser Cys Asn Gln Gly Pro Tyr Pro Leu Val Gln Ala Val Lys
370 375 380

Arg Ser Leu Gly Ser Leu
385 390

<210> 295

<211> 943

<212> PRT

<213> Artificial Sequence

<220>

<223> CLCA2__Homo_sapiens__Q9UQC9

<400> 295

Met Thr Gln Arg Ser Ile Ala Gly Pro Ile Cys Asn Leu Lys Phe Val
1 5 10 15

Thr Leu Leu Val Ala Leu Ser Ser Glu Leu Pro Phe Leu Gly Ala Gly
20 25 30

Val Gln Leu Gln Asp Asn Gly Tyr Asn Gly Leu Leu Ile Ala Ile Asn
35 40 45

Pro Gln Val Pro Glu Asn Gln Asn Leu Ile Ser Asn Ile Lys Glu Met
50 55 60

Ile Thr Glu Ala Ser Phe Tyr Leu Phe Asn Ala Thr Lys Arg Arg Val
65 70 75 80

Phe Phe Arg Asn Ile Lys Ile Leu Ile Pro Ala Thr Trp Lys Ala Asn
85 90 95

Asn Asn Ser Lys Ile Lys Gln Glu Ser Tyr Glu Lys Ala Asn Val Ile
100 105 110

Val Thr Asp Trp Tyr Gly Ala His Gly Asp Asp Pro Tyr Thr Leu Gln
115 120 125

Tyr Arg Gly Cys Gly Lys Glu Gly Lys Tyr Ile His Phe Thr Pro Asn
130 135 140

Phe Leu Leu Asn Asp Asn Leu Thr Ala Gly Tyr Gly Ser Arg Gly Arg
145 150 155 160

ITI-08-PCT_Sequence_Listing_ST25.txt

Val	Phe	Val	His	Glu	Trp	Ala	His	Leu	Arg	Trp	Gly	Val	Phe	Asp	Glu	165	170	175
Tyr	Asn	Asn	Asp	Lys	Pro	Phe	Tyr	Ile	Asn	Gly	Gln	Asn	Gln	Ile	Lys	180	185	190
Val	Thr	Arg	Cys	Ser	Ser	Asp	Ile	Thr	Gly	Ile	Phe	Val	Cys	Glu	Lys	195	200	205
Gly	Pro	Cys	Pro	Gln	Glu	Asn	Cys	Ile	Ile	Ser	Lys	Leu	Phe	Lys	Glu	210	215	220
Gly	Cys	Thr	Phe	Ile	Tyr	Asn	Ser	Thr	Gln	Asn	Ala	Thr	Ala	Ser	Ile	225	230	235
Met	Phe	Met	Gln	Ser	Leu	Ser	Ser	Val	Val	Glu	Phe	Cys	Asn	Ala	Ser	245	250	255
Thr	His	Asn	Gln	Glu	Ala	Pro	Asn	Leu	Gln	Asn	Gln	Met	Cys	Ser	Leu	260	265	270
Arg	Ser	Ala	Trp	Asp	Val	Ile	Thr	Asp	Ser	Ala	Asp	Phe	His	His	Ser	275	280	285
Phe	Pro	Met	Asn	Gly	Thr	Glu	Leu	Pro	Pro	Pro	Pro	Thr	Phe	Ser	Leu	290	295	300
Val	Gln	Ala	Gly	Asp	Lys	Val	Val	Cys	Leu	Val	Leu	Asp	Val	Ser	Ser	305	310	315
Lys	Met	Ala	Glu	Ala	Asp	Arg	Leu	Leu	Gln	Leu	Gln	Gln	Ala	Ala	Glu	325	330	335
Phe	Tyr	Leu	Met	Gln	Ile	Val	Glu	Ile	His	Thr	Phe	Val	Gly	Ile	Ala	340	345	350
Ser	Phe	Asp	Ser	Lys	Gly	Glu	Ile	Arg	Ala	Gln	Leu	His	Gln	Ile	Asn	355	360	365
Ser	Asn	Asp	Asp	Arg	Lys	Leu	Leu	Val	Ser	Tyr	Leu	Pro	Thr	Thr	Val	370	375	380
Ser	Ala	Lys	Thr	Asp	Ile	Ser	Ile	Cys	Ser	Gly	Leu	Lys	Lys	Gly	Phe	385	390	395
Glu	Val	Val	Glu	Lys	Leu	Asn	Gly	Lys	Ala	Tyr	Gly	Ser	Val	Met	Ile	405	410	415
Leu	Val	Thr	Ser	Gly	Asp	Asp	Lys	Leu	Leu	Gly	Asn	Cys	Leu	Pro	Thr	420	425	430

ITI-08-PCT_Sequence_Listing_ST25.txt

Val Leu Ser Ser Gly Ser Thr Ile His Ser Ile Ala Leu Gly Ser Ser
 435 440 445
 Ala Ala Pro Asn Leu Glu Glu Leu Ser Arg Leu Thr Gly Gly Leu Lys
 450 455 460
 Phe Phe Val Pro Asp Ile Ser Asn Ser Asn Ser Met Ile Asp Ala Phe
 465 470 475 480
 Ser Arg Ile Ser Ser Gly Thr Gly Asp Ile Phe Gln Gln His Ile Gln
 485 490 495
 Leu Glu Ser Thr Gly Glu Asn Val Lys Pro His His Gln Leu Lys Asn
 500 505 510
 Thr Val Thr Val Asp Asn Thr Val Gly Asn Asp Thr Met Phe Leu Val
 515 520 525
 Thr Trp Gln Ala Ser Gly Pro Pro Glu Ile Ile Leu Phe Asp Pro Asp
 530 535 540
 Gly Arg Lys Tyr Tyr Thr Asn Asn Phe Ile Thr Asn Leu Thr Phe Arg
 545 550 555 560
 Thr Ala Ser Leu Trp Ile Pro Gly Thr Ala Lys Pro Gly His Trp Thr
 565 570 575
 Tyr Thr Leu Asn Asn Thr His His Ser Leu Gln Ala Leu Lys Val Thr
 580 585 590
 Val Thr Ser Arg Ala Ser Asn Ser Ala Val Pro Pro Ala Thr Val Glu
 595 600 605
 Ala Phe Val Glu Arg Asp Ser Leu His Phe Pro His Pro Val Met Ile
 610 615 620
 Tyr Ala Asn Val Lys Gln Gly Phe Tyr Pro Ile Leu Asn Ala Thr Val
 625 630 635 640
 Thr Ala Thr Val Glu Pro Glu Thr Gly Asp Pro Val Thr Leu Arg Leu
 645 650 655
 Leu Asp Asp Gly Ala Gly Ala Asp Val Ile Lys Asn Asp Gly Ile Tyr
 660 665 670
 Ser Arg Tyr Phe Phe Ser Phe Ala Ala Asn Gly Arg Tyr Ser Leu Lys
 675 680 685
 Val His Val Asn His Ser Pro Ser Ile Ser Thr Pro Ala His Ser Ile
 690 695 700
 Pro Gly Ser His Ala Met Tyr Val Pro Gly Tyr Thr Ala Asn Gly Asn

ITI-08-PCT_Sequence_Listing_ST25.txt

```

705              710              715              720
Ile Gln Met Asn Ala Pro Arg Lys Ser Val Gly Arg Asn Glu Glu Glu
              725              730              735
Arg Lys Trp Gly Phe Ser Arg Val Ser Ser Gly Gly Ser Phe Ser Val
              740              745              750
Leu Gly Val Pro Ala Gly Pro His Pro Asp Val Phe Pro Pro Cys Lys
              755              760              765
Ile Ile Asp Leu Glu Ala Val Lys Val Glu Glu Glu Leu Thr Leu Ser
              770              775              780
Trp Thr Ala Pro Gly Glu Asp Phe Asp Gln Gly Gln Ala Thr Ser Tyr
785              790              795              800
Glu Ile Arg Met Ser Lys Ser Leu Gln Asn Ile Gln Asp Asp Phe Asn
              805              810              815
Asn Ala Ile Leu Val Asn Thr Ser Lys Arg Asn Pro Gln Gln Ala Gly
              820              825              830
Ile Arg Glu Ile Phe Thr Phe Ser Pro Gln Ile Ser Thr Asn Gly Pro
              835              840              845
Glu His Gln Pro Asn Gly Glu Thr His Glu Ser His Arg Ile Tyr Val
              850              855              860
Ala Ile Arg Ala Met Asp Arg Asn Ser Leu Gln Ser Ala Val Ser Asn
865              870              875              880
Ile Ala Gln Ala Pro Leu Phe Ile Pro Pro Asn Ser Asp Pro Val Pro
              885              890              895
Ala Arg Asp Tyr Leu Ile Leu Lys Gly Val Leu Thr Ala Met Gly Leu
              900              905              910
Ile Gly Ile Ile Cys Leu Ile Ile Val Val Thr His His Thr Leu Ser
              915              920              925
Arg Lys Lys Arg Ala Asp Lys Lys Glu Asn Gly Thr Lys Leu Leu
              930              935              940

```

<210> 296

<211> 235

<212> PRT

<213> Artificial Sequence

<220>

<223> CML28__Homo_sapiens__Q9NQ4

ITI-08-PCT_Sequence_Listing_ST25.txt

<400> 296

```

Met Glu Glu Glu Thr His Thr Asp Ala Lys Ile Arg Ala Glu Asn Gly
1      5      10      15

Thr Gly Ser Ser Pro Arg Gly Pro Gly Cys Ser Leu Arg His Phe Ala
      20      25      30

Cys Glu Gln Asn Leu Leu Ser Arg Pro Asp Gly Ser Ala Ser Phe Leu
      35      40      45

Gln Gly Asp Thr Ser Val Leu Ala Gly Val Tyr Gly Pro Ala Glu Val
      50      55      60

Lys Val Ser Lys Glu Ile Phe Asn Lys Ala Thr Leu Glu Val Ile Leu
65      70      75      80

Arg Pro Lys Ile Gly Leu Pro Gly Val Ala Glu Lys Ser Arg Glu Arg
      85      90      95

Leu Ile Arg Asn Thr Cys Glu Ala Val Val Leu Gly Thr Leu His Pro
      100      105      110

Arg Thr Ser Ile Thr Val Val Leu Gln Val Val Ser Asp Ala Gly Ser
      115      120      125

Leu Leu Ala Cys Cys Leu Asn Ala Ala Cys Met Ala Leu Val Asp Ala
      130      135      140

Gly Val Pro Met Arg Ala Leu Phe Cys Gly Val Ala Cys Ala Leu Asp
145      150      155      160

Ser Asp Gly Thr Leu Val Leu Asp Pro Thr Ser Lys Gln Glu Lys Glu
      165      170      175

Ala Arg Ala Val Leu Thr Phe Ala Leu Asp Ser Val Glu Arg Lys Leu
      180      185      190

Leu Met Ser Ser Thr Lys Gly Leu Tyr Ser Asp Thr Glu Leu Gln Gln
      195      200      205

Cys Leu Ala Ala Ala Gln Ala Ala Ser Gln His Val Phe Arg Phe Tyr
      210      215      220

Arg Glu Ser Leu Gln Arg Arg Tyr Ser Lys Ser
225      230      235

```

<210> 297

<211> 583

<212> PRT

<213> Artificial Sequence

ITI-08-PCT_Sequence_Listing_ST25.txt

<220>

<223> CML66__Homo_sapiens__Q96RS6

<400> 297

Met Glu Val Ala Ala Asn Cys Ser Leu Arg Val Lys Arg Pro Leu Leu
1 5 10 15

Asp Pro Arg Phe Glu Gly Tyr Lys Leu Ser Leu Glu Pro Leu Pro Cys
20 25 30

Tyr Gln Leu Glu Leu Asp Ala Ala Val Ala Glu Val Lys Leu Arg Asp
35 40 45

Asp Gln Tyr Thr Leu Glu His Met His Ala Phe Gly Met Tyr Asn Tyr
50 55 60

Leu His Cys Asp Ser Trp Tyr Gln Asp Ser Val Tyr Tyr Ile Asp Thr
65 70 75 80

Leu Gly Arg Ile Met Asn Leu Thr Val Met Leu Asp Thr Ala Leu Gly
85 90 95

Lys Pro Arg Glu Val Phe Arg Leu Pro Thr Asp Leu Thr Ala Cys Asp
100 105 110

Asn Arg Leu Cys Ala Ser Ile His Phe Ser Ser Ser Thr Trp Val Thr
115 120 125

Leu Ser Asp Gly Thr Gly Arg Leu Tyr Val Ile Gly Thr Gly Glu Arg
130 135 140

Gly Asn Ser Ala Ser Glu Lys Trp Glu Ile Met Phe Asn Glu Glu Leu
145 150 155 160

Gly Asp Pro Phe Ile Ile Ile His Ser Ile Ser Leu Leu Asn Ala Glu
165 170 175

Glu His Ser Ile Ala Thr Leu Leu Leu Arg Ile Glu Lys Glu Glu Leu
180 185 190

Asp Met Lys Gly Ser Gly Phe Tyr Val Ser Leu Glu Trp Val Thr Ile
195 200 205

Ser Lys Lys Asn Gln Asp Asn Lys Lys Tyr Glu Ile Ile Lys Arg Asp
210 215 220

Ile Leu Arg Gly Lys Ser Val Pro His Tyr Ala Ala Ile Glu Pro Asp
225 230 235 240

Gly Asn Gly Leu Met Ile Val Ser Tyr Lys Ser Leu Thr Phe Val Gln
245 250 255

ITI-08-PCT_Sequence_Listing_ST25.txt

Ala	Gly	Gln	Asp	Leu	Glu	Glu	Asn	Met	Asp	Glu	Asp	Ile	Ser	Glu	Lys	260	265	270
Ile	Lys	Glu	Pro	Leu	Tyr	Tyr	Trp	Gln	Gln	Thr	Glu	Asp	Asp	Leu	Thr	275	280	285
Val	Thr	Ile	Arg	Leu	Pro	Glu	Asp	Ser	Thr	Lys	Glu	Asp	Ile	Gln	Ile	290	295	300
Gln	Phe	Leu	Pro	Asp	His	Ile	Asn	Ile	Val	Leu	Lys	Asp	His	Gln	Phe	305	310	315
Leu	Glu	Gly	Lys	Leu	Tyr	Ser	Ser	Ile	Asp	His	Glu	Ser	Ser	Thr	Trp	325	330	335
Ile	Ile	Lys	Glu	Ser	Asn	Ser	Leu	Glu	Ile	Ser	Leu	Ile	Lys	Lys	Asn	340	345	350
Glu	Gly	Leu	Thr	Trp	Pro	Glu	Leu	Val	Ile	Gly	Asp	Lys	Gln	Gly	Glu	355	360	365
Leu	Ile	Arg	Asp	Ser	Ala	Gln	Cys	Ala	Ala	Ile	Ala	Glu	Arg	Leu	Met	370	375	380
His	Leu	Thr	Ser	Glu	Glu	Leu	Asn	Pro	Asn	Pro	Asp	Lys	Glu	Lys	Pro	385	390	395
Pro	Cys	Asn	Ala	Gln	Glu	Leu	Glu	Glu	Cys	Asp	Ile	Phe	Phe	Glu	Glu	405	410	415
Ser	Ser	Ser	Leu	Cys	Arg	Phe	Asp	Gly	Asn	Thr	Leu	Lys	Thr	Thr	His	420	425	430
Val	Val	Asn	Leu	Gly	Ser	Asn	Gln	Tyr	Leu	Phe	Ser	Val	Ile	Val	Asp	435	440	445
Pro	Lys	Glu	Met	Pro	Cys	Phe	Cys	Leu	Arg	His	Asp	Val	Asp	Ala	Leu	450	455	460
Leu	Trp	Gln	Pro	His	Ser	Ser	Lys	Gln	Asp	Asp	Met	Trp	Glu	His	Ile	465	470	475
Ala	Thr	Phe	Asn	Ala	Leu	Gly	Tyr	Val	Gln	Ala	Ser	Lys	Arg	Asp	Lys	485	490	495
Lys	Phe	Phe	Ala	Cys	Ala	Pro	Asn	Tyr	Ser	Tyr	Ala	Ala	Leu	Cys	Glu	500	505	510
Cys	Leu	Arg	Arg	Val	Phe	Ile	Tyr	Arg	Gln	Pro	Ala	Pro	Met	Ser	Thr	515	520	525

ITI-08-PCT_Sequence_Listing_ST25.txt

Val Leu Tyr Asn Arg Lys Glu Gly Arg Gln Val Gly Gln Val Ala Lys
530 535 540

Gln Gln Val Ala Ser Leu Glu Thr Asn Asp Pro Ile Leu Gly Phe Gln
545 550 555 560

Ala Thr Asn Glu Arg Leu Phe Val Leu Thr Thr Lys Asn Leu Phe Leu
565 570 575

Ile Lys Val Asn Thr Glu Asn
580

<210> 298

<211> 520

<212> PRT

<213> Artificial Sequence

<220>

<223> COA-1/m__Homo_sapiens__Q5T124

<400> 298

Met Ser Ser Pro Leu Ala Ser Leu Ser Lys Thr Arg Lys Val Pro Leu
1 5 10 15

Pro Ser Glu Pro Met Asn Pro Gly Arg Arg Gly Ile Arg Ile Tyr Gly
20 25 30

Asp Glu Asp Glu Val Asp Met Leu Ser Asp Gly Cys Gly Ser Glu Glu
35 40 45

Lys Ile Ser Val Pro Ser Cys Tyr Gly Gly Ile Gly Ala Pro Val Ser
50 55 60

Arg Gln Val Pro Ala Ser His Asp Ser Glu Leu Met Ala Phe Met Thr
65 70 75 80

Arg Lys Leu Trp Asp Leu Glu Gln Gln Val Lys Ala Gln Thr Asp Glu
85 90 95

Ile Leu Ser Lys Asp Gln Lys Ile Ala Ala Leu Glu Asp Leu Val Gln
100 105 110

Thr Leu Arg Pro His Pro Ala Glu Ala Thr Leu Gln Arg Gln Glu Glu
115 120 125

Leu Glu Thr Met Cys Val Gln Leu Gln Arg Gln Val Arg Glu Met Glu
130 135 140

Arg Phe Leu Ser Asp Tyr Gly Leu Gln Trp Val Gly Glu Pro Met Asp
145 150 155 160

ITI-08-PCT_Sequence_Listing_ST25.txt

Gln Glu Asp Ser Glu Ser Lys Thr Val Ser Glu His Gly Glu Arg Asp
165 170 175

Trp Met Thr Ala Lys Lys Phe Trp Lys Pro Gly Asp Ser Leu Ala Pro
180 185 190

Pro Glu Val Asp Phe Asp Arg Leu Leu Ala Ser Leu Gln Asp Leu Ser
195 200 205

Glu Leu Val Val Glu Gly Asp Thr Gln Val Thr Pro Val Pro Gly Gly
210 215 220

Ala Arg Leu Arg Thr Leu Glu Pro Ile Pro Leu Lys Leu Tyr Arg Asn
225 230 235 240

Gly Ile Met Met Phe Asp Gly Pro Phe Gln Pro Phe Tyr Asp Pro Ser
245 250 255

Thr Gln Arg Cys Leu Arg Asp Ile Leu Asp Gly Phe Phe Pro Ser Glu
260 265 270

Leu Gln Arg Leu Tyr Pro Asn Gly Val Pro Phe Lys Val Ser Asp Leu
275 280 285

Arg Asn Gln Val Tyr Leu Glu Asp Gly Leu Asp Pro Phe Pro Gly Glu
290 295 300

Gly Arg Val Val Gly Arg Gln Leu Met His Lys Ala Leu Asp Arg Val
305 310 315 320

Glu Glu His Pro Gly Ser Arg Met Thr Ala Glu Lys Phe Leu Asn Arg
325 330 335

Leu Pro Lys Phe Val Ile Arg Gln Gly Glu Val Ile Asp Ile Arg Gly
340 345 350

Pro Ile Arg Asp Thr Leu Gln Asn Cys Cys Pro Leu Pro Ala Arg Ile
355 360 365

Gln Glu Ile Val Val Glu Thr Pro Thr Leu Ala Ala Glu Arg Glu Arg
370 375 380

Ser Gln Glu Ser Pro Asn Thr Pro Ala Pro Pro Leu Ser Met Leu Arg
385 390 395 400

Ile Lys Ser Glu Asn Gly Glu Gln Ala Phe Leu Leu Met Met Gln Pro
405 410 415

Asp Asn Thr Ile Gly Asp Val Arg Ala Leu Leu Ala Gln Ala Arg Val
420 425 430

Met Asp Ala Ser Ala Phe Glu Ile Phe Ser Thr Phe Pro Pro Thr Leu

ITI-08-PCT_Sequence_Listing_ST25.txt

```

435                               440                               445
Tyr Gln Asp Asp Thr Leu Thr Leu Gln Ala Ala Gly Leu Val Pro Lys
450                               455                               460
Ala Ala Leu Leu Leu Arg Ala Arg Arg Ala Pro Lys Ser Ser Leu Lys
465                               470                               475                               480
Phe Ser Pro Gly Pro Cys Pro Gly Pro Gly Pro Gly Pro Ser Pro Gly
485                               490                               495
Pro Gly Pro Gly Pro Ser Pro Gly Pro Gly Pro Gly Pro Ser Pro Cys
500                               505                               510
Pro Gly Pro Ser Pro Ser Pro Gln
515                               520
<210> 299
<211> 142
<212> PRT
<213> Artificial Sequence
<220>
<223> coactosin-like_protein__Homo_sapiens__Q14019
<400> 299
Met Ala Thr Lys Ile Asp Lys Glu Ala Cys Arg Ala Ala Tyr Asn Leu
1                               5                               10                               15
Val Arg Asp Asp Gly Ser Ala Val Ile Trp Val Thr Phe Lys Tyr Asp
20                               25                               30
Gly Ser Thr Ile Val Pro Gly Glu Gln Gly Ala Glu Tyr Gln His Phe
35                               40                               45
Ile Gln Gln Cys Thr Asp Asp Val Arg Leu Phe Ala Phe Val Arg Phe
50                               55                               60
Thr Thr Gly Asp Ala Met Ser Lys Arg Ser Lys Phe Ala Leu Ile Thr
65                               70                               75                               80
Trp Ile Gly Glu Asn Val Ser Gly Leu Gln Arg Ala Lys Thr Gly Thr
85                               90                               95
Asp Lys Thr Leu Val Lys Glu Val Val Gln Asn Phe Ala Lys Glu Phe
100                              105                              110
Val Ile Ser Asp Arg Lys Glu Leu Glu Glu Asp Phe Ile Lys Ser Glu
115                              120                              125
Leu Lys Lys Ala Gly Gly Ala Asn Tyr Asp Ala Gln Thr Glu

```

ITI-08-PCT_Sequence_Listing_ST25.txt

130

135

140

<210> 300

<211> 164

<212> PRT

<213> Artificial Sequence

<220>

<223> collagen_XXIII__Homo_sapiens__L8EAS4

<400> 300

Met Ala Thr Arg Asp Pro Trp Val Trp Met Ala Ser Pro Asp Phe Gln
1 5 10 15

Ala Arg Lys Gly Lys Arg Val His Gln Glu Thr Leu Ala Pro Gly Glu
20 25 30

Thr Lys Asp Lys Met Glu Leu Leu Gly Leu Arg Gly Pro Leu Asp Leu
35 40 45

Leu Gly Pro Gly Ala Leu Leu Ala Thr Leu Gly Lys Met Ala Pro Gly
50 55 60

Glu His Lys Ala Gln Arg Ala Pro Lys Glu Ser Pro Asp Lys Thr Ala
65 70 75 80

Arg Trp Ala Gln Arg Asp Pro Gln Gly Pro Arg Val Ser Leu Glu Tyr
85 90 95

Leu Glu Arg Arg Ala Thr Met Gly His Gln Ala Ser Leu Asp His Gln
100 105 110

Gly Pro Arg Ala Ser Gln Gly Ala Trp Gly Leu Gly Glu Arg Thr Val
115 120 125

Trp Thr Val Pro Gln Asp Arg Arg Gly Ser Leu Ala Thr Glu Ala Arg
130 135 140

Met Glu Leu Gln Gly Pro Gly Val Pro Gln Ala Ser Arg Ala Ser Arg
145 150 155 160

Glu Thr Gln Trp

<210> 301

<211> 540

<212> PRT

<213> Artificial Sequence

<220>

<223> collagen_XXIII__Homo_sapiens__Q86Y22

ITI-08-PCT_Sequence_Listing_ST25.txt

<400> 301

```

Met Gly Pro Gly Glu Arg Ala Gly Gly Gly Gly Asp Ala Gly Lys Gly
1      5      10
Asn Ala Ala Gly Gly Gly Gly Gly Arg Ser Ala Thr Thr Ala Gly
20      25      30
Ser Arg Ala Val Ser Ala Leu Cys Leu Leu Leu Ser Val Gly Ser Ala
35      40      45
Ala Ala Cys Leu Leu Leu Gly Val Gln Ala Ala Ala Leu Gln Gly Arg
50      55      60
Val Ala Ala Leu Glu Glu Glu Arg Glu Leu Leu Arg Arg Ala Gly Pro
65      70      75      80
Pro Gly Ala Leu Asp Ala Trp Ala Glu Pro His Leu Glu Arg Leu Leu
85      90      95
Arg Glu Lys Leu Asp Gly Leu Ala Lys Ile Arg Thr Ala Arg Glu Ala
100     105     110
Pro Ser Glu Cys Val Cys Pro Pro Gly Pro Pro Gly Arg Arg Gly Lys
115     120     125
Pro Gly Arg Arg Gly Asp Pro Gly Pro Pro Gly Gln Ser Gly Arg Asp
130     135     140
Gly Tyr Pro Gly Pro Leu Gly Leu Asp Gly Lys Pro Gly Leu Pro Gly
145     150     155     160
Pro Lys Gly Glu Lys Gly Ala Pro Gly Asp Phe Gly Pro Arg Gly Asp
165     170     175
Gln Gly Gln Asp Gly Ala Ala Gly Pro Pro Gly Pro Pro Gly Pro Pro
180     185     190
Gly Ala Arg Gly Pro Pro Gly Asp Thr Gly Lys Asp Gly Pro Arg Gly
195     200     205
Ala Gln Gly Pro Ala Gly Pro Lys Gly Glu Pro Gly Gln Asp Gly Glu
210     215     220
Met Gly Pro Lys Gly Pro Pro Gly Pro Lys Gly Glu Pro Gly Val Pro
225     230     235     240
Gly Lys Lys Gly Asp Asp Gly Thr Pro Ser Gln Pro Gly Pro Pro Gly
245     250     255
Pro Lys Gly Glu Pro Gly Ser Met Gly Pro Arg Gly Glu Asn Gly Val
260     265     270

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Asp Gly Ala Pro Gly Pro Lys Gly Glu Pro Gly His Arg Gly Thr Asp
 275 280 285
 Gly Ala Ala Gly Pro Arg Gly Ala Pro Gly Leu Lys Gly Glu Gln Gly
 290 295 300
 Asp Thr Val Val Ile Asp Tyr Asp Gly Arg Ile Leu Asp Ala Leu Lys
 305 310 315 320
 Gly Pro Pro Gly Pro Gln Gly Pro Pro Gly Pro Pro Gly Ile Pro Gly
 325 330 335
 Ala Lys Gly Glu Leu Gly Leu Pro Gly Ala Pro Gly Ile Asp Gly Glu
 340 345 350
 Lys Gly Pro Lys Gly Gln Lys Gly Asp Pro Gly Glu Pro Gly Pro Ala
 355 360 365
 Gly Leu Lys Gly Glu Ala Gly Glu Met Gly Leu Ser Gly Leu Pro Gly
 370 375 380
 Ala Asp Gly Leu Lys Gly Glu Lys Gly Glu Ser Ala Ser Asp Ser Leu
 385 390 395 400
 Gln Glu Ser Leu Ala Gln Leu Ile Val Glu Pro Gly Pro Pro Gly Pro
 405 410 415
 Pro Gly Pro Pro Gly Pro Met Gly Leu Gln Gly Ile Gln Gly Pro Lys
 420 425 430
 Gly Leu Asp Gly Ala Lys Gly Glu Lys Gly Ala Ser Gly Glu Arg Gly
 435 440 445
 Pro Ser Gly Leu Pro Gly Pro Val Gly Pro Pro Gly Leu Ile Gly Leu
 450 455 460
 Pro Gly Thr Lys Gly Glu Lys Gly Arg Pro Gly Glu Pro Gly Leu Asp
 465 470 475 480
 Gly Phe Pro Gly Pro Arg Gly Glu Lys Gly Asp Arg Ser Glu Arg Gly
 485 490 495
 Glu Lys Gly Glu Arg Gly Val Pro Gly Arg Lys Gly Val Lys Gly Gln
 500 505 510
 Lys Gly Glu Pro Gly Pro Pro Gly Leu Asp Gln Pro Cys Pro Val Gly
 515 520 525
 Pro Asp Gly Leu Pro Val Pro Gly Cys Trp His Lys
 530 535 540

ITI-08-PCT_Sequence_Listing_ST25.txt

```

<210> 302
<211> 163
<212> PRT
<213> Artificial Sequence

<220>
<223> COX-2__Homo_sapiens__Q6ZYK7

<400> 302

Met Leu Ala Arg Ala Leu Leu Leu Cys Ala Val Leu Ala Leu Ser His
1          5          10          15

Thr Ala Asn Pro Cys Cys Ser His Pro Cys Gln Asn Arg Gly Val Cys
          20          25          30

Met Ser Val Gly Phe Asp Gln Tyr Lys Cys Asp Cys Thr Arg Thr Gly
          35          40          45

Phe Tyr Gly Glu Asn Cys Ser Thr Pro Glu Phe Leu Thr Arg Ile Lys
          50          55          60

Leu Phe Leu Lys Pro Thr Pro Asn Thr Val His Tyr Ile Leu Thr His
65          70          75          80

Phe Lys Gly Phe Trp Asn Val Val Asn Asn Ile Pro Phe Leu Arg Asn
          85          90          95

Ala Ile Met Ser Tyr Val Leu Thr Ser Arg Ser His Leu Ile Asp Ser
          100          105          110

Pro Pro Thr Tyr Asn Ala Asp Tyr Gly Tyr Lys Ser Trp Glu Ala Phe
          115          120          125

Ser Asn Leu Ser Tyr Tyr Thr Arg Ala Leu Pro Pro Val Pro Asp Asp
          130          135          140

Cys Pro Thr Pro Leu Gly Val Lys Ala Leu His Ala Ser Val Phe Gln
145          150          155          160

Asp Arg Ser

```

```

<210> 303
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> CP1B1__Homo_sapiens__Q16678

<400> 303

```

ITI-08-PCT_Sequence_Listing_ST25.txt

```

Met Gly Thr Ser Leu Ser Pro Asn Asp Pro Trp Pro Leu Asn Pro Leu
1      5      10      15

Ser Ile Gln Gln Thr Thr Leu Leu Leu Leu Ser Val Leu Ala Thr
      20      25      30

Val His Val Gly Gln Arg Leu Leu Arg Gln Arg Arg Arg Gln Leu Arg
      35      40      45

Ser Ala Pro Pro Gly Pro Phe Ala Trp Pro Leu Ile Gly Asn Ala Ala
      50      55      60

Ala Val Gly Gln Ala Ala His Leu Ser Phe Ala Arg Leu Ala Arg Arg
65      70      75      80

Tyr Gly Asp Val Phe Gln Ile Arg Leu Gly Ser Cys Pro Ile Val Val
      85      90      95

Leu Asn Gly Glu Arg Ala Ile His Gln Ala Leu Val Gln Gln Gly Ser
      100      105      110

Ala Phe Ala Asp Arg Pro Ala Phe Ala Ser Phe Arg Val Val Ser Gly
      115      120      125

Gly Arg Ser Met Ala Phe Gly His Tyr Ser Glu His Trp Lys Val Gln
      130      135      140

Arg Arg Ala Ala His Ser Met Met Arg Asn Phe Phe Thr Arg Gln Pro
145      150      155      160

Arg Ser Arg Gln Val Leu Glu Gly His Val Leu Ser Glu Ala Arg Glu
      165      170      175

Leu Val Ala Leu Leu Val Arg Gly Ser Ala Asp Gly Ala Phe Leu Asp
      180      185      190

Pro Arg Pro Leu Thr Val Val Ala Val Ala Asn Val Met Ser Ala Val
      195      200      205

Cys Phe Gly Cys Arg Tyr Ser His Asp Asp Pro Glu Phe Arg Glu Leu
      210      215      220

Leu Ser His Asn Glu Glu Phe Gly Arg Thr Val Gly Ala Gly Ser Leu
225      230      235      240

Val Asp Val Met Pro Trp Leu Gln Tyr Phe Pro Asn Pro Val Arg Thr
      245      250      255

Val Phe Arg Glu Phe Glu Gln Leu Asn Arg Asn Phe Ser Asn Phe Ile
      260      265      270

Leu Asp Lys Phe Leu Arg His Cys Glu Ser Leu Arg Pro Gly Ala Ala

```

ITI-08-PCT_Sequence_Listing_ST25.txt

```

275                280                285
Pro Arg Asp Met Met Asp Ala Phe Ile Leu Ser Ala Glu Lys Lys Ala
 290                295                300
Ala Gly Asp Ser His Gly Gly Gly Ala Arg Leu Asp Leu Glu Asn Val
305                310                315                320
Pro Ala Thr Ile Thr Asp Ile Phe Gly Ala Ser Gln Asp Thr Leu Ser
                325                330                335
Thr Ala Leu Gln Trp Leu Leu Leu Leu Phe Thr Arg Tyr Pro Asp Val
                340                345                350
Gln Thr Arg Val Gln Ala Glu Leu Asp Gln Val Val Gly Arg Asp Arg
                355                360                365
Leu Pro Cys Met Gly Asp Gln Pro Asn Leu Pro Tyr Val Leu Ala Phe
 370                375                380
Leu Tyr Glu Ala Met Arg Phe Ser Ser Phe Val Pro Val Thr Ile Pro
385                390                395                400
His Ala Thr Thr Ala Asn Thr Ser Val Leu Gly Tyr His Ile Pro Lys
                405                410                415
Asp Thr Val Val Phe Val Asn Gln Trp Ser Val Asn His Asp Pro Leu
                420                425                430
Lys Trp Pro Asn Pro Glu Asn Phe Asp Pro Ala Arg Phe Leu Asp Lys
                435                440                445
Asp Gly Leu Ile Asn Lys Asp Leu Thr Ser Arg Val Met Ile Phe Ser
 450                455                460
Val Gly Lys Arg Arg Cys Ile Gly Glu Glu Leu Ser Lys Met Gln Leu
465                470                475                480
Phe Leu Phe Ile Ser Ile Leu Ala His Gln Cys Asp Phe Arg Ala Asn
                485                490                495
Pro Asn Glu Pro Ala Lys Met Asn Phe Ser Tyr Gly Leu Thr Ile Lys
                500                505                510
Pro Lys Ser Phe Lys Val Asn Val Thr Leu Arg Glu Ser Met Glu Leu
                515                520                525
Leu Asp Ser Ala Val Gln Asn Leu Gln Ala Lys Glu Thr Cys Gln
 530                535                540

```

<210> 304

<211> 110

ITI-08-PCT_Sequence_Listing_ST25.txt

<212> PRT

<213> Artificial Sequence

<220>

<223> CSAG2__Homo_sapiens__Q9Y5P2-2

<400> 304

Met Trp Met Gly Leu Ile Gln Leu Val Glu Gly Val Lys Arg Lys Asp
1 5 10 15

Gln Gly Phe Leu Glu Lys Glu Phe Tyr His Lys Thr Asn Ile Lys Met
20 25 30

Arg Cys Glu Phe Leu Ala Cys Trp Pro Ala Phe Thr Val Leu Gly Glu
35 40 45

Ala Trp Arg Asp Gln Val Asp Trp Ser Arg Leu Leu Arg Asp Ala Gly
50 55 60

Leu Val Lys Met Ser Arg Lys Pro Arg Ala Ser Ser Pro Leu Ser Asn
65 70 75 80

Asn His Pro Pro Thr Pro Lys Arg Phe Pro Arg Gln Pro Gly Arg Glu
85 90 95

Lys Gly Pro Ile Lys Glu Val Pro Gly Thr Lys Gly Ser Pro
100 105 110

<210> 305

<211> 127

<212> PRT

<213> Artificial Sequence

<220>

<223> CSAG2__Homo_sapiens__Q9Y5P2

<400> 305

Met Trp Met Gly Leu Ile Gln Leu Val Glu Gly Val Lys Arg Lys Asp
1 5 10 15

Gln Gly Phe Leu Glu Lys Glu Phe Tyr His Lys Thr Asn Ile Lys Met
20 25 30

Arg Cys Glu Phe Leu Ala Cys Trp Pro Ala Phe Thr Val Leu Gly Glu
35 40 45

Ala Trp Arg Asp Gln Val Asp Trp Ser Arg Leu Leu Arg Asp Ala Gly
50 55 60

Leu Val Lys Met Ser Arg Lys Pro Arg Ala Ser Ser Pro Leu Ser Asn

ITI-08-PCT_Sequence_Listing_ST25.txt

```

65              70              75              80
Asn His Pro Pro Thr Pro Lys Arg Arg Gly Ser Gly Arg His Pro Leu
      85              90              95

Asn Pro Gly Pro Glu Ala Leu Ser Lys Phe Pro Arg Gln Pro Gly Arg
      100             105             110

Glu Lys Gly Pro Ile Lys Glu Val Pro Gly Thr Lys Gly Ser Pro
      115             120             125

<210> 306
<211> 189
<212> PRT
<213> Artificial Sequence

<220>
<223> CT45A1__Homo_sapiens__Q5HYN5

<400> 306

Met Thr Asp Lys Thr Glu Lys Val Ala Val Asp Pro Glu Thr Val Phe
1              5              10              15

Lys Arg Pro Arg Glu Cys Asp Ser Pro Ser Tyr Gln Lys Arg Gln Arg
      20              25              30

Met Ala Leu Leu Ala Arg Lys Gln Gly Ala Gly Asp Ser Leu Ile Ala
      35              40              45

Gly Ser Ala Met Ser Lys Ala Lys Lys Leu Met Thr Gly His Ala Ile
      50              55              60

Pro Pro Ser Gln Leu Asp Ser Gln Ile Asp Asp Phe Thr Gly Phe Ser
65              70              75              80

Lys Asp Arg Met Met Gln Lys Pro Gly Ser Asn Ala Pro Val Gly Gly
      85              90              95

Asn Val Thr Ser Ser Phe Ser Gly Asp Asp Leu Glu Cys Arg Glu Thr
      100             105             110

Ala Ser Ser Pro Lys Ser Gln Arg Glu Ile Asn Ala Asp Ile Lys Arg
      115             120             125

Lys Leu Val Lys Glu Leu Arg Cys Val Gly Gln Lys Tyr Glu Lys Ile
      130             135             140

Phe Glu Met Leu Glu Gly Val Gln Gly Pro Thr Ala Val Arg Lys Arg
145             150             155             160

Phe Phe Glu Ser Ile Ile Lys Glu Ala Ala Arg Cys Met Arg Arg Asp

```

ITI-08-PCT_Sequence_Listing_ST25.txt

165 170 175

Phe Val Lys His Leu Lys Lys Lys Leu Lys Arg Met Ile
180 185

<210> 307
<211> 264
<212> PRT
<213> Artificial Sequence

<220>
<223> CT55__Homo_sapiens__Q8WUE5

<400> 307

Met Leu Arg Leu Leu Arg Leu Ala Leu Ala Phe Tyr Gly Arg Thr Ala
1 5 10 15

Asp Pro Ala Glu Arg Gln Gly Pro Gln Gln Gln Gly Leu Pro Gln Gly
20 25 30

Asp Thr Gln Leu Thr Thr Val Gln Gly Val Val Thr Ser Phe Cys Gly
35 40 45

Asp Tyr Gly Met Ile Asp Glu Ser Ile Tyr Phe Ser Ser Asp Val Val
50 55 60

Thr Gly Asn Val Pro Leu Lys Val Gly Gln Lys Val Asn Val Val Val
65 70 75 80

Glu Glu Asp Lys Pro His Tyr Gly Leu Arg Ala Ile Lys Val Asp Val
85 90 95

Val Pro Arg His Leu Tyr Gly Ala Gly Pro Ser Asp Ser Gly Thr Arg
100 105 110

Val Leu Ile Gly Cys Val Thr Ser Ile Asn Glu Asp Asn Ile Tyr Ile
115 120 125

Ser Asn Ser Ile Tyr Phe Ser Ile Ala Ile Val Ser Glu Asp Phe Val
130 135 140

Pro Tyr Lys Gly Asp Leu Leu Glu Val Glu Tyr Ser Thr Glu Pro Gly
145 150 155 160

Ile Ser Asn Ile Lys Ala Thr Ser Val Lys Pro Ile Arg Cys Ile His
165 170 175

Thr Glu Glu Val Cys Ile Thr Ser Val His Gly Arg Asn Gly Val Ile
180 185 190

Asp Tyr Thr Ile Phe Phe Thr Leu Asp Ser Val Lys Leu Pro Asp Gly

ITI-08-PCT_Sequence_Listing_ST25.txt

195

200

205

Tyr Val Pro Gln Val Asp Asp Ile Val Asn Val Val Met Val Glu Ser
 210 215 220

Ile Gln Phe Cys Phe Ile Trp Arg Ala Ile Ser Ile Thr Pro Val His
 225 230 235 240

Lys Ser Ser Ser Gly Phe Gln Asp Asp Gly Gly Leu Gly Arg Pro Lys
 245 250 255

Arg Glu Arg Arg Ser Gln Ser Ile
 260

<210> 308

<211> 947

<212> PRT

<213> Artificial Sequence

<220>

<223> CT-_9/BRD6__Homo_sapiens__Q58F21

<400> 308

Met Ser Leu Pro Ser Arg Gln Thr Ala Ile Ile Val Asn Pro Pro Pro
 1 5 10 15

Pro Glu Tyr Ile Asn Thr Lys Lys Asn Gly Arg Leu Thr Asn Gln Leu
 20 25 30

Gln Tyr Leu Gln Lys Val Val Leu Lys Asp Leu Trp Lys His Ser Phe
 35 40 45

Ser Trp Pro Phe Gln Arg Pro Val Asp Ala Val Lys Leu Gln Leu Pro
 50 55 60

Asp Tyr Tyr Thr Ile Ile Lys Asn Pro Met Asp Leu Asn Thr Ile Lys
 65 70 75 80

Lys Arg Leu Glu Asn Lys Tyr Tyr Ala Lys Ala Ser Glu Cys Ile Glu
 85 90 95

Asp Phe Asn Thr Met Phe Ser Asn Cys Tyr Leu Tyr Asn Lys Pro Gly
 100 105 110

Asp Asp Ile Val Leu Met Ala Gln Ala Leu Glu Lys Leu Phe Met Gln
 115 120 125

Lys Leu Ser Gln Met Pro Gln Glu Glu Gln Val Val Gly Val Lys Glu
 130 135 140

Arg Ile Lys Lys Gly Thr Gln Gln Asn Ile Ala Val Ser Ser Ala Lys

ITI-08-PCT_Sequence_Listing_ST25.txt

145		150		155		160													
Glu	Lys	Ser	Ser	Pro	Ser	Ala	Thr	Glu	Lys	Val	Phe	Lys	Gln	Gln	Glu				
				165					170					175					
Ile	Pro	Ser	Val	Phe	Pro	Lys	Thr	Ser	Ile	Ser	Pro	Leu	Asn	Val	Val				
			180					185					190						
Gln	Gly	Ala	Ser	Val	Asn	Ser	Ser	Ser	Gln	Thr	Ala	Ala	Gln	Val	Thr				
		195					200					205							
Lys	Gly	Val	Lys	Arg	Lys	Ala	Asp	Thr	Thr	Thr	Pro	Ala	Thr	Ser	Ala				
	210					215					220								
Val	Lys	Ala	Ser	Ser	Glu	Phe	Ser	Pro	Thr	Phe	Thr	Glu	Lys	Ser	Val				
225					230					235					240				
Ala	Leu	Pro	Pro	Ile	Lys	Glu	Asn	Met	Pro	Lys	Asn	Val	Leu	Pro	Asp				
				245					250					255					
Ser	Gln	Gln	Gln	Tyr	Asn	Val	Val	Lys	Thr	Val	Lys	Val	Thr	Glu	Gln				
			260					265					270						
Leu	Arg	His	Cys	Ser	Glu	Ile	Leu	Lys	Glu	Met	Leu	Ala	Lys	Lys	His				
		275					280					285							
Phe	Ser	Tyr	Ala	Trp	Pro	Phe	Tyr	Asn	Pro	Val	Asp	Val	Asn	Ala	Leu				
	290					295					300								
Gly	Leu	His	Asn	Tyr	Tyr	Asp	Val	Val	Lys	Asn	Pro	Met	Asp	Leu	Gly				
305					310					315				320					
Thr	Ile	Lys	Glu	Lys	Met	Asp	Asn	Gln	Glu	Tyr	Lys	Asp	Ala	Tyr	Lys				
				325					330					335					
Phe	Ala	Ala	Asp	Val	Arg	Leu	Met	Phe	Met	Asn	Cys	Tyr	Lys	Tyr	Asn				
			340					345					350						
Pro	Pro	Asp	His	Glu	Val	Val	Thr	Met	Ala	Arg	Met	Leu	Gln	Asp	Val				
		355					360					365							
Phe	Glu	Thr	His	Phe	Ser	Lys	Ile	Pro	Ile	Glu	Pro	Val	Glu	Ser	Met				
	370					375					380								
Pro	Leu	Cys	Tyr	Ile	Lys	Thr	Asp	Ile	Thr	Glu	Thr	Thr	Gly	Arg	Glu				
385					390					395					400				
Asn	Thr	Asn	Glu	Ala	Ser	Ser	Glu	Gly	Asn	Ser	Ser	Asp	Asp	Ser	Glu				
				405					410					415					
Asp	Glu	Arg	Val	Lys	Arg	Leu	Ala	Lys	Leu	Gln	Glu	Gln	Leu	Lys	Ala				
			420					425					430						

ITI-08-PCT_Sequence_Listing_ST25.txt

Val	His	Gln	Gln	Leu	Gln	Val	Leu	Ser	Gln	Val	Pro	Phe	Arg	Lys	Leu
435						440						445			
Asn	Lys	Lys	Lys	Glu	Lys	Ser	Lys	Lys	Glu	Lys	Lys	Lys	Glu	Lys	Val
450						455						460			
Asn	Asn	Ser	Asn	Glu	Asn	Pro	Arg	Lys	Met	Cys	Glu	Gln	Met	Arg	Leu
465						470						475			
Lys	Glu	Lys	Ser	Lys	Arg	Asn	Gln	Pro	Lys	Lys	Arg	Lys	Gln	Gln	Phe
				485						490				495	
Ile	Gly	Leu	Lys	Ser	Glu	Asp	Glu	Asp	Asn	Ala	Lys	Pro	Met	Asn	Tyr
		500						505				510			
Asp	Glu	Lys	Arg	Gln	Leu	Ser	Leu	Asn	Ile	Asn	Lys	Leu	Pro	Gly	Asp
515						520						525			
Lys	Leu	Gly	Arg	Val	Val	His	Ile	Ile	Gln	Ser	Arg	Glu	Pro	Ser	Leu
530						535						540			
Ser	Asn	Ser	Asn	Pro	Asp	Glu	Ile	Glu	Ile	Asp	Phe	Glu	Thr	Leu	Lys
545						550						555		560	
Ala	Ser	Thr	Leu	Arg	Glu	Leu	Glu	Lys	Tyr	Val	Ser	Ala	Cys	Leu	Arg
				565						570				575	
Lys	Arg	Pro	Leu	Lys	Pro	Pro	Ala	Lys	Lys	Ile	Met	Met	Ser	Lys	Glu
		580						585				590			
Glu	Leu	His	Ser	Gln	Lys	Lys	Gln	Glu	Leu	Glu	Lys	Arg	Leu	Leu	Asp
595						600						605			
Val	Asn	Asn	Gln	Leu	Asn	Ser	Arg	Lys	Arg	Gln	Thr	Lys	Ser	Asp	Lys
610						615						620			
Thr	Gln	Pro	Ser	Lys	Ala	Val	Glu	Asn	Val	Ser	Arg	Leu	Ser	Glu	Ser
625				630						635				640	
Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Glu	Ser	Glu	Ser	Ser	Ser	Ser	Asp
				645						650				655	
Leu	Ser	Ser	Ser	Asp	Ser	Ser	Asp	Ser	Glu	Ser	Glu	Met	Phe	Pro	Lys
		660						665				670			
Phe	Thr	Glu	Val	Lys	Pro	Asn	Asp	Ser	Pro	Ser	Lys	Glu	Asn	Val	Lys
675						680						685			
Lys	Met	Lys	Asn	Glu	Cys	Ile	Pro	Pro	Glu	Gly	Arg	Thr	Gly	Val	Thr
690						695						700			

ITI-08-PCT_Sequence_Listing_ST25.txt

Gln Ile Gly Tyr Cys Val Gln Asp Thr Thr Ser Ala Asn Thr Thr Leu
705 710 715 720

Val His Gln Thr Thr Pro Ser His Val Met Pro Pro Asn His His Gln
725 730 735

Leu Ala Phe Asn Tyr Gln Glu Leu Glu His Leu Gln Thr Val Lys Asn
740 745 750

Ile Ser Pro Leu Gln Ile Leu Pro Pro Ser Gly Asp Ser Glu Gln Leu
755 760 765

Ser Asn Gly Ile Thr Val Met His Pro Ser Gly Asp Ser Asp Thr Thr
770 775 780

Met Leu Glu Ser Glu Cys Gln Ala Pro Val Gln Lys Asp Ile Lys Ile
785 790 795 800

Lys Asn Ala Asp Ser Trp Lys Ser Leu Gly Lys Pro Val Lys Pro Ser
805 810 815

Gly Val Met Lys Ser Ser Asp Glu Leu Phe Asn Gln Phe Arg Lys Ala
820 825 830

Ala Ile Glu Lys Glu Val Lys Ala Arg Thr Gln Glu Leu Ile Arg Lys
835 840 845

His Leu Glu Gln Asn Thr Lys Glu Leu Lys Ala Ser Gln Glu Asn Gln
850 855 860

Arg Asp Leu Gly Asn Gly Leu Thr Val Glu Ser Phe Ser Asn Lys Ile
865 870 875 880

Gln Asn Lys Cys Ser Gly Glu Glu Gln Lys Glu His Gln Gln Ser Ser
885 890 895

Glu Ala Gln Asp Lys Ser Lys Leu Trp Leu Leu Lys Asp Arg Asp Leu
900 905 910

Ala Arg Gln Lys Glu Gln Glu Arg Arg Arg Arg Glu Ala Met Val Gly
915 920 925

Thr Ile Asp Met Thr Leu Gln Ser Asp Ile Met Thr Met Phe Glu Asn
930 935 940

Asn Phe Asp
945

<210> 309

<211> 180

<212> PRT

<213> Artificial Sequence

ITI-08-PCT_Sequence_Listing_ST25.txt

<220>

<223> CTAG2_Isoform_LAGE-1A__Homo_sapiens__075638-2

<400> 309

Met Gln Ala Glu Gly Arg Gly Thr Gly Gly Ser Thr Gly Asp Ala Asp
1 5 10 15

Gly Pro Gly Gly Pro Gly Ile Pro Asp Gly Pro Gly Gly Asn Ala Gly
20 25 30

Gly Pro Gly Glu Ala Gly Ala Thr Gly Gly Arg Gly Pro Arg Gly Ala
35 40 45

Gly Ala Ala Arg Ala Ser Gly Pro Arg Gly Gly Ala Pro Arg Gly Pro
50 55 60

His Gly Gly Ala Ala Ser Ala Gln Asp Gly Arg Cys Pro Cys Gly Ala
65 70 75 80

Arg Arg Pro Asp Ser Arg Leu Leu Glu Leu His Ile Thr Met Pro Phe
85 90 95

Ser Ser Pro Met Glu Ala Glu Leu Val Arg Arg Ile Leu Ser Arg Asp
100 105 110

Ala Ala Pro Leu Pro Arg Pro Gly Ala Val Leu Lys Asp Phe Thr Val
115 120 125

Ser Gly Asn Leu Leu Phe Ile Arg Leu Thr Ala Ala Asp His Arg Gln
130 135 140

Leu Gln Leu Ser Ile Ser Ser Cys Leu Gln Gln Leu Ser Leu Leu Met
145 150 155 160

Trp Ile Thr Gln Cys Phe Leu Pro Val Phe Leu Ala Gln Ala Pro Ser
165 170 175

Gly Gln Arg Arg
180

<210> 310

<211> 210

<212> PRT

<213> Artificial Sequence

<220>

<223> CTAG2_Isoform_LAGE-1B__Homo_sapiens__075638

<400> 310

ITI-08-PCT_Sequence_Listing_ST25.txt

```

Met Gln Ala Glu Gly Gln Gly Thr Gly Gly Ser Thr Gly Asp Ala Asp
1           5           10           15

Gly Pro Gly Gly Pro Gly Ile Pro Asp Gly Pro Gly Gly Asn Ala Gly
          20           25           30

Gly Pro Gly Glu Ala Gly Ala Thr Gly Gly Arg Gly Pro Arg Gly Ala
          35           40           45

Gly Ala Ala Arg Ala Ser Gly Pro Arg Gly Gly Ala Pro Arg Gly Pro
          50           55           60

His Gly Gly Ala Ala Ser Ala Gln Asp Gly Arg Cys Pro Cys Gly Ala
65           70           75           80

Arg Arg Pro Asp Ser Arg Leu Leu Gln Leu His Ile Thr Met Pro Phe
          85           90           95

Ser Ser Pro Met Glu Ala Glu Leu Val Arg Arg Ile Leu Ser Arg Asp
          100          105          110

Ala Ala Pro Leu Pro Arg Pro Gly Ala Val Leu Lys Asp Phe Thr Val
          115          120          125

Ser Gly Asn Leu Leu Phe Met Ser Val Arg Asp Gln Asp Arg Glu Gly
          130          135          140

Ala Gly Arg Met Arg Val Val Gly Trp Gly Leu Gly Ser Ala Ser Pro
145           150           155           160

Glu Gly Gln Lys Ala Arg Asp Leu Arg Thr Pro Lys His Lys Val Ser
          165          170          175

Glu Gln Arg Pro Gly Thr Pro Gly Pro Pro Pro Pro Glu Gly Ala Gln
          180          185          190

Gly Asp Gly Cys Arg Gly Val Ala Phe Asn Val Met Phe Ser Ala Pro
          195          200          205

His Ile
          210

```

```

<210> 311
<211> 663
<212> PRT
<213> Artificial Sequence

<220>
<223> CTCFL__Homo_sapiens__Q8NI51

<400> 311

```

ITI-08-PCT_Sequence_Listing_ST25.txt

```

Met Ala Ala Thr Glu Ile Ser Val Leu Ser Glu Gln Phe Thr Lys Ile
1          5          10          15

Lys Glu Leu Glu Leu Met Pro Glu Lys Gly Leu Lys Glu Glu Glu Lys
          20          25          30

Asp Gly Val Cys Arg Glu Lys Asp His Arg Ser Pro Ser Glu Leu Glu
          35          40          45

Ala Glu Arg Thr Ser Gly Ala Phe Gln Asp Ser Val Leu Glu Glu Glu
          50          55          60

Val Glu Leu Val Leu Ala Pro Ser Glu Glu Ser Glu Lys Tyr Ile Leu
65          70          75          80

Thr Leu Gln Thr Val His Phe Thr Ser Glu Ala Val Glu Leu Gln Asp
          85          90          95

Met Ser Leu Leu Ser Ile Gln Gln Gln Glu Gly Val Gln Val Val Val
          100          105          110

Gln Gln Pro Gly Pro Gly Leu Leu Trp Leu Glu Glu Gly Pro Arg Gln
          115          120          125

Ser Leu Gln Gln Cys Val Ala Ile Ser Ile Gln Gln Glu Leu Tyr Ser
          130          135          140

Pro Gln Glu Met Glu Val Leu Gln Phe His Ala Leu Glu Glu Asn Val
145          150          155          160

Met Val Ala Ser Glu Asp Ser Lys Leu Ala Val Ser Leu Ala Glu Thr
          165          170          175

Thr Gly Leu Ile Lys Leu Glu Glu Glu Gln Glu Lys Asn Gln Leu Leu
          180          185          190

Ala Glu Arg Thr Lys Glu Gln Leu Phe Phe Val Glu Thr Met Ser Gly
          195          200          205

Asp Glu Arg Ser Asp Glu Ile Val Leu Thr Val Ser Asn Ser Asn Val
          210          215          220

Glu Glu Gln Glu Asp Gln Pro Thr Ala Gly Gln Ala Asp Ala Glu Lys
225          230          235          240

Ala Lys Ser Thr Lys Asn Gln Arg Lys Thr Lys Gly Ala Lys Gly Thr
          245          250          255

Phe His Cys Asp Val Cys Met Phe Thr Ser Ser Arg Met Ser Ser Phe
          260          265          270

Asn Arg His Met Lys Thr His Thr Ser Glu Lys Pro His Leu Cys His

```

ITI-08-PCT_Sequence_Listing_ST25.txt

```

275                280                285
Leu Cys Leu Lys Thr Phe Arg Thr Val Thr Leu Leu Arg Asn His Val
290                295                300
Asn Thr His Thr Gly Thr Arg Pro Tyr Lys Cys Asn Asp Cys Asn Met
305                310                315                320
Ala Phe Val Thr Ser Gly Glu Leu Val Arg His Arg Arg Tyr Lys His
325                330                335
Thr His Glu Lys Pro Phe Lys Cys Ser Met Cys Lys Tyr Ala Ser Val
340                345                350
Glu Ala Ser Lys Leu Lys Arg His Val Arg Ser His Thr Gly Glu Arg
355                360                365
Pro Phe Gln Cys Cys Gln Cys Ser Tyr Ala Ser Arg Asp Thr Tyr Lys
370                375                380
Leu Lys Arg His Met Arg Thr His Ser Gly Glu Lys Pro Tyr Glu Cys
385                390                395                400
His Ile Cys His Thr Arg Phe Thr Gln Ser Gly Thr Met Lys Ile His
405                410                415
Ile Leu Gln Lys His Gly Glu Asn Val Pro Lys Tyr Gln Cys Pro His
420                425                430
Cys Ala Thr Ile Ile Ala Arg Lys Ser Asp Leu Arg Val His Met Arg
435                440                445
Asn Leu His Ala Tyr Ser Ala Ala Glu Leu Lys Cys Arg Tyr Cys Ser
450                455                460
Ala Val Phe His Glu Arg Tyr Ala Leu Ile Gln His Gln Lys Thr His
465                470                475                480
Lys Asn Glu Lys Arg Phe Lys Cys Lys His Cys Ser Tyr Ala Cys Lys
485                490                495
Gln Glu Arg His Met Thr Ala His Ile Arg Thr His Thr Gly Glu Lys
500                505                510
Pro Phe Thr Cys Leu Ser Cys Asn Lys Cys Phe Arg Gln Lys Gln Leu
515                520                525
Leu Asn Ala His Phe Arg Lys Tyr His Asp Ala Asn Phe Ile Pro Thr
530                535                540
Val Tyr Lys Cys Ser Lys Cys Gly Lys Gly Phe Ser Arg Trp Ile Asn
545                550                555                560

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Leu His Arg His Ser Glu Lys Cys Gly Ser Gly Glu Ala Lys Ser Ala
565 570 575

Ala Ser Gly Lys Gly Arg Arg Thr Arg Lys Arg Lys Gln Thr Ile Leu
580 585 590

Lys Glu Ala Thr Lys Gly Gln Lys Glu Ala Ala Lys Gly Trp Lys Glu
595 600 605

Ala Ala Asn Gly Asp Glu Ala Ala Ala Glu Glu Ala Ser Thr Thr Lys
610 615 620

Gly Glu Gln Phe Pro Gly Glu Met Phe Pro Val Ala Cys Arg Glu Thr
625 630 635 640

Thr Ala Arg Val Lys Glu Glu Val Asp Glu Gly Val Thr Cys Glu Met
645 650 655

Leu Leu Asn Thr Met Asp Lys
660

<210> 312
<211> 715
<212> PRT
<213> Artificial Sequence

<220>
<223> Cten__Homo_sapiens__Q8IZW8

<400> 312

Met Ser Gln Val Met Ser Ser Pro Leu Leu Ala Gly Gly His Ala Val
1 5 10 15

Ser Leu Ala Pro Cys Asp Glu Pro Arg Arg Thr Leu His Pro Ala Pro
20 25 30

Ser Pro Ser Leu Pro Pro Gln Cys Ser Tyr Tyr Thr Thr Glu Gly Trp
35 40 45

Gly Ala Gln Ala Leu Met Ala Pro Val Pro Cys Met Gly Pro Pro Gly
50 55 60

Arg Leu Gln Gln Ala Pro Gln Val Glu Ala Lys Ala Thr Cys Phe Leu
65 70 75 80

Pro Ser Pro Gly Glu Lys Ala Leu Gly Thr Pro Glu Asp Leu Asp Ser
85 90 95

Tyr Ile Asp Phe Ser Leu Glu Ser Leu Asn Gln Met Ile Leu Glu Leu
100 105 110

ITI-08-PCT_Sequence_Listing_ST25.txt

Asp	Pro	Thr	Phe	Gln	Leu	Leu	Pro	Pro	Gly	Thr	Gly	Gly	Ser	Gln	Ala	115	120	125
Glu	Leu	Ala	Gln	Ser	Thr	Met	Ser	Met	Arg	Lys	Lys	Glu	Glu	Ser	Glu	130	135	140
Ala	Leu	Asp	Ile	Lys	Tyr	Ile	Glu	Val	Thr	Ser	Ala	Arg	Ser	Arg	Cys	145	150	155
His	Asp	Gly	Pro	Gln	His	Cys	Ser	Ser	Pro	Ser	Val	Thr	Pro	Pro	Phe	165	170	175
Gly	Ser	Leu	Arg	Ser	Gly	Gly	Leu	Leu	Leu	Ser	Arg	Asp	Val	Pro	Arg	180	185	190
Glu	Thr	Arg	Ser	Ser	Ser	Glu	Ser	Leu	Ile	Phe	Ser	Gly	Asn	Gln	Gly	195	200	205
Arg	Gly	His	Gln	Arg	Pro	Leu	Pro	Pro	Ser	Glu	Gly	Leu	Ser	Pro	Arg	210	215	220
Pro	Pro	Asn	Ser	Pro	Ser	Ile	Ser	Ile	Pro	Cys	Met	Gly	Ser	Lys	Ala	225	230	235
Ser	Ser	Pro	His	Gly	Leu	Gly	Ser	Pro	Leu	Val	Ala	Ser	Pro	Arg	Leu	245	250	255
Glu	Lys	Arg	Leu	Gly	Gly	Leu	Ala	Pro	Gln	Arg	Gly	Ser	Arg	Ile	Ser	260	265	270
Val	Leu	Ser	Ala	Ser	Pro	Val	Ser	Asp	Val	Ser	Tyr	Met	Phe	Gly	Ser	275	280	285
Ser	Gln	Ser	Leu	Leu	His	Ser	Ser	Asn	Ser	Ser	His	Gln	Ser	Ser	Ser	290	295	300
Arg	Ser	Leu	Glu	Ser	Pro	Ala	Asn	Ser	Ser	Ser	Ser	Leu	His	Ser	Leu	305	310	315
Gly	Ser	Val	Ser	Leu	Cys	Thr	Arg	Pro	Ser	Asp	Phe	Gln	Ala	Pro	Arg	325	330	335
Asn	Pro	Thr	Leu	Thr	Met	Gly	Gln	Pro	Arg	Thr	Pro	His	Ser	Pro	Pro	340	345	350
Leu	Ala	Lys	Glu	His	Ala	Ser	Ser	Cys	Pro	Pro	Ser	Ile	Thr	Asn	Ser	355	360	365
Met	Val	Asp	Ile	Pro	Ile	Val	Leu	Ile	Asn	Gly	Cys	Pro	Glu	Pro	Gly	370	375	380

ITI-08-PCT_Sequence_Listing_ST25.txt

Ser	Ser	Pro	Pro	Gln	Arg	Thr	Pro	Gly	His	Gln	Asn	Ser	Val	Gln	Pro	385	390	395	400
Gly	Ala	Ala	Ser	Pro	Ser	Asn	Pro	Cys	Pro	Ala	Thr	Arg	Ser	Asn	Ser	405	410	415	
Gln	Thr	Leu	Ser	Asp	Ala	Pro	Phe	Thr	Thr	Cys	Pro	Glu	Gly	Pro	Ala	420	425	430	
Arg	Asp	Met	Gln	Pro	Thr	Met	Lys	Phe	Val	Met	Asp	Thr	Ser	Lys	Tyr	435	440	445	
Trp	Phe	Lys	Pro	Asn	Ile	Thr	Arg	Glu	Gln	Ala	Ile	Glu	Leu	Leu	Arg	450	455	460	
Lys	Glu	Glu	Pro	Gly	Ala	Phe	Val	Ile	Arg	Asp	Ser	Ser	Ser	Tyr	Arg	465	470	475	480
Gly	Ser	Phe	Gly	Leu	Ala	Leu	Lys	Val	Gln	Glu	Val	Pro	Ala	Ser	Ala	485	490	495	
Gln	Ser	Arg	Pro	Gly	Glu	Asp	Ser	Asn	Asp	Leu	Ile	Arg	His	Phe	Leu	500	505	510	
Ile	Glu	Ser	Ser	Ala	Lys	Gly	Val	His	Leu	Lys	Gly	Ala	Asp	Glu	Glu	515	520	525	
Pro	Tyr	Phe	Gly	Ser	Leu	Ser	Ala	Phe	Val	Cys	Gln	His	Ser	Ile	Met	530	535	540	
Ala	Leu	Ala	Leu	Pro	Cys	Lys	Leu	Thr	Ile	Pro	Gln	Arg	Glu	Leu	Gly	545	550	555	560
Gly	Ala	Asp	Gly	Ala	Ser	Asp	Ser	Thr	Asp	Ser	Pro	Ala	Ser	Cys	Gln	565	570	575	
Lys	Lys	Ser	Ala	Gly	Cys	His	Thr	Leu	Tyr	Leu	Ser	Ser	Val	Ser	Val	580	585	590	
Glu	Thr	Leu	Thr	Gly	Ala	Leu	Ala	Val	Gln	Lys	Ala	Ile	Ser	Thr	Thr	595	600	605	
Phe	Glu	Arg	Asp	Ile	Leu	Pro	Thr	Pro	Thr	Val	Val	His	Phe	Lys	Val	610	615	620	
Thr	Glu	Gln	Gly	Ile	Thr	Leu	Thr	Asp	Val	Gln	Arg	Lys	Val	Phe	Phe	625	630	635	640
Arg	Arg	His	Tyr	Pro	Leu	Thr	Thr	Leu	Arg	Phe	Cys	Gly	Met	Asp	Pro	645	650	655	
Glu	Gln	Arg	Lys	Trp	Gln	Lys	Tyr	Cys	Lys	Pro	Ser	Trp	Ile	Phe	Gly				

ITI-08-PCT_Sequence_Listing_ST25.txt

660

665

670

Phe Val Ala Lys Ser Gln Thr Glu Pro Gln Glu Asn Val Cys His Leu
675 680 685

Phe Ala Glu Tyr Asp Met Val Gln Pro Ala Ser Gln Val Ile Gly Leu
690 695 700

Val Thr Ala Leu Leu Gln Asp Ala Glu Arg Met
705 710 715

<210> 313

<211> 433

<212> PRT

<213> Artificial Sequence

<220>

<223> cyclin_B1__Homo_sapiens__P14635

<400> 313

Met Ala Leu Arg Val Thr Arg Asn Ser Lys Ile Asn Ala Glu Asn Lys
1 5 10 15

Ala Lys Ile Asn Met Ala Gly Ala Lys Arg Val Pro Thr Ala Pro Ala
20 25 30

Ala Thr Ser Lys Pro Gly Leu Arg Pro Arg Thr Ala Leu Gly Asp Ile
35 40 45

Gly Asn Lys Val Ser Glu Gln Leu Gln Ala Lys Met Pro Met Lys Lys
50 55 60

Glu Ala Lys Pro Ser Ala Thr Gly Lys Val Ile Asp Lys Lys Leu Pro
65 70 75 80

Lys Pro Leu Glu Lys Val Pro Met Leu Val Pro Val Pro Val Ser Glu
85 90 95

Pro Val Pro Glu Pro Glu Pro Glu Pro Glu Pro Val Lys Glu
100 105 110

Glu Lys Leu Ser Pro Glu Pro Ile Leu Val Asp Thr Ala Ser Pro Ser
115 120 125

Pro Met Glu Thr Ser Gly Cys Ala Pro Ala Glu Glu Asp Leu Cys Gln
130 135 140

Ala Phe Ser Asp Val Ile Leu Ala Val Asn Asp Val Asp Ala Glu Asp
145 150 155 160

Gly Ala Asp Pro Asn Leu Cys Ser Glu Tyr Val Lys Asp Ile Tyr Ala

ITI-08-PCT_Sequence_Listing_ST25.txt

165

170

175

Tyr Leu Arg Gln Leu Glu Glu Glu Gln Ala Val Arg Pro Lys Tyr Leu
 180 185 190

Leu Gly Arg Glu Val Thr Gly Asn Met Arg Ala Ile Leu Ile Asp Trp
 195 200 205

Leu Val Gln Val Gln Met Lys Phe Arg Leu Leu Gln Glu Thr Met Tyr
 210 215 220

Met Thr Val Ser Ile Ile Asp Arg Phe Met Gln Asn Asn Cys Val Pro
 225 230 235 240

Lys Lys Met Leu Gln Leu Val Gly Val Thr Ala Met Phe Ile Ala Ser
 245 250 255

Lys Tyr Glu Glu Met Tyr Pro Pro Glu Ile Gly Asp Phe Ala Phe Val
 260 265 270

Thr Asp Asn Thr Tyr Thr Lys His Gln Ile Arg Gln Met Glu Met Lys
 275 280 285

Ile Leu Arg Ala Leu Asn Phe Gly Leu Gly Arg Pro Leu Pro Leu His
 290 295 300

Phe Leu Arg Arg Ala Ser Lys Ile Gly Glu Val Asp Val Glu Gln His
 305 310 315 320

Thr Leu Ala Lys Tyr Leu Met Glu Leu Thr Met Leu Asp Tyr Asp Met
 325 330 335

Val His Phe Pro Pro Ser Gln Ile Ala Ala Gly Ala Phe Cys Leu Ala
 340 345 350

Leu Lys Ile Leu Asp Asn Gly Glu Trp Thr Pro Thr Leu Gln His Tyr
 355 360 365

Leu Ser Tyr Thr Glu Glu Ser Leu Leu Pro Val Met Gln His Leu Ala
 370 375 380

Lys Asn Val Val Met Val Asn Gln Gly Leu Thr Lys His Met Thr Val
 385 390 395 400

Lys Asn Lys Tyr Ala Thr Ser Lys His Ala Lys Ile Ser Thr Leu Pro
 405 410 415

Gln Leu Asn Ser Ala Leu Val Gln Asp Leu Ala Lys Ala Val Ala Lys
 420 425 430

Val

ITI-08-PCT_Sequence_Listing_ST25.txt

```

<210> 314
<211> 295
<212> PRT
<213> Artificial Sequence

<220>
<223> cyclin_D1__Homo_sapiens__P24385

<400> 314

Met Glu His Gln Leu Leu Cys Cys Glu Val Glu Thr Ile Arg Arg Ala
1          5          10          15

Tyr Pro Asp Ala Asn Leu Leu Asn Asp Arg Val Leu Arg Ala Met Leu
          20          25          30

Lys Ala Glu Glu Thr Cys Ala Pro Ser Val Ser Tyr Phe Lys Cys Val
          35          40          45

Gln Lys Glu Val Leu Pro Ser Met Arg Lys Ile Val Ala Thr Trp Met
          50          55          60

Leu Glu Val Cys Glu Glu Gln Lys Cys Glu Glu Glu Val Phe Pro Leu
65          70          75          80

Ala Met Asn Tyr Leu Asp Arg Phe Leu Ser Leu Glu Pro Val Lys Lys
          85          90          95

Ser Arg Leu Gln Leu Leu Gly Ala Thr Cys Met Phe Val Ala Ser Lys
          100         105         110

Met Lys Glu Thr Ile Pro Leu Thr Ala Glu Lys Leu Cys Ile Tyr Thr
          115         120         125

Asp Asn Ser Ile Arg Pro Glu Glu Leu Leu Gln Met Glu Leu Leu Leu
          130         135         140

Val Asn Lys Leu Lys Trp Asn Leu Ala Ala Met Thr Pro His Asp Phe
145          150         155         160

Ile Glu His Phe Leu Ser Lys Met Pro Glu Ala Glu Glu Asn Lys Gln
          165         170         175

Ile Ile Arg Lys His Ala Gln Thr Phe Val Ala Leu Cys Ala Thr Asp
          180         185         190

Val Lys Phe Ile Ser Asn Pro Pro Ser Met Val Ala Ala Gly Ser Val
          195         200         205

Val Ala Ala Val Gln Gly Leu Asn Leu Arg Ser Pro Asn Asn Phe Leu
210          215         220

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Ser Tyr Tyr Arg Leu Thr Arg Phe Leu Ser Arg Val Ile Lys Cys Asp
225 230 235 240

Pro Asp Cys Leu Arg Ala Cys Gln Glu Gln Ile Glu Ala Leu Leu Glu
245 250 255

Ser Ser Leu Arg Gln Ala Gln Gln Asn Met Asp Pro Lys Ala Ala Glu
260 265 270

Glu Glu Glu Glu Glu Glu Glu Glu Val Asp Leu Ala Cys Thr Pro Thr
275 280 285

Asp Val Arg Asp Val Asp Ile
290 295

<210> 315

<211> 216

<212> PRT

<213> Artificial Sequence

<220>

<223> cyp-B__Homo_sapiens__P23284

<400> 315

Met Leu Arg Leu Ser Glu Arg Asn Met Lys Val Leu Leu Ala Ala Ala
1 5 10 15

Leu Ile Ala Gly Ser Val Phe Phe Leu Leu Leu Pro Gly Pro Ser Ala
20 25 30

Ala Asp Glu Lys Lys Lys Gly Pro Lys Val Thr Val Lys Val Tyr Phe
35 40 45

Asp Leu Arg Ile Gly Asp Glu Asp Val Gly Arg Val Ile Phe Gly Leu
50 55 60

Phe Gly Lys Thr Val Pro Lys Thr Val Asp Asn Phe Val Ala Leu Ala
65 70 75 80

Thr Gly Glu Lys Gly Phe Gly Tyr Lys Asn Ser Lys Phe His Arg Val
85 90 95

Ile Lys Asp Phe Met Ile Gln Gly Gly Asp Phe Thr Arg Gly Asp Gly
100 105 110

Thr Gly Gly Lys Ser Ile Tyr Gly Glu Arg Phe Pro Asp Glu Asn Phe
115 120 125

Lys Leu Lys His Tyr Gly Pro Gly Trp Val Ser Met Ala Asn Ala Gly
130 135 140

ITI-08-PCT_Sequence_Listing_ST25.txt

Lys Asp Thr Asn Gly Ser Gln Phe Phe Ile Thr Thr Val Lys Thr Ala
145 150 155 160

Trp Leu Asp Gly Lys His Val Val Phe Gly Lys Val Leu Glu Gly Met
165 170 175

Glu Val Val Arg Lys Val Glu Ser Thr Lys Thr Asp Ser Arg Asp Lys
180 185 190

Pro Leu Lys Asp Val Ile Ile Ala Asp Cys Gly Lys Ile Glu Val Glu
195 200 205

Lys Pro Phe Ala Ile Ala Lys Glu
210 215

<210> 316

<211> 347

<212> PRT

<213> Artificial Sequence

<220>

<223> DAM-10__Homo_sapiens__P43366

<400> 316

Met Pro Arg Gly Gln Lys Ser Lys Leu Arg Ala Arg Glu Lys Arg Arg
1 5 10 15

Lys Ala Arg Glu Glu Thr Gln Gly Leu Lys Val Ala His Ala Thr Ala
20 25 30

Ala Glu Lys Glu Glu Cys Pro Ser Ser Ser Pro Val Leu Gly Asp Thr
35 40 45

Pro Thr Ser Ser Pro Ala Ala Gly Ile Pro Gln Lys Pro Gln Gly Ala
50 55 60

Pro Pro Thr Thr Thr Ala Ala Ala Ala Val Ser Cys Thr Glu Ser Asp
65 70 75 80

Glu Gly Ala Lys Cys Gln Gly Glu Glu Asn Ala Ser Phe Ser Gln Ala
85 90 95

Thr Thr Ser Thr Glu Ser Ser Val Lys Asp Pro Val Ala Trp Glu Ala
100 105 110

Gly Met Leu Met His Phe Ile Leu Arg Lys Tyr Lys Met Arg Glu Pro
115 120 125

Ile Met Lys Ala Asp Met Leu Lys Val Val Asp Glu Lys Tyr Lys Asp
130 135 140

ITI-08-PCT_Sequence_Listing_ST25.txt

His Phe Thr Glu Ile Leu Asn Gly Ala Ser Arg Arg Leu Glu Leu Val
145 150 155 160

Phe Gly Leu Asp Leu Lys Glu Asp Asn Pro Ser Gly His Thr Tyr Thr
165 170 175

Leu Val Ser Lys Leu Asn Leu Thr Asn Asp Gly Asn Leu Ser Asn Asp
180 185 190

Trp Asp Phe Pro Arg Asn Gly Leu Leu Met Pro Leu Leu Gly Val Ile
195 200 205

Phe Leu Lys Gly Asn Ser Ala Thr Glu Glu Glu Ile Trp Lys Phe Met
210 215 220

Asn Val Leu Gly Ala Tyr Asp Gly Glu Glu His Leu Ile Tyr Gly Glu
225 230 235 240

Pro Arg Lys Phe Ile Thr Gln Asp Leu Val Gln Glu Lys Tyr Leu Lys
245 250 255

Tyr Glu Gln Val Pro Asn Ser Asp Pro Pro Arg Tyr Gln Phe Leu Trp
260 265 270

Gly Pro Arg Ala Tyr Ala Glu Thr Thr Lys Met Lys Val Leu Glu Phe
275 280 285

Leu Ala Lys Met Asn Gly Ala Thr Pro Arg Asp Phe Pro Ser His Tyr
290 295 300

Glu Glu Ala Leu Arg Asp Glu Glu Glu Arg Ala Gln Val Arg Ser Ser
305 310 315 320

Val Arg Ala Arg Arg Arg Thr Thr Ala Thr Thr Phe Arg Ala Arg Ser
325 330 335

Arg Ala Pro Phe Ser Arg Ser Ser His Pro Met
340 345

<210> 317

<211> 811

<212> PRT

<213> Artificial Sequence

<220>

<223> DEP1A__Homo_sapiens__Q5TB30

<400> 317

Met Glu Ser Gln Gly Val Pro Pro Gly Pro Tyr Arg Ala Thr Lys Leu
1 5 10 15

Trp	Asn	Glu	Val	Thr	Thr	Ser	Phe	Arg	Ala	Gly	Met	Pro	Leu	Arg	Lys
			20					25				30			
His	Arg	Gln	His	Phe	Lys	Lys	Tyr	Gly	Asn	Cys	Phe	Thr	Ala	Gly	Glu
		35					40					45			
Ala	Val	Asp	Trp	Leu	Tyr	Asp	Leu	Leu	Arg	Asn	Asn	Ser	Asn	Phe	Gly
	50					55					60				
Pro	Glu	Val	Thr	Arg	Gln	Gln	Thr	Ile	Gln	Leu	Leu	Arg	Lys	Phe	Leu
65					70					75					80
Lys	Asn	His	Val	Ile	Glu	Asp	Ile	Lys	Gly	Arg	Trp	Gly	Ser	Glu	Asn
				85					90					95	
Val	Asp	Asp	Asn	Asn	Gln	Leu	Phe	Arg	Phe	Pro	Ala	Thr	Ser	Pro	Leu
			100					105					110		
Lys	Thr	Leu	Pro	Arg	Arg	Tyr	Pro	Glu	Leu	Arg	Lys	Asn	Asn	Ile	Glu
		115					120					125			
Asn	Phe	Ser	Lys	Asp	Lys	Asp	Ser	Ile	Phe	Lys	Leu	Arg	Asn	Leu	Ser
	130					135					140				
Arg	Arg	Thr	Pro	Lys	Arg	His	Gly	Leu	His	Leu	Ser	Gln	Glu	Asn	Gly
145					150					155					160
Glu	Lys	Ile	Lys	His	Glu	Ile	Ile	Asn	Glu	Asp	Gln	Glu	Asn	Ala	Ile
				165					170					175	
Asp	Asn	Arg	Glu	Leu	Ser	Gln	Glu	Asp	Val	Glu	Glu	Val	Trp	Arg	Tyr
			180					185					190		
Val	Ile	Leu	Ile	Tyr	Leu	Gln	Thr	Ile	Leu	Gly	Val	Pro	Ser	Leu	Glu
		195					200					205			
Glu	Val	Ile	Asn	Pro	Lys	Gln	Val	Ile	Pro	Gln	Tyr	Ile	Met	Tyr	Asn
	210					215					220				
Met	Ala	Asn	Thr	Ser	Lys	Arg	Gly	Val	Val	Ile	Leu	Gln	Asn	Lys	Ser
225					230					235					240
Asp	Asp	Leu	Pro	His	Trp	Val	Leu	Ser	Ala	Met	Lys	Cys	Leu	Ala	Asn
				245					250					255	
Trp	Pro	Arg	Ser	Asn	Asp	Met	Asn	Asn	Pro	Thr	Tyr	Val	Gly	Phe	Glu
			260					265					270		
Arg	Asp	Val	Phe	Arg	Thr	Ile	Ala	Asp	Tyr	Phe	Leu	Asp	Leu	Pro	Glu
		275					280					285			
Pro	Leu	Leu	Thr	Phe	Glu	Tyr	Tyr	Glu	Leu	Phe	Val	Asn	Ile	Leu	Val

ITI-08-PCT_Sequence_Listing_ST25.txt

```

290          295          300
Val Cys Gly Tyr Ile Thr Val Ser Asp Arg Ser Ser Gly Ile His Lys
305          310          315
Ile Gln Asp Asp Pro Gln Ser Ser Lys Phe Leu His Leu Asn Asn Leu
          325          330          335
Asn Ser Phe Lys Ser Thr Glu Cys Leu Leu Leu Ser Leu Leu His Arg
          340          345          350
Glu Lys Asn Lys Glu Glu Ser Asp Ser Thr Glu Arg Leu Gln Ile Ser
          355          360          365
Asn Pro Gly Phe Gln Glu Arg Cys Ala Lys Lys Met Gln Leu Val Asn
          370          375          380
Leu Arg Asn Arg Arg Val Ser Ala Asn Asp Ile Met Gly Gly Ser Cys
385          390          395          400
His Asn Leu Ile Gly Leu Ser Asn Met His Asp Leu Ser Ser Asn Ser
          405          410          415
Lys Pro Arg Cys Cys Ser Leu Glu Gly Ile Val Asp Val Pro Gly Asn
          420          425          430
Ser Ser Lys Glu Ala Ser Ser Val Phe His Gln Ser Phe Pro Asn Ile
          435          440          445
Glu Gly Gln Asn Asn Lys Leu Phe Leu Glu Ser Lys Pro Lys Gln Glu
          450          455          460
Phe Leu Leu Asn Leu His Ser Glu Glu Asn Ile Gln Lys Pro Phe Ser
465          470          475          480
Ala Gly Phe Lys Arg Thr Ser Thr Leu Thr Val Gln Asp Gln Glu Glu
          485          490          495
Leu Cys Asn Gly Lys Cys Lys Ser Lys Gln Leu Cys Arg Ser Gln Ser
          500          505          510
Leu Leu Leu Arg Ser Ser Thr Arg Arg Asn Ser Tyr Ile Asn Thr Pro
          515          520          525
Val Ala Glu Ile Ile Met Lys Pro Asn Val Gly Gln Gly Ser Thr Ser
          530          535          540
Val Gln Thr Ala Met Glu Ser Glu Leu Gly Glu Ser Ser Ala Thr Ile
545          550          555          560
Asn Lys Arg Leu Cys Lys Ser Thr Ile Glu Leu Ser Glu Asn Ser Leu
          565          570          575

```

ITI-08-PCT_Sequence_Listing_ST25.txt

```

Leu Pro Ala Ser Ser Met Leu Thr Gly Thr Gln Ser Leu Leu Gln Pro
      580                      585                      590

His Leu Glu Arg Val Ala Ile Asp Ala Leu Gln Leu Cys Cys Leu Leu
      595                      600                      605

Leu Pro Pro Pro Asn Arg Arg Lys Leu Gln Leu Leu Met Arg Met Ile
      610                      615                      620

Ser Arg Met Ser Gln Asn Val Asp Met Pro Lys Leu His Asp Ala Met
      625                      630                      635                      640

Gly Thr Arg Ser Leu Met Ile His Thr Phe Ser Arg Cys Val Leu Cys
      645                      650                      655

Cys Ala Glu Glu Val Asp Leu Asp Glu Leu Leu Ala Gly Arg Leu Val
      660                      665                      670

Ser Phe Leu Met Asp His His Gln Glu Ile Leu Gln Val Pro Ser Tyr
      675                      680                      685

Leu Gln Thr Ala Val Glu Lys His Leu Asp Tyr Leu Lys Lys Gly His
      690                      695                      700

Ile Glu Asn Pro Gly Asp Gly Leu Phe Ala Pro Leu Pro Thr Tyr Ser
      705                      710                      715                      720

Tyr Cys Lys Gln Ile Ser Ala Gln Glu Phe Asp Glu Gln Lys Val Ser
      725                      730                      735

Thr Ser Gln Ala Ala Ile Ala Glu Leu Leu Glu Asn Ile Ile Lys Asn
      740                      745                      750

Arg Ser Leu Pro Leu Lys Glu Lys Arg Lys Lys Leu Lys Gln Phe Gln
      755                      760                      765

Lys Glu Tyr Pro Leu Ile Tyr Gln Lys Arg Phe Pro Thr Thr Glu Ser
      770                      775                      780

Glu Ala Ala Leu Phe Gly Asp Lys Pro Thr Ile Lys Gln Pro Met Leu
      785                      790                      795                      800

Ile Leu Arg Lys Pro Lys Phe Arg Ser Leu Arg
      805                      810

```

<210> 318
 <211> 98
 <212> PRT
 <213> Artificial Sequence

<220>

ITI-08-PCT_Sequence_Listing_ST25.txt

<223> E7__Human_papillomavirus_type_16__P03129

<400> 318

Met His Gly Asp Thr Pro Thr Leu His Glu Tyr Met Leu Asp Leu Gln
1 5 10 15

Pro Glu Thr Thr Asp Leu Tyr Cys Tyr Glu Gln Leu Asn Asp Ser Ser
20 25 30

Glu Glu Glu Asp Glu Ile Asp Gly Pro Ala Gly Gln Ala Glu Pro Asp
35 40 45

Arg Ala His Tyr Asn Ile Val Thr Phe Cys Cys Lys Cys Asp Ser Thr
50 55 60

Leu Arg Leu Cys Val Gln Ser Thr His Val Asp Ile Arg Thr Leu Glu
65 70 75 80

Asp Leu Leu Met Gly Thr Leu Gly Ile Val Cys Pro Ile Cys Ser Gln
85 90 95

Lys Pro

<210> 319

<211> 105

<212> PRT

<213> Artificial Sequence

<220>

<223> E7__Human_papillomavirus_type_18__P06788

<400> 319

Met His Gly Pro Lys Ala Thr Leu Gln Asp Ile Val Leu His Leu Glu
1 5 10 15

Pro Gln Asn Glu Ile Pro Val Asp Leu Leu Cys His Glu Gln Leu Ser
20 25 30

Asp Ser Glu Glu Glu Asn Asp Glu Ile Asp Gly Val Asn His Gln His
35 40 45

Leu Pro Ala Arg Arg Ala Glu Pro Gln Arg His Thr Met Leu Cys Met
50 55 60

Cys Cys Lys Cys Glu Ala Arg Ile Lys Leu Val Val Glu Ser Ser Ala
65 70 75 80

Asp Asp Leu Arg Ala Phe Gln Gln Leu Phe Leu Asn Thr Leu Ser Phe
85 90 95

ITI-08-PCT_Sequence_Listing_ST25.txt

Val Cys Pro Trp Cys Ala Ser Gln Gln
100 105

<210> 320
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> E7__Human_papillomavirus_type_31__P17387

<400> 320

Met Arg Gly Glu Thr Pro Thr Leu Gln Asp Tyr Val Leu Asp Leu Gln
1 5 10 15

Pro Glu Ala Thr Asp Leu His Cys Tyr Glu Gln Leu Pro Asp Ser Ser
20 25 30

Asp Glu Glu Asp Val Ile Asp Ser Pro Ala Gly Gln Ala Glu Pro Asp
35 40 45

Thr Ser Asn Tyr Asn Ile Val Thr Phe Cys Cys Gln Cys Lys Ser Thr
50 55 60

Leu Arg Leu Cys Val Gln Ser Thr Gln Val Asp Ile Arg Ile Leu Gln
65 70 75 80

Glu Leu Leu Met Gly Ser Phe Gly Ile Val Cys Pro Asn Cys Ser Thr
85 90 95

Arg Leu

<210> 321
<211> 97
<212> PRT
<213> Artificial Sequence

<220>
<223> E7__Human_papillomavirus_type_33__P06429

<400> 321

Met Arg Gly His Lys Pro Thr Leu Lys Glu Tyr Val Leu Asp Leu Tyr
1 5 10 15

Pro Glu Pro Thr Asp Leu Tyr Cys Tyr Glu Gln Leu Ser Asp Ser Ser
20 25 30

Asp Glu Asp Glu Gly Leu Asp Arg Pro Asp Gly Gln Ala Gln Pro Ala
35 40 45

ITI-08-PCT_Sequence_Listing_ST25.txt

Thr Ala Asp Tyr Tyr Ile Val Thr Cys Cys His Thr Cys Asn Thr Thr
50 55 60

Val Arg Leu Cys Val Asn Ser Thr Ala Ser Asp Leu Arg Thr Ile Gln
65 70 75 80

Gln Leu Leu Met Gly Thr Val Asn Ile Val Cys Pro Thr Cys Ala Gln
85 90 95

Gln

<210> 322
<211> 99
<212> PRT
<213> Artificial Sequence

<220>
<223> E7__Human_papillomavirus_type_35__P27230

<400> 322

Met His Gly Glu Ile Thr Thr Leu Gln Asp Tyr Val Leu Asp Leu Glu
1 5 10 15

Pro Glu Ala Thr Asp Leu Tyr Cys Tyr Glu Gln Leu Cys Asp Ser Ser
20 25 30

Glu Glu Glu Glu Asp Thr Ile Asp Gly Pro Ala Gly Gln Ala Lys Pro
35 40 45

Asp Thr Ser Asn Tyr Asn Ile Val Thr Ser Cys Cys Lys Cys Glu Ala
50 55 60

Thr Leu Arg Leu Cys Val Gln Ser Thr His Ile Asp Ile Arg Lys Leu
65 70 75 80

Glu Asp Leu Leu Met Gly Thr Phe Gly Ile Val Cys Pro Gly Cys Ser
85 90 95

Gln Arg Ala

<210> 323
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> E7__Human_papillomavirus_type_39__P24837

<400> 323

Met Arg Gly Pro Lys Pro Thr Leu Gln Glu Ile Val Leu Asp Leu Cys

ITI-08-PCT_Sequence_Listing_ST25.txt

```

1           5           10           15
Pro Tyr Asn Glu Ile Gln Pro Val Asp Leu Val Cys His Glu Gln Leu
      20           25           30
Gly Glu Ser Glu Asp Glu Ile Asp Glu Pro Asp His Ala Val Asn His
      35           40           45
Gln His Gln Leu Leu Ala Arg Arg Asp Glu Pro Gln Arg His Thr Ile
      50           55           60
Gln Cys Ser Cys Cys Lys Cys Asn Asn Thr Leu Gln Leu Val Val Glu
65           70           75           80
Ala Ser Arg Asp Thr Leu Arg Gln Leu Gln Gln Leu Phe Met Asp Ser
      85           90           95
Leu Gly Phe Val Cys Pro Trp Cys Ala Thr Ala Asn Gln
      100           105

```

<210> 324
 <211> 106
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> E7__Human_papillomavirus_type_45__P21736

<400> 324

```

Met His Gly Pro Arg Glu Thr Leu Gln Glu Ile Val Leu His Leu Glu
1           5           10           15
Pro Gln Asn Glu Leu Asp Pro Val Asp Leu Leu Cys Tyr Glu Gln Leu
      20           25           30
Ser Glu Ser Glu Glu Glu Asn Asp Glu Ala Asp Gly Val Ser His Ala
      35           40           45
Gln Leu Pro Ala Arg Arg Ala Glu Pro Gln Arg His Lys Ile Leu Cys
      50           55           60
Val Cys Cys Lys Cys Asp Gly Arg Ile Glu Leu Thr Val Glu Ser Ser
65           70           75           80
Ala Glu Asp Leu Arg Thr Leu Gln Gln Leu Phe Leu Ser Thr Leu Ser
      85           90           95
Phe Val Cys Pro Trp Cys Ala Thr Asn Gln
      100           105

```

<210> 325

ITI-08-PCT_Sequence_Listing_ST25.txt

<211> 101
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> E7__Human_papillomavirus_type_51__P26558
 <400> 325

```
Met Arg Gly Asn Val Pro Gln Leu Lys Asp Val Val Leu His Leu Thr
1              5              10              15

Pro Gln Thr Glu Ile Asp Leu Gln Cys Tyr Glu Gln Phe Asp Ser Ser
          20              25              30

Glu Glu Glu Asp Glu Val Asp Asn Met Arg Asp Gln Leu Pro Glu Arg
          35              40              45

Arg Ala Gly Gln Ala Thr Cys Tyr Arg Ile Glu Ala Pro Cys Cys Arg
          50              55              60

Cys Ser Ser Val Val Gln Leu Ala Val Glu Ser Ser Gly Asp Thr Leu
65              70              75              80

Arg Val Val Gln Gln Met Leu Met Gly Glu Leu Ser Leu Val Cys Pro
          85              90              95

Cys Cys Ala Asn Asn
          100
```

<210> 326
 <211> 99
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> E7__Human_papillomavirus_type_52__P36831
 <400> 326

```
Met Arg Gly Asp Lys Ala Thr Ile Lys Asp Tyr Ile Leu Asp Leu Gln
1              5              10              15

Pro Glu Thr Thr Asp Leu His Cys Tyr Glu Gln Leu Gly Asp Ser Ser
          20              25              30

Asp Glu Glu Asp Thr Asp Gly Val Asp Arg Pro Asp Gly Gln Ala Glu
          35              40              45

Gln Ala Thr Ser Asn Tyr Tyr Ile Val Thr Tyr Cys His Ser Cys Asp
          50              55              60
```

ITI-08-PCT_Sequence_Listing_ST25.txt

Ser Thr Leu Arg Leu Cys Ile His Ser Thr Ala Thr Asp Leu Arg Thr
65 70 75 80

Leu Gln Gln Met Leu Leu Gly Thr Leu Gln Val Val Cys Pro Gly Cys
85 90 95

Ala Arg Leu

<210> 327
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> E7__Human_papillomavirus_type_56__P36833

<400> 327

Met His Gly Lys Val Pro Thr Leu Gln Asp Val Val Leu Glu Leu Thr
1 5 10 15

Pro Gln Thr Glu Ile Asp Leu Gln Cys Asn Glu Gln Leu Asp Ser Ser
20 25 30

Glu Asp Glu Asp Glu Asp Glu Val Asp His Leu Gln Glu Arg Pro Gln
35 40 45

Gln Ala Arg Gln Ala Lys Gln His Thr Cys Tyr Leu Ile His Val Pro
50 55 60

Cys Cys Glu Cys Lys Phe Val Val Gln Leu Asp Ile Gln Ser Thr Lys
65 70 75 80

Glu Asp Leu Arg Val Val Gln Gln Leu Leu Met Gly Ala Leu Thr Val
85 90 95

Thr Cys Pro Leu Cys Ala Ser Ser Asn
100 105

<210> 328
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> E7__Human_papillomavirus_type_58__Q9QCZ1

<400> 328

Met Arg Gly Asn Asn Pro Thr Leu Arg Glu Tyr Ile Leu Asp Leu His
1 5 10 15

ITI-08-PCT_Sequence_Listing_ST25.txt

Pro Glu Pro Thr Asp Leu Phe Cys Tyr Glu Gln Leu Cys Asp Ser Ser
20 25 30

Asp Glu Asp Glu Ile Gly Leu Asp Arg Pro Asp Gly Gln Ala Gln Pro
35 40 45

Ala Thr Ala Asn Tyr Tyr Ile Val Thr Cys Cys Tyr Thr Cys Asp Thr
50 55 60

Thr Val Arg Leu Cys Ile Asn Ser Thr Thr Thr Asp Val Arg Thr Leu
65 70 75 80

Gln Gln Leu Leu Met Gly Thr Cys Thr Ile Val Cys Pro Ser Cys Ala
85 90 95

Gln Gln

<210> 329

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> E7__Human_papillomavirus_type_59__Q81965

<400> 329

Met His Gly Pro Lys Ala Thr Leu Cys Asp Ile Val Leu Asp Leu Glu
1 5 10 15

Pro Gln Asn Tyr Glu Glu Val Asp Leu Val Cys Tyr Glu Gln Leu Pro
20 25 30

Asp Ser Asp Ser Glu Asn Glu Lys Asp Glu Pro Asp Gly Val Asn His
35 40 45

Pro Leu Leu Leu Ala Arg Arg Ala Glu Pro Gln Arg His Asn Ile Val
50 55 60

Cys Val Cys Cys Lys Cys Asn Asn Gln Leu Gln Leu Val Val Glu Thr
65 70 75 80

Ser Gln Asp Gly Leu Arg Ala Leu Gln Gln Leu Phe Met Asp Thr Leu
85 90 95

Ser Phe Val Cys Pro Leu Cys Ala Ala Asn Gln
100 105

<210> 330

<211> 105

<212> PRT

<213> Artificial Sequence

ITI-08-PCT_Sequence_Listing_ST25.txt

<220>

<223> E7__Human_papillomavirus_type_66__Q80956

<400> 330

Met His Gly Lys Val Pro Thr Leu Gln Glu Val Ile Leu Glu Leu Ala
1 5 10 15

Pro Gln Thr Glu Ile Asp Leu Gln Cys Asn Glu Gln Leu Asp Ser Ser
20 25 30

Glu Asp Glu Asp Glu Asp Glu Ile Asp His Leu Leu Glu Arg Pro Gln
35 40 45

Gln Ala Arg Gln Ala Glu Gln His Lys Cys Tyr Leu Ile His Val Pro
50 55 60

Cys Cys Lys Cys Glu Leu Val Val Gln Leu Asp Ile Gln Ser Thr Lys
65 70 75 80

Glu Glu Leu Arg Val Val Gln Gln Leu Leu Met Gly Ala Leu Thr Val
85 90 95

Thr Cys Pro Leu Cys Ala Ser Ser Lys
100 105

<210> 331

<211> 463

<212> PRT

<213> Artificial Sequence

<220>

<223> EF1A2__Homo_sapiens__Q05639

<400> 331

Met Gly Lys Glu Lys Thr His Ile Asn Ile Val Val Ile Gly His Val
1 5 10 15

Asp Ser Gly Lys Ser Thr Thr Thr Gly His Leu Ile Tyr Lys Cys Gly
20 25 30

Gly Ile Asp Lys Arg Thr Ile Glu Lys Phe Glu Lys Glu Ala Ala Glu
35 40 45

Met Gly Lys Gly Ser Phe Lys Tyr Ala Trp Val Leu Asp Lys Leu Lys
50 55 60

Ala Glu Arg Glu Arg Gly Ile Thr Ile Asp Ile Ser Leu Trp Lys Phe
65 70 75 80

ITI-08-PCT_Sequence_Listing_ST25.txt

Glu	Thr	Thr	Lys	Tyr	Tyr	Ile	Thr	Ile	Ile	Asp	Ala	Pro	Gly	His	Arg	
				85					90					95		
Asp	Phe	Ile	Lys	Asn	Met	Ile	Thr	Gly	Thr	Ser	Gln	Ala	Asp	Cys	Ala	
			100					105					110			
Val	Leu	Ile	Val	Ala	Ala	Gly	Val	Gly	Glu	Phe	Glu	Ala	Gly	Ile	Ser	
		115					120					125				
Lys	Asn	Gly	Gln	Thr	Arg	Glu	His	Ala	Leu	Leu	Ala	Tyr	Thr	Leu	Gly	
	130					135					140					
Val	Lys	Gln	Leu	Ile	Val	Gly	Val	Asn	Lys	Met	Asp	Ser	Thr	Glu	Pro	
145					150				155						160	
Ala	Tyr	Ser	Glu	Lys	Arg	Tyr	Asp	Glu	Ile	Val	Lys	Glu	Val	Ser	Ala	
				165					170					175		
Tyr	Ile	Lys	Lys	Ile	Gly	Tyr	Asn	Pro	Ala	Thr	Val	Pro	Phe	Val	Pro	
			180					185					190			
Ile	Ser	Gly	Trp	His	Gly	Asp	Asn	Met	Leu	Glu	Pro	Ser	Pro	Asn	Met	
		195					200					205				
Pro	Trp	Phe	Lys	Gly	Trp	Lys	Val	Glu	Arg	Lys	Glu	Gly	Asn	Ala	Ser	
	210					215					220					
Gly	Val	Ser	Leu	Leu	Glu	Ala	Leu	Asp	Thr	Ile	Leu	Pro	Pro	Thr	Arg	
225					230					235					240	
Pro	Thr	Asp	Lys	Pro	Leu	Arg	Leu	Pro	Leu	Gln	Asp	Val	Tyr	Lys	Ile	
				245					250					255		
Gly	Gly	Ile	Gly	Thr	Val	Pro	Val	Gly	Arg	Val	Glu	Thr	Gly	Ile	Leu	
			260					265					270			
Arg	Pro	Gly	Met	Val	Val	Thr	Phe	Ala	Pro	Val	Asn	Ile	Thr	Thr	Glu	
		275					280					285				
Val	Lys	Ser	Val	Glu	Met	His	His	Glu	Ala	Leu	Ser	Glu	Ala	Leu	Pro	
	290					295					300					
Gly	Asp	Asn	Val	Gly	Phe	Asn	Val	Lys	Asn	Val	Ser	Val	Lys	Asp	Ile	
305					310				315						320	
Arg	Arg	Gly	Asn	Val	Cys	Gly	Asp	Ser	Lys	Ser	Asp	Pro	Pro	Gln	Glu	
				325					330					335		
Ala	Ala	Gln	Phe	Thr	Ser	Gln	Val	Ile	Ile	Leu	Asn	His	Pro	Gly	Gln	
			340					345					350			
Ile	Ser	Ala	Gly	Tyr	Ser	Pro	Val	Ile	Asp	Cys	His	Thr	Ala	His	Ile	

ITI-08-PCT_Sequence_Listing_ST25.txt

355

360

365

Ala Cys Lys Phe Ala Glu Leu Lys Glu Lys Ile Asp Arg Arg Ser Gly
370 375 380

Lys Lys Leu Glu Asp Asn Pro Lys Ser Leu Lys Ser Gly Asp Ala Ala
385 390 395 400

Ile Val Glu Met Val Pro Gly Lys Pro Met Cys Val Glu Ser Phe Ser
405 410 415

Gln Tyr Pro Pro Leu Gly Arg Phe Ala Val Arg Asp Met Arg Gln Thr
420 425 430

Val Ala Val Gly Val Ile Lys Asn Val Glu Lys Lys Ser Gly Gly Ala
435 440 445

Gly Lys Val Thr Lys Ser Ala Gln Lys Ala Gln Lys Ala Gly Lys
450 455 460

<210> 332

<211> 972

<212> PRT

<213> Artificial Sequence

<220>

<223> EFTUD2/m__Homo_sapiens__Q15029

<400> 332

Met Asp Thr Asp Leu Tyr Asp Glu Phe Gly Asn Tyr Ile Gly Pro Glu
1 5 10 15

Leu Asp Ser Asp Glu Asp Asp Asp Glu Leu Gly Arg Glu Thr Lys Asp
20 25 30

Leu Asp Glu Met Asp Asp Asp Asp Asp Asp Asp Val Gly Asp His
35 40 45

Asp Asp Asp His Pro Gly Met Glu Val Val Leu His Glu Asp Lys Lys
50 55 60

Tyr Tyr Pro Thr Ala Glu Glu Val Tyr Gly Pro Glu Val Glu Thr Ile
65 70 75 80

Val Gln Glu Glu Asp Thr Gln Pro Leu Thr Glu Pro Ile Ile Lys Pro
85 90 95

Val Lys Thr Lys Lys Phe Thr Leu Met Glu Gln Thr Leu Pro Val Thr
100 105 110

Val Tyr Glu Met Asp Phe Leu Ala Asp Leu Met Asp Asn Ser Glu Leu

ITI-08-PCT_Sequence_Listing_ST25.txt

115						120						125			
Ile	Arg	Asn	Val	Thr	Leu	Cys	Gly	His	Leu	His	His	Gly	Lys	Thr	Cys
130						135						140			
Phe	Val	Asp	Cys	Leu	Ile	Glu	Gln	Thr	His	Pro	Glu	Ile	Arg	Lys	Arg
145					150					155					160
Tyr	Asp	Gln	Asp	Leu	Cys	Tyr	Thr	Asp	Ile	Leu	Phe	Thr	Glu	Gln	Glu
				165					170					175	
Arg	Gly	Val	Gly	Ile	Lys	Ser	Thr	Pro	Val	Thr	Val	Val	Leu	Pro	Asp
			180					185					190		
Thr	Lys	Gly	Lys	Ser	Tyr	Leu	Phe	Asn	Ile	Met	Asp	Thr	Pro	Gly	His
		195					200					205			
Val	Asn	Phe	Ser	Asp	Glu	Val	Thr	Ala	Gly	Leu	Arg	Ile	Ser	Asp	Gly
	210					215					220				
Val	Val	Leu	Phe	Ile	Asp	Ala	Ala	Glu	Gly	Val	Met	Leu	Asn	Thr	Glu
225					230					235					240
Arg	Leu	Ile	Lys	His	Ala	Val	Gln	Glu	Arg	Leu	Ala	Val	Thr	Val	Cys
				245					250					255	
Ile	Asn	Lys	Ile	Asp	Arg	Leu	Ile	Leu	Glu	Leu	Lys	Leu	Pro	Pro	Thr
			260					265					270		
Asp	Ala	Tyr	Tyr	Lys	Leu	Arg	His	Ile	Val	Asp	Glu	Val	Asn	Gly	Leu
		275					280					285			
Ile	Ser	Met	Tyr	Ser	Thr	Asp	Glu	Asn	Leu	Ile	Leu	Ser	Pro	Leu	Leu
	290					295					300				
Gly	Asn	Val	Cys	Phe	Ser	Ser	Ser	Gln	Tyr	Ser	Ile	Cys	Phe	Thr	Leu
305					310					315					320
Gly	Ser	Phe	Ala	Lys	Ile	Tyr	Ala	Asp	Thr	Phe	Gly	Asp	Ile	Asn	Tyr
				325					330					335	
Gln	Glu	Phe	Ala	Lys	Arg	Leu	Trp	Gly	Asp	Ile	Tyr	Phe	Asn	Pro	Lys
			340					345					350		
Thr	Arg	Lys	Phe	Thr	Lys	Lys	Ala	Pro	Thr	Ser	Ser	Ser	Gln	Arg	Ser
		355					360						365		
Phe	Val	Glu	Phe	Ile	Leu	Glu	Pro	Leu	Tyr	Lys	Ile	Leu	Ala	Gln	Val
	370					375					380				
Val	Gly	Asp	Val	Asp	Thr	Ser	Leu	Pro	Arg	Thr	Leu	Asp	Glu	Leu	Gly
385					390					395					400

ITI-08-PCT_Sequence_Listing_ST25.txt

Ile	His	Leu	Thr	Lys	Glu	Glu	Leu	Lys	Leu	Asn	Ile	Arg	Pro	Leu	Leu	405	410	415	
Arg	Leu	Val	Cys	Lys	Lys	Phe	Phe	Gly	Glu	Phe	Thr	Gly	Phe	Val	Asp	420	425	430	
Met	Cys	Val	Gln	His	Ile	Pro	Ser	Pro	Lys	Val	Gly	Ala	Lys	Pro	Lys	435	440	445	
Ile	Glu	His	Thr	Tyr	Thr	Gly	Gly	Val	Asp	Ser	Asp	Leu	Gly	Glu	Ala	450	455	460	
Met	Ser	Asp	Cys	Asp	Pro	Asp	Gly	Pro	Leu	Met	Cys	His	Thr	Thr	Lys	465	470	475	480
Met	Tyr	Ser	Thr	Asp	Asp	Gly	Val	Gln	Phe	His	Ala	Phe	Gly	Arg	Val	485	490	495	
Leu	Ser	Gly	Thr	Ile	His	Ala	Gly	Gln	Pro	Val	Lys	Val	Leu	Gly	Glu	500	505	510	
Asn	Tyr	Thr	Leu	Glu	Asp	Glu	Glu	Asp	Ser	Gln	Ile	Cys	Thr	Val	Gly	515	520	525	
Arg	Leu	Trp	Ile	Ser	Val	Ala	Arg	Tyr	His	Ile	Glu	Val	Asn	Arg	Val	530	535	540	
Pro	Ala	Gly	Asn	Trp	Val	Leu	Ile	Glu	Gly	Val	Asp	Gln	Pro	Ile	Val	545	550	555	560
Lys	Thr	Ala	Thr	Ile	Thr	Glu	Pro	Arg	Gly	Asn	Glu	Glu	Ala	Gln	Ile	565	570	575	
Phe	Arg	Pro	Leu	Lys	Phe	Asn	Thr	Thr	Ser	Val	Ile	Lys	Ile	Ala	Val	580	585	590	
Glu	Pro	Val	Asn	Pro	Ser	Glu	Leu	Pro	Lys	Met	Leu	Asp	Gly	Leu	Arg	595	600	605	
Lys	Val	Asn	Lys	Ser	Tyr	Pro	Ser	Leu	Thr	Thr	Lys	Val	Glu	Glu	Ser	610	615	620	
Gly	Glu	His	Val	Ile	Leu	Gly	Thr	Gly	Glu	Leu	Tyr	Leu	Asp	Cys	Val	625	630	635	640
Met	His	Asp	Leu	Arg	Lys	Met	Tyr	Ser	Glu	Ile	Asp	Ile	Lys	Val	Ala	645	650	655	
Asp	Pro	Val	Val	Thr	Phe	Cys	Glu	Thr	Val	Val	Glu	Thr	Ser	Ser	Leu	660	665	670	

ITI-08-PCT_Sequence_Listing_ST25.txt

Lys Cys Phe Ala Glu Thr Pro Asn Lys Lys Asn Lys Ile Thr Met Ile
 675 680 685
 Ala Glu Pro Leu Glu Lys Gly Leu Ala Glu Asp Ile Glu Asn Glu Val
 690 695 700
 Val Gln Ile Thr Trp Asn Arg Lys Lys Leu Gly Glu Phe Phe Gln Thr
 705 710 715 720
 Lys Tyr Asp Trp Asp Leu Leu Ala Ala Arg Ser Ile Trp Ala Phe Gly
 725 730 735
 Pro Asp Ala Thr Gly Pro Asn Ile Leu Val Asp Asp Thr Leu Pro Ser
 740 745 750
 Glu Val Asp Lys Ala Leu Leu Gly Ser Val Lys Asp Ser Ile Val Gln
 755 760 765
 Gly Phe Gln Trp Gly Thr Arg Glu Gly Pro Leu Cys Asp Glu Leu Ile
 770 775 780
 Arg Asn Val Lys Phe Lys Ile Leu Asp Ala Val Val Ala Gln Glu Pro
 785 790 795 800
 Leu His Arg Gly Gly Gly Gln Ile Ile Pro Thr Ala Arg Arg Val Val
 805 810 815
 Tyr Ser Ala Phe Leu Met Ala Thr Pro Arg Leu Met Glu Pro Tyr Tyr
 820 825 830
 Phe Val Glu Val Gln Ala Pro Ala Asp Cys Val Ser Ala Val Tyr Thr
 835 840 845
 Val Leu Ala Arg Arg Arg Gly His Val Thr Gln Asp Ala Pro Ile Pro
 850 855 860
 Gly Ser Pro Leu Tyr Thr Ile Lys Ala Phe Ile Pro Ala Ile Asp Ser
 865 870 875 880
 Phe Gly Phe Glu Thr Asp Leu Arg Thr His Thr Gln Gly Gln Ala Phe
 885 890 895
 Ser Leu Ser Val Phe His His Trp Gln Ile Val Pro Gly Asp Pro Leu
 900 905 910
 Asp Lys Ser Ile Val Ile Arg Pro Leu Glu Pro Gln Pro Ala Pro His
 915 920 925
 Leu Ala Arg Glu Phe Met Ile Lys Thr Arg Arg Arg Lys Gly Leu Ser
 930 935 940
 Glu Asp Val Ser Ile Ser Lys Phe Phe Asp Asp Pro Met Leu Leu Glu

ITI-08-PCT_Sequence_Listing_ST25.txt

945 950 955 960

Leu Ala Lys Gln Asp Val Val Leu Asn Tyr Pro Met
965 970

<210> 333
<211> 657
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFR__Homo_sapiens__A0A0B4J1Y5

<400> 333

Met Arg Pro Ser Gly Thr Ala Gly Ala Ala Leu Leu Ala Leu Leu Ala
1 5 10 15

Ala Leu Cys Pro Ala Ser Arg Ala Leu Glu Glu Lys Lys Val Cys Gln
20 25 30

Gly Thr Ser Asn Lys Leu Thr Gln Leu Gly Thr Phe Glu Asp His Phe
35 40 45

Leu Ser Leu Gln Arg Met Phe Asn Asn Cys Glu Val Val Leu Gly Asn
50 55 60

Leu Glu Ile Thr Tyr Val Gln Arg Asn Tyr Asp Leu Ser Phe Leu Lys
65 70 75 80

Thr Ile Gln Glu Val Ala Gly Tyr Val Leu Ile Ala Leu Asn Thr Val
85 90 95

Glu Arg Ile Pro Leu Glu Asn Leu Gln Ile Ile Arg Gly Asn Met Tyr
100 105 110

Tyr Glu Asn Ser Tyr Ala Leu Ala Val Leu Ser Asn Tyr Asp Ala Asn
115 120 125

Lys Thr Gly Leu Lys Glu Leu Pro Met Arg Asn Leu Gln Glu Ile Leu
130 135 140

His Gly Ala Val Arg Phe Ser Asn Asn Pro Ala Leu Cys Asn Val Glu
145 150 155 160

Ser Ile Gln Trp Arg Asp Ile Val Ser Ser Asp Phe Leu Ser Asn Met
165 170 175

Ser Met Asp Phe Gln Asn His Leu Gly Ser Cys Gln Lys Cys Asp Pro
180 185 190

Ser Cys Pro Asn Gly Ser Cys Trp Gly Ala Gly Glu Glu Asn Cys Gln

ITI-08-PCT_Sequence_Listing_ST25.txt

```

195                200                205
Lys Leu Thr Lys Ile Ile Cys Ala Gln Gln Cys Ser Gly Arg Cys Arg
210                215                220
Gly Lys Ser Pro Ser Asp Cys Cys His Asn Gln Cys Ala Ala Gly Cys
225                230                235                240
Thr Gly Pro Arg Glu Ser Asp Cys Leu Val Cys Arg Lys Phe Arg Asp
245                250                255
Glu Ala Thr Cys Lys Asp Thr Cys Pro Pro Leu Met Leu Tyr Asn Pro
260                265                270
Thr Thr Tyr Gln Met Asp Val Asn Pro Glu Gly Lys Tyr Ser Phe Gly
275                280                285
Ala Thr Cys Val Lys Lys Cys Pro Arg Asn Tyr Val Val Thr Asp His
290                295                300
Gly Ser Cys Val Arg Ala Cys Gly Ala Asp Ser Tyr Glu Met Glu Glu
305                310                315                320
Asp Gly Val Arg Lys Cys Lys Lys Cys Glu Gly Pro Cys Arg Lys Val
325                330                335
Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu Ser Ile Asn
340                345                350
Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile Ser Gly Asp
355                360                365
Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe Thr His Thr
370                375                380
Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr Val Lys Glu
385                390                395                400
Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn Arg Thr Asp
405                410                415
Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg Thr Lys Gln
420                425                430
His Gly Gln Phe Ser Leu Ala Val Val Ser Leu Asn Ile Thr Ser Leu
435                440                445
Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val Ile Ile Ser
450                455                460
Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp Lys Lys Leu
465                470                475                480

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn Arg Gly Glu
485 490 495

Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu Cys Ser Pro
500 505 510

Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser Cys Arg Asn
515 520 525

Val Ser Arg Gly Arg Glu Cys Val Asp Lys Cys Asn Leu Leu Glu Gly
530 535 540

Glu Pro Arg Glu Phe Val Glu Asn Ser Glu Cys Ile Gln Cys His Pro
545 550 555 560

Glu Cys Leu Pro Gln Ala Met Asn Ile Thr Cys Thr Gly Arg Gly Pro
565 570 575

Asp Asn Cys Ile Gln Cys Ala His Tyr Ile Asp Gly Pro His Cys Val
580 585 590

Lys Thr Cys Pro Ala Gly Val Met Gly Glu Asn Asn Thr Leu Val Trp
595 600 605

Lys Tyr Ala Asp Ala Gly His Val Cys His Leu Cys His Pro Asn Cys
610 615 620

Thr Tyr Gly Cys Thr Gly Pro Gly Leu Glu Gly Cys Pro Thr Asn Gly
625 630 635 640

Ser Tyr Ile Val Ser His Phe Pro Arg Ser Phe Tyr Lys Met Ser Val
645 650 655

His

<210> 334

<211> 1136

<212> PRT

<213> Artificial Sequence

<220>

<223> EGFR__Homo_sapiens__E7BSV0

<400> 334

Met Arg Pro Ser Gly Thr Ala Gly Ala Ala Leu Leu Ala Leu Leu Ala
1 5 10 15

Ala Leu Cys Pro Ala Ser Arg Ala Leu Glu Glu Lys Lys Val Cys Gln
20 25 30

Gly 35	Thr	Ser	Asn	Lys	Leu	Thr	Gln	Leu	Gly	Thr	Phe	Glu	Asp	His	Phe
Leu 50	Ser	Leu	Gln	Arg	Met	Phe	Asn	Asn	Cys	Glu	Val	Val	Leu	Gly	Asn
Leu 65	Glu	Ile	Thr	Tyr	Val	Gln	Arg	Asn	Tyr	Asp	Leu	Ser	Phe	Leu	Lys
Thr	Ile	Gln	Glu	Val	Ala	Gly	Tyr	Val	Leu	Ile	Ala	Leu	Asn	Thr	Val
Glu	Arg	Ile	Pro	Leu	Glu	Asn	Leu	Gln	Ile	Ile	Arg	Gly	Asn	Met	Tyr
Tyr	Glu	Asn	Ser	Tyr	Ala	Leu	Ala	Val	Leu	Ser	Asn	Tyr	Asp	Ala	Asn
Lys	Thr	Gly	Leu	Lys	Glu	Leu	Pro	Met	Arg	Asn	Leu	Gln	Glu	Ile	Leu
His	Gly	Ala	Val	Arg	Phe	Ser	Asn	Asn	Pro	Ala	Leu	Cys	Asn	Val	Glu
Ser	Ile	Gln	Trp	Arg	Asp	Ile	Val	Ser	Ser	Asp	Phe	Leu	Ser	Asn	Met
Ser	Met	Asp	Phe	Gln	Asn	His	Leu	Gly	Ser	Cys	Gln	Lys	Cys	Asp	Pro
Ser	Cys	Pro	Asn	Gly	Ser	Cys	Trp	Gly	Ala	Gly	Glu	Glu	Asn	Cys	Gln
Lys	Leu	Thr	Lys	Ile	Ile	Cys	Ala	Gln	Gln	Cys	Ser	Gly	Arg	Cys	Arg
Gly	Lys	Ser	Pro	Ser	Asp	Cys	Cys	His	Asn	Gln	Cys	Ala	Ala	Gly	Cys
Thr	Gly	Pro	Arg	Glu	Ser	Asp	Cys	Leu	Val	Cys	Arg	Lys	Phe	Arg	Asp
Glu	Ala	Thr	Cys	Lys	Asp	Thr	Cys	Pro	Pro	Leu	Met	Leu	Tyr	Asn	Pro
Thr	Thr	Tyr	Gln	Met	Asp	Val	Asn	Pro	Glu	Gly	Lys	Tyr	Ser	Phe	Gly
Ala	Thr	Cys	Val	Lys	Lys	Cys	Pro	Arg	Asn	Tyr	Val	Val	Thr	Asp	His
Gly	Ser	Cys	Val	Arg	Ala	Cys	Gly	Ala	Asp	Ser	Tyr	Glu	Met	Glu	Glu

ITI-08-PCT_Sequence_Listing_ST25.txt

```

305          310          315          320
Asp Gly Val Arg Lys Cys Lys Lys Cys Glu Gly Pro Cys Arg Lys Val
          325          330          335

Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu Ser Ile Asn
          340          345          350

Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile Ser Gly Asp
          355          360          365

Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe Thr His Thr
          370          375          380

Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr Val Lys Glu
385          390          395          400

Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn Arg Thr Asp
          405          410          415

Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg Thr Lys Gln
          420          425          430

His Gly Gln Phe Ser Leu Ala Val Val Ser Leu Asn Ile Thr Ser Leu
          435          440          445

Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val Ile Ile Ser
          450          455          460

Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp Lys Lys Leu
465          470          475          480

Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn Arg Gly Glu
          485          490          495

Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu Cys Ser Pro
          500          505          510

Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser Cys Arg Asn
          515          520          525

Val Ser Arg Gly Arg Glu Cys Val Asp Lys Cys Asn Leu Leu Glu Gly
          530          535          540

Glu Pro Arg Glu Phe Val Glu Asn Ser Glu Cys Ile Gln Cys His Pro
545          550          555          560

Glu Cys Leu Pro Gln Ala Met Asn Ile Thr Cys Thr Gly Arg Gly Pro
          565          570          575

Asp Asn Cys Ile Gln Cys Ala His Tyr Ile Asp Gly Pro His Cys Val
          580          585          590

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Lys Thr Cys Pro Ala Gly Val Met Gly Glu Asn Asn Thr Leu Val Trp
 595 600 605
 Lys Tyr Ala Asp Ala Gly His Val Cys His Leu Cys His Pro Asn Cys
 610 615 620
 Thr Tyr Gly Cys Thr Gly Pro Gly Leu Glu Gly Cys Pro Thr Asn Gly
 625 630 635 640
 Pro Lys Ile Pro Ser Ile Ala Thr Gly Met Val Gly Ala Leu Leu Leu
 645 650 655
 Leu Leu Val Val Ala Leu Gly Ile Gly Leu Phe Met Arg Arg Arg His
 660 665 670
 Ile Val Arg Lys Arg Thr Leu Arg Arg Leu Leu Gln Glu Arg Glu Leu
 675 680 685
 Val Glu Pro Leu Thr Pro Ser Gly Glu Ala Pro Asn Gln Ala Leu Leu
 690 695 700
 Arg Ile Leu Lys Glu Thr Glu Phe Lys Lys Ile Lys Val Leu Gly Ser
 705 710 715 720
 Gly Ala Phe Gly Thr Val Tyr Lys Gly Leu Trp Ile Pro Glu Gly Glu
 725 730 735
 Lys Val Lys Ile Pro Val Ala Ile Lys Glu Leu Arg Glu Ala Thr Ser
 740 745 750
 Pro Lys Ala Asn Lys Glu Ile Leu Asp Glu Ala Tyr Val Met Ala Ser
 755 760 765
 Val Asp Asn Pro His Val Cys Arg Leu Leu Gly Ile Cys Leu Thr Ser
 770 775 780
 Thr Val Gln Leu Ile Thr Gln Leu Met Pro Phe Gly Cys Leu Leu Asp
 785 790 795 800
 Tyr Val Arg Glu His Lys Asp Asn Ile Gly Ser Gln Tyr Leu Leu Asn
 805 810 815
 Trp Cys Val Gln Ile Ala Lys Gly Met Asn Tyr Leu Glu Asp Arg Arg
 820 825 830
 Leu Val His Arg Asp Leu Ala Ala Arg Asn Val Leu Val Lys Thr Pro
 835 840 845
 Gln His Val Lys Ile Thr Asp Phe Gly Leu Ala Lys Leu Leu Gly Ala
 850 855 860

ITI-08-PCT_Sequence_Listing_ST25.txt

Glu Glu Lys Glu Tyr His Ala Glu Gly Gly Lys Val Pro Ile Lys Trp
 865 870 875 880
 Met Ala Leu Glu Ser Ile Leu His Arg Ile Tyr Thr His Gln Ser Asp
 885 890 895
 Val Trp Ser Tyr Gly Val Thr Val Trp Glu Leu Met Thr Phe Gly Ser
 900 905 910
 Lys Pro Tyr Asp Gly Ile Pro Ala Ser Glu Ile Ser Ser Ile Leu Glu
 915 920 925
 Lys Gly Glu Arg Leu Pro Gln Pro Pro Ile Cys Thr Ile Asp Val Tyr
 930 935 940
 Met Ile Met Val Lys Cys Trp Met Ile Asp Ala Asp Ser Arg Pro Lys
 945 950 955 960
 Phe Arg Glu Leu Ile Ile Glu Phe Ser Lys Met Ala Arg Asp Pro Gln
 965 970 975
 Arg Tyr Leu Val Ile Gln Gly Asp Glu Arg Met His Leu Pro Ser Pro
 980 985 990
 Thr Asp Ser Asn Phe Tyr Arg Ala Leu Met Asp Glu Glu Asp Met Asp
 995 1000 1005
 Asp Val Val Asp Ala Asp Glu Tyr Leu Ile Pro Gln Gln Gly Phe
 1010 1015 1020
 Phe Ser Ser Pro Ser Thr Ser Arg Thr Pro Leu Leu Ser Ser Leu
 1025 1030 1035
 Ser Ala Thr Ser Asn Asn Ser Thr Val Ala Cys Ile Asp Arg Asn
 1040 1045 1050
 Gly Leu Gln Ser Cys Pro Ile Lys Glu Asp Ser Phe Leu Gln Arg
 1055 1060 1065
 Tyr Ser Ser Asp Pro Thr Gly Ala Leu Thr Glu Asp Ser Ile Asp
 1070 1075 1080
 Asp Thr Phe Leu Pro Val Pro Gly Glu Trp Leu Val Trp Lys Gln
 1085 1090 1095
 Ser Cys Ser Ser Thr Ser Ser Thr His Ser Ala Ala Ala Ser Leu
 1100 1105 1110
 Gln Cys Pro Ser Gln Val Leu Pro Pro Ala Ser Pro Glu Gly Glu
 1115 1120 1125
 Thr Val Ala Asp Leu Gln Thr Gln

ITI-08-PCT_Sequence_Listing_ST25.txt

1130

1135

<210> 335
<211> 49
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFR__Homo_sapiens__L0R6G1

<400> 335

Met Cys Ala Thr Cys Ala Ile Gln Thr Ala Pro Thr Gly Pro Asn Lys
1 5 10 15

Ser Ser Leu Ser Asp Phe Ser Leu Pro Leu Lys Leu His Phe Leu Ser
20 25 30

Thr Ile Ser Ile Ser Pro Phe Ala Ser Asn Lys Val Leu Thr Leu Phe
35 40 45

Ile

<210> 336
<211> 405
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFR__Homo_sapiens__P00533-2

<400> 336

Met Arg Pro Ser Gly Thr Ala Gly Ala Ala Leu Leu Ala Leu Ala
1 5 10 15

Ala Leu Cys Pro Ala Ser Arg Ala Leu Glu Glu Lys Lys Val Cys Gln
20 25 30

Gly Thr Ser Asn Lys Leu Thr Gln Leu Gly Thr Phe Glu Asp His Phe
35 40 45

Leu Ser Leu Gln Arg Met Phe Asn Asn Cys Glu Val Val Leu Gly Asn
50 55 60

Leu Glu Ile Thr Tyr Val Gln Arg Asn Tyr Asp Leu Ser Phe Leu Lys
65 70 75 80

Thr Ile Gln Glu Val Ala Gly Tyr Val Leu Ile Ala Leu Asn Thr Val
85 90 95

Glu Arg Ile Pro Leu Glu Asn Leu Gln Ile Ile Arg Gly Asn Met Tyr

ITI-08-PCT_Sequence_Listing_ST25.txt

100	105	110																	
Tyr	Glu	Asn	Ser	Tyr	Ala	Leu	Ala	Val	Leu	Ser	Asn	Tyr	Asp	Ala	Asn				
		115					120					125							
Lys	Thr	Gly	Leu	Lys	Glu	Leu	Pro	Met	Arg	Asn	Leu	Gln	Glu	Ile	Leu				
	130					135					140								
His	Gly	Ala	Val	Arg	Phe	Ser	Asn	Asn	Pro	Ala	Leu	Cys	Asn	Val	Glu				
145					150					155					160				
Ser	Ile	Gln	Trp	Arg	Asp	Ile	Val	Ser	Ser	Asp	Phe	Leu	Ser	Asn	Met				
				165					170					175					
Ser	Met	Asp	Phe	Gln	Asn	His	Leu	Gly	Ser	Cys	Gln	Lys	Cys	Asp	Pro				
			180					185					190						
Ser	Cys	Pro	Asn	Gly	Ser	Cys	Trp	Gly	Ala	Gly	Glu	Glu	Asn	Cys	Gln				
		195					200					205							
Lys	Leu	Thr	Lys	Ile	Ile	Cys	Ala	Gln	Gln	Cys	Ser	Gly	Arg	Cys	Arg				
	210					215					220								
Gly	Lys	Ser	Pro	Ser	Asp	Cys	Cys	His	Asn	Gln	Cys	Ala	Ala	Gly	Cys				
225					230					235					240				
Thr	Gly	Pro	Arg	Glu	Ser	Asp	Cys	Leu	Val	Cys	Arg	Lys	Phe	Arg	Asp				
				245					250					255					
Glu	Ala	Thr	Cys	Lys	Asp	Thr	Cys	Pro	Pro	Leu	Met	Leu	Tyr	Asn	Pro				
			260					265					270						
Thr	Thr	Tyr	Gln	Met	Asp	Val	Asn	Pro	Glu	Gly	Lys	Tyr	Ser	Phe	Gly				
		275					280					285							
Ala	Thr	Cys	Val	Lys	Lys	Cys	Pro	Arg	Asn	Tyr	Val	Val	Thr	Asp	His				
	290					295					300								
Gly	Ser	Cys	Val	Arg	Ala	Cys	Gly	Ala	Asp	Ser	Tyr	Glu	Met	Glu	Glu				
305					310				315					320					
Asp	Gly	Val	Arg	Lys	Cys	Lys	Lys	Cys	Glu	Gly	Pro	Cys	Arg	Lys	Val				
				325					330					335					
Cys	Asn	Gly	Ile	Gly	Ile	Gly	Glu	Phe	Lys	Asp	Ser	Leu	Ser	Ile	Asn				
			340				345						350						
Ala	Thr	Asn	Ile	Lys	His	Phe	Lys	Asn	Cys	Thr	Ser	Ile	Ser	Gly	Asp				
		355					360					365							
Leu	His	Ile	Leu	Pro	Val	Ala	Phe	Arg	Gly	Asp	Ser	Phe	Thr	His	Thr				
	370					375					380								

ITI-08-PCT_Sequence_Listing_ST25.txt

Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr Val Lys Glu
385 390 395 400

Ile Thr Gly Leu Ser
405

<210> 337
<211> 1210
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFR__Homo_sapiens__P00533

<400> 337

Met Arg Pro Ser Gly Thr Ala Gly Ala Ala Leu Leu Ala Leu Leu Ala
1 5 10 15

Ala Leu Cys Pro Ala Ser Arg Ala Leu Glu Glu Lys Lys Val Cys Gln
20 25 30

Gly Thr Ser Asn Lys Leu Thr Gln Leu Gly Thr Phe Glu Asp His Phe
35 40 45

Leu Ser Leu Gln Arg Met Phe Asn Asn Cys Glu Val Val Leu Gly Asn
50 55 60

Leu Glu Ile Thr Tyr Val Gln Arg Asn Tyr Asp Leu Ser Phe Leu Lys
65 70 75 80

Thr Ile Gln Glu Val Ala Gly Tyr Val Leu Ile Ala Leu Asn Thr Val
85 90 95

Glu Arg Ile Pro Leu Glu Asn Leu Gln Ile Ile Arg Gly Asn Met Tyr
100 105 110

Tyr Glu Asn Ser Tyr Ala Leu Ala Val Leu Ser Asn Tyr Asp Ala Asn
115 120 125

Lys Thr Gly Leu Lys Glu Leu Pro Met Arg Asn Leu Gln Glu Ile Leu
130 135 140

His Gly Ala Val Arg Phe Ser Asn Asn Pro Ala Leu Cys Asn Val Glu
145 150 155 160

Ser Ile Gln Trp Arg Asp Ile Val Ser Ser Asp Phe Leu Ser Asn Met
165 170 175

Ser Met Asp Phe Gln Asn His Leu Gly Ser Cys Gln Lys Cys Asp Pro
180 185 190

ITI-08-PCT_Sequence_Listing_ST25.txt

Ser	Cys	Pro	Asn	Gly	Ser	Cys	Trp	Gly	Ala	Gly	Glu	Glu	Asn	Cys	Gln	195	200	205
Lys	Leu	Thr	Lys	Ile	Ile	Cys	Ala	Gln	Gln	Cys	Ser	Gly	Arg	Cys	Arg	210	215	220
Gly	Lys	Ser	Pro	Ser	Asp	Cys	Cys	His	Asn	Gln	Cys	Ala	Ala	Gly	Cys	225	230	235
Thr	Gly	Pro	Arg	Glu	Ser	Asp	Cys	Leu	Val	Cys	Arg	Lys	Phe	Arg	Asp	245	250	255
Glu	Ala	Thr	Cys	Lys	Asp	Thr	Cys	Pro	Pro	Leu	Met	Leu	Tyr	Asn	Pro	260	265	270
Thr	Thr	Tyr	Gln	Met	Asp	Val	Asn	Pro	Glu	Gly	Lys	Tyr	Ser	Phe	Gly	275	280	285
Ala	Thr	Cys	Val	Lys	Lys	Cys	Pro	Arg	Asn	Tyr	Val	Val	Thr	Asp	His	290	295	300
Gly	Ser	Cys	Val	Arg	Ala	Cys	Gly	Ala	Asp	Ser	Tyr	Glu	Met	Glu	Glu	305	310	315
Asp	Gly	Val	Arg	Lys	Cys	Lys	Lys	Cys	Glu	Gly	Pro	Cys	Arg	Lys	Val	325	330	335
Cys	Asn	Gly	Ile	Gly	Ile	Gly	Glu	Phe	Lys	Asp	Ser	Leu	Ser	Ile	Asn	340	345	350
Ala	Thr	Asn	Ile	Lys	His	Phe	Lys	Asn	Cys	Thr	Ser	Ile	Ser	Gly	Asp	355	360	365
Leu	His	Ile	Leu	Pro	Val	Ala	Phe	Arg	Gly	Asp	Ser	Phe	Thr	His	Thr	370	375	380
Pro	Pro	Leu	Asp	Pro	Gln	Glu	Leu	Asp	Ile	Leu	Lys	Thr	Val	Lys	Glu	385	390	395
Ile	Thr	Gly	Phe	Leu	Leu	Ile	Gln	Ala	Trp	Pro	Glu	Asn	Arg	Thr	Asp	405	410	415
Leu	His	Ala	Phe	Glu	Asn	Leu	Glu	Ile	Ile	Arg	Gly	Arg	Thr	Lys	Gln	420	425	430
His	Gly	Gln	Phe	Ser	Leu	Ala	Val	Val	Ser	Leu	Asn	Ile	Thr	Ser	Leu	435	440	445
Gly	Leu	Arg	Ser	Leu	Lys	Glu	Ile	Ser	Asp	Gly	Asp	Val	Ile	Ile	Ser	450	455	460

ITI-08-PCT_Sequence_Listing_ST25.txt

Gly	Asn	Lys	Asn	Leu	Cys	Tyr	Ala	Asn	Thr	Ile	Asn	Trp	Lys	Lys	Leu	465	470	475	480
Phe	Gly	Thr	Ser	Gly	Gln	Lys	Thr	Lys	Ile	Ile	Ser	Asn	Arg	Gly	Glu	485	490	495	
Asn	Ser	Cys	Lys	Ala	Thr	Gly	Gln	Val	Cys	His	Ala	Leu	Cys	Ser	Pro	500	505	510	
Glu	Gly	Cys	Trp	Gly	Pro	Glu	Pro	Arg	Asp	Cys	Val	Ser	Cys	Arg	Asn	515	520	525	
Val	Ser	Arg	Gly	Arg	Glu	Cys	Val	Asp	Lys	Cys	Asn	Leu	Leu	Glu	Gly	530	535	540	
Glu	Pro	Arg	Glu	Phe	Val	Glu	Asn	Ser	Glu	Cys	Ile	Gln	Cys	His	Pro	545	550	555	560
Glu	Cys	Leu	Pro	Gln	Ala	Met	Asn	Ile	Thr	Cys	Thr	Gly	Arg	Gly	Pro	565	570	575	
Asp	Asn	Cys	Ile	Gln	Cys	Ala	His	Tyr	Ile	Asp	Gly	Pro	His	Cys	Val	580	585	590	
Lys	Thr	Cys	Pro	Ala	Gly	Val	Met	Gly	Glu	Asn	Asn	Thr	Leu	Val	Trp	595	600	605	
Lys	Tyr	Ala	Asp	Ala	Gly	His	Val	Cys	His	Leu	Cys	His	Pro	Asn	Cys	610	615	620	
Thr	Tyr	Gly	Cys	Thr	Gly	Pro	Gly	Leu	Glu	Gly	Cys	Pro	Thr	Asn	Gly	625	630	635	640
Pro	Lys	Ile	Pro	Ser	Ile	Ala	Thr	Gly	Met	Val	Gly	Ala	Leu	Leu	Leu	645	650	655	
Leu	Leu	Val	Val	Ala	Leu	Gly	Ile	Gly	Leu	Phe	Met	Arg	Arg	Arg	His	660	665	670	
Ile	Val	Arg	Lys	Arg	Thr	Leu	Arg	Arg	Leu	Leu	Gln	Glu	Arg	Glu	Leu	675	680	685	
Val	Glu	Pro	Leu	Thr	Pro	Ser	Gly	Glu	Ala	Pro	Asn	Gln	Ala	Leu	Leu	690	695	700	
Arg	Ile	Leu	Lys	Glu	Thr	Glu	Phe	Lys	Lys	Ile	Lys	Val	Leu	Gly	Ser	705	710	715	720
Gly	Ala	Phe	Gly	Thr	Val	Tyr	Lys	Gly	Leu	Trp	Ile	Pro	Glu	Gly	Glu	725	730	735	
Lys	Val	Lys	Ile	Pro	Val	Ala	Ile	Lys	Glu	Leu	Arg	Glu	Ala	Thr	Ser				

ITI-08-PCT_Sequence_Listing_ST25.txt

```

740                               745                               750
Pro Lys Ala Asn Lys Glu Ile Leu Asp Glu Ala Tyr Val Met Ala Ser
755                               760                               765
Val Asp Asn Pro His Val Cys Arg Leu Leu Gly Ile Cys Leu Thr Ser
770                               775                               780
Thr Val Gln Leu Ile Thr Gln Leu Met Pro Phe Gly Cys Leu Leu Asp
785                               790                               795                               800
Tyr Val Arg Glu His Lys Asp Asn Ile Gly Ser Gln Tyr Leu Leu Asn
805                               810                               815
Trp Cys Val Gln Ile Ala Lys Gly Met Asn Tyr Leu Glu Asp Arg Arg
820                               825                               830
Leu Val His Arg Asp Leu Ala Ala Arg Asn Val Leu Val Lys Thr Pro
835                               840                               845
Gln His Val Lys Ile Thr Asp Phe Gly Leu Ala Lys Leu Leu Gly Ala
850                               855                               860
Glu Glu Lys Glu Tyr His Ala Glu Gly Gly Lys Val Pro Ile Lys Trp
865                               870                               875                               880
Met Ala Leu Glu Ser Ile Leu His Arg Ile Tyr Thr His Gln Ser Asp
885                               890                               895
Val Trp Ser Tyr Gly Val Thr Val Trp Glu Leu Met Thr Phe Gly Ser
900                               905                               910
Lys Pro Tyr Asp Gly Ile Pro Ala Ser Glu Ile Ser Ser Ile Leu Glu
915                               920                               925
Lys Gly Glu Arg Leu Pro Gln Pro Pro Ile Cys Thr Ile Asp Val Tyr
930                               935                               940
Met Ile Met Val Lys Cys Trp Met Ile Asp Ala Asp Ser Arg Pro Lys
945                               950                               955                               960
Phe Arg Glu Leu Ile Ile Glu Phe Ser Lys Met Ala Arg Asp Pro Gln
965                               970                               975
Arg Tyr Leu Val Ile Gln Gly Asp Glu Arg Met His Leu Pro Ser Pro
980                               985                               990
Thr Asp Ser Asn Phe Tyr Arg Ala Leu Met Asp Glu Glu Asp Met Asp
995                               1000                               1005
Asp Val Val Asp Ala Asp Glu Tyr Leu Ile Pro Gln Gln Gly Phe
1010                               1015                               1020

```

ITI-08-PCT_Sequence_Listing_ST25.txt

```

Phe Ser  Ser Pro Ser Thr Ser  Arg Thr Pro Leu Leu  Ser Ser Leu
 1025                      1030                      1035

Ser Ala  Thr Ser Asn Asn Ser  Thr Val Ala Cys Ile  Asp Arg Asn
 1040                      1045                      1050

Gly Leu  Gln Ser Cys Pro Ile  Lys Glu Asp Ser Phe  Leu Gln Arg
 1055                      1060                      1065

Tyr Ser  Ser Asp Pro Thr Gly  Ala Leu Thr Glu Asp  Ser Ile Asp
 1070                      1075                      1080

Asp Thr  Phe Leu Pro Val Pro  Glu Tyr Ile Asn Gln  Ser Val Pro
 1085                      1090                      1095

Lys Arg  Pro Ala Gly Ser Val  Gln Asn Pro Val Tyr  His Asn Gln
 1100                      1105                      1110

Pro Leu  Asn Pro Ala Pro Ser  Arg Asp Pro His Tyr  Gln Asp Pro
 1115                      1120                      1125

His Ser  Thr Ala Val Gly Asn  Pro Glu Tyr Leu Asn  Thr Val Gln
 1130                      1135                      1140

Pro Thr  Cys Val Asn Ser Thr  Phe Asp Ser Pro Ala  His Trp Ala
 1145                      1150                      1155

Gln Lys  Gly Ser His Gln Ile  Ser Leu Asp Asn Pro  Asp Tyr Gln
 1160                      1165                      1170

Gln Asp  Phe Phe Pro Lys Glu  Ala Lys Pro Asn Gly  Ile Phe Lys
 1175                      1180                      1185

Gly Ser  Thr Ala Glu Asn Ala  Glu Tyr Leu Arg Val  Ala Pro Gln
 1190                      1195                      1200

Ser Ser  Glu Phe Ile Gly Ala
 1205                      1210

```

<210> 338

<211> 464

<212> PRT

<213> Artificial Sequence

<220>

<223> EGFR__Homo_sapiens__Q147T7

<400> 338

```

Met Ala Ala Glu Asp Val Ile Ile Cys Ala Gln Gln Cys Ser Gly Arg
 1           5           10          15

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Cys	Arg	Gly	Lys	Ser	Pro	Ser	Asp	Cys	Cys	His	Asn	Gln	Cys	Ala	Ala		
			20					25					30				
Gly	Cys	Thr	Gly	Pro	Arg	Glu	Ser	Asp	Cys	Leu	Val	Cys	Arg	Lys	Phe		
		35					40					45					
Arg	Asp	Glu	Ala	Thr	Cys	Lys	Asp	Thr	Cys	Pro	Pro	Leu	Met	Leu	Tyr		
	50					55					60						
Asn	Pro	Thr	Thr	Tyr	Gln	Met	Asp	Val	Asn	Pro	Glu	Gly	Lys	Tyr	Ser		
65					70				75						80		
Phe	Gly	Ala	Thr	Cys	Val	Lys	Lys	Cys	Pro	Arg	Asn	Tyr	Val	Val	Thr		
				85					90					95			
Asp	His	Gly	Ser	Cys	Val	Arg	Ala	Cys	Gly	Ala	Asp	Ser	Tyr	Glu	Met		
			100					105					110				
Glu	Glu	Asp	Gly	Val	Arg	Lys	Cys	Lys	Lys	Cys	Glu	Gly	Pro	Cys	Arg		
		115					120					125					
Lys	Val	Cys	Asn	Gly	Ile	Gly	Ile	Gly	Glu	Phe	Lys	Asp	Ser	Leu	Ser		
	130					135					140						
Ile	Asn	Ala	Thr	Asn	Ile	Lys	His	Phe	Lys	Asn	Cys	Thr	Ser	Ile	Ser		
145					150				155						160		
Gly	Asp	Leu	His	Ile	Leu	Pro	Val	Ala	Phe	Arg	Gly	Asp	Ser	Phe	Thr		
				165					170					175			
His	Thr	Pro	Pro	Leu	Asp	Pro	Gln	Glu	Leu	Asp	Ile	Leu	Lys	Thr	Val		
			180					185					190				
Lys	Glu	Ile	Thr	Gly	Phe	Leu	Leu	Ile	Gln	Ala	Trp	Pro	Glu	Asn	Arg		
		195					200					205					
Thr	Asp	Leu	His	Ala	Phe	Glu	Asn	Leu	Glu	Ile	Ile	Arg	Gly	Arg	Thr		
	210					215					220						
Lys	Gln	His	Gly	Gln	Phe	Ser	Leu	Ala	Val	Val	Ser	Leu	Asn	Ile	Thr		
225					230					235					240		
Ser	Leu	Gly	Leu	Arg	Ser	Leu	Lys	Glu	Ile	Ser	Asp	Gly	Asp	Val	Ile		
				245					250					255			
Ile	Ser	Gly	Asn	Lys	Asn	Leu	Cys	Tyr	Ala	Asn	Thr	Ile	Asn	Trp	Lys		
			260					265					270				
Lys	Leu	Phe	Gly	Thr	Ser	Gly	Gln	Lys	Thr	Lys	Ile	Ile	Ser	Asn	Arg		
		275					280					285					

ITI-08-PCT_Sequence_Listing_ST25.txt

Gly Glu Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu Cys
290 295 300

Ser Pro Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser Cys
305 310 315 320

Arg Asn Val Ser Arg Gly Arg Glu Cys Val Asp Lys Cys Asn Leu Leu
325 330 335

Glu Gly Glu Pro Arg Glu Phe Val Glu Asn Ser Glu Cys Ile Gln Cys
340 345 350

His Pro Glu Cys Leu Pro Gln Ala Met Asn Ile Thr Cys Thr Gly Arg
355 360 365

Gly Pro Asp Asn Cys Ile Gln Cys Ala His Tyr Ile Asp Gly Pro His
370 375 380

Cys Val Lys Thr Cys Pro Ala Gly Val Met Gly Glu Asn Asn Thr Leu
385 390 395 400

Val Trp Lys Tyr Ala Asp Ala Gly His Val Cys His Leu Cys His Pro
405 410 415

Asn Cys Thr Tyr Gly Cys Thr Gly Pro Gly Leu Glu Gly Cys Pro Thr
420 425 430

Asn Gly Pro Lys Ile Pro Ser Ile Ala Thr Gly Met Val Gly Ala Leu
435 440 445

Leu Leu Leu Leu Val Val Ala Leu Gly Ile Gly Pro Leu His Gly Arg
450 455 460

<210> 339

<211> 1091

<212> PRT

<213> Artificial Sequence

<220>

<223> EGFR__Homo_sapiens__Q504U8

<400> 339

Met Arg Pro Ser Gly Thr Ala Gly Ala Ala Leu Leu Ala Leu Leu Ala
1 5 10 15

Ala Leu Cys Pro Ala Ser Arg Ala Leu Glu Glu Lys Lys Val Cys Gln
20 25 30

Gly Thr Ser Asn Lys Leu Thr Gln Leu Gly Thr Phe Glu Asp His Phe
35 40 45

ITI-08-PCT_Sequence_Listing_ST25.txt

```

Leu Ser Leu Gln Arg Met Phe Asn Asn Cys Glu Val Val Leu Gly Asn
 50                      55                      60

Leu Glu Ile Thr Tyr Val Gln Arg Asn Tyr Asp Leu Ser Phe Leu Lys
65                      70                      75                      80

Thr Ile Gln Glu Val Ala Gly Tyr Val Leu Ile Ala Leu Asn Thr Val
                        85                      90                      95

Glu Arg Ile Pro Leu Glu Asn Leu Gln Ile Ile Arg Gly Asn Met Tyr
                        100                    105                    110

Tyr Glu Asn Ser Tyr Ala Leu Ala Val Leu Ser Asn Tyr Asp Ala Asn
      115                    120                    125

Lys Thr Gly Leu Lys Glu Leu Pro Met Arg Asn Leu Gln Gly Gln Lys
130                      135                      140

Cys Asp Pro Ser Cys Pro Asn Gly Ser Cys Trp Gly Ala Gly Glu Glu
145                      150                    155                      160

Asn Cys Gln Lys Leu Thr Lys Ile Ile Cys Ala Gln Gln Cys Ser Gly
                        165                    170                    175

Arg Cys Arg Gly Lys Ser Pro Ser Asp Cys Cys His Asn Gln Cys Ala
      180                    185                    190

Ala Gly Cys Thr Gly Pro Arg Glu Ser Asp Cys Leu Val Cys Arg Lys
      195                    200                    205

Phe Arg Asp Glu Ala Thr Cys Lys Asp Thr Cys Pro Pro Leu Met Leu
210                      215                    220

Tyr Asn Pro Thr Thr Tyr Gln Met Asp Val Asn Pro Glu Gly Lys Tyr
225                      230                    235                    240

Ser Phe Gly Ala Thr Cys Val Lys Lys Cys Pro Arg Asn Tyr Val Val
                        245                    250                    255

Thr Asp His Gly Ser Cys Val Arg Ala Cys Gly Ala Asp Ser Tyr Glu
      260                    265                    270

Met Glu Glu Asp Gly Val Arg Lys Cys Lys Lys Cys Glu Gly Pro Cys
      275                    280                    285

Arg Lys Val Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu
290                      295                    300

Ser Ile Asn Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile
305                      310                    315                    320

Ser Gly Asp Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe

```


ITI-08-PCT_Sequence_Listing_ST25.txt

325 330 335

Thr His Thr Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr
340 345 350

Val Lys Glu Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn
355 360 365

Arg Thr Asp Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg
370 375 380

Thr Lys Gln His Gly Gln Phe Ser Leu Ala Val Val Ser Leu Asn Ile
385 390 395 400

Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val
405 410 415

Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp
420 425 430

Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn
435 440 445

Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu
450 455 460

Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser
465 470 475 480

Cys Arg Asn Val Ser Arg Gly Arg Glu Cys Val Asp Lys Cys Asn Leu
485 490 495

Leu Glu Gly Glu Pro Arg Glu Phe Val Glu Asn Ser Glu Cys Ile Gln
500 505 510

Cys His Pro Glu Cys Leu Pro Gln Ala Met Asn Ile Thr Cys Thr Gly
515 520 525

Arg Gly Pro Asp Asn Cys Ile Gln Cys Ala His Tyr Ile Asp Gly Pro
530 535 540

His Cys Val Lys Thr Cys Pro Ala Gly Val Met Gly Glu Asn Asn Thr
545 550 555 560

Leu Val Trp Lys Tyr Ala Asp Ala Gly His Val Cys His Leu Cys His
565 570 575

Pro Asn Cys Thr Tyr Gly Cys Thr Gly Pro Gly Leu Glu Gly Cys Pro
580 585 590

Thr Asn Gly Pro Lys Ile Pro Ser Ile Ala Thr Gly Met Val Gly Ala
595 600 605

ITI-08-PCT_Sequence_Listing_ST25.txt

```

Leu Leu Leu Leu Leu Val Val Ala Leu Gly Ile Gly Leu Phe Met Arg
 610                      615                      620

Arg Arg His Ile Val Arg Lys Arg Thr Leu Arg Arg Leu Leu Gln Glu
625                      630                      635                      640

Arg Glu Leu Val Glu Pro Leu Thr Pro Ser Gly Glu Ala Pro Asn Gln
                      645                      650                      655

Ala Leu Leu Arg Ile Leu Lys Glu Thr Glu Phe Lys Lys Ile Lys Val
                      660                      665                      670

Leu Gly Ser Gly Ala Phe Gly Thr Val Tyr Lys Gly Leu Trp Ile Pro
 675                      680                      685

Glu Gly Glu Lys Val Lys Ile Pro Val Ala Ile Lys Glu Leu Arg Glu
690                      695                      700

Ala Thr Ser Pro Lys Ala Asn Lys Glu Ile Leu Asp Glu Ala Tyr Val
705                      710                      715                      720

Met Ala Ser Val Asp Asn Pro His Val Cys Arg Leu Leu Gly Ile Cys
                      725                      730                      735

Leu Thr Ser Thr Val Gln Leu Ile Thr Gln Leu Met Pro Phe Gly Cys
 740                      745                      750

Leu Leu Asp Tyr Val Arg Glu His Lys Asp Asn Ile Gly Ser Gln Tyr
755                      760                      765

Leu Leu Asn Trp Cys Val Gln Ile Ala Lys Gly Met Asn Tyr Leu Glu
770                      775                      780

Asp Arg Arg Leu Val His Arg Asp Leu Ala Ala Arg Asn Val Leu Val
785                      790                      795                      800

Lys Thr Pro Gln His Val Lys Ile Thr Asp Phe Gly Leu Ala Lys Leu
                      805                      810                      815

Leu Gly Ala Glu Glu Lys Glu Tyr His Ala Glu Gly Gly Lys Val Pro
 820                      825                      830

Ile Lys Trp Met Ala Leu Glu Ser Ile Leu His Arg Ile Tyr Thr His
835                      840                      845

Gln Ser Asp Val Trp Ser Tyr Gly Val Thr Val Trp Glu Leu Met Thr
850                      855                      860

Phe Gly Ser Lys Pro Tyr Asp Gly Ile Pro Ala Ser Glu Ile Ser Ser
865                      870                      875                      880

```

ITI-08-PCT_Sequence_Listing_ST25.txt

```

Ile Leu Glu Lys Gly Glu Arg Leu Pro Gln Pro Pro Ile Cys Thr Ile
      885                      890                      895

Asp Val Tyr Met Ile Met Val Lys Cys Trp Met Ile Asp Ala Asp Ser
      900                      905                      910

Arg Pro Lys Phe Arg Glu Leu Ile Ile Glu Phe Ser Lys Met Ala Arg
      915                      920                      925

Asp Pro Gln Arg Tyr Leu Val Ile Gln Gly Asp Glu Arg Met His Leu
      930                      935                      940

Pro Ser Pro Thr Asp Ser Asn Phe Tyr Arg Ala Leu Met Asp Glu Glu
  945                      950                      955                      960

Asp Met Asp Asp Val Val Asp Ala Asp Glu Tyr Leu Ile Pro Gln Gln
      965                      970                      975

Gly Phe Phe Ser Ser Pro Ser Thr Ser Arg Thr Pro Leu Leu Ser Ser
      980                      985                      990

Leu Ser Ala Thr Ser Asn Asn Ser Thr Val Ala Cys Ile Asp Arg Asn
      995                      1000                     1005

Gly Leu Gln Ser Cys Pro Ile Lys Glu Asp Ser Phe Leu Gln Arg
  1010                      1015                      1020

Tyr Ser Ser Asp Pro Thr Gly Ala Leu Thr Glu Asp Ser Ile Asp
  1025                      1030                      1035

Asp Thr Phe Leu Pro Val Pro Gly Glu Trp Leu Val Trp Lys Gln
  1040                      1045                      1050

Ser Cys Ser Ser Thr Ser Ser Thr His Ser Ala Ala Ala Ser Leu
  1055                      1060                      1065

Gln Cys Pro Ser Gln Val Leu Pro Pro Ala Ser Pro Glu Gly Glu
  1070                      1075                      1080

Thr Val Ala Asp Leu Gln Thr Gln
  1085                      1090

<210> 340
<211> 71
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFR__Homo_sapiens__Q8NDU8

<400> 340

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Met Arg Pro Ser Gly Thr Ala Gly Ala Ala Leu Leu Ala Leu Leu Ala
1 5 10 15

Ala Leu Cys Pro Ala Ser Arg Ala Leu Glu Glu Lys Lys Gly Lys Gly
20 25 30

Val Ser Arg Arg Leu Pro Arg Arg Pro Arg Ile Ala Pro Arg Thr Pro
35 40 45

Gln Pro Ala Gln Pro Arg Thr Gly Ala Pro Ala Arg Ala Arg Ala Pro
50 55 60

Ala Arg Pro Phe Leu Phe Pro
65 70

<210> 341

<211> 239

<212> PRT

<213> Artificial Sequence

<220>

<223> EGLN3__Homo_sapiens__Q9H6Z9

<400> 341

Met Pro Leu Gly His Ile Met Arg Leu Asp Leu Glu Lys Ile Ala Leu
1 5 10 15

Glu Tyr Ile Val Pro Cys Leu His Glu Val Gly Phe Cys Tyr Leu Asp
20 25 30

Asn Phe Leu Gly Glu Val Val Gly Asp Cys Val Leu Glu Arg Val Lys
35 40 45

Gln Leu His Cys Thr Gly Ala Leu Arg Asp Gly Gln Leu Ala Gly Pro
50 55 60

Arg Ala Gly Val Ser Lys Arg His Leu Arg Gly Asp Gln Ile Thr Trp
65 70 75 80

Ile Gly Gly Asn Glu Glu Gly Cys Glu Ala Ile Ser Phe Leu Leu Ser
85 90 95

Leu Ile Asp Arg Leu Val Leu Tyr Cys Gly Ser Arg Leu Gly Lys Tyr
100 105 110

Tyr Val Lys Glu Arg Ser Lys Ala Met Val Ala Cys Tyr Pro Gly Asn
115 120 125

Gly Thr Gly Tyr Val Arg His Val Asp Asn Pro Asn Gly Asp Gly Arg
130 135 140

ITI-08-PCT_Sequence_Listing_ST25.txt

Cys Ile Thr Cys Ile Tyr Tyr Leu Asn Lys Asn Trp Asp Ala Lys Leu
145 150 155 160

His Gly Gly Ile Leu Arg Ile Phe Pro Glu Gly Lys Ser Phe Ile Ala
165 170 175

Asp Val Glu Pro Ile Phe Asp Arg Leu Leu Phe Phe Trp Ser Asp Arg
180 185 190

Arg Asn Pro His Glu Val Gln Pro Ser Tyr Ala Thr Arg Tyr Ala Met
195 200 205

Thr Val Trp Tyr Phe Asp Ala Glu Glu Arg Ala Glu Ala Lys Lys Lys
210 215 220

Phe Arg Asn Leu Thr Arg Lys Thr Glu Ser Ala Leu Thr Glu Asp
225 230 235

<210> 342

<211> 521

<212> PRT

<213> Artificial Sequence

<220>

<223> ELF2/m__Homo_sapiens__B7Z720

<400> 342

Met Ala Thr Ser Leu His Glu Gly Pro Thr Asn Gln Leu Asp Leu Leu
1 5 10 15

Ile Arg Ala Val Glu Ala Ser Val His Ser Ser Asn Ala His Cys Thr
20 25 30

Asp Lys Thr Ile Glu Ala Ala Glu Ala Leu Leu His Met Glu Ser Pro
35 40 45

Thr Cys Leu Arg Asp Ser Arg Ser Pro Glu Phe Ile His Ala Ala Met
50 55 60

Arg Pro Asp Val Ile Thr Glu Thr Val Val Glu Val Ser Thr Glu Glu
65 70 75 80

Ser Glu Pro Met Asp Thr Ser Pro Ile Pro Thr Ser Pro Asp Ser His
85 90 95

Glu Pro Met Lys Lys Lys Lys Val Gly Arg Lys Pro Lys Thr Gln Gln
100 105 110

Ser Pro Ile Ser Asn Gly Ser Pro Glu Leu Gly Ile Lys Lys Lys Pro
115 120 125

ITI-08-PCT_Sequence_Listing_ST25.txt

Arg	Glu	Gly	Lys	Gly	Asn	Thr	Thr	Tyr	Leu	Trp	Glu	Phe	Leu	Leu	Asp	130	135	140	
Leu	Leu	Gln	Asp	Lys	Asn	Thr	Cys	Pro	Arg	Tyr	Ile	Lys	Trp	Thr	Gln	145	150	155	160
Arg	Glu	Lys	Gly	Ile	Phe	Lys	Leu	Val	Asp	Ser	Lys	Ala	Val	Ser	Lys	165	170	175	
Leu	Trp	Gly	Lys	His	Lys	Asn	Lys	Pro	Asp	Met	Asn	Tyr	Glu	Thr	Met	180	185	190	
Gly	Arg	Ala	Leu	Arg	Tyr	Tyr	Tyr	Gln	Arg	Gly	Ile	Leu	Ala	Lys	Val	195	200	205	
Glu	Gly	Gln	Arg	Leu	Val	Tyr	Gln	Phe	Lys	Asp	Met	Pro	Lys	Asn	Ile	210	215	220	
Val	Val	Ile	Asp	Asp	Asp	Lys	Ser	Glu	Thr	Cys	Asn	Glu	Asp	Leu	Ala	225	230	235	240
Gly	Thr	Thr	Asp	Glu	Lys	Ser	Leu	Glu	Arg	Val	Ser	Leu	Ser	Ala	Glu	245	250	255	
Ser	Leu	Leu	Lys	Ala	Ala	Ser	Ser	Val	Arg	Ser	Gly	Lys	Asn	Ser	Ser	260	265	270	
Pro	Ile	Asn	Cys	Ser	Arg	Ala	Glu	Lys	Gly	Val	Ala	Arg	Val	Val	Asn	275	280	285	
Ile	Thr	Ser	Pro	Gly	His	Asp	Ala	Ser	Ser	Arg	Ser	Pro	Thr	Thr	Thr	290	295	300	
Ala	Ser	Val	Ser	Ala	Thr	Ala	Ala	Pro	Arg	Thr	Val	Arg	Val	Ala	Met	305	310	315	320
Gln	Val	Pro	Val	Val	Met	Thr	Ser	Leu	Gly	Gln	Lys	Ile	Ser	Thr	Val	325	330	335	
Ala	Val	Gln	Ser	Val	Asn	Ala	Gly	Ala	Pro	Leu	Ile	Thr	Ser	Thr	Ser	340	345	350	
Pro	Thr	Thr	Ala	Thr	Ser	Pro	Lys	Val	Val	Ile	Gln	Thr	Ile	Pro	Thr	355	360	365	
Val	Met	Pro	Ala	Ser	Thr	Glu	Asn	Gly	Asp	Lys	Ile	Thr	Met	Gln	Pro	370	375	380	
Ala	Lys	Ile	Ile	Thr	Ile	Pro	Ala	Thr	Gln	Leu	Ala	Gln	Cys	Gln	Leu	385	390	395	400
Gln	Thr	Lys	Ser	Asn	Leu	Thr	Gly	Ser	Gly	Ser	Ile	Asn	Ile	Val	Gly				

ITI-08-PCT_Sequence_Listing_ST25.txt

405 410 415

Thr Pro Leu Ala Val Arg Ala Leu Thr Pro Val Ser Ile Ala His Gly
420 425 430

Thr Pro Val Met Arg Leu Ser Met Pro Thr Gln Gln Ala Ser Gly Gln
435 440 445

Thr Pro Pro Arg Val Ile Ser Ala Val Ile Lys Gly Pro Glu Val Lys
450 455 460

Ser Glu Ala Val Ala Lys Lys Gln Glu His Asp Val Lys Thr Leu Gln
465 470 475 480

Leu Val Glu Glu Lys Pro Ala Asp Gly Asn Lys Thr Val Thr His Val
485 490 495

Val Val Val Ser Ala Pro Ser Ala Ile Ala Leu Pro Val Thr Met Lys
500 505 510

Thr Glu Gly Leu Val Thr Cys Glu Lys
515 520

<210> 343

<211> 269

<212> PRT

<213> Artificial Sequence

<220>

<223> EMMPRIN__Homo_sapiens__Q54A51

<400> 343

Met Ala Ala Ala Leu Phe Val Leu Leu Gly Phe Ala Leu Leu Gly Thr
1 5 10 15

His Gly Ala Ser Gly Ala Ala Gly Thr Val Phe Thr Thr Val Glu Asp
20 25 30

Leu Gly Ser Lys Ile Leu Leu Thr Cys Ser Leu Asn Asp Ser Ala Thr
35 40 45

Glu Val Thr Gly His Arg Trp Leu Lys Gly Gly Val Val Leu Lys Glu
50 55 60

Asp Ala Leu Pro Gly Gln Lys Thr Glu Phe Lys Val Asp Ser Asp Asp
65 70 75 80

Gln Trp Gly Glu Tyr Ser Cys Val Phe Leu Pro Glu Pro Met Gly Thr
85 90 95

Ala Asn Ile Gln Leu His Gly Pro Pro Arg Val Lys Ala Val Lys Ser

ITI-08-PCT_Sequence_Listing_ST25.txt

100

105

110

Ser Glu His Ile Asn Glu Gly Glu Thr Ala Met Leu Val Cys Lys Ser
115 120 125

Glu Ser Val Pro Pro Val Thr Asp Trp Ala Trp Tyr Lys Ile Thr Asp
130 135 140

Ser Glu Asp Lys Ala Leu Met Asn Gly Ser Glu Ser Arg Phe Phe Val
145 150 155 160

Ser Ser Ser Gln Gly Arg Ser Glu Leu His Ile Glu Asn Leu Asn Met
165 170 175

Glu Ala Asp Pro Gly Gln Tyr Arg Cys Asn Gly Thr Ser Ser Lys Gly
180 185 190

Ser Asp Gln Ala Ile Ile Thr Leu Arg Val Arg Ser His Leu Ala Ala
195 200 205

Leu Trp Pro Phe Leu Gly Ile Val Ala Glu Val Leu Val Leu Val Thr
210 215 220

Ile Ile Phe Ile Tyr Glu Lys Arg Arg Lys Pro Glu Asp Val Leu Asp
225 230 235 240

Asp Asp Asp Ala Gly Ser Ala Pro Leu Lys Ser Ser Gly Gln His Gln
245 250 255

Asn Asp Lys Gly Lys Asn Val Arg Gln Arg Asn Ser Ser
260 265

<210> 344

<211> 314

<212> PRT

<213> Artificial Sequence

<220>

<223> EpCam__Homo_sapiens__P16422

<400> 344

Met Ala Pro Pro Gln Val Leu Ala Phe Gly Leu Leu Leu Ala Ala Ala
1 5 10 15

Thr Ala Thr Phe Ala Ala Ala Gln Glu Glu Cys Val Cys Glu Asn Tyr
20 25 30

Lys Leu Ala Val Asn Cys Phe Val Asn Asn Asn Arg Gln Cys Gln Cys
35 40 45

Thr Ser Val Gly Ala Gln Asn Thr Val Ile Cys Ser Lys Leu Ala Ala

ITI-08-PCT_Sequence_Listing_ST25.txt

50

55

60

Lys Cys Leu Val Met Lys Ala Glu Met Asn Gly Ser Lys Leu Gly Arg
65 70 75 80

Arg Ala Lys Pro Glu Gly Ala Leu Gln Asn Asn Asp Gly Leu Tyr Asp
85 90 95

Pro Asp Cys Asp Glu Ser Gly Leu Phe Lys Ala Lys Gln Cys Asn Gly
100 105 110

Thr Ser Met Cys Trp Cys Val Asn Thr Ala Gly Val Arg Arg Thr Asp
115 120 125

Lys Asp Thr Glu Ile Thr Cys Ser Glu Arg Val Arg Thr Tyr Trp Ile
130 135 140

Ile Ile Glu Leu Lys His Lys Ala Arg Glu Lys Pro Tyr Asp Ser Lys
145 150 155 160

Ser Leu Arg Thr Ala Leu Gln Lys Glu Ile Thr Thr Arg Tyr Gln Leu
165 170 175

Asp Pro Lys Phe Ile Thr Ser Ile Leu Tyr Glu Asn Asn Val Ile Thr
180 185 190

Ile Asp Leu Val Gln Asn Ser Ser Gln Lys Thr Gln Asn Asp Val Asp
195 200 205

Ile Ala Asp Val Ala Tyr Tyr Phe Glu Lys Asp Val Lys Gly Glu Ser
210 215 220

Leu Phe His Ser Lys Lys Met Asp Leu Thr Val Asn Gly Glu Gln Leu
225 230 235 240

Asp Leu Asp Pro Gly Gln Thr Leu Ile Tyr Tyr Val Asp Glu Lys Ala
245 250 255

Pro Glu Phe Ser Met Gln Gly Leu Lys Ala Gly Val Ile Ala Val Ile
260 265 270

Val Val Val Val Ile Ala Val Val Ala Gly Ile Val Val Leu Val Ile
275 280 285

Ser Arg Lys Lys Arg Met Ala Lys Tyr Glu Lys Ala Glu Ile Lys Glu
290 295 300

Met Gly Glu Met His Arg Glu Leu Asn Ala
305 310

<210> 345

<211> 976

ITI-08-PCT_Sequence_Listing_ST25.txt

<212> PRT

<213> Artificial Sequence

<220>

<223> EphA2__Homo_sapiens__P29317

<400> 345

Met Glu Leu Gln Ala Ala Arg Ala Cys Phe Ala Leu Leu Trp Gly Cys
1 5 10 15

Ala Leu Ala Ala Ala Ala Ala Ala Gln Gly Lys Glu Val Val Leu Leu
20 25 30

Asp Phe Ala Ala Ala Gly Gly Glu Leu Gly Trp Leu Thr His Pro Tyr
35 40 45

Gly Lys Gly Trp Asp Leu Met Gln Asn Ile Met Asn Asp Met Pro Ile
50 55 60

Tyr Met Tyr Ser Val Cys Asn Val Met Ser Gly Asp Gln Asp Asn Trp
65 70 75 80

Leu Arg Thr Asn Trp Val Tyr Arg Gly Glu Ala Glu Arg Ile Phe Ile
85 90 95

Glu Leu Lys Phe Thr Val Arg Asp Cys Asn Ser Phe Pro Gly Gly Ala
100 105 110

Ser Ser Cys Lys Glu Thr Phe Asn Leu Tyr Tyr Ala Glu Ser Asp Leu
115 120 125

Asp Tyr Gly Thr Asn Phe Gln Lys Arg Leu Phe Thr Lys Ile Asp Thr
130 135 140

Ile Ala Pro Asp Glu Ile Thr Val Ser Ser Asp Phe Glu Ala Arg His
145 150 155 160

Val Lys Leu Asn Val Glu Glu Arg Ser Val Gly Pro Leu Thr Arg Lys
165 170 175

Gly Phe Tyr Leu Ala Phe Gln Asp Ile Gly Ala Cys Val Ala Leu Leu
180 185 190

Ser Val Arg Val Tyr Tyr Lys Lys Cys Pro Glu Leu Leu Gln Gly Leu
195 200 205

Ala His Phe Pro Glu Thr Ile Ala Gly Ser Asp Ala Pro Ser Leu Ala
210 215 220

Thr Val Ala Gly Thr Cys Val Asp His Ala Val Val Pro Pro Gly Gly
225 230 235 240

ITI-08-PCT_Sequence_Listing_ST25.txt

Glu	Glu	Pro	Arg	Met	His	Cys	Ala	Val	Asp	Gly	Glu	Trp	Leu	Val	Pro	
				245					250					255		
Ile	Gly	Gln	Cys	Leu	Cys	Gln	Ala	Gly	Tyr	Glu	Lys	Val	Glu	Asp	Ala	
			260					265					270			
Cys	Gln	Ala	Cys	Ser	Pro	Gly	Phe	Phe	Lys	Phe	Glu	Ala	Ser	Glu	Ser	
		275					280					285				
Pro	Cys	Leu	Glu	Cys	Pro	Glu	His	Thr	Leu	Pro	Ser	Pro	Glu	Gly	Ala	
	290					295					300					
Thr	Ser	Cys	Glu	Cys	Glu	Glu	Gly	Phe	Phe	Arg	Ala	Pro	Gln	Asp	Pro	
305					310					315					320	
Ala	Ser	Met	Pro	Cys	Thr	Arg	Pro	Pro	Ser	Ala	Pro	His	Tyr	Leu	Thr	
				325					330					335		
Ala	Val	Gly	Met	Gly	Ala	Lys	Val	Glu	Leu	Arg	Trp	Thr	Pro	Pro	Gln	
			340					345					350			
Asp	Ser	Gly	Gly	Arg	Glu	Asp	Ile	Val	Tyr	Ser	Val	Thr	Cys	Glu	Gln	
		355					360					365				
Cys	Trp	Pro	Glu	Ser	Gly	Glu	Cys	Gly	Pro	Cys	Glu	Ala	Ser	Val	Arg	
	370					375					380					
Tyr	Ser	Glu	Pro	Pro	His	Gly	Leu	Thr	Arg	Thr	Ser	Val	Thr	Val	Ser	
385					390					395					400	
Asp	Leu	Glu	Pro	His	Met	Asn	Tyr	Thr	Phe	Thr	Val	Glu	Ala	Arg	Asn	
				405					410					415		
Gly	Val	Ser	Gly	Leu	Val	Thr	Ser	Arg	Ser	Phe	Arg	Thr	Ala	Ser	Val	
			420					425					430			
Ser	Ile	Asn	Gln	Thr	Glu	Pro	Pro	Lys	Val	Arg	Leu	Glu	Gly	Arg	Ser	
		435					440					445				
Thr	Thr	Ser	Leu	Ser	Val	Ser	Trp	Ser	Ile	Pro	Pro	Pro	Gln	Gln	Ser	
	450					455					460					
Arg	Val	Trp	Lys	Tyr	Glu	Val	Thr	Tyr	Arg	Lys	Lys	Gly	Asp	Ser	Asn	
465					470				475						480	
Ser	Tyr	Asn	Val	Arg	Arg	Thr	Glu	Gly	Phe	Ser	Val	Thr	Leu	Asp	Asp	
				485					490					495		
Leu	Ala	Pro	Asp	Thr	Thr	Tyr	Leu	Val	Gln	Val	Gln	Ala	Leu	Thr	Gln	
			500				505						510			

ITI-08-PCT_Sequence_Listing_ST25.txt

Glu	Gly	Gln	Gly	Ala	Gly	Ser	Lys	Val	His	Glu	Phe	Gln	Thr	Leu	Ser	515	520	525
Pro	Glu	Gly	Ser	Gly	Asn	Leu	Ala	Val	Ile	Gly	Gly	Val	Ala	Val	Gly	530	535	540
Val	Val	Leu	Leu	Leu	Val	Leu	Ala	Gly	Val	Gly	Phe	Phe	Ile	His	Arg	545	550	555
Arg	Arg	Lys	Asn	Gln	Arg	Ala	Arg	Gln	Ser	Pro	Glu	Asp	Val	Tyr	Phe	565	570	575
Ser	Lys	Ser	Glu	Gln	Leu	Lys	Pro	Leu	Lys	Thr	Tyr	Val	Asp	Pro	His	580	585	590
Thr	Tyr	Glu	Asp	Pro	Asn	Gln	Ala	Val	Leu	Lys	Phe	Thr	Thr	Glu	Ile	595	600	605
His	Pro	Ser	Cys	Val	Thr	Arg	Gln	Lys	Val	Ile	Gly	Ala	Gly	Glu	Phe	610	615	620
Gly	Glu	Val	Tyr	Lys	Gly	Met	Leu	Lys	Thr	Ser	Ser	Gly	Lys	Lys	Glu	625	630	635
Val	Pro	Val	Ala	Ile	Lys	Thr	Leu	Lys	Ala	Gly	Tyr	Thr	Glu	Lys	Gln	645	650	655
Arg	Val	Asp	Phe	Leu	Gly	Glu	Ala	Gly	Ile	Met	Gly	Gln	Phe	Ser	His	660	665	670
His	Asn	Ile	Ile	Arg	Leu	Glu	Gly	Val	Ile	Ser	Lys	Tyr	Lys	Pro	Met	675	680	685
Met	Ile	Ile	Thr	Glu	Tyr	Met	Glu	Asn	Gly	Ala	Leu	Asp	Lys	Phe	Leu	690	695	700
Arg	Glu	Lys	Asp	Gly	Glu	Phe	Ser	Val	Leu	Gln	Leu	Val	Gly	Met	Leu	705	710	715
Arg	Gly	Ile	Ala	Ala	Gly	Met	Lys	Tyr	Leu	Ala	Asn	Met	Asn	Tyr	Val	725	730	735
His	Arg	Asp	Leu	Ala	Ala	Arg	Asn	Ile	Leu	Val	Asn	Ser	Asn	Leu	Val	740	745	750
Cys	Lys	Val	Ser	Asp	Phe	Gly	Leu	Ser	Arg	Val	Leu	Glu	Asp	Asp	Pro	755	760	765
Glu	Ala	Thr	Tyr	Thr	Thr	Ser	Gly	Gly	Lys	Ile	Pro	Ile	Arg	Trp	Thr	770	775	780
Ala	Pro	Glu	Ala	Ile	Ser	Tyr	Arg	Lys	Phe	Thr	Ser	Ala	Ser	Asp	Val			

ITI-08-PCT_Sequence_Listing_ST25.txt

```

785              790              795              800
Trp Ser Phe Gly Ile Val Met Trp Glu Val Met Thr Tyr Gly Glu Arg
      805              810
Pro Tyr Trp Glu Leu Ser Asn His Glu Val Met Lys Ala Ile Asn Asp
      820              825              830
Gly Phe Arg Leu Pro Thr Pro Met Asp Cys Pro Ser Ala Ile Tyr Gln
      835              840              845
Leu Met Met Gln Cys Trp Gln Gln Glu Arg Ala Arg Arg Pro Lys Phe
      850              855              860
Ala Asp Ile Val Ser Ile Leu Asp Lys Leu Ile Arg Ala Pro Asp Ser
865              870              875              880
Leu Lys Thr Leu Ala Asp Phe Asp Pro Arg Val Ser Ile Arg Leu Pro
      885              890              895
Ser Thr Ser Gly Ser Glu Gly Val Pro Phe Arg Thr Val Ser Glu Trp
      900              905              910
Leu Glu Ser Ile Lys Met Gln Gln Tyr Thr Glu His Phe Met Ala Ala
      915              920              925
Gly Tyr Thr Ala Ile Glu Lys Val Val Gln Met Thr Asn Asp Asp Ile
      930              935              940
Lys Arg Ile Gly Val Arg Leu Pro Gly His Gln Lys Arg Ile Ala Tyr
945              950              955              960
Ser Leu Leu Gly Leu Lys Asp Gln Val Asn Thr Val Gly Ile Pro Ile
      965              970              975

```

<210> 346
 <211> 983
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> EphA3__Homo_sapiens__P29320

<400> 346

```

Met Asp Cys Gln Leu Ser Ile Leu Leu Leu Leu Ser Cys Ser Val Leu
1              5              10              15
Asp Ser Phe Gly Glu Leu Ile Pro Gln Pro Ser Asn Glu Val Asn Leu
      20              25              30
Leu Asp Ser Lys Thr Ile Gln Gly Glu Leu Gly Trp Ile Ser Tyr Pro

```

ITI-08-PCT_Sequence_Listing_ST25.txt

```

35          40          45
Ser His Gly Trp Glu Glu Ile Ser Gly Val Asp Glu His Tyr Thr Pro
50          55          60

Ile Arg Thr Tyr Gln Val Cys Asn Val Met Asp His Ser Gln Asn Asn
65          70          75          80

Trp Leu Arg Thr Asn Trp Val Pro Arg Asn Ser Ala Gln Lys Ile Tyr
85          90          95

Val Glu Leu Lys Phe Thr Leu Arg Asp Cys Asn Ser Ile Pro Leu Val
100         105         110

Leu Gly Thr Cys Lys Glu Thr Phe Asn Leu Tyr Tyr Met Glu Ser Asp
115         120         125

Asp Asp His Gly Val Lys Phe Arg Glu His Gln Phe Thr Lys Ile Asp
130         135         140

Thr Ile Ala Ala Asp Glu Ser Phe Thr Gln Met Asp Leu Gly Asp Arg
145         150         155         160

Ile Leu Lys Leu Asn Thr Glu Ile Arg Glu Val Gly Pro Val Asn Lys
165         170         175

Lys Gly Phe Tyr Leu Ala Phe Gln Asp Val Gly Ala Cys Val Ala Leu
180         185         190

Val Ser Val Arg Val Tyr Phe Lys Lys Cys Pro Phe Thr Val Lys Asn
195         200         205

Leu Ala Met Phe Pro Asp Thr Val Pro Met Asp Ser Gln Ser Leu Val
210         215         220

Glu Val Arg Gly Ser Cys Val Asn Asn Ser Lys Glu Glu Asp Pro Pro
225         230         235         240

Arg Met Tyr Cys Ser Thr Glu Gly Glu Trp Leu Val Pro Ile Gly Lys
245         250         255

Cys Ser Cys Asn Ala Gly Tyr Glu Glu Arg Gly Phe Met Cys Gln Ala
260         265         270

Cys Arg Pro Gly Phe Tyr Lys Ala Leu Asp Gly Asn Met Lys Cys Ala
275         280         285

Lys Cys Pro Pro His Ser Ser Thr Gln Glu Asp Gly Ser Met Asn Cys
290         295         300

Arg Cys Glu Asn Asn Tyr Phe Arg Ala Asp Lys Asp Pro Pro Ser Met
305         310         315         320

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Ala	Cys	Thr	Arg	Pro	Pro	Ser	Ser	Pro	Arg	Asn	Val	Ile	Ser	Asn	Ile	
				325					330					335		
Asn	Glu	Thr	Ser	Val	Ile	Leu	Asp	Trp	Ser	Trp	Pro	Leu	Asp	Thr	Gly	
			340					345					350			
Gly	Arg	Lys	Asp	Val	Thr	Phe	Asn	Ile	Ile	Cys	Lys	Lys	Cys	Gly	Trp	
		355					360					365				
Asn	Ile	Lys	Gln	Cys	Glu	Pro	Cys	Ser	Pro	Asn	Val	Arg	Phe	Leu	Pro	
	370					375					380					
Arg	Gln	Phe	Gly	Leu	Thr	Asn	Thr	Thr	Val	Thr	Val	Thr	Asp	Leu	Leu	
385					390				395						400	
Ala	His	Thr	Asn	Tyr	Thr	Phe	Glu	Ile	Asp	Ala	Val	Asn	Gly	Val	Ser	
			405						410					415		
Glu	Leu	Ser	Ser	Pro	Pro	Arg	Gln	Phe	Ala	Ala	Val	Ser	Ile	Thr	Thr	
			420					425					430			
Asn	Gln	Ala	Ala	Pro	Ser	Pro	Val	Leu	Thr	Ile	Lys	Lys	Asp	Arg	Thr	
	435						440					445				
Ser	Arg	Asn	Ser	Ile	Ser	Leu	Ser	Trp	Gln	Glu	Pro	Glu	His	Pro	Asn	
	450					455					460					
Gly	Ile	Ile	Leu	Asp	Tyr	Glu	Val	Lys	Tyr	Tyr	Glu	Lys	Gln	Glu	Gln	
465				470					475						480	
Glu	Thr	Ser	Tyr	Thr	Ile	Leu	Arg	Ala	Arg	Gly	Thr	Asn	Val	Thr	Ile	
			485						490					495		
Ser	Ser	Leu	Lys	Pro	Asp	Thr	Ile	Tyr	Val	Phe	Gln	Ile	Arg	Ala	Arg	
			500					505					510			
Thr	Ala	Ala	Gly	Tyr	Gly	Thr	Asn	Ser	Arg	Lys	Phe	Glu	Phe	Glu	Thr	
	515						520					525				
Ser	Pro	Asp	Ser	Phe	Ser	Ile	Ser	Gly	Glu	Ser	Ser	Gln	Val	Val	Met	
	530					535					540					
Ile	Ala	Ile	Ser	Ala	Ala	Val	Ala	Ile	Ile	Leu	Leu	Thr	Val	Val	Ile	
545				550						555					560	
Tyr	Val	Leu	Ile	Gly	Arg	Phe	Cys	Gly	Tyr	Lys	Ser	Lys	His	Gly	Ala	
			565					570						575		
Asp	Glu	Lys	Arg	Leu	His	Phe	Gly	Asn	Gly	His	Leu	Lys	Leu	Pro	Gly	
			580					585					590			

ITI-08-PCT_Sequence_Listing_ST25.txt

Leu Arg Thr Tyr Val Asp Pro His Thr Tyr Glu Asp Pro Thr Gln Ala
 595 600 605
 Val His Glu Phe Ala Lys Glu Leu Asp Ala Thr Asn Ile Ser Ile Asp
 610 615 620
 Lys Val Val Gly Ala Gly Glu Phe Gly Glu Val Cys Ser Gly Arg Leu
 625 630 635 640
 Lys Leu Pro Ser Lys Lys Glu Ile Ser Val Ala Ile Lys Thr Leu Lys
 645 650 655
 Val Gly Tyr Thr Glu Lys Gln Arg Arg Asp Phe Leu Gly Glu Ala Ser
 660 665 670
 Ile Met Gly Gln Phe Asp His Pro Asn Ile Ile Arg Leu Glu Gly Val
 675 680 685
 Val Thr Lys Ser Lys Pro Val Met Ile Val Thr Glu Tyr Met Glu Asn
 690 695 700
 Gly Ser Leu Asp Ser Phe Leu Arg Lys His Asp Ala Gln Phe Thr Val
 705 710 715 720
 Ile Gln Leu Val Gly Met Leu Arg Gly Ile Ala Ser Gly Met Lys Tyr
 725 730 735
 Leu Ser Asp Met Gly Tyr Val His Arg Asp Leu Ala Ala Arg Asn Ile
 740 745 750
 Leu Ile Asn Ser Asn Leu Val Cys Lys Val Ser Asp Phe Gly Leu Ser
 755 760 765
 Arg Val Leu Glu Asp Asp Pro Glu Ala Ala Tyr Thr Thr Arg Gly Gly
 770 775 780
 Lys Ile Pro Ile Arg Trp Thr Ser Pro Glu Ala Ile Ala Tyr Arg Lys
 785 790 795 800
 Phe Thr Ser Ala Ser Asp Val Trp Ser Tyr Gly Ile Val Leu Trp Glu
 805 810 815
 Val Met Ser Tyr Gly Glu Arg Pro Tyr Trp Glu Met Ser Asn Gln Asp
 820 825 830
 Val Ile Lys Ala Val Asp Glu Gly Tyr Arg Leu Pro Pro Pro Met Asp
 835 840 845
 Cys Pro Ala Ala Leu Tyr Gln Leu Met Leu Asp Cys Trp Gln Lys Asp
 850 855 860
 Arg Asn Asn Arg Pro Lys Phe Glu Gln Ile Val Ser Ile Leu Asp Lys

ITI-08-PCT_Sequence_Listing_ST25.txt

```

865                870                875                880
Leu Ile Arg Asn Pro Gly Ser Leu Lys Ile Ile Thr Ser Ala Ala Ala
                885                890                895

Arg Pro Ser Asn Leu Leu Leu Asp Gln Ser Asn Val Asp Ile Thr Thr
                900                905                910

Phe Arg Thr Thr Gly Asp Trp Leu Asn Gly Val Trp Thr Ala His Cys
                915                920                925

Lys Glu Ile Phe Thr Gly Val Glu Tyr Ser Ser Cys Asp Thr Ile Ala
                930                935                940

Lys Ile Ser Thr Asp Asp Met Lys Lys Val Gly Val Thr Val Val Gly
945                950                955                960

Pro Gln Lys Lys Ile Ile Ser Ser Ile Lys Ala Leu Glu Thr Gln Ser
                965                970                975

Lys Asn Gly Pro Val Pro Val
                980

```

```

<210> 347
<211> 983
<212> PRT
<213> Artificial Sequence

<220>
<223> EphA3__Homo_sapiens__Q6P4R6

<400> 347

```

```

Met Asp Cys Gln Leu Ser Ile Leu Leu Leu Leu Ser Cys Ser Val Leu
1                5                10                15

Asp Ser Phe Gly Glu Leu Ile Pro Gln Pro Ser Asn Glu Val Asn Leu
                20                25                30

Leu Asp Ser Lys Thr Ile Gln Gly Glu Leu Gly Trp Ile Ser Tyr Pro
                35                40                45

Ser His Gly Trp Glu Glu Ile Ser Gly Val Asp Glu His Tyr Thr Pro
                50                55                60

Ile Arg Thr Tyr Gln Val Cys Asn Val Met Asp His Ser Gln Asn Asn
65                70                75                80

Trp Leu Arg Thr Asn Trp Val Pro Arg Asn Ser Ala Gln Lys Ile Tyr
                85                90                95

Val Glu Leu Lys Phe Thr Leu Arg Asp Cys Asn Ser Ile Pro Leu Val

```

ITI-08-PCT_Sequence_Listing_ST25.txt

100	105	110															
Leu	Gly	Thr	Cys	Lys	Glu	Thr	Phe	Asn	Leu	Tyr	Tyr	Met	Glu	Ser	Asp		
	115						120					125					
Asp	Asp	His	Gly	Val	Lys	Phe	Arg	Glu	His	Gln	Phe	Thr	Lys	Ile	Asp		
	130					135					140						
Thr	Ile	Ala	Ala	Asp	Glu	Ser	Phe	Thr	Gln	Met	Asp	Leu	Gly	Asp	Arg		
145				150						155					160		
Ile	Leu	Lys	Leu	Asn	Thr	Glu	Ile	Arg	Glu	Val	Gly	Pro	Val	Asn	Lys		
				165					170					175			
Lys	Gly	Phe	Tyr	Leu	Ala	Phe	Gln	Asp	Val	Gly	Ala	Cys	Val	Ala	Leu		
		180						185					190				
Val	Ser	Val	Arg	Val	Tyr	Phe	Lys	Lys	Cys	Pro	Phe	Thr	Val	Lys	Asn		
	195						200					205					
Leu	Ala	Met	Phe	Pro	Asp	Thr	Val	Pro	Met	Asp	Ser	Gln	Ser	Leu	Val		
	210					215					220						
Glu	Val	Arg	Gly	Ser	Cys	Val	Asn	Asn	Ser	Lys	Glu	Glu	Asp	Pro	Pro		
225					230					235					240		
Arg	Met	Tyr	Cys	Ser	Thr	Glu	Gly	Glu	Trp	Leu	Val	Pro	Ile	Gly	Lys		
				245					250					255			
Cys	Ser	Cys	Asn	Ala	Gly	Tyr	Glu	Glu	Arg	Gly	Phe	Met	Cys	Gln	Ala		
			260					265					270				
Cys	Arg	Pro	Gly	Phe	Tyr	Lys	Ala	Leu	Asp	Gly	Asn	Met	Lys	Cys	Ala		
	275						280					285					
Lys	Cys	Pro	Pro	His	Ser	Ser	Thr	Gln	Glu	Asp	Gly	Ser	Met	Asn	Cys		
	290					295					300						
Arg	Cys	Glu	Asn	Asn	Tyr	Phe	Arg	Ala	Asp	Lys	Asp	Pro	Pro	Ser	Met		
305					310					315					320		
Ala	Cys	Thr	Arg	Pro	Pro	Ser	Ser	Pro	Arg	Asn	Val	Ile	Ser	Asn	Ile		
				325					330					335			
Asn	Glu	Thr	Ser	Val	Ile	Leu	Asp	Trp	Ser	Trp	Pro	Leu	Asp	Thr	Gly		
			340					345					350				
Gly	Arg	Lys	Asp	Val	Thr	Phe	Asn	Ile	Ile	Cys	Lys	Lys	Cys	Gly	Trp		
	355						360					365					
Asn	Ile	Lys	Gln	Cys	Glu	Pro	Cys	Ser	Pro	Asn	Val	Arg	Phe	Leu	Pro		
	370					375					380						

ITI-08-PCT_Sequence_Listing_ST25.txt

Arg Gln Phe Gly Leu Thr Asn Thr Thr Val Thr Val Thr Asp Leu Leu
 385 390 395 400
 Ala His Thr Asn Tyr Thr Phe Glu Ile Asp Ala Val Asn Gly Val Ser
 405 410 415
 Glu Leu Ser Ser Pro Pro Arg Gln Phe Ala Ala Val Ser Ile Thr Thr
 420 425 430
 Asn Gln Ala Ala Pro Ser Pro Val Leu Thr Ile Lys Lys Asp Arg Thr
 435 440 445
 Ser Arg Asn Ser Ile Ser Leu Ser Trp Gln Glu Pro Glu His Pro Asn
 450 455 460
 Gly Ile Ile Leu Asp Tyr Glu Val Lys Tyr Tyr Glu Lys Gln Glu Gln
 465 470 475 480
 Glu Thr Ser Tyr Thr Ile Leu Arg Ala Arg Gly Thr Asn Val Thr Ile
 485 490 495
 Ser Ser Leu Lys Pro Asp Thr Ile Tyr Val Phe Gln Ile Arg Ala Arg
 500 505 510
 Thr Ala Ala Gly Tyr Gly Thr Asn Ser Arg Lys Phe Glu Phe Glu Thr
 515 520 525
 Ser Pro Asp Ser Phe Ser Ile Ser Gly Glu Ser Ser Gln Val Val Met
 530 535 540
 Ile Ala Ile Ser Ala Ala Val Ala Ile Ile Leu Leu Thr Val Val Ile
 545 550 555 560
 Tyr Val Leu Ile Gly Arg Phe Cys Gly Tyr Lys Ser Lys His Gly Ala
 565 570 575
 Asp Glu Lys Arg Leu His Phe Gly Asn Gly His Leu Lys Leu Pro Gly
 580 585 590
 Leu Arg Thr Tyr Val Asp Pro His Thr Tyr Glu Asp Pro Thr Gln Thr
 595 600 605
 Val His Glu Phe Ala Lys Glu Leu Asp Ala Thr Asn Ile Ser Ile Asp
 610 615 620
 Lys Val Val Gly Ala Gly Glu Phe Gly Glu Val Cys Ser Gly Arg Leu
 625 630 635 640
 Lys Leu Pro Ser Lys Lys Glu Ile Ser Val Ala Ile Lys Thr Leu Lys
 645 650 655

ITI-08-PCT_Sequence_Listing_ST25.txt

Val	Gly	Tyr	Thr	Glu	Lys	Gln	Arg	Arg	Asp	Phe	Leu	Gly	Glu	Ala	Ser	660	665	670
Ile	Met	Gly	Gln	Phe	Asp	His	Pro	Asn	Ile	Ile	Arg	Leu	Glu	Gly	Val	675	680	685
Val	Thr	Lys	Ser	Lys	Pro	Val	Met	Ile	Val	Thr	Glu	Tyr	Met	Glu	Asn	690	695	700
Gly	Ser	Leu	Asp	Ser	Phe	Leu	Arg	Lys	His	Asp	Ala	Gln	Phe	Thr	Val	705	710	715
Ile	Gln	Leu	Val	Gly	Met	Leu	Arg	Gly	Ile	Ala	Ser	Gly	Met	Lys	Tyr	725	730	735
Leu	Ser	Asp	Met	Gly	Tyr	Val	His	Arg	Asp	Leu	Ala	Ala	Arg	Asn	Ile	740	745	750
Leu	Ile	Asn	Ser	Asn	Leu	Val	Cys	Lys	Val	Ser	Asp	Phe	Gly	Leu	Ser	755	760	765
Arg	Val	Leu	Glu	Asp	Asp	Pro	Glu	Ala	Ala	Tyr	Thr	Thr	Arg	Gly	Gly	770	775	780
Lys	Ile	Pro	Ile	Arg	Trp	Thr	Ser	Pro	Glu	Ala	Ile	Ala	Tyr	Arg	Lys	785	790	795
Phe	Thr	Ser	Ala	Ser	Asp	Val	Trp	Ser	Tyr	Gly	Ile	Val	Leu	Trp	Glu	805	810	815
Val	Met	Ser	Tyr	Gly	Glu	Arg	Pro	Tyr	Trp	Glu	Met	Ser	Asn	Gln	Asp	820	825	830
Val	Ile	Lys	Ala	Val	Asp	Glu	Gly	Tyr	Arg	Leu	Pro	Pro	Pro	Met	Asp	835	840	845
Cys	Pro	Ala	Ala	Leu	Tyr	Gln	Leu	Met	Leu	Asp	Cys	Trp	Gln	Lys	Asp	850	855	860
Arg	Asn	Asn	Arg	Pro	Lys	Phe	Glu	Gln	Ile	Val	Ser	Ile	Leu	Asp	Lys	865	870	875
Leu	Ile	Arg	Asn	Pro	Gly	Ser	Leu	Lys	Ile	Ile	Thr	Ser	Ala	Ala	Ala	885	890	895
Arg	Pro	Ser	Asn	Leu	Leu	Leu	Asp	Gln	Ser	Asn	Val	Asp	Ile	Thr	Thr	900	905	910
Phe	Arg	Thr	Thr	Gly	Asp	Trp	Leu	Asn	Gly	Val	Trp	Thr	Ala	His	Cys	915	920	925
Lys	Glu	Ile	Phe	Thr	Gly	Val	Glu	Tyr	Ser	Ser	Cys	Asp	Thr	Ile	Ala			

ITI-08-PCT_Sequence_Listing_ST25.txt

930

935

940

Lys Ile Ser Thr Asp Asp Met Lys Lys Val Gly Val Thr Val Val Gly
945 950 955 960

Pro Gln Lys Lys Ile Ile Ser Ser Ile Lys Ala Leu Glu Thr Gln Ser
965 970 975

Lys Asn Gly Pro Val Pro Val
980

<210> 348

<211> 462

<212> PRT

<213> Artificial Sequence

<220>

<223> ErbB3__Homo_sapiens__B3KWG5

<400> 348

Met Pro Met Ser Thr Ile Leu Pro Val Thr Ser Pro Cys Leu Pro Ala
1 5 10 15

Thr Gly Val Thr Val Trp Glu Leu Met Thr Phe Gly Ala Glu Pro Tyr
20 25 30

Ala Gly Leu Arg Leu Ala Glu Val Pro Asp Leu Leu Glu Lys Gly Glu
35 40 45

Arg Leu Ala Gln Pro Gln Ile Cys Thr Ile Asp Val Tyr Met Val Met
50 55 60

Val Lys Cys Trp Met Ile Asp Glu Asn Ile Arg Pro Thr Phe Lys Glu
65 70 75 80

Leu Ala Asn Glu Phe Thr Arg Met Ala Arg Asp Pro Pro Arg Tyr Leu
85 90 95

Val Ile Lys Arg Glu Ser Gly Pro Gly Ile Ala Pro Gly Pro Glu Pro
100 105 110

His Gly Leu Thr Asn Lys Lys Leu Glu Glu Val Glu Leu Glu Pro Glu
115 120 125

Leu Asp Leu Asp Leu Asp Leu Glu Ala Glu Glu Asp Asn Leu Ala Thr
130 135 140

Thr Thr Leu Gly Ser Ala Leu Ser Leu Pro Val Gly Thr Leu Asn Arg
145 150 155 160

Pro Arg Gly Ser Gln Ser Leu Leu Ser Pro Ser Ser Gly Tyr Met Pro

ITI-08-PCT_Sequence_Listing_ST25.txt

165

170

175

Met Asn Gln Gly Asn Leu Gly Glu Ser Cys Gln Glu Ser Ala Val Ser
 180 185 190

Gly Ser Ser Glu Arg Cys Pro Arg Pro Val Ser Leu His Pro Met Pro
 195 200 205

Arg Gly Cys Leu Ala Ser Glu Ser Ser Glu Gly His Val Thr Gly Ser
 210 215 220

Glu Ala Glu Leu Gln Glu Lys Val Ser Met Cys Arg Ser Arg Ser Arg
 225 230 235 240

Ser Arg Ser Pro Arg Pro Arg Gly Asp Ser Ala Tyr His Ser Gln Arg
 245 250 255

His Ser Leu Leu Thr Pro Val Thr Pro Leu Ser Pro Pro Gly Leu Glu
 260 265 270

Glu Glu Asp Val Asn Gly Tyr Val Met Pro Asp Thr His Leu Lys Gly
 275 280 285

Thr Pro Ser Ser Arg Glu Gly Thr Leu Ser Ser Val Gly Leu Ser Ser
 290 295 300

Val Leu Gly Thr Glu Glu Glu Asp Glu Asp Glu Glu Tyr Glu Tyr Met
 305 310 315 320

Asn Arg Arg Arg Arg His Ser Pro Pro His Pro Pro Arg Pro Ser Ser
 325 330 335

Leu Glu Glu Leu Gly Tyr Glu Tyr Met Asp Val Gly Ser Asp Leu Ser
 340 345 350

Ala Ser Leu Gly Ser Thr Gln Ser Cys Pro Leu His Pro Val Pro Ile
 355 360 365

Met Pro Thr Ala Gly Thr Thr Pro Asp Glu Asp Tyr Glu Tyr Met Asn
 370 375 380

Arg Gln Arg Asp Gly Gly Gly Pro Gly Gly Asp Tyr Ala Ala Met Gly
 385 390 395 400

Ala Cys Pro Ala Ser Glu Gln Gly Tyr Glu Glu Met Arg Ala Phe Gln
 405 410 415

Gly Pro Gly His Gln Ala Pro His Val His Tyr Ala Arg Leu Lys Thr
 420 425 430

Leu Arg Ser Leu Glu Ala Thr Asp Ser Ala Phe Asp Asn Pro Asp Tyr
 435 440 445

ITI-08-PCT_Sequence_Listing_ST25.txt

Trp His Ser Arg Leu Phe Pro Lys Ala Asn Ala Gln Arg Thr
 450 455 460

<210> 349
 <211> 921
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> ErbB3__Homo_sapiens__B4DGQ7

<400> 349

Met Arg Ala Asn Asp Ala Leu Gln Val Leu Gly Leu Leu Phe Ser Leu
 1 5 10 15

Ala Arg Gly Ser Glu Val Gly Asn Ser Gln Ala Val Cys Pro Gly Thr
 20 25 30

Leu Asn Gly Leu Ser Val Thr Gly Asp Ala Glu Asn Gln Tyr Gln Thr
 35 40 45

Leu Tyr Lys Leu Tyr Glu Arg Cys Glu Val Val Met Gly Asn Leu Glu
 50 55 60

Ile Val Leu Thr Gly His Asn Ala Asp Leu Ser Phe Leu Gln Trp Ile
 65 70 75 80

Arg Glu Val Thr Gly Tyr Val Leu Val Ala Met Asn Glu Phe Ser Thr
 85 90 95

Leu Pro Leu Pro Asn Leu Arg Val Val Arg Gly Thr Gln Val Tyr Asp
 100 105 110

Gly Lys Phe Ala Ile Phe Val Met Leu Asn Tyr Asn Thr Asn Ser Ser
 115 120 125

His Ala Leu Arg Gln Leu Arg Leu Thr Gln Leu Thr Glu Ile Leu Ser
 130 135 140

Gly Gly Val Tyr Ile Glu Lys Asn Asp Lys Leu Cys His Met Asp Thr
 145 150 155 160

Ile Asp Trp Arg Asp Ile Val Arg Asp Arg Asp Ala Glu Ile Val Val
 165 170 175

Lys Asp Asn Gly Arg Ser Cys Pro Pro Cys His Glu Val Cys Lys Gly
 180 185 190

Arg Cys Trp Gly Pro Gly Ser Glu Asp Cys Gln Thr Leu Thr Lys Thr
 195 200 205

ITI-08-PCT_Sequence_Listing_ST25.txt

Ile	Cys	Ala	Pro	Gln	Cys	Asn	Gly	His	Cys	Phe	Gly	Pro	Asn	Pro	Asn	210	215	220
Gln	Cys	Cys	His	Asp	Glu	Cys	Ala	Gly	Gly	Cys	Ser	Gly	Pro	Gln	Asp	225	230	235
Thr	Asp	Cys	Phe	Ala	Cys	Arg	His	Phe	Asn	Asp	Ser	Gly	Ala	Cys	Val	245	250	255
Pro	Arg	Cys	Pro	Gln	Pro	Leu	Val	Tyr	Asn	Lys	Leu	Thr	Phe	Gln	Leu	260	265	270
Glu	Pro	Asn	Pro	His	Thr	Lys	Tyr	Gln	Tyr	Gly	Gly	Val	Cys	Val	Ala	275	280	285
Ser	Cys	Pro	His	Asn	Phe	Val	Val	Asp	Gln	Thr	Ser	Cys	Val	Arg	Ala	290	295	300
Cys	Pro	Pro	Asp	Lys	Met	Glu	Val	Asp	Lys	Asn	Gly	Leu	Lys	Met	Cys	305	310	315
Glu	Pro	Cys	Gly	Gly	Leu	Cys	Pro	Lys	Ala	Cys	Glu	Gly	Thr	Gly	Ser	325	330	335
Gly	Ser	Arg	Phe	Gln	Thr	Val	Asp	Ser	Ser	Asn	Ile	Asp	Gly	Phe	Val	340	345	350
Asn	Cys	Thr	Lys	Ile	Leu	Gly	Asn	Leu	Asp	Phe	Leu	Ile	Thr	Gly	Leu	355	360	365
Asn	Gly	Asp	Pro	Trp	His	Lys	Ile	Pro	Ala	Leu	Asp	Pro	Glu	Lys	Leu	370	375	380
Asn	Val	Phe	Arg	Thr	Val	Arg	Glu	Ile	Thr	Gly	Tyr	Leu	Asn	Ile	Gln	385	390	395
Ser	Trp	Pro	Pro	His	Met	His	Asn	Phe	Ser	Val	Phe	Ser	Asn	Leu	Thr	405	410	415
Thr	Ile	Gly	Gly	Arg	Ser	Leu	Tyr	Asn	Arg	Gly	Phe	Ser	Leu	Leu	Ile	420	425	430
Met	Lys	Asn	Leu	Asn	Val	Thr	Ser	Leu	Gly	Phe	Arg	Ser	Leu	Lys	Glu	435	440	445
Ile	Ser	Ala	Gly	Arg	Ile	Tyr	Ile	Ser	Ala	Asn	Arg	Gln	Leu	Cys	Tyr	450	455	460
His	His	Ser	Leu	Asn	Trp	Thr	Lys	Val	Leu	Arg	Gly	Pro	Thr	Glu	Glu	465	470	475

ITI-08-PCT_Sequence_Listing_ST25.txt

Arg	Leu	Asp	Ile	Lys	His	Asn	Arg	Pro	Arg	Arg	Asp	Cys	Val	Ala	Glu	485	490	495
Gly	Lys	Val	Cys	Asp	Pro	Leu	Cys	Ser	Ser	Gly	Gly	Cys	Trp	Gly	Pro	500	505	510
Gly	Pro	Gly	Gln	Cys	Leu	Ser	Cys	Arg	Asn	Tyr	Ser	Arg	Gly	Gly	Val	515	520	525
Cys	Val	Thr	His	Cys	Asn	Phe	Leu	Asn	Gly	Glu	Pro	Arg	Glu	Phe	Ala	530	535	540
His	Glu	Ala	Glu	Cys	Phe	Ser	Cys	His	Pro	Glu	Cys	Gln	Pro	Met	Glu	545	550	555
Gly	Thr	Ala	Thr	Cys	Asn	Gly	Ser	Gly	Ser	Asp	Thr	Cys	Ala	Gln	Cys	565	570	575
Ala	His	Phe	Arg	Asp	Gly	Pro	His	Cys	Val	Ser	Ser	Cys	Pro	His	Gly	580	585	590
Val	Leu	Gly	Ala	Lys	Gly	Pro	Ile	Tyr	Lys	Tyr	Pro	Asp	Val	Gln	Asn	595	600	605
Glu	Cys	Arg	Pro	Cys	His	Glu	Asn	Cys	Thr	Gln	Gly	Cys	Lys	Gly	Pro	610	615	620
Glu	Leu	Gln	Asp	Cys	Leu	Gly	Gln	Thr	Leu	Val	Leu	Ile	Gly	Lys	Thr	625	630	635
His	Leu	Thr	Met	Ala	Leu	Thr	Val	Ile	Ala	Gly	Leu	Val	Val	Ile	Phe	645	650	655
Met	Met	Leu	Gly	Gly	Thr	Phe	Leu	Tyr	Trp	Arg	Gly	Arg	Arg	Ile	Gln	660	665	670
Asn	Lys	Arg	Ala	Met	Arg	Arg	Tyr	Leu	Glu	Arg	Gly	Glu	Ser	Ile	Glu	675	680	685
Pro	Leu	Asp	Pro	Ser	Glu	Lys	Ala	Asn	Lys	Val	Leu	Ala	Arg	Ile	Phe	690	695	700
Lys	Glu	Thr	Glu	Leu	Arg	Lys	Leu	Lys	Val	Leu	Gly	Ser	Gly	Val	Phe	705	710	715
Gly	Thr	Val	His	Lys	Gly	Val	Trp	Ile	Pro	Glu	Gly	Glu	Ser	Ile	Lys	725	730	735
Ile	Pro	Val	Cys	Ile	Lys	Val	Ile	Glu	Asp	Lys	Ser	Gly	Arg	Gln	Ser	740	745	750
Phe	Gln	Ala	Val	Thr	Asp	His	Met	Leu	Ala	Ile	Gly	Ser	Leu	Asp	His			

ITI-08-PCT_Sequence_Listing_ST25.txt

755

760

765

Ala His Ile Val Arg Leu Leu Gly Leu Cys Pro Gly Ser Ser Leu Gln
770 775 780

Leu Val Thr Gln Tyr Leu Pro Leu Gly Ser Leu Leu Asp His Val Arg
785 790 795 800

Gln His Arg Gly Ala Leu Gly Pro Gln Leu Leu Leu Asn Trp Gly Val
805 810 815

Gln Ile Ala Lys Gly Met Tyr Tyr Leu Glu Glu His Gly Met Val His
820 825 830

Arg Asn Leu Ala Ala Arg Asn Val Leu Leu Lys Ser Pro Ser Gln Val
835 840 845

Gln Val Ala Asp Phe Gly Val Ala Asp Leu Leu Pro Pro Asp Asp Lys
850 855 860

Gln Leu Leu Tyr Ser Glu Ala Lys Thr Pro Ile Lys Trp Met Ala Leu
865 870 875 880

Glu Ser Ile His Phe Gly Lys Tyr Thr His Gln Ser Asp Val Trp Ser
885 890 895

Tyr Gly Gln Cys Ile Trp Met Pro Ser Leu Pro Ser Leu Ala Pro Val
900 905 910

Ser Asn Leu Pro Phe Glu Thr Pro Ser
915 920

<210> 350
<211> 1308
<212> PRT
<213> Artificial Sequence

<220>
<223> ERBB4__Homo_sapiens__Q15303

<400> 350

Met Lys Pro Ala Thr Gly Leu Trp Val Trp Val Ser Leu Leu Val Ala
1 5 10 15

Ala Gly Thr Val Gln Pro Ser Asp Ser Gln Ser Val Cys Ala Gly Thr
20 25 30

Glu Asn Lys Leu Ser Ser Leu Ser Asp Leu Glu Gln Gln Tyr Arg Ala
35 40 45

Leu Arg Lys Tyr Tyr Glu Asn Cys Glu Val Val Met Gly Asn Leu Glu

ITI-08-PCT_Sequence_Listing_ST25.txt

50	55	60													
Ile	Thr	Ser	Ile	Glu	His	Asn	Arg	Asp	Leu	Ser	Phe	Leu	Arg	Ser	Val
65					70					75					80
Arg	Glu	Val	Thr	Gly	Tyr	Val	Leu	Val	Ala	Leu	Asn	Gln	Phe	Arg	Tyr
				85					90					95	
Leu	Pro	Leu	Glu	Asn	Leu	Arg	Ile	Ile	Arg	Gly	Thr	Lys	Leu	Tyr	Glu
			100					105					110		
Asp	Arg	Tyr	Ala	Leu	Ala	Ile	Phe	Leu	Asn	Tyr	Arg	Lys	Asp	Gly	Asn
		115					120					125			
Phe	Gly	Leu	Gln	Glu	Leu	Gly	Leu	Lys	Asn	Leu	Thr	Glu	Ile	Leu	Asn
	130					135					140				
Gly	Gly	Val	Tyr	Val	Asp	Gln	Asn	Lys	Phe	Leu	Cys	Tyr	Ala	Asp	Thr
145					150					155					160
Ile	His	Trp	Gln	Asp	Ile	Val	Arg	Asn	Pro	Trp	Pro	Ser	Asn	Leu	Thr
				165					170					175	
Leu	Val	Ser	Thr	Asn	Gly	Ser	Ser	Gly	Cys	Gly	Arg	Cys	His	Lys	Ser
			180					185					190		
Cys	Thr	Gly	Arg	Cys	Trp	Gly	Pro	Thr	Glu	Asn	His	Cys	Gln	Thr	Leu
		195					200					205			
Thr	Arg	Thr	Val	Cys	Ala	Glu	Gln	Cys	Asp	Gly	Arg	Cys	Tyr	Gly	Pro
	210					215					220				
Tyr	Val	Ser	Asp	Cys	Cys	His	Arg	Glu	Cys	Ala	Gly	Gly	Cys	Ser	Gly
225					230					235					240
Pro	Lys	Asp	Thr	Asp	Cys	Phe	Ala	Cys	Met	Asn	Phe	Asn	Asp	Ser	Gly
				245					250					255	
Ala	Cys	Val	Thr	Gln	Cys	Pro	Gln	Thr	Phe	Val	Tyr	Asn	Pro	Thr	Thr
			260					265					270		
Phe	Gln	Leu	Glu	His	Asn	Phe	Asn	Ala	Lys	Tyr	Thr	Tyr	Gly	Ala	Phe
		275					280					285			
Cys	Val	Lys	Lys	Cys	Pro	His	Asn	Phe	Val	Val	Asp	Ser	Ser	Ser	Cys
	290					295					300				
Val	Arg	Ala	Cys	Pro	Ser	Ser	Lys	Met	Glu	Val	Glu	Glu	Asn	Gly	Ile
305					310					315					320
Lys	Met	Cys	Lys	Pro	Cys	Thr	Asp	Ile	Cys	Pro	Lys	Ala	Cys	Asp	Gly
				325					330					335	

ITI-08-PCT_Sequence_Listing_ST25.txt

Ile	Gly	Thr	Gly	Ser	Leu	Met	Ser	Ala	Gln	Thr	Val	Asp	Ser	Ser	Asn	340	345	350	
Ile	Asp	Lys	Phe	Ile	Asn	Cys	Thr	Lys	Ile	Asn	Gly	Asn	Leu	Ile	Phe	355	360	365	
Leu	Val	Thr	Gly	Ile	His	Gly	Asp	Pro	Tyr	Asn	Ala	Ile	Glu	Ala	Ile	370	375	380	
Asp	Pro	Glu	Lys	Leu	Asn	Val	Phe	Arg	Thr	Val	Arg	Glu	Ile	Thr	Gly	385	390	395	400
Phe	Leu	Asn	Ile	Gln	Ser	Trp	Pro	Pro	Asn	Met	Thr	Asp	Phe	Ser	Val	405	410	415	
Phe	Ser	Asn	Leu	Val	Thr	Ile	Gly	Gly	Arg	Val	Leu	Tyr	Ser	Gly	Leu	420	425	430	
Ser	Leu	Leu	Ile	Leu	Lys	Gln	Gln	Gly	Ile	Thr	Ser	Leu	Gln	Phe	Gln	435	440	445	
Ser	Leu	Lys	Glu	Ile	Ser	Ala	Gly	Asn	Ile	Tyr	Ile	Thr	Asp	Asn	Ser	450	455	460	
Asn	Leu	Cys	Tyr	Tyr	His	Thr	Ile	Asn	Trp	Thr	Thr	Leu	Phe	Ser	Thr	465	470	475	480
Ile	Asn	Gln	Arg	Ile	Val	Ile	Arg	Asp	Asn	Arg	Lys	Ala	Glu	Asn	Cys	485	490	495	
Thr	Ala	Glu	Gly	Met	Val	Cys	Asn	His	Leu	Cys	Ser	Ser	Asp	Gly	Cys	500	505	510	
Trp	Gly	Pro	Gly	Pro	Asp	Gln	Cys	Leu	Ser	Cys	Arg	Arg	Phe	Ser	Arg	515	520	525	
Gly	Arg	Ile	Cys	Ile	Glu	Ser	Cys	Asn	Leu	Tyr	Asp	Gly	Glu	Phe	Arg	530	535	540	
Glu	Phe	Glu	Asn	Gly	Ser	Ile	Cys	Val	Glu	Cys	Asp	Pro	Gln	Cys	Glu	545	550	555	560
Lys	Met	Glu	Asp	Gly	Leu	Leu	Thr	Cys	His	Gly	Pro	Gly	Pro	Asp	Asn	565	570	575	
Cys	Thr	Lys	Cys	Ser	His	Phe	Lys	Asp	Gly	Pro	Asn	Cys	Val	Glu	Lys	580	585	590	
Cys	Pro	Asp	Gly	Leu	Gln	Gly	Ala	Asn	Ser	Phe	Ile	Phe	Lys	Tyr	Ala	595	600	605	

ITI-08-PCT_Sequence_Listing_ST25.txt

Asp	Pro	Asp	Arg	Glu	Cys	His	Pro	Cys	His	Pro	Asn	Cys	Thr	Gln	Gly	610	615	620
Cys	Asn	Gly	Pro	Thr	Ser	His	Asp	Cys	Ile	Tyr	Tyr	Pro	Trp	Thr	Gly	625	630	635
His	Ser	Thr	Leu	Pro	Gln	His	Ala	Arg	Thr	Pro	Leu	Ile	Ala	Ala	Gly	645	650	655
Val	Ile	Gly	Gly	Leu	Phe	Ile	Leu	Val	Ile	Val	Gly	Leu	Thr	Phe	Ala	660	665	670
Val	Tyr	Val	Arg	Arg	Lys	Ser	Ile	Lys	Lys	Lys	Arg	Ala	Leu	Arg	Arg	675	680	685
Phe	Leu	Glu	Thr	Glu	Leu	Val	Glu	Pro	Leu	Thr	Pro	Ser	Gly	Thr	Ala	690	695	700
Pro	Asn	Gln	Ala	Gln	Leu	Arg	Ile	Leu	Lys	Glu	Thr	Glu	Leu	Lys	Arg	705	710	715
Val	Lys	Val	Leu	Gly	Ser	Gly	Ala	Phe	Gly	Thr	Val	Tyr	Lys	Gly	Ile	725	730	735
Trp	Val	Pro	Glu	Gly	Glu	Thr	Val	Lys	Ile	Pro	Val	Ala	Ile	Lys	Ile	740	745	750
Leu	Asn	Glu	Thr	Thr	Gly	Pro	Lys	Ala	Asn	Val	Glu	Phe	Met	Asp	Glu	755	760	765
Ala	Leu	Ile	Met	Ala	Ser	Met	Asp	His	Pro	His	Leu	Val	Arg	Leu	Leu	770	775	780
Gly	Val	Cys	Leu	Ser	Pro	Thr	Ile	Gln	Leu	Val	Thr	Gln	Leu	Met	Pro	785	790	795
His	Gly	Cys	Leu	Leu	Glu	Tyr	Val	His	Glu	His	Lys	Asp	Asn	Ile	Gly	805	810	815
Ser	Gln	Leu	Leu	Leu	Asn	Trp	Cys	Val	Gln	Ile	Ala	Lys	Gly	Met	Met	820	825	830
Tyr	Leu	Glu	Glu	Arg	Arg	Leu	Val	His	Arg	Asp	Leu	Ala	Ala	Arg	Asn	835	840	845
Val	Leu	Val	Lys	Ser	Pro	Asn	His	Val	Lys	Ile	Thr	Asp	Phe	Gly	Leu	850	855	860
Ala	Arg	Leu	Leu	Glu	Gly	Asp	Glu	Lys	Glu	Tyr	Asn	Ala	Asp	Gly	Gly	865	870	875
Lys	Met	Pro	Ile	Lys	Trp	Met	Ala	Leu	Glu	Cys	Ile	His	Tyr	Arg	Lys			

ITI-08-PCT_Sequence_Listing_ST25.txt

885

890

895

Phe Thr His Gln Ser Asp Val Trp Ser Tyr Gly Val Thr Ile Trp Glu
 900 905 910

Leu Met Thr Phe Gly Gly Lys Pro Tyr Asp Gly Ile Pro Thr Arg Glu
 915 920 925

Ile Pro Asp Leu Leu Glu Lys Gly Glu Arg Leu Pro Gln Pro Pro Ile
 930 935 940

Cys Thr Ile Asp Val Tyr Met Val Met Val Lys Cys Trp Met Ile Asp
 945 950 955 960

Ala Asp Ser Arg Pro Lys Phe Lys Glu Leu Ala Ala Glu Phe Ser Arg
 965 970 975

Met Ala Arg Asp Pro Gln Arg Tyr Leu Val Ile Gln Gly Asp Asp Arg
 980 985 990

Met Lys Leu Pro Ser Pro Asn Asp Ser Lys Phe Phe Gln Asn Leu Leu
 995 1000 1005

Asp Glu Glu Asp Leu Glu Asp Met Met Asp Ala Glu Glu Tyr Leu
 1010 1015 1020

Val Pro Gln Ala Phe Asn Ile Pro Pro Pro Ile Tyr Thr Ser Arg
 1025 1030 1035

Ala Arg Ile Asp Ser Asn Arg Ser Glu Ile Gly His Ser Pro Pro
 1040 1045 1050

Pro Ala Tyr Thr Pro Met Ser Gly Asn Gln Phe Val Tyr Arg Asp
 1055 1060 1065

Gly Gly Phe Ala Ala Glu Gln Gly Val Ser Val Pro Tyr Arg Ala
 1070 1075 1080

Pro Thr Ser Thr Ile Pro Glu Ala Pro Val Ala Gln Gly Ala Thr
 1085 1090 1095

Ala Glu Ile Phe Asp Asp Ser Cys Cys Asn Gly Thr Leu Arg Lys
 1100 1105 1110

Pro Val Ala Pro His Val Gln Glu Asp Ser Ser Thr Gln Arg Tyr
 1115 1120 1125

Ser Ala Asp Pro Thr Val Phe Ala Pro Glu Arg Ser Pro Arg Gly
 1130 1135 1140

Glu Leu Asp Glu Glu Gly Tyr Met Thr Pro Met Arg Asp Lys Pro
 1145 1150 1155

ITI-08-PCT_Sequence_Listing_ST25.txt

Lys Gln Glu Tyr Leu Asn Pro Val Glu Glu Asn Pro Phe Val Ser
1160 1165 1170

Arg Arg Lys Asn Gly Asp Leu Gln Ala Leu Asp Asn Pro Glu Tyr
1175 1180 1185

His Asn Ala Ser Asn Gly Pro Pro Lys Ala Glu Asp Glu Tyr Val
1190 1195 1200

Asn Glu Pro Leu Tyr Leu Asn Thr Phe Ala Asn Thr Leu Gly Lys
1205 1210 1215

Ala Glu Tyr Leu Lys Asn Asn Ile Leu Ser Met Pro Glu Lys Ala
1220 1225 1230

Lys Lys Ala Phe Asp Asn Pro Asp Tyr Trp Asn His Ser Leu Pro
1235 1240 1245

Pro Arg Ser Thr Leu Gln His Pro Asp Tyr Leu Gln Glu Tyr Ser
1250 1255 1260

Thr Lys Tyr Phe Tyr Lys Gln Asn Gly Arg Ile Arg Pro Ile Val
1265 1270 1275

Ala Glu Asn Pro Glu Tyr Leu Ser Glu Phe Ser Leu Lys Pro Gly
1280 1285 1290

Thr Val Leu Pro Pro Pro Pro Tyr Arg His Arg Asn Thr Val Val
1295 1300 1305

<210> 351
<211> 486
<212> PRT
<213> Artificial Sequence

<220>
<223> ERG__Homo_sapiens__P11308

<400> 351

Met Ile Gln Thr Val Pro Asp Pro Ala Ala His Ile Lys Glu Ala Leu
1 5 10 15

Ser Val Val Ser Glu Asp Gln Ser Leu Phe Glu Cys Ala Tyr Gly Thr
20 25 30

Pro His Leu Ala Lys Thr Glu Met Thr Ala Ser Ser Ser Ser Asp Tyr
35 40 45

Gly Gln Thr Ser Lys Met Ser Pro Arg Val Pro Gln Gln Asp Trp Leu
50 55 60

ITI-08-PCT_Sequence_Listing_ST25.txt

Ser	Gln	Pro	Pro	Ala	Arg	Val	Thr	Ile	Lys	Met	Glu	Cys	Asn	Pro	Ser	65	70	75	80
Gln	Val	Asn	Gly	Ser	Arg	Asn	Ser	Pro	Asp	Glu	Cys	Ser	Val	Ala	Lys	85	90	95	
Gly	Gly	Lys	Met	Val	Gly	Ser	Pro	Asp	Thr	Val	Gly	Met	Asn	Tyr	Gly	100	105	110	
Ser	Tyr	Met	Glu	Glu	Lys	His	Met	Pro	Pro	Pro	Asn	Met	Thr	Thr	Asn	115	120	125	
Glu	Arg	Arg	Val	Ile	Val	Pro	Ala	Asp	Pro	Thr	Leu	Trp	Ser	Thr	Asp	130	135	140	
His	Val	Arg	Gln	Trp	Leu	Glu	Trp	Ala	Val	Lys	Glu	Tyr	Gly	Leu	Pro	145	150	155	160
Asp	Val	Asn	Ile	Leu	Leu	Phe	Gln	Asn	Ile	Asp	Gly	Lys	Glu	Leu	Cys	165	170	175	
Lys	Met	Thr	Lys	Asp	Asp	Phe	Gln	Arg	Leu	Thr	Pro	Ser	Tyr	Asn	Ala	180	185	190	
Asp	Ile	Leu	Leu	Ser	His	Leu	His	Tyr	Leu	Arg	Glu	Thr	Pro	Leu	Pro	195	200	205	
His	Leu	Thr	Ser	Asp	Asp	Val	Asp	Lys	Ala	Leu	Gln	Asn	Ser	Pro	Arg	210	215	220	
Leu	Met	His	Ala	Arg	Asn	Thr	Gly	Gly	Ala	Ala	Phe	Ile	Phe	Pro	Asn	225	230	235	240
Thr	Ser	Val	Tyr	Pro	Glu	Ala	Thr	Gln	Arg	Ile	Thr	Thr	Arg	Pro	Asp	245	250	255	
Leu	Pro	Tyr	Glu	Pro	Pro	Arg	Arg	Ser	Ala	Trp	Thr	Gly	His	Gly	His	260	265	270	
Pro	Thr	Pro	Gln	Ser	Lys	Ala	Ala	Gln	Pro	Ser	Pro	Ser	Thr	Val	Pro	275	280	285	
Lys	Thr	Glu	Asp	Gln	Arg	Pro	Gln	Leu	Asp	Pro	Tyr	Gln	Ile	Leu	Gly	290	295	300	
Pro	Thr	Ser	Ser	Arg	Leu	Ala	Asn	Pro	Gly	Ser	Gly	Gln	Ile	Gln	Leu	305	310	315	320
Trp	Gln	Phe	Leu	Leu	Glu	Leu	Leu	Ser	Asp	Ser	Ser	Asn	Ser	Ser	Cys	325	330	335	

ITI-08-PCT_Sequence_Listing_ST25.txt

Ile Thr Trp Glu Gly Thr Asn Gly Glu Phe Lys Met Thr Asp Pro Asp
340 345 350

Glu Val Ala Arg Arg Trp Gly Glu Arg Lys Ser Lys Pro Asn Met Asn
355 360 365

Tyr Asp Lys Leu Ser Arg Ala Leu Arg Tyr Tyr Tyr Asp Lys Asn Ile
370 375 380

Met Thr Lys Val His Gly Lys Arg Tyr Ala Tyr Lys Phe Asp Phe His
385 390 395 400

Gly Ile Ala Gln Ala Leu Gln Pro His Pro Pro Glu Ser Ser Leu Tyr
405 410 415

Lys Tyr Pro Ser Asp Leu Pro Tyr Met Gly Ser Tyr His Ala His Pro
420 425 430

Gln Lys Met Asn Phe Val Ala Pro His Pro Pro Ala Leu Pro Val Thr
435 440 445

Ser Ser Ser Phe Phe Ala Ala Pro Asn Pro Tyr Trp Asn Ser Pro Thr
450 455 460

Gly Gly Ile Tyr Pro Asn Thr Arg Leu Pro Thr Ser His Met Pro Ser
465 470 475 480

His Leu Gly Thr Tyr Tyr
485

<210> 352
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> ETV6__Homo_sapiens__P41212

<400> 352

Met Ser Glu Thr Pro Ala Gln Cys Ser Ile Lys Gln Glu Arg Ile Ser
1 5 10 15

Tyr Thr Pro Pro Glu Ser Pro Val Pro Ser Tyr Ala Ser Ser Thr Pro
20 25 30

Leu His Val Pro Val Pro Arg Ala Leu Arg Met Glu Glu Asp Ser Ile
35 40 45

Arg Leu Pro Ala His Leu Arg Leu Gln Pro Ile Tyr Trp Ser Arg Asp
50 55 60

ITI-08-PCT_Sequence_Listing_ST25.txt

Asp	Val	Ala	Gln	Trp	Leu	Lys	Trp	Ala	Glu	Asn	Glu	Phe	Ser	Leu	Arg	65	70	75	80
Pro	Ile	Asp	Ser	Asn	Thr	Phe	Glu	Met	Asn	Gly	Lys	Ala	Leu	Leu	Leu	85	90	95	
Leu	Thr	Lys	Glu	Asp	Phe	Arg	Tyr	Arg	Ser	Pro	His	Ser	Gly	Asp	Val	100	105	110	
Leu	Tyr	Glu	Leu	Leu	Gln	His	Ile	Leu	Lys	Gln	Arg	Lys	Pro	Arg	Ile	115	120	125	
Leu	Phe	Ser	Pro	Phe	Phe	His	Pro	Gly	Asn	Ser	Ile	His	Thr	Gln	Pro	130	135	140	
Glu	Val	Ile	Leu	His	Gln	Asn	His	Glu	Glu	Asp	Asn	Cys	Val	Gln	Arg	145	150	155	160
Thr	Pro	Arg	Pro	Ser	Val	Asp	Asn	Val	His	His	Asn	Pro	Pro	Thr	Ile	165	170	175	
Glu	Leu	Leu	His	Arg	Ser	Arg	Ser	Pro	Ile	Thr	Thr	Asn	His	Arg	Pro	180	185	190	
Ser	Pro	Asp	Pro	Glu	Gln	Arg	Pro	Leu	Arg	Ser	Pro	Leu	Asp	Asn	Met	195	200	205	
Ile	Arg	Arg	Leu	Ser	Pro	Ala	Glu	Arg	Ala	Gln	Gly	Pro	Arg	Pro	His	210	215	220	
Gln	Glu	Asn	Asn	His	Gln	Glu	Ser	Tyr	Pro	Leu	Ser	Val	Ser	Pro	Met	225	230	235	240
Glu	Asn	Asn	His	Cys	Pro	Ala	Ser	Ser	Glu	Ser	His	Pro	Lys	Pro	Ser	245	250	255	
Ser	Pro	Arg	Gln	Glu	Ser	Thr	Arg	Val	Ile	Gln	Leu	Met	Pro	Ser	Pro	260	265	270	
Ile	Met	His	Pro	Leu	Ile	Leu	Asn	Pro	Arg	His	Ser	Val	Asp	Phe	Lys	275	280	285	
Gln	Ser	Arg	Leu	Ser	Glu	Asp	Gly	Leu	His	Arg	Glu	Gly	Lys	Pro	Ile	290	295	300	
Asn	Leu	Ser	His	Arg	Glu	Asp	Leu	Ala	Tyr	Met	Asn	His	Ile	Met	Val	305	310	315	320
Ser	Val	Ser	Pro	Pro	Glu	Glu	His	Ala	Met	Pro	Ile	Gly	Arg	Ile	Ala	325	330	335	
Asp	Cys	Arg	Leu	Leu	Trp	Asp	Tyr	Val	Tyr	Gln	Leu	Leu	Ser	Asp	Ser				

ITI-08-PCT_Sequence_Listing_ST25.txt

340

345

350

Arg Tyr Glu Asn Phe Ile Arg Trp Glu Asp Lys Glu Ser Lys Ile Phe
355 360 365

Arg Ile Val Asp Pro Asn Gly Leu Ala Arg Leu Trp Gly Asn His Lys
370 375 380

Asn Arg Thr Asn Met Thr Tyr Glu Lys Met Ser Arg Ala Leu Arg His
385 390 395 400

Tyr Tyr Lys Leu Asn Ile Ile Arg Lys Glu Pro Gly Gln Arg Leu Leu
405 410 415

Phe Arg Phe Met Lys Thr Pro Asp Glu Ile Met Ser Gly Arg Thr Asp
420 425 430

Arg Leu Glu His Leu Glu Ser Gln Glu Leu Asp Glu Gln Ile Tyr Gln
435 440 445

Glu Asp Glu Cys
450

<210> 353

<211> 656

<212> PRT

<213> Artificial Sequence

<220>

<223> EWS__Homo_sapiens__Q01844

<400> 353

Met Ala Ser Thr Asp Tyr Ser Thr Tyr Ser Gln Ala Ala Ala Gln Gln
1 5 10 15

Gly Tyr Ser Ala Tyr Thr Ala Gln Pro Thr Gln Gly Tyr Ala Gln Thr
20 25 30

Thr Gln Ala Tyr Gly Gln Gln Ser Tyr Gly Thr Tyr Gly Gln Pro Thr
35 40 45

Asp Val Ser Tyr Thr Gln Ala Gln Thr Thr Ala Thr Tyr Gly Gln Thr
50 55 60

Ala Tyr Ala Thr Ser Tyr Gly Gln Pro Pro Thr Gly Tyr Thr Thr Pro
65 70 75 80

Thr Ala Pro Gln Ala Tyr Ser Gln Pro Val Gln Gly Tyr Gly Thr Gly
85 90 95

Ala Tyr Asp Thr Thr Thr Ala Thr Val Thr Thr Thr Gln Ala Ser Tyr

ITI-08-PCT_Sequence_Listing_ST25.txt

100	105	110																	
Ala	Ala	Gln	Ser	Ala	Tyr	Gly	Thr	Gln	Pro	Ala	Tyr	Pro	Ala	Tyr	Gly				
	115					120					125								
Gln	Gln	Pro	Ala	Ala	Thr	Ala	Pro	Thr	Arg	Pro	Gln	Asp	Gly	Asn	Lys				
	130					135					140								
Pro	Thr	Glu	Thr	Ser	Gln	Pro	Gln	Ser	Ser	Thr	Gly	Gly	Tyr	Asn	Gln				
145					150					155					160				
Pro	Ser	Leu	Gly	Tyr	Gly	Gln	Ser	Asn	Tyr	Ser	Tyr	Pro	Gln	Val	Pro				
				165					170					175					
Gly	Ser	Tyr	Pro	Met	Gln	Pro	Val	Thr	Ala	Pro	Pro	Ser	Tyr	Pro	Pro				
			180					185					190						
Thr	Ser	Tyr	Ser	Ser	Thr	Gln	Pro	Thr	Ser	Tyr	Asp	Gln	Ser	Ser	Tyr				
	195						200					205							
Ser	Gln	Gln	Asn	Thr	Tyr	Gly	Gln	Pro	Ser	Ser	Tyr	Gly	Gln	Gln	Ser				
	210					215					220								
Ser	Tyr	Gly	Gln	Gln	Ser	Ser	Tyr	Gly	Gln	Gln	Pro	Pro	Thr	Ser	Tyr				
225					230					235					240				
Pro	Pro	Gln	Thr	Gly	Ser	Tyr	Ser	Gln	Ala	Pro	Ser	Gln	Tyr	Ser	Gln				
				245					250					255					
Gln	Ser	Ser	Ser	Tyr	Gly	Gln	Gln	Ser	Ser	Phe	Arg	Gln	Asp	His	Pro				
			260					265					270						
Ser	Ser	Met	Gly	Val	Tyr	Gly	Gln	Glu	Ser	Gly	Gly	Phe	Ser	Gly	Pro				
		275					280					285							
Gly	Glu	Asn	Arg	Ser	Met	Ser	Gly	Pro	Asp	Asn	Arg	Gly	Arg	Gly	Arg				
	290					295					300								
Gly	Gly	Phe	Asp	Arg	Gly	Gly	Met	Ser	Arg	Gly	Gly	Arg	Gly	Gly	Gly				
305					310				315						320				
Arg	Gly	Gly	Met	Gly	Ser	Ala	Gly	Glu	Arg	Gly	Gly	Phe	Asn	Lys	Pro				
				325					330					335					
Gly	Gly	Pro	Met	Asp	Glu	Gly	Pro	Asp	Leu	Asp	Leu	Gly	Pro	Pro	Val				
			340					345					350						
Asp	Pro	Asp	Glu	Asp	Ser	Asp	Asn	Ser	Ala	Ile	Tyr	Val	Gln	Gly	Leu				
		355					360					365							
Asn	Asp	Ser	Val	Thr	Leu	Asp	Asp	Leu	Ala	Asp	Phe	Phe	Lys	Gln	Cys				
	370					375					380								

ITI-08-PCT_Sequence_Listing_ST25.txt

Gly	Val	Val	Lys	Met	Asn	Lys	Arg	Thr	Gly	Gln	Pro	Met	Ile	His	Ile	385	390	395	400
Tyr	Leu	Asp	Lys	Glu	Thr	Gly	Lys	Pro	Lys	Gly	Asp	Ala	Thr	Val	Ser	405	410	415	
Tyr	Glu	Asp	Pro	Pro	Thr	Ala	Lys	Ala	Ala	Val	Glu	Trp	Phe	Asp	Gly	420	425	430	
Lys	Asp	Phe	Gln	Gly	Ser	Lys	Leu	Lys	Val	Ser	Leu	Ala	Arg	Lys	Lys	435	440	445	
Pro	Pro	Met	Asn	Ser	Met	Arg	Gly	Gly	Leu	Pro	Pro	Arg	Glu	Gly	Arg	450	455	460	
Gly	Met	Pro	Pro	Pro	Leu	Arg	Gly	Gly	Pro	Gly	Gly	Pro	Gly	Gly	Pro	465	470	475	480
Gly	Gly	Pro	Met	Gly	Arg	Met	Gly	Gly	Arg	Gly	Gly	Asp	Arg	Gly	Gly	485	490	495	
Phe	Pro	Pro	Arg	Gly	Pro	Arg	Gly	Ser	Arg	Gly	Asn	Pro	Ser	Gly	Gly	500	505	510	
Gly	Asn	Val	Gln	His	Arg	Ala	Gly	Asp	Trp	Gln	Cys	Pro	Asn	Pro	Gly	515	520	525	
Cys	Gly	Asn	Gln	Asn	Phe	Ala	Trp	Arg	Thr	Glu	Cys	Asn	Gln	Cys	Lys	530	535	540	
Ala	Pro	Lys	Pro	Glu	Gly	Phe	Leu	Pro	Pro	Pro	Phe	Pro	Pro	Pro	Gly	545	550	555	560
Gly	Asp	Arg	Gly	Arg	Gly	Gly	Pro	Gly	Gly	Met	Arg	Gly	Gly	Arg	Gly	565	570	575	
Gly	Leu	Met	Asp	Arg	Gly	Gly	Pro	Gly	Gly	Met	Phe	Arg	Gly	Gly	Arg	580	585	590	
Gly	Gly	Asp	Arg	Gly	Gly	Phe	Arg	Gly	Gly	Arg	Gly	Met	Asp	Arg	Gly	595	600	605	
Gly	Phe	Gly	Gly	Gly	Arg	Arg	Gly	Gly	Pro	Gly	Gly	Pro	Pro	Gly	Pro	610	615	620	
Leu	Met	Glu	Gln	Met	Gly	Gly	Arg	Arg	Gly	Gly	Arg	Gly	Gly	Pro	Gly	625	630	635	640
Lys	Met	Asp	Lys	Gly	Glu	His	Arg	Gln	Glu	Arg	Arg	Asp	Arg	Pro	Tyr	645	650	655	

ITI-08-PCT_Sequence_Listing_ST25.txt

<210> 354

<211> 665

<212> PRT

<213> Artificial Sequence

<220>

<223> EZH2__Homo_sapiens__F2YMM1

<400> 354

Met Gly Gln Thr Gly Lys Lys Ser Glu Lys Gly Pro Val Cys Trp Arg
1 5 10 15

Lys Arg Val Lys Ser Glu Tyr Met Arg Leu Arg Gln Leu Lys Arg Phe
20 25 30

Arg Arg Ala Asp Glu Val Lys Ser Met Phe Ser Ser Asn Arg Gln Lys
35 40 45

Ile Leu Glu Arg Thr Glu Ile Leu Asn Gln Glu Trp Lys Gln Arg Arg
50 55 60

Ile Gln Pro Val His Ile Leu Thr Ser Val Ser Ser Leu Arg Gly Thr
65 70 75 80

Arg Glu Val Glu Asp Glu Thr Val Leu His Asn Ile Pro Tyr Met Gly
85 90 95

Asp Glu Val Leu Asp Gln Asp Gly Thr Phe Ile Glu Glu Leu Ile Lys
100 105 110

Asn Tyr Asp Gly Lys Val His Gly Asp Arg Glu Cys Gly Phe Ile Asn
115 120 125

Asp Glu Ile Phe Val Glu Leu Val Asn Ala Leu Gly Gln Tyr Asn Asp
130 135 140

Asp Asp Asp Asp Asp Asp Gly Asp Asp Pro Glu Glu Arg Glu Glu Lys
145 150 155 160

Gln Lys Asp Leu Glu Asp His Arg Asp Asp Lys Glu Ser Arg Pro Pro
165 170 175

Arg Lys Phe Pro Ser Asp Lys Ile Phe Glu Ala Ile Ser Ser Met Phe
180 185 190

Pro Asp Lys Gly Thr Ala Glu Glu Leu Lys Glu Lys Tyr Lys Glu Leu
195 200 205

Thr Glu Gln Gln Leu Pro Gly Ala Leu Pro Pro Glu Cys Thr Pro Asn
210 215 220

ITI-08-PCT_Sequence_Listing_ST25.txt

Ile	Asp	Gly	Pro	Asn	Ala	Lys	Ser	Val	Gln	Arg	Glu	Gln	Ser	Leu	His	225	230	235	240
Ser	Phe	His	Thr	Leu	Phe	Cys	Arg	Arg	Cys	Phe	Lys	Tyr	Asp	Cys	Phe	245	250	255	
Leu	His	Pro	Phe	His	Ala	Thr	Pro	Asn	Thr	Tyr	Lys	Arg	Lys	Asn	Thr	260	265	270	
Glu	Thr	Ala	Leu	Asp	Asn	Lys	Pro	Cys	Gly	Pro	Gln	Cys	Tyr	Gln	His	275	280	285	
Leu	Glu	Gly	Ala	Lys	Glu	Phe	Ala	Ala	Ala	Leu	Thr	Ala	Glu	Arg	Ile	290	295	300	
Lys	Thr	Pro	Pro	Lys	Arg	Pro	Gly	Gly	Arg	Arg	Arg	Gly	Arg	Leu	Pro	305	310	315	320
Asn	Asn	Ser	Ser	Arg	Pro	Ser	Thr	Pro	Thr	Ile	Asn	Val	Leu	Glu	Ser	325	330	335	
Lys	Asp	Thr	Asp	Ser	Asp	Arg	Glu	Ala	Gly	Thr	Glu	Thr	Gly	Gly	Glu	340	345	350	
Asn	Asn	Asp	Lys	Glu	Glu	Glu	Glu	Lys	Lys	Asp	Glu	Thr	Ser	Ser	Ser	355	360	365	
Ser	Glu	Ala	Asn	Ser	Arg	Cys	Gln	Thr	Pro	Ile	Lys	Met	Lys	Pro	Asn	370	375	380	
Ile	Glu	Pro	Pro	Glu	Asn	Val	Glu	Trp	Ser	Gly	Ala	Glu	Ala	Ser	Met	385	390	395	400
Phe	Arg	Val	Leu	Ile	Gly	Thr	Tyr	Tyr	Asp	Asn	Phe	Cys	Ala	Ile	Ala	405	410	415	
Arg	Leu	Ile	Gly	Thr	Lys	Thr	Cys	Arg	Gln	Val	Tyr	Glu	Phe	Arg	Val	420	425	430	
Lys	Glu	Ser	Ser	Ile	Ile	Ala	Pro	Ala	Pro	Ala	Glu	Asp	Val	Asp	Thr	435	440	445	
Pro	Pro	Arg	Lys	Lys	Lys	Arg	Lys	His	Arg	Leu	Trp	Ala	Ala	His	Cys	450	455	460	
Arg	Lys	Ile	Gln	Leu	Lys	Lys	Gly	Gln	Asn	Arg	Phe	Pro	Gly	Cys	Arg	465	470	475	480
Cys	Lys	Ala	Gln	Cys	Asn	Thr	Lys	Gln	Cys	Pro	Cys	Tyr	Leu	Ala	Val	485	490	495	
Arg	Glu	Cys	Asp	Pro	Asp	Leu	Cys	Leu	Thr	Cys	Gly	Ala	Ala	Asp	His				

ITI-08-PCT_Sequence_Listing_ST25.txt

500

505

510

Trp Asp Ser Lys Asn Val Ser Cys Lys Asn Cys Ser Ile Gln Arg Gly
515 520 525

Ser Lys Lys His Leu Leu Leu Ala Pro Ser Asp Val Ala Gly Trp Gly
530 535 540

Ile Phe Ile Lys Asp Pro Val Gln Lys Asn Glu Phe Ile Ser Glu Tyr
545 550 555 560

Cys Gly Glu Ile Ile Ser Gln Asp Glu Ala Asp Arg Arg Gly Lys Val
565 570 575

Tyr Asp Lys Tyr Met Cys Ser Phe Leu Phe Asn Leu Asn Asn Asp Phe
580 585 590

Val Val Asp Ala Thr Arg Lys Gly Asn Lys Ile Arg Phe Ala Asn His
595 600 605

Ser Val Asn Pro Asn Cys Tyr Ala Lys Val Met Met Val Asn Gly Asp
610 615 620

His Arg Ile Gly Ile Phe Ala Lys Arg Ala Ile Gln Thr Gly Glu Glu
625 630 635 640

Leu Phe Phe Asp Tyr Arg Tyr Ser Gln Ala Asp Ala Leu Lys Tyr Val
645 650 655

Gly Ile Glu Arg Glu Met Glu Ile Pro
660 665

<210> 355

<211> 334

<212> PRT

<213> Artificial Sequence

<220>

<223> EZH2__Homo_sapiens__G3XAL2

<400> 355

Met Gly Gln Thr Gly Lys Lys Ser Glu Lys Gly Pro Val Cys Trp Arg
1 5 10 15

Lys Arg Val Lys Ser Glu Tyr Met Arg Leu Arg Gln Leu Lys Arg Phe
20 25 30

Arg Arg Ala Asp Glu Val Lys Ser Met Phe Ser Ser Asn Arg Gln Lys
35 40 45

Ile Leu Glu Arg Thr Glu Ile Leu Asn Gln Glu Trp Lys Gln Arg Arg

ITI-08-PCT_Sequence_Listing_ST25.txt

50						55						60					
Ile	Gln	Pro	Val	His	Ile	Leu	Thr	Ser	Val	Ser	Ser	Leu	Arg	Gly	Thr		
65					70					75					80		
Arg	Glu	Cys	Ser	Val	Thr	Ser	Asp	Leu	Asp	Phe	Pro	Thr	Gln	Val	Ile		
				85					90					95			
Pro	Leu	Lys	Thr	Leu	Asn	Ala	Val	Ala	Ser	Val	Pro	Ile	Met	Tyr	Ser		
			100					105					110				
Trp	Ser	Pro	Leu	Gln	Gln	Asn	Phe	Met	Val	Glu	Asp	Glu	Thr	Val	Leu		
		115					120					125					
His	Asn	Ile	Pro	Tyr	Met	Gly	Asp	Glu	Val	Leu	Asp	Gln	Asp	Gly	Thr		
	130					135					140						
Phe	Ile	Glu	Glu	Leu	Ile	Lys	Asn	Tyr	Asp	Gly	Lys	Val	His	Gly	Asp		
145					150					155					160		
Arg	Glu	Cys	Gly	Phe	Ile	Asn	Asp	Glu	Ile	Phe	Val	Glu	Leu	Val	Asn		
				165					170					175			
Ala	Leu	Gly	Gln	Tyr	Asn	Asp	Asp	Asp	Asp	Asp	Asp	Asp	Gly	Asp	Asp		
			180					185					190				
Pro	Glu	Glu	Arg	Glu	Glu	Lys	Gln	Lys	Asp	Leu	Glu	Asp	His	Arg	Asp		
		195					200					205					
Asp	Lys	Glu	Ser	Arg	Pro	Pro	Arg	Lys	Phe	Pro	Ser	Asp	Lys	Ile	Phe		
	210					215					220						
Glu	Ala	Ile	Ser	Ser	Met	Phe	Pro	Asp	Lys	Gly	Thr	Ala	Glu	Glu	Leu		
225					230					235					240		
Lys	Glu	Lys	Tyr	Lys	Glu	Leu	Thr	Glu	Gln	Gln	Leu	Pro	Gly	Ala	Leu		
				245					250					255			
Pro	Pro	Glu	Cys	Thr	Pro	Asn	Ile	Asp	Gly	Pro	Asn	Ala	Lys	Ser	Val		
			260					265					270				
Gln	Arg	Glu	Gln	Ser	Leu	His	Ser	Phe	His	Thr	Leu	Phe	Cys	Arg	Arg		
		275					280					285					
Cys	Phe	Lys	Tyr	Asp	Cys	Phe	Leu	His	Pro	Phe	His	Ala	Thr	Pro	Asn		
	290					295					300						
Thr	Tyr	Lys	Arg	Lys	Asn	Thr	Glu	Thr	Ala	Leu	Asp	Asn	Lys	Pro	Cys		
305					310					315					320		
Gly	Pro	Gln	Cys	Tyr	Gln	His	Leu	Pro	Leu	Leu	Pro	Arg	Asn				
				325					330								

ITI-08-PCT_Sequence_Listing_ST25.txt

<210> 356
 <211> 64
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> EZH2__Homo_sapiens__L0R855

<400> 356

Met	Pro	Leu	Val	Asn	Ile	Met	Met	Met	Thr	Met	Met	Met	Met	Glu	Thr
1				5					10					15	
Ile	Leu	Lys	Lys	Glu	Lys	Lys	Ser	Arg	Lys	Ile	Trp	Arg	Ile	Thr	Glu
			20					25					30		
Met	Ile	Lys	Lys	Ala	Ala	His	Leu	Gly	Asn	Phe	Leu	Leu	Ile	Lys	Phe
			35				40					45			
Leu	Lys	Pro	Phe	Pro	Gln	Cys	Phe	Gln	Ile	Arg	Ala	Gln	Gln	Lys	Asn
	50					55					60				

<210> 357
 <211> 746
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> EZH2__Homo_sapiens__Q15910

<400> 357

Met	Gly	Gln	Thr	Gly	Lys	Lys	Ser	Glu	Lys	Gly	Pro	Val	Cys	Trp	Arg
1				5					10					15	
Lys	Arg	Val	Lys	Ser	Glu	Tyr	Met	Arg	Leu	Arg	Gln	Leu	Lys	Arg	Phe
			20					25					30		
Arg	Arg	Ala	Asp	Glu	Val	Lys	Ser	Met	Phe	Ser	Ser	Asn	Arg	Gln	Lys
		35					40					45			
Ile	Leu	Glu	Arg	Thr	Glu	Ile	Leu	Asn	Gln	Glu	Trp	Lys	Gln	Arg	Arg
	50					55					60				
Ile	Gln	Pro	Val	His	Ile	Leu	Thr	Ser	Val	Ser	Ser	Leu	Arg	Gly	Thr
65					70				75					80	
Arg	Glu	Cys	Ser	Val	Thr	Ser	Asp	Leu	Asp	Phe	Pro	Thr	Gln	Val	Ile
				85					90					95	
Pro	Leu	Lys	Thr	Leu	Asn	Ala	Val	Ala	Ser	Val	Pro	Ile	Met	Tyr	Ser

ITI-08-PCT_Sequence_Listing_ST25.txt

```

100          105          110
Trp Ser Pro Leu Gln Gln Asn Phe Met Val Glu Asp Glu Thr Val Leu
115          120          125
His Asn Ile Pro Tyr Met Gly Asp Glu Val Leu Asp Gln Asp Gly Thr
130          135          140
Phe Ile Glu Glu Leu Ile Lys Asn Tyr Asp Gly Lys Val His Gly Asp
145          150          155          160
Arg Glu Cys Gly Phe Ile Asn Asp Glu Ile Phe Val Glu Leu Val Asn
165          170          175
Ala Leu Gly Gln Tyr Asn Asp Asp Asp Asp Asp Asp Gly Asp Asp
180          185          190
Pro Glu Glu Arg Glu Glu Lys Gln Lys Asp Leu Glu Asp His Arg Asp
195          200          205
Asp Lys Glu Ser Arg Pro Pro Arg Lys Phe Pro Ser Asp Lys Ile Phe
210          215          220
Glu Ala Ile Ser Ser Met Phe Pro Asp Lys Gly Thr Ala Glu Glu Leu
225          230          235          240
Lys Glu Lys Tyr Lys Glu Leu Thr Glu Gln Gln Leu Pro Gly Ala Leu
245          250          255
Pro Pro Glu Cys Thr Pro Asn Ile Asp Gly Pro Asn Ala Lys Ser Val
260          265          270
Gln Arg Glu Gln Ser Leu His Ser Phe His Thr Leu Phe Cys Arg Arg
275          280          285
Cys Phe Lys Tyr Asp Cys Phe Leu His Pro Phe His Ala Thr Pro Asn
290          295          300
Thr Tyr Lys Arg Lys Asn Thr Glu Thr Ala Leu Asp Asn Lys Pro Cys
305          310          315          320
Gly Pro Gln Cys Tyr Gln His Leu Glu Gly Ala Lys Glu Phe Ala Ala
325          330          335
Ala Leu Thr Ala Glu Arg Ile Lys Thr Pro Pro Lys Arg Pro Gly Gly
340          345          350
Arg Arg Arg Gly Arg Leu Pro Asn Asn Ser Ser Arg Pro Ser Thr Pro
355          360          365
Thr Ile Asn Val Leu Glu Ser Lys Asp Thr Asp Ser Asp Arg Glu Ala
370          375          380

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Gly	Thr	Glu	Thr	Gly	Gly	Glu	Asn	Asn	Asp	Lys	Glu	Glu	Glu	Glu	Lys	385	390	395	400
Lys	Asp	Glu	Thr	Ser	Ser	Ser	Ser	Glu	Ala	Asn	Ser	Arg	Cys	Gln	Thr	405	410	415	
Pro	Ile	Lys	Met	Lys	Pro	Asn	Ile	Glu	Pro	Pro	Glu	Asn	Val	Glu	Trp	420	425	430	
Ser	Gly	Ala	Glu	Ala	Ser	Met	Phe	Arg	Val	Leu	Ile	Gly	Thr	Tyr	Tyr	435	440	445	
Asp	Asn	Phe	Cys	Ala	Ile	Ala	Arg	Leu	Ile	Gly	Thr	Lys	Thr	Cys	Arg	450	455	460	
Gln	Val	Tyr	Glu	Phe	Arg	Val	Lys	Glu	Ser	Ser	Ile	Ile	Ala	Pro	Ala	465	470	475	480
Pro	Ala	Glu	Asp	Val	Asp	Thr	Pro	Pro	Arg	Lys	Lys	Lys	Arg	Lys	His	485	490	495	
Arg	Leu	Trp	Ala	Ala	His	Cys	Arg	Lys	Ile	Gln	Leu	Lys	Lys	Asp	Gly	500	505	510	
Ser	Ser	Asn	His	Val	Tyr	Asn	Tyr	Gln	Pro	Cys	Asp	His	Pro	Arg	Gln	515	520	525	
Pro	Cys	Asp	Ser	Ser	Cys	Pro	Cys	Val	Ile	Ala	Gln	Asn	Phe	Cys	Glu	530	535	540	
Lys	Phe	Cys	Gln	Cys	Ser	Ser	Glu	Cys	Gln	Asn	Arg	Phe	Pro	Gly	Cys	545	550	555	560
Arg	Cys	Lys	Ala	Gln	Cys	Asn	Thr	Lys	Gln	Cys	Pro	Cys	Tyr	Leu	Ala	565	570	575	
Val	Arg	Glu	Cys	Asp	Pro	Asp	Leu	Cys	Leu	Thr	Cys	Gly	Ala	Ala	Asp	580	585	590	
His	Trp	Asp	Ser	Lys	Asn	Val	Ser	Cys	Lys	Asn	Cys	Ser	Ile	Gln	Arg	595	600	605	
Gly	Ser	Lys	Lys	His	Leu	Leu	Leu	Ala	Pro	Ser	Asp	Val	Ala	Gly	Trp	610	615	620	
Gly	Ile	Phe	Ile	Lys	Asp	Pro	Val	Gln	Lys	Asn	Glu	Phe	Ile	Ser	Glu	625	630	635	640
Tyr	Cys	Gly	Glu	Ile	Ile	Ser	Gln	Asp	Glu	Ala	Asp	Arg	Arg	Gly	Lys	645	650	655	

ITI-08-PCT_Sequence_Listing_ST25.txt

Val Tyr Asp Lys Tyr Met Cys Ser Phe Leu Phe Asn Leu Asn Asn Asp
660 665 670

Phe Val Val Asp Ala Thr Arg Lys Gly Asn Lys Ile Arg Phe Ala Asn
675 680 685

His Ser Val Asn Pro Asn Cys Tyr Ala Lys Val Met Met Val Asn Gly
690 695 700

Asp His Arg Ile Gly Ile Phe Ala Lys Arg Ala Ile Gln Thr Gly Glu
705 710 715 720

Glu Leu Phe Phe Asp Tyr Arg Tyr Ser Gln Ala Asp Ala Leu Lys Tyr
725 730 735

Val Gly Ile Glu Arg Glu Met Glu Ile Pro
740 745

<210> 358
<211> 707
<212> PRT
<213> Artificial Sequence

<220>
<223> EZH2__Homo_sapiens__S4S3R8

<400> 358

Met Gly Gln Thr Gly Lys Lys Ser Glu Lys Gly Pro Val Cys Trp Arg
1 5 10 15

Lys Arg Val Lys Ser Glu Tyr Met Arg Leu Arg Gln Leu Lys Arg Phe
20 25 30

Arg Arg Ala Asp Glu Val Lys Ser Met Phe Ser Ser Asn Arg Gln Lys
35 40 45

Ile Leu Glu Arg Thr Glu Ile Leu Asn Gln Glu Trp Lys Gln Arg Arg
50 55 60

Ile Gln Pro Val His Ile Leu Thr Ser Val Ser Ser Leu Arg Gly Thr
65 70 75 80

Arg Glu Val Glu Asp Glu Thr Val Leu His Asn Ile Pro Tyr Met Gly
85 90 95

Asp Glu Val Leu Asp Gln Asp Gly Thr Phe Ile Glu Glu Leu Ile Lys
100 105 110

Asn Tyr Asp Gly Lys Val His Gly Asp Arg Glu Cys Gly Phe Ile Asn
115 120 125

ITI-08-PCT_Sequence_Listing_ST25.txt

Asp	Glu	Ile	Phe	Val	Glu	Leu	Val	Asn	Ala	Leu	Gly	Gln	Tyr	Asn	Asp	130	135	140	
Asp	Asp	Asp	Asp	Asp	Asp	Gly	Asp	Asp	Pro	Glu	Glu	Arg	Glu	Glu	Lys	145	150	155	160
Gln	Lys	Asp	Leu	Glu	Asp	His	Arg	Asp	Asp	Lys	Glu	Ser	Arg	Pro	Pro	165	170	175	
Arg	Lys	Phe	Pro	Ser	Asp	Lys	Ile	Phe	Glu	Ala	Ile	Ser	Ser	Met	Phe	180	185	190	
Pro	Asp	Lys	Gly	Thr	Ala	Glu	Glu	Leu	Lys	Glu	Lys	Tyr	Lys	Glu	Leu	195	200	205	
Thr	Glu	Gln	Gln	Leu	Pro	Gly	Ala	Leu	Pro	Pro	Glu	Cys	Thr	Pro	Asn	210	215	220	
Ile	Asp	Gly	Pro	Asn	Ala	Lys	Ser	Val	Gln	Arg	Glu	Gln	Ser	Leu	His	225	230	235	240
Ser	Phe	His	Thr	Leu	Phe	Cys	Arg	Arg	Cys	Phe	Lys	Tyr	Asp	Cys	Phe	245	250	255	
Leu	His	Pro	Phe	His	Ala	Thr	Pro	Asn	Thr	Tyr	Lys	Arg	Lys	Asn	Thr	260	265	270	
Glu	Thr	Ala	Leu	Asp	Asn	Lys	Pro	Cys	Gly	Pro	Gln	Cys	Tyr	Gln	His	275	280	285	
Leu	Glu	Gly	Ala	Lys	Glu	Phe	Ala	Ala	Ala	Leu	Thr	Ala	Glu	Arg	Ile	290	295	300	
Lys	Thr	Pro	Pro	Lys	Arg	Pro	Gly	Gly	Arg	Arg	Arg	Gly	Arg	Leu	Pro	305	310	315	320
Asn	Asn	Ser	Ser	Arg	Pro	Ser	Thr	Pro	Thr	Ile	Asn	Val	Leu	Glu	Ser	325	330	335	
Lys	Asp	Thr	Asp	Ser	Asp	Arg	Glu	Ala	Gly	Thr	Glu	Thr	Gly	Gly	Glu	340	345	350	
Asn	Asn	Asp	Lys	Glu	Glu	Glu	Glu	Lys	Lys	Asp	Glu	Thr	Ser	Ser	Ser	355	360	365	
Ser	Glu	Ala	Asn	Ser	Arg	Cys	Gln	Thr	Pro	Ile	Lys	Met	Lys	Pro	Asn	370	375	380	
Ile	Glu	Pro	Pro	Glu	Asn	Val	Glu	Trp	Ser	Gly	Ala	Glu	Ala	Ser	Met	385	390	395	400
Phe	Arg	Val	Leu	Ile	Gly	Thr	Tyr	Tyr	Asp	Asn	Phe	Cys	Ala	Ile	Ala				

ITI-08-PCT_Sequence_Listing_ST25.txt

405 410 415

Arg Leu Ile Gly Thr Lys Thr Cys Arg Gln Val Tyr Glu Phe Arg Val
420 425 430

Lys Glu Ser Ser Ile Ile Ala Pro Ala Pro Ala Glu Asp Val Asp Thr
435 440 445

Pro Pro Arg Lys Lys Lys Arg Lys His Arg Leu Trp Ala Ala His Cys
450 455 460

Arg Lys Ile Gln Leu Lys Lys Asp Gly Ser Ser Asn His Val Tyr Asn
465 470 475 480

Tyr Gln Pro Cys Asp His Pro Arg Gln Pro Cys Asp Ser Ser Cys Pro
485 490 495

Cys Val Ile Ala Gln Asn Phe Cys Glu Lys Phe Cys Gln Cys Ser Ser
500 505 510

Glu Cys Gln Asn Arg Phe Pro Gly Cys Arg Cys Lys Ala Gln Cys Asn
515 520 525

Thr Lys Gln Cys Pro Cys Tyr Leu Ala Val Arg Glu Cys Asp Pro Asp
530 535 540

Leu Cys Leu Thr Cys Gly Ala Ala Asp His Trp Asp Ser Lys Asn Val
545 550 555 560

Ser Cys Lys Asn Cys Ser Ile Gln Arg Gly Ser Lys Lys His Leu Leu
565 570 575

Leu Ala Pro Ser Asp Val Ala Gly Trp Gly Ile Phe Ile Lys Asp Pro
580 585 590

Val Gln Lys Asn Glu Phe Ile Ser Glu Tyr Cys Gly Glu Ile Ile Ser
595 600 605

Gln Asp Glu Ala Asp Arg Arg Gly Lys Val Tyr Asp Lys Tyr Met Cys
610 615 620

Ser Phe Leu Phe Asn Leu Asn Asn Asp Phe Val Val Asp Ala Thr Arg
625 630 635 640

Lys Gly Asn Lys Ile Arg Phe Ala Asn His Ser Val Asn Pro Asn Cys
645 650 655

Tyr Ala Lys Val Met Met Val Asn Gly Asp His Arg Ile Gly Ile Phe
660 665 670

Ala Lys Arg Ala Ile Gln Thr Gly Glu Glu Leu Phe Phe Asp Tyr Arg
675 680 685

ITI-08-PCT_Sequence_Listing_ST25.txt

Tyr Ser Gln Ala Asp Ala Leu Lys Tyr Val Gly Ile Glu Arg Glu Met
690 695 700

Glu Ile Pro
705

<210> 359
<211> 132
<212> PRT
<213> Artificial Sequence

<220>
<223> FABP7__Homo_sapiens__015540

<400> 359

Met Val Glu Ala Phe Cys Ala Thr Trp Lys Leu Thr Asn Ser Gln Asn
1 5 10 15

Phe Asp Glu Tyr Met Lys Ala Leu Gly Val Gly Phe Ala Thr Arg Gln
20 25 30

Val Gly Asn Val Thr Lys Pro Thr Val Ile Ile Ser Gln Glu Gly Asp
35 40 45

Lys Val Val Ile Arg Thr Leu Ser Thr Phe Lys Asn Thr Glu Ile Ser
50 55 60

Phe Gln Leu Gly Glu Glu Phe Asp Glu Thr Thr Ala Asp Asp Arg Asn
65 70 75 80

Cys Lys Ser Val Val Ser Leu Asp Gly Asp Lys Leu Val His Ile Gln
85 90 95

Lys Trp Asp Gly Lys Glu Thr Asn Phe Val Arg Glu Ile Lys Asp Gly
100 105 110

Lys Met Val Met Thr Leu Thr Phe Gly Asp Val Val Ala Val Arg His
115 120 125

Tyr Glu Lys Ala
130

<210> 360
<211> 254
<212> PRT
<213> Artificial Sequence

<220>
<223> FCGR3A_Version_1__Homo_sapiens__P08637

ITI-08-PCT_Sequence_Listing_ST25.txt

<400> 360

```

Met Trp Gln Leu Leu Leu Pro Thr Ala Leu Leu Leu Leu Val Ser Ala
1      5      10      15

Gly Met Arg Thr Glu Asp Leu Pro Lys Ala Val Val Phe Leu Glu Pro
      20      25      30

Gln Trp Tyr Arg Val Leu Glu Lys Asp Ser Val Thr Leu Lys Cys Gln
      35      40      45

Gly Ala Tyr Ser Pro Glu Asp Asn Ser Thr Gln Trp Phe His Asn Glu
      50      55      60

Ser Leu Ile Ser Ser Gln Ala Ser Ser Tyr Phe Ile Asp Ala Ala Thr
65      70      75      80

Val Asp Asp Ser Gly Glu Tyr Arg Cys Gln Thr Asn Leu Ser Thr Leu
      85      90      95

Ser Asp Pro Val Gln Leu Glu Val His Ile Gly Trp Leu Leu Leu Gln
      100      105      110

Ala Pro Arg Trp Val Phe Lys Glu Glu Asp Pro Ile His Leu Arg Cys
      115      120      125

His Ser Trp Lys Asn Thr Ala Leu His Lys Val Thr Tyr Leu Gln Asn
      130      135      140

Gly Lys Gly Arg Lys Tyr Phe His His Asn Ser Asp Phe Tyr Ile Pro
145      150      155      160

Lys Ala Thr Leu Lys Asp Ser Gly Ser Tyr Phe Cys Arg Gly Leu Phe
      165      170      175

Gly Ser Lys Asn Val Ser Ser Glu Thr Val Asn Ile Thr Ile Thr Gln
      180      185      190

Gly Leu Ala Val Ser Thr Ile Ser Ser Phe Phe Pro Pro Gly Tyr Gln
      195      200      205

Val Ser Phe Cys Leu Val Met Val Leu Leu Phe Ala Val Asp Thr Gly
      210      215      220

Leu Tyr Phe Ser Val Lys Thr Asn Ile Arg Ser Ser Thr Arg Asp Trp
225      230      235      240

Lys Asp His Lys Phe Lys Trp Arg Lys Asp Pro Gln Asp Lys
      245      250

```

<210> 361

<211> 290

ITI-08-PCT_Sequence_Listing_ST25.txt

<212> PRT

<213> Artificial Sequence

<220>

<223> FCGR3A_Version_2__Homo_sapiens__CCDS1232.1

<400> 361

Met Gly Gly Gly Ala Gly Glu Arg Leu Phe Thr Ser Ser Cys Leu Val
1 5 10 15

Gly Leu Val Pro Leu Gly Leu Arg Ile Ser Leu Val Thr Cys Pro Leu
20 25 30

Gln Cys Gly Ile Met Trp Gln Leu Leu Leu Pro Thr Ala Leu Leu Leu
35 40 45

Leu Val Ser Ala Gly Met Arg Thr Glu Asp Leu Pro Lys Ala Val Val
50 55 60

Phe Leu Glu Pro Gln Trp Tyr Arg Val Leu Glu Lys Asp Ser Val Thr
65 70 75 80

Leu Lys Cys Gln Gly Ala Tyr Ser Pro Glu Asp Asn Ser Thr Gln Trp
85 90 95

Phe His Asn Glu Ser Leu Ile Ser Ser Gln Ala Ser Ser Tyr Phe Ile
100 105 110

Asp Ala Ala Thr Val Asp Asp Ser Gly Glu Tyr Arg Cys Gln Thr Asn
115 120 125

Leu Ser Thr Leu Ser Asp Pro Val Gln Leu Glu Val His Ile Gly Trp
130 135 140

Leu Leu Leu Gln Ala Pro Arg Trp Val Phe Lys Glu Glu Asp Pro Ile
145 150 155 160

His Leu Arg Cys His Ser Trp Lys Asn Thr Ala Leu His Lys Val Thr
165 170 175

Tyr Leu Gln Asn Gly Lys Gly Arg Lys Tyr Phe His His Asn Ser Asp
180 185 190

Phe Tyr Ile Pro Lys Ala Thr Leu Lys Asp Ser Gly Ser Tyr Phe Cys
195 200 205

Arg Gly Leu Phe Gly Ser Lys Asn Val Ser Ser Glu Thr Val Asn Ile
210 215 220

Thr Ile Thr Gln Gly Leu Ala Val Ser Thr Ile Ser Ser Phe Phe Pro
225 230 235 240

ITI-08-PCT_Sequence_Listing_ST25.txt

Pro Gly Tyr Gln Val Ser Phe Cys Leu Val Met Val Leu Leu Phe Ala
245 250 255

Val Asp Thr Gly Leu Tyr Phe Ser Val Lys Thr Asn Ile Arg Ser Ser
260 265 270

Thr Arg Asp Trp Lys Asp His Lys Phe Lys Trp Arg Lys Asp Pro Gln
275 280 285

Asp Lys
290

<210> 362

<211> 268

<212> PRT

<213> Artificial Sequence

<220>

<223> FGF5__Homo_sapiens__P12034

<400> 362

Met Ser Leu Ser Phe Leu Leu Leu Leu Phe Phe Ser His Leu Ile Leu
1 5 10 15

Ser Ala Trp Ala His Gly Glu Lys Arg Leu Ala Pro Lys Gly Gln Pro
20 25 30

Gly Pro Ala Ala Thr Asp Arg Asn Pro Arg Gly Ser Ser Ser Arg Gln
35 40 45

Ser Ser Ser Ser Ala Met Ser Ser Ser Ser Ala Ser Ser Ser Pro Ala
50 55 60

Ala Ser Leu Gly Ser Gln Gly Ser Gly Leu Glu Gln Ser Ser Phe Gln
65 70 75 80

Trp Ser Pro Ser Gly Arg Arg Thr Gly Ser Leu Tyr Cys Arg Val Gly
85 90 95

Ile Gly Phe His Leu Gln Ile Tyr Pro Asp Gly Lys Val Asn Gly Ser
100 105 110

His Glu Ala Asn Met Leu Ser Val Leu Glu Ile Phe Ala Val Ser Gln
115 120 125

Gly Ile Val Gly Ile Arg Gly Val Phe Ser Asn Lys Phe Leu Ala Met
130 135 140

Ser Lys Lys Gly Lys Leu His Ala Ser Ala Lys Phe Thr Asp Asp Cys
145 150 155 160

ITI-08-PCT_Sequence_Listing_ST25.txt

Lys Phe Arg Glu Arg Phe Gln Glu Asn Ser Tyr Asn Thr Tyr Ala Ser
165 170 175

Ala Ile His Arg Thr Glu Lys Thr Gly Arg Glu Trp Tyr Val Ala Leu
180 185 190

Asn Lys Arg Gly Lys Ala Lys Arg Gly Cys Ser Pro Arg Val Lys Pro
195 200 205

Gln His Ile Ser Thr His Phe Leu Pro Arg Phe Lys Gln Ser Glu Gln
210 215 220

Pro Glu Leu Ser Phe Thr Val Thr Val Pro Glu Lys Lys Lys Pro Pro
225 230 235 240

Ser Pro Ile Lys Pro Lys Ile Pro Leu Ser Ala Pro Arg Lys Asn Thr
245 250 255

Asn Ser Val Lys Tyr Arg Leu Lys Phe Arg Phe Gly
260 265

<210> 363
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<223> FGF5__Homo_sapiens__Q60518

<400> 363

Met Ser Thr Arg Cys Gly Glu Ala Gly Arg Ala Arg Gly Thr Gln Pro
1 5 10 15

His Arg Gly Tyr Arg Ala Gln Asn Gln Pro Tyr Lys Met His Leu Gly
20 25 30

Pro Pro Arg Leu Glu Glu
35

<210> 364
<211> 821
<212> PRT
<213> Artificial Sequence

<220>
<223> FGFR2__Homo_sapiens__P21802

<400> 364

Met Val Ser Trp Gly Arg Phe Ile Cys Leu Val Val Val Thr Met Ala

ITI-08-PCT_Sequence_Listing_ST25.txt

```

1           5           10           15
Thr Leu Ser Leu Ala Arg Pro Ser Phe Ser Leu Val Glu Asp Thr Thr
      20           25           30
Leu Glu Pro Glu Glu Pro Pro Thr Lys Tyr Gln Ile Ser Gln Pro Glu
      35           40           45
Val Tyr Val Ala Ala Pro Gly Glu Ser Leu Glu Val Arg Cys Leu Leu
      50           55           60
Lys Asp Ala Ala Val Ile Ser Trp Thr Lys Asp Gly Val His Leu Gly
      65           70           75           80
Pro Asn Asn Arg Thr Val Leu Ile Gly Glu Tyr Leu Gln Ile Lys Gly
      85           90           95
Ala Thr Pro Arg Asp Ser Gly Leu Tyr Ala Cys Thr Ala Ser Arg Thr
      100          105          110
Val Asp Ser Glu Thr Trp Tyr Phe Met Val Asn Val Thr Asp Ala Ile
      115          120          125
Ser Ser Gly Asp Asp Glu Asp Asp Thr Asp Gly Ala Glu Asp Phe Val
      130          135          140
Ser Glu Asn Ser Asn Asn Lys Arg Ala Pro Tyr Trp Thr Asn Thr Glu
      145          150          155          160
Lys Met Glu Lys Arg Leu His Ala Val Pro Ala Ala Asn Thr Val Lys
      165          170          175
Phe Arg Cys Pro Ala Gly Gly Asn Pro Met Pro Thr Met Arg Trp Leu
      180          185          190
Lys Asn Gly Lys Glu Phe Lys Gln Glu His Arg Ile Gly Gly Tyr Lys
      195          200          205
Val Arg Asn Gln His Trp Ser Leu Ile Met Glu Ser Val Val Pro Ser
      210          215          220
Asp Lys Gly Asn Tyr Thr Cys Val Val Glu Asn Glu Tyr Gly Ser Ile
      225          230          235          240
Asn His Thr Tyr His Leu Asp Val Val Glu Arg Ser Pro His Arg Pro
      245          250          255
Ile Leu Gln Ala Gly Leu Pro Ala Asn Ala Ser Thr Val Val Gly Gly
      260          265          270
Asp Val Glu Phe Val Cys Lys Val Tyr Ser Asp Ala Gln Pro His Ile
      275          280          285

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Gln	Trp	Ile	Lys	His	Val	Glu	Lys	Asn	Gly	Ser	Lys	Tyr	Gly	Pro	Asp	290	295	300
Gly	Leu	Pro	Tyr	Leu	Lys	Val	Leu	Lys	Ala	Ala	Gly	Val	Asn	Thr	Thr	305	310	315
Asp	Lys	Glu	Ile	Glu	Val	Leu	Tyr	Ile	Arg	Asn	Val	Thr	Phe	Glu	Asp	325	330	335
Ala	Gly	Glu	Tyr	Thr	Cys	Leu	Ala	Gly	Asn	Ser	Ile	Gly	Ile	Ser	Phe	340	345	350
His	Ser	Ala	Trp	Leu	Thr	Val	Leu	Pro	Ala	Pro	Gly	Arg	Glu	Lys	Glu	355	360	365
Ile	Thr	Ala	Ser	Pro	Asp	Tyr	Leu	Glu	Ile	Ala	Ile	Tyr	Cys	Ile	Gly	370	375	380
Val	Phe	Leu	Ile	Ala	Cys	Met	Val	Val	Thr	Val	Ile	Leu	Cys	Arg	Met	385	390	395
Lys	Asn	Thr	Thr	Lys	Lys	Pro	Asp	Phe	Ser	Ser	Gln	Pro	Ala	Val	His	405	410	415
Lys	Leu	Thr	Lys	Arg	Ile	Pro	Leu	Arg	Arg	Gln	Val	Thr	Val	Ser	Ala	420	425	430
Glu	Ser	Ser	Ser	Ser	Met	Asn	Ser	Asn	Thr	Pro	Leu	Val	Arg	Ile	Thr	435	440	445
Thr	Arg	Leu	Ser	Ser	Thr	Ala	Asp	Thr	Pro	Met	Leu	Ala	Gly	Val	Ser	450	455	460
Glu	Tyr	Glu	Leu	Pro	Glu	Asp	Pro	Lys	Trp	Glu	Phe	Pro	Arg	Asp	Lys	465	470	475
Leu	Thr	Leu	Gly	Lys	Pro	Leu	Gly	Glu	Gly	Cys	Phe	Gly	Gln	Val	Val	485	490	495
Met	Ala	Glu	Ala	Val	Gly	Ile	Asp	Lys	Asp	Lys	Pro	Lys	Glu	Ala	Val	500	505	510
Thr	Val	Ala	Val	Lys	Met	Leu	Lys	Asp	Asp	Ala	Thr	Glu	Lys	Asp	Leu	515	520	525
Ser	Asp	Leu	Val	Ser	Glu	Met	Glu	Met	Met	Lys	Met	Ile	Gly	Lys	His	530	535	540
Lys	Asn	Ile	Ile	Asn	Leu	Leu	Gly	Ala	Cys	Thr	Gln	Asp	Gly	Pro	Leu	545	550	555

ITI-08-PCT_Sequence_Listing_ST25.txt

Tyr Val Ile Val Glu Tyr Ala Ser Lys Gly Asn Leu Arg Glu Tyr Leu
 565 570 575
 Arg Ala Arg Arg Pro Pro Gly Met Glu Tyr Ser Tyr Asp Ile Asn Arg
 580 585 590
 Val Pro Glu Glu Gln Met Thr Phe Lys Asp Leu Val Ser Cys Thr Tyr
 595 600 605
 Gln Leu Ala Arg Gly Met Glu Tyr Leu Ala Ser Gln Lys Cys Ile His
 610 615 620
 Arg Asp Leu Ala Ala Arg Asn Val Leu Val Thr Glu Asn Asn Val Met
 625 630 635 640
 Lys Ile Ala Asp Phe Gly Leu Ala Arg Asp Ile Asn Asn Ile Asp Tyr
 645 650 655
 Tyr Lys Lys Thr Thr Asn Gly Arg Leu Pro Val Lys Trp Met Ala Pro
 660 665 670
 Glu Ala Leu Phe Asp Arg Val Tyr Thr His Gln Ser Asp Val Trp Ser
 675 680 685
 Phe Gly Val Leu Met Trp Glu Ile Phe Thr Leu Gly Gly Ser Pro Tyr
 690 695 700
 Pro Gly Ile Pro Val Glu Glu Leu Phe Lys Leu Leu Lys Glu Gly His
 705 710 715 720
 Arg Met Asp Lys Pro Ala Asn Cys Thr Asn Glu Leu Tyr Met Met Met
 725 730 735
 Arg Asp Cys Trp His Ala Val Pro Ser Gln Arg Pro Thr Phe Lys Gln
 740 745 750
 Leu Val Glu Asp Leu Asp Arg Ile Leu Thr Leu Thr Thr Asn Glu Glu
 755 760 765
 Tyr Leu Asp Leu Ser Gln Pro Leu Glu Gln Tyr Ser Pro Ser Tyr Pro
 770 775 780
 Asp Thr Arg Ser Ser Cys Ser Ser Gly Asp Asp Ser Val Phe Ser Pro
 785 790 795 800
 Asp Pro Met Pro Tyr Glu Pro Cys Leu Pro Gln Tyr Pro His Ile Asn
 805 810 815
 Gly Ser Val Lys Thr
 820

<210> 365

ITI-08-PCT_Sequence_Listing_ST25.txt

<211> 635

<212> PRT

<213> Artificial Sequence

<220>

<223> fibronectin__Homo_sapiens__A0A024R5I6

<400> 365

Met Ala Pro Pro Leu Leu Leu Leu Leu Ala Ser Gly Ala Ala Ala
1 5 10 15

Cys Pro Leu Pro Cys Val Cys Gln Asn Leu Ser Glu Ser Leu Ser Thr
20 25 30

Leu Cys Ala His Arg Gly Leu Leu Phe Val Pro Pro Asn Val Asp Arg
35 40 45

Arg Thr Val Glu Leu Arg Leu Ala Asp Asn Phe Ile Gln Ala Leu Gly
50 55 60

Pro Pro Asp Phe Arg Asn Met Thr Gly Leu Val Asp Leu Thr Leu Ser
65 70 75 80

Arg Asn Ala Ile Thr Arg Ile Gly Ala Arg Ala Phe Gly Asp Leu Glu
85 90 95

Ser Leu Arg Ser Leu His Leu Asp Gly Asn Arg Leu Val Glu Leu Gly
100 105 110

Thr Gly Ser Leu Arg Gly Pro Val Asn Leu Gln His Leu Ile Leu Ser
115 120 125

Gly Asn Gln Leu Gly Arg Ile Ala Pro Gly Ala Phe Asp Asp Phe Leu
130 135 140

Glu Ser Leu Glu Asp Leu Asp Leu Ser Tyr Asn Asn Leu Arg Gln Val
145 150 155 160

Pro Trp Ala Gly Ile Gly Ala Met Pro Ala Leu His Thr Leu Asn Leu
165 170 175

Asp His Asn Leu Ile Asp Ala Leu Pro Pro Gly Ala Phe Ala Gln Leu
180 185 190

Gly Gln Leu Ser Arg Leu Asp Leu Thr Ser Asn Arg Leu Ala Thr Leu
195 200 205

Ala Pro Asp Pro Leu Phe Ser Arg Gly Arg Asp Ala Glu Ala Ser Pro
210 215 220

Ala Pro Leu Val Leu Ser Phe Ser Gly Asn Pro Leu His Cys Asn Cys

ITI-08-PCT_Sequence_Listing_ST25.txt

```

225                230                235                240
Glu Leu Leu Trp Leu Arg Arg Leu Ala Arg Pro Asp Asp Leu Glu Thr
      245                250                255
Cys Ala Ser Pro Pro Gly Leu Ala Gly Arg Tyr Phe Trp Ala Val Pro
      260                265                270
Glu Gly Glu Phe Ser Cys Glu Pro Pro Leu Ile Ala Arg His Thr Gln
      275                280                285
Arg Leu Trp Val Leu Glu Gly Gln Arg Ala Thr Leu Arg Cys Arg Ala
      290                295                300
Leu Gly Asp Pro Ala Pro Thr Met His Trp Val Gly Pro Asp Asp Arg
305                310                315                320
Leu Val Gly Asn Ser Ser Arg Ala Arg Ala Phe Pro Asn Gly Thr Leu
      325                330                335
Glu Ile Gly Val Thr Gly Ala Gly Asp Ala Gly Gly Tyr Thr Cys Ile
      340                345                350
Ala Thr Asn Pro Ala Gly Glu Ala Thr Ala Arg Val Glu Leu Arg Val
      355                360                365
Leu Ala Leu Pro His Gly Gly Asn Ser Ser Ala Glu Gly Gly Arg Pro
      370                375                380
Gly Pro Ser Asp Ile Ala Ala Ser Ala Arg Thr Ala Ala Glu Gly Glu
385                390                395                400
Gly Thr Leu Glu Ser Glu Pro Ala Val Gln Val Thr Glu Val Thr Ala
      405                410                415
Thr Ser Gly Leu Val Ser Trp Gly Pro Gly Arg Pro Ala Asp Pro Val
      420                425                430
Trp Met Phe Gln Ile Gln Tyr Asn Ser Ser Glu Asp Glu Thr Leu Ile
      435                440                445
Tyr Arg Ile Val Pro Ala Ser Ser His His Phe Leu Leu Lys His Leu
      450                455                460
Val Pro Gly Ala Asp Tyr Asp Leu Cys Leu Leu Ala Leu Ser Pro Ala
465                470                475                480
Ala Gly Pro Ser Asp Leu Thr Ala Thr Arg Leu Leu Gly Cys Ala His
      485                490                495
Phe Ser Thr Leu Pro Ala Ser Pro Leu Cys His Ala Leu Gln Ala His
      500                505                510

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Val Leu Gly Gly Thr Leu Thr Val Ala Val Gly Gly Val Leu Val Ala
515 520 525

Ala Leu Leu Val Phe Thr Val Ala Leu Leu Val Arg Gly Arg Gly Ala
530 535 540

Gly Asn Gly Arg Leu Pro Leu Lys Leu Ser His Val Gln Ser Gln Thr
545 550 555 560

Asn Gly Gly Pro Ser Pro Thr Pro Lys Ala His Pro Pro Arg Ser Pro
565 570 575

Pro Pro Arg Pro Gln Arg Ser Cys Ser Leu Asp Leu Gly Asp Ala Gly
580 585 590

Cys Tyr Gly Tyr Ala Arg Arg Leu Gly Gly Ala Trp Ala Arg Arg Ser
595 600 605

His Ser Val His Gly Gly Leu Leu Gly Ala Gly Cys Arg Gly Val Gly
610 615 620

Gly Ser Ala Glu Arg Leu Glu Glu Ser Val Val
625 630 635

<210> 366

<211> 1098

<212> PRT

<213> Artificial Sequence

<220>

<223> fibronectin__Homo_sapiens__A0A024RB01

<400> 366

Met Pro Pro Arg Gln Pro Pro Arg Gln Ala Gly Gly Gly Leu Ser Arg
1 5 10 15

Glu Phe Gly Lys Leu Leu Pro Ala Leu Ser His Ser Pro Leu Gly Gly
20 25 30

Leu Gly Ser Gly Ser Gly Ser Val Ala Pro Gly Gln Gly Arg Ala Gly
35 40 45

Ala Met Gly Ser Arg Thr Pro Glu Ser Pro Leu His Ala Val Gln Leu
50 55 60

Arg Trp Gly Pro Arg Arg Arg Pro Pro Leu Leu Pro Leu Leu Leu Leu
65 70 75 80

Leu Leu Pro Pro Pro Pro Arg Val Gly Gly Phe Asn Leu Asp Ala Glu
85 90 95

ITI-08-PCT_Sequence_Listing_ST25.txt

Ala	Pro	Ala	Val	Leu	Ser	Gly	Pro	Pro	Gly	Ser	Phe	Phe	Gly	Phe	Ser	100	105	110
Val	Glu	Phe	Tyr	Arg	Pro	Gly	Thr	Asp	Gly	Val	Ser	Val	Leu	Val	Gly	115	120	125
Ala	Pro	Lys	Ala	Asn	Thr	Ser	Gln	Pro	Gly	Val	Leu	Gln	Gly	Gly	Ala	130	135	140
Val	Tyr	Leu	Cys	Pro	Trp	Gly	Ala	Ser	Pro	Thr	Gln	Cys	Thr	Pro	Ile	145	150	155
Glu	Phe	Asp	Ser	Lys	Gly	Ser	Arg	Leu	Leu	Glu	Ser	Ser	Leu	Ser	Ser	165	170	175
Ser	Glu	Gly	Glu	Glu	Pro	Val	Glu	Tyr	Lys	Ser	Leu	Gln	Trp	Phe	Gly	180	185	190
Ala	Thr	Val	Arg	Ala	His	Gly	Ser	Ser	Ile	Leu	Ala	Cys	Ala	Pro	Leu	195	200	205
Tyr	Ser	Trp	Arg	Thr	Glu	Lys	Glu	Pro	Leu	Ser	Asp	Pro	Val	Gly	Thr	210	215	220
Cys	Tyr	Leu	Ser	Thr	Asp	Asn	Phe	Thr	Arg	Ile	Leu	Glu	Tyr	Ala	Pro	225	230	235
Cys	Arg	Ser	Asp	Phe	Ser	Trp	Ala	Ala	Gly	Gln	Gly	Tyr	Cys	Gln	Gly	245	250	255
Gly	Phe	Ser	Ala	Glu	Phe	Thr	Lys	Thr	Gly	Arg	Val	Val	Leu	Gly	Gly	260	265	270
Pro	Gly	Ser	Tyr	Phe	Trp	Gln	Gly	Gln	Ile	Leu	Ser	Ala	Thr	Gln	Glu	275	280	285
Gln	Ile	Ala	Glu	Ser	Tyr	Tyr	Pro	Glu	Tyr	Leu	Ile	Asn	Leu	Val	Gln	290	295	300
Gly	Gln	Leu	Gln	Thr	Arg	Gln	Ala	Ser	Ser	Ile	Tyr	Asp	Asp	Ser	Tyr	305	310	315
Leu	Gly	Tyr	Ser	Val	Ala	Val	Gly	Glu	Phe	Ser	Gly	Asp	Asp	Thr	Glu	325	330	335
Asp	Phe	Val	Ala	Gly	Val	Pro	Lys	Gly	Asn	Leu	Thr	Tyr	Gly	Tyr	Val	340	345	350
Thr	Ile	Leu	Asn	Gly	Ser	Asp	Ile	Arg	Ser	Leu	Tyr	Asn	Phe	Ser	Gly	355	360	365

ITI-08-PCT_Sequence_Listing_ST25.txt

Glu Gln Met Ala Ser Tyr Phe Gly Tyr Ala Val Ala Ala Thr Asp Val
 370 375 380
 Asn Gly Asp Gly Leu Asp Asp Leu Leu Val Gly Ala Pro Leu Leu Met
 385 390 395 400
 Asp Arg Thr Pro Asp Gly Arg Pro Gln Glu Val Gly Arg Val Tyr Val
 405 410 415
 Tyr Leu Gln His Pro Ala Gly Ile Glu Pro Thr Pro Thr Leu Thr Leu
 420 425 430
 Thr Gly His Asp Glu Phe Gly Arg Phe Gly Ser Ser Leu Thr Pro Leu
 435 440 445
 Gly Asp Leu Asp Gln Asp Gly Tyr Asn Asp Val Ala Ile Gly Ala Pro
 450 455 460
 Phe Gly Gly Glu Thr Gln Gln Gly Val Val Phe Val Phe Pro Gly Gly
 465 470 475 480
 Pro Gly Gly Leu Gly Ser Lys Pro Ser Gln Val Leu Gln Pro Leu Trp
 485 490 495
 Ala Ala Ser His Thr Pro Asp Phe Phe Gly Ser Ala Leu Arg Gly Gly
 500 505 510
 Arg Asp Leu Asp Gly Asn Gly Tyr Pro Asp Leu Ile Val Gly Ser Phe
 515 520 525
 Gly Val Asp Lys Ala Val Val Tyr Arg Gly Arg Pro Ile Val Ser Ala
 530 535 540
 Ser Ala Ser Leu Thr Ile Phe Pro Ala Met Phe Asn Pro Glu Glu Arg
 545 550 555 560
 Ser Cys Ser Leu Glu Gly Asn Pro Val Ala Cys Ile Asn Leu Ser Phe
 565 570 575
 Cys Leu Asn Ala Ser Gly Lys His Val Ala Asp Ser Ile Gly Phe Thr
 580 585 590
 Val Glu Leu Gln Leu Asp Trp Gln Lys Gln Lys Gly Gly Val Arg Arg
 595 600 605
 Ala Leu Phe Leu Ala Ser Arg Gln Ala Thr Leu Thr Gln Thr Leu Leu
 610 615 620
 Ile Gln Asn Gly Ala Arg Glu Asp Cys Arg Glu Met Lys Ile Tyr Leu
 625 630 635 640
 Arg Asn Glu Ser Glu Phe Arg Asp Lys Leu Ser Pro Ile His Ile Ala

ITI-08-PCT_Sequence_Listing_ST25.txt

645 650 655

Leu Asn Phe Ser Leu Asp Pro Gln Ala Pro Val Asp Ser His Gly Leu
660 665 670

Arg Pro Ala Leu His Tyr Gln Ser Lys Ser Arg Ile Glu Asp Lys Ala
675 680 685

Gln Ile Leu Leu Asp Cys Gly Glu Asp Asn Ile Cys Val Pro Asp Leu
690 695 700

Gln Leu Glu Val Phe Gly Glu Gln Asn His Val Tyr Leu Gly Asp Lys
705 710 715 720

Asn Ala Leu Asn Leu Thr Phe His Ala Gln Asn Val Gly Glu Gly Gly
725 730 735

Ala Tyr Glu Ala Glu Leu Arg Val Thr Ala Pro Pro Glu Ala Glu Tyr
740 745 750

Ser Gly Leu Val Arg His Pro Gly Asn Phe Ser Ser Leu Ser Cys Asp
755 760 765

Tyr Phe Ala Val Asn Gln Ser Arg Leu Leu Val Cys Asp Leu Gly Asn
770 775 780

Pro Met Lys Ala Gly Ala Ser Leu Trp Gly Gly Leu Arg Phe Thr Val
785 790 795 800

Pro His Leu Arg Asp Thr Lys Lys Thr Ile Gln Phe Asp Phe Gln Ile
805 810 815

Leu Ser Lys Asn Leu Asn Asn Ser Gln Ser Asp Val Val Ser Phe Arg
820 825 830

Leu Ser Val Glu Ala Gln Ala Gln Val Thr Leu Asn Gly Val Ser Lys
835 840 845

Pro Glu Ala Val Leu Phe Pro Val Ser Asp Trp His Pro Arg Asp Gln
850 855 860

Pro Gln Lys Glu Glu Asp Leu Gly Pro Ala Val His His Val Tyr Glu
865 870 875 880

Leu Ile Asn Gln Gly Pro Ser Ser Ile Ser Gln Gly Val Leu Glu Leu
885 890 895

Ser Cys Pro Gln Ala Leu Glu Gly Gln Gln Leu Leu Tyr Val Thr Arg
900 905 910

Val Thr Gly Leu Asn Cys Thr Thr Asn His Pro Ile Asn Pro Lys Gly
915 920 925

ITI-08-PCT_Sequence_Listing_ST25.txt

Leu Glu Leu Asp Pro Glu Gly Ser Leu His His Gln Gln Lys Arg Glu
 930 935 940
 Ala Pro Ser Arg Ser Ser Ala Ser Ser Gly Pro Gln Ile Leu Lys Cys
 945 950 955 960
 Pro Glu Ala Glu Cys Phe Arg Leu Arg Cys Glu Leu Gly Pro Leu His
 965 970 975
 Gln Gln Glu Ser Gln Ser Leu Gln Leu His Phe Arg Val Trp Ala Lys
 980 985 990
 Thr Phe Leu Gln Arg Glu His Gln Pro Phe Ser Leu Gln Cys Glu Ala
 995 1000 1005
 Val Tyr Lys Ala Leu Lys Met Pro Tyr Arg Ile Leu Pro Arg Gln
 1010 1015 1020
 Leu Pro Gln Lys Glu Arg Gln Val Ala Thr Ala Val Gln Trp Thr
 1025 1030 1035
 Lys Ala Glu Gly Ser Tyr Gly Val Pro Leu Trp Ile Ile Ile Leu
 1040 1045 1050
 Ala Ile Leu Phe Gly Leu Leu Leu Leu Gly Leu Leu Ile Tyr Ile
 1055 1060 1065
 Leu Tyr Lys Leu Gly Phe Phe Lys Arg Ser Leu Pro Tyr Gly Thr
 1070 1075 1080
 Ala Met Glu Lys Ala Gln Leu Lys Pro Pro Ala Thr Ser Asp Ala
 1085 1090 1095
 <210> 367
 <211> 1198
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> fibronectin__Homo_sapiens__A0A024RDT9
 <400> 367
 Met Ala Glu His Pro Pro Leu Leu Asp Thr Thr Gln Ile Leu Ser Ser
 1 5 10 15
 Asp Ile Ser Leu Leu Ser Ala Pro Ile Val Ser Ala Asp Gly Thr Gln
 20 25 30
 Gln Val Ile Leu Val Gln Val Asn Pro Gly Glu Ala Phe Thr Ile Arg
 35 40 45

ITI-08-PCT_Sequence_Listing_ST25.txt

Arg	Glu	Asp	Gly	Gln	Phe	Gln	Cys	Ile	Thr	Gly	Pro	Ala	Gln	Val	Pro	50	55	60	
Met	Met	Ser	Pro	Asn	Gly	Ser	Val	Pro	Pro	Ile	Tyr	Val	Pro	Pro	Gly	65	70	75	80
Tyr	Ala	Pro	Gln	Val	Ile	Glu	Asp	Asn	Gly	Val	Arg	Arg	Val	Val	Val	85	90	95	
Val	Pro	Gln	Ala	Pro	Glu	Phe	His	Pro	Gly	Ser	His	Thr	Val	Leu	His	100	105	110	
Arg	Ser	Pro	His	Pro	Pro	Leu	Pro	Gly	Phe	Ile	Pro	Val	Pro	Thr	Met	115	120	125	
Met	Pro	Pro	Pro	Pro	Arg	His	Met	Tyr	Ser	Pro	Val	Thr	Gly	Ala	Gly	130	135	140	
Asp	Met	Thr	Thr	Gln	Tyr	Met	Pro	Gln	Tyr	Gln	Ser	Ser	Gln	Val	Tyr	145	150	155	160
Gly	Asp	Val	Asp	Ala	His	Ser	Thr	His	Gly	Arg	Ser	Asn	Phe	Arg	Asp	165	170	175	
Glu	Arg	Ser	Ser	Lys	Thr	Tyr	Glu	Arg	Leu	Gln	Lys	Lys	Leu	Lys	Asp	180	185	190	
Arg	Gln	Gly	Thr	Gln	Lys	Asp	Lys	Met	Ser	Ser	Pro	Pro	Ser	Ser	Pro	195	200	205	
Gln	Lys	Cys	Pro	Ser	Pro	Ile	Asn	Glu	His	Asn	Gly	Leu	Ile	Lys	Gly	210	215	220	
Gln	Ile	Ala	Gly	Gly	Ile	Asn	Thr	Gly	Ser	Ala	Lys	Ile	Lys	Ser	Gly	225	230	235	240
Lys	Gly	Lys	Gly	Gly	Thr	Gln	Val	Asp	Thr	Glu	Ile	Glu	Glu	Lys	Asp	245	250	255	
Glu	Glu	Thr	Lys	Ala	Phe	Glu	Ala	Leu	Leu	Ser	Asn	Ile	Val	Lys	Pro	260	265	270	
Val	Ala	Ser	Asp	Ile	Gln	Ala	Arg	Thr	Val	Val	Leu	Thr	Trp	Ser	Pro	275	280	285	
Pro	Ser	Ser	Leu	Ile	Asn	Gly	Glu	Thr	Asp	Glu	Ser	Ser	Val	Pro	Glu	290	295	300	
Leu	Tyr	Gly	Tyr	Glu	Val	Leu	Ile	Ser	Ser	Thr	Gly	Lys	Asp	Gly	Lys	305	310	315	320

ITI-08-PCT_Sequence_Listing_ST25.txt

Tyr Lys Ser Val Tyr Val Gly Glu Glu Thr Asn Ile Thr Leu Asn Asp
 325 330 335
 Leu Lys Pro Ala Met Asp Tyr His Ala Lys Val Gln Ala Glu Tyr Asn
 340 345 350
 Ser Ile Lys Gly Thr Pro Ser Glu Ala Glu Ile Phe Thr Thr Leu Ser
 355 360 365
 Cys Glu Pro Asp Ile Pro Asn Pro Pro Arg Ile Ala Asn Arg Thr Lys
 370 375 380
 Asn Ser Leu Thr Leu Gln Trp Lys Ala Pro Ser Asp Asn Gly Ser Lys
 385 390 395 400
 Ile Gln Asn Phe Val Leu Glu Trp Asp Glu Gly Lys Gly Asn Gly Glu
 405 410 415
 Phe Cys Gln Cys Tyr Met Gly Ser Gln Lys Gln Phe Lys Ile Thr Lys
 420 425 430
 Leu Ser Pro Ala Met Gly Cys Lys Phe Arg Leu Ser Ala Arg Asn Asp
 435 440 445
 Tyr Gly Thr Ser Gly Phe Ser Glu Glu Val Leu Tyr Tyr Thr Ser Gly
 450 455 460
 Cys Ala Pro Ser Met Pro Ala Ser Pro Val Leu Thr Lys Ala Gly Ile
 465 470 475 480
 Thr Trp Leu Ser Leu Gln Trp Ser Lys Pro Ser Gly Thr Pro Ser Asp
 485 490 495
 Glu Gly Ile Ser Tyr Ile Leu Glu Met Glu Glu Glu Thr Ser Gly Tyr
 500 505 510
 Gly Phe Lys Pro Lys Tyr Asp Gly Glu Asp Leu Ala Tyr Thr Val Lys
 515 520 525
 Asn Leu Arg Arg Ser Thr Lys Tyr Lys Phe Lys Val Ile Ala Tyr Asn
 530 535 540
 Ser Glu Gly Lys Ser Asn Pro Ser Glu Val Val Glu Phe Thr Thr Cys
 545 550 555 560
 Pro Asp Lys Pro Gly Ile Pro Val Lys Pro Ser Val Lys Gly Lys Ile
 565 570 575
 His Ser His Ser Phe Lys Ile Thr Trp Asp Pro Pro Lys Asp Asn Gly
 580 585 590
 Gly Ala Thr Ile Asn Lys Tyr Val Val Glu Met Ala Glu Gly Ser Asn

ITI-08-PCT_Sequence_Listing_ST25.txt

```

595                                     600                                     605
Gly Asn Lys Trp Glu Met Ile Tyr Ser Gly Ala Thr Arg Glu His Leu
610                                     615                                     620
Cys Asp Arg Leu Asn Pro Gly Cys Phe Tyr Arg Leu Arg Val Tyr Cys
625                                     630                                     635                                     640
Ile Ser Asp Gly Gly Gln Ser Ala Val Ser Glu Ser Leu Leu Val Gln
645                                     650                                     655
Thr Pro Ala Val Pro Pro Gly Pro Cys Leu Pro Pro Arg Leu Gln Gly
660                                     665                                     670
Arg Pro Lys Ala Lys Glu Ile Gln Leu Arg Trp Gly Pro Pro Leu Val
675                                     680                                     685
Asp Gly Gly Ser Pro Ile Ser Cys Tyr Ser Val Glu Met Ser Pro Ile
690                                     695                                     700
Glu Lys Asp Glu Pro Arg Glu Val Tyr Gln Gly Ser Glu Val Glu Cys
705                                     710                                     715                                     720
Thr Val Ser Ser Leu Leu Pro Gly Lys Thr Tyr Ser Phe Arg Leu Arg
725                                     730                                     735
Ala Ala Asn Lys Met Gly Phe Gly Pro Phe Ser Glu Lys Cys Asp Ile
740                                     745                                     750
Thr Thr Ala Pro Gly Pro Pro Asp Gln Cys Lys Pro Pro Gln Val Thr
755                                     760                                     765
Cys Arg Ser Ala Thr Cys Ala Gln Val Asn Trp Glu Val Pro Leu Ser
770                                     775                                     780
Asn Gly Thr Asp Val Thr Glu Tyr Arg Leu Glu Trp Gly Gly Val Glu
785                                     790                                     795                                     800
Gly Ser Met Gln Ile Cys Tyr Cys Gly Pro Gly Leu Ser Tyr Glu Ile
805                                     810                                     815
Lys Gly Leu Ser Pro Ala Thr Thr Tyr Tyr Cys Arg Val Gln Ala Leu
820                                     825                                     830
Ser Val Val Gly Ala Gly Pro Phe Ser Glu Val Val Ala Cys Val Thr
835                                     840                                     845
Pro Pro Ser Val Pro Gly Ile Val Thr Cys Leu Gln Glu Ile Ser Asp
850                                     855                                     860
Asp Glu Ile Glu Asn Pro His Tyr Ser Pro Ser Thr Cys Leu Ala Ile
865                                     870                                     875                                     880

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Ser	Trp	Glu	Lys	Pro	Cys	Asp	His	Gly	Ser	Glu	Ile	Leu	Ala	Tyr	Ser		
				885					890					895			
Ile	Asp	Phe	Gly	Asp	Lys	Gln	Ser	Leu	Thr	Val	Gly	Lys	Val	Thr	Ser		
			900					905					910				
Tyr	Ile	Ile	Asn	Asn	Leu	Gln	Pro	Asp	Thr	Thr	Tyr	Arg	Ile	Arg	Ile		
			915				920					925					
Gln	Ala	Leu	Asn	Ser	Leu	Gly	Ala	Gly	Pro	Phe	Ser	His	Met	Ile	Lys		
	930					935					940						
Leu	Lys	Thr	Lys	Pro	Leu	Pro	Pro	Asp	Pro	Pro	Arg	Leu	Glu	Cys	Val		
945					950					955					960		
Ala	Phe	Ser	His	Gln	Asn	Leu	Lys	Leu	Lys	Trp	Gly	Glu	Gly	Thr	Pro		
				965					970						975		
Lys	Thr	Leu	Ser	Thr	Asp	Ser	Ile	Gln	Tyr	His	Leu	Gln	Met	Glu	Asp		
			980					985					990				
Lys	Asn	Gly	Arg	Phe	Val	Ser	Leu	Tyr	Arg	Gly	Pro	Cys	His	Thr	Tyr		
		995					1000					1005					
Lys	Val	Gln	Arg	Leu	Asn	Glu	Ser	Thr	Ser	Tyr	Lys	Phe	Cys	Ile			
	1010					1015					1020						
Gln	Ala	Cys	Asn	Glu	Ala	Gly	Glu	Gly	Pro	Leu	Ser	Gln	Glu	Tyr			
	1025					1030					1035						
Ile	Phe	Thr	Thr	Pro	Lys	Ser	Val	Pro	Ala	Ala	Leu	Lys	Ala	Pro			
	1040					1045					1050						
Lys	Ile	Glu	Lys	Val	Asn	Asp	His	Ile	Cys	Glu	Ile	Thr	Trp	Glu			
	1055					1060					1065						
Cys	Leu	Gln	Pro	Met	Lys	Gly	Asp	Pro	Val	Ile	Tyr	Ser	Leu	Gln			
	1070					1075					1080						
Val	Met	Leu	Gly	Lys	Asp	Ser	Glu	Phe	Lys	Gln	Ile	Tyr	Lys	Gly			
	1085					1090					1095						
Pro	Asp	Ser	Ser	Phe	Arg	Tyr	Ser	Ser	Leu	Gln	Leu	Asn	Cys	Glu			
	1100					1105					1110						
Tyr	Arg	Phe	Arg	Val	Cys	Ala	Ile	Arg	Gln	Cys	Gln	Asp	Ser	Leu			
	1115					1120					1125						
Gly	His	Gln	Asp	Leu	Val	Gly	Pro	Tyr	Ser	Thr	Thr	Val	Leu	Phe			
	1130					1135					1140						

ITI-08-PCT_Sequence_Listing_ST25.txt

Ile Ser Gln Arg Thr Glu Pro Pro Ala Ser Thr Asn Arg Asp Thr
1145 1150 1155

Val Glu Ser Thr Arg Thr Arg Arg Ala Leu Ser Asp Glu Gln Cys
1160 1165 1170

Ala Ala Val Ile Leu Val Leu Phe Ala Phe Phe Ser Ile Leu Ile
1175 1180 1185

Ala Phe Ile Ile Gln Tyr Phe Val Ile Lys
1190 1195

<210> 368
<211> 1142
<212> PRT
<213> Artificial Sequence

<220>
<223> fibronectin__Homo_sapiens__A0A024RDV5

<400> 368

Met Ser Gly Pro Ala Gln Val Pro Met Met Ser Pro Asn Gly Ser Val
1 5 10 15

Pro Pro Ile Tyr Val Pro Pro Gly Tyr Ala Pro Gln Val Ile Glu Asp
20 25 30

Asn Gly Val Arg Arg Val Val Val Val Pro Gln Ala Pro Glu Phe His
35 40 45

Pro Gly Ser His Thr Val Leu His Arg Ser Pro His Pro Pro Leu Pro
50 55 60

Gly Phe Ile Pro Val Pro Thr Met Met Pro Pro Pro Pro Arg His Met
65 70 75 80

Tyr Ser Pro Val Thr Gly Ala Gly Asp Met Thr Thr Gln Tyr Met Pro
85 90 95

Gln Tyr Gln Ser Ser Gln Val Tyr Gly Asp Val Asp Ala His Ser Thr
100 105 110

His Gly Arg Ser Asn Phe Arg Asp Glu Arg Ser Ser Lys Thr Tyr Glu
115 120 125

Arg Leu Gln Lys Lys Leu Lys Asp Arg Gln Gly Thr Gln Lys Asp Lys
130 135 140

Met Ser Ser Pro Pro Ser Ser Pro Gln Lys Cys Pro Ser Pro Ile Asn
145 150 155 160

ITI-08-PCT_Sequence_Listing_ST25.txt

Glu His Asn Gly Leu Ile Lys Gly Gln Ile Ala Gly Gly Ile Asn Thr
165 170 175

Gly Ser Ala Lys Ile Lys Ser Gly Lys Gly Lys Gly Gly Thr Gln Val
180 185 190

Asp Thr Glu Ile Glu Glu Lys Asp Glu Glu Thr Lys Ala Phe Glu Ala
195 200 205

Leu Leu Ser Asn Ile Val Lys Pro Val Ala Ser Asp Ile Gln Ala Arg
210 215 220

Thr Val Val Leu Thr Trp Ser Pro Pro Ser Ser Leu Ile Asn Gly Glu
225 230 235 240

Thr Asp Glu Ser Ser Val Pro Glu Leu Tyr Gly Tyr Glu Val Leu Ile
245 250 255

Ser Ser Thr Gly Lys Asp Gly Lys Tyr Lys Ser Val Tyr Val Gly Glu
260 265 270

Glu Thr Asn Ile Thr Leu Asn Asp Leu Lys Pro Ala Met Asp Tyr His
275 280 285

Ala Lys Val Gln Ala Glu Tyr Asn Ser Ile Lys Gly Thr Pro Ser Glu
290 295 300

Ala Glu Ile Phe Thr Thr Leu Ser Cys Glu Pro Asp Ile Pro Asn Pro
305 310 315 320

Pro Arg Ile Ala Asn Arg Thr Lys Asn Ser Leu Thr Leu Gln Trp Lys
325 330 335

Ala Pro Ser Asp Asn Gly Ser Lys Ile Gln Asn Phe Val Leu Glu Trp
340 345 350

Asp Glu Gly Lys Gly Asn Gly Glu Phe Cys Gln Cys Tyr Met Gly Ser
355 360 365

Gln Lys Gln Phe Lys Ile Thr Lys Leu Ser Pro Ala Met Gly Cys Lys
370 375 380

Phe Arg Leu Ser Ala Arg Asn Asp Tyr Gly Thr Ser Gly Phe Ser Glu
385 390 395 400

Glu Val Leu Tyr Tyr Thr Ser Gly Cys Ala Pro Ser Met Pro Ala Ser
405 410 415

Pro Val Leu Thr Lys Ala Gly Ile Thr Trp Leu Ser Leu Gln Trp Ser
420 425 430

Lys Pro Ser Gly Thr Pro Ser Asp Glu Gly Ile Ser Tyr Ile Leu Glu

435 440 445

Page 610

ITI-08-PCT_Sequence_Listing_ST25.txt

Val	Asn	Trp	Glu	Val	Pro	Leu	Ser	Asn	Gly	Thr	Asp	Val	Thr	Glu	Tyr	725	730	735
Arg	Leu	Glu	Trp	Gly	Gly	Val	Glu	Gly	Ser	Met	Gln	Ile	Cys	Tyr	Cys	740	745	750
Gly	Pro	Gly	Leu	Ser	Tyr	Glu	Ile	Lys	Gly	Leu	Ser	Pro	Ala	Thr	Thr	755	760	765
Tyr	Tyr	Cys	Arg	Val	Gln	Ala	Leu	Ser	Val	Val	Gly	Ala	Gly	Pro	Phe	770	775	780
Ser	Glu	Val	Val	Ala	Cys	Val	Thr	Pro	Pro	Ser	Val	Pro	Gly	Ile	Val	785	790	800
Thr	Cys	Leu	Gln	Glu	Ile	Ser	Asp	Asp	Glu	Ile	Glu	Asn	Pro	His	Tyr	805	810	815
Ser	Pro	Ser	Thr	Cys	Leu	Ala	Ile	Ser	Trp	Glu	Lys	Pro	Cys	Asp	His	820	825	830
Gly	Ser	Glu	Ile	Leu	Ala	Tyr	Ser	Ile	Asp	Phe	Gly	Asp	Lys	Gln	Ser	835	840	845
Leu	Thr	Val	Gly	Lys	Val	Thr	Ser	Tyr	Ile	Ile	Asn	Asn	Leu	Gln	Pro	850	855	860
Asp	Thr	Thr	Tyr	Arg	Ile	Arg	Ile	Gln	Ala	Leu	Asn	Ser	Leu	Gly	Ala	865	870	875
Gly	Pro	Phe	Ser	His	Met	Ile	Lys	Leu	Lys	Thr	Lys	Pro	Leu	Pro	Pro	885	890	895
Asp	Pro	Pro	Arg	Leu	Glu	Cys	Val	Ala	Phe	Ser	His	Gln	Asn	Leu	Lys	900	905	910
Leu	Lys	Trp	Gly	Glu	Gly	Thr	Pro	Lys	Thr	Leu	Ser	Thr	Asp	Ser	Ile	915	920	925
Gln	Tyr	His	Leu	Gln	Met	Glu	Asp	Lys	Asn	Gly	Arg	Phe	Val	Ser	Leu	930	935	940
Tyr	Arg	Gly	Pro	Cys	His	Thr	Tyr	Lys	Val	Gln	Arg	Leu	Asn	Glu	Ser	945	950	955
Thr	Ser	Tyr	Lys	Phe	Cys	Ile	Gln	Ala	Cys	Asn	Glu	Ala	Gly	Glu	Gly	965	970	975
Pro	Leu	Ser	Gln	Glu	Tyr	Ile	Phe	Thr	Thr	Pro	Lys	Ser	Val	Pro	Ala	980	985	990

ITI-08-PCT_Sequence_Listing_ST25.txt

Ala Leu Lys Ala Pro Lys Ile Glu Lys Val Asn Asp His Ile Cys Glu
995 1000 1005

Ile Thr Trp Glu Cys Leu Gln Pro Met Lys Gly Asp Pro Val Ile
1010 1015 1020

Tyr Ser Leu Gln Val Met Leu Gly Lys Asp Ser Glu Phe Lys Gln
1025 1030 1035

Ile Tyr Lys Gly Pro Asp Ser Ser Phe Arg Tyr Ser Ser Leu Gln
1040 1045 1050

Leu Asn Cys Glu Tyr Arg Phe Arg Val Cys Ala Ile Arg Gln Cys
1055 1060 1065

Gln Asp Ser Leu Gly His Gln Asp Leu Val Gly Pro Tyr Ser Thr
1070 1075 1080

Thr Val Leu Phe Ile Ser Gln Arg Thr Glu Pro Pro Ala Ser Thr
1085 1090 1095

Asn Arg Asp Thr Val Glu Ser Thr Arg Thr Arg Arg Ala Leu Ser
1100 1105 1110

Asp Glu Gln Cys Ala Ala Val Ile Leu Val Leu Phe Ala Phe Phe
1115 1120 1125

Ser Ile Leu Ile Ala Phe Ile Ile Gln Tyr Phe Val Ile Lys
1130 1135 1140

<210> 369

<211> 339

<212> PRT

<213> Artificial Sequence

<220>

<223> fibronectin__Homo_sapiens__A6NH44

<400> 369

Met Pro Pro Ser Lys Pro His Pro Pro Val Val Gly Lys Val Thr His
1 5 10 15

His Ser Ile Glu Leu Tyr Trp Asp Leu Glu Lys Lys Ala Lys Arg Gln
20 25 30

Gly Pro Gln Glu Gln Trp Phe Arg Phe Ser Ile Glu Glu Glu Asp Pro
35 40 45

Lys Met His Thr Tyr Gly Ile Ile Tyr Thr Gly Tyr Ala Thr Lys His
50 55 60

ITI-08-PCT_Sequence_Listing_ST25.txt

Val	Val	Glu	Gly	Leu	Glu	Pro	Arg	Thr	Leu	Tyr	Arg	Phe	Arg	Leu	Lys	65	70	75	80
Val	Thr	Ser	Pro	Ser	Gly	Glu	Cys	Glu	Tyr	Ser	Pro	Leu	Val	Ser	Val	85	90	95	
Ser	Thr	Thr	Arg	Glu	Pro	Ile	Ser	Ser	Glu	His	Leu	His	Arg	Ala	Val	100	105	110	
Ser	Val	Asn	Asp	Glu	Asp	Leu	Leu	Val	Arg	Ile	Leu	Gln	Gly	Gly	Arg	115	120	125	
Val	Lys	Val	Asp	Val	Pro	Asn	Lys	Phe	Gly	Phe	Thr	Ala	Leu	Met	Val	130	135	140	
Ala	Ala	Gln	Lys	Gly	Tyr	Thr	Arg	Leu	Val	Lys	Ile	Leu	Val	Ser	Asn	145	150	155	160
Gly	Thr	Asp	Val	Asn	Leu	Lys	Asn	Gly	Ser	Gly	Lys	Asp	Ser	Leu	Met	165	170	175	
Leu	Ala	Cys	Tyr	Ala	Gly	His	Leu	Asp	Val	Val	Lys	Tyr	Leu	Arg	Arg	180	185	190	
His	Gly	Ala	Ser	Trp	Gln	Ala	Arg	Asp	Leu	Gly	Gly	Cys	Thr	Ala	Leu	195	200	205	
His	Trp	Ala	Ala	Asp	Gly	Gly	His	Cys	Ser	Val	Ile	Glu	Trp	Met	Ile	210	215	220	
Lys	Asp	Gly	Cys	Glu	Val	Asp	Val	Val	Asp	Thr	Gly	Ser	Gly	Trp	Thr	225	230	235	240
Pro	Leu	Met	Arg	Val	Ser	Ala	Val	Ser	Gly	Asn	Gln	Arg	Val	Ala	Ser	245	250	255	
Leu	Leu	Ile	Asp	Ala	Gly	Ala	Asn	Val	Asn	Val	Lys	Asp	Arg	Asn	Gly	260	265	270	
Lys	Thr	Pro	Leu	Met	Val	Ala	Val	Leu	Asn	Asn	His	Glu	Glu	Leu	Val	275	280	285	
Gln	Leu	Leu	Leu	Asp	Lys	Gly	Ala	Asp	Ala	Ser	Val	Lys	Asn	Glu	Phe	290	295	300	
Gly	Lys	Gly	Val	Leu	Glu	Met	Ala	Arg	Val	Phe	Asp	Arg	Gln	Ser	Val	305	310	315	320
Val	Ser	Leu	Leu	Glu	Glu	Arg	Lys	Lys	Lys	Gln	Arg	Pro	Lys	Lys	Ser	325	330	335	
Cys	Val	Cys																	

ITI-08-PCT_Sequence_Listing_ST25.txt

<210> 370
 <211> 1049
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fibronectin__Homo_sapiens__A8K6A5

<400> 370

```

Met Gly Ser Arg Thr Pro Glu Ser Pro Leu His Ala Val Gln Leu Arg
1           5           10           15

Trp Gly Pro Arg Arg Arg Pro Pro Leu Leu Pro Leu Leu Leu Leu
20           25           30

Leu Pro Pro Pro Pro Arg Val Gly Gly Phe Asn Leu Asp Ala Glu Ala
35           40           45

Pro Ala Val Leu Ser Gly Pro Pro Gly Ser Phe Phe Gly Phe Ser Val
50           55           60

Glu Phe Tyr Arg Pro Gly Thr Asp Gly Val Ser Val Leu Val Gly Ala
65           70           75           80

Pro Lys Ala Asn Thr Ser Gln Pro Gly Val Leu Gln Gly Gly Ala Val
85           90           95

Tyr Leu Cys Pro Trp Gly Ala Ser Pro Thr Gln Cys Thr Pro Ile Glu
100          105          110

Phe Asp Ser Lys Gly Ser Arg Leu Leu Glu Ser Ser Leu Ser Ser Ser
115          120          125

Glu Gly Glu Glu Pro Val Glu Tyr Lys Ser Leu Gln Trp Phe Gly Ala
130          135          140

Thr Val Arg Ala His Gly Ser Ser Ile Leu Ala Cys Ala Pro Leu Tyr
145          150          155          160

Ser Trp Arg Thr Glu Lys Glu Pro Leu Ser Asp Pro Val Gly Thr Cys
165          170          175

Tyr Leu Ser Thr Asp Asn Phe Thr Arg Ile Leu Glu Tyr Ala Pro Cys
180          185          190

Arg Ser Asp Phe Ser Trp Ala Ala Gly Gln Gly Tyr Cys Gln Gly Gly
195          200          205

Phe Ser Ala Glu Phe Thr Lys Thr Gly Arg Val Val Leu Gly Gly Pro
210          215          220
    
```

ITI-08-PCT_Sequence_Listing_ST25.txt

Gly	Ser	Tyr	Phe	Trp	Gln	Gly	Gln	Ile	Leu	Ser	Ala	Thr	Gln	Glu	Gln	225	230	235	240
Ile	Ala	Glu	Ser	Tyr	Tyr	Pro	Glu	Tyr	Leu	Ile	Asn	Leu	Val	Gln	Gly	245	250	255	
Gln	Leu	Gln	Thr	Arg	Gln	Ala	Ser	Ser	Ile	Tyr	Asp	Asp	Ser	Tyr	Leu	260	265	270	
Gly	Tyr	Ser	Val	Ala	Val	Gly	Glu	Phe	Ser	Gly	Asp	Asp	Thr	Glu	Asp	275	280	285	
Phe	Val	Ala	Gly	Val	Pro	Lys	Gly	Asn	Leu	Thr	Tyr	Gly	Tyr	Val	Thr	290	295	300	
Ile	Leu	Asn	Gly	Ser	Asp	Ile	Arg	Ser	Leu	Tyr	Asn	Phe	Ser	Gly	Glu	305	310	315	320
Gln	Met	Ala	Ser	Tyr	Phe	Ala	Tyr	Ala	Val	Ala	Ala	Thr	Asp	Val	Asn	325	330	335	
Gly	Asp	Gly	Leu	Asp	Asp	Leu	Leu	Val	Gly	Ala	Pro	Leu	Leu	Met	Asp	340	345	350	
Arg	Thr	Pro	Asp	Gly	Arg	Pro	Gln	Glu	Val	Gly	Arg	Val	Tyr	Val	Tyr	355	360	365	
Leu	Gln	His	Pro	Ala	Gly	Ile	Glu	Ser	Thr	Pro	Thr	Leu	Thr	Leu	Thr	370	375	380	
Gly	His	Asp	Glu	Phe	Gly	Arg	Phe	Gly	Ser	Ser	Leu	Thr	Pro	Leu	Gly	385	390	395	400
Asp	Leu	Asp	Gln	Asp	Gly	Tyr	Asn	Asp	Val	Ala	Ile	Gly	Ala	Pro	Phe	405	410	415	
Gly	Gly	Glu	Thr	Gln	Gln	Gly	Val	Val	Phe	Val	Phe	Pro	Gly	Gly	Pro	420	425	430	
Gly	Gly	Leu	Gly	Ser	Lys	Pro	Ser	Gln	Val	Leu	Gln	Pro	Leu	Trp	Ala	435	440	445	
Ala	Ser	His	Thr	Pro	Asp	Phe	Phe	Gly	Ser	Ala	Leu	Arg	Gly	Gly	Arg	450	455	460	
Asp	Leu	Asp	Gly	Asn	Gly	Tyr	Pro	Asp	Leu	Ile	Val	Gly	Ser	Phe	Gly	465	470	475	480
Val	Asp	Lys	Ala	Val	Val	Tyr	Arg	Gly	Arg	Pro	Ile	Val	Ser	Ala	Ser	485	490	495	

ITI-08-PCT_Sequence_Listing_ST25.txt

Ala	Ser	Leu	Thr	Ile	Phe	Pro	Ala	Met	Phe	Asn	Pro	Glu	Glu	Arg	Ser		
			500					505					510				
Cys	Ser	Leu	Glu	Gly	Asn	Pro	Val	Ala	Cys	Ile	Asn	Leu	Ser	Phe	Cys		
		515					520					525					
Leu	Asn	Ala	Ser	Gly	Lys	His	Val	Ala	Asp	Ser	Ile	Gly	Phe	Thr	Val		
	530					535					540						
Glu	Leu	Gln	Leu	Asp	Trp	Gln	Lys	Gln	Lys	Gly	Gly	Val	Arg	Arg	Ala		
545					550					555					560		
Leu	Phe	Leu	Ala	Ser	Arg	Gln	Ala	Thr	Leu	Thr	Gln	Thr	Leu	Leu	Ile		
				565					570						575		
Gln	Asn	Gly	Ala	Arg	Glu	Asp	Cys	Arg	Glu	Met	Lys	Ile	Tyr	Leu	Arg		
			580					585					590				
Asn	Glu	Ser	Glu	Phe	Arg	Asp	Lys	Leu	Ser	Pro	Ile	His	Ile	Ala	Leu		
		595					600					605					
Asn	Phe	Ser	Leu	Asp	Pro	Gln	Ala	Pro	Val	Asp	Ser	His	Gly	Leu	Arg		
	610					615					620						
Pro	Ala	Leu	His	Tyr	Gln	Ser	Lys	Ser	Arg	Ile	Glu	Asp	Lys	Ala	Gln		
625					630					635					640		
Ile	Leu	Leu	Gly	Cys	Gly	Glu	Asp	Asn	Ile	Cys	Val	Pro	Asp	Leu	Gln		
				645					650					655			
Leu	Glu	Val	Phe	Gly	Glu	Gln	Asn	His	Val	Tyr	Leu	Gly	Asp	Lys	Asn		
			660					665					670				
Ala	Leu	Asn	Leu	Thr	Phe	His	Ala	Gln	Asn	Val	Gly	Glu	Gly	Gly	Ala		
		675					680					685					
Tyr	Glu	Ala	Glu	Leu	Arg	Val	Thr	Ala	Pro	Pro	Glu	Ala	Glu	Tyr	Ser		
	690					695					700						
Gly	Leu	Val	Arg	His	Pro	Gly	Asn	Phe	Ser	Ser	Leu	Ser	Cys	Asp	Tyr		
705					710					715					720		
Phe	Ala	Val	Asn	Gln	Ser	Arg	Leu	Leu	Val	Cys	Asp	Leu	Gly	Asn	Pro		
			725						730					735			
Met	Lys	Ala	Gly	Ala	Ser	Leu	Trp	Gly	Gly	Leu	Arg	Phe	Thr	Val	Pro		
			740					745					750				
His	Leu	Arg	Asp	Thr	Lys	Lys	Thr	Ile	Gln	Phe	Asp	Phe	Gln	Ile	Leu		
		755					760					765					
Ser	Lys	Asn	Leu	Asn	Asn	Ser	Gln	Ser	Asp	Val	Val	Ser	Phe	Arg	Leu		

ITI-08-PCT_Sequence_Listing_ST25.txt

770

775

780

Ser Val Glu Ala Gln Ala Gln Val Thr Leu Asn Gly Val Ser Lys Pro
 785 790 795 800

Glu Ala Val Leu Phe Pro Val Ser Asp Trp His Pro Arg Asp Gln Pro
 805 810 815

Gln Glu Glu Glu Asp Leu Gly Pro Ala Val His His Val Tyr Glu Leu
 820 825 830

Ile Asn Gln Gly Pro Ser Ser Ile Ser Gln Gly Val Leu Glu Leu Ser
 835 840 845

Cys Pro Gln Ala Leu Glu Gly Gln Gln Leu Leu Tyr Val Thr Arg Val
 850 855 860

Thr Gly Leu Asn Cys Thr Thr Asn His Pro Ile Asn Pro Lys Gly Leu
 865 870 875 880

Glu Leu Asp Pro Glu Gly Ser Leu His His Gln Gln Lys Arg Glu Ala
 885 890 895

Pro Ser Arg Ser Ser Ala Ser Ser Gly Pro Gln Ile Leu Lys Cys Pro
 900 905 910

Glu Ala Glu Cys Phe Arg Leu Arg Cys Glu Leu Gly Pro Leu His Gln
 915 920 925

Gln Glu Ser Gln Ser Leu Gln Leu His Phe Arg Val Trp Ala Lys Thr
 930 935 940

Phe Leu Gln Arg Glu His Gln Pro Phe Ser Leu Gln Cys Glu Ala Val
 945 950 955 960

Tyr Lys Ala Leu Lys Met Pro Tyr Arg Ile Leu Pro Arg Gln Leu Pro
 965 970 975

Gln Lys Glu Arg Gln Val Ala Thr Ala Val Gln Trp Thr Lys Ala Glu
 980 985 990

Gly Ser Tyr Gly Val Pro Leu Trp Ile Ile Ile Leu Ala Ile Leu Phe
 995 1000 1005

Gly Leu Leu Leu Leu Gly Leu Leu Ile Tyr Ile Leu Tyr Lys Leu
 1010 1015 1020

Gly Phe Phe Lys Arg Ser Leu Pro Tyr Gly Thr Ala Met Glu Lys
 1025 1030 1035

Ala Gln Leu Lys Pro Pro Ala Thr Ser Asp Ala
 1040 1045

ITI-08-PCT_Sequence_Listing_ST25.txt

<210> 371
 <211> 1049
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fibronectin__Homo_sapiens__B2R627

<400> 371

```

Met Gly Ser Arg Thr Pro Glu Ser Pro Leu His Ala Val Gln Leu Arg
1          5          10          15

Trp Gly Pro Arg Arg Arg Pro Pro Leu Leu Pro Leu Leu Leu Leu
20          25          30

Leu Pro Pro Pro Pro Arg Val Gly Gly Phe Asn Leu Asp Ala Glu Ala
35          40          45

Pro Ala Val Leu Ser Gly Pro Pro Gly Ser Phe Phe Gly Phe Ser Val
50          55          60

Glu Phe Tyr Arg Pro Gly Thr Asp Gly Val Ser Val Leu Val Gly Ala
65          70          75          80

Pro Lys Ala Asn Thr Ser Gln Pro Gly Val Leu Gln Gly Gly Ala Val
85          90          95

Tyr Leu Cys Pro Trp Gly Ala Ser Pro Thr Gln Cys Thr Pro Ile Glu
100         105         110

Phe Asp Ser Lys Gly Ser Arg Leu Leu Glu Ser Ser Leu Ser Ser Ser
115         120         125

Glu Gly Glu Glu Pro Val Glu Tyr Lys Ser Leu Gln Trp Phe Gly Ala
130         135         140

Thr Val Arg Ala His Gly Ser Ser Ile Leu Ala Cys Ala Pro Leu Tyr
145         150         155         160

Ser Trp Arg Thr Glu Lys Glu Pro Leu Ser Asp Pro Val Gly Thr Cys
165         170         175

Tyr Leu Ser Thr Asp Asn Phe Thr Arg Ile Leu Glu Tyr Ala Pro Cys
180         185         190

Arg Ser Asp Phe Ser Trp Ala Ala Gly Gln Gly Tyr Cys Gln Gly Gly
195         200         205

Phe Ser Ala Glu Phe Thr Lys Thr Gly Arg Val Val Leu Gly Gly Pro
210         215         220
    
```

ITI-08-PCT_Sequence_Listing_ST25.txt

Gly	Ser	Tyr	Phe	Trp	Gln	Gly	Gln	Ile	Leu	Ser	Ala	Thr	Gln	Glu	Gln	225	230	235	240
Ile	Ala	Glu	Ser	Tyr	Tyr	Pro	Glu	Tyr	Leu	Ile	Asn	Leu	Val	Gln	Gly	245	250	255	
Gln	Leu	Gln	Thr	Arg	Gln	Ala	Ser	Ser	Ile	Tyr	Asp	Asp	Ser	Tyr	Leu	260	265	270	
Gly	Tyr	Ser	Val	Ala	Val	Gly	Glu	Phe	Ser	Gly	Asp	Asp	Thr	Glu	Asp	275	280	285	
Phe	Val	Ala	Gly	Val	Pro	Lys	Gly	Asn	Leu	Thr	Tyr	Gly	Tyr	Val	Thr	290	295	300	
Ile	Leu	Asn	Gly	Ser	Asp	Ile	Arg	Ser	Leu	Tyr	Asn	Phe	Ser	Gly	Glu	305	310	315	320
Gln	Met	Ala	Ser	Tyr	Phe	Gly	Tyr	Ala	Val	Ala	Ala	Thr	Asp	Val	Asn	325	330	335	
Gly	Asp	Gly	Leu	Asp	Asp	Leu	Leu	Val	Gly	Ala	Pro	Leu	Leu	Met	Asp	340	345	350	
Arg	Thr	Pro	Asp	Gly	Arg	Pro	Gln	Gly	Val	Gly	Arg	Val	Tyr	Val	Tyr	355	360	365	
Leu	Gln	His	Pro	Ala	Gly	Ile	Glu	Pro	Thr	Pro	Thr	Leu	Thr	Leu	Thr	370	375	380	
Gly	His	Asp	Glu	Phe	Gly	Arg	Phe	Gly	Ser	Ser	Leu	Thr	Pro	Leu	Gly	385	390	395	400
Asp	Leu	Asp	Gln	Asp	Gly	Tyr	Asn	Asp	Val	Ala	Ile	Gly	Ala	Pro	Phe	405	410	415	
Gly	Gly	Glu	Thr	Gln	Gln	Gly	Val	Val	Phe	Val	Phe	Pro	Gly	Gly	Pro	420	425	430	
Gly	Gly	Leu	Gly	Ser	Lys	Leu	Ser	Gln	Val	Leu	Gln	Pro	Leu	Trp	Ala	435	440	445	
Ala	Ser	His	Thr	Pro	Asp	Phe	Phe	Gly	Ser	Ala	Leu	Arg	Gly	Gly	Arg	450	455	460	
Asp	Leu	Asp	Gly	Asn	Gly	Tyr	Pro	Asp	Leu	Ile	Val	Gly	Ser	Phe	Gly	465	470	475	480
Val	Asp	Lys	Ala	Val	Val	Tyr	Arg	Gly	Arg	Pro	Ile	Val	Ser	Ala	Ser	485	490	495	

ITI-08-PCT_Sequence_Listing_ST25.txt

Ala	Ser	Leu	Thr	Ile	Phe	Pro	Ala	Met	Phe	Asn	Pro	Glu	Glu	Arg	Ser	500	505	510
Cys	Ser	Leu	Glu	Gly	Asn	Pro	Val	Ala	Cys	Ile	Asn	Leu	Ser	Phe	Cys	515	520	525
Leu	Asn	Ala	Ser	Gly	Lys	His	Val	Ala	Asp	Ser	Ile	Gly	Phe	Thr	Val	530	535	540
Glu	Leu	Gln	Leu	Asp	Trp	Gln	Lys	Gln	Lys	Gly	Gly	Val	Arg	Arg	Ala	545	550	555
Leu	Phe	Leu	Ala	Ser	Arg	Gln	Ala	Thr	Leu	Thr	Gln	Thr	Leu	Leu	Ile	565	570	575
Gln	Asn	Gly	Ala	Arg	Glu	Asp	Cys	Arg	Glu	Met	Lys	Ile	Tyr	Leu	Arg	580	585	590
Asn	Glu	Ser	Glu	Phe	Arg	Asp	Lys	Leu	Ser	Pro	Ile	His	Ile	Ala	Leu	595	600	605
Asn	Phe	Ser	Leu	Asp	Pro	Gln	Ala	Pro	Val	Asp	Ser	His	Gly	Leu	Arg	610	615	620
Pro	Ala	Leu	His	Tyr	Gln	Ser	Lys	Ser	Arg	Ile	Glu	Asp	Lys	Ala	Gln	625	630	635
Ile	Leu	Leu	Asp	Cys	Gly	Glu	Asp	Asn	Ile	Cys	Val	Pro	Asp	Leu	Gln	645	650	655
Leu	Glu	Val	Phe	Gly	Glu	Gln	Asn	His	Val	Tyr	Leu	Gly	Asp	Lys	Asn	660	665	670
Ala	Leu	Asn	Leu	Thr	Phe	His	Ala	Gln	Asn	Val	Gly	Glu	Gly	Gly	Ala	675	680	685
Tyr	Glu	Ala	Glu	Leu	Arg	Val	Thr	Ala	Pro	Pro	Glu	Ala	Glu	Tyr	Ser	690	695	700
Gly	Leu	Val	Arg	His	Pro	Gly	Asn	Phe	Ser	Ser	Leu	Ser	Cys	Asp	Tyr	705	710	715
Phe	Ala	Val	Asn	Gln	Ser	Arg	Leu	Leu	Val	Cys	Asp	Leu	Gly	Asn	Pro	725	730	735
Met	Lys	Ala	Gly	Ala	Ser	Leu	Trp	Gly	Gly	Leu	Arg	Phe	Thr	Val	Pro	740	745	750
His	Leu	Arg	Asp	Thr	Lys	Lys	Thr	Ile	Gln	Phe	Asp	Phe	Gln	Ile	Leu	755	760	765
Ser	Lys	Asn	Leu	Asn	Asn	Ser	Gln	Ser	Asp	Val	Val	Ser	Phe	Arg	Leu			

ITI-08-PCT_Sequence_Listing_ST25.txt

770

775

780

Ser Val Glu Ala Gln Ala Gln Val Thr Leu Asn Gly Val Ser Lys Pro
 785 790 795 800

Glu Ala Val Leu Phe Pro Val Ser Asp Trp His Pro Arg Asp Gln Pro
 805 810 815

Gln Lys Glu Glu Asp Leu Gly Pro Ala Val His His Val Tyr Glu Leu
 820 825 830

Ile Asn Gln Gly Pro Ser Ser Ile Ser Gln Gly Val Leu Glu Leu Ser
 835 840 845

Cys Pro Gln Ala Leu Glu Gly Gln Gln Leu Leu Tyr Val Thr Arg Val
 850 855 860

Thr Gly Leu Asn Cys Thr Thr Asn His Pro Ile Asn Pro Lys Gly Leu
 865 870 875 880

Glu Leu Asp Pro Glu Gly Ser Leu His His Gln Gln Lys Arg Glu Ala
 885 890 895

Pro Ser Arg Ser Ser Ala Ser Ser Gly Pro Gln Ile Leu Lys Cys Pro
 900 905 910

Glu Ala Glu Cys Phe Arg Leu Arg Cys Glu Leu Gly Pro Leu His Gln
 915 920 925

Gln Glu Ser Gln Ser Leu Gln Leu His Phe Arg Val Trp Ala Lys Thr
 930 935 940

Phe Leu Gln Arg Glu His Gln Pro Phe Ser Leu Gln Cys Glu Ala Val
 945 950 955 960

Tyr Lys Ala Leu Lys Met Pro Tyr Arg Ile Leu Pro Arg Gln Leu Pro
 965 970 975

Gln Lys Glu Arg Gln Val Ala Thr Ala Val Gln Trp Thr Lys Ala Glu
 980 985 990

Gly Ser Tyr Gly Val Pro Leu Trp Ile Ile Ile Leu Ala Ile Leu Phe
 995 1000 1005

Gly Leu Leu Leu Leu Gly Leu Leu Ile Tyr Ile Leu Tyr Lys Leu
 1010 1015 1020

Gly Phe Phe Lys Arg Ser Leu Pro Tyr Gly Thr Ala Met Glu Lys
 1025 1030 1035

Ala Gln Leu Lys Pro Pro Ala Thr Ser Asp Ala
 1040 1045

ITI-08-PCT_Sequence_Listing_ST25.txt

<210> 372
 <211> 466
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fibronectin__Homo_sapiens__B3KXM5

<400> 372

```

Met Leu Ser Leu Arg Gln Arg Met Met His Ala Arg Phe Arg Asn Pro
1          5          10          15

Leu Ser Arg Gln Pro Ala Arg Pro Ser Tyr Arg Gln Gly Tyr Asn Gly
          20          25          30

Arg Pro Asn Val Glu Gly Lys Val Leu Pro Gly Ser Asn Gly Lys Pro
          35          40          45

Asn Gly Gln Arg Ile Ile Asn Gly Pro Gln Gly Thr Lys Trp Val Val
50          55          60

Asp Leu Asp Arg Gly Leu Val Leu Asn Ala Glu Gly Arg Tyr Leu Gln
65          70          75          80

Asp Ser His Gly Asn Pro Leu Arg Ile Lys Leu Gly Gly Asp Gly Arg
          85          90          95

Thr Ile Val Asp Leu Glu Gly Thr Pro Val Val Ser Pro Asp Gly Leu
          100          105          110

Pro Leu Phe Gly Gln Gly Arg His Gly Thr Pro Leu Ala Asn Ala Gln
          115          120          125

Asp Lys Pro Ile Leu Ser Leu Gly Gly Lys Pro Leu Val Gly Leu Glu
          130          135          140

Val Ile Lys Lys Thr Thr His Pro Pro Thr Thr Thr Met Gln Pro Thr
145          150          155          160

Thr Thr Thr Thr Pro Leu Pro Thr Thr Thr Thr Pro Arg Pro Thr Thr
          165          170          175

Ala Thr Thr Arg Arg Thr Thr Thr Arg Arg Pro Thr Thr Thr Val Arg
          180          185          190

Thr Thr Thr Arg Thr Thr Thr Thr Thr Thr Pro Lys Pro Thr Thr Pro
          195          200          205

Ile Pro Thr Cys Pro Pro Gly Thr Leu Glu Arg His Asp Asp Asp Gly
210          215          220
    
```

ITI-08-PCT_Sequence_Listing_ST25.txt

```

Asn Leu Ile Met Ser Ser Asn Gly Ile Pro Glu Cys Tyr Ala Glu Glu
225                      230                      235                      240

Asp Glu Phe Ser Gly Leu Glu Thr Asp Thr Ala Val Pro Thr Glu Glu
                      245                      250                      255

Ala Tyr Val Ile Tyr Asp Glu Asp Tyr Glu Phe Glu Thr Ser Arg Pro
                      260                      265                      270

Pro Thr Thr Thr Glu Pro Ser Thr Thr Ala Thr Thr Pro Arg Val Ile
                      275                      280                      285

Pro Glu Glu Gly Ala Ile Ser Ser Phe Pro Glu Glu Glu Phe Asp Leu
290                      295                      300

Ala Gly Arg Lys Arg Phe Val Ala Pro Tyr Val Thr Tyr Leu Asn Lys
305                      310                      315                      320

Asp Pro Ser Ala Pro Cys Ser Leu Thr Asp Ala Leu Asp His Phe Gln
                      325                      330                      335

Val Asp Ser Leu Asp Glu Ile Ile Pro Asn Asp Leu Lys Lys Ser Asp
                      340                      345                      350

Leu Pro Pro Gln His Ala Pro Arg Asn Ile Thr Val Val Ala Val Glu
                      355                      360                      365

Gly Cys His Ser Phe Val Ile Val Asp Trp Asp Lys Ala Thr Pro Gly
370                      375                      380

Asp Val Val Thr Gly Tyr Leu Val Tyr Ser Ala Ser Tyr Glu Asp Phe
385                      390                      395                      400

Ile Arg Asn Lys Trp Ser Thr Gln Ala Ser Ser Val Thr His Leu Pro
                      405                      410                      415

Ile Glu Asn Leu Lys Pro Asn Thr Arg Tyr Tyr Phe Lys Val Gln Ala
                      420                      425                      430

Gln Asn Pro His Gly Tyr Gly Pro Ile Ser Pro Ser Val Ser Phe Val
                      435                      440                      445

Thr Glu Ser Asp Asn Pro Leu Leu Val Val Arg Pro Pro Gly Gly Glu
450                      455                      460

Pro Ile
465

<210> 373
<211> 156
<212> PRT

```

ITI-08-PCT_Sequence_Listing_ST25.txt

<213> Artificial Sequence

<220>

<223> fibronectin__Homo_sapiens__B4DIC5

<400> 373

Met Glu Glu Gln Arg Asn Glu Glu Ile Gln Ser Phe Ile Tyr Ser Leu
1 5 10 15

Lys Gln Met Leu Leu Asn Val Glu Ala Asn Ser Ala Lys Val Gln Glu
20 25 30

Asp Leu Glu Ala Glu Phe Gln Ser Leu Phe Ser Leu Leu Glu Glu Leu
35 40 45

Lys Glu Gly Met Leu Met Lys Ile Lys Gln Asp Arg Ala Ser Arg Thr
50 55 60

Tyr Glu Leu Gln Asn Gln Leu Ala Ala Cys Thr Arg Ala Leu Glu Ser
65 70 75 80

Ser Glu Glu Leu Leu Glu Thr Ala Asn Gln Thr Leu Gln Ala Met Asp
85 90 95

Ser Glu Asp Phe Pro Gln Ala Ala Lys Gln Ile Lys Asp Gly Val Thr
100 105 110

Met Ala Pro Ala Phe Arg Leu Ser Leu Lys Ala Lys Val Ser Asp Asn
115 120 125

Met Ser His Leu Met Val Asp Phe Ala Gln Glu Arg Gln Met Leu Gln
130 135 140

Ala Leu Lys Phe Leu Pro Gly Glu Arg Gly Thr His
145 150 155

<210> 374

<211> 306

<212> PRT

<213> Artificial Sequence

<220>

<223> fibronectin__Homo_sapiens__B4DN21

<400> 374

Met Ile Phe Glu Glu His Gly Phe Arg Arg Thr Thr Pro Pro Thr Thr
1 5 10 15

Ala Thr Pro Ile Arg His Arg Pro Arg Pro Tyr Pro Pro Asn Val Gly
20 25 30

ITI-08-PCT_Sequence_Listing_ST25.txt

Gln Glu Ala Leu Ser Gln Thr Thr Ile Ser Trp Ala Pro Phe Gln Asp
 35 40 45
 Thr Ser Glu Tyr Ile Ile Ser Cys His Pro Val Gly Thr Asp Glu Glu
 50 55 60
 Pro Leu Gln Phe Arg Val Pro Gly Thr Ser Thr Ser Ala Thr Leu Thr
 65 70 75 80
 Gly Leu Thr Arg Gly Ala Thr Tyr Asn Ile Ile Val Glu Ala Leu Lys
 85 90 95
 Asp Gln Gln Arg His Lys Val Arg Glu Glu Val Val Thr Val Gly Asn
 100 105 110
 Ser Val Asn Glu Gly Leu Asn Gln Pro Thr Asp Asp Ser Cys Phe Asp
 115 120 125
 Pro Tyr Thr Val Ser His Tyr Ala Val Gly Asp Glu Trp Glu Arg Met
 130 135 140
 Ser Glu Ser Gly Phe Lys Leu Leu Cys Gln Cys Leu Gly Phe Gly Ser
 145 150 155 160
 Gly His Phe Arg Cys Asp Ser Ser Arg Trp Cys His Asp Asn Gly Val
 165 170 175
 Asn Tyr Lys Ile Gly Glu Lys Trp Asp Arg Gln Gly Glu Asn Gly Gln
 180 185 190
 Met Met Ser Cys Thr Cys Leu Gly Asn Gly Lys Gly Glu Phe Lys Cys
 195 200 205
 Asp Pro His Glu Ala Thr Cys Tyr Asp Asp Gly Lys Thr Tyr His Val
 210 215 220
 Gly Glu Gln Trp Gln Lys Glu Tyr Leu Gly Ala Ile Cys Ser Cys Thr
 225 230 235 240
 Cys Phe Gly Gly Gln Arg Gly Trp Arg Cys Asp Asn Cys Arg Arg Pro
 245 250 255
 Gly Gly Glu Pro Ser Pro Glu Gly Thr Thr Gly Gln Ser Tyr Asn Gln
 260 265 270
 Tyr Ser Gln Arg Tyr His Gln Arg Thr Asn Thr Asn Val Asn Cys Pro
 275 280 285
 Ile Glu Cys Phe Met Pro Leu Asp Val Gln Ala Asp Arg Glu Asp Ser
 290 295 300

ITI-08-PCT_Sequence_Listing_ST25.txt

Arg Glu
305

<210> 375
<211> 639
<212> PRT
<213> Artificial Sequence

<220>
<223> fibronectin__Homo_sapiens__B4DS98

<400> 375

Met Glu Lys Ile Leu Phe Tyr Leu Phe Leu Ile Gly Ile Ala Val Lys
1 5 10 15

Ala Gln Ile Cys Pro Lys Arg Cys Val Cys Gln Ile Leu Ser Pro Asn
20 25 30

Leu Ala Thr Leu Cys Ala Lys Lys Gly Leu Leu Phe Val Pro Pro Asn
35 40 45

Ile Asp Arg Arg Thr Val Glu Leu Arg Leu Ala Asp Asn Phe Val Thr
50 55 60

Asn Ile Lys Arg Lys Asp Phe Ala Asn Met Thr Ser Leu Val Asp Leu
65 70 75 80

Thr Leu Ser Arg Asn Thr Ile Ser Phe Ile Thr Pro His Ala Phe Ala
85 90 95

Asp Leu Arg Asn Leu Arg Ser Leu His Leu Asn Ser Asn Arg Leu Thr
100 105 110

Lys Ile Thr Asn Asp Met Phe Ser Gly Leu Ser Asn Leu His His Leu
115 120 125

Ile Leu Asn Asn Asn Gln Leu Thr Leu Ile Ser Ser Thr Ala Phe Asp
130 135 140

Asp Val Phe Ala Leu Glu Glu Leu Asp Leu Ser Tyr Asn Asn Leu Glu
145 150 155 160

Thr Ile Pro Trp Asp Ala Val Glu Lys Met Val Ser Leu His Thr Leu
165 170 175

Ser Leu Asp His Asn Met Ile Asp Asn Ile Pro Lys Gly Thr Phe Ser
180 185 190

His Leu His Lys Met Thr Arg Leu Asp Val Thr Ser Asn Lys Leu Gln
195 200 205

ITI-08-PCT_Sequence_Listing_ST25.txt

Lys Leu Pro Pro Asp Pro Leu Phe Gln Arg Ala Gln Val Leu Ala Thr
 210 215 220
 Ser Gly Ile Ile Ser Pro Ser Thr Phe Ala Leu Ser Phe Gly Gly Asn
 225 230 235 240
 Pro Leu His Cys Asn Cys Glu Leu Leu Trp Leu Arg Arg Leu Ser Arg
 245 250 255
 Glu Tyr Asp Leu Glu Thr Cys Ala Ser Pro Pro Leu Leu Thr Gly Arg
 260 265 270
 Tyr Phe Trp Ser Ile Pro Glu Glu Glu Phe Leu Cys Glu Pro Pro Leu
 275 280 285
 Ile Thr Arg His Thr His Glu Met Arg Val Leu Glu Gly Gln Arg Ala
 290 295 300
 Thr Leu Arg Cys Lys Ala Arg Gly Asp Pro Glu Pro Ala Ile His Trp
 305 310 315 320
 Ile Ser Pro Glu Gly Lys Leu Ile Ser Asn Ala Thr Arg Ser Leu Val
 325 330 335
 Tyr Asp Asn Gly Thr Leu Asp Ile Leu Ile Thr Thr Val Lys Asp Thr
 340 345 350
 Gly Ala Phe Thr Cys Ile Ala Ser Asn Pro Ala Gly Glu Ala Thr Gln
 355 360 365
 Ile Val Asp Leu His Ile Ile Lys Leu Pro His Leu Leu Asn Ser Thr
 370 375 380
 Asn His Ile His Glu Pro Asp Pro Gly Ser Ser Asp Ile Ser Thr Ser
 385 390 395 400
 Thr Lys Ser Gly Ser Asn Thr Ser Ser Ser Asn Asp Gly Ile Thr Ser
 405 410 415
 Leu Thr Ala Thr Arg Val Val Gly Cys Ile Gln Phe Thr Thr Glu Gln
 420 425 430
 Asp Tyr Val Arg Cys His Phe Met Gln Ser Gln Phe Leu Gly Gly Thr
 435 440 445
 Met Ile Ile Ile Ile Gly Gly Ile Ile Val Ala Ser Val Leu Val Phe
 450 455 460
 Ile Ile Ile Leu Met Ile Arg Tyr Lys Val Cys Asn Asn Asn Gly Gln
 465 470 475 480
 His Lys Val Thr Lys Val Ser Asn Val Tyr Ser Gln Thr Asn Gly Ala

ITI-08-PCT_Sequence_Listing_ST25.txt

485 490 495

Gln Ile Gln Gly Cys Ser Val Thr Leu Pro Gln Ser Val Ser Lys Gln
500 505 510

Ala Val Gly His Glu Glu Asn Ala Gln Cys Cys Lys Ala Thr Ser Asp
515 520 525

Asn Val Ile Gln Ser Ser Glu Thr Cys Ser Ser Gln Asp Ser Ala Thr
530 535 540

Thr Thr Ser Ala Leu Pro Pro Ser Trp Thr Ser Ser Thr Ser Val Ser
545 550 555 560

Gln Lys Gln Lys Arg Lys Thr Gly Thr Lys Pro Ser Thr Glu Pro Gln
565 570 575

Asn Glu Ala Val Thr Asn Val Glu Ser Gln Asn Thr Asn Arg Asn Asn
580 585 590

Ser Thr Ala Leu Gln Leu Ala Ser Arg Pro Pro Asp Ser Val Thr Glu
595 600 605

Gly Pro Thr Ser Lys Arg Ala His Ile Lys Pro Asn Ala Leu Leu Thr
610 615 620

Asn Val Asp Gln Ile Val Gln Glu Thr Gln Arg Leu Glu Leu Ile
625 630 635

<210> 376
<211> 337
<212> PRT
<213> Artificial Sequence

<220>
<223> fibronectin__Homo_sapiens__B4DTH2

<400> 376

Met Ile Phe Glu Glu His Gly Phe Arg Arg Thr Thr Pro Pro Thr Thr
1 5 10 15

Ala Thr Pro Ile Arg His Arg Pro Arg Pro Tyr Pro Pro Asn Val Gly
20 25 30

Glu Glu Ile Gln Ile Gly His Ile Pro Arg Glu Asp Val Asp Tyr His
35 40 45

Leu Tyr Pro His Gly Pro Gly Leu Asn Pro Asn Ala Ser Thr Gly Gln
50 55 60

Glu Ala Leu Ser Gln Thr Thr Ile Ser Trp Ala Pro Phe Gln Asp Thr

ITI-08-PCT_Sequence_Listing_ST25.txt

```

65              70              75              80
Ser Glu Tyr Ile Ile Ser Cys His Pro Val Gly Thr Asp Glu Glu Pro
              85              90              95
Leu Gln Phe Arg Val Pro Gly Thr Ser Thr Ser Ala Thr Leu Thr Gly
              100              105              110
Leu Thr Arg Gly Ala Thr Tyr Asn Ile Ile Val Glu Ala Leu Lys Asp
              115              120              125
Gln Gln Arg His Lys Val Arg Glu Glu Val Val Thr Val Gly Asn Ser
              130              135              140
Val Asn Glu Gly Leu Asn Gln Pro Thr Asp Asp Ser Cys Phe Asp Pro
145              150              155              160
Tyr Thr Val Ser His Tyr Ala Val Gly Asp Glu Trp Glu Arg Met Ser
              165              170              175
Glu Ser Gly Phe Lys Leu Leu Cys Gln Cys Leu Gly Phe Gly Ser Gly
              180              185              190
His Phe Arg Cys Asp Ser Ser Arg Trp Cys His Asp Asn Gly Val Asn
              195              200              205
Tyr Lys Ile Gly Glu Lys Trp Asp Arg Gln Gly Glu Asn Gly Gln Met
              210              215              220
Met Ser Cys Thr Cys Leu Gly Asn Gly Lys Gly Glu Phe Lys Cys Asp
225              230              235              240
Pro His Glu Ala Thr Cys Tyr Asp Asp Gly Lys Thr Tyr His Val Gly
              245              250              255
Glu Gln Trp Gln Lys Glu Tyr Leu Gly Ala Ile Cys Ser Cys Thr Cys
              260              265              270
Phe Gly Gly Gln Arg Gly Trp Arg Cys Asp Asn Cys Arg Arg Pro Gly
              275              280              285
Gly Glu Pro Ser Pro Glu Gly Thr Thr Gly Gln Ser Tyr Asn Gln Tyr
              290              295              300
Ser Gln Arg Tyr His Gln Arg Thr Asn Thr Asn Val Asn Cys Pro Ile
305              310              315              320
Glu Cys Phe Met Pro Leu Asp Val Gln Ala Asp Arg Glu Asp Ser Arg
              325              330              335
Glu

```


ITI-08-PCT_Sequence_Listing_ST25.txt

<210> 377

<211> 1014

<212> PRT

<213> Artificial Sequence

<220>

<223> fibronectin__Homo_sapiens__B4DTK1

<400> 377

Met Arg Val Thr Trp Ala Pro Pro Pro Ser Ile Asp Leu Thr Asn Phe
1 5 10 15

Leu Val Arg Tyr Ser Pro Val Lys Asn Glu Glu Asp Val Ala Glu Leu
20 25 30

Ser Ile Ser Pro Ser Asp Asn Ala Val Val Leu Thr Asn Leu Leu Pro
35 40 45

Gly Thr Glu Tyr Val Val Ser Val Ser Ser Val Tyr Glu Gln His Glu
50 55 60

Ser Thr Pro Leu Arg Gly Arg Gln Lys Thr Gly Leu Asp Ser Pro Thr
65 70 75 80

Gly Ile Asp Phe Ser Asp Ile Thr Gly Asn Ser Phe Thr Val His Trp
85 90 95

Ile Ala Pro Arg Ala Thr Ile Thr Gly Tyr Arg Ile Arg His His Pro
100 105 110

Glu His Phe Ser Gly Arg Pro Arg Glu Asp Arg Val Pro His Ser Arg
115 120 125

Asn Ser Ile Thr Leu Thr Asn Leu Thr Pro Gly Thr Glu Tyr Val Val
130 135 140

Ser Ile Val Ala Leu Asn Gly Arg Glu Glu Ser Pro Leu Leu Ile Gly
145 150 155 160

Gln Gln Ser Thr Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala
165 170 175

Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Val Thr
180 185 190

Val Arg Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro
195 200 205

Val Gln Glu Phe Thr Val Pro Gly Ser Lys Ser Thr Ala Thr Ile Ser
210 215 220

ITI-08-PCT_Sequence_Listing_ST25.txt

Gly	Leu	Lys	Pro	Gly	Val	Asp	Tyr	Thr	Ile	Thr	Val	Tyr	Ala	Val	Thr	225	230	235	240
Gly	Arg	Gly	Asp	Ser	Pro	Ala	Ser	Ser	Lys	Pro	Ile	Ser	Ile	Asn	Tyr	245	250	255	
Arg	Thr	Glu	Ile	Asp	Lys	Pro	Ser	Gln	Met	Gln	Val	Thr	Asp	Val	Gln	260	265	270	
Asp	Asn	Ser	Ile	Ser	Val	Lys	Trp	Leu	Pro	Ser	Ser	Ser	Pro	Val	Thr	275	280	285	
Gly	Tyr	Arg	Val	Thr	Thr	Thr	Pro	Lys	Asn	Gly	Pro	Gly	Pro	Thr	Lys	290	295	300	
Thr	Lys	Thr	Ala	Gly	Pro	Asp	Gln	Thr	Glu	Met	Thr	Ile	Glu	Gly	Leu	305	310	315	320
Gln	Pro	Thr	Val	Glu	Tyr	Val	Val	Ser	Val	Tyr	Ala	Gln	Asn	Pro	Ser	325	330	335	
Gly	Glu	Ser	Gln	Pro	Leu	Val	Gln	Thr	Ala	Val	Thr	Thr	Ile	Pro	Ala	340	345	350	
Pro	Thr	Asp	Leu	Lys	Phe	Thr	Gln	Val	Thr	Pro	Thr	Ser	Leu	Ser	Ala	355	360	365	
Gln	Trp	Thr	Pro	Pro	Asn	Val	Gln	Leu	Thr	Gly	Tyr	Arg	Val	Arg	Val	370	375	380	
Thr	Pro	Lys	Glu	Lys	Thr	Gly	Pro	Met	Lys	Glu	Ile	Asn	Leu	Ala	Pro	385	390	395	400
Asp	Ser	Ser	Ser	Val	Val	Val	Ser	Gly	Leu	Met	Val	Ala	Thr	Lys	Tyr	405	410	415	
Glu	Val	Ser	Val	Tyr	Ala	Leu	Lys	Asp	Thr	Leu	Thr	Ser	Arg	Pro	Ala	420	425	430	
Gln	Gly	Val	Val	Thr	Thr	Leu	Glu	Asn	Val	Ser	Pro	Pro	Arg	Arg	Ala	435	440	445	
Arg	Val	Thr	Asp	Ala	Thr	Glu	Thr	Thr	Ile	Thr	Ile	Ser	Trp	Arg	Thr	450	455	460	
Lys	Thr	Glu	Thr	Ile	Thr	Gly	Phe	Gln	Val	Asp	Ala	Val	Pro	Ala	Asn	465	470	475	480
Gly	Gln	Thr	Pro	Ile	Gln	Arg	Thr	Ile	Lys	Pro	Asp	Val	Arg	Ser	Tyr	485	490	495	
Thr	Ile	Thr	Gly	Leu	Gln	Pro	Gly	Thr	Asp	Tyr	Lys	Ile	Tyr	Leu	Tyr				

ITI-08-PCT_Sequence_Listing_ST25.txt

500

505

510

Thr Leu Asn Asp Asn Ala Arg Ser Ser Pro Val Val Ile Asp Ala Ser
 515 520 525

Thr Ala Ile Asp Ala Pro Ser Asn Leu Arg Phe Leu Ala Thr Thr Pro
 530 535 540

Asn Ser Leu Leu Val Ser Trp Gln Pro Pro Arg Ala Arg Ile Thr Gly
 545 550 555 560

Tyr Ile Ile Lys Tyr Glu Lys Pro Gly Ser Pro Pro Arg Glu Val Val
 565 570 575

Pro Arg Pro Arg Pro Gly Val Thr Glu Ala Thr Ile Thr Gly Leu Glu
 580 585 590

Pro Gly Thr Glu Tyr Thr Ile Tyr Val Ile Ala Leu Lys Asn Asn Gln
 595 600 605

Lys Ser Glu Pro Leu Ile Gly Arg Lys Lys Thr Asp Glu Leu Pro Gln
 610 615 620

Leu Val Thr Leu Pro His Pro Asn Leu His Gly Pro Glu Ile Leu Asp
 625 630 635 640

Val Pro Ser Thr Val Gln Lys Thr Pro Phe Val Thr His Pro Gly Tyr
 645 650 655

Asp Thr Gly Asn Gly Ile Gln Leu Pro Gly Thr Ser Gly Gln Gln Pro
 660 665 670

Ser Val Gly Gln Gln Met Ile Phe Glu Glu His Gly Phe Arg Arg Thr
 675 680 685

Thr Pro Pro Thr Thr Ala Thr Pro Ile Arg His Arg Pro Arg Pro Tyr
 690 695 700

Pro Pro Asn Val Gly Glu Glu Ile Gln Ile Gly His Ile Pro Arg Glu
 705 710 715 720

Asp Val Asp Tyr His Leu Tyr Pro His Gly Pro Gly Leu Asn Pro Asn
 725 730 735

Ala Ser Thr Gly Gln Glu Ala Leu Ser Gln Thr Thr Ile Ser Trp Ala
 740 745 750

Pro Phe Gln Asp Thr Ser Glu Tyr Ile Ile Ser Cys His Pro Val Gly
 755 760 765

Thr Asp Glu Glu Pro Leu Gln Phe Arg Val Pro Gly Thr Ser Thr Ser
 770 775 780

ITI-08-PCT_Sequence_Listing_ST25.txt

```

Ala Thr Leu Thr Gly Leu Thr Arg Gly Ala Thr Tyr Asn Ile Ile Val
785                      790                      795                      800

Glu Ala Leu Lys Asp Gln Gln Arg His Lys Val Arg Glu Glu Val Val
                        805                      810                      815

Thr Val Gly Asn Ser Val Asn Glu Gly Leu Asn Gln Pro Thr Asp Asp
                        820                      825                      830

Ser Cys Phe Asp Pro Tyr Thr Val Ser His Tyr Ala Val Gly Asp Glu
                        835                      840                      845

Trp Glu Arg Met Ser Glu Ser Gly Phe Lys Leu Leu Cys Gln Cys Leu
850                      855                      860

Gly Phe Gly Ser Gly His Phe Arg Cys Asp Ser Ser Arg Trp Cys His
865                      870                      875

Asp Asn Gly Val Asn Tyr Lys Ile Gly Glu Lys Trp Asp Arg Gln Gly
                        885                      890                      895

Glu Asn Gly Gln Met Met Ser Cys Thr Cys Leu Gly Asn Gly Lys Gly
900                      905                      910

Glu Phe Lys Cys Asp Pro His Glu Ala Thr Cys Tyr Asp Asp Gly Lys
915                      920                      925

Thr Tyr His Val Gly Glu Gln Trp Gln Lys Glu Tyr Leu Gly Ala Ile
930                      935                      940

Cys Ser Cys Thr Cys Phe Gly Gly Gln Arg Gly Trp Arg Cys Asp Asn
945                      950                      955                      960

Cys Arg Arg Pro Gly Gly Glu Pro Ser Pro Glu Gly Thr Thr Gly Gln
965                      970                      975

Ser Tyr Asn Gln Tyr Ser Gln Arg Tyr His Gln Arg Thr Asn Thr Asn
980                      985                      990

Val Asn Cys Pro Ile Glu Cys Phe Met Pro Leu Asp Val Gln Ala Asp
995                      1000                     1005

Arg Glu Asp Ser Arg Glu
1010

```

```

<210> 378
<211> 894
<212> PRT
<213> Artificial Sequence

```

<220>

ITI-08-PCT_Sequence_Listing_ST25.txt

<223> fibronectin__Homo_sapiens__B4DU16

<400> 378

```

Met Arg Val Thr Trp Ala Pro Pro Pro Ser Ile Asp Leu Thr Asn Phe
1          5          10          15

Leu Val Arg Tyr Ser Pro Val Lys Asn Glu Glu Asp Val Ala Glu Leu
          20          25          30

Ser Ile Ser Pro Ser Asp Asn Ala Val Val Leu Thr Asn Leu Leu Pro
          35          40          45

Gly Thr Glu Tyr Val Val Ser Val Ser Ser Val Tyr Glu Gln His Glu
          50          55          60

Ser Thr Pro Leu Arg Gly Arg Gln Lys Thr Gly Leu Asp Ser Pro Thr
65          70          75          80

Gly Ile Asp Phe Ser Asp Ile Thr Ala Asn Ser Phe Thr Val His Trp
          85          90          95

Ile Ala Pro Arg Ala Thr Ile Thr Gly Tyr Arg Ile Arg His His Pro
          100          105          110

Glu His Phe Ser Gly Arg Pro Arg Glu Asp Arg Val Pro His Ser Arg
          115          120          125

Asn Ser Ile Thr Leu Thr Asn Leu Thr Pro Gly Thr Glu Tyr Val Val
          130          135          140

Ser Ile Val Ala Leu Asn Gly Arg Glu Glu Ser Pro Leu Leu Ile Gly
145          150          155          160

Gln Gln Ser Thr Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala
          165          170          175

Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Val Thr
          180          185          190

Val Arg Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro
          195          200          205

Val Gln Glu Phe Thr Val Pro Gly Ser Lys Ser Thr Ala Thr Ile Ser
          210          215          220

Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Thr
225          230          235          240

Gly Arg Gly Asp Ser Pro Ala Ser Ser Lys Pro Ile Ser Ile Asn Tyr
          245          250          255

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Arg	Thr	Glu	Ile	Asp	Lys	Pro	Ser	Gln	Met	Gln	Val	Thr	Asp	Val	Gln	260	265	270
Asp	Asn	Ser	Ile	Ser	Val	Lys	Trp	Leu	Pro	Ser	Ser	Ser	Pro	Val	Thr	275	280	285
Gly	Tyr	Arg	Val	Thr	Thr	Thr	Pro	Lys	Asn	Gly	Pro	Gly	Pro	Thr	Lys	290	295	300
Thr	Lys	Thr	Ala	Gly	Pro	Asp	Gln	Thr	Glu	Met	Thr	Ile	Glu	Gly	Leu	305	310	315
His	Pro	Thr	Val	Glu	Tyr	Val	Val	Ser	Val	Tyr	Ala	Gln	Asn	Pro	Ser	325	330	335
Gly	Glu	Ser	Gln	Pro	Leu	Val	Gln	Thr	Ala	Val	Thr	Thr	Ile	Pro	Ala	340	345	350
Pro	Thr	Asp	Leu	Lys	Phe	Thr	Gln	Val	Thr	Pro	Thr	Ser	Leu	Ser	Ala	355	360	365
Gln	Trp	Thr	Pro	Pro	Asn	Val	Gln	Leu	Thr	Gly	Tyr	Arg	Val	Arg	Val	370	375	380
Thr	Pro	Lys	Glu	Lys	Thr	Gly	Pro	Met	Lys	Glu	Ile	Asn	Leu	Ala	Pro	385	390	395
Asp	Ser	Ser	Ser	Val	Val	Val	Ser	Gly	Leu	Met	Val	Ala	Thr	Lys	Tyr	405	410	415
Glu	Val	Ser	Val	Tyr	Ala	Leu	Lys	Asp	Thr	Leu	Thr	Ser	Arg	Pro	Ala	420	425	430
Gln	Gly	Val	Val	Thr	Thr	Leu	Glu	Asn	Val	Ser	Pro	Pro	Arg	Arg	Ala	435	440	445
Arg	Val	Thr	Asp	Ala	Thr	Glu	Thr	Thr	Ile	Thr	Ile	Ser	Trp	Arg	Thr	450	455	460
Lys	Thr	Glu	Thr	Ile	Thr	Gly	Phe	Gln	Val	Asp	Ala	Val	Pro	Ala	Asn	465	470	475
Gly	Gln	Thr	Pro	Ile	Gln	Arg	Thr	Ile	Lys	Pro	Asp	Val	Arg	Ser	Tyr	485	490	495
Thr	Ile	Thr	Gly	Leu	Gln	Pro	Gly	Thr	Asp	Tyr	Lys	Ile	Tyr	Leu	Tyr	500	505	510
Thr	Leu	Asn	Asp	Asn	Ala	Arg	Ser	Ser	Pro	Val	Val	Ile	Asp	Ala	Ser	515	520	525
Thr	Ala	Ile	Asp	Ala	Pro	Ser	Asn	Leu	Arg	Phe	Leu	Ala	Thr	Thr	Pro			

ITI-08-PCT_Sequence_Listing_ST25.txt

```

530          535          540
Asn Ser Leu Leu Val Ser Trp Gln Pro Pro Arg Ala Arg Ile Thr Gly
545          550          555          560
Tyr Ile Ile Lys Tyr Glu Lys Pro Gly Ser Pro Pro Arg Glu Val Val
565          570          575
Pro Arg Pro Arg Pro Gly Val Thr Glu Ala Thr Ile Thr Gly Leu Glu
580          585          590
Pro Gly Thr Glu Tyr Thr Ile Tyr Val Ile Ala Leu Lys Asn Asn Gln
595          600          605
Lys Ser Glu Pro Leu Ile Gly Arg Lys Lys Thr Gly Gln Glu Ala Leu
610          615          620
Ser Gln Thr Thr Ile Ser Trp Ala Pro Phe Gln Asp Thr Ser Glu Tyr
625          630          635          640
Ile Ile Ser Cys His Pro Val Gly Thr Asp Glu Glu Pro Leu Gln Phe
645          650          655
Arg Val Pro Gly Thr Ser Thr Ser Ala Thr Leu Thr Gly Leu Thr Arg
660          665          670
Gly Ala Thr Tyr Asn Ile Ile Val Glu Ala Leu Lys Asp Gln Gln Arg
675          680          685
His Lys Val Arg Glu Glu Val Ile Thr Val Gly Asn Ser Val Asn Glu
690          695          700
Gly Leu Asn Gln Pro Thr Asp Asp Ser Cys Phe Asp Pro Tyr Thr Val
705          710          715          720
Ser His Tyr Ala Val Gly Asp Glu Trp Glu Arg Met Ser Glu Ser Gly
725          730          735
Phe Lys Leu Leu Cys Gln Cys Leu Gly Phe Gly Ser Gly His Phe Arg
740          745          750
Cys Asp Ser Ser Arg Trp Cys His Asp Asn Gly Val Asn Tyr Lys Ile
755          760          765
Gly Glu Lys Trp Asp Arg Gln Gly Glu Asn Gly Gln Met Met Ser Cys
770          775          780
Thr Cys Leu Gly Asn Gly Lys Gly Glu Phe Lys Cys Asp Pro His Glu
785          790          795          800
Ala Thr Cys Tyr Asp Asp Gly Lys Thr Tyr His Val Gly Glu Gln Trp
805          810          815

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Gln Lys Glu Tyr Leu Gly Ala Ile Cys Ser Cys Thr Cys Phe Gly Gly
820 825 830

Gln Arg Gly Trp Arg Cys Asp Asn Cys Arg Arg Pro Gly Gly Glu Pro
835 840 845

Ser Pro Glu Gly Thr Thr Gly Gln Ser Tyr Asn Gln Tyr Ser Gln Arg
850 855 860

Tyr His Gln Arg Thr Asn Thr Asn Val Asn Cys Pro Ile Glu Cys Phe
865 870 875 880

Met Pro Leu Asp Val Gln Ala Asp Arg Glu Asp Ser Arg Glu
885 890

<210> 379

<211> 383

<212> PRT

<213> Artificial Sequence

<220>

<223> fibronectin__Homo_sapiens__B7Z3W5

<400> 379

Met Ala Ser Ala Phe Arg Leu Ser Leu Lys Pro Lys Val Ser Asp Asn
1 5 10 15

Met Thr His Leu Met Val Asp Phe Ser Gln Glu Arg Gln Met Leu Gln
20 25 30

Thr Leu Lys Phe Leu Pro Val Pro Lys Ala Pro Glu Ile Asp Pro Val
35 40 45

Glu Cys Leu Val Ala Asp Asn Ser Val Thr Val Ala Trp Arg Met Pro
50 55 60

Glu Glu Asp Asn Lys Ile Asp His Phe Ile Leu Glu His Arg Lys Thr
65 70 75 80

Asn Phe Asp Gly Leu Pro Arg Val Lys Asp Glu Arg Cys Trp Glu Ile
85 90 95

Ile Asp Asn Ile Lys Gly Thr Glu Tyr Thr Leu Ser Gly Leu Lys Phe
100 105 110

Asp Ser Lys Tyr Met Asn Phe Arg Val Arg Ala Cys Asn Lys Ala Val
115 120 125

Ala Gly Glu Tyr Ser Asp Pro Val Thr Leu Glu Thr Lys Ala Leu Asn
130 135 140

ITI-08-PCT_Sequence_Listing_ST25.txt

Phe Asn Leu Asp Asn Ser Ser Ser His Leu Asn Leu Lys Val Glu Asp
145 150 155 160

Thr Cys Val Glu Trp Asp Pro Thr Gly Gly Lys Gly Gln Glu Ser Lys
165 170 175

Ile Lys Gly Lys Glu Asn Lys Gly Ser Val His Val Thr Ser Leu Lys
180 185 190

Lys His Thr Ser Gly Thr Pro Ser Pro Lys Arg Thr Ser Val Gly Ser
195 200 205

Arg Pro Pro Ala Val Arg Gly Ser Arg Asp Arg Phe Thr Gly Glu Ser
210 215 220

Tyr Thr Val Leu Gly Asp Thr Ala Ile Glu Ser Gly Gln His Tyr Trp
225 230 235 240

Glu Val Lys Ala Gln Lys Asp Cys Lys Ser Tyr Ser Val Gly Val Ala
245 250 255

Tyr Lys Thr Leu Gly Lys Phe Asp Gln Leu Gly Lys Thr Asn Thr Ser
260 265 270

Trp Cys Ile His Val Asn Asn Trp Leu Gln Asn Thr Phe Ala Ala Lys
275 280 285

His Asn Asn Lys Val Lys Ala Leu Asp Val Thr Val Pro Glu Lys Ile
290 295 300

Gly Val Phe Cys Asp Phe Asp Gly Gly Gln Leu Ser Phe Tyr Asp Ala
305 310 315 320

Asn Ser Lys Gln Leu Leu Tyr Ser Phe Lys Thr Lys Phe Thr Gln Pro
325 330 335

Val Leu Pro Gly Phe Met Val Trp Cys Gly Gly Leu Ser Leu Ser Thr
340 345 350

Gly Met Gln Val Pro Ser Ala Val Arg Thr Leu Gln Lys Ser Glu Asn
355 360 365

Gly Met Thr Gly Ser Ala Ser Ser Leu Asn Asn Val Val Thr Gln
370 375 380

<210> 380

<211> 146

<212> PRT

<213> Artificial Sequence

<220>

ITI-08-PCT_Sequence_Listing_ST25.txt

<223> fibronectin__Homo_sapiens__B7Z939

<400> 380

Met Pro Pro Ser Lys Pro His Pro Pro Val Val Gly Lys Val Thr His
1 5 10 15

His Ser Ile Glu Leu Tyr Trp Asp Leu Glu Lys Lys Ala Lys Arg Gln
20 25 30

Gly Pro Gln Glu Gln Trp Phe Arg Phe Ser Ile Glu Glu Glu Asp Pro
35 40 45

Lys Met His Thr Tyr Gly Ile Ile Tyr Thr Gly Tyr Ala Thr Lys His
50 55 60

Val Val Glu Gly Leu Glu Pro Arg Thr Leu Tyr Arg Phe Arg Leu Lys
65 70 75 80

Val Thr Ser Pro Ser Gly Glu Cys Glu Tyr Ser Pro Leu Val Ser Val
85 90 95

Ser Thr Thr Ser Glu Tyr Ser Asp Arg Pro His Ser Pro Leu Ser Arg
100 105 110

Ser Met Glu Met Thr Ser Asn Leu Glu Lys Ile Phe Cys Leu Ser Phe
115 120 125

Gly Leu Thr Arg Ser Arg Asn Asp Thr Ile Phe Lys His Cys Asn Asn
130 135 140

Ile Cys
145

<210> 381

<211> 684

<212> PRT

<213> Artificial Sequence

<220>

<223> fibronectin__Homo_sapiens__G5E9X3

<400> 381

Met Ala Glu His Pro Pro Leu Leu Asp Thr Thr Gln Ile Leu Ser Ser
1 5 10 15

Asp Ile Ser Leu Leu Ser Ala Pro Ile Val Ser Ala Asp Gly Thr Gln
20 25 30

Gln Val Ile Leu Val Gln Val Asn Pro Gly Glu Ala Phe Thr Ile Arg
35 40 45

ITI-08-PCT_Sequence_Listing_ST25.txt

Arg	Glu	Asp	Gly	Gln	Phe	Gln	Cys	Ile	Thr	Gly	Pro	Ala	Gln	Val	Pro	50	55	60	
Met	Met	Ser	Pro	Asn	Gly	Ser	Val	Pro	Pro	Ile	Tyr	Val	Pro	Pro	Gly	65	70	75	80
Tyr	Ala	Pro	Gln	Val	Ile	Glu	Asp	Asn	Gly	Val	Arg	Arg	Val	Val	Val	85	90	95	
Val	Pro	Gln	Ala	Pro	Glu	Phe	His	Pro	Gly	Ser	His	Thr	Val	Leu	His	100	105	110	
Arg	Ser	Pro	His	Pro	Pro	Leu	Pro	Gly	Phe	Ile	Pro	Val	Pro	Thr	Met	115	120	125	
Met	Pro	Pro	Pro	Pro	Arg	His	Met	Tyr	Ser	Pro	Val	Thr	Gly	Ala	Gly	130	135	140	
Asp	Met	Thr	Thr	Gln	Tyr	Met	Pro	Gln	Tyr	Gln	Ser	Ser	Gln	Val	Tyr	145	150	155	160
Gly	Asp	Val	Asp	Ala	His	Ser	Thr	His	Gly	Arg	Ser	Asn	Phe	Arg	Asp	165	170	175	
Glu	Arg	Ser	Ser	Lys	Thr	Tyr	Glu	Arg	Leu	Gln	Lys	Lys	Leu	Lys	Asp	180	185	190	
Arg	Gln	Gly	Thr	Gln	Lys	Asp	Lys	Met	Ser	Ser	Pro	Pro	Ser	Ser	Pro	195	200	205	
Gln	Lys	Cys	Pro	Ser	Pro	Ile	Asn	Glu	His	Asn	Gly	Leu	Ile	Lys	Gly	210	215	220	
Gln	Ile	Ala	Gly	Gly	Ile	Asn	Thr	Gly	Ser	Ala	Lys	Ile	Lys	Ser	Gly	225	230	235	240
Lys	Gly	Lys	Gly	Gly	Thr	Gln	Val	Asp	Thr	Glu	Ile	Glu	Glu	Lys	Asp	245	250	255	
Glu	Glu	Thr	Lys	Ala	Phe	Glu	Ala	Leu	Leu	Ser	Asn	Ile	Val	Lys	Pro	260	265	270	
Val	Ala	Ser	Asp	Ile	Gln	Ala	Arg	Thr	Val	Val	Leu	Thr	Trp	Ser	Pro	275	280	285	
Pro	Ser	Ser	Leu	Ile	Asn	Gly	Glu	Thr	Asp	Glu	Ser	Ser	Val	Pro	Glu	290	295	300	
Leu	Tyr	Gly	Tyr	Glu	Val	Leu	Ile	Ser	Ser	Thr	Gly	Lys	Asp	Gly	Lys	305	310	315	320

ITI-08-PCT_Sequence_Listing_ST25.txt

Tyr Lys Ser Val Tyr Val Gly Glu Glu Thr Asn Ile Thr Leu Asn Asp
 325 330 335
 Leu Lys Pro Ala Met Asp Tyr His Ala Lys Val Gln Ala Glu Tyr Asn
 340 345 350
 Ser Ile Lys Gly Thr Pro Ser Glu Ala Glu Ile Phe Thr Thr Leu Ser
 355 360 365
 Cys Glu Pro Asp Ile Pro Asn Pro Pro Arg Ile Ala Asn Arg Thr Lys
 370 375 380
 Asn Ser Leu Thr Leu Gln Trp Lys Ala Pro Ser Asp Asn Gly Ser Lys
 385 390 395 400
 Ile Gln Asn Phe Val Leu Glu Trp Asp Glu Gly Lys Gly Asn Gly Glu
 405 410 415
 Phe Cys Gln Cys Tyr Met Gly Ser Gln Lys Gln Phe Lys Ile Thr Lys
 420 425 430
 Leu Ser Pro Ala Met Gly Cys Lys Phe Arg Leu Ser Ala Arg Asn Asp
 435 440 445
 Tyr Gly Thr Ser Gly Phe Ser Glu Glu Val Leu Tyr Tyr Thr Ser Gly
 450 455 460
 Cys Ala Pro Ser Met Pro Ala Ser Pro Val Leu Thr Lys Ala Gly Ile
 465 470 475 480
 Thr Trp Leu Ser Leu Gln Trp Ser Lys Pro Ser Gly Thr Pro Ser Asp
 485 490 495
 Glu Gly Ile Ser Tyr Ile Leu Glu Met Glu Glu Glu Thr Ser Gly Tyr
 500 505 510
 Gly Phe Lys Pro Lys Tyr Asp Gly Glu Asp Leu Ala Tyr Thr Val Lys
 515 520 525
 Asn Leu Arg Arg Ser Thr Lys Tyr Lys Phe Lys Val Ile Ala Tyr Asn
 530 535 540
 Ser Glu Gly Lys Ser Asn Pro Ser Glu Val Val Glu Phe Thr Thr Cys
 545 550 555 560
 Pro Asp Lys Pro Gly Ile Pro Val Lys Pro Ser Val Lys Gly Lys Ile
 565 570 575
 His Ser His Ser Phe Lys Ile Thr Trp Asp Pro Pro Lys Asp Asn Gly
 580 585 590
 Gly Ala Thr Ile Asn Lys Tyr Val Val Glu Met Ala Glu Gly Ser Asn

ITI-08-PCT_Sequence_Listing_ST25.txt

595

600

605

Gly Asn Lys Trp Glu Met Ile Tyr Ser Gly Ala Thr Arg Glu His Leu
610 615 620

Cys Asp Arg Leu Asn Pro Gly Cys Phe Tyr Arg Leu Arg Val Tyr Cys
625 630 635 640

Ile Ser Asp Gly Gly Gln Ser Ala Val Ser Glu Ser Leu Leu Val Gln
645 650 655

Thr Pro Ala Val Pro Pro Gly Pro Cys Leu Pro Pro Arg Leu Gln Gly
660 665 670

Arg Pro Lys Ala Lys Glu Ile Gln Thr Pro Ser Gly
675 680

<210> 382

<211> 163

<212> PRT

<213> Artificial Sequence

<220>

<223> fibronectin__Homo_sapiens__Q9H382

<400> 382

Met Ser Glu Ser Gly Phe Lys Leu Leu Cys Gln Cys Leu Gly Phe Gly
1 5 10 15

Ser Gly His Phe Arg Cys Asp Ser Ser Arg Trp Cys His Asp Asn Gly
20 25 30

Val Asn Tyr Lys Ile Gly Glu Lys Trp Asp Arg Gln Gly Glu Asn Gly
35 40 45

Gln Met Met Ser Cys Thr Cys Leu Gly Asn Gly Lys Gly Glu Phe Lys
50 55 60

Cys Asp Pro His Glu Ala Thr Cys Tyr Asp Asp Gly Lys Thr Tyr His
65 70 75 80

Val Gly Glu Gln Trp Gln Lys Glu Tyr Leu Gly Ala Ile Cys Ser Cys
85 90 95

Thr Cys Phe Gly Gly Gln Arg Gly Trp Arg Cys Asp Asn Cys Arg Arg
100 105 110

Pro Gly Gly Glu Pro Ser Pro Glu Gly Thr Thr Gly Gln Ser Tyr Asn
115 120 125

Gln Tyr Ser Gln Arg Tyr His Gln Arg Thr Asn Thr Asn Val Asn Cys

ITI-08-PCT_Sequence_Listing_ST25.txt

130

135

140

Pro Ile Glu Cys Phe Met Pro Leu Asp Val Gln Ala Asp Arg Glu Asp
145 150 155 160

Ser Arg Glu

<210> 383

<211> 380

<212> PRT

<213> Artificial Sequence

<220>

<223> FOS__Homo_sapiens__P01100

<400> 383

Met Met Phe Ser Gly Phe Asn Ala Asp Tyr Glu Ala Ser Ser Ser Arg
1 5 10 15

Cys Ser Ser Ala Ser Pro Ala Gly Asp Ser Leu Ser Tyr Tyr His Ser
20 25 30

Pro Ala Asp Ser Phe Ser Ser Met Gly Ser Pro Val Asn Ala Gln Asp
35 40 45

Phe Cys Thr Asp Leu Ala Val Ser Ser Ala Asn Phe Ile Pro Thr Val
50 55 60

Thr Ala Ile Ser Thr Ser Pro Asp Leu Gln Trp Leu Val Gln Pro Ala
65 70 75 80

Leu Val Ser Ser Val Ala Pro Ser Gln Thr Arg Ala Pro His Pro Phe
85 90 95

Gly Val Pro Ala Pro Ser Ala Gly Ala Tyr Ser Arg Ala Gly Val Val
100 105 110

Lys Thr Met Thr Gly Gly Arg Ala Gln Ser Ile Gly Arg Arg Gly Lys
115 120 125

Val Glu Gln Leu Ser Pro Glu Glu Glu Glu Lys Arg Arg Ile Arg Arg
130 135 140

Glu Arg Asn Lys Met Ala Ala Ala Lys Cys Arg Asn Arg Arg Arg Glu
145 150 155 160

Leu Thr Asp Thr Leu Gln Ala Glu Thr Asp Gln Leu Glu Asp Glu Lys
165 170 175

Ser Ala Leu Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys
180 185 190

ITI-08-PCT_Sequence_Listing_ST25.txt

Leu Glu Phe Ile Leu Ala Ala His Arg Pro Ala Cys Lys Ile Pro Asp
195 200 205

Asp Leu Gly Phe Pro Glu Glu Met Ser Val Ala Ser Leu Asp Leu Thr
210 215 220

Gly Gly Leu Pro Glu Val Ala Thr Pro Glu Ser Glu Glu Ala Phe Thr
225 230 235 240

Leu Pro Leu Leu Asn Asp Pro Glu Pro Lys Pro Ser Val Glu Pro Val
245 250 255

Lys Ser Ile Ser Ser Met Glu Leu Lys Thr Glu Pro Phe Asp Asp Phe
260 265 270

Leu Phe Pro Ala Ser Ser Arg Pro Ser Gly Ser Glu Thr Ala Arg Ser
275 280 285

Val Pro Asp Met Asp Leu Ser Gly Ser Phe Tyr Ala Ala Asp Trp Glu
290 295 300

Pro Leu His Ser Gly Ser Leu Gly Met Gly Pro Met Ala Thr Glu Leu
305 310 315 320

Glu Pro Leu Cys Thr Pro Val Val Thr Cys Thr Pro Ser Cys Thr Ala
325 330 335

Tyr Thr Ser Ser Phe Val Phe Thr Tyr Pro Glu Ala Asp Ser Phe Pro
340 345 350

Ser Cys Ala Ala Ala His Arg Lys Gly Ser Ser Ser Asn Glu Pro Ser
355 360 365

Ser Asp Ser Leu Ser Ser Pro Thr Leu Leu Ala Leu
370 375 380

<210> 384

<211> 431

<212> PRT

<213> Artificial Sequence

<220>

<223> FOXP3__Homo_sapiens__Q9BZS1

<400> 384

Met Pro Asn Pro Arg Pro Gly Lys Pro Ser Ala Pro Ser Leu Ala Leu
1 5 10 15

Gly Pro Ser Pro Gly Ala Ser Pro Ser Trp Arg Ala Ala Pro Lys Ala
20 25 30

ITI-08-PCT_Sequence_Listing_ST25.txt

Ser Asp Leu Leu Gly Ala Arg Gly Pro Gly Gly Thr Phe Gln Gly Arg
35 40 45

Asp Leu Arg Gly Gly Ala His Ala Ser Ser Ser Ser Leu Asn Pro Met
50 55 60

Pro Pro Ser Gln Leu Gln Leu Pro Thr Leu Pro Leu Val Met Val Ala
65 70 75 80

Pro Ser Gly Ala Arg Leu Gly Pro Leu Pro His Leu Gln Ala Leu Leu
85 90 95

Gln Asp Arg Pro His Phe Met His Gln Leu Ser Thr Val Asp Ala His
100 105 110

Ala Arg Thr Pro Val Leu Gln Val His Pro Leu Glu Ser Pro Ala Met
115 120 125

Ile Ser Leu Thr Pro Pro Thr Thr Ala Thr Gly Val Phe Ser Leu Lys
130 135 140

Ala Arg Pro Gly Leu Pro Pro Gly Ile Asn Val Ala Ser Leu Glu Trp
145 150 155 160

Val Ser Arg Glu Pro Ala Leu Leu Cys Thr Phe Pro Asn Pro Ser Ala
165 170 175

Pro Arg Lys Asp Ser Thr Leu Ser Ala Val Pro Gln Ser Ser Tyr Pro
180 185 190

Leu Leu Ala Asn Gly Val Cys Lys Trp Pro Gly Cys Glu Lys Val Phe
195 200 205

Glu Glu Pro Glu Asp Phe Leu Lys His Cys Gln Ala Asp His Leu Leu
210 215 220

Asp Glu Lys Gly Arg Ala Gln Cys Leu Leu Gln Arg Glu Met Val Gln
225 230 235 240

Ser Leu Glu Gln Gln Leu Val Leu Glu Lys Glu Lys Leu Ser Ala Met
245 250 255

Gln Ala His Leu Ala Gly Lys Met Ala Leu Thr Lys Ala Ser Ser Val
260 265 270

Ala Ser Ser Asp Lys Gly Ser Cys Cys Ile Val Ala Ala Gly Ser Gln
275 280 285

Gly Pro Val Val Pro Ala Trp Ser Gly Pro Arg Glu Ala Pro Asp Ser
290 295 300

ITI-08-PCT_Sequence_Listing_ST25.txt

Leu Phe Ala Val Arg Arg His Leu Trp Gly Ser His Gly Asn Ser Thr
305 310 315 320

Phe Pro Glu Phe Leu His Asn Met Asp Tyr Phe Lys Phe His Asn Met
325 330 335

Arg Pro Pro Phe Thr Tyr Ala Thr Leu Ile Arg Trp Ala Ile Leu Glu
340 345 350

Ala Pro Glu Lys Gln Arg Thr Leu Asn Glu Ile Tyr His Trp Phe Thr
355 360 365

Arg Met Phe Ala Phe Phe Arg Asn His Pro Ala Thr Trp Lys Asn Ala
370 375 380

Ile Arg His Asn Leu Ser Leu His Lys Cys Phe Val Arg Val Glu Ser
385 390 395 400

Glu Lys Gly Ala Val Trp Thr Val Asp Glu Leu Glu Phe Arg Lys Lys
405 410 415

Arg Ser Gln Arg Pro Ser Arg Cys Ser Asn Pro Thr Pro Gly Pro
420 425 430

<210> 385

<211> 365

<212> PRT

<213> Artificial Sequence

<220>

<223> FUT1__Homo_sapiens__P19526

<400> 385

Met Trp Leu Arg Ser His Arg Gln Leu Cys Leu Ala Phe Leu Leu Val
1 5 10 15

Cys Val Leu Ser Val Ile Phe Phe Leu His Ile His Gln Asp Ser Phe
20 25 30

Pro His Gly Leu Gly Leu Ser Ile Leu Cys Pro Asp Arg Arg Leu Val
35 40 45

Thr Pro Pro Val Ala Ile Phe Cys Leu Pro Gly Thr Ala Met Gly Pro
50 55 60

Asn Ala Ser Ser Ser Cys Pro Gln His Pro Ala Ser Leu Ser Gly Thr
65 70 75 80

Trp Thr Val Tyr Pro Asn Gly Arg Phe Gly Asn Gln Met Gly Gln Tyr
85 90 95

ITI-08-PCT_Sequence_Listing_ST25.txt

Ala Thr Leu Leu Ala Leu Ala Gln Leu Asn Gly Arg Arg Ala Phe Ile
100 105 110

Leu Pro Ala Met His Ala Ala Leu Ala Pro Val Phe Arg Ile Thr Leu
115 120 125

Pro Val Leu Ala Pro Glu Val Asp Ser Arg Thr Pro Trp Arg Glu Leu
130 135 140

Gln Leu His Asp Trp Met Ser Glu Glu Tyr Ala Asp Leu Arg Asp Pro
145 150 155 160

Phe Leu Lys Leu Ser Gly Phe Pro Cys Ser Trp Thr Phe Phe His His
165 170 175

Leu Arg Glu Gln Ile Arg Arg Glu Phe Thr Leu His Asp His Leu Arg
180 185 190

Glu Glu Ala Gln Ser Val Leu Gly Gln Leu Arg Leu Gly Arg Thr Gly
195 200 205

Asp Arg Pro Arg Thr Phe Val Gly Val His Val Arg Arg Gly Asp Tyr
210 215 220

Leu Gln Val Met Pro Gln Arg Trp Lys Gly Val Val Gly Asp Ser Ala
225 230 235 240

Tyr Leu Arg Gln Ala Met Asp Trp Phe Arg Ala Arg His Glu Ala Pro
245 250 255

Val Phe Val Val Thr Ser Asn Gly Met Glu Trp Cys Lys Glu Asn Ile
260 265 270

Asp Thr Ser Gln Gly Asp Val Thr Phe Ala Gly Asp Gly Gln Glu Ala
275 280 285

Thr Pro Trp Lys Asp Phe Ala Leu Leu Thr Gln Cys Asn His Thr Ile
290 295 300

Met Thr Ile Gly Thr Phe Gly Phe Trp Ala Ala Tyr Leu Ala Gly Gly
305 310 315 320

Asp Thr Val Tyr Leu Ala Asn Phe Thr Leu Pro Asp Ser Glu Phe Leu
325 330 335

Lys Ile Phe Lys Pro Glu Ala Ala Phe Leu Pro Glu Trp Val Gly Ile
340 345 350

Asn Ala Asp Leu Ser Pro Leu Trp Thr Leu Ala Lys Pro
355 360 365

<210> 386

ITI-08-PCT_Sequence_Listing_ST25.txt

<211> 459

<212> PRT

<213> Artificial Sequence

<220>

<223> G250__Homo_sapiens__Q16790

<400> 386

Met Ala Pro Leu Cys Pro Ser Pro Trp Leu Pro Leu Leu Ile Pro Ala
1 5 10 15

Pro Ala Pro Gly Leu Thr Val Gln Leu Leu Leu Ser Leu Leu Leu Leu
20 25 30

Val Pro Val His Pro Gln Arg Leu Pro Arg Met Gln Glu Asp Ser Pro
35 40 45

Leu Gly Gly Gly Ser Ser Gly Glu Asp Asp Pro Leu Gly Glu Glu Asp
50 55 60

Leu Pro Ser Glu Glu Asp Ser Pro Arg Glu Glu Asp Pro Pro Gly Glu
65 70 75 80

Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro
85 90 95

Glu Val Lys Pro Lys Ser Glu Glu Glu Gly Ser Leu Lys Leu Glu Asp
100 105 110

Leu Pro Thr Val Glu Ala Pro Gly Asp Pro Gln Glu Pro Gln Asn Asn
115 120 125

Ala His Arg Asp Lys Glu Gly Asp Asp Gln Ser His Trp Arg Tyr Gly
130 135 140

Gly Asp Pro Pro Trp Pro Arg Val Ser Pro Ala Cys Ala Gly Arg Phe
145 150 155 160

Gln Ser Pro Val Asp Ile Arg Pro Gln Leu Ala Ala Phe Cys Pro Ala
165 170 175

Leu Arg Pro Leu Glu Leu Leu Gly Phe Gln Leu Pro Pro Leu Pro Glu
180 185 190

Leu Arg Leu Arg Asn Asn Gly His Ser Val Gln Leu Thr Leu Pro Pro
195 200 205

Gly Leu Glu Met Ala Leu Gly Pro Gly Arg Glu Tyr Arg Ala Leu Gln
210 215 220

Leu His Leu His Trp Gly Ala Ala Gly Arg Pro Gly Ser Glu His Thr

ITI-08-PCT_Sequence_Listing_ST25.txt

```

225                230                235                240
Val Glu Gly His Arg Phe Pro Ala Glu Ile His Val Val His Leu Ser
                245                250                255

Thr Ala Phe Ala Arg Val Asp Glu Ala Leu Gly Arg Pro Gly Gly Leu
                260                265                270

Ala Val Leu Ala Ala Phe Leu Glu Glu Gly Pro Glu Glu Asn Ser Ala
                275                280                285

Tyr Glu Gln Leu Leu Ser Arg Leu Glu Glu Ile Ala Glu Glu Gly Ser
    290                295                300

Glu Thr Gln Val Pro Gly Leu Asp Ile Ser Ala Leu Leu Pro Ser Asp
    305                310                315                320

Phe Ser Arg Tyr Phe Gln Tyr Glu Gly Ser Leu Thr Thr Pro Pro Cys
                325                330                335

Ala Gln Gly Val Ile Trp Thr Val Phe Asn Gln Thr Val Met Leu Ser
                340                345                350

Ala Lys Gln Leu His Thr Leu Ser Asp Thr Leu Trp Gly Pro Gly Asp
                355                360                365

Ser Arg Leu Gln Leu Asn Phe Arg Ala Thr Gln Pro Leu Asn Gly Arg
    370                375                380

Val Ile Glu Ala Ser Phe Pro Ala Gly Val Asp Ser Ser Pro Arg Ala
    385                390                395                400

Ala Glu Pro Val Gln Leu Asn Ser Cys Leu Ala Ala Gly Asp Ile Leu
                405                410                415

Ala Leu Val Phe Gly Leu Leu Phe Ala Val Thr Ser Val Ala Phe Leu
                420                425                430

Val Gln Met Arg Arg Gln His Arg Arg Gly Thr Lys Gly Gly Val Ser
                435                440                445

Tyr Arg Pro Ala Glu Val Ala Glu Thr Gly Ala
    450                455

```

<210> 387

<211> 138

<212> PRT

<213> Artificial Sequence

<220>

<223> GAGE-1__Homo_sapiens__AAA82744

ITI-08-PCT_Sequence_Listing_ST25.txt

<400> 387

Met Ser Trp Arg Gly Arg Ser Thr Tyr Arg Pro Arg Pro Arg Arg Tyr
1 5 10 15

Val Glu Pro Pro Glu Met Ile Gly Pro Met Arg Pro Glu Gln Phe Ser
20 25 30

Asp Glu Val Glu Pro Ala Thr Pro Glu Glu Gly Glu Pro Ala Thr Gln
35 40 45

Arg Gln Asp Pro Ala Ala Ala Gln Glu Gly Glu Asp Glu Gly Ala Ser
50 55 60

Ala Gly Gln Gly Pro Lys Pro Glu Ala Asp Ser Gln Glu Gln Gly His
65 70 75 80

Pro Gln Thr Gly Cys Glu Cys Glu Asp Gly Pro Asp Gly Gln Glu Met
85 90 95

Asp Pro Pro Asn Pro Glu Glu Val Lys Thr Pro Glu Glu Glu Met Arg
100 105 110

Ser His Tyr Val Ala Gln Thr Gly Ile Leu Trp Leu Leu Met Asn Asn
115 120 125

Cys Phe Leu Asn Leu Ser Pro Arg Lys Pro
130 135

<210> 388

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<223> GAGE-2__Homo_sapiens__Q6NT46

<400> 388

Met Ser Trp Arg Gly Arg Ser Thr Tyr Arg Pro Arg Pro Arg Arg Tyr
1 5 10 15

Val Glu Pro Pro Glu Met Ile Gly Pro Met Arg Pro Glu Gln Phe Ser
20 25 30

Asp Glu Val Glu Pro Ala Thr Pro Glu Glu Gly Glu Pro Ala Thr Gln
35 40 45

Arg Gln Asp Pro Ala Ala Ala Gln Glu Gly Gln Asp Glu Gly Ala Ser
50 55 60

Ala Gly Gln Gly Pro Lys Pro Glu Ala His Ser Gln Glu Gln Gly His

65 70 75 80

Pro Gln Thr Gly Cys Glu Cys Glu Asp Gly Pro Asp Gly Gln Glu Met
 85 90 95

Asp Pro Pro Asn Pro Glu Glu Val Lys Thr Pro Glu Glu Gly Glu Lys
 100 105 110

Gln Ser Gln Cys
 115

<210>	389
<211>	118
<212>	PRT
<213>	Artificial Sequence

<220>
<223> GAGE-3 Homo sapiens Q13067

<400> 389

Met Asn Leu Ser Arg Gly Lys Ser Thr Tyr Tyr Trp Pro Arg Pro Arg
1 5 10 15

Arg Tyr Val Gln Pro Pro Glu Val Ile Gly Pro Met Arg Pro Glu Gln
20 25 30

Phe Ser Asp Glu Val Glu Pro Ala Thr Pro Glu Glu Gly Glu Pro Ala
35 40 45

Thr Gln Arg Gln Asp Pro Ala Ala Ala Gln Glu Gly Glu Asp Glu Gly
50 55 60

Ala Ser Ala Gly Gln Gly Pro Lys Pro Glu Ala Asp Ser Gln Glu Gln
65 70 75 80

Gly His Pro Gln Thr Gly Cys Glu Cys Glu Asp Gly Pro Asp Gly Gln
85 90 95

Glu Met Asp Pro Pro Asn Pro Glu Glu Val Lys Thr Pro Glu Glu Gly
100 105 110

Glu Lys Gln Ser Gln Cys
115

<210>	390
<211>	117
<212>	PRT
<213>	Artificial Sequence

<220>
<223> GAGE-4 Homo sapiens Q13068

ITI-08-PCT_Sequence_Listing_ST25.txt

<400> 390

```

Met Ser Trp Arg Gly Arg Ser Thr Tyr Tyr Trp Pro Arg Pro Arg Arg
1          5          10          15

Tyr Val Gln Pro Pro Glu Met Ile Gly Pro Met Arg Pro Glu Gln Phe
          20          25          30

Ser Asp Glu Val Glu Pro Ala Thr Pro Glu Glu Gly Glu Pro Ala Thr
          35          40          45

Gln Arg Gln Asp Pro Ala Ala Ala Gln Glu Gly Glu Asp Glu Gly Ala
50          55          60

Ser Ala Gly Gln Gly Pro Lys Pro Glu Ala Asp Ser Gln Glu Gln Gly
65          70          75          80

His Pro Gln Thr Gly Cys Glu Cys Glu Asp Gly Pro Asp Gly Gln Glu
          85          90          95

Met Asp Pro Pro Asn Pro Glu Glu Val Lys Thr Pro Glu Glu Gly Glu
          100          105          110

Gly Gln Ser Gln Cys
          115

```

<210> 391

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> GAGE-5__Homo_sapiens__Q13069

<400> 391

```

Met Ser Trp Arg Gly Arg Ser Thr Tyr Tyr Trp Pro Arg Pro Arg Arg
1          5          10          15

Tyr Val Gln Pro Pro Glu Val Ile Gly Pro Met Arg Pro Glu Gln Phe
          20          25          30

Ser Asp Glu Val Glu Pro Ala Thr Pro Glu Glu Gly Glu Pro Ala Thr
          35          40          45

Gln Arg Gln Asp Pro Ala Ala Ala Gln Glu Gly Glu Asp Glu Gly Ala
50          55          60

Ser Ala Gly Gln Gly Pro Lys Pro Glu Ala Asp Ser Gln Glu Gln Gly
65          70          75          80

```

ITI-08-PCT_Sequence_Listing_ST25.txt

His Pro Gln Thr Gly Cys Glu Cys Glu Asp Gly Pro Asp Gly Gln Glu
85 90 95

Met Asp Pro Pro Asn Pro Glu Glu Val Lys Thr Pro Glu Glu Gly Glu
100 105 110

Lys Gln Ser Gln Cys
115

<210> 392
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> GAGE-6__Homo_sapiens__Q13070

<400> 392

Met Ser Trp Arg Gly Arg Ser Thr Tyr Tyr Trp Pro Arg Pro Arg Arg
1 5 10 15

Tyr Val Gln Pro Pro Glu Val Ile Gly Pro Met Arg Pro Glu Gln Phe
20 25 30

Ser Asp Glu Val Glu Pro Ala Thr Pro Glu Glu Gly Glu Pro Ala Thr
35 40 45

Gln Arg Gln Asp Pro Ala Ala Ala Gln Glu Gly Glu Asp Glu Gly Ala
50 55 60

Ser Ala Gly Gln Gly Pro Lys Pro Glu Ala Asp Ser Gln Glu Gln Gly
65 70 75 80

His Pro Gln Thr Gly Cys Glu Cys Glu Asp Gly Pro Asp Gly Gln Glu
85 90 95

Val Asp Pro Pro Asn Pro Glu Glu Val Lys Thr Pro Glu Glu Gly Glu
100 105 110

Lys Gln Ser Gln Cys
115

<210> 393
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> GAGE7b__Homo_sapiens__076087

<400> 393

ITI-08-PCT_Sequence_Listing_ST25.txt

```

Met Ser Trp Arg Gly Arg Ser Thr Tyr Tyr Trp Pro Arg Pro Arg Arg
1           5           10           15

Tyr Val Gln Pro Pro Glu Met Ile Gly Pro Met Arg Pro Glu Gln Phe
          20           25           30

Ser Asp Glu Val Glu Pro Ala Thr Pro Glu Glu Gly Glu Pro Ala Thr
          35           40           45

Gln Arg Gln Asp Pro Ala Ala Ala Gln Glu Gly Glu Asp Glu Gly Ala
          50           55           60

Ser Ala Gly Gln Gly Pro Lys Pro Glu Ala His Ser Gln Glu Gln Gly
65           70           75           80

His Pro Gln Thr Gly Cys Glu Cys Glu Asp Gly Pro Asp Gly Gln Glu
          85           90           95

Met Asp Pro Pro Asn Pro Glu Glu Val Lys Thr Pro Glu Glu Gly Glu
          100          105          110

Lys Gln Ser Gln Cys
          115

```

```

<210> 394
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> GAGE-8_(GAGE-2D)__Homo_sapiens__Q9UEU5

<400> 394

```

```

Met Ser Trp Arg Gly Arg Ser Thr Tyr Arg Pro Arg Pro Arg Arg Tyr
1           5           10           15

Val Glu Pro Pro Glu Met Ile Gly Pro Met Arg Pro Glu Gln Phe Ser
          20           25           30

Asp Glu Val Glu Pro Ala Thr Pro Glu Glu Gly Glu Pro Ala Thr Gln
          35           40           45

Arg Gln Asp Pro Ala Ala Ala Gln Glu Gly Glu Asp Glu Gly Ala Ser
          50           55           60

Ala Gly Gln Gly Pro Lys Pro Glu Ala Asp Ser Gln Glu Gln Gly His
65           70           75           80

Pro Gln Thr Gly Cys Glu Cys Glu Asp Gly Pro Asp Gly Gln Glu Met
          85           90           95

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Asp Pro Pro Asn Pro Glu Glu Val Lys Thr Pro Glu Glu Gly Glu Lys
100 105 110

Gln Ser Gln Cys
115

<210> 395

<211> 447

<212> PRT

<213> Artificial Sequence

<220>

<223> GASR__Homo_sapiens__P32239

<400> 395

Met Glu Leu Leu Lys Leu Asn Arg Ser Val Gln Gly Thr Gly Pro Gly
1 5 10 15

Pro Gly Ala Ser Leu Cys Arg Pro Gly Ala Pro Leu Leu Asn Ser Ser
20 25 30

Ser Val Gly Asn Leu Ser Cys Glu Pro Pro Arg Ile Arg Gly Ala Gly
35 40 45

Thr Arg Glu Leu Glu Leu Ala Ile Arg Ile Thr Leu Tyr Ala Val Ile
50 55 60

Phe Leu Met Ser Val Gly Gly Asn Met Leu Ile Ile Val Val Leu Gly
65 70 75 80

Leu Ser Arg Arg Leu Arg Thr Val Thr Asn Ala Phe Leu Leu Ser Leu
85 90 95

Ala Val Ser Asp Leu Leu Leu Ala Val Ala Cys Met Pro Phe Thr Leu
100 105 110

Leu Pro Asn Leu Met Gly Thr Phe Ile Phe Gly Thr Val Ile Cys Lys
115 120 125

Ala Val Ser Tyr Leu Met Gly Val Ser Val Ser Val Ser Thr Leu Ser
130 135 140

Leu Val Ala Ile Ala Leu Glu Arg Tyr Ser Ala Ile Cys Arg Pro Leu
145 150 155 160

Gln Ala Arg Val Trp Gln Thr Arg Ser His Ala Ala Arg Val Ile Val
165 170 175

Ala Thr Trp Leu Leu Ser Gly Leu Leu Met Val Pro Tyr Pro Val Tyr
180 185 190

ITI-08-PCT_Sequence_Listing_ST25.txt

```

Thr Val Val Gln Pro Val Gly Pro Arg Val Leu Gln Cys Val His Arg
    195                200                205

Trp Pro Ser Ala Arg Val Arg Gln Thr Trp Ser Val Leu Leu Leu Leu
    210                215                220

Leu Leu Phe Phe Ile Pro Gly Val Val Met Ala Val Ala Tyr Gly Leu
    225                230                235                240

Ile Ser Arg Glu Leu Tyr Leu Gly Leu Arg Phe Asp Gly Asp Ser Asp
    245                250                255

Ser Asp Ser Gln Ser Arg Val Arg Asn Gln Gly Gly Leu Pro Gly Ala
    260                265                270

Val His Gln Asn Gly Arg Cys Arg Pro Glu Thr Gly Ala Val Gly Glu
    275                280                285

Asp Ser Asp Gly Cys Tyr Val Gln Leu Pro Arg Ser Arg Pro Ala Leu
    290                295                300

Glu Leu Thr Ala Leu Thr Ala Pro Gly Pro Gly Ser Gly Ser Arg Pro
    305                310                315                320

Thr Gln Ala Lys Leu Leu Ala Lys Lys Arg Val Val Arg Met Leu Leu
    325                330                335

Val Ile Val Val Leu Phe Phe Leu Cys Trp Leu Pro Val Tyr Ser Ala
    340                345                350

Asn Thr Trp Arg Ala Phe Asp Gly Pro Gly Ala His Arg Ala Leu Ser
    355                360                365

Gly Ala Pro Ile Ser Phe Ile His Leu Leu Ser Tyr Ala Ser Ala Cys
    370                375                380

Val Asn Pro Leu Val Tyr Cys Phe Met His Arg Arg Phe Arg Gln Ala
    385                390                395                400

Cys Leu Glu Thr Cys Ala Arg Cys Cys Pro Arg Pro Pro Arg Ala Arg
    405                410                415

Pro Arg Ala Leu Pro Asp Glu Asp Pro Pro Thr Pro Ser Ile Ala Ser
    420                425                430

Leu Ser Arg Leu Ser Tyr Thr Thr Ile Ser Thr Leu Gly Pro Gly
    435                440                445

```

<210> 396

<211> 741

<212> PRT

ITI-08-PCT_Sequence_Listing_ST25.txt

<213> Artificial Sequence

<220>

<223> GnT-V__Homo_sapiens__Q09328

<400> 396

Met Ala Leu Phe Thr Pro Trp Lys Leu Ser Ser Gln Lys Leu Gly Phe
1 5 10 15

Phe Leu Val Thr Phe Gly Phe Ile Trp Gly Met Met Leu Leu His Phe
20 25 30

Thr Ile Gln Gln Arg Thr Gln Pro Glu Ser Ser Ser Met Leu Arg Glu
35 40 45

Gln Ile Leu Asp Leu Ser Lys Arg Tyr Ile Lys Ala Leu Ala Glu Glu
50 55 60

Asn Arg Asn Val Val Asp Gly Pro Tyr Ala Gly Val Met Thr Ala Tyr
65 70 75 80

Asp Leu Lys Lys Thr Leu Ala Val Leu Leu Asp Asn Ile Leu Gln Arg
85 90 95

Ile Gly Lys Leu Glu Ser Lys Val Asp Asn Leu Val Val Asn Gly Thr
100 105 110

Gly Thr Asn Ser Thr Asn Ser Thr Thr Ala Val Pro Ser Leu Val Ala
115 120 125

Leu Glu Lys Ile Asn Val Ala Asp Ile Ile Asn Gly Ala Gln Glu Lys
130 135 140

Cys Val Leu Pro Pro Met Asp Gly Tyr Pro His Cys Glu Gly Lys Ile
145 150 155 160

Lys Trp Met Lys Asp Met Trp Arg Ser Asp Pro Cys Tyr Ala Asp Tyr
165 170 175

Gly Val Asp Gly Ser Thr Cys Ser Phe Phe Ile Tyr Leu Ser Glu Val
180 185 190

Glu Asn Trp Cys Pro His Leu Pro Trp Arg Ala Lys Asn Pro Tyr Glu
195 200 205

Glu Ala Asp His Asn Ser Leu Ala Glu Ile Arg Thr Asp Phe Asn Ile
210 215 220

Leu Tyr Ser Met Met Lys Lys His Glu Glu Phe Arg Trp Met Arg Leu
225 230 235 240

ITI-08-PCT_Sequence_Listing_ST25.txt

Arg Ile Arg Arg Met Ala Asp Ala Trp Ile Gln Ala Ile Lys Ser Leu
245 250 255

Ala Glu Lys Gln Asn Leu Glu Lys Arg Lys Arg Lys Lys Val Leu Val
260 265 270

His Leu Gly Leu Leu Thr Lys Glu Ser Gly Phe Lys Ile Ala Glu Thr
275 280 285

Ala Phe Ser Gly Gly Pro Leu Gly Glu Leu Val Gln Trp Ser Asp Leu
290 295 300

Ile Thr Ser Leu Tyr Leu Leu Gly His Asp Ile Arg Ile Ser Ala Ser
305 310 315 320

Leu Ala Glu Leu Lys Glu Ile Met Lys Lys Val Val Gly Asn Arg Ser
325 330 335

Gly Cys Pro Thr Val Gly Asp Arg Ile Val Glu Leu Ile Tyr Ile Asp
340 345 350

Ile Val Gly Leu Ala Gln Phe Lys Lys Thr Leu Gly Pro Ser Trp Val
355 360 365

His Tyr Gln Cys Met Leu Arg Val Leu Asp Ser Phe Gly Thr Glu Pro
370 375 380

Glu Phe Asn His Ala Asn Tyr Ala Gln Ser Lys Gly His Lys Thr Pro
385 390 395 400

Trp Gly Lys Trp Asn Leu Asn Pro Gln Gln Phe Tyr Thr Met Phe Pro
405 410 415

His Thr Pro Asp Asn Ser Phe Leu Gly Phe Val Val Glu Gln His Leu
420 425 430

Asn Ser Ser Asp Ile His His Ile Asn Glu Ile Lys Arg Gln Asn Gln
435 440 445

Ser Leu Val Tyr Gly Lys Val Asp Ser Phe Trp Lys Asn Lys Lys Ile
450 455 460

Tyr Leu Asp Ile Ile His Thr Tyr Met Glu Val His Ala Thr Val Tyr
465 470 475 480

Gly Ser Ser Thr Lys Asn Ile Pro Ser Tyr Val Lys Asn His Gly Ile
485 490 495

Leu Ser Gly Arg Asp Leu Gln Phe Leu Leu Arg Glu Thr Lys Leu Phe
500 505 510

Val Gly Leu Gly Phe Pro Tyr Glu Gly Pro Ala Pro Leu Glu Ala Ile

ITI-08-PCT_Sequence_Listing_ST25.txt

```

515                               520                               525
Ala Asn Gly Cys Ala Phe Leu Asn Pro Lys Phe Asn Pro Pro Lys Ser
530                               535                               540
Ser Lys Asn Thr Asp Phe Phe Ile Gly Lys Pro Thr Leu Arg Glu Leu
545                               550                               555                               560
Thr Ser Gln His Pro Tyr Ala Glu Val Phe Ile Gly Arg Pro His Val
565                               570                               575
Trp Thr Val Asp Leu Asn Asn Gln Glu Glu Val Glu Asp Ala Val Lys
580                               585                               590
Ala Ile Leu Asn Gln Lys Ile Glu Pro Tyr Met Pro Tyr Glu Phe Thr
595                               600                               605
Cys Glu Gly Met Leu Gln Arg Ile Asn Ala Phe Ile Glu Lys Gln Asp
610                               615                               620
Phe Cys His Gly Gln Val Met Trp Pro Pro Leu Ser Ala Leu Gln Val
625                               630                               635                               640
Lys Leu Ala Glu Pro Gly Gln Ser Cys Lys Gln Val Cys Gln Glu Ser
645                               650                               655
Gln Leu Ile Cys Glu Pro Ser Phe Phe Gln His Leu Asn Lys Asp Lys
660                               665                               670
Asp Met Leu Lys Tyr Lys Val Thr Cys Gln Ser Ser Glu Leu Ala Lys
675                               680                               685
Asp Ile Leu Val Pro Ser Phe Asp Pro Lys Asn Lys His Cys Val Phe
690                               695                               700
Gln Gly Asp Leu Leu Leu Phe Ser Cys Ala Gly Ala His Pro Arg His
705                               710                               715                               720
Gln Arg Val Cys Pro Cys Arg Asp Phe Ile Lys Gly Gln Val Ala Leu
725                               730                               735
Cys Lys Asp Cys Leu
740

```

<210> 397

<211> 580

<212> PRT

<213> Artificial Sequence

<220>

<223> GPC3__Homo_sapiens__I6QTG3

ITI-08-PCT_Sequence_Listing_ST25.txt

<400> 397

Met	Ala	Gly	Thr	Val	Arg	Thr	Ala	Cys	Leu	Val	Val	Ala	Met	Leu	Leu	1	5	10	15
Ser	Leu	Asp	Phe	Pro	Gly	Gln	Ala	Gln	Pro	Pro	Pro	Pro	Pro	Pro	Asp	20	25	30	
Ala	Thr	Cys	His	Gln	Val	Arg	Ser	Phe	Phe	Gln	Arg	Leu	Gln	Pro	Gly	35	40	45	
Leu	Lys	Trp	Val	Pro	Glu	Thr	Pro	Val	Pro	Gly	Ser	Asp	Leu	Gln	Val	50	55	60	
Cys	Leu	Pro	Lys	Gly	Pro	Thr	Cys	Cys	Ser	Arg	Lys	Met	Glu	Glu	Lys	65	70	75	80
Tyr	Gln	Leu	Thr	Ala	Arg	Leu	Asn	Met	Glu	Gln	Leu	Leu	Gln	Ser	Ala	85	90	95	
Ser	Met	Glu	Leu	Lys	Phe	Leu	Ile	Ile	Gln	Asn	Ala	Ala	Val	Phe	Gln	100	105	110	
Glu	Ala	Phe	Glu	Ile	Val	Val	Arg	His	Ala	Lys	Asn	Tyr	Thr	Asn	Ala	115	120	125	
Met	Phe	Lys	Asn	Asn	Tyr	Pro	Ser	Leu	Thr	Pro	Gln	Ala	Phe	Glu	Phe	130	135	140	
Val	Gly	Glu	Phe	Phe	Thr	Asp	Val	Ser	Leu	Tyr	Ile	Leu	Gly	Ser	Asp	145	150	155	160
Ile	Asn	Val	Asp	Asp	Met	Val	Asn	Glu	Leu	Phe	Asp	Ser	Leu	Phe	Pro	165	170	175	
Val	Ile	Tyr	Thr	Gln	Leu	Met	Asn	Pro	Gly	Leu	Pro	Asp	Ser	Ala	Leu	180	185	190	
Asp	Ile	Asn	Glu	Cys	Leu	Arg	Gly	Ala	Arg	Arg	Asp	Leu	Lys	Val	Phe	195	200	205	
Gly	Asn	Phe	Pro	Lys	Leu	Ile	Met	Thr	Gln	Val	Ser	Lys	Ser	Leu	Gln	210	215	220	
Val	Thr	Arg	Ile	Phe	Leu	Gln	Ala	Leu	Asn	Leu	Gly	Ile	Glu	Val	Ile	225	230	235	240
Asn	Thr	Thr	Asp	His	Leu	Lys	Phe	Ser	Lys	Asp	Cys	Gly	Arg	Met	Leu	245	250	255	
Thr	Arg	Met	Trp	Tyr	Cys	Ser	Tyr	Cys	Gln	Gly	Leu	Met	Met	Val	Lys	260	265	270	

ITI-08-PCT_Sequence_Listing_ST25.txt

Pro Cys Gly Gly Tyr Cys Asn Val Val Met Gln Gly Cys Met Ala Gly
275 280 285

Val Val Glu Ile Asp Lys Tyr Trp Arg Glu Tyr Ile Leu Ser Leu Glu
290 295 300

Glu Leu Val Asn Gly Met Tyr Arg Ile Tyr Asp Met Glu Asn Val Leu
305 310 315 320

Leu Gly Leu Phe Ser Thr Ile His Asp Ser Ile Gln Tyr Val Gln Lys
325 330 335

Asn Ala Gly Lys Leu Thr Thr Thr Ile Gly Lys Leu Cys Ala His Ser
340 345 350

Gln Gln Arg Gln Tyr Arg Ser Ala Tyr Tyr Pro Glu Asp Leu Phe Ile
355 360 365

Asp Lys Lys Val Leu Lys Val Ala His Val Glu His Glu Glu Thr Leu
370 375 380

Ser Ser Arg Arg Arg Glu Leu Ile Gln Lys Leu Lys Ser Phe Ile Ser
385 390 395 400

Phe Tyr Ser Ala Leu Pro Gly Tyr Ile Cys Ser His Ser Pro Val Ala
405 410 415

Glu Asn Asp Thr Leu Cys Trp Asn Gly Gln Glu Leu Val Glu Arg Tyr
420 425 430

Ser Gln Lys Ala Ala Arg Asn Gly Met Lys Asn Gln Phe Asn Leu His
435 440 445

Glu Leu Lys Met Lys Gly Pro Glu Pro Val Val Ser Gln Ile Ile Asp
450 455 460

Lys Leu Lys His Ile Asn Gln Leu Leu Arg Thr Met Ser Met Pro Lys
465 470 475 480

Gly Arg Val Leu Asp Lys Asn Leu Asp Glu Glu Gly Phe Glu Ser Gly
485 490 495

Asp Cys Gly Asp Asp Glu Asp Glu Cys Ile Gly Gly Ser Gly Asp Gly
500 505 510

Met Ile Lys Val Lys Asn Gln Leu Arg Phe Leu Ala Glu Leu Ala Tyr
515 520 525

Asp Leu Asp Val Asp Asp Ala Pro Gly Asn Ser Gln Gln Ala Thr Pro
530 535 540

ITI-08-PCT_Sequence_Listing_ST25.txt

Lys Asp Asn Glu Ile Ser Thr Phe His Asn Leu Gly Asn Val His Ser
545 550 555 560

Pro Leu Lys Leu Leu Thr Ser Met Ala Ile Ser Val Val Cys Phe Phe
565 570 575

Phe Leu Val His
580

<210> 398

<211> 580

<212> PRT

<213> Artificial Sequence

<220>

<223> GPC3__Homo_sapiens__P51654

<400> 398

Met Ala Gly Thr Val Arg Thr Ala Cys Leu Val Val Ala Met Leu Leu
1 5 10 15

Ser Leu Asp Phe Pro Gly Gln Ala Gln Pro Pro Pro Pro Pro Pro Asp
20 25 30

Ala Thr Cys His Gln Val Arg Ser Phe Phe Gln Arg Leu Gln Pro Gly
35 40 45

Leu Lys Trp Val Pro Glu Thr Pro Val Pro Gly Ser Asp Leu Gln Val
50 55 60

Cys Leu Pro Lys Gly Pro Thr Cys Cys Ser Arg Lys Met Glu Glu Lys
65 70 75 80

Tyr Gln Leu Thr Ala Arg Leu Asn Met Glu Gln Leu Leu Gln Ser Ala
85 90 95

Ser Met Glu Leu Lys Phe Leu Ile Ile Gln Asn Ala Ala Val Phe Gln
100 105 110

Glu Ala Phe Glu Ile Val Val Arg His Ala Lys Asn Tyr Thr Asn Ala
115 120 125

Met Phe Lys Asn Asn Tyr Pro Ser Leu Thr Pro Gln Ala Phe Glu Phe
130 135 140

Val Gly Glu Phe Phe Thr Asp Val Ser Leu Tyr Ile Leu Gly Ser Asp
145 150 155 160

Ile Asn Val Asp Asp Met Val Asn Glu Leu Phe Asp Ser Leu Phe Pro
165 170 175

ITI-08-PCT_Sequence_Listing_ST25.txt

Val	Ile	Tyr	Thr	Gln	Leu	Met	Asn	Pro	Gly	Leu	Pro	Asp	Ser	Ala	Leu	180	185	190
Asp	Ile	Asn	Glu	Cys	Leu	Arg	Gly	Ala	Arg	Arg	Asp	Leu	Lys	Val	Phe	195	200	205
Gly	Asn	Phe	Pro	Lys	Leu	Ile	Met	Thr	Gln	Val	Ser	Lys	Ser	Leu	Gln	210	215	220
Val	Thr	Arg	Ile	Phe	Leu	Gln	Ala	Leu	Asn	Leu	Gly	Ile	Glu	Val	Ile	225	230	235
Asn	Thr	Thr	Asp	His	Leu	Lys	Phe	Ser	Lys	Asp	Cys	Gly	Arg	Met	Leu	245	250	255
Thr	Arg	Met	Trp	Tyr	Cys	Ser	Tyr	Cys	Gln	Gly	Leu	Met	Met	Val	Lys	260	265	270
Pro	Cys	Gly	Gly	Tyr	Cys	Asn	Val	Val	Met	Gln	Gly	Cys	Met	Ala	Gly	275	280	285
Val	Val	Glu	Ile	Asp	Lys	Tyr	Trp	Arg	Glu	Tyr	Ile	Leu	Ser	Leu	Glu	290	295	300
Glu	Leu	Val	Asn	Gly	Met	Tyr	Arg	Ile	Tyr	Asp	Met	Glu	Asn	Val	Leu	305	310	315
Leu	Gly	Leu	Phe	Ser	Thr	Ile	His	Asp	Ser	Ile	Gln	Tyr	Val	Gln	Lys	325	330	335
Asn	Ala	Gly	Lys	Leu	Thr	Thr	Thr	Ile	Gly	Lys	Leu	Cys	Ala	His	Ser	340	345	350
Gln	Gln	Arg	Gln	Tyr	Arg	Ser	Ala	Tyr	Tyr	Pro	Glu	Asp	Leu	Phe	Ile	355	360	365
Asp	Lys	Lys	Val	Leu	Lys	Val	Ala	His	Val	Glu	His	Glu	Glu	Thr	Leu	370	375	380
Ser	Ser	Arg	Arg	Arg	Glu	Leu	Ile	Gln	Lys	Leu	Lys	Ser	Phe	Ile	Ser	385	390	395
Phe	Tyr	Ser	Ala	Leu	Pro	Gly	Tyr	Ile	Cys	Ser	His	Ser	Pro	Val	Ala	405	410	415
Glu	Asn	Asp	Thr	Leu	Cys	Trp	Asn	Gly	Gln	Glu	Leu	Val	Glu	Arg	Tyr	420	425	430
Ser	Gln	Lys	Ala	Ala	Arg	Asn	Gly	Met	Lys	Asn	Gln	Phe	Asn	Leu	His	435	440	445
Glu	Leu	Lys	Met	Lys	Gly	Pro	Glu	Pro	Val	Val	Ser	Gln	Ile	Ile	Asp			

ITI-08-PCT_Sequence_Listing_ST25.txt

450

455

460

Lys Leu Lys His Ile Asn Gln Leu Leu Arg Thr Met Ser Met Pro Lys
465 470 475 480

Gly Arg Val Leu Asp Lys Asn Leu Asp Glu Glu Gly Phe Glu Ser Gly
485 490 495

Asp Cys Gly Asp Asp Glu Asp Glu Cys Ile Gly Gly Ser Gly Asp Gly
500 505 510

Met Ile Lys Val Lys Asn Gln Leu Arg Phe Leu Ala Glu Leu Ala Tyr
515 520 525

Asp Leu Asp Val Asp Asp Ala Pro Gly Asn Ser Gln Gln Ala Thr Pro
530 535 540

Lys Asp Asn Glu Ile Ser Thr Phe His Asn Leu Gly Asn Val His Ser
545 550 555 560

Pro Leu Lys Leu Leu Thr Ser Met Ala Ile Ser Val Val Cys Phe Phe
565 570 575

Phe Leu Val His
580

<210> 399

<211> 580

<212> PRT

<213> Artificial Sequence

<220>

<223> GPC3__Homo_sapiens__Q8IYG2

<400> 399

Met Ala Gly Thr Val Arg Thr Ala Cys Leu Val Val Ala Met Leu Leu
1 5 10 15

Ser Leu Asp Phe Pro Gly Gln Ala Gln Pro Pro Pro Pro Pro Pro Asp
20 25 30

Ala Thr Cys His Gln Val Arg Ser Phe Phe Gln Arg Leu Gln Pro Gly
35 40 45

Leu Lys Trp Val Pro Glu Thr Pro Val Pro Gly Ser Asp Leu Gln Val
50 55 60

Cys Leu Pro Lys Gly Pro Thr Cys Cys Ser Arg Lys Met Glu Glu Lys
65 70 75 80

Tyr Gln Leu Thr Ala Arg Leu Asn Met Glu Gln Leu Leu Gln Ser Ala

ITI-08-PCT_Sequence_Listing_ST25.txt

85

90

95

Ser Met Glu Leu Lys Phe Leu Ile Ile Gln Asn Ala Ala Val Phe Gln
 100 105 110

Glu Ala Phe Glu Ile Val Val Arg His Ala Lys Asn Tyr Thr Asn Ala
 115 120 125

Met Phe Lys Asn Asn Tyr Pro Ser Leu Thr Pro Gln Ala Phe Glu Phe
 130 135 140

Val Gly Glu Phe Phe Thr Asp Val Ser Leu Tyr Ile Leu Gly Ser Asp
 145 150 155 160

Ile Asn Val Asp Asp Met Val Asn Glu Leu Phe Asp Ser Leu Phe Pro
 165 170 175

Val Ile Tyr Thr Gln Leu Met Asn Pro Gly Leu Pro Asp Ser Ala Leu
 180 185 190

Asp Ile Asn Glu Cys Leu Arg Gly Ala Arg Arg Asp Leu Lys Val Phe
 195 200 205

Gly Asn Phe Pro Lys Leu Ile Met Thr Gln Val Ser Lys Ser Leu Gln
 210 215 220

Val Thr Arg Ile Phe Leu Gln Ala Leu Asn Leu Gly Ile Glu Val Ile
 225 230 235 240

Asn Thr Thr Asp His Leu Lys Phe Ser Lys Asp Cys Gly Arg Met Leu
 245 250 255

Thr Arg Met Trp Tyr Cys Ser Tyr Cys Gln Gly Leu Met Met Val Lys
 260 265 270

Pro Cys Gly Gly Tyr Cys Asn Val Val Met Gln Gly Cys Met Ala Gly
 275 280 285

Val Val Glu Ile Asp Lys Tyr Trp Arg Glu Tyr Ile Leu Ser Leu Glu
 290 295 300

Glu Leu Val Asn Gly Met Tyr Arg Ile Tyr Asp Met Glu Asn Val Leu
 305 310 315 320

Leu Gly Leu Phe Ser Thr Ile His Asp Ser Ile Gln Tyr Val Gln Lys
 325 330 335

Asn Ala Gly Lys Leu Thr Thr Thr Ile Gly Lys Leu Cys Ala His Ser
 340 345 350

Gln Gln Arg Gln Tyr Arg Phe Ala Tyr Tyr Pro Glu Asp Leu Phe Ile
 355 360 365

ITI-08-PCT_Sequence_Listing_ST25.txt

Asp Lys Lys Val Leu Lys Val Ala His Val Glu His Glu Glu Thr Leu
 370 375 380
 Ser Ser Arg Arg Arg Glu Leu Ile Gln Lys Leu Lys Ser Phe Ile Ser
 385 390 395 400
 Phe Tyr Ser Ala Leu Pro Gly Tyr Ile Cys Ser His Ser Pro Val Ala
 405 410 415
 Glu Asn Asp Thr Leu Cys Trp Asn Gly Gln Glu Leu Val Glu Arg Tyr
 420 425 430
 Ser Gln Lys Ala Ala Arg Asn Gly Met Lys Asn Gln Phe Asn Leu His
 435 440 445
 Glu Leu Lys Met Lys Gly Pro Glu Pro Val Val Ser Gln Ile Ile Asp
 450 455 460
 Lys Leu Lys His Ile Asn Gln Leu Leu Arg Thr Met Ser Met Pro Lys
 465 470 475 480
 Gly Arg Val Leu Asp Lys Asn Leu Asp Glu Glu Gly Phe Glu Ser Gly
 485 490 495
 Asp Cys Gly Asp Asp Glu Asp Glu Cys Ile Gly Gly Ser Gly Asp Gly
 500 505 510
 Met Ile Lys Val Lys Asn Gln Leu Arg Phe Leu Ala Glu Leu Ala Tyr
 515 520 525
 Asp Leu Asp Val Asp Asp Ala Pro Gly Asn Ser Gln Gln Ala Thr Pro
 530 535 540
 Lys Asp Asn Glu Ile Ser Thr Phe His Asn Leu Gly Asn Val His Ser
 545 550 555 560
 Pro Leu Lys Leu Leu Thr Ser Met Ala Ile Ser Val Val Cys Phe Phe
 565 570 575
 Phe Leu Val His
 580

<210> 400
 <211> 560
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> GPNMB/m__Homo_sapiens__A0A024RA55

<400> 400

ITI-08-PCT_Sequence_Listing_ST25.txt

```

Met Glu Cys Leu Tyr Tyr Phe Leu Gly Phe Leu Leu Leu Ala Ala Arg
1          5          10          15

Leu Pro Leu Asp Ala Ala Lys Arg Phe His Asp Val Leu Gly Asn Glu
          20          25          30

Arg Pro Ser Ala Tyr Met Arg Glu His Asn Gln Leu Asn Gly Trp Ser
          35          40          45

Ser Asp Glu Asn Asp Trp Asn Glu Lys Leu Tyr Pro Val Trp Lys Arg
          50          55          60

Gly Asp Met Arg Trp Lys Asn Ser Trp Lys Gly Gly Arg Val Gln Ala
65          70          75          80

Val Leu Thr Ser Asp Ser Pro Ala Leu Val Gly Ser Asn Ile Thr Phe
          85          90          95

Ala Val Asn Leu Ile Phe Pro Arg Cys Gln Lys Glu Asp Ala Asn Gly
          100          105          110

Asn Ile Val Tyr Glu Lys Asn Cys Arg Asn Glu Ala Gly Leu Ser Ala
          115          120          125

Asp Pro Tyr Val Tyr Asn Trp Thr Ala Trp Ser Glu Asp Ser Asp Gly
          130          135          140

Glu Asn Gly Thr Gly Gln Ser His His Asn Val Phe Pro Asp Gly Lys
145          150          155          160

Pro Phe Pro His His Pro Gly Trp Arg Arg Trp Asn Phe Ile Tyr Val
          165          170          175

Phe His Thr Leu Gly Gln Tyr Phe Gln Lys Leu Gly Arg Cys Ser Val
          180          185          190

Arg Val Ser Val Asn Thr Ala Asn Val Thr Leu Gly Pro Gln Leu Met
          195          200          205

Glu Val Thr Val Tyr Arg Arg His Gly Arg Ala Tyr Val Pro Ile Ala
          210          215          220

Gln Val Lys Asp Val Tyr Val Val Thr Asp Gln Ile Pro Val Phe Val
225          230          235          240

Thr Met Phe Gln Lys Asn Asp Arg Asn Ser Ser Asp Glu Thr Phe Leu
          245          250          255

Lys Asp Leu Pro Ile Met Phe Asp Val Leu Ile His Asp Pro Ser His
          260          265          270

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Phe Leu Asn Tyr Ser Thr Ile Asn Tyr Lys Trp Ser Phe Gly Asp Asn
 275 280 285
 Thr Gly Leu Phe Val Ser Thr Asn His Thr Val Asn His Thr Tyr Val
 290 295 300
 Leu Asn Gly Thr Phe Ser Leu Asn Leu Thr Val Lys Ala Ala Ala Pro
 305 310 315 320
 Gly Pro Cys Pro Pro Pro Pro Pro Pro Arg Pro Ser Lys Pro Thr
 325 330 335
 Pro Ser Leu Gly Pro Ala Gly Asp Asn Pro Leu Glu Leu Ser Arg Ile
 340 345 350
 Pro Asp Glu Asn Cys Gln Ile Asn Arg Tyr Gly His Phe Gln Ala Thr
 355 360 365
 Ile Thr Ile Val Glu Gly Ile Leu Glu Val Asn Ile Ile Gln Met Thr
 370 375 380
 Asp Val Leu Met Pro Val Pro Trp Pro Glu Ser Ser Leu Ile Asp Phe
 385 390 395 400
 Val Val Thr Cys Gln Gly Ser Ile Pro Thr Glu Val Cys Thr Ile Ile
 405 410 415
 Ser Asp Pro Thr Cys Glu Ile Thr Gln Asn Thr Val Cys Ser Pro Val
 420 425 430
 Asp Val Asp Glu Met Cys Leu Leu Thr Val Arg Arg Thr Phe Asn Gly
 435 440 445
 Ser Gly Thr Tyr Cys Val Asn Leu Thr Leu Gly Asp Asp Thr Ser Leu
 450 455 460
 Ala Leu Thr Ser Thr Leu Ile Ser Val Pro Asp Arg Asp Pro Ala Ser
 465 470 475 480
 Pro Leu Arg Met Ala Asn Ser Ala Leu Ile Ser Val Gly Cys Leu Ala
 485 490 495
 Ile Phe Val Thr Val Ile Ser Leu Leu Val Tyr Lys Lys His Lys Glu
 500 505 510
 Tyr Asn Pro Ile Glu Asn Ser Pro Gly Asn Val Val Arg Ser Lys Gly
 515 520 525
 Leu Ser Val Phe Leu Asn Arg Ala Lys Ala Val Phe Phe Pro Gly Asn
 530 535 540
 Gln Glu Lys Asp Pro Leu Leu Lys Asn Gln Glu Phe Lys Gly Val Ser

ITI-08-PCT_Sequence_Listing_ST25.txt

545 550 555 560

<210> 401
<211> 572
<212> PRT
<213> Artificial Sequence

<220>
<223> GPNMB/m__Homo_sapiens__Q14956

<400> 401

Met Glu Cys Leu Tyr Tyr Phe Leu Gly Phe Leu Leu Leu Ala Ala Arg
1 5 10 15

Leu Pro Leu Asp Ala Ala Lys Arg Phe His Asp Val Leu Gly Asn Glu
20 25 30

Arg Pro Ser Ala Tyr Met Arg Glu His Asn Gln Leu Asn Gly Trp Ser
35 40 45

Ser Asp Glu Asn Asp Trp Asn Glu Lys Leu Tyr Pro Val Trp Lys Arg
50 55 60

Gly Asp Met Arg Trp Lys Asn Ser Trp Lys Gly Gly Arg Val Gln Ala
65 70 75 80

Val Leu Thr Ser Asp Ser Pro Ala Leu Val Gly Ser Asn Ile Thr Phe
85 90 95

Ala Val Asn Leu Ile Phe Pro Arg Cys Gln Lys Glu Asp Ala Asn Gly
100 105 110

Asn Ile Val Tyr Glu Lys Asn Cys Arg Asn Glu Ala Gly Leu Ser Ala
115 120 125

Asp Pro Tyr Val Tyr Asn Trp Thr Ala Trp Ser Glu Asp Ser Asp Gly
130 135 140

Glu Asn Gly Thr Gly Gln Ser His His Asn Val Phe Pro Asp Gly Lys
145 150 155 160

Pro Phe Pro His His Pro Gly Trp Arg Arg Trp Asn Phe Ile Tyr Val
165 170 175

Phe His Thr Leu Gly Gln Tyr Phe Gln Lys Leu Gly Arg Cys Ser Val
180 185 190

Arg Val Ser Val Asn Thr Ala Asn Val Thr Leu Gly Pro Gln Leu Met
195 200 205

Glu Val Thr Val Tyr Arg Arg His Gly Arg Ala Tyr Val Pro Ile Ala

ITI-08-PCT_Sequence_Listing_ST25.txt

210						215						220					
Gln	Val	Lys	Asp	Val	Tyr	Val	Val	Thr	Asp	Gln	Ile	Pro	Val	Phe	Val		
225					230					235						240	
Thr	Met	Phe	Gln	Lys	Asn	Asp	Arg	Asn	Ser	Ser	Asp	Glu	Thr	Phe	Leu		
				245					250					255			
Lys	Asp	Leu	Pro	Ile	Met	Phe	Asp	Val	Leu	Ile	His	Asp	Pro	Ser	His		
			260					265					270				
Phe	Leu	Asn	Tyr	Ser	Thr	Ile	Asn	Tyr	Lys	Trp	Ser	Phe	Gly	Asp	Asn		
		275					280					285					
Thr	Gly	Leu	Phe	Val	Ser	Thr	Asn	His	Thr	Val	Asn	His	Thr	Tyr	Val		
	290					295					300						
Leu	Asn	Gly	Thr	Phe	Ser	Leu	Asn	Leu	Thr	Val	Lys	Ala	Ala	Ala	Pro		
305					310					315					320		
Gly	Pro	Cys	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Arg	Pro	Ser	Lys	Pro	Thr		
				325					330					335			
Pro	Ser	Leu	Ala	Thr	Thr	Leu	Lys	Ser	Tyr	Asp	Ser	Asn	Thr	Pro	Gly		
			340					345					350				
Pro	Ala	Gly	Asp	Asn	Pro	Leu	Glu	Leu	Ser	Arg	Ile	Pro	Asp	Glu	Asn		
		355					360					365					
Cys	Gln	Ile	Asn	Arg	Tyr	Gly	His	Phe	Gln	Ala	Thr	Ile	Thr	Ile	Val		
	370					375					380						
Glu	Gly	Ile	Leu	Glu	Val	Asn	Ile	Ile	Gln	Met	Thr	Asp	Val	Leu	Met		
385					390					395					400		
Pro	Val	Pro	Trp	Pro	Glu	Ser	Ser	Leu	Ile	Asp	Phe	Val	Val	Thr	Cys		
				405					410					415			
Gln	Gly	Ser	Ile	Pro	Thr	Glu	Val	Cys	Thr	Ile	Ile	Ser	Asp	Pro	Thr		
			420					425					430				
Cys	Glu	Ile	Thr	Gln	Asn	Thr	Val	Cys	Ser	Pro	Val	Asp	Val	Asp	Glu		
		435					440					445					
Met	Cys	Leu	Leu	Thr	Val	Arg	Arg	Thr	Phe	Asn	Gly	Ser	Gly	Thr	Tyr		
	450					455					460						
Cys	Val	Asn	Leu	Thr	Leu	Gly	Asp	Asp	Thr	Ser	Leu	Ala	Leu	Thr	Ser		
465					470					475					480		
Thr	Leu	Ile	Ser	Val	Pro	Asp	Arg	Asp	Pro	Ala	Ser	Pro	Leu	Arg	Met		
				485					490					495			

ITI-08-PCT_Sequence_Listing_ST25.txt

Ala Asn Ser Ala Leu Ile Ser Val Gly Cys Leu Ala Ile Phe Val Thr
500 505 510

Val Ile Ser Leu Leu Val Tyr Lys Lys His Lys Glu Tyr Asn Pro Ile
515 520 525

Glu Asn Ser Pro Gly Asn Val Val Arg Ser Lys Gly Leu Ser Val Phe
530 535 540

Leu Asn Arg Ala Lys Ala Val Phe Phe Pro Gly Asn Gln Glu Lys Asp
545 550 555 560

Pro Leu Leu Lys Asn Gln Glu Phe Lys Gly Val Ser
565 570

<210> 402

<211> 206

<212> PRT

<213> Artificial Sequence

<220>

<223> GPNMB/m__Homo_sapiens__Q8IXJ5

<400> 402

Met Glu Cys Leu Tyr Tyr Phe Leu Gly Phe Leu Leu Leu Ala Ala Arg
1 5 10 15

Leu Pro Leu Asp Ala Ala Lys Arg Phe His Asp Val Leu Gly Asn Glu
20 25 30

Arg Pro Ser Ala Tyr Met Arg Glu His Asn Gln Leu Asn Gly Trp Ser
35 40 45

Ser Asp Glu Asn Asp Trp Asn Glu Lys Leu Tyr Pro Val Trp Lys Arg
50 55 60

Gly Asp Met Arg Trp Lys Asn Ser Trp Lys Gly Gly Arg Val Gln Ala
65 70 75 80

Val Leu Thr Ser Asp Ser Pro Ala Leu Val Gly Ser Asn Ile Thr Phe
85 90 95

Ala Val Asn Leu Ile Phe Pro Arg Cys Gln Lys Glu Asp Ala Asn Gly
100 105 110

Asn Ile Val Tyr Glu Lys Asn Cys Arg Asn Glu Ala Gly Leu Ser Ala
115 120 125

Asp Pro Tyr Val Tyr Asn Trp Thr Ala Trp Ser Glu Asp Ser Asp Gly
130 135 140

ITI-08-PCT_Sequence_Listing_ST25.txt

Glu Asn Gly Thr Gly Gln Ser His His Asn Val Phe Pro Asp Gly Lys
145 150 155 160

Pro Phe Pro His His Pro Gly Trp Arg Arg Trp Asn Phe Ile Tyr Val
165 170 175

Phe His Thr Leu Asp Trp Leu Leu Gln Thr Pro Lys Leu Leu Tyr
180 185 190

Leu Ser Leu Lys Phe Gln Pro Ser Leu Phe Leu Leu Tyr Asn
195 200 205

<210> 403

<211> 206

<212> PRT

<213> Artificial Sequence

<220>

<223> GPNMB/m__Homo_sapiens__Q96F58

<400> 403

Met Glu Cys Leu Tyr Tyr Phe Leu Gly Phe Leu Leu Leu Ala Ala Arg
1 5 10 15

Leu Pro Leu Asp Ala Ala Lys Arg Phe His Asp Val Leu Gly Asn Glu
20 25 30

Arg Pro Ser Ala Tyr Met Arg Glu His Asn Gln Leu Asn Gly Trp Ser
35 40 45

Ser Asp Glu Asn Asp Trp Asn Glu Lys Leu Tyr Pro Val Trp Lys Arg
50 55 60

Gly Asp Met Arg Trp Lys Asn Ser Trp Lys Gly Gly Arg Val Gln Ala
65 70 75 80

Val Leu Thr Ser Asp Ser Pro Ala Leu Val Gly Ser Asn Ile Thr Phe
85 90 95

Ala Val Asn Leu Ile Phe Pro Arg Cys Gln Lys Glu Asp Ala Asn Gly
100 105 110

Asn Ile Val Tyr Glu Lys Asn Cys Arg Asn Glu Ala Gly Leu Ser Ala
115 120 125

Asp Pro Tyr Val Tyr Asn Trp Thr Ala Trp Ser Glu Asp Ser Asp Gly
130 135 140

Glu Asn Gly Thr Gly Gln Ser His His Asn Val Phe Pro Asp Gly Lys
145 150 155 160

ITI-08-PCT_Sequence_Listing_ST25.txt

Pro Phe Pro His His Pro Gly Trp Arg Arg Trp Asn Phe Ile Tyr Val
165 170 175

Phe His Thr Leu Gly Trp Leu Leu Gln Thr Pro Lys Leu Leu Leu Tyr
180 185 190

Leu Ser Leu Lys Phe Gln Pro Ser Leu Phe Leu Leu Tyr Asn
195 200 205

<210> 404

<211> 879

<212> PRT

<213> Artificial Sequence

<220>

<223> GRM3__Homo_sapiens__Q14832

<400> 404

Met Lys Met Leu Thr Arg Leu Gln Val Leu Thr Leu Ala Leu Phe Ser
1 5 10 15

Lys Gly Phe Leu Leu Ser Leu Gly Asp His Asn Phe Leu Arg Arg Glu
20 25 30

Ile Lys Ile Glu Gly Asp Leu Val Leu Gly Gly Leu Phe Pro Ile Asn
35 40 45

Glu Lys Gly Thr Gly Thr Glu Glu Cys Gly Arg Ile Asn Glu Asp Arg
50 55 60

Gly Ile Gln Arg Leu Glu Ala Met Leu Phe Ala Ile Asp Glu Ile Asn
65 70 75 80

Lys Asp Asp Tyr Leu Leu Pro Gly Val Lys Leu Gly Val His Ile Leu
85 90 95

Asp Thr Cys Ser Arg Asp Thr Tyr Ala Leu Glu Gln Ser Leu Glu Phe
100 105 110

Val Arg Ala Ser Leu Thr Lys Val Asp Glu Ala Glu Tyr Met Cys Pro
115 120 125

Asp Gly Ser Tyr Ala Ile Gln Glu Asn Ile Pro Leu Leu Ile Ala Gly
130 135 140

Val Ile Gly Gly Ser Tyr Ser Ser Val Ser Ile Gln Val Ala Asn Leu
145 150 155 160

Leu Arg Leu Phe Gln Ile Pro Gln Ile Ser Tyr Ala Ser Thr Ser Ala
165 170 175

ITI-08-PCT_Sequence_Listing_ST25.txt

Lys	Leu	Ser	Asp	Lys	Ser	Arg	Tyr	Asp	Tyr	Phe	Ala	Arg	Thr	Val	Pro	
			180					185					190			
Pro	Asp	Phe	Tyr	Gln	Ala	Lys	Ala	Met	Ala	Glu	Ile	Leu	Arg	Phe	Phe	
		195					200					205				
Asn	Trp	Thr	Tyr	Val	Ser	Thr	Val	Ala	Ser	Glu	Gly	Asp	Tyr	Gly	Glu	
	210					215					220					
Thr	Gly	Ile	Glu	Ala	Phe	Glu	Gln	Glu	Ala	Arg	Leu	Arg	Asn	Ile	Cys	
225					230					235					240	
Ile	Ala	Thr	Ala	Glu	Lys	Val	Gly	Arg	Ser	Asn	Ile	Arg	Lys	Ser	Tyr	
			245						250					255		
Asp	Ser	Val	Ile	Arg	Glu	Leu	Leu	Gln	Lys	Pro	Asn	Ala	Arg	Val	Val	
			260					265					270			
Val	Leu	Phe	Met	Arg	Ser	Asp	Asp	Ser	Arg	Glu	Leu	Ile	Ala	Ala	Ala	
		275					280					285				
Ser	Arg	Ala	Asn	Ala	Ser	Phe	Thr	Trp	Val	Ala	Ser	Asp	Gly	Trp	Gly	
	290					295					300					
Ala	Gln	Glu	Ser	Ile	Ile	Lys	Gly	Ser	Glu	His	Val	Ala	Tyr	Gly	Ala	
305					310					315					320	
Ile	Thr	Leu	Glu	Leu	Ala	Ser	Gln	Pro	Val	Arg	Gln	Phe	Asp	Arg	Tyr	
			325					330						335		
Phe	Gln	Ser	Leu	Asn	Pro	Tyr	Asn	Asn	His	Arg	Asn	Pro	Trp	Phe	Arg	
			340					345					350			
Asp	Phe	Trp	Glu	Gln	Lys	Phe	Gln	Cys	Ser	Leu	Gln	Asn	Lys	Arg	Asn	
		355					360					365				
His	Arg	Arg	Val	Cys	Asp	Lys	His	Leu	Ala	Ile	Asp	Ser	Ser	Asn	Tyr	
	370					375					380					
Glu	Gln	Glu	Ser	Lys	Ile	Met	Phe	Val	Val	Asn	Ala	Val	Tyr	Ala	Met	
385					390					395					400	
Ala	His	Ala	Leu	His	Lys	Met	Gln	Arg	Thr	Leu	Cys	Pro	Asn	Thr	Thr	
			405						410					415		
Lys	Leu	Cys	Asp	Ala	Met	Lys	Ile	Leu	Asp	Gly	Lys	Lys	Leu	Tyr	Lys	
			420					425					430			
Asp	Tyr	Leu	Leu	Lys	Ile	Asn	Phe	Thr	Ala	Pro	Phe	Asn	Pro	Asn	Lys	
		435					440					445				

ITI-08-PCT_Sequence_Listing_ST25.txt

Asp	Ala	Asp	Ser	Ile	Val	Lys	Phe	Asp	Thr	Phe	Gly	Asp	Gly	Met	Gly
450						455					460				
Arg	Tyr	Asn	Val	Phe	Asn	Phe	Gln	Asn	Val	Gly	Gly	Lys	Tyr	Ser	Tyr
465					470					475					480
Leu	Lys	Val	Gly	His	Trp	Ala	Glu	Thr	Leu	Ser	Leu	Asp	Val	Asn	Ser
				485					490					495	
Ile	His	Trp	Ser	Arg	Asn	Ser	Val	Pro	Thr	Ser	Gln	Cys	Ser	Asp	Pro
			500					505					510		
Cys	Ala	Pro	Asn	Glu	Met	Lys	Asn	Met	Gln	Pro	Gly	Asp	Val	Cys	Cys
		515					520					525			
Trp	Ile	Cys	Ile	Pro	Cys	Glu	Pro	Tyr	Glu	Tyr	Leu	Ala	Asp	Glu	Phe
	530					535					540				
Thr	Cys	Met	Asp	Cys	Gly	Ser	Gly	Gln	Trp	Pro	Thr	Ala	Asp	Leu	Thr
545					550					555					560
Gly	Cys	Tyr	Asp	Leu	Pro	Glu	Asp	Tyr	Ile	Arg	Trp	Glu	Asp	Ala	Trp
				565					570					575	
Ala	Ile	Gly	Pro	Val	Thr	Ile	Ala	Cys	Leu	Gly	Phe	Met	Cys	Thr	Cys
			580					585					590		
Met	Val	Val	Thr	Val	Phe	Ile	Lys	His	Asn	Asn	Thr	Pro	Leu	Val	Lys
		595					600					605			
Ala	Ser	Gly	Arg	Glu	Leu	Cys	Tyr	Ile	Leu	Leu	Phe	Gly	Val	Gly	Leu
	610					615					620				
Ser	Tyr	Cys	Met	Thr	Phe	Phe	Phe	Ile	Ala	Lys	Pro	Ser	Pro	Val	Ile
625					630					635					640
Cys	Ala	Leu	Arg	Arg	Leu	Gly	Leu	Gly	Ser	Ser	Phe	Ala	Ile	Cys	Tyr
				645					650					655	
Ser	Ala	Leu	Leu	Thr	Lys	Thr	Asn	Cys	Ile	Ala	Arg	Ile	Phe	Asp	Gly
			660					665					670		
Val	Lys	Asn	Gly	Ala	Gln	Arg	Pro	Lys	Phe	Ile	Ser	Pro	Ser	Ser	Gln
		675					680					685			
Val	Phe	Ile	Cys	Leu	Gly	Leu	Ile	Leu	Val	Gln	Ile	Val	Met	Val	Ser
	690					695					700				
Val	Trp	Leu	Ile	Leu	Glu	Ala	Pro	Gly	Thr	Arg	Arg	Tyr	Thr	Leu	Ala
705					710					715					720
Glu	Lys	Arg	Glu	Thr	Val	Ile	Leu	Lys	Cys	Asn	Val	Lys	Asp	Ser	Ser

ITI-08-PCT_Sequence_Listing_ST25.txt

725 730 735

Met Leu Ile Ser Leu Thr Tyr Asp Val Ile Leu Val Ile Leu Cys Thr
740 745 750

Val Tyr Ala Phe Lys Thr Arg Lys Cys Pro Glu Asn Phe Asn Glu Ala
755 760 765

Lys Phe Ile Gly Phe Thr Met Tyr Thr Thr Cys Ile Ile Trp Leu Ala
770 775 780

Phe Leu Pro Ile Phe Tyr Val Thr Ser Ser Asp Tyr Arg Val Gln Thr
785 790 795 800

Thr Thr Met Cys Ile Ser Val Ser Leu Ser Gly Phe Val Val Leu Gly
805 810 815

Cys Leu Phe Ala Pro Lys Val His Ile Ile Leu Phe Gln Pro Gln Lys
820 825 830

Asn Val Val Thr His Arg Leu His Leu Asn Arg Phe Ser Val Ser Gly
835 840 845

Thr Gly Thr Thr Tyr Ser Gln Ser Ser Ala Ser Thr Tyr Val Pro Thr
850 855 860

Val Cys Asn Gly Arg Glu Val Leu Asp Ser Thr Thr Ser Ser Leu
865 870 875

<210> 405
<211> 648
<212> PRT
<213> Artificial Sequence

<220>
<223> HAGE__Homo_sapiens__Q9NXZ2

<400> 405

Met Ser His His Gly Gly Ala Pro Lys Ala Ser Thr Trp Val Val Ala
1 5 10 15

Ser Arg Arg Ser Ser Thr Val Ser Arg Ala Pro Glu Arg Arg Pro Ala
20 25 30

Glu Glu Leu Asn Arg Thr Gly Pro Glu Gly Tyr Ser Val Gly Arg Gly
35 40 45

Gly Arg Trp Arg Gly Thr Ser Arg Pro Pro Glu Ala Val Ala Ala Gly
50 55 60

His Glu Glu Leu Pro Leu Cys Phe Ala Leu Lys Ser His Phe Val Gly

ITI-08-PCT_Sequence_Listing_ST25.txt

```

65              70              75              80
Ala Val Ile Gly Arg Gly Gly Ser Lys Ile Lys Asn Ile Gln Ser Thr
      85              90              95
Thr Asn Thr Thr Ile Gln Ile Ile Gln Glu Gln Pro Glu Ser Leu Val
      100              105              110
Lys Ile Phe Gly Ser Lys Ala Met Gln Thr Lys Ala Lys Ala Val Ile
      115              120              125
Asp Asn Phe Val Lys Lys Leu Glu Glu Asn Tyr Asn Ser Glu Cys Gly
      130              135              140
Ile Asp Thr Ala Phe Gln Pro Ser Val Gly Lys Asp Gly Ser Thr Asp
145              150              155              160
Asn Asn Val Val Ala Gly Asp Arg Pro Leu Ile Asp Trp Asp Gln Ile
      165              170              175
Arg Glu Glu Gly Leu Lys Trp Gln Lys Thr Lys Trp Ala Asp Leu Pro
      180              185              190
Pro Ile Lys Lys Asn Phe Tyr Lys Glu Ser Thr Ala Thr Ser Ala Met
      195              200              205
Ser Lys Val Glu Ala Asp Ser Trp Arg Lys Glu Asn Phe Asn Ile Thr
      210              215              220
Trp Asp Asp Leu Lys Asp Gly Glu Lys Arg Pro Ile Pro Asn Pro Thr
225              230              235              240
Cys Thr Phe Asp Asp Ala Phe Gln Cys Tyr Pro Glu Val Met Glu Asn
      245              250              255
Ile Lys Lys Ala Gly Phe Gln Lys Pro Thr Pro Ile Gln Ser Gln Ala
      260              265              270
Trp Pro Ile Val Leu Gln Gly Ile Asp Leu Ile Gly Val Ala Gln Thr
      275              280              285
Gly Thr Gly Lys Thr Leu Cys Tyr Leu Met Pro Gly Phe Ile His Leu
      290              295              300
Val Leu Gln Pro Ser Leu Lys Gly Gln Arg Asn Arg Pro Gly Met Leu
305              310              315              320
Val Leu Thr Pro Thr Arg Glu Leu Ala Leu Gln Val Glu Gly Glu Cys
      325              330              335
Cys Lys Tyr Ser Tyr Lys Gly Leu Arg Ser Val Cys Val Tyr Gly Gly
      340              345              350

```


ITI-08-PCT_Sequence_Listing_ST25.txt

Gly	Asn	Arg	Asp	Glu	Gln	Ile	Glu	Glu	Leu	Lys	Lys	Gly	Val	Asp	Ile		
		355					360					365					
Ile	Ile	Ala	Thr	Pro	Gly	Arg	Leu	Asn	Asp	Leu	Gln	Met	Ser	Asn	Phe		
	370					375					380						
Val	Asn	Leu	Lys	Asn	Ile	Thr	Tyr	Leu	Val	Leu	Asp	Glu	Ala	Asp	Lys		
385					390					395					400		
Met	Leu	Asp	Met	Gly	Phe	Glu	Pro	Gln	Ile	Met	Lys	Ile	Leu	Leu	Asp		
				405					410					415			
Val	Arg	Pro	Asp	Arg	Gln	Thr	Val	Met	Thr	Ser	Ala	Thr	Trp	Pro	His		
			420					425					430				
Ser	Val	His	Arg	Leu	Ala	Gln	Ser	Tyr	Leu	Lys	Glu	Pro	Met	Ile	Val		
	435						440					445					
Tyr	Val	Gly	Thr	Leu	Asp	Leu	Val	Ala	Val	Ser	Ser	Val	Lys	Gln	Asn		
	450					455					460						
Ile	Ile	Val	Thr	Thr	Glu	Glu	Glu	Lys	Trp	Ser	His	Met	Gln	Thr	Phe		
465					470				475						480		
Leu	Gln	Ser	Met	Ser	Ser	Thr	Asp	Lys	Val	Ile	Val	Phe	Val	Ser	Arg		
				485					490					495			
Lys	Ala	Val	Ala	Asp	His	Leu	Ser	Ser	Asp	Leu	Ile	Leu	Gly	Asn	Ile		
			500					505					510				
Ser	Val	Glu	Ser	Leu	His	Gly	Asp	Arg	Glu	Gln	Arg	Asp	Arg	Glu	Lys		
	515						520					525					
Ala	Leu	Glu	Asn	Phe	Lys	Thr	Gly	Lys	Val	Arg	Ile	Leu	Ile	Ala	Thr		
	530					535					540						
Asp	Leu	Ala	Ser	Arg	Gly	Leu	Asp	Val	His	Asp	Val	Thr	His	Val	Tyr		
545					550					555					560		
Asn	Phe	Asp	Phe	Pro	Arg	Asn	Ile	Glu	Glu	Tyr	Val	His	Arg	Ile	Gly		
				565					570					575			
Arg	Thr	Gly	Arg	Ala	Gly	Arg	Thr	Gly	Val	Ser	Ile	Thr	Thr	Leu	Thr		
			580					585					590				
Arg	Asn	Asp	Trp	Arg	Val	Ala	Ser	Glu	Leu	Ile	Asn	Ile	Leu	Glu	Arg		
	595						600					605					
Ala	Asn	Gln	Ser	Ile	Pro	Glu	Glu	Leu	Val	Ser	Met	Ala	Glu	Arg	Phe		
	610					615					620						

ITI-08-PCT_Sequence_Listing_ST25.txt

Lys Ala His Gln Gln Lys Arg Glu Met Glu Arg Lys Met Glu Arg Pro
625 630 635 640

Gln Gly Arg Pro Lys Lys Phe His
645

<210> 406

<211> 402

<212> PRT

<213> Artificial Sequence

<220>

<223> hepsin__Homo_sapiens__B2ZDQ2

<400> 406

Met Ala Gln Lys Glu Gly Gly Arg Thr Val Pro Cys Cys Ser Arg Pro
1 5 10 15

Lys Val Ala Ala Leu Thr Ala Gly Thr Leu Leu Leu Leu Thr Ala Ile
20 25 30

Gly Ala Ala Ser Trp Ala Ile Val Ala Val Leu Leu Arg Ser Asp Gln
35 40 45

Glu Pro Leu Tyr Pro Val Gln Val Ser Ser Ala Asp Ala Arg Leu Met
50 55 60

Val Phe Asp Lys Thr Glu Gly Thr Trp Arg Leu Leu Cys Ser Ser Arg
65 70 75 80

Ser Asn Ala Arg Val Ala Gly Leu Ser Cys Glu Glu Met Gly Phe Leu
85 90 95

Arg Ala Leu Thr His Ser Glu Leu Asp Val Arg Thr Ala Gly Ala Asn
100 105 110

Gly Thr Ser Gly Phe Phe Cys Val Asp Glu Gly Arg Leu Pro His Thr
115 120 125

Gln Arg Leu Leu Glu Val Ile Ser Val Cys Asp Cys Pro Arg Gly Arg
130 135 140

Phe Leu Ala Ala Ile Cys Gln Asp Cys Gly Arg Arg Lys Leu Pro Val
145 150 155 160

Asp Arg Ile Val Gly Gly Arg Asp Thr Ser Leu Gly Arg Trp Pro Trp
165 170 175

Gln Val Ser Leu Arg Tyr Asp Gly Ala His Leu Cys Gly Gly Ser Leu
180 185 190

ITI-08-PCT_Sequence_Listing_ST25.txt

Leu Ser Gly Asp Trp Val Leu Thr Ala Ala His Cys Phe Pro Glu Arg
195 200 205

Asn Arg Val Leu Ser Arg Trp Arg Val Phe Ala Gly Ala Val Ala Gln
210 215 220

Ala Ser Pro His Gly Leu Gln Leu Gly Val Gln Ala Val Val Tyr His
225 230 235 240

Gly Gly Tyr Leu Pro Phe Arg Asp Pro Asn Ser Glu Glu Asn Ser Asn
245 250 255

Asp Ile Ala Leu Val His Leu Ser Ser Pro Leu Pro Leu Thr Glu Tyr
260 265 270

Ile Gln Pro Val Cys Leu Pro Ala Ala Gly Gln Ala Leu Val Asp Gly
275 280 285

Lys Ile Cys Thr Val Thr Gly Trp Gly Asn Thr Gln Tyr Tyr Gly Gln
290 295 300

Gln Ala Gly Val Leu Gln Glu Ala Arg Val Pro Ile Ile Ser Asn Asp
305 310 315 320

Val Cys Asn Gly Ala Asp Phe Tyr Gly Asn Gln Ile Lys Pro Lys Met
325 330 335

Phe Cys Ala Gly Tyr Pro Glu Gly Gly Ile Asp Ala Cys Gln Gly Asp
340 345 350

Ser Gly Gly Pro Phe Val Cys Glu Asp Ser Ile Ser Arg Thr Pro Arg
355 360 365

Trp Arg Leu Cys Gly Ile Val Ser Trp Gly Thr Gly Cys Ala Leu Ala
370 375 380

Gln Lys Pro Gly Val Tyr Thr Lys Val Ser Asp Phe Arg Glu Trp Ile
385 390 395 400

Phe Gln

<210> 407

<211> 417

<212> PRT

<213> Artificial Sequence

<220>

<223> hepsin__Homo_sapiens__P05981

<400> 407

Met Ala Gln Lys Glu Gly Gly Arg Thr Val Pro Cys Cys Ser Arg Pro

ITI-08-PCT_Sequence_Listing_ST25.txt

1		5		10		15										
Lys	Val	Ala	Ala	Leu	Thr	Ala	Gly	Thr	Leu	Leu	Leu	Leu	Thr	Ala	Ile	
		20					25						30			
Gly	Ala	Ala	Ser	Trp	Ala	Ile	Val	Ala	Val	Leu	Leu	Arg	Ser	Asp	Gln	
		35					40					45				
Glu	Pro	Leu	Tyr	Pro	Val	Gln	Val	Ser	Ser	Ala	Asp	Ala	Arg	Leu	Met	
	50					55					60					
Val	Phe	Asp	Lys	Thr	Glu	Gly	Thr	Trp	Arg	Leu	Leu	Cys	Ser	Ser	Arg	
65					70					75					80	
Ser	Asn	Ala	Arg	Val	Ala	Gly	Leu	Ser	Cys	Glu	Glu	Met	Gly	Phe	Leu	
			85						90					95		
Arg	Ala	Leu	Thr	His	Ser	Glu	Leu	Asp	Val	Arg	Thr	Ala	Gly	Ala	Asn	
			100					105					110			
Gly	Thr	Ser	Gly	Phe	Phe	Cys	Val	Asp	Glu	Gly	Arg	Leu	Pro	His	Thr	
		115					120					125				
Gln	Arg	Leu	Leu	Glu	Val	Ile	Ser	Val	Cys	Asp	Cys	Pro	Arg	Gly	Arg	
	130					135					140					
Phe	Leu	Ala	Ala	Ile	Cys	Gln	Asp	Cys	Gly	Arg	Arg	Lys	Leu	Pro	Val	
145					150					155					160	
Asp	Arg	Ile	Val	Gly	Gly	Arg	Asp	Thr	Ser	Leu	Gly	Arg	Trp	Pro	Trp	
			165						170					175		
Gln	Val	Ser	Leu	Arg	Tyr	Asp	Gly	Ala	His	Leu	Cys	Gly	Gly	Ser	Leu	
		180						185					190			
Leu	Ser	Gly	Asp	Trp	Val	Leu	Thr	Ala	Ala	His	Cys	Phe	Pro	Glu	Arg	
		195					200					205				
Asn	Arg	Val	Leu	Ser	Arg	Trp	Arg	Val	Phe	Ala	Gly	Ala	Val	Ala	Gln	
	210					215					220					
Ala	Ser	Pro	His	Gly	Leu	Gln	Leu	Gly	Val	Gln	Ala	Val	Val	Tyr	His	
225					230					235					240	
Gly	Gly	Tyr	Leu	Pro	Phe	Arg	Asp	Pro	Asn	Ser	Glu	Glu	Asn	Ser	Asn	
			245						250					255		
Asp	Ile	Ala	Leu	Val	His	Leu	Ser	Ser	Pro	Leu	Pro	Leu	Thr	Glu	Tyr	
		260						265					270			
Ile	Gln	Pro	Val	Cys	Leu	Pro	Ala	Ala	Gly	Gln	Ala	Leu	Val	Asp	Gly	
	275						280					285				

ITI-08-PCT_Sequence_Listing_ST25.txt

Lys Ile Cys Thr Val Thr Gly Trp Gly Asn Thr Gln Tyr Tyr Gly Gln
290 295 300

Gln Ala Gly Val Leu Gln Glu Ala Arg Val Pro Ile Ile Ser Asn Asp
305 310 315 320

Val Cys Asn Gly Ala Asp Phe Tyr Gly Asn Gln Ile Lys Pro Lys Met
325 330 335

Phe Cys Ala Gly Tyr Pro Glu Gly Gly Ile Asp Ala Cys Gln Gly Asp
340 345 350

Ser Gly Gly Pro Phe Val Cys Glu Asp Ser Ile Ser Arg Thr Pro Arg
355 360 365

Trp Arg Leu Cys Gly Ile Val Ser Trp Gly Thr Gly Cys Ala Leu Ala
370 375 380

Gln Lys Pro Gly Val Tyr Thr Lys Val Ser Asp Phe Arg Glu Trp Ile
385 390 395 400

Phe Gln Ala Ile Lys Thr His Ser Glu Ala Ser Gly Met Val Thr Gln
405 410 415

Leu

<210> 408

<211> 979

<212> PRT

<213> Artificial Sequence

<220>

<223> Her2/neu__Homo_sapiens__B4DTR1

<400> 408

Met Glu Leu Ala Ala Leu Cys Arg Trp Gly Leu Leu Leu Ala Leu Leu
1 5 10 15

Pro Pro Gly Ala Ala Ser Thr Gln Asp Asn Tyr Leu Ser Thr Asp Val
20 25 30

Gly Ser Cys Thr Leu Val Cys Pro Leu His Asn Gln Glu Val Thr Ala
35 40 45

Glu Asp Gly Thr Gln Arg Cys Glu Lys Cys Ser Lys Pro Cys Ala Arg
50 55 60

Val Cys Tyr Gly Leu Gly Met Glu His Leu Arg Glu Val Arg Ala Val
65 70 75 80

ITI-08-PCT_Sequence_Listing_ST25.txt

Thr	Ser	Ala	Asn	Ile	Gln	Glu	Phe	Ala	Gly	Cys	Lys	Lys	Ile	Phe	Gly	85	90	95
Ser	Leu	Ala	Phe	Leu	Pro	Glu	Ser	Phe	Asp	Gly	Asp	Pro	Ala	Ser	Asn	100	105	110
Thr	Ala	Pro	Leu	Gln	Pro	Glu	Gln	Leu	Gln	Val	Phe	Glu	Thr	Leu	Glu	115	120	125
Glu	Ile	Thr	Gly	Tyr	Leu	Tyr	Ile	Ser	Ala	Trp	Pro	Asp	Ser	Leu	Pro	130	135	140
Asp	Leu	Ser	Val	Phe	Gln	Asn	Leu	Gln	Val	Ile	Arg	Gly	Arg	Ile	Leu	145	150	155
His	Asn	Gly	Ala	Tyr	Ser	Leu	Thr	Leu	Gln	Gly	Leu	Gly	Ile	Ser	Trp	165	170	175
Leu	Gly	Leu	Arg	Ser	Leu	Arg	Glu	Leu	Gly	Ser	Gly	Leu	Ala	Leu	Ile	180	185	190
His	His	Asn	Thr	His	Leu	Cys	Phe	Val	His	Thr	Val	Pro	Trp	Asp	Gln	195	200	205
Leu	Phe	Arg	Asn	Pro	His	Gln	Ala	Leu	Leu	His	Thr	Ala	Asn	Arg	Pro	210	215	220
Glu	Asp	Glu	Cys	Val	Gly	Glu	Gly	Leu	Ala	Cys	His	Gln	Leu	Cys	Ala	225	230	235
Arg	Gly	His	Cys	Trp	Gly	Pro	Gly	Pro	Thr	Gln	Cys	Val	Asn	Cys	Ser	245	250	255
Gln	Phe	Leu	Arg	Gly	Gln	Glu	Cys	Val	Glu	Glu	Cys	Arg	Val	Leu	Gln	260	265	270
Gly	Leu	Pro	Arg	Glu	Tyr	Val	Asn	Ala	Arg	His	Cys	Leu	Pro	Cys	His	275	280	285
Pro	Glu	Cys	Gln	Pro	Gln	Asn	Gly	Ser	Val	Thr	Cys	Phe	Gly	Pro	Glu	290	295	300
Ala	Asp	Gln	Cys	Val	Ala	Cys	Ala	His	Tyr	Lys	Asp	Pro	Pro	Phe	Cys	305	310	315
Val	Ala	Arg	Cys	Pro	Ser	Gly	Val	Lys	Pro	Asp	Leu	Ser	Tyr	Met	Pro	325	330	335
Ile	Trp	Lys	Phe	Pro	Asp	Glu	Glu	Gly	Ala	Cys	Gln	Pro	Cys	Pro	Ile	340	345	350
Asn	Cys	Thr	His	Ser	Cys	Val	Asp	Leu	Asp	Asp	Lys	Gly	Cys	Pro	Ala			

ITI-08-PCT_Sequence_Listing_ST25.txt

```

355                               360                               365
Glu Gln Arg Ala Ser Pro Leu Thr Ser Ile Ile Ser Ala Val Val Gly
370                               375                               380
Ile Leu Leu Val Val Val Leu Gly Val Val Phe Gly Ile Leu Ile Lys
385                               390                               395                               400
Arg Arg Gln Gln Lys Ile Arg Lys Tyr Thr Met Arg Arg Leu Leu Gln
405                               410                               415
Glu Thr Glu Leu Val Glu Pro Leu Thr Pro Ser Gly Ala Met Pro Asn
420                               425                               430
Gln Ala Gln Met Arg Ile Leu Lys Glu Thr Glu Leu Arg Lys Val Lys
435                               440                               445
Val Leu Gly Ser Gly Ala Phe Gly Thr Val Tyr Lys Gly Ile Trp Ile
450                               455                               460
Pro Asp Gly Glu Asn Val Lys Ile Pro Val Ala Ile Lys Val Leu Arg
465                               470                               475                               480
Glu Asn Thr Ser Pro Lys Ala Asn Lys Glu Ile Leu Asp Glu Ala Tyr
485                               490                               495
Val Met Ala Gly Val Gly Ser Pro Tyr Val Ser Arg Leu Leu Gly Ile
500                               505                               510
Cys Leu Thr Ser Thr Val Gln Leu Val Thr Gln Leu Met Pro Tyr Gly
515                               520                               525
Cys Leu Leu Asp His Val Arg Glu Asn Arg Gly Arg Leu Gly Ser Gln
530                               535                               540
Asp Leu Leu Asn Trp Cys Met Gln Ile Ala Lys Gly Met Ser Tyr Leu
545                               550                               555                               560
Glu Asp Val Arg Leu Val His Arg Asp Leu Ala Ala Arg Asn Val Leu
565                               570                               575
Val Lys Ser Pro Asn His Val Lys Ile Thr Asp Phe Gly Leu Ala Arg
580                               585                               590
Leu Leu Asp Ile Asp Glu Thr Glu Tyr His Ala Asp Gly Gly Lys Val
595                               600                               605
Pro Ile Lys Trp Met Ala Leu Glu Ser Ile Leu Arg Arg Arg Phe Thr
610                               615                               620
His Gln Ser Asp Val Trp Ser Tyr Gly Val Thr Val Trp Glu Leu Met
625                               630                               635                               640

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Thr	Phe	Gly	Ala	Lys	Pro	Tyr	Asp	Gly	Ile	Pro	Ala	Arg	Glu	Ile	Pro	645	650	655
Asp	Leu	Leu	Glu	Lys	Gly	Glu	Arg	Leu	Pro	Gln	Pro	Pro	Ile	Cys	Thr	660	665	670
Ile	Asp	Val	Tyr	Met	Ile	Met	Val	Lys	Cys	Trp	Met	Ile	Asp	Ser	Glu	675	680	685
Cys	Arg	Pro	Arg	Phe	Arg	Glu	Leu	Val	Ser	Glu	Phe	Ser	Arg	Met	Ala	690	695	700
Arg	Asp	Pro	Gln	Arg	Phe	Val	Val	Ile	Gln	Asn	Glu	Asp	Leu	Gly	Pro	705	710	715
Ala	Ser	Pro	Leu	Asp	Ser	Thr	Phe	Tyr	Arg	Ser	Leu	Leu	Glu	Asp	Asp	725	730	735
Asp	Met	Gly	Asp	Leu	Val	Asp	Ala	Glu	Glu	Tyr	Leu	Val	Pro	Gln	Gln	740	745	750
Gly	Phe	Phe	Cys	Pro	Asp	Pro	Ala	Pro	Gly	Ala	Gly	Gly	Met	Val	His	755	760	765
His	Arg	His	Arg	Ser	Ser	Ser	Thr	Arg	Ser	Gly	Gly	Gly	Asp	Leu	Thr	770	775	780
Leu	Gly	Leu	Glu	Pro	Ser	Glu	Glu	Glu	Ala	Pro	Arg	Ser	Pro	Leu	Ala	785	790	795
Pro	Ser	Glu	Gly	Ala	Gly	Ser	Asp	Val	Phe	Asp	Gly	Asp	Leu	Gly	Met	805	810	815
Gly	Ala	Ala	Lys	Gly	Leu	Gln	Ser	Leu	Pro	Thr	His	Asp	Pro	Ser	Pro	820	825	830
Leu	Gln	Arg	Tyr	Ser	Glu	Asp	Pro	Thr	Val	Pro	Leu	Pro	Ser	Glu	Thr	835	840	845
Asp	Gly	Tyr	Val	Ala	Pro	Leu	Thr	Cys	Ser	Pro	Gln	Pro	Glu	Tyr	Val	850	855	860
Asn	Gln	Pro	Asp	Val	Arg	Pro	Gln	Pro	Pro	Ser	Pro	Arg	Glu	Gly	Pro	865	870	875
Leu	Pro	Ala	Ala	Arg	Pro	Ala	Gly	Ala	Thr	Leu	Glu	Arg	Pro	Lys	Thr	885	890	895
Leu	Ser	Pro	Gly	Lys	Asn	Gly	Val	Val	Lys	Asp	Val	Phe	Ala	Phe	Gly	900	905	910

ITI-08-PCT_Sequence_Listing_ST25.txt

Gly Ala Val Glu Asn Pro Glu Tyr Leu Thr Pro Gln Gly Gly Ala Ala
 915 920 925

Pro Gln Pro His Pro Pro Pro Ala Phe Ser Pro Ala Phe Asp Asn Leu
 930 935 940

Tyr Tyr Trp Asp Gln Asp Pro Pro Glu Arg Gly Ala Pro Pro Ser Thr
 945 950 955 960

Phe Lys Gly Thr Pro Thr Ala Glu Asn Pro Glu Tyr Leu Gly Leu Asp
 965 970 975

Val Pro Val

<210> 409
 <211> 87
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Her2/neu__Homo_sapiens__L8E8G2

<400> 409

Met Met Arg Met Lys Thr Phe Val Met Ile His Phe His Leu Met Asn
 1 5 10 15

Gly Gly Lys Ala Lys Leu Tyr Ser Arg Pro His Ala Lys Leu Leu Pro
 20 25 30

Glu Gln Arg Val Thr Asp Lys Thr Gly Ala Pro Val Glu Trp Pro Gly
 35 40 45

Gln Thr Gln Cys Ser Thr Glu Thr Gln Thr Leu Ala Ala Met Pro Ala
 50 55 60

Gln Ala Val Met Arg Val Thr Cys Thr Val Val Asp Met His Lys Ser
 65 70 75 80

Glu Cys Ala Pro Ala Gln Thr
 85

<210> 410
 <211> 1255
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Her2/neu__Homo_sapiens__P04626

<400> 410

ITI-08-PCT_Sequence_Listing_ST25.txt

Met	Glu	Leu	Ala	Ala	Leu	Cys	Arg	Trp	Gly	Leu	Leu	Leu	Ala	Leu	Leu		
1				5					10					15			
Pro	Pro	Gly	Ala	Ala	Ser	Thr	Gln	Val	Cys	Thr	Gly	Thr	Asp	Met	Lys		
			20					25					30				
Leu	Arg	Leu	Pro	Ala	Ser	Pro	Glu	Thr	His	Leu	Asp	Met	Leu	Arg	His		
		35					40					45					
Leu	Tyr	Gln	Gly	Cys	Gln	Val	Val	Gln	Gly	Asn	Leu	Glu	Leu	Thr	Tyr		
	50					55					60						
Leu	Pro	Thr	Asn	Ala	Ser	Leu	Ser	Phe	Leu	Gln	Asp	Ile	Gln	Glu	Val		
65					70					75					80		
Gln	Gly	Tyr	Val	Leu	Ile	Ala	His	Asn	Gln	Val	Arg	Gln	Val	Pro	Leu		
				85					90					95			
Gln	Arg	Leu	Arg	Ile	Val	Arg	Gly	Thr	Gln	Leu	Phe	Glu	Asp	Asn	Tyr		
			100					105					110				
Ala	Leu	Ala	Val	Leu	Asp	Asn	Gly	Asp	Pro	Leu	Asn	Asn	Thr	Thr	Pro		
		115					120					125					
Val	Thr	Gly	Ala	Ser	Pro	Gly	Gly	Leu	Arg	Glu	Leu	Gln	Leu	Arg	Ser		
	130					135					140						
Leu	Thr	Glu	Ile	Leu	Lys	Gly	Gly	Val	Leu	Ile	Gln	Arg	Asn	Pro	Gln		
145					150					155					160		
Leu	Cys	Tyr	Gln	Asp	Thr	Ile	Leu	Trp	Lys	Asp	Ile	Phe	His	Lys	Asn		
				165					170					175			
Asn	Gln	Leu	Ala	Leu	Thr	Leu	Ile	Asp	Thr	Asn	Arg	Ser	Arg	Ala	Cys		
			180					185					190				
His	Pro	Cys	Ser	Pro	Met	Cys	Lys	Gly	Ser	Arg	Cys	Trp	Gly	Glu	Ser		
		195					200					205					
Ser	Glu	Asp	Cys	Gln	Ser	Leu	Thr	Arg	Thr	Val	Cys	Ala	Gly	Gly	Cys		
	210					215					220						
Ala	Arg	Cys	Lys	Gly	Pro	Leu	Pro	Thr	Asp	Cys	Cys	His	Glu	Gln	Cys		
225					230					235					240		
Ala	Ala	Gly	Cys	Thr	Gly	Pro	Lys	His	Ser	Asp	Cys	Leu	Ala	Cys	Leu		
				245					250					255			
His	Phe	Asn	His	Ser	Gly	Ile	Cys	Glu	Leu	His	Cys	Pro	Ala	Leu	Val		
			260					265					270				
Thr	Tyr	Asn	Thr	Asp	Thr	Phe	Glu	Ser	Met	Pro	Asn	Pro	Glu	Gly	Arg		

ITI-08-PCT_Sequence_Listing_ST25.txt

```

275                280                285
Tyr Thr Phe Gly Ala Ser Cys Val Thr Ala Cys Pro Tyr Asn Tyr Leu
290                295                300
Ser Thr Asp Val Gly Ser Cys Thr Leu Val Cys Pro Leu His Asn Gln
305                310                315                320
Glu Val Thr Ala Glu Asp Gly Thr Gln Arg Cys Glu Lys Cys Ser Lys
325                330                335
Pro Cys Ala Arg Val Cys Tyr Gly Leu Gly Met Glu His Leu Arg Glu
340                345                350
Val Arg Ala Val Thr Ser Ala Asn Ile Gln Glu Phe Ala Gly Cys Lys
355                360                365
Lys Ile Phe Gly Ser Leu Ala Phe Leu Pro Glu Ser Phe Asp Gly Asp
370                375                380
Pro Ala Ser Asn Thr Ala Pro Leu Gln Pro Glu Gln Leu Gln Val Phe
385                390                395                400
Glu Thr Leu Glu Glu Ile Thr Gly Tyr Leu Tyr Ile Ser Ala Trp Pro
405                410                415
Asp Ser Leu Pro Asp Leu Ser Val Phe Gln Asn Leu Gln Val Ile Arg
420                425                430
Gly Arg Ile Leu His Asn Gly Ala Tyr Ser Leu Thr Leu Gln Gly Leu
435                440                445
Gly Ile Ser Trp Leu Gly Leu Arg Ser Leu Arg Glu Leu Gly Ser Gly
450                455                460
Leu Ala Leu Ile His His Asn Thr His Leu Cys Phe Val His Thr Val
465                470                475                480
Pro Trp Asp Gln Leu Phe Arg Asn Pro His Gln Ala Leu Leu His Thr
485                490                495
Ala Asn Arg Pro Glu Asp Glu Cys Val Gly Glu Gly Leu Ala Cys His
500                505                510
Gln Leu Cys Ala Arg Gly His Cys Trp Gly Pro Gly Pro Thr Gln Cys
515                520                525
Val Asn Cys Ser Gln Phe Leu Arg Gly Gln Glu Cys Val Glu Glu Cys
530                535                540
Arg Val Leu Gln Gly Leu Pro Arg Glu Tyr Val Asn Ala Arg His Cys
545                550                555                560

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Leu	Pro	Cys	His	Pro	Glu	Cys	Gln	Pro	Gln	Asn	Gly	Ser	Val	Thr	Cys	565	570	575
Phe	Gly	Pro	Glu	Ala	Asp	Gln	Cys	Val	Ala	Cys	Ala	His	Tyr	Lys	Asp	580	585	590
Pro	Pro	Phe	Cys	Val	Ala	Arg	Cys	Pro	Ser	Gly	Val	Lys	Pro	Asp	Leu	595	600	605
Ser	Tyr	Met	Pro	Ile	Trp	Lys	Phe	Pro	Asp	Glu	Glu	Gly	Ala	Cys	Gln	610	615	620
Pro	Cys	Pro	Ile	Asn	Cys	Thr	His	Ser	Cys	Val	Asp	Leu	Asp	Asp	Lys	625	630	635
Gly	Cys	Pro	Ala	Glu	Gln	Arg	Ala	Ser	Pro	Leu	Thr	Ser	Ile	Ile	Ser	645	650	655
Ala	Val	Val	Gly	Ile	Leu	Leu	Val	Val	Val	Leu	Gly	Val	Val	Phe	Gly	660	665	670
Ile	Leu	Ile	Lys	Arg	Arg	Gln	Gln	Lys	Ile	Arg	Lys	Tyr	Thr	Met	Arg	675	680	685
Arg	Leu	Leu	Gln	Glu	Thr	Glu	Leu	Val	Glu	Pro	Leu	Thr	Pro	Ser	Gly	690	695	700
Ala	Met	Pro	Asn	Gln	Ala	Gln	Met	Arg	Ile	Leu	Lys	Glu	Thr	Glu	Leu	705	710	715
Arg	Lys	Val	Lys	Val	Leu	Gly	Ser	Gly	Ala	Phe	Gly	Thr	Val	Tyr	Lys	725	730	735
Gly	Ile	Trp	Ile	Pro	Asp	Gly	Glu	Asn	Val	Lys	Ile	Pro	Val	Ala	Ile	740	745	750
Lys	Val	Leu	Arg	Glu	Asn	Thr	Ser	Pro	Lys	Ala	Asn	Lys	Glu	Ile	Leu	755	760	765
Asp	Glu	Ala	Tyr	Val	Met	Ala	Gly	Val	Gly	Ser	Pro	Tyr	Val	Ser	Arg	770	775	780
Leu	Leu	Gly	Ile	Cys	Leu	Thr	Ser	Thr	Val	Gln	Leu	Val	Thr	Gln	Leu	785	790	795
Met	Pro	Tyr	Gly	Cys	Leu	Leu	Asp	His	Val	Arg	Glu	Asn	Arg	Gly	Arg	805	810	815
Leu	Gly	Ser	Gln	Asp	Leu	Leu	Asn	Trp	Cys	Met	Gln	Ile	Ala	Lys	Gly	820	825	830

ITI-08-PCT_Sequence_Listing_ST25.txt

Met Ser Tyr Leu Glu Asp Val Arg Leu Val His Arg Asp Leu Ala Ala
835 840 845

Arg Asn Val Leu Val Lys Ser Pro Asn His Val Lys Ile Thr Asp Phe
850 855 860

Gly Leu Ala Arg Leu Leu Asp Ile Asp Glu Thr Glu Tyr His Ala Asp
865 870 875 880

Gly Gly Lys Val Pro Ile Lys Trp Met Ala Leu Glu Ser Ile Leu Arg
885 890 895

Arg Arg Phe Thr His Gln Ser Asp Val Trp Ser Tyr Gly Val Thr Val
900 905 910

Trp Glu Leu Met Thr Phe Gly Ala Lys Pro Tyr Asp Gly Ile Pro Ala
915 920 925

Arg Glu Ile Pro Asp Leu Leu Glu Lys Gly Glu Arg Leu Pro Gln Pro
930 935 940

Pro Ile Cys Thr Ile Asp Val Tyr Met Ile Met Val Lys Cys Trp Met
945 950 955 960

Ile Asp Ser Glu Cys Arg Pro Arg Phe Arg Glu Leu Val Ser Glu Phe
965 970 975

Ser Arg Met Ala Arg Asp Pro Gln Arg Phe Val Val Ile Gln Asn Glu
980 985 990

Asp Leu Gly Pro Ala Ser Pro Leu Asp Ser Thr Phe Tyr Arg Ser Leu
995 1000 1005

Leu Glu Asp Asp Asp Met Gly Asp Leu Val Asp Ala Glu Glu Tyr
1010 1015 1020

Leu Val Pro Gln Gln Gly Phe Phe Cys Pro Asp Pro Ala Pro Gly
1025 1030 1035

Ala Gly Gly Met Val His His Arg His Arg Ser Ser Ser Thr Arg
1040 1045 1050

Ser Gly Gly Gly Asp Leu Thr Leu Gly Leu Glu Pro Ser Glu Glu
1055 1060 1065

Glu Ala Pro Arg Ser Pro Leu Ala Pro Ser Glu Gly Ala Gly Ser
1070 1075 1080

Asp Val Phe Asp Gly Asp Leu Gly Met Gly Ala Ala Lys Gly Leu
1085 1090 1095

Gln Ser Leu Pro Thr His Asp Pro Ser Pro Leu Gln Arg Tyr Ser

ITI-08-PCT_Sequence_Listing_ST25.txt

1100		1105		1110
Glu Asp Pro Thr Val Pro Leu Pro Ser Glu Thr Asp Gly Tyr Val				
1115		1120		1125
Ala Pro Leu Thr Cys Ser Pro Gln Pro Glu Tyr Val Asn Gln Pro				
1130		1135		1140
Asp Val Arg Pro Gln Pro Pro Ser Pro Arg Glu Gly Pro Leu Pro				
1145		1150		1155
Ala Ala Arg Pro Ala Gly Ala Thr Leu Glu Arg Pro Lys Thr Leu				
1160		1165		1170
Ser Pro Gly Lys Asn Gly Val Val Lys Asp Val Phe Ala Phe Gly				
1175		1180		1185
Gly Ala Val Glu Asn Pro Glu Tyr Leu Thr Pro Gln Gly Gly Ala				
1190		1195		1200
Ala Pro Gln Pro His Pro Pro Pro Ala Phe Ser Pro Ala Phe Asp				
1205		1210		1215
Asn Leu Tyr Tyr Trp Asp Gln Asp Pro Pro Glu Arg Gly Ala Pro				
1220		1225		1230
Pro Ser Thr Phe Lys Gly Thr Pro Thr Ala Glu Asn Pro Glu Tyr				
1235		1240		1245
Leu Gly Leu Asp Val Pro Val				
1250		1255		

<210> 411

<211> 419

<212> PRT

<213> Artificial Sequence

<220>

<223> Her2/neu__Homo_sapiens__Q9UK79

<400> 411

Met Glu Leu Ala Ala Leu Cys Arg Trp Gly Leu Leu Leu Ala Leu Leu			
1	5	10	15
Pro Pro Gly Ala Ala Ser Thr Gln Val Cys Thr Gly Thr Asp Met Lys			
20	25	30	
Leu Arg Leu Pro Ala Ser Pro Glu Thr His Leu Asp Met Leu Arg His			
35	40	45	
Leu Tyr Gln Gly Cys Gln Val Val Gln Gly Asn Leu Glu Leu Thr Tyr			

ITI-08-PCT_Sequence_Listing_ST25.txt

50		55		60															
Leu	Pro	Thr	Asn	Ala	Ser	Leu	Ser	Phe	Leu	Gln	Asp	Ile	Gln	Glu	Val				
65					70					75					80				
Gln	Gly	Tyr	Val	Leu	Ile	Ala	His	Asn	Gln	Val	Arg	Gln	Val	Pro	Leu				
				85					90					95					
Gln	Arg	Leu	Arg	Ile	Val	Arg	Gly	Thr	Gln	Leu	Phe	Glu	Asp	Asn	Tyr				
			100					105					110						
Ala	Leu	Ala	Val	Leu	Asp	Asn	Gly	Asp	Pro	Leu	Asn	Asn	Thr	Thr	Pro				
		115					120					125							
Val	Thr	Gly	Ala	Ser	Pro	Gly	Gly	Leu	Arg	Glu	Leu	Gln	Leu	Arg	Ser				
	130					135					140								
Leu	Thr	Glu	Ile	Leu	Lys	Gly	Gly	Val	Leu	Ile	Gln	Arg	Asn	Pro	Gln				
145					150					155					160				
Leu	Cys	Tyr	Gln	Asp	Thr	Ile	Leu	Trp	Lys	Asp	Ile	Phe	His	Lys	Asn				
				165					170					175					
Asn	Gln	Leu	Ala	Leu	Thr	Leu	Ile	Asp	Thr	Asn	Arg	Ser	Arg	Ala	Cys				
			180					185					190						
His	Pro	Cys	Ser	Pro	Met	Cys	Lys	Gly	Ser	Arg	Cys	Trp	Gly	Glu	Ser				
		195					200					205							
Ser	Glu	Asp	Cys	Gln	Ser	Leu	Thr	Arg	Thr	Val	Cys	Ala	Gly	Gly	Cys				
	210					215					220								
Ala	Arg	Cys	Lys	Gly	Pro	Leu	Pro	Thr	Asp	Cys	Cys	His	Glu	Gln	Cys				
225					230					235					240				
Ala	Ala	Gly	Cys	Thr	Gly	Pro	Lys	His	Ser	Asp	Cys	Leu	Ala	Cys	Leu				
				245					250					255					
His	Phe	Asn	His	Ser	Gly	Ile	Cys	Glu	Leu	His	Cys	Pro	Ala	Leu	Val				
			260					265					270						
Thr	Tyr	Asn	Thr	Asp	Thr	Phe	Glu	Ser	Met	Pro	Asn	Pro	Glu	Gly	Arg				
		275					280					285							
Tyr	Thr	Phe	Gly	Ala	Ser	Cys	Val	Thr	Ala	Cys	Pro	Tyr	Asn	Tyr	Leu				
	290					295					300								
Ser	Thr	Asp	Val	Gly	Ser	Cys	Thr	Leu	Val	Cys	Pro	Leu	His	Asn	Gln				
305					310					315					320				
Glu	Val	Thr	Ala	Glu	Asp	Gly	Thr	Gln	Arg	Cys	Glu	Lys	Cys	Ser	Lys				
				325					330					335					

ITI-08-PCT_Sequence_Listing_ST25.txt

Pro Cys Ala Arg Gly Thr His Ser Leu Pro Pro Arg Pro Ala Ala Val
340 345 350

Pro Val Pro Leu Arg Met Gln Pro Gly Pro Ala His Pro Val Leu Ser
355 360 365

Phe Leu Arg Pro Ser Trp Asp Leu Val Ser Ala Phe Tyr Ser Leu Pro
370 375 380

Leu Ala Pro Leu Ser Pro Thr Ser Val Pro Ile Ser Pro Val Ser Val
385 390 395 400

Gly Arg Gly Pro Asp Pro Asp Ala His Val Ala Val Asp Leu Ser Arg
405 410 415

Tyr Glu Gly

<210> 412
<211> 182
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-A2/m__Homo_sapiens__Q95387

<400> 412

Gly Ser His Ser Met Arg Tyr Phe Phe Thr Ser Val Ser Arg Pro Gly
1 5 10 15

Arg Gly Glu Pro Arg Phe Ile Ala Val Gly Tyr Val Asp Asp Thr Gln
20 25 30

Phe Val Arg Phe Asp Ser Asp Ala Ala Ser Gln Arg Met Glu Pro Arg
35 40 45

Ala Pro Trp Ile Glu Gln Glu Gly Pro Glu Tyr Trp Asp Gly Glu Thr
50 55 60

Arg Lys Val Lys Ala His Ser Gln Thr His Arg Val Asp Leu Gly Thr
65 70 75 80

Leu Arg Gly Tyr Tyr Asn Gln Ser Glu Ala Gly Ser His Thr Val Gln
85 90 95

Arg Met Tyr Gly Cys Asp Val Gly Ser Asp Trp Arg Phe Leu Arg Gly
100 105 110

Tyr His Gln Tyr Ala Tyr Asp Gly Lys Asp Tyr Ile Ala Leu Lys Glu
115 120 125

ITI-08-PCT_Sequence_Listing_ST25.txt

Asp Leu Arg Ser Trp Thr Ala Ala Asp Met Ala Ala Gln Thr Thr Lys
130 135 140

His Lys Trp Glu Thr Ala His Val Ala Glu Gln Leu Arg Ala Tyr Leu
145 150 155 160

Glu Gly Thr Cys Val Glu Trp Leu Arg Arg Tyr Leu Glu Asn Gly Lys
165 170 175

Glu Thr Leu Gln Arg Thr
180

<210> 413

<211> 181

<212> PRT

<213> Artificial Sequence

<220>

<223> HLA-A2/m__Homo_sapiens__Q9MYF8

<400> 413

Ser His Ser Met Arg Tyr Phe Phe Thr Ser Val Ser Arg Pro Gly Arg
1 5 10 15

Gly Glu Pro Arg Phe Ile Ala Val Gly Tyr Val Asp Asp Thr Gln Phe
20 25 30

Val Arg Phe Asp Ser Asp Ala Ala Ser Gln Arg Met Glu Pro Arg Ala
35 40 45

Pro Trp Ile Glu Gln Glu Gly Pro Glu Tyr Trp Asp Gly Glu Thr Arg
50 55 60

Lys Val Lys Ala His Ser Gln Thr His Arg Val Asp Leu Gly Thr Leu
65 70 75 80

Arg Gly Tyr Tyr Asn Gln Ser Glu Ala Gly Ser His Thr Val Gln Arg
85 90 95

Met Tyr Gly Cys Asp Val Gly Ser Asp Trp Arg Phe Leu Arg Gly Tyr
100 105 110

His Gln Tyr Ala Tyr Asp Gly Lys Asp Tyr Ile Ala Leu Lys Glu Asp
115 120 125

Leu Arg Ser Trp Thr Ala Ala Asp Met Ala Ala Gln Thr Thr Lys His
130 135 140

Lys Trp Glu Ala Ala His Val Ala Glu Gln Leu Arg Ala Tyr Leu Glu
145 150 155 160

ITI-08-PCT_Sequence_Listing_ST25.txt

Gly Thr Cys Val Glu Trp Leu Arg Arg Tyr Leu Glu Asn Gly Lys Glu
165 170 175

Thr Leu Gln Arg Thr
180

<210> 414
<211> 234
<212> PRT
<213> Artificial Sequence

<220>
<223> homeobox_NKX3.1__Homo_sapiens__Q99801

<400> 414

Met Leu Arg Val Pro Glu Pro Arg Pro Gly Glu Ala Lys Ala Glu Gly
1 5 10 15

Ala Ala Pro Pro Thr Pro Ser Lys Pro Leu Thr Ser Phe Leu Ile Gln
20 25 30

Asp Ile Leu Arg Asp Gly Ala Gln Arg Gln Gly Gly Arg Thr Ser Ser
35 40 45

Gln Arg Gln Arg Asp Pro Glu Pro Glu Pro Glu Pro Glu Pro Glu Gly
50 55 60

Gly Arg Ser Arg Ala Gly Ala Gln Asn Asp Gln Leu Ser Thr Gly Pro
65 70 75 80

Arg Ala Ala Pro Glu Glu Ala Glu Thr Leu Ala Glu Thr Glu Pro Glu
85 90 95

Arg His Leu Gly Ser Tyr Leu Leu Asp Ser Glu Asn Thr Ser Gly Ala
100 105 110

Leu Pro Arg Leu Pro Gln Thr Pro Lys Gln Pro Gln Lys Arg Ser Arg
115 120 125

Ala Ala Phe Ser His Thr Gln Val Ile Glu Leu Glu Arg Lys Phe Ser
130 135 140

His Gln Lys Tyr Leu Ser Ala Pro Glu Arg Ala His Leu Ala Lys Asn
145 150 155 160

Leu Lys Leu Thr Glu Thr Gln Val Lys Ile Trp Phe Gln Asn Arg Arg
165 170 175

Tyr Lys Thr Lys Arg Lys Gln Leu Ser Ser Glu Leu Gly Asp Leu Glu
180 185 190

ITI-08-PCT_Sequence_Listing_ST25.txt

Lys His Ser Ser Leu Pro Ala Leu Lys Glu Glu Ala Phe Ser Arg Ala
195 200 205

Ser Leu Val Ser Val Tyr Asn Ser Tyr Pro Tyr Tyr Pro Tyr Leu Tyr
210 215 220

Cys Val Gly Ser Trp Ser Pro Ala Phe Trp
225 230

<210> 415

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> HOM-TES-85__Homo_sapiens__B2RBQ6

<400> 415

Met Ala Ser Phe Arg Lys Leu Thr Leu Ser Glu Lys Val Pro Pro Asn
1 5 10 15

His Pro Ser Arg Lys Lys Val Asn Phe Leu Asp Met Ser Leu Asp Asp
20 25 30

Ile Ile Ile Tyr Lys Glu Leu Glu Gly Thr Asn Ala Glu Glu Glu Lys
35 40 45

Asn Lys Arg Gln Asn His Ser Lys Lys Glu Ser Pro Ser Arg Gln Gln
50 55 60

Ser Lys Ala His Arg His Arg His Arg Arg Asp Tyr Ser Arg Cys Arg
65 70 75 80

Ser Asn Ser Glu Glu Gly Asn His Asp Lys Lys Pro Ser Gln Lys Pro
85 90 95

Ser Gly Phe Lys Ser Gly Gln His Pro Leu Asn Gly Gln Pro Leu Ile
100 105 110

Glu Gln Glu Lys Cys Ser Asp Asn Tyr Glu Ala Gln Ala Glu Lys Asn
115 120 125

Gln Gly Gln Ser Glu Gly Asn Gln His Gln Ser Glu Gly Asn Pro Asp
130 135 140

Lys Ser Glu Glu Ser Gln Gly Gln Pro Glu Glu Asn His His Ser Glu
145 150 155 160

Arg Ser Arg Asn His Leu Glu Arg Ser Leu Ser Gln Ser Asp Arg Ser
165 170 175

ITI-08-PCT_Sequence_Listing_ST25.txt

Gln Gly Gln Leu Lys Arg His His Pro Gln Tyr Glu Arg Ser His Gly
180 185 190

Gln Tyr Lys Arg Ser His Gly Gln Ser Glu Arg Ser His Gly His Ser
195 200 205

Glu Arg Ser His Gly His Ser Glu Arg Ser His Gly His Ser Glu Arg
210 215 220

Ser His Gly His Ser Lys Arg Ser Arg Ser Gln Gly Asp Leu Val Asp
225 230 235 240

Thr Gln Ser Asp Leu Ile Ala Thr Gln Arg Asp Leu Ile Ala Thr Gln
245 250 255

Lys Asp Leu Ile Ala Thr Gln Arg Asp Leu Ile Ala Thr Gln Arg Asp
260 265 270

Leu Ile Val Thr Gln Arg Asp Leu Val Ala Thr Glu Arg Asp Leu Ile
275 280 285

Asn Gln Ser Gly Arg Ser His Gly Gln Ser Glu Arg His Gln Arg Tyr
290 295 300

Ser Thr Gly Lys Asn Thr Ile Thr Thr
305 310

<210> 416

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> HOM-TES-85__Homo_sapiens__Q9P127

<400> 416

Met Ala Ser Phe Arg Lys Leu Thr Leu Ser Glu Lys Val Pro Pro Asn
1 5 10 15

His Pro Ser Arg Lys Lys Val Asn Phe Leu Asp Met Ser Leu Asp Asp
20 25 30

Ile Ile Ile Tyr Lys Glu Leu Glu Gly Thr Asn Ala Glu Glu Glu Lys
35 40 45

Asn Lys Arg Gln Asn His Ser Lys Lys Glu Ser Pro Ser Arg Gln Gln
50 55 60

Ser Lys Ala His Arg His Arg His Arg Arg Gly Tyr Ser Arg Cys Arg
65 70 75 80

ITI-08-PCT_Sequence_Listing_ST25.txt

Ser Asn Ser Glu Glu Gly Asn His Asp Lys Lys Pro Ser Gln Lys Pro
85 90 95

Ser Gly Phe Lys Ser Gly Gln His Pro Leu Asn Gly Gln Pro Leu Ile
100 105 110

Glu Gln Glu Lys Cys Ser Asp Asn Tyr Glu Ala Gln Ala Glu Lys Asn
115 120 125

Gln Gly Gln Ser Glu Gly Asn Gln His Gln Ser Glu Gly Asn Pro Asp
130 135 140

Lys Ser Glu Glu Ser Gln Gly Gln Pro Glu Glu Asn His His Ser Glu
145 150 155 160

Arg Ser Arg Asn His Leu Glu Arg Ser Leu Ser Gln Ser Asp Arg Ser
165 170 175

Gln Gly Gln Leu Lys Arg His His Pro Gln Tyr Glu Arg Ser His Gly
180 185 190

Gln Tyr Lys Arg Ser His Gly Gln Ser Glu Arg Ser His Gly His Ser
195 200 205

Glu Arg Ser His Gly His Ser Glu Arg Ser His Gly His Ser Glu Arg
210 215 220

Ser His Gly His Ser Lys Arg Ser Arg Ser Gln Gly Asp Leu Val Asp
225 230 235 240

Thr Gln Ser Asp Leu Ile Ala Thr Gln Arg Asp Leu Ile Ala Thr Gln
245 250 255

Lys Asp Leu Ile Ala Thr Gln Arg Asp Leu Ile Ala Thr Gln Arg Asp
260 265 270

Leu Ile Val Thr Gln Arg Asp Leu Val Ala Thr Glu Arg Asp Leu Ile
275 280 285

Asn Gln Ser Gly Arg Ser His Gly Gln Ser Glu Arg His Gln Arg Tyr
290 295 300

Ser Thr Gly Lys Asn Thr Ile Thr Thr
305 310

<210> 417

<211> 127

<212> PRT

<213> Artificial Sequence

<220>

<223> HPG1__Homo_sapiens__12543784

ITI-08-PCT_Sequence_Listing_ST25.txt

<400> 417

Met Ile Lys Lys Asn Leu Lys Lys Leu Gly Ile Glu Glu Thr Tyr Leu
1 5 10 15

Asn Ile Ile Lys Ala Ile Tyr Asp Arg Pro Thr Ala Ser Ile Gln Lys
20 25 30

Thr Glu Asn Leu Ser Thr Lys Thr Gly Thr Ser Gln Glu Tyr His Leu
35 40 45

Ser Pro Leu Trp Phe Tyr Ile Val Leu Glu Ile Leu Ala Ser Thr Ile
50 55 60

Arg Gln Glu Lys Asn Leu Lys Asp Ile His Thr Glu Lys Glu Glu Val
65 70 75 80

Lys Leu Ser Leu Phe Ala Asp Ala Met Ile Leu Tyr Leu Lys Lys Pro
85 90 95

Asn Asp Ser Thr Arg Lys Leu Leu Glu Leu Ile Lys Lys Ile His Ser
100 105 110

Ser Cys Arg Ile Lys Ile Asn Ile His Phe Ala Phe Cys Ser Gln
115 120 125

<210> 418

<211> 641

<212> PRT

<213> Artificial Sequence

<220>

<223> HS71A__Homo_sapiens__P0DMV8

<400> 418

Met Ala Lys Ala Ala Ala Ile Gly Ile Asp Leu Gly Thr Thr Tyr Ser
1 5 10 15

Cys Val Gly Val Phe Gln His Gly Lys Val Glu Ile Ile Ala Asn Asp
20 25 30

Gln Gly Asn Arg Thr Thr Pro Ser Tyr Val Ala Phe Thr Asp Thr Glu
35 40 45

Arg Leu Ile Gly Asp Ala Ala Lys Asn Gln Val Ala Leu Asn Pro Gln
50 55 60

Asn Thr Val Phe Asp Ala Lys Arg Leu Ile Gly Arg Lys Phe Gly Asp
65 70 75 80

ITI-08-PCT_Sequence_Listing_ST25.txt

Pro	Val	Val	Gln	Ser	Asp	Met	Lys	His	Trp	Pro	Phe	Gln	Val	Ile	Asn	85	90	95
Asp	Gly	Asp	Lys	Pro	Lys	Val	Gln	Val	Ser	Tyr	Lys	Gly	Glu	Thr	Lys	100	105	110
Ala	Phe	Tyr	Pro	Glu	Glu	Ile	Ser	Ser	Met	Val	Leu	Thr	Lys	Met	Lys	115	120	125
Glu	Ile	Ala	Glu	Ala	Tyr	Leu	Gly	Tyr	Pro	Val	Thr	Asn	Ala	Val	Ile	130	135	140
Thr	Val	Pro	Ala	Tyr	Phe	Asn	Asp	Ser	Gln	Arg	Gln	Ala	Thr	Lys	Asp	145	150	155
Ala	Gly	Val	Ile	Ala	Gly	Leu	Asn	Val	Leu	Arg	Ile	Ile	Asn	Glu	Pro	165	170	175
Thr	Ala	Ala	Ala	Ile	Ala	Tyr	Gly	Leu	Asp	Arg	Thr	Gly	Lys	Gly	Glu	180	185	190
Arg	Asn	Val	Leu	Ile	Phe	Asp	Leu	Gly	Gly	Gly	Thr	Phe	Asp	Val	Ser	195	200	205
Ile	Leu	Thr	Ile	Asp	Asp	Gly	Ile	Phe	Glu	Val	Lys	Ala	Thr	Ala	Gly	210	215	220
Asp	Thr	His	Leu	Gly	Gly	Glu	Asp	Phe	Asp	Asn	Arg	Leu	Val	Asn	His	225	230	235
Phe	Val	Glu	Glu	Phe	Lys	Arg	Lys	His	Lys	Lys	Asp	Ile	Ser	Gln	Asn	245	250	255
Lys	Arg	Ala	Val	Arg	Arg	Leu	Arg	Thr	Ala	Cys	Glu	Arg	Ala	Lys	Arg	260	265	270
Thr	Leu	Ser	Ser	Ser	Thr	Gln	Ala	Ser	Leu	Glu	Ile	Asp	Ser	Leu	Phe	275	280	285
Glu	Gly	Ile	Asp	Phe	Tyr	Thr	Ser	Ile	Thr	Arg	Ala	Arg	Phe	Glu	Glu	290	295	300
Leu	Cys	Ser	Asp	Leu	Phe	Arg	Ser	Thr	Leu	Glu	Pro	Val	Glu	Lys	Ala	305	310	315
Leu	Arg	Asp	Ala	Lys	Leu	Asp	Lys	Ala	Gln	Ile	His	Asp	Leu	Val	Leu	325	330	335
Val	Gly	Gly	Ser	Thr	Arg	Ile	Pro	Lys	Val	Gln	Lys	Leu	Leu	Gln	Asp	340	345	350
Phe	Phe	Asn	Gly	Arg	Asp	Leu	Asn	Lys	Ser	Ile	Asn	Pro	Asp	Glu	Ala			

ITI-08-PCT_Sequence_Listing_ST25.txt

```

355                               360                               365
Val Ala Tyr Gly Ala Ala Val Gln Ala Ala Ile Leu Met Gly Asp Lys
370                               375                               380

Ser Glu Asn Val Gln Asp Leu Leu Leu Leu Asp Val Ala Pro Leu Ser
385                               390                               395                               400

Leu Gly Leu Glu Thr Ala Gly Gly Val Met Thr Ala Leu Ile Lys Arg
405                               410                               415

Asn Ser Thr Ile Pro Thr Lys Gln Thr Gln Ile Phe Thr Thr Tyr Ser
420                               425                               430

Asp Asn Gln Pro Gly Val Leu Ile Gln Val Tyr Glu Gly Glu Arg Ala
435                               440                               445

Met Thr Lys Asp Asn Asn Leu Leu Gly Arg Phe Glu Leu Ser Gly Ile
450                               455                               460

Pro Pro Ala Pro Arg Gly Val Pro Gln Ile Glu Val Thr Phe Asp Ile
465                               470                               475                               480

Asp Ala Asn Gly Ile Leu Asn Val Thr Ala Thr Asp Lys Ser Thr Gly
485                               490                               495

Lys Ala Asn Lys Ile Thr Ile Thr Asn Asp Lys Gly Arg Leu Ser Lys
500                               505                               510

Glu Glu Ile Glu Arg Met Val Gln Glu Ala Glu Lys Tyr Lys Ala Glu
515                               520                               525

Asp Glu Val Gln Arg Glu Arg Val Ser Ala Lys Asn Ala Leu Glu Ser
530                               535                               540

Tyr Ala Phe Asn Met Lys Ser Ala Val Glu Asp Glu Gly Leu Lys Gly
545                               550                               555                               560

Lys Ile Ser Glu Ala Asp Lys Lys Lys Val Leu Asp Lys Cys Gln Glu
565                               570                               575

Val Ile Ser Trp Leu Asp Ala Asn Thr Leu Ala Glu Lys Asp Glu Phe
580                               585                               590

Glu His Lys Arg Lys Glu Leu Glu Gln Val Cys Asn Pro Ile Ile Ser
595                               600                               605

Gly Leu Tyr Gln Gly Ala Gly Gly Pro Gly Pro Gly Gly Phe Gly Ala
610                               615                               620

Gln Gly Pro Lys Gly Gly Ser Gly Ser Gly Pro Thr Ile Glu Glu Val
625                               630                               635                               640

```


ITI-08-PCT_Sequence_Listing_ST25.txt

Asp

<210> 419

<211> 641

<212> PRT

<213> Artificial Sequence

<220>

<223> HS71B__Homo_sapiens__P0DMV9

<400> 419

Met Ala Lys Ala Ala Ala Ile Gly Ile Asp Leu Gly Thr Thr Tyr Ser
1 5 10 15

Cys Val Gly Val Phe Gln His Gly Lys Val Glu Ile Ile Ala Asn Asp
20 25 30

Gln Gly Asn Arg Thr Thr Pro Ser Tyr Val Ala Phe Thr Asp Thr Glu
35 40 45

Arg Leu Ile Gly Asp Ala Ala Lys Asn Gln Val Ala Leu Asn Pro Gln
50 55 60

Asn Thr Val Phe Asp Ala Lys Arg Leu Ile Gly Arg Lys Phe Gly Asp
65 70 75 80

Pro Val Val Gln Ser Asp Met Lys His Trp Pro Phe Gln Val Ile Asn
85 90 95

Asp Gly Asp Lys Pro Lys Val Gln Val Ser Tyr Lys Gly Glu Thr Lys
100 105 110

Ala Phe Tyr Pro Glu Glu Ile Ser Ser Met Val Leu Thr Lys Met Lys
115 120 125

Glu Ile Ala Glu Ala Tyr Leu Gly Tyr Pro Val Thr Asn Ala Val Ile
130 135 140

Thr Val Pro Ala Tyr Phe Asn Asp Ser Gln Arg Gln Ala Thr Lys Asp
145 150 155 160

Ala Gly Val Ile Ala Gly Leu Asn Val Leu Arg Ile Ile Asn Glu Pro
165 170 175

Thr Ala Ala Ala Ile Ala Tyr Gly Leu Asp Arg Thr Gly Lys Gly Glu
180 185 190

Arg Asn Val Leu Ile Phe Asp Leu Gly Gly Gly Thr Phe Asp Val Ser
195 200 205

ITI-08-PCT_Sequence_Listing_ST25.txt

```

Ile Leu Thr Ile Asp Asp Gly Ile Phe Glu Val Lys Ala Thr Ala Gly
 210                215                220

Asp Thr His Leu Gly Gly Glu Asp Phe Asp Asn Arg Leu Val Asn His
225                230                235                240

Phe Val Glu Glu Phe Lys Arg Lys His Lys Lys Asp Ile Ser Gln Asn
                245                250                255

Lys Arg Ala Val Arg Arg Leu Arg Thr Ala Cys Glu Arg Ala Lys Arg
                260                265                270

Thr Leu Ser Ser Ser Thr Gln Ala Ser Leu Glu Ile Asp Ser Leu Phe
 275                280                285

Glu Gly Ile Asp Phe Tyr Thr Ser Ile Thr Arg Ala Arg Phe Glu Glu
 290                295                300

Leu Cys Ser Asp Leu Phe Arg Ser Thr Leu Glu Pro Val Glu Lys Ala
305                310                315                320

Leu Arg Asp Ala Lys Leu Asp Lys Ala Gln Ile His Asp Leu Val Leu
                325                330                335

Val Gly Gly Ser Thr Arg Ile Pro Lys Val Gln Lys Leu Leu Gln Asp
 340                345                350

Phe Phe Asn Gly Arg Asp Leu Asn Lys Ser Ile Asn Pro Asp Glu Ala
 355                360                365

Val Ala Tyr Gly Ala Ala Val Gln Ala Ala Ile Leu Met Gly Asp Lys
 370                375                380

Ser Glu Asn Val Gln Asp Leu Leu Leu Leu Asp Val Ala Pro Leu Ser
385                390                395                400

Leu Gly Leu Glu Thr Ala Gly Gly Val Met Thr Ala Leu Ile Lys Arg
                405                410                415

Asn Ser Thr Ile Pro Thr Lys Gln Thr Gln Ile Phe Thr Thr Tyr Ser
 420                425                430

Asp Asn Gln Pro Gly Val Leu Ile Gln Val Tyr Glu Gly Glu Arg Ala
 435                440                445

Met Thr Lys Asp Asn Asn Leu Leu Gly Arg Phe Glu Leu Ser Gly Ile
 450                455                460

Pro Pro Ala Pro Arg Gly Val Pro Gln Ile Glu Val Thr Phe Asp Ile
465                470                475                480

Asp Ala Asn Gly Ile Leu Asn Val Thr Ala Thr Asp Lys Ser Thr Gly

```

ITI-08-PCT_Sequence_Listing_ST25.txt

485 490 495

Lys Ala Asn Lys Ile Thr Ile Thr Asn Asp Lys Gly Arg Leu Ser Lys
500 505 510

Glu Glu Ile Glu Arg Met Val Gln Glu Ala Glu Lys Tyr Lys Ala Glu
515 520 525

Asp Glu Val Gln Arg Glu Arg Val Ser Ala Lys Asn Ala Leu Glu Ser
530 535 540

Tyr Ala Phe Asn Met Lys Ser Ala Val Glu Asp Glu Gly Leu Lys Gly
545 550 555 560

Lys Ile Ser Glu Ala Asp Lys Lys Lys Val Leu Asp Lys Cys Gln Glu
565 570 575

Val Ile Ser Trp Leu Asp Ala Asn Thr Leu Ala Glu Lys Asp Glu Phe
580 585 590

Glu His Lys Arg Lys Glu Leu Glu Gln Val Cys Asn Pro Ile Ile Ser
595 600 605

Gly Leu Tyr Gln Gly Ala Gly Gly Pro Gly Pro Gly Gly Phe Gly Ala
610 615 620

Gln Gly Pro Lys Gly Gly Ser Gly Ser Gly Pro Thr Ile Glu Glu Val
625 630 635 640

Asp

<210> 420

<211> 208

<212> PRT

<213> Artificial Sequence

<220>

<223> HST-2__Homo_sapiens__P10767

<400> 420

Met Ala Leu Gly Gln Lys Leu Phe Ile Thr Met Ser Arg Gly Ala Gly
1 5 10 15

Arg Leu Gln Gly Thr Leu Trp Ala Leu Val Phe Leu Gly Ile Leu Val
20 25 30

Gly Met Val Val Pro Ser Pro Ala Gly Thr Arg Ala Asn Asn Thr Leu
35 40 45

Leu Asp Ser Arg Gly Trp Gly Thr Leu Leu Ser Arg Ser Arg Ala Gly
50 55 60

ITI-08-PCT_Sequence_Listing_ST25.txt

Leu Ala Gly Glu Ile Ala Gly Val Asn Trp Glu Ser Gly Tyr Leu Val
65 70 75 80

Gly Ile Lys Arg Gln Arg Arg Leu Tyr Cys Asn Val Gly Ile Gly Phe
85 90 95

His Leu Gln Val Leu Pro Asp Gly Arg Ile Ser Gly Thr His Glu Glu
100 105 110

Asn Pro Tyr Ser Leu Leu Glu Ile Ser Thr Val Glu Arg Gly Val Val
115 120 125

Ser Leu Phe Gly Val Arg Ser Ala Leu Phe Val Ala Met Asn Ser Lys
130 135 140

Gly Arg Leu Tyr Ala Thr Pro Ser Phe Gln Glu Glu Cys Lys Phe Arg
145 150 155 160

Glu Thr Leu Leu Pro Asn Asn Tyr Asn Ala Tyr Glu Ser Asp Leu Tyr
165 170 175

Gln Gly Thr Tyr Ile Ala Leu Ser Lys Tyr Gly Arg Val Lys Arg Gly
180 185 190

Ser Lys Val Ser Pro Ile Met Thr Val Thr His Phe Leu Pro Arg Ile
195 200 205

<210> 421

<211> 523

<212> PRT

<213> Artificial Sequence

<220>

<223> hTERT__Homo_sapiens__094807

<400> 421

Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
1 5 10 15

His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
20 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu
65 70 75 80

ITI-08-PCT_Sequence_Listing_ST25.txt

Val	Ala	Arg	Val	Leu	Gln	Arg	Leu	Cys	Glu	Arg	Gly	Ala	Lys	Asn	Val	85	90	95
Leu	Ala	Phe	Gly	Phe	Ala	Leu	Leu	Asp	Gly	Ala	Arg	Gly	Gly	Pro	Pro	100	105	110
Glu	Ala	Phe	Thr	Thr	Ser	Val	Arg	Ser	Tyr	Leu	Pro	Asn	Thr	Val	Thr	115	120	125
Asp	Ala	Leu	Arg	Gly	Ser	Gly	Ala	Trp	Gly	Leu	Leu	Leu	Arg	Arg	Val	130	135	140
Gly	Asp	Asp	Val	Leu	Val	His	Leu	Leu	Ala	Arg	Cys	Ala	Leu	Phe	Val	145	150	155
Leu	Val	Ala	Pro	Ser	Cys	Ala	Tyr	Gln	Val	Cys	Gly	Pro	Pro	Leu	Tyr	165	170	175
Gln	Leu	Gly	Ala	Ala	Thr	Gln	Ala	Arg	Pro	Pro	Pro	His	Ala	Ser	Gly	180	185	190
Pro	Arg	Arg	Arg	Leu	Gly	Cys	Glu	Arg	Ala	Trp	Asn	His	Ser	Val	Arg	195	200	205
Glu	Ala	Gly	Val	Pro	Leu	Gly	Leu	Pro	Ala	Pro	Gly	Ala	Arg	Arg	Arg	210	215	220
Gly	Gly	Ser	Ala	Ser	Arg	Ser	Leu	Pro	Leu	Pro	Lys	Arg	Pro	Arg	Arg	225	230	235
Gly	Ala	Ala	Pro	Glu	Pro	Glu	Arg	Thr	Pro	Val	Gly	Gln	Gly	Ser	Trp	245	250	255
Ala	His	Pro	Gly	Arg	Thr	Arg	Gly	Pro	Ser	Asp	Arg	Gly	Phe	Cys	Val	260	265	270
Val	Ser	Pro	Ala	Arg	Pro	Ala	Glu	Glu	Ala	Thr	Ser	Leu	Glu	Gly	Ala	275	280	285
Leu	Ser	Gly	Thr	Arg	His	Ser	His	Pro	Ser	Val	Gly	Arg	Gln	His	His	290	295	300
Ala	Gly	Pro	Pro	Ser	Thr	Ser	Arg	Pro	Pro	Arg	Pro	Trp	Asp	Thr	Pro	305	310	315
Cys	Pro	Pro	Val	Tyr	Ala	Glu	Thr	Lys	His	Phe	Leu	Tyr	Ser	Ser	Gly	325	330	335
Asp	Lys	Glu	Gln	Leu	Arg	Pro	Ser	Phe	Leu	Leu	Ser	Ser	Leu	Arg	Pro	340	345	350

ITI-08-PCT_Sequence_Listing_ST25.txt

Ile Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser
355 360 365

Ser Pro Gly Cys Gln Gly Leu Pro Ala Gly Cys Pro Ala Cys Pro Ser
370 375 380

Ala Thr Gly Lys Cys Gly Pro Cys Phe Trp Ser Cys Leu Gly Thr Thr
385 390 395 400

Arg Ser Ala Pro Thr Gly Cys Ser Ser Arg Arg Thr Ala Arg Cys Glu
405 410 415

Leu Arg Ser Pro Gln Gln Pro Val Ser Val Pro Gly Arg Ser Pro Arg
420 425 430

Ala Leu Trp Arg Pro Pro Arg Arg Arg Thr Gln Thr Pro Val Ala Trp
435 440 445

Cys Ser Cys Ser Ala Ser Thr Ala Pro Leu Ala Gly Val Arg Leu Arg
450 455 460

Ala Gly Leu Pro Ala Pro Ala Gly Ala Pro Arg Pro Leu Gly Leu Gln
465 470 475 480

Ala Gln Arg Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu
485 490 495

Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser
500 505 510

Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro
515 520

<210> 422
<211> 559
<212> PRT
<213> Artificial Sequence

<220>
<223> iCE__Homo_sapiens__000748

<400> 422

Met Arg Leu His Arg Leu Arg Ala Arg Leu Ser Ala Val Ala Cys Gly
1 5 10 15

Leu Leu Leu Leu Leu Val Arg Gly Gln Gly Gln Asp Ser Ala Ser Pro
20 25 30

Ile Arg Thr Thr His Thr Gly Gln Val Leu Gly Ser Leu Val His Val
35 40 45

ITI-08-PCT_Sequence_Listing_ST25.txt

Lys Gly Ala Asn Ala Gly Val Gln Thr Phe Leu Gly Ile Pro Phe Ala
 50 55 60
 Lys Pro Pro Leu Gly Pro Leu Arg Phe Ala Pro Pro Glu Pro Pro Glu
 65 70 75 80
 Ser Trp Ser Gly Val Arg Asp Gly Thr Thr His Pro Ala Met Cys Leu
 85 90 95
 Gln Asp Leu Thr Ala Val Glu Ser Glu Phe Leu Ser Gln Phe Asn Met
 100 105 110
 Thr Phe Pro Ser Asp Ser Met Ser Glu Asp Cys Leu Tyr Leu Ser Ile
 115 120 125
 Tyr Thr Pro Ala His Ser His Glu Gly Ser Asn Leu Pro Val Met Val
 130 135 140
 Trp Ile His Gly Gly Ala Leu Val Phe Gly Met Ala Ser Leu Tyr Asp
 145 150 155 160
 Gly Ser Met Leu Ala Ala Leu Glu Asn Val Val Val Val Ile Ile Gln
 165 170 175
 Tyr Arg Leu Gly Val Leu Gly Phe Phe Ser Thr Gly Asp Lys His Ala
 180 185 190
 Thr Gly Asn Trp Gly Tyr Leu Asp Gln Val Ala Ala Leu Arg Trp Val
 195 200 205
 Gln Gln Asn Ile Ala His Phe Gly Gly Asn Pro Asp Arg Val Thr Ile
 210 215 220
 Phe Gly Glu Ser Ala Gly Gly Thr Ser Val Ser Ser Leu Val Val Ser
 225 230 235 240
 Pro Ile Ser Gln Gly Leu Phe His Gly Ala Ile Met Glu Ser Gly Val
 245 250 255
 Ala Leu Leu Pro Gly Leu Ile Ala Ser Ser Ala Asp Val Ile Ser Thr
 260 265 270
 Val Val Ala Asn Leu Ser Ala Cys Asp Gln Val Asp Ser Glu Ala Leu
 275 280 285
 Val Gly Cys Leu Arg Gly Lys Ser Lys Glu Glu Ile Leu Ala Ile Asn
 290 295 300
 Lys Pro Phe Lys Met Ile Pro Gly Val Val Asp Gly Val Phe Leu Pro
 305 310 315 320
 Arg His Pro Gln Glu Leu Leu Ala Ser Ala Asp Phe Gln Pro Val Pro

ITI-08-PCT_Sequence_Listing_ST25.txt

325 330 335

Ser Ile Val Gly Val Asn Asn Asn Glu Phe Gly Trp Leu Ile Pro Lys
340 345 350

Val Met Arg Ile Tyr Asp Thr Gln Lys Glu Met Asp Arg Glu Ala Ser
355 360 365

Gln Ala Ala Leu Gln Lys Met Leu Thr Leu Leu Met Leu Pro Pro Thr
370 375 380

Phe Gly Asp Leu Leu Arg Glu Glu Tyr Ile Gly Asp Asn Gly Asp Pro
385 390 395 400

Gln Thr Leu Gln Ala Gln Phe Gln Glu Met Met Ala Asp Ser Met Phe
405 410 415

Val Ile Pro Ala Leu Gln Val Ala His Phe Gln Cys Ser Arg Ala Pro
420 425 430

Val Tyr Phe Tyr Glu Phe Gln His Gln Pro Ser Trp Leu Lys Asn Ile
435 440 445

Arg Pro Pro His Met Lys Ala Asp His Gly Asp Glu Leu Pro Phe Val
450 455 460

Phe Arg Ser Phe Phe Gly Gly Asn Tyr Ile Lys Phe Thr Glu Glu Glu
465 470 475 480

Glu Gln Leu Ser Arg Lys Met Met Lys Tyr Trp Ala Asn Phe Ala Arg
485 490 495

Asn Gly Asn Pro Asn Gly Glu Gly Leu Pro His Trp Pro Leu Phe Asp
500 505 510

Gln Glu Glu Gln Tyr Leu Gln Leu Asn Leu Gln Pro Ala Val Gly Arg
515 520 525

Ala Leu Lys Ala His Arg Leu Gln Phe Trp Lys Lys Ala Leu Pro Gln
530 535 540

Lys Ile Gln Glu Leu Glu Glu Pro Glu Glu Arg His Thr Glu Leu
545 550 555

<210> 423

<211> 579

<212> PRT

<213> Artificial Sequence

<220>

<223> IF2B3__Homo_sapiens__000425

ITI-08-PCT_Sequence_Listing_ST25.txt

<400> 423

```

Met Asn Lys Leu Tyr Ile Gly Asn Leu Ser Glu Asn Ala Ala Pro Ser
1      5      10      15

Asp Leu Glu Ser Ile Phe Lys Asp Ala Lys Ile Pro Val Ser Gly Pro
      20      25      30

Phe Leu Val Lys Thr Gly Tyr Ala Phe Val Asp Cys Pro Asp Glu Ser
      35      40      45

Trp Ala Leu Lys Ala Ile Glu Ala Leu Ser Gly Lys Ile Glu Leu His
      50      55      60

Gly Lys Pro Ile Glu Val Glu His Ser Val Pro Lys Arg Gln Arg Ile
65      70      75      80

Arg Lys Leu Gln Ile Arg Asn Ile Pro Pro His Leu Gln Trp Glu Val
      85      90      95

Leu Asp Ser Leu Leu Val Gln Tyr Gly Val Val Glu Ser Cys Glu Gln
      100      105      110

Val Asn Thr Asp Ser Glu Thr Ala Val Val Asn Val Thr Tyr Ser Ser
      115      120      125

Lys Asp Gln Ala Arg Gln Ala Leu Asp Lys Leu Asn Gly Phe Gln Leu
      130      135      140

Glu Asn Phe Thr Leu Lys Val Ala Tyr Ile Pro Asp Glu Met Ala Ala
145      150      155      160

Gln Gln Asn Pro Leu Gln Gln Pro Arg Gly Arg Arg Gly Leu Gly Gln
      165      170      175

Arg Gly Ser Ser Arg Gln Gly Ser Pro Gly Ser Val Ser Lys Gln Lys
      180      185      190

Pro Cys Asp Leu Pro Leu Arg Leu Leu Val Pro Thr Gln Phe Val Gly
      195      200      205

Ala Ile Ile Gly Lys Glu Gly Ala Thr Ile Arg Asn Ile Thr Lys Gln
      210      215      220

Thr Gln Ser Lys Ile Asp Val His Arg Lys Glu Asn Ala Gly Ala Ala
225      230      235      240

Glu Lys Ser Ile Thr Ile Leu Ser Thr Pro Glu Gly Thr Ser Ala Ala
      245      250      255

Cys Lys Ser Ile Leu Glu Ile Met His Lys Glu Ala Gln Asp Ile Lys
      260      265      270

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Phe	Thr	Glu	Glu	Ile	Pro	Leu	Lys	Ile	Leu	Ala	His	Asn	Asn	Phe	Val	275	280	285
Gly	Arg	Leu	Ile	Gly	Lys	Glu	Gly	Arg	Asn	Leu	Lys	Lys	Ile	Glu	Gln	290	295	300
Asp	Thr	Asp	Thr	Lys	Ile	Thr	Ile	Ser	Pro	Leu	Gln	Glu	Leu	Thr	Leu	305	310	315
Tyr	Asn	Pro	Glu	Arg	Thr	Ile	Thr	Val	Lys	Gly	Asn	Val	Glu	Thr	Cys	325	330	335
Ala	Lys	Ala	Glu	Glu	Glu	Ile	Met	Lys	Lys	Ile	Arg	Glu	Ser	Tyr	Glu	340	345	350
Asn	Asp	Ile	Ala	Ser	Met	Asn	Leu	Gln	Ala	His	Leu	Ile	Pro	Gly	Leu	355	360	365
Asn	Leu	Asn	Ala	Leu	Gly	Leu	Phe	Pro	Pro	Thr	Ser	Gly	Met	Pro	Pro	370	375	380
Pro	Thr	Ser	Gly	Pro	Pro	Ser	Ala	Met	Thr	Pro	Pro	Tyr	Pro	Gln	Phe	385	390	395
Glu	Gln	Ser	Glu	Thr	Glu	Thr	Val	His	Leu	Phe	Ile	Pro	Ala	Leu	Ser	405	410	415
Val	Gly	Ala	Ile	Ile	Gly	Lys	Gln	Gly	Gln	His	Ile	Lys	Gln	Leu	Ser	420	425	430
Arg	Phe	Ala	Gly	Ala	Ser	Ile	Lys	Ile	Ala	Pro	Ala	Glu	Ala	Pro	Asp	435	440	445
Ala	Lys	Val	Arg	Met	Val	Ile	Ile	Thr	Gly	Pro	Pro	Glu	Ala	Gln	Phe	450	455	460
Lys	Ala	Gln	Gly	Arg	Ile	Tyr	Gly	Lys	Ile	Lys	Glu	Glu	Asn	Phe	Val	465	470	475
Ser	Pro	Lys	Glu	Glu	Val	Lys	Leu	Glu	Ala	His	Ile	Arg	Val	Pro	Ser	485	490	495
Phe	Ala	Ala	Gly	Arg	Val	Ile	Gly	Lys	Gly	Gly	Lys	Thr	Val	Asn	Glu	500	505	510
Leu	Gln	Asn	Leu	Ser	Ser	Ala	Glu	Val	Val	Val	Pro	Arg	Asp	Gln	Thr	515	520	525
Pro	Asp	Glu	Asn	Asp	Gln	Val	Val	Val	Lys	Ile	Thr	Gly	His	Phe	Tyr	530	535	540

ITI-08-PCT_Sequence_Listing_ST25.txt

Ala Cys Gln Val Ala Gln Arg Lys Ile Gln Glu Ile Leu Thr Gln Val
545 550 555 560

Lys Gln His Gln Gln Gln Lys Ala Leu Gln Ser Gly Pro Pro Gln Ser
565 570 575

Arg Arg Lys

<210> 424

<211> 380

<212> PRT

<213> Artificial Sequence

<220>

<223> IL-13Ra2__Homo_sapiens__Q14627

<400> 424

Met Ala Phe Val Cys Leu Ala Ile Gly Cys Leu Tyr Thr Phe Leu Ile
1 5 10 15

Ser Thr Thr Phe Gly Cys Thr Ser Ser Ser Asp Thr Glu Ile Lys Val
20 25 30

Asn Pro Pro Gln Asp Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr
35 40 45

Leu Tyr Leu Gln Trp Gln Pro Pro Leu Ser Leu Asp His Phe Lys Glu
50 55 60

Cys Thr Val Glu Tyr Glu Leu Lys Tyr Arg Asn Ile Gly Ser Glu Thr
65 70 75 80

Trp Lys Thr Ile Ile Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp
85 90 95

Leu Asn Lys Gly Ile Glu Ala Lys Ile His Thr Leu Leu Pro Trp Gln
100 105 110

Cys Thr Asn Gly Ser Glu Val Gln Ser Ser Trp Ala Glu Thr Thr Tyr
115 120 125

Trp Ile Ser Pro Gln Gly Ile Pro Glu Thr Lys Val Gln Asp Met Asp
130 135 140

Cys Val Tyr Tyr Asn Trp Gln Tyr Leu Leu Cys Ser Trp Lys Pro Gly
145 150 155 160

Ile Gly Val Leu Leu Asp Thr Asn Tyr Asn Leu Phe Tyr Trp Tyr Glu
165 170 175

Gly Leu Asp His Ala Leu Gln Cys Val Asp Tyr Ile Lys Ala Asp Gly

ITI-08-PCT_Sequence_Listing_ST25.txt

180

185

190

Gln Asn Ile Gly Cys Arg Phe Pro Tyr Leu Glu Ala Ser Asp Tyr Lys
195 200 205

Asp Phe Tyr Ile Cys Val Asn Gly Ser Ser Glu Asn Lys Pro Ile Arg
210 215 220

Ser Ser Tyr Phe Thr Phe Gln Leu Gln Asn Ile Val Lys Pro Leu Pro
225 230 235 240

Pro Val Tyr Leu Thr Phe Thr Arg Glu Ser Ser Cys Glu Ile Lys Leu
245 250 255

Lys Trp Ser Ile Pro Leu Gly Pro Ile Pro Ala Arg Cys Phe Asp Tyr
260 265 270

Glu Ile Glu Ile Arg Glu Asp Asp Thr Thr Leu Val Thr Ala Thr Val
275 280 285

Glu Asn Glu Thr Tyr Thr Leu Lys Thr Thr Asn Glu Thr Arg Gln Leu
290 295 300

Cys Phe Val Val Arg Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly
305 310 315 320

Ile Trp Ser Glu Trp Ser Asp Lys Gln Cys Trp Glu Gly Glu Asp Leu
325 330 335

Ser Lys Lys Thr Leu Leu Arg Phe Trp Leu Pro Phe Gly Phe Ile Leu
340 345 350

Ile Leu Val Ile Phe Val Thr Gly Leu Leu Leu Arg Lys Pro Asn Thr
355 360 365

Tyr Pro Lys Met Ile Pro Glu Phe Phe Cys Asp Thr
370 375 380

<210> 425

<211> 272

<212> PRT

<213> Artificial Sequence

<220>

<223> IL2-RA__Homo_sapiens__P01589

<400> 425

Met Asp Ser Tyr Leu Leu Met Trp Gly Leu Leu Thr Phe Ile Met Val
1 5 10 15

Pro Gly Cys Gln Ala Glu Leu Cys Asp Asp Asp Pro Pro Glu Ile Pro

20 25 30

Ser Gly Leu Thr Trp Gln Arg Arg Gln Arg Lys Ser Arg Arg Thr Ile
260 265 270

<210>	426
<211>	551
<212>	PRT
<213>	Artificial Sequence

ITI-08-PCT_Sequence_Listing_ST25.txt

<220>

<223> IL2-RB__Homo_sapiens__P14784

<400> 426

```

Met Ala Ala Pro Ala Leu Ser Trp Arg Leu Pro Leu Leu Ile Leu Leu
1          5          10          15

Leu Pro Leu Ala Thr Ser Trp Ala Ser Ala Ala Val Asn Gly Thr Ser
          20          25          30

Gln Phe Thr Cys Phe Tyr Asn Ser Arg Ala Asn Ile Ser Cys Val Trp
          35          40          45

Ser Gln Asp Gly Ala Leu Gln Asp Thr Ser Cys Gln Val His Ala Trp
          50          55          60

Pro Asp Arg Arg Arg Trp Asn Gln Thr Cys Glu Leu Leu Pro Val Ser
65          70          75          80

Gln Ala Ser Trp Ala Cys Asn Leu Ile Leu Gly Ala Pro Asp Ser Gln
          85          90          95

Lys Leu Thr Thr Val Asp Ile Val Thr Leu Arg Val Leu Cys Arg Glu
          100          105          110

Gly Val Arg Trp Arg Val Met Ala Ile Gln Asp Phe Lys Pro Phe Glu
          115          120          125

Asn Leu Arg Leu Met Ala Pro Ile Ser Leu Gln Val Val His Val Glu
          130          135          140

Thr His Arg Cys Asn Ile Ser Trp Glu Ile Ser Gln Ala Ser His Tyr
145          150          155          160

Phe Glu Arg His Leu Glu Phe Glu Ala Arg Thr Leu Ser Pro Gly His
          165          170          175

Thr Trp Glu Glu Ala Pro Leu Leu Thr Leu Lys Gln Lys Gln Glu Trp
          180          185          190

Ile Cys Leu Glu Thr Leu Thr Pro Asp Thr Gln Tyr Glu Phe Gln Val
          195          200          205

Arg Val Lys Pro Leu Gln Gly Glu Phe Thr Thr Trp Ser Pro Trp Ser
          210          215          220

Gln Pro Leu Ala Phe Arg Thr Lys Pro Ala Ala Leu Gly Lys Asp Thr
225          230          235          240

Ile Pro Trp Leu Gly His Leu Leu Val Gly Leu Ser Gly Ala Phe Gly
          245          250          255

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Phe	Ile	Ile	Leu	Val	Tyr	Leu	Leu	Ile	Asn	Cys	Arg	Asn	Thr	Gly	Pro	
			260					265					270			
Trp	Leu	Lys	Lys	Val	Leu	Lys	Cys	Asn	Thr	Pro	Asp	Pro	Ser	Lys	Phe	
		275					280					285				
Phe	Ser	Gln	Leu	Ser	Ser	Glu	His	Gly	Gly	Asp	Val	Gln	Lys	Trp	Leu	
	290					295					300					
Ser	Ser	Pro	Phe	Pro	Ser	Ser	Ser	Phe	Ser	Pro	Gly	Gly	Leu	Ala	Pro	
305					310					315					320	
Glu	Ile	Ser	Pro	Leu	Glu	Val	Leu	Glu	Arg	Asp	Lys	Val	Thr	Gln	Leu	
			325						330					335		
Leu	Leu	Gln	Gln	Asp	Lys	Val	Pro	Glu	Pro	Ala	Ser	Leu	Ser	Ser	Asn	
			340					345					350			
His	Ser	Leu	Thr	Ser	Cys	Phe	Thr	Asn	Gln	Gly	Tyr	Phe	Phe	Phe	His	
		355					360					365				
Leu	Pro	Asp	Ala	Leu	Glu	Ile	Glu	Ala	Cys	Gln	Val	Tyr	Phe	Thr	Tyr	
	370					375					380					
Asp	Pro	Tyr	Ser	Glu	Glu	Asp	Pro	Asp	Glu	Gly	Val	Ala	Gly	Ala	Pro	
385					390					395					400	
Thr	Gly	Ser	Ser	Pro	Gln	Pro	Leu	Gln	Pro	Leu	Ser	Gly	Glu	Asp	Asp	
				405				410						415		
Ala	Tyr	Cys	Thr	Phe	Pro	Ser	Arg	Asp	Asp	Leu	Leu	Leu	Phe	Ser	Pro	
			420					425					430			
Ser	Leu	Leu	Gly	Gly	Pro	Ser	Pro	Pro	Ser	Thr	Ala	Pro	Gly	Gly	Ser	
		435					440					445				
Gly	Ala	Gly	Glu	Glu	Arg	Met	Pro	Pro	Ser	Leu	Gln	Glu	Arg	Val	Pro	
	450					455					460					
Arg	Asp	Trp	Asp	Pro	Gln	Pro	Leu	Gly	Pro	Pro	Thr	Pro	Gly	Val	Pro	
465					470				475						480	
Asp	Leu	Val	Asp	Phe	Gln	Pro	Pro	Pro	Glu	Leu	Val	Leu	Arg	Glu	Ala	
				485					490					495		
Gly	Glu	Glu	Val	Pro	Asp	Ala	Gly	Pro	Arg	Glu	Gly	Val	Ser	Phe	Pro	
			500					505					510			
Trp	Ser	Arg	Pro	Pro	Gly	Gln	Gly	Glu	Phe	Arg	Ala	Leu	Asn	Ala	Arg	
		515				520						525				

ITI-08-PCT_Sequence_Listing_ST25.txt

Leu Pro Leu Asn Thr Asp Ala Tyr Leu Ser Leu Gln Glu Leu Gln Gly
530 535 540

Gln Asp Pro Thr His Leu Val
545 550

<210> 427
<211> 369
<212> PRT
<213> Artificial Sequence

<220>
<223> IL2-RG__Homo_sapiens__P31785

<400> 427

Met Leu Lys Pro Ser Leu Pro Phe Thr Ser Leu Leu Phe Leu Gln Leu
1 5 10 15

Pro Leu Leu Gly Val Gly Leu Asn Thr Thr Ile Leu Thr Pro Asn Gly
20 25 30

Asn Glu Asp Thr Thr Ala Asp Phe Phe Leu Thr Thr Met Pro Thr Asp
35 40 45

Ser Leu Ser Val Ser Thr Leu Pro Leu Pro Glu Val Gln Cys Phe Val
50 55 60

Phe Asn Val Glu Tyr Met Asn Cys Thr Trp Asn Ser Ser Ser Glu Pro
65 70 75 80

Gln Pro Thr Asn Leu Thr Leu His Tyr Trp Tyr Lys Asn Ser Asp Asn
85 90 95

Asp Lys Val Gln Lys Cys Ser His Tyr Leu Phe Ser Glu Glu Ile Thr
100 105 110

Ser Gly Cys Gln Leu Gln Lys Lys Glu Ile His Leu Tyr Gln Thr Phe
115 120 125

Val Val Gln Leu Gln Asp Pro Arg Glu Pro Arg Arg Gln Ala Thr Gln
130 135 140

Met Leu Lys Leu Gln Asn Leu Val Ile Pro Trp Ala Pro Glu Asn Leu
145 150 155 160

Thr Leu His Lys Leu Ser Glu Ser Gln Leu Glu Leu Asn Trp Asn Asn
165 170 175

Arg Phe Leu Asn His Cys Leu Glu His Leu Val Gln Tyr Arg Thr Asp
180 185 190

ITI-08-PCT_Sequence_Listing_ST25.txt

Trp Asp His Ser Trp Thr Glu Gln Ser Val Asp Tyr Arg His Lys Phe
195 200 205

Ser Leu Pro Ser Val Asp Gly Gln Lys Arg Tyr Thr Phe Arg Val Arg
210 215 220

Ser Arg Phe Asn Pro Leu Cys Gly Ser Ala Gln His Trp Ser Glu Trp
225 230 235 240

Ser His Pro Ile His Trp Gly Ser Asn Thr Ser Lys Glu Asn Pro Phe
245 250 255

Leu Phe Ala Leu Glu Ala Val Val Ile Ser Val Gly Ser Met Gly Leu
260 265 270

Ile Ile Ser Leu Leu Cys Val Tyr Phe Trp Leu Glu Arg Thr Met Pro
275 280 285

Arg Ile Pro Thr Leu Lys Asn Leu Glu Asp Leu Val Thr Glu Tyr His
290 295 300

Gly Asn Phe Ser Ala Trp Ser Gly Val Ser Lys Gly Leu Ala Glu Ser
305 310 315 320

Leu Gln Pro Asp Tyr Ser Glu Arg Leu Cys Leu Val Ser Glu Ile Pro
325 330 335

Pro Lys Gly Gly Ala Leu Gly Glu Gly Pro Gly Ala Ser Pro Cys Asn
340 345 350

Gln His Ser Pro Tyr Trp Ala Pro Pro Cys Tyr Thr Leu Lys Pro Glu
355 360 365

Thr

<210> 428
<211> 184
<212> PRT
<213> Artificial Sequence

<220>
<223> IMP3__Homo_sapiens__Q9NV31

<400> 428

Met Val Arg Lys Leu Lys Phe His Glu Gln Lys Leu Leu Lys Gln Val
1 5 10 15

Asp Phe Leu Asn Trp Glu Val Thr Asp His Asn Leu His Glu Leu Arg
20 25 30

Val Leu Arg Arg Tyr Arg Leu Gln Arg Arg Glu Asp Tyr Thr Arg Tyr

ITI-08-PCT_Sequence_Listing_ST25.txt

```

35          40          45
Asn Gln Leu Ser Arg Ala Val Arg Glu Leu Ala Arg Arg Leu Arg Asp
50          55          60
Leu Pro Glu Arg Asp Gln Phe Arg Val Arg Ala Ser Ala Ala Leu Leu
65          70          75          80
Asp Lys Leu Tyr Ala Leu Gly Leu Val Pro Thr Arg Gly Ser Leu Glu
85          90          95
Leu Cys Asp Phe Val Thr Ala Ser Ser Phe Cys Arg Arg Arg Leu Pro
100         105         110
Thr Val Leu Leu Lys Leu Arg Met Ala Gln His Leu Gln Ala Ala Val
115         120         125
Ala Phe Val Glu Gln Gly His Val Arg Val Gly Pro Asp Val Val Thr
130         135         140
Asp Pro Ala Phe Leu Val Thr Arg Ser Met Glu Asp Phe Val Thr Trp
145         150         155         160
Val Asp Ser Ser Lys Ile Lys Arg His Val Leu Glu Tyr Asn Glu Glu
165         170         175
Arg Asp Asp Phe Asp Leu Glu Ala
180

```

```

<210> 429
<211> 1049
<212> PRT
<213> Artificial Sequence

<220>
<223> ITA5__Homo_sapiens__P08648

<400> 429

```

```

Met Gly Ser Arg Thr Pro Glu Ser Pro Leu His Ala Val Gln Leu Arg
1          5          10          15
Trp Gly Pro Arg Arg Arg Pro Pro Leu Leu Pro Leu Leu Leu Leu Leu
20         25         30
Leu Pro Pro Pro Pro Arg Val Gly Gly Phe Asn Leu Asp Ala Glu Ala
35         40         45
Pro Ala Val Leu Ser Gly Pro Pro Gly Ser Phe Phe Gly Phe Ser Val
50         55         60
Glu Phe Tyr Arg Pro Gly Thr Asp Gly Val Ser Val Leu Val Gly Ala

```

ITI-08-PCT_Sequence_Listing_ST25.txt

65						70						75				80
Pro	Lys	Ala	Asn	Thr	Ser	Gln	Pro	Gly	Val	Leu	Gln	Gly	Gly	Ala	Val	
				85					90					95		
Tyr	Leu	Cys	Pro	Trp	Gly	Ala	Ser	Pro	Thr	Gln	Cys	Thr	Pro	Ile	Glu	
			100					105					110			
Phe	Asp	Ser	Lys	Gly	Ser	Arg	Leu	Leu	Glu	Ser	Ser	Leu	Ser	Ser	Ser	
		115					120					125				
Glu	Gly	Glu	Glu	Pro	Val	Glu	Tyr	Lys	Ser	Leu	Gln	Trp	Phe	Gly	Ala	
	130					135					140					
Thr	Val	Arg	Ala	His	Gly	Ser	Ser	Ile	Leu	Ala	Cys	Ala	Pro	Leu	Tyr	
145					150					155					160	
Ser	Trp	Arg	Thr	Glu	Lys	Glu	Pro	Leu	Ser	Asp	Pro	Val	Gly	Thr	Cys	
				165					170					175		
Tyr	Leu	Ser	Thr	Asp	Asn	Phe	Thr	Arg	Ile	Leu	Glu	Tyr	Ala	Pro	Cys	
			180					185					190			
Arg	Ser	Asp	Phe	Ser	Trp	Ala	Ala	Gly	Gln	Gly	Tyr	Cys	Gln	Gly	Gly	
		195					200					205				
Phe	Ser	Ala	Glu	Phe	Thr	Lys	Thr	Gly	Arg	Val	Val	Leu	Gly	Gly	Pro	
	210					215					220					
Gly	Ser	Tyr	Phe	Trp	Gln	Gly	Gln	Ile	Leu	Ser	Ala	Thr	Gln	Glu	Gln	
225					230					235					240	
Ile	Ala	Glu	Ser	Tyr	Tyr	Pro	Glu	Tyr	Leu	Ile	Asn	Leu	Val	Gln	Gly	
				245					250					255		
Gln	Leu	Gln	Thr	Arg	Gln	Ala	Ser	Ser	Ile	Tyr	Asp	Asp	Ser	Tyr	Leu	
			260					265					270			
Gly	Tyr	Ser	Val	Ala	Val	Gly	Glu	Phe	Ser	Gly	Asp	Asp	Thr	Glu	Asp	
		275					280					285				
Phe	Val	Ala	Gly	Val	Pro	Lys	Gly	Asn	Leu	Thr	Tyr	Gly	Tyr	Val	Thr	
	290					295					300					
Ile	Leu	Asn	Gly	Ser	Asp	Ile	Arg	Ser	Leu	Tyr	Asn	Phe	Ser	Gly	Glu	
305					310					315					320	
Gln	Met	Ala	Ser	Tyr	Phe	Gly	Tyr	Ala	Val	Ala	Ala	Thr	Asp	Val	Asn	
				325					330					335		
Gly	Asp	Gly	Leu	Asp	Asp	Leu	Leu	Val	Gly	Ala	Pro	Leu	Leu	Met	Asp	
			340					345					350			

ITI-08-PCT_Sequence_Listing_ST25.txt

Arg Thr Pro Asp Gly Arg Pro Gln Glu Val Gly Arg Val Tyr Val Tyr
 355 360 365
 Leu Gln His Pro Ala Gly Ile Glu Pro Thr Pro Thr Leu Thr Leu Thr
 370 375 380
 Gly His Asp Glu Phe Gly Arg Phe Gly Ser Ser Leu Thr Pro Leu Gly
 385 390 395 400
 Asp Leu Asp Gln Asp Gly Tyr Asn Asp Val Ala Ile Gly Ala Pro Phe
 405 410 415
 Gly Gly Glu Thr Gln Gln Gly Val Val Phe Val Phe Pro Gly Gly Pro
 420 425 430
 Gly Gly Leu Gly Ser Lys Pro Ser Gln Val Leu Gln Pro Leu Trp Ala
 435 440 445
 Ala Ser His Thr Pro Asp Phe Phe Gly Ser Ala Leu Arg Gly Gly Arg
 450 455 460
 Asp Leu Asp Gly Asn Gly Tyr Pro Asp Leu Ile Val Gly Ser Phe Gly
 465 470 475 480
 Val Asp Lys Ala Val Val Tyr Arg Gly Arg Pro Ile Val Ser Ala Ser
 485 490 495
 Ala Ser Leu Thr Ile Phe Pro Ala Met Phe Asn Pro Glu Glu Arg Ser
 500 505 510
 Cys Ser Leu Glu Gly Asn Pro Val Ala Cys Ile Asn Leu Ser Phe Cys
 515 520 525
 Leu Asn Ala Ser Gly Lys His Val Ala Asp Ser Ile Gly Phe Thr Val
 530 535 540
 Glu Leu Gln Leu Asp Trp Gln Lys Gln Lys Gly Gly Val Arg Arg Ala
 545 550 555 560
 Leu Phe Leu Ala Ser Arg Gln Ala Thr Leu Thr Gln Thr Leu Leu Ile
 565 570 575
 Gln Asn Gly Ala Arg Glu Asp Cys Arg Glu Met Lys Ile Tyr Leu Arg
 580 585 590
 Asn Glu Ser Glu Phe Arg Asp Lys Leu Ser Pro Ile His Ile Ala Leu
 595 600 605
 Asn Phe Ser Leu Asp Pro Gln Ala Pro Val Asp Ser His Gly Leu Arg
 610 615 620

ITI-08-PCT_Sequence_Listing_ST25.txt

```

Pro Ala Leu His Tyr Gln Ser Lys Ser Arg Ile Glu Asp Lys Ala Gln
625                               630                               635                               640

Ile Leu Leu Asp Cys Gly Glu Asp Asn Ile Cys Val Pro Asp Leu Gln
                               645                               650                               655

Leu Glu Val Phe Gly Glu Gln Asn His Val Tyr Leu Gly Asp Lys Asn
                               660                               665                               670

Ala Leu Asn Leu Thr Phe His Ala Gln Asn Val Gly Glu Gly Gly Ala
                               675                               680                               685

Tyr Glu Ala Glu Leu Arg Val Thr Ala Pro Pro Glu Ala Glu Tyr Ser
690                               695                               700

Gly Leu Val Arg His Pro Gly Asn Phe Ser Ser Leu Ser Cys Asp Tyr
705                               710                               715                               720

Phe Ala Val Asn Gln Ser Arg Leu Leu Val Cys Asp Leu Gly Asn Pro
                               725                               730                               735

Met Lys Ala Gly Ala Ser Leu Trp Gly Gly Leu Arg Phe Thr Val Pro
                               740                               745                               750

His Leu Arg Asp Thr Lys Lys Thr Ile Gln Phe Asp Phe Gln Ile Leu
755                               760                               765

Ser Lys Asn Leu Asn Asn Ser Gln Ser Asp Val Val Ser Phe Arg Leu
770                               775                               780

Ser Val Glu Ala Gln Ala Gln Val Thr Leu Asn Gly Val Ser Lys Pro
785                               790                               795                               800

Glu Ala Val Leu Phe Pro Val Ser Asp Trp His Pro Arg Asp Gln Pro
                               805                               810                               815

Gln Lys Glu Glu Asp Leu Gly Pro Ala Val His His Val Tyr Glu Leu
                               820                               825                               830

Ile Asn Gln Gly Pro Ser Ser Ile Ser Gln Gly Val Leu Glu Leu Ser
835                               840                               845

Cys Pro Gln Ala Leu Glu Gly Gln Gln Leu Leu Tyr Val Thr Arg Val
850                               855                               860

Thr Gly Leu Asn Cys Thr Thr Asn His Pro Ile Asn Pro Lys Gly Leu
865                               870                               875                               880

Glu Leu Asp Pro Glu Gly Ser Leu His His Gln Gln Lys Arg Glu Ala
                               885                               890                               895

Pro Ser Arg Ser Ser Ala Ser Ser Gly Pro Gln Ile Leu Lys Cys Pro

```

ITI-08-PCT_Sequence_Listing_ST25.txt

900

905

910

Glu Ala Glu Cys Phe Arg Leu Arg Cys Glu Leu Gly Pro Leu His Gln
915 920 925

Gln Glu Ser Gln Ser Leu Gln Leu His Phe Arg Val Trp Ala Lys Thr
930 935 940

Phe Leu Gln Arg Glu His Gln Pro Phe Ser Leu Gln Cys Glu Ala Val
945 950 955 960

Tyr Lys Ala Leu Lys Met Pro Tyr Arg Ile Leu Pro Arg Gln Leu Pro
965 970 975

Gln Lys Glu Arg Gln Val Ala Thr Ala Val Gln Trp Thr Lys Ala Glu
980 985 990

Gly Ser Tyr Gly Val Pro Leu Trp Ile Ile Ile Leu Ala Ile Leu Phe
995 1000 1005

Gly Leu Leu Leu Gly Leu Leu Ile Tyr Ile Leu Tyr Lys Leu
1010 1015 1020

Gly Phe Phe Lys Arg Ser Leu Pro Tyr Gly Thr Ala Met Glu Lys
1025 1030 1035

Ala Gln Leu Lys Pro Pro Ala Thr Ser Asp Ala
1040 1045

<210> 430

<211> 798

<212> PRT

<213> Artificial Sequence

<220>

<223> ITB1__Homo_sapiens__P05556

<400> 430

Met Asn Leu Gln Pro Ile Phe Trp Ile Gly Leu Ile Ser Ser Val Cys
1 5 10 15

Cys Val Phe Ala Gln Thr Asp Glu Asn Arg Cys Leu Lys Ala Asn Ala
20 25 30

Lys Ser Cys Gly Glu Cys Ile Gln Ala Gly Pro Asn Cys Gly Trp Cys
35 40 45

Thr Asn Ser Thr Phe Leu Gln Glu Gly Met Pro Thr Ser Ala Arg Cys
50 55 60

Asp Asp Leu Glu Ala Leu Lys Lys Lys Gly Cys Pro Pro Asp Asp Ile

65				70				75				80			
Glu	Asn	Pro	Arg	Gly 85	Ser	Lys	Asp	Ile	Lys 90	Lys	Asn	Lys	Asn	Val 95	Thr
Asn	Arg	Ser	Lys 100	Gly	Thr	Ala	Glu	Lys 105	Leu	Lys	Pro	Glu	Asp 110	Ile	Thr
Gln	Ile	Gln 115	Pro	Gln	Gln	Leu	Val 120	Leu	Arg	Leu	Arg	Ser 125	Gly	Glu	Pro
Gln	Thr 130	Phe	Thr	Leu	Lys	Phe 135	Lys	Arg	Ala	Glu	Asp 140	Tyr	Pro	Ile	Asp
Leu 145	Tyr	Tyr	Leu	Met	Asp 150	Leu	Ser	Tyr	Ser	Met 155	Lys	Asp	Asp	Leu	Glu 160
Asn	Val	Lys	Ser	Leu 165	Gly	Thr	Asp	Leu	Met 170	Asn	Glu	Met	Arg	Arg 175	Ile
Thr	Ser	Asp	Phe 180	Arg	Ile	Gly	Phe	Gly 185	Ser	Phe	Val	Glu	Lys 190	Thr	Val
Met	Pro	Tyr 195	Ile	Ser	Thr	Thr	Pro 200	Ala	Lys	Leu	Arg	Asn 205	Pro	Cys	Thr
Ser	Glu 210	Gln	Asn	Cys	Thr	Ser 215	Pro	Phe	Ser	Tyr	Lys 220	Asn	Val	Leu	Ser
Leu 225	Thr	Asn	Lys	Gly	Glu 230	Val	Phe	Asn	Glu	Leu 235	Val	Gly	Lys	Gln	Arg 240
Ile	Ser	Gly	Asn	Leu 245	Asp	Ser	Pro	Glu	Gly 250	Gly	Phe	Asp	Ala	Ile 255	Met
Gln	Val	Ala 260	Val	Cys	Gly	Ser	Leu 265	Ile	Gly	Trp	Arg	Asn	Val 270	Thr	Arg
Leu	Leu 275	Val	Phe	Ser	Thr	Asp	Ala 280	Gly	Phe	His	Phe	Ala 285	Gly	Asp	Gly
Lys	Leu 290	Gly	Gly	Ile	Val	Leu 295	Pro	Asn	Asp	Gly	Gln 300	Cys	His	Leu	Glu
Asn 305	Asn	Met	Tyr	Thr	Met 310	Ser	His	Tyr	Tyr	Asp 315	Tyr	Pro	Ser	Ile	Ala 320
His	Leu	Val	Gln 325	Lys	Leu	Ser	Glu	Asn	Asn 330	Ile	Gln	Thr	Ile	Phe 335	Ala
Val	Thr	Glu	Glu 340	Phe	Gln	Pro	Val	Tyr 345	Lys	Glu	Leu	Lys	Asn 350	Leu	Ile

ITI-08-PCT_Sequence_Listing_ST25.txt

Pro	Lys	Ser	Ala	Val	Gly	Thr	Leu	Ser	Ala	Asn	Ser	Ser	Asn	Val	Ile	355	360	365	
Gln	Leu	Ile	Ile	Asp	Ala	Tyr	Asn	Ser	Leu	Ser	Ser	Glu	Val	Ile	Leu	370	375	380	
Glu	Asn	Gly	Lys	Leu	Ser	Glu	Gly	Val	Thr	Ile	Ser	Tyr	Lys	Ser	Tyr	385	390	395	400
Cys	Lys	Asn	Gly	Val	Asn	Gly	Thr	Gly	Glu	Asn	Gly	Arg	Lys	Cys	Ser	405	410	415	
Asn	Ile	Ser	Ile	Gly	Asp	Glu	Val	Gln	Phe	Glu	Ile	Ser	Ile	Thr	Ser	420	425	430	
Asn	Lys	Cys	Pro	Lys	Lys	Asp	Ser	Asp	Ser	Phe	Lys	Ile	Arg	Pro	Leu	435	440	445	
Gly	Phe	Thr	Glu	Glu	Val	Glu	Val	Ile	Leu	Gln	Tyr	Ile	Cys	Glu	Cys	450	455	460	
Glu	Cys	Gln	Ser	Glu	Gly	Ile	Pro	Glu	Ser	Pro	Lys	Cys	His	Glu	Gly	465	470	475	480
Asn	Gly	Thr	Phe	Glu	Cys	Gly	Ala	Cys	Arg	Cys	Asn	Glu	Gly	Arg	Val	485	490	495	
Gly	Arg	His	Cys	Glu	Cys	Ser	Thr	Asp	Glu	Val	Asn	Ser	Glu	Asp	Met	500	505	510	
Asp	Ala	Tyr	Cys	Arg	Lys	Glu	Asn	Ser	Ser	Glu	Ile	Cys	Ser	Asn	Asn	515	520	525	
Gly	Glu	Cys	Val	Cys	Gly	Gln	Cys	Val	Cys	Arg	Lys	Arg	Asp	Asn	Thr	530	535	540	
Asn	Glu	Ile	Tyr	Ser	Gly	Lys	Phe	Cys	Glu	Cys	Asp	Asn	Phe	Asn	Cys	545	550	555	560
Asp	Arg	Ser	Asn	Gly	Leu	Ile	Cys	Gly	Gly	Asn	Gly	Val	Cys	Lys	Cys	565	570	575	
Arg	Val	Cys	Glu	Cys	Asn	Pro	Asn	Tyr	Thr	Gly	Ser	Ala	Cys	Asp	Cys	580	585	590	
Ser	Leu	Asp	Thr	Ser	Thr	Cys	Glu	Ala	Ser	Asn	Gly	Gln	Ile	Cys	Asn	595	600	605	
Gly	Arg	Gly	Ile	Cys	Glu	Cys	Gly	Val	Cys	Lys	Cys	Thr	Asp	Pro	Lys	610	615	620	

ITI-08-PCT_Sequence_Listing_ST25.txt

Phe Gln Gly Gln Thr Cys Glu Met Cys Gln Thr Cys Leu Gly Val Cys
625 630 635 640

Ala Glu His Lys Glu Cys Val Gln Cys Arg Ala Phe Asn Lys Gly Glu
645 650 655

Lys Lys Asp Thr Cys Thr Gln Glu Cys Ser Tyr Phe Asn Ile Thr Lys
660 665 670

Val Glu Ser Arg Asp Lys Leu Pro Gln Pro Val Gln Pro Asp Pro Val
675 680 685

Ser His Cys Lys Glu Lys Asp Val Asp Asp Cys Trp Phe Tyr Phe Thr
690 695 700

Tyr Ser Val Asn Gly Asn Asn Glu Val Met Val His Val Val Glu Asn
705 710 715 720

Pro Glu Cys Pro Thr Gly Pro Asp Ile Ile Pro Ile Val Ala Gly Val
725 730 735

Val Ala Gly Ile Val Leu Ile Gly Leu Ala Leu Leu Leu Ile Trp Lys
740 745 750

Leu Leu Met Ile Ile His Asp Arg Arg Glu Phe Ala Lys Phe Glu Lys
755 760 765

Glu Lys Met Asn Ala Lys Trp Asp Thr Gly Glu Asn Pro Ile Tyr Lys
770 775 780

Ser Ala Val Thr Thr Val Val Asn Pro Lys Tyr Glu Gly Lys
785 790 795

<210> 431

<211> 788

<212> PRT

<213> Artificial Sequence

<220>

<223> ITB6__Homo_sapiens__P18564

<400> 431

Met Gly Ile Glu Leu Leu Cys Leu Phe Phe Leu Phe Leu Gly Arg Asn
1 5 10 15

Asp His Val Gln Gly Gly Cys Ala Leu Gly Gly Ala Glu Thr Cys Glu
20 25 30

Asp Cys Leu Leu Ile Gly Pro Gln Cys Ala Trp Cys Ala Gln Glu Asn
35 40 45

ITI-08-PCT_Sequence_Listing_ST25.txt

Phe	Thr	His	Pro	Ser	Gly	Val	Gly	Glu	Arg	Cys	Asp	Thr	Pro	Ala	Asn	50	55	60	
Leu	Leu	Ala	Lys	Gly	Cys	Gln	Leu	Asn	Phe	Ile	Glu	Asn	Pro	Val	Ser	65	70	75	80
Gln	Val	Glu	Ile	Leu	Lys	Asn	Lys	Pro	Leu	Ser	Val	Gly	Arg	Gln	Lys	85	90	95	
Asn	Ser	Ser	Asp	Ile	Val	Gln	Ile	Ala	Pro	Gln	Ser	Leu	Ile	Leu	Lys	100	105	110	
Leu	Arg	Pro	Gly	Gly	Ala	Gln	Thr	Leu	Gln	Val	His	Val	Arg	Gln	Thr	115	120	125	
Glu	Asp	Tyr	Pro	Val	Asp	Leu	Tyr	Tyr	Leu	Met	Asp	Leu	Ser	Ala	Ser	130	135	140	
Met	Asp	Asp	Asp	Leu	Asn	Thr	Ile	Lys	Glu	Leu	Gly	Ser	Arg	Leu	Ser	145	150	155	160
Lys	Glu	Met	Ser	Lys	Leu	Thr	Ser	Asn	Phe	Arg	Leu	Gly	Phe	Gly	Ser	165	170	175	
Phe	Val	Glu	Lys	Pro	Val	Ser	Pro	Phe	Val	Lys	Thr	Thr	Pro	Glu	Glu	180	185	190	
Ile	Ala	Asn	Pro	Cys	Ser	Ser	Ile	Pro	Tyr	Phe	Cys	Leu	Pro	Thr	Phe	195	200	205	
Gly	Phe	Lys	His	Ile	Leu	Pro	Leu	Thr	Asn	Asp	Ala	Glu	Arg	Phe	Asn	210	215	220	
Glu	Ile	Val	Lys	Asn	Gln	Lys	Ile	Ser	Ala	Asn	Ile	Asp	Thr	Pro	Glu	225	230	235	240
Gly	Gly	Phe	Asp	Ala	Ile	Met	Gln	Ala	Ala	Val	Cys	Lys	Glu	Lys	Ile	245	250	255	
Gly	Trp	Arg	Asn	Asp	Ser	Leu	His	Leu	Leu	Val	Phe	Val	Ser	Asp	Ala	260	265	270	
Asp	Ser	His	Phe	Gly	Met	Asp	Ser	Lys	Leu	Ala	Gly	Ile	Val	Ile	Pro	275	280	285	
Asn	Asp	Gly	Leu	Cys	His	Leu	Asp	Ser	Lys	Asn	Glu	Tyr	Ser	Met	Ser	290	295	300	
Thr	Val	Leu	Glu	Tyr	Pro	Thr	Ile	Gly	Gln	Leu	Ile	Asp	Lys	Leu	Val	305	310	315	320
Gln	Asn	Asn	Val	Leu	Leu	Ile	Phe	Ala	Val	Thr	Gln	Glu	Gln	Val	His				

ITI-08-PCT_Sequence_Listing_ST25.txt

325 330 335

Leu Tyr Glu Asn Tyr Ala Lys Leu Ile Pro Gly Ala Thr Val Gly Leu
340 345 350

Leu Gln Lys Asp Ser Gly Asn Ile Leu Gln Leu Ile Ile Ser Ala Tyr
355 360 365

Glu Glu Leu Arg Ser Glu Val Glu Leu Glu Val Leu Gly Asp Thr Glu
370 375 380

Gly Leu Asn Leu Ser Phe Thr Ala Ile Cys Asn Asn Gly Thr Leu Phe
385 390 395 400

Gln His Gln Lys Lys Cys Ser His Met Lys Val Gly Asp Thr Ala Ser
405 410 415

Phe Ser Val Thr Val Asn Ile Pro His Cys Glu Arg Arg Ser Arg His
420 425 430

Ile Ile Ile Lys Pro Val Gly Leu Gly Asp Ala Leu Glu Leu Leu Val
435 440 445

Ser Pro Glu Cys Asn Cys Asp Cys Gln Lys Glu Val Glu Val Asn Ser
450 455 460

Ser Lys Cys His His Gly Asn Gly Ser Phe Gln Cys Gly Val Cys Ala
465 470 475 480

Cys His Pro Gly His Met Gly Pro Arg Cys Glu Cys Gly Glu Asp Met
485 490 495

Leu Ser Thr Asp Ser Cys Lys Glu Ala Pro Asp His Pro Ser Cys Ser
500 505 510

Gly Arg Gly Asp Cys Tyr Cys Gly Gln Cys Ile Cys His Leu Ser Pro
515 520 525

Tyr Gly Asn Ile Tyr Gly Pro Tyr Cys Gln Cys Asp Asn Phe Ser Cys
530 535 540

Val Arg His Lys Gly Leu Leu Cys Gly Gly Asn Gly Asp Cys Asp Cys
545 550 555 560

Gly Glu Cys Val Cys Arg Ser Gly Trp Thr Gly Glu Tyr Cys Asn Cys
565 570 575

Thr Thr Ser Thr Asp Ser Cys Val Ser Glu Asp Gly Val Leu Cys Ser
580 585 590

Gly Arg Gly Asp Cys Val Cys Gly Lys Cys Val Cys Thr Asn Pro Gly
595 600 605

ITI-08-PCT_Sequence_Listing_ST25.txt

Ala Ser Gly Pro Thr Cys Glu Arg Cys Pro Thr Cys Gly Asp Pro Cys
610 615 620

Asn Ser Lys Arg Ser Cys Ile Glu Cys His Leu Ser Ala Ala Gly Gln
625 630 635 640

Ala Arg Glu Glu Cys Val Asp Lys Cys Lys Leu Ala Gly Ala Thr Ile
645 650 655

Ser Glu Glu Glu Asp Phe Ser Lys Asp Gly Ser Val Ser Cys Ser Leu
660 665 670

Gln Gly Glu Asn Glu Cys Leu Ile Thr Phe Leu Ile Thr Thr Asp Asn
675 680 685

Glu Gly Lys Thr Ile Ile His Ser Ile Asn Glu Lys Asp Cys Pro Lys
690 695 700

Pro Pro Asn Ile Pro Met Ile Met Leu Gly Val Ser Leu Ala Ile Leu
705 710 715 720

Leu Ile Gly Val Val Leu Leu Cys Ile Trp Lys Leu Leu Val Ser Phe
725 730 735

His Asp Arg Lys Glu Val Ala Lys Phe Glu Ala Glu Arg Ser Lys Ala
740 745 750

Lys Trp Gln Thr Gly Thr Asn Pro Leu Tyr Arg Gly Ser Thr Ser Thr
755 760 765

Phe Lys Asn Val Thr Tyr Lys His Arg Glu Lys Gln Lys Val Asp Leu
770 775 780

Ser Thr Asp Cys
785

<210> 432

<211> 261

<212> PRT

<213> Artificial Sequence

<220>

<223> kallikrein-2__Homo_sapiens__A0A024R4J4

<400> 432

Met Trp Asp Leu Val Leu Ser Ile Ala Leu Ser Val Gly Cys Thr Gly
1 5 10 15

Ala Val Pro Leu Ile Gln Ser Arg Ile Val Gly Gly Trp Glu Cys Glu
20 25 30

ITI-08-PCT_Sequence_Listing_ST25.txt

Lys His Ser Gln Pro Trp Gln Val Ala Val Tyr Ser His Gly Trp Ala
35 40 45

His Cys Gly Gly Val Leu Val His Pro Gln Trp Val Leu Thr Ala Ala
50 55 60

His Cys Leu Lys Lys Asn Ser Gln Val Trp Leu Gly Arg His Asn Leu
65 70 75 80

Phe Glu Pro Glu Asp Thr Gly Gln Arg Val Pro Val Ser His Ser Phe
85 90 95

Pro	His	Pro	Leu	Tyr	Asn	Met	Ser	Leu	Leu	Lys	His	Gln	Ser	Leu	Arg
			100					105					110		

Pro Asp Glu Asp Ser Ser His Asp Leu Met Leu Leu Arg Leu Ser Glu
115 120 125

Pro Ala Lys Ile Thr Asp Val Val Lys Val Leu Gly Leu Pro Thr Gln
130 135 140

Glu Pro Ala Leu Gly Thr Thr Cys Tyr Ala Ser Gly Trp Gly Ser Ile
145 150 155 160

Glu Pro Glu Glu Phe Leu Arg Pro Arg Ser Leu Gln Cys Val Ser Leu
165 170 175

His Leu Leu Ser Asn Asp Met Cys Ala Arg Ala Tyr Ser Glu Lys Val
180 185 190

Thr Glu Phe Met Leu Cys Ala Gly Leu Trp Thr Gly Gly Lys Asp Thr
195 200 205

Cys Gly Gly Asp Ser Gly Gly Pro Leu Val Cys Asn Gly Val Leu Gln
210 215 220

Gly Ile Thr Ser Trp Gly Pro Glu Pro Cys Ala Leu Pro Glu Lys Pro
225 230 235 240

Ala Val Tyr Thr Lys Val Val His Tyr Arg Lys Trp Ile Lys Asp Thr
245 250 255

Ile Ala Ala Asn Pro
260

$\langle 210 \rangle$ 433

$\langle 211 \rangle$ 223

<212> PRT

<213> Artificial Sequence

 $\langle 220 \rangle$

ITI-08-PCT_Sequence_Listing_ST25.txt

<223> kallikrein-2__Homo_sapiens__A0A024R4N3

<400> 433

Met Trp Asp Leu Val Leu Ser Ile Ala Leu Ser Val Gly Cys Thr Gly
1 5 10 15

Ala Val Pro Leu Ile Gln Ser Arg Ile Val Gly Gly Trp Glu Cys Glu
20 25 30

Lys His Ser Gln Pro Trp Gln Val Ala Val Tyr Ser His Gly Trp Ala
35 40 45

His Cys Gly Gly Val Leu Val His Pro Gln Trp Val Leu Thr Ala Ala
50 55 60

His Cys Leu Lys Lys Asn Ser Gln Val Trp Leu Gly Arg His Asn Leu
65 70 75 80

Phe Glu Pro Glu Asp Thr Gly Gln Arg Val Pro Val Ser His Ser Phe
85 90 95

Pro His Pro Leu Tyr Asn Met Ser Leu Leu Lys His Gln Ser Leu Arg
100 105 110

Pro Asp Glu Asp Ser Ser His Asp Leu Met Leu Leu Arg Leu Ser Glu
115 120 125

Pro Ala Lys Ile Thr Asp Val Val Lys Val Leu Gly Leu Pro Thr Gln
130 135 140

Glu Pro Ala Leu Gly Thr Thr Cys Tyr Ala Ser Gly Trp Gly Ser Ile
145 150 155 160

Glu Pro Glu Glu Phe Leu Arg Pro Arg Ser Leu Gln Cys Val Ser Leu
165 170 175

His Leu Leu Ser Asn Asp Met Cys Ala Arg Ala Tyr Ser Glu Lys Val
180 185 190

Thr Glu Phe Met Leu Cys Ala Gly Leu Trp Thr Gly Gly Lys Asp Thr
195 200 205

Cys Gly Val Ser His Pro Tyr Ser Gln His Leu Glu Gly Lys Gly
210 215 220

<210> 434

<211> 62

<212> PRT

<213> Artificial Sequence

<220>

ITI-08-PCT_Sequence_Listing_ST25.txt

<223> kallikrein-2__Homo_sapiens__B0AZU9

<400> 434

Met Ser Leu Leu Lys His Gln Ser Leu Arg Pro Asp Glu Asp Ser Ser
1 5 10 15

His Asp Leu Met Leu Leu Arg Leu Ser Glu Pro Ala Lys Ile Thr Asp
20 25 30

Val Val Lys Val Leu Gly Leu Pro Thr Gln Glu Pro Ala Leu Gly Thr
35 40 45

Thr Cys Tyr Ala Ser Gly Trp Gly Ser Ile Glu Pro Glu Glu
50 55 60

<210> 435

<211> 244

<212> PRT

<213> Artificial Sequence

<220>

<223> kallikrein-2__Homo_sapiens__B4DU77

<400> 435

Met Gly Thr Leu Trp Gly Cys Pro Gly Ala Pro Pro Val Gly Ala His
1 5 10 15

Ser Cys Pro Leu Pro Lys Glu Val Ser Arg Thr Leu Gly Ser Gly Glu
20 25 30

Gly Met Ala Val Ser His Arg Asn Asn Ser Gly Met Leu Pro Pro Gly
35 40 45

Ser Leu Leu Arg Asn Ser Gln Val Trp Leu Gly Arg His Asn Leu Phe
50 55 60

Glu Pro Glu Asp Thr Gly Arg Arg Val Pro Val Ser His Ser Phe Pro
65 70 75 80

His Pro Leu Tyr Asn Met Ser Leu Leu Lys His Gln Ser Leu Arg Pro
85 90 95

Asp Glu Asp Ser Ser His Asp Leu Met Leu Leu Arg Leu Ser Glu Pro
100 105 110

Ala Lys Ile Thr Asp Val Val Lys Val Leu Gly Leu Pro Thr Gln Glu
115 120 125

Pro Ala Leu Gly Thr Thr Cys Tyr Ala Ser Gly Trp Gly Ser Ile Glu
130 135 140

ITI-08-PCT_Sequence_Listing_ST25.txt

Pro Glu Glu Phe Leu Arg Pro Arg Ser Leu Gln Cys Val Ser Leu His
145 150 155 160

Leu Leu Ser Asn Asp Met Cys Ala Arg Ala Tyr Ser Glu Lys Val Thr
165 170 175

Glu Phe Met Leu Cys Ala Gly Leu Trp Thr Gly Gly Lys Asp Thr Cys
180 185 190

Gly Gly Asp Ser Gly Gly Pro Leu Val Cys Asn Gly Val Leu Gln Gly
195 200 205

Ile Thr Ser Trp Gly Pro Glu Pro Cys Ala Leu Pro Glu Lys Pro Ala
210 215 220

Val Tyr Thr Lys Val Val His Tyr Arg Lys Trp Ile Lys Asp Thr Ile
225 230 235 240

Ala Ala Asn Pro

<210> 436

<211> 261

<212> PRT

<213> Artificial Sequence

<220>

<223> kallikrein-2__Homo_sapiens__P20151

<400> 436

Met Trp Asp Leu Val Leu Ser Ile Ala Leu Ser Val Gly Cys Thr Gly
1 5 10 15

Ala Val Pro Leu Ile Gln Ser Arg Ile Val Gly Gly Trp Glu Cys Glu
20 25 30

Lys His Ser Gln Pro Trp Gln Val Ala Val Tyr Ser His Gly Trp Ala
35 40 45

His Cys Gly Gly Val Leu Val His Pro Gln Trp Val Leu Thr Ala Ala
50 55 60

His Cys Leu Lys Lys Asn Ser Gln Val Trp Leu Gly Arg His Asn Leu
65 70 75 80

Phe Glu Pro Glu Asp Thr Gly Gln Arg Val Pro Val Ser His Ser Phe
85 90 95

Pro His Pro Leu Tyr Asn Met Ser Leu Leu Lys His Gln Ser Leu Arg
100 105 110

ITI-08-PCT_Sequence_Listing_ST25.txt

Pro Asp Glu Asp Ser Ser His Asp Leu Met Leu Leu Arg Leu Ser Glu
115 120 125

Pro Ala Lys Ile Thr Asp Val Val Lys Val Leu Gly Leu Pro Thr Gln
130 135 140

Glu Pro Ala Leu Gly Thr Thr Cys Tyr Ala Ser Gly Trp Gly Ser Ile
145 150 155 160

Glu Pro Glu Glu Phe Leu Arg Pro Arg Ser Leu Gln Cys Val Ser Leu
165 170 175

His Leu Leu Ser Asn Asp Met Cys Ala Arg Ala Tyr Ser Glu Lys Val
180 185 190

Thr Glu Phe Met Leu Cys Ala Gly Leu Trp Thr Gly Gly Lys Asp Thr
195 200 205

Cys Gly Gly Asp Ser Gly Gly Pro Leu Val Cys Asn Gly Val Leu Gln
210 215 220

Gly Ile Thr Ser Trp Gly Pro Glu Pro Cys Ala Leu Pro Glu Lys Pro
225 230 235 240

Ala Val Tyr Thr Lys Val Val His Tyr Arg Lys Trp Ile Lys Asp Thr
245 250 255

Ile Ala Ala Asn Pro
260

<210> 437
<211> 49
<212> PRT
<213> Artificial Sequence

<220>
<223> kallikrein-2__Homo_sapiens__Q6T774

<400> 437

Met Trp Asp Leu Val Leu Ser Ile Ala Leu Ser Val Gly Cys Thr Gly
1 5 10 15

Ile Ala Arg Ser Gly Trp Val Gly Thr Thr Cys Leu Ser Leu Lys Thr
20 25 30

Gln Ala Arg Gly Ser Leu Ser Ala Thr Ala Ser His Thr Arg Ser Thr
35 40 45

Ile

<210> 438

ITI-08-PCT_Sequence_Listing_ST25.txt

<211> 180
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> kallikrein-2__Homo_sapiens__Q6T775
 <400> 438

```

Met Trp Asp Leu Val Leu Ser Ile Ala Leu Ser Val Gly Cys Thr Gly
1           5           10           15

Ala Val Pro Leu Ile Gln Ser Arg Ile Val Gly Gly Trp Glu Cys Glu
          20           25           30

Lys His Ser Gln Pro Trp Gln Val Ala Val Tyr Ser His Gly Trp Ala
          35           40           45

His Cys Gly Gly Val Leu Val His Pro Gln Trp Val Leu Thr Ala Ala
          50           55           60

His Cys Leu Lys Lys Asn Ser Gln Val Trp Leu Gly Arg His Asn Leu
65           70           75           80

Phe Glu Pro Glu Asp Thr Gly Gln Arg Val Pro Val Ser His Ser Phe
          85           90           95

Pro His Pro Leu Tyr Asn Met Ser Leu Leu Lys His Gln Ser Leu Arg
          100          105          110

Pro Asp Glu Asp Ser Ser His Asp Leu Met Leu Leu Arg Leu Ser Glu
          115          120          125

Pro Ala Lys Ile Thr Asp Val Val Lys Val Leu Gly Leu Pro Thr Gln
          130          135          140

Glu Pro Ala Leu Gly Thr Thr Cys Tyr Ala Ser Gly Trp Gly Ser Ile
145          150          155          160

Glu Pro Glu Glu Cys Thr Pro Gly Pro Asp Gly Val Ala Gly Ser Pro
          165          170          175

Asp Ala Trp Val
          180
    
```

<210> 439
 <211> 254
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> kallikrein-4__Homo_sapiens__A0A0C4DFQ5

ITI-08-PCT_Sequence_Listing_ST25.txt

<400> 439

Met	Ala	Thr	Ala	Gly	Asn	Pro	Trp	Gly	Trp	Phe	Leu	Gly	Tyr	Leu	Ile
1				5				10						15	
Leu	Gly	Val	Ala	Gly	Ser	Leu	Val	Ser	Gly	Ser	Cys	Ser	Gln	Ile	Ile
			20					25					30		
Asn	Gly	Glu	Asp	Cys	Ser	Pro	His	Ser	Gln	Pro	Trp	Gln	Ala	Ala	Leu
		35					40					45			
Val	Met	Glu	Asn	Glu	Leu	Phe	Cys	Ser	Gly	Val	Leu	Val	His	Pro	Gln
	50					55					60				
Trp	Val	Leu	Ser	Ala	Ala	His	Cys	Phe	Gln	Asn	Ser	Tyr	Thr	Ile	Gly
65					70					75					80
Leu	Gly	Leu	His	Ser	Leu	Glu	Ala	Asp	Gln	Glu	Pro	Gly	Ser	Gln	Met
				85					90					95	
Val	Glu	Ala	Ser	Leu	Ser	Val	Arg	His	Pro	Glu	Tyr	Asn	Arg	Pro	Leu
			100					105					110		
Leu	Ala	Asn	Asp	Leu	Met	Leu	Ile	Lys	Leu	Asp	Glu	Ser	Val	Ser	Glu
		115					120					125			
Ser	Asp	Thr	Ile	Arg	Ser	Ile	Ser	Ile	Ala	Ser	Gln	Cys	Pro	Thr	Ala
	130					135					140				
Gly	Asn	Ser	Cys	Leu	Val	Ser	Gly	Trp	Gly	Leu	Leu	Ala	Asn	Gly	Arg
145					150					155					160
Met	Pro	Thr	Val	Leu	Gln	Cys	Val	Asn	Val	Ser	Val	Val	Ser	Glu	Glu
				165					170					175	
Val	Cys	Ser	Lys	Leu	Tyr	Asp	Pro	Leu	Tyr	His	Pro	Ser	Met	Phe	Cys
			180					185					190		
Ala	Gly	Gly	Gly	Gln	Asp	Gln	Lys	Asp	Ser	Cys	Asn	Gly	Asp	Ser	Gly
		195					200					205			
Gly	Pro	Leu	Ile	Cys	Asn	Gly	Tyr	Leu	Gln	Gly	Leu	Val	Ser	Phe	Gly
	210					215					220				
Lys	Ala	Pro	Cys	Gly	Gln	Val	Gly	Val	Pro	Gly	Val	Tyr	Thr	Asn	Leu
225					230					235					240
Cys	Lys	Phe	Thr	Glu	Trp	Ile	Glu	Lys	Thr	Val	Gln	Ala	Ser		
				245					250						

<210> 440

ITI-08-PCT_Sequence_Listing_ST25.txt

<211> 75
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> kallikrein-4__Homo_sapiens__Q5BQA0

<400> 440

Met Ala Thr Ala Gly Asn Pro Trp Gly Trp Phe Leu Gly Tyr Leu Ile
 1 5 10 15

Leu Gly Val Ala Gly Ser Leu Val Ser Gly Ser Cys Ser Gln Ile Ile
 20 25 30

Asn Gly Glu Asp Cys Ser Pro His Ser Gln Pro Trp Gln Ala Ala Leu
 35 40 45

Val Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln
 50 55 60

Trp Val Leu Ser Ala Ala His Cys Phe Gln Lys
 65 70 75

<210> 441
 <211> 195
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> kallikrein-4__Homo_sapiens__Q96PT0

<400> 441

Met Ala Thr Ala Gly Asn Pro Trp Gly Trp Phe Leu Gly Tyr Leu Ile
 1 5 10 15

Leu Gly Val Ala Gly Ser Leu Val Ser Gly Ser Cys Ser Gln Ile Ile
 20 25 30

Asn Gly Glu Asp Cys Ser Pro His Ser Gln Pro Trp Gln Ala Ala Leu
 35 40 45

Val Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln
 50 55 60

Trp Val Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly
 65 70 75 80

Leu Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met
 85 90 95

ITI-08-PCT_Sequence_Listing_ST25.txt

Val Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro Leu
100 105 110

Leu Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu
115 120 125

Ser Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala
130 135 140

Gly Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly Glu
145 150 155 160

Leu Thr Gly Val Cys Leu Pro Ser Ser Arg Arg Ser Ser Ala Gln Ser
165 170 175

Arg Gly Leu Thr Gln Ser Ser Ala Ser Gln Ala Glu Cys Leu Pro Cys
180 185 190

Cys Ser Ala
195

<210> 442
<211> 159
<212> PRT
<213> Artificial Sequence

<220>
<223> kallikrein-4__Homo_sapiens__Q96PT1

<400> 442

Met Ala Thr Ala Gly Asn Pro Trp Gly Trp Phe Leu Gly Tyr Leu Ile
1 5 10 15

Leu Gly Val Ala Gly Ser Leu Val Ser Gly Ser Cys Ser Gln Ile Ile
20 25 30

Asn Gly Glu Asp Cys Ser Pro His Ser Gln Pro Trp Gln Ala Ala Leu
35 40 45

Val Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln
50 55 60

Trp Val Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly
65 70 75 80

Leu Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met
85 90 95

Val Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro Leu
100 105 110

ITI-08-PCT_Sequence_Listing_ST25.txt

Leu Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu
115 120 125

Ser Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala
130 135 140

Gly Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly
145 150 155

<210> 443

<211> 254

<212> PRT

<213> Artificial Sequence

<220>

<223> kallikrein-4__Homo_sapiens__Q9Y5K2

<400> 443

Met Ala Thr Ala Gly Asn Pro Trp Gly Trp Phe Leu Gly Tyr Leu Ile
1 5 10 15

Leu Gly Val Ala Gly Ser Leu Val Ser Gly Ser Cys Ser Gln Ile Ile
20 25 30

Asn Gly Glu Asp Cys Ser Pro His Ser Gln Pro Trp Gln Ala Ala Leu
35 40 45

Val Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln
50 55 60

Trp Val Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly
65 70 75 80

Leu Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met
85 90 95

Val Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro Leu
100 105 110

Leu Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu
115 120 125

Ser Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala
130 135 140

Gly Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly Arg
145 150 155 160

Met Pro Thr Val Leu Gln Cys Val Asn Val Ser Val Val Ser Glu Glu
165 170 175

ITI-08-PCT_Sequence_Listing_ST25.txt

Val Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe Cys
180 185 190

Ala Gly Gly Gly His Asp Gln Lys Asp Ser Cys Asn Gly Asp Ser Gly
195 200 205

Gly Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe Gly
210 215 220

Lys Ala Pro Cys Gly Gln Val Gly Val Pro Gly Val Tyr Thr Asn Leu
225 230 235 240

Cys Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser
245 250

<210> 444

<211> 890

<212> PRT

<213> Artificial Sequence

<220>

<223> KI20A__Homo_sapiens__095235

<400> 444

Met Ser Gln Gly Ile Leu Ser Pro Pro Ala Gly Leu Leu Ser Asp Asp
1 5 10 15

Asp Val Val Val Ser Pro Met Phe Glu Ser Thr Ala Ala Asp Leu Gly
20 25 30

Ser Val Val Arg Lys Asn Leu Leu Ser Asp Cys Ser Val Val Ser Thr
35 40 45

Ser Leu Glu Asp Lys Gln Gln Val Pro Ser Glu Asp Ser Met Glu Lys
50 55 60

Val Lys Val Tyr Leu Arg Val Arg Pro Leu Leu Pro Ser Glu Leu Glu
65 70 75 80

Arg Gln Glu Asp Gln Gly Cys Val Arg Ile Glu Asn Val Glu Thr Leu
85 90 95

Val Leu Gln Ala Pro Lys Asp Ser Phe Ala Leu Lys Ser Asn Glu Arg
100 105 110

Gly Ile Gly Gln Ala Thr His Arg Phe Thr Phe Ser Gln Ile Phe Gly
115 120 125

Pro Glu Val Gly Gln Ala Ser Phe Phe Asn Leu Thr Val Lys Glu Met
130 135 140

ITI-08-PCT_Sequence_Listing_ST25.txt

Val	Lys	Asp	Val	Leu	Lys	Gly	Gln	Asn	Trp	Leu	Ile	Tyr	Thr	Tyr	Gly	145	150	155	160
Val	Thr	Asn	Ser	Gly	Lys	Thr	His	Thr	Ile	Gln	Gly	Thr	Ile	Lys	Asp	165	170	175	
Gly	Gly	Ile	Leu	Pro	Arg	Ser	Leu	Ala	Leu	Ile	Phe	Asn	Ser	Leu	Gln	180	185	190	
Gly	Gln	Leu	His	Pro	Thr	Pro	Asp	Leu	Lys	Pro	Leu	Leu	Ser	Asn	Glu	195	200	205	
Val	Ile	Trp	Leu	Asp	Ser	Lys	Gln	Ile	Arg	Gln	Glu	Glu	Met	Lys	Lys	210	215	220	
Leu	Ser	Leu	Leu	Asn	Gly	Gly	Leu	Gln	Glu	Glu	Glu	Leu	Ser	Thr	Ser	225	230	235	240
Leu	Lys	Arg	Ser	Val	Tyr	Ile	Glu	Ser	Arg	Ile	Gly	Thr	Ser	Thr	Ser	245	250	255	
Phe	Asp	Ser	Gly	Ile	Ala	Gly	Leu	Ser	Ser	Ile	Ser	Gln	Cys	Thr	Ser	260	265	270	
Ser	Ser	Gln	Leu	Asp	Glu	Thr	Ser	His	Arg	Trp	Ala	Gln	Pro	Asp	Thr	275	280	285	
Ala	Pro	Leu	Pro	Val	Pro	Ala	Asn	Ile	Arg	Phe	Ser	Ile	Trp	Ile	Ser	290	295	300	
Phe	Phe	Glu	Ile	Tyr	Asn	Glu	Leu	Leu	Tyr	Asp	Leu	Leu	Glu	Pro	Pro	305	310	315	320
Ser	Gln	Gln	Arg	Lys	Arg	Gln	Thr	Leu	Arg	Leu	Cys	Glu	Asp	Gln	Asn	325	330	335	
Gly	Asn	Pro	Tyr	Val	Lys	Asp	Leu	Asn	Trp	Ile	His	Val	Gln	Asp	Ala	340	345	350	
Glu	Glu	Ala	Trp	Lys	Leu	Leu	Lys	Val	Gly	Arg	Lys	Asn	Gln	Ser	Phe	355	360	365	
Ala	Ser	Thr	His	Leu	Asn	Gln	Asn	Ser	Ser	Arg	Ser	His	Ser	Ile	Phe	370	375	380	
Ser	Ile	Arg	Ile	Leu	His	Leu	Gln	Gly	Glu	Gly	Asp	Ile	Val	Pro	Lys	385	390	395	400
Ile	Ser	Glu	Leu	Ser	Leu	Cys	Asp	Leu	Ala	Gly	Ser	Glu	Arg	Cys	Lys	405	410	415	
Asp	Gln	Lys	Ser	Gly	Glu	Arg	Leu	Lys	Glu	Ala	Gly	Asn	Ile	Asn	Thr				

ITI-08-PCT_Sequence_Listing_ST25.txt

```

420                               425                               430
Ser Leu His Thr Leu Gly Arg Cys Ile Ala Ala Leu Arg Gln Asn Gln
435                               440                               445

Gln Asn Arg Ser Lys Gln Asn Leu Val Pro Phe Arg Asp Ser Lys Leu
450                               455                               460

Thr Arg Val Phe Gln Gly Phe Phe Thr Gly Arg Gly Arg Ser Cys Met
465                               470                               475                               480

Ile Val Asn Val Asn Pro Cys Ala Ser Thr Tyr Asp Glu Thr Leu His
485                               490                               495

Val Ala Lys Phe Ser Ala Ile Ala Ser Gln Leu Val His Ala Pro Pro
500                               505                               510

Met Gln Leu Gly Phe Pro Ser Leu His Ser Phe Ile Lys Glu His Ser
515                               520                               525

Leu Gln Val Ser Pro Ser Leu Glu Lys Gly Ala Lys Ala Asp Thr Gly
530                               535                               540

Leu Asp Asp Asp Ile Glu Asn Glu Ala Asp Ile Ser Met Tyr Gly Lys
545                               550                               555                               560

Glu Glu Leu Leu Gln Val Val Glu Ala Met Lys Thr Leu Leu Leu Lys
565                               570                               575

Glu Arg Gln Glu Lys Leu Gln Leu Glu Met His Leu Arg Asp Glu Ile
580                               585                               590

Cys Asn Glu Met Val Glu Gln Met Gln Gln Arg Glu Gln Trp Cys Ser
595                               600                               605

Glu His Leu Asp Thr Gln Lys Glu Leu Leu Glu Glu Met Tyr Glu Glu
610                               615                               620

Lys Leu Asn Ile Leu Lys Glu Ser Leu Thr Ser Phe Tyr Gln Glu Glu
625                               630                               635                               640

Ile Gln Glu Arg Asp Glu Lys Ile Glu Glu Leu Glu Ala Leu Leu Gln
645                               650                               655

Glu Ala Arg Gln Gln Ser Val Ala His Gln Gln Ser Gly Ser Glu Leu
660                               665                               670

Ala Leu Arg Arg Ser Gln Arg Leu Ala Ala Ser Ala Ser Thr Gln Gln
675                               680                               685

Leu Gln Glu Val Lys Ala Lys Leu Gln Gln Cys Lys Ala Glu Leu Asn
690                               695                               700

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Ser Thr Thr Glu Glu Leu His Lys Tyr Gln Lys Met Leu Glu Pro Pro
705 710 715 720

Pro Ser Ala Lys Pro Phe Thr Ile Asp Val Asp Lys Lys Leu Glu Glu
725 730 735

Gly Gln Lys Asn Ile Arg Leu Leu Arg Thr Glu Leu Gln Lys Leu Gly
740 745 750

Glu Ser Leu Gln Ser Ala Glu Arg Ala Cys Cys His Ser Thr Gly Ala
755 760 765

Gly Lys Leu Arg Gln Ala Leu Thr Thr Cys Asp Asp Ile Leu Ile Lys
770 775 780

Gln Asp Gln Thr Leu Ala Glu Leu Gln Asn Asn Met Val Leu Val Lys
785 790 795 800

Leu Asp Leu Arg Lys Lys Ala Ala Cys Ile Ala Glu Gln Tyr His Thr
805 810 815

Val Leu Lys Leu Gln Gly Gln Val Ser Ala Lys Lys Arg Leu Gly Thr
820 825 830

Asn Gln Glu Asn Gln Gln Pro Asn Gln Gln Pro Pro Gly Lys Lys Pro
835 840 845

Phe Leu Arg Asn Leu Leu Pro Arg Thr Pro Thr Cys Gln Ser Ser Thr
850 855 860

Asp Cys Ser Pro Tyr Ala Arg Ile Leu Arg Ser Arg Arg Ser Pro Leu
865 870 875 880

Leu Lys Ser Gly Pro Phe Gly Lys Lys Tyr
885 890

<210> 445

<211> 370

<212> PRT

<213> Artificial Sequence

<220>

<223> KIAA0205__Homo_sapiens__Q92604

<400> 445

Met Ala Ile Thr Leu Glu Glu Ala Pro Trp Leu Gly Trp Leu Leu Val
1 5 10 15

Lys Ala Leu Met Arg Phe Ala Phe Met Val Val Asn Asn Leu Val Ala
20 25 30

ITI-08-PCT_Sequence_Listing_ST25.txt

Ile	Pro	Ser	Tyr	Ile	Cys	Tyr	Val	Ile	Ile	Leu	Gln	Pro	Leu	Arg	Val
		35					40					45			
Leu	Asp	Ser	Lys	Arg	Phe	Trp	Tyr	Ile	Glu	Gly	Ile	Met	Tyr	Lys	Trp
	50					55					60				
Leu	Leu	Gly	Met	Val	Ala	Ser	Trp	Gly	Trp	Tyr	Ala	Gly	Tyr	Thr	Val
65					70					75					80
Met	Glu	Trp	Gly	Glu	Asp	Ile	Lys	Ala	Val	Ser	Lys	Asp	Glu	Ala	Val
				85					90					95	
Met	Leu	Val	Asn	His	Gln	Ala	Thr	Gly	Asp	Val	Cys	Thr	Leu	Met	Met
			100					105					110		
Cys	Leu	Gln	Asp	Lys	Gly	Leu	Val	Val	Ala	Gln	Met	Met	Trp	Leu	Met
		115					120					125			
Asp	His	Ile	Phe	Lys	Tyr	Thr	Asn	Phe	Gly	Ile	Val	Ser	Leu	Val	His
	130					135					140				
Gly	Asp	Phe	Phe	Ile	Arg	Gln	Gly	Arg	Ser	Tyr	Arg	Asp	Gln	Gln	Leu
145					150					155					160
Leu	Leu	Leu	Lys	Lys	His	Leu	Glu	Asn	Asn	Tyr	Arg	Ser	Arg	Asp	Arg
				165					170					175	
Lys	Trp	Ile	Val	Leu	Phe	Pro	Glu	Gly	Gly	Phe	Leu	Arg	Lys	Arg	Arg
			180					185					190		
Glu	Thr	Ser	Gln	Ala	Phe	Ala	Lys	Lys	Asn	Asn	Leu	Pro	Phe	Leu	Thr
		195					200					205			
Asn	Val	Thr	Leu	Pro	Arg	Ser	Gly	Ala	Thr	Lys	Ile	Ile	Leu	Asn	Ala
	210					215					220				
Leu	Val	Ala	Gln	Gln	Lys	Asn	Gly	Ser	Pro	Ala	Gly	Gly	Asp	Ala	Lys
225					230					235					240
Glu	Leu	Asp	Ser	Lys	Ser	Lys	Gly	Leu	Gln	Trp	Ile	Ile	Asp	Thr	Thr
				245					250					255	
Ile	Ala	Tyr	Pro	Lys	Ala	Glu	Pro	Ile	Asp	Ile	Gln	Thr	Trp	Ile	Leu
			260					265					270		
Gly	Tyr	Arg	Lys	Pro	Thr	Val	Thr	His	Val	His	Tyr	Arg	Ile	Phe	Pro
		275					280					285			
Ile	Lys	Asp	Val	Pro	Leu	Glu	Thr	Asp	Asp	Leu	Thr	Thr	Trp	Leu	Tyr
	290					295					300				

ITI-08-PCT_Sequence_Listing_ST25.txt

Gln Arg Phe Val Glu Lys Glu Asp Leu Leu Ser His Phe Tyr Glu Thr
305 310 315 320

Gly Ala Phe Pro Pro Ser Lys Gly His Lys Glu Ala Val Ser Arg Glu
325 330 335

Met Thr Leu Ser Asn Leu Trp Ile Phe Leu Ile Gln Ser Phe Ala Phe
340 345 350

Leu Ser Gly Tyr Met Trp Tyr Asn Ile Ile Gln Tyr Phe Tyr His Cys
355 360 365

Leu Phe
370

<210> 446

<211> 725

<212> PRT

<213> Artificial Sequence

<220>

<223> KIF2C__Homo_sapiens__Q99661

<400> 446

Met Ala Met Asp Ser Ser Leu Gln Ala Arg Leu Phe Pro Gly Leu Ala
1 5 10 15

Ile Lys Ile Gln Arg Ser Asn Gly Leu Ile His Ser Ala Asn Val Arg
20 25 30

Thr Val Asn Leu Glu Lys Ser Cys Val Ser Val Glu Trp Ala Glu Gly
35 40 45

Gly Ala Thr Lys Gly Lys Glu Ile Asp Phe Asp Asp Val Ala Ala Ile
50 55 60

Asn Pro Glu Leu Leu Gln Leu Leu Pro Leu His Pro Lys Asp Asn Leu
65 70 75 80

Pro Leu Gln Glu Asn Val Thr Ile Gln Lys Gln Lys Arg Arg Ser Val
85 90 95

Asn Ser Lys Ile Pro Ala Pro Lys Glu Ser Leu Arg Ser Arg Ser Thr
100 105 110

Arg Met Ser Thr Val Ser Glu Leu Arg Ile Thr Ala Gln Glu Asn Asp
115 120 125

Met Glu Val Glu Leu Pro Ala Ala Ala Asn Ser Arg Lys Gln Phe Ser
130 135 140

ITI-08-PCT_Sequence_Listing_ST25.txt

Val	Pro	Pro	Ala	Pro	Thr	Arg	Pro	Ser	Cys	Pro	Ala	Val	Ala	Glu	Ile	145	150	155	160
Pro	Leu	Arg	Met	Val	Ser	Glu	Glu	Met	Glu	Glu	Gln	Val	His	Ser	Ile	165	170	175	
Arg	Gly	Ser	Ser	Ser	Ala	Asn	Pro	Val	Asn	Ser	Val	Arg	Arg	Lys	Ser	180	185	190	
Cys	Leu	Val	Lys	Glu	Val	Glu	Lys	Met	Lys	Asn	Lys	Arg	Glu	Glu	Lys	195	200	205	
Lys	Ala	Gln	Asn	Ser	Glu	Met	Arg	Met	Lys	Arg	Ala	Gln	Glu	Tyr	Asp	210	215	220	
Ser	Ser	Phe	Pro	Asn	Trp	Glu	Phe	Ala	Arg	Met	Ile	Lys	Glu	Phe	Arg	225	230	235	240
Ala	Thr	Leu	Glu	Cys	His	Pro	Leu	Thr	Met	Thr	Asp	Pro	Ile	Glu	Glu	245	250	255	
His	Arg	Ile	Cys	Val	Cys	Val	Arg	Lys	Arg	Pro	Leu	Asn	Lys	Gln	Glu	260	265	270	
Leu	Ala	Lys	Lys	Glu	Ile	Asp	Val	Ile	Ser	Ile	Pro	Ser	Lys	Cys	Leu	275	280	285	
Leu	Leu	Val	His	Glu	Pro	Lys	Leu	Lys	Val	Asp	Leu	Thr	Lys	Tyr	Leu	290	295	300	
Glu	Asn	Gln	Ala	Phe	Cys	Phe	Asp	Phe	Ala	Phe	Asp	Glu	Thr	Ala	Ser	305	310	315	320
Asn	Glu	Val	Val	Tyr	Arg	Phe	Thr	Ala	Arg	Pro	Leu	Val	Gln	Thr	Ile	325	330	335	
Phe	Glu	Gly	Gly	Lys	Ala	Thr	Cys	Phe	Ala	Tyr	Gly	Gln	Thr	Gly	Ser	340	345	350	
Gly	Lys	Thr	His	Thr	Met	Gly	Gly	Asp	Leu	Ser	Gly	Lys	Ala	Gln	Asn	355	360	365	
Ala	Ser	Lys	Gly	Ile	Tyr	Ala	Met	Ala	Ser	Arg	Asp	Val	Phe	Leu	Leu	370	375	380	
Lys	Asn	Gln	Pro	Cys	Tyr	Arg	Lys	Leu	Gly	Leu	Glu	Val	Tyr	Val	Thr	385	390	395	400
Phe	Phe	Glu	Ile	Tyr	Asn	Gly	Lys	Leu	Phe	Asp	Leu	Leu	Asn	Lys	Lys	405	410	415	
Ala	Lys	Leu	Arg	Val	Leu	Glu	Asp	Gly	Lys	Gln	Gln	Val	Gln	Val	Val				

ITI-08-PCT_Sequence_Listing_ST25.txt

420	425	430																
Gly	Leu	Gln	Glu	His	Leu	Val	Asn	Ser	Ala	Asp	Asp	Val	Ile	Lys	Met			
	435						440					445						
Ile	Asp	Met	Gly	Ser	Ala	Cys	Arg	Thr	Ser	Gly	Gln	Thr	Phe	Ala	Asn			
	450					455					460							
Ser	Asn	Ser	Ser	Arg	Ser	His	Ala	Cys	Phe	Gln	Ile	Ile	Leu	Arg	Ala			
465					470					475								
Lys	Gly	Arg	Met	His	Gly	Lys	Phe	Ser	Leu	Val	Asp	Leu	Ala	Gly	Asn			
				485					490									
Glu	Arg	Gly	Ala	Asp	Thr	Ser	Ser	Ala	Asp	Arg	Gln	Thr	Arg	Met	Glu			
			500					505										
Gly	Ala	Glu	Ile	Asn	Lys	Ser	Leu	Leu	Ala	Leu	Lys	Glu	Cys	Ile	Arg			
	515							520										
Ala	Leu	Gly	Gln	Asn	Lys	Ala	His	Thr	Pro	Phe	Arg	Glu	Ser	Lys	Leu			
	530							535										
Thr	Gln	Val	Leu	Arg	Asp	Ser	Phe	Ile	Gly	Glu	Asn	Ser	Arg	Thr	Cys			
545					550							555						
Met	Ile	Ala	Thr	Ile	Ser	Pro	Gly	Ile	Ser	Ser	Cys	Glu	Tyr	Thr	Leu			
				565							570							
Asn	Thr	Leu	Arg	Tyr	Ala	Asp	Arg	Val	Lys	Glu	Leu	Ser	Pro	His	Ser			
			580							585								
Gly	Pro	Ser	Gly	Glu	Gln	Leu	Ile	Gln	Met	Glu	Thr	Glu	Glu	Met	Glu			
	595							600										
Ala	Cys	Ser	Asn	Gly	Ala	Leu	Ile	Pro	Gly	Asn	Leu	Ser	Lys	Glu	Glu			
	610							615										
Glu	Glu	Leu	Ser	Ser	Gln	Met	Ser	Ser	Phe	Asn	Glu	Ala	Met	Thr	Gln			
625					630							635						
Ile	Arg	Glu	Leu	Glu	Glu	Lys	Ala	Met	Glu	Glu	Leu	Lys	Glu	Ile	Ile			
				645							650							
Gln	Gln	Gly	Pro	Asp	Trp	Leu	Glu	Leu	Ser	Glu	Met	Thr	Glu	Gln	Pro			
			660							665								
Asp	Tyr	Asp	Leu	Glu	Thr	Phe	Val	Asn	Lys	Ala	Glu	Ser	Ala	Leu	Ala			
	675							680										
Gln	Gln	Ala	Lys	His	Phe	Ser	Ala	Leu	Arg	Asp	Val	Ile	Lys	Ala	Leu			
	690							695										

ITI-08-PCT_Sequence_Listing_ST25.txt

Arg Leu Ala Met Gln Leu Glu Glu Gln Ala Ser Arg Gln Ile Ser Ser
705 710 715 720

Lys Lys Arg Pro Gln
725

<210> 447
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> KK-LC-1__Homo_sapiens__Q5H943

<400> 447

Met Asn Phe Tyr Leu Leu Leu Ala Ser Ser Ile Leu Cys Ala Leu Ile
1 5 10 15

Val Phe Trp Lys Tyr Arg Arg Phe Gln Arg Asn Thr Gly Glu Met Ser
20 25 30

Ser Asn Ser Thr Ala Leu Ala Leu Val Arg Pro Ser Ser Ser Gly Leu
35 40 45

Ile Asn Ser Asn Thr Asp Asn Asn Leu Ala Val Tyr Asp Leu Ser Arg
50 55 60

Asp Ile Leu Asn Asn Phe Pro His Ser Ile Ala Arg Gln Lys Arg Ile
65 70 75 80

Leu Val Asn Leu Ser Met Val Glu Asn Lys Leu Val Glu Leu Glu His
85 90 95

Thr Leu Leu Ser Lys Gly Phe Arg Gly Ala Ser Pro His Arg Lys Ser
100 105 110

Thr

<210> 448
<211> 860
<212> PRT
<213> Artificial Sequence

<220>
<223> LDLR__Homo_sapiens__P01130

<400> 448

Met Gly Pro Trp Gly Trp Lys Leu Arg Trp Thr Val Ala Leu Leu Leu
1 5 10 15

ITI-08-PCT_Sequence_Listing_ST25.txt

Ala	Ala	Ala	Gly	Thr	Ala	Val	Gly	Asp	Arg	Cys	Glu	Arg	Asn	Glu	Phe	20	25	30
Gln	Cys	Gln	Asp	Gly	Lys	Cys	Ile	Ser	Tyr	Lys	Trp	Val	Cys	Asp	Gly	35	40	45
Ser	Ala	Glu	Cys	Gln	Asp	Gly	Ser	Asp	Glu	Ser	Gln	Glu	Thr	Cys	Leu	50	55	60
Ser	Val	Thr	Cys	Lys	Ser	Gly	Asp	Phe	Ser	Cys	Gly	Gly	Arg	Val	Asn	65	70	75
Arg	Cys	Ile	Pro	Gln	Phe	Trp	Arg	Cys	Asp	Gly	Gln	Val	Asp	Cys	Asp	85	90	95
Asn	Gly	Ser	Asp	Glu	Gln	Gly	Cys	Pro	Pro	Lys	Thr	Cys	Ser	Gln	Asp	100	105	110
Glu	Phe	Arg	Cys	His	Asp	Gly	Lys	Cys	Ile	Ser	Arg	Gln	Phe	Val	Cys	115	120	125
Asp	Ser	Asp	Arg	Asp	Cys	Leu	Asp	Gly	Ser	Asp	Glu	Ala	Ser	Cys	Pro	130	135	140
Val	Leu	Thr	Cys	Gly	Pro	Ala	Ser	Phe	Gln	Cys	Asn	Ser	Ser	Thr	Cys	145	150	155
Ile	Pro	Gln	Leu	Trp	Ala	Cys	Asp	Asn	Asp	Pro	Asp	Cys	Glu	Asp	Gly	165	170	175
Ser	Asp	Glu	Trp	Pro	Gln	Arg	Cys	Arg	Gly	Leu	Tyr	Val	Phe	Gln	Gly	180	185	190
Asp	Ser	Ser	Pro	Cys	Ser	Ala	Phe	Glu	Phe	His	Cys	Leu	Ser	Gly	Glu	195	200	205
Cys	Ile	His	Ser	Ser	Trp	Arg	Cys	Asp	Gly	Gly	Pro	Asp	Cys	Lys	Asp	210	215	220
Lys	Ser	Asp	Glu	Glu	Asn	Cys	Ala	Val	Ala	Thr	Cys	Arg	Pro	Asp	Glu	225	230	235
Phe	Gln	Cys	Ser	Asp	Gly	Asn	Cys	Ile	His	Gly	Ser	Arg	Gln	Cys	Asp	245	250	255
Arg	Glu	Tyr	Asp	Cys	Lys	Asp	Met	Ser	Asp	Glu	Val	Gly	Cys	Val	Asn	260	265	270
Val	Thr	Leu	Cys	Glu	Gly	Pro	Asn	Lys	Phe	Lys	Cys	His	Ser	Gly	Glu	275	280	285

ITI-08-PCT_Sequence_Listing_ST25.txt

Cys Ile Thr Leu Asp Lys Val Cys Asn Met Ala Arg Asp Cys Arg Asp
290 295 300

Trp Ser Asp Glu Pro Ile Lys Glu Cys Gly Thr Asn Glu Cys Leu Asp
305 310 315 320

Asn Asn Gly Gly Cys Ser His Val Cys Asn Asp Leu Lys Ile Gly Tyr
325 330 335

Glu Cys Leu Cys Pro Asp Gly Phe Gln Leu Val Ala Gln Arg Arg Cys
340 345 350

Glu Asp Ile Asp Glu Cys Gln Asp Pro Asp Thr Cys Ser Gln Leu Cys
355 360 365

Val Asn Leu Glu Gly Gly Tyr Lys Cys Gln Cys Glu Glu Gly Phe Gln
370 375 380

Leu Asp Pro His Thr Lys Ala Cys Lys Ala Val Gly Ser Ile Ala Tyr
385 390 395 400

Leu Phe Phe Thr Asn Arg His Glu Val Arg Lys Met Thr Leu Asp Arg
405 410 415

Ser Glu Tyr Thr Ser Leu Ile Pro Asn Leu Arg Asn Val Val Ala Leu
420 425 430

Asp Thr Glu Val Ala Ser Asn Arg Ile Tyr Trp Ser Asp Leu Ser Gln
435 440 445

Arg Met Ile Cys Ser Thr Gln Leu Asp Arg Ala His Gly Val Ser Ser
450 455 460

Tyr Asp Thr Val Ile Ser Arg Asp Ile Gln Ala Pro Asp Gly Leu Ala
465 470 475 480

Val Asp Trp Ile His Ser Asn Ile Tyr Trp Thr Asp Ser Val Leu Gly
485 490 495

Thr Val Ser Val Ala Asp Thr Lys Gly Val Lys Arg Lys Thr Leu Phe
500 505 510

Arg Glu Asn Gly Ser Lys Pro Arg Ala Ile Val Val Asp Pro Val His
515 520 525

Gly Phe Met Tyr Trp Thr Asp Trp Gly Thr Pro Ala Lys Ile Lys Lys
530 535 540

Gly Gly Leu Asn Gly Val Asp Ile Tyr Ser Leu Val Thr Glu Asn Ile
545 550 555 560

Gln Trp Pro Asn Gly Ile Thr Leu Asp Leu Leu Ser Gly Arg Leu Tyr

ITI-08-PCT_Sequence_Listing_ST25.txt

565

570

575

Trp Val Asp Ser Lys Leu His Ser Ile Ser Ser Ile Asp Val Asn Gly
 580 585 590

Gly Asn Arg Lys Thr Ile Leu Glu Asp Glu Lys Arg Leu Ala His Pro
 595 600 605

Phe Ser Leu Ala Val Phe Glu Asp Lys Val Phe Trp Thr Asp Ile Ile
 610 615 620

Asn Glu Ala Ile Phe Ser Ala Asn Arg Leu Thr Gly Ser Asp Val Asn
 625 630 635 640

Leu Leu Ala Glu Asn Leu Leu Ser Pro Glu Asp Met Val Leu Phe His
 645 650 655

Asn Leu Thr Gln Pro Arg Gly Val Asn Trp Cys Glu Arg Thr Thr Leu
 660 665 670

Ser Asn Gly Gly Cys Gln Tyr Leu Cys Leu Pro Ala Pro Gln Ile Asn
 675 680 685

Pro His Ser Pro Lys Phe Thr Cys Ala Cys Pro Asp Gly Met Leu Leu
 690 695 700

Ala Arg Asp Met Arg Ser Cys Leu Thr Glu Ala Glu Ala Ala Val Ala
 705 710 715 720

Thr Gln Glu Thr Ser Thr Val Arg Leu Lys Val Ser Ser Thr Ala Val
 725 730 735

Arg Thr Gln His Thr Thr Thr Arg Pro Val Pro Asp Thr Ser Arg Leu
 740 745 750

Pro Gly Ala Thr Pro Gly Leu Thr Thr Val Glu Ile Val Thr Met Ser
 755 760 765

His Gln Ala Leu Gly Asp Val Ala Gly Arg Gly Asn Glu Lys Lys Pro
 770 775 780

Ser Ser Val Arg Ala Leu Ser Ile Val Leu Pro Ile Val Leu Leu Val
 785 790 795 800

Phe Leu Cys Leu Gly Val Phe Leu Leu Trp Lys Asn Trp Arg Leu Lys
 805 810 815

Asn Ile Asn Ser Ile Asn Phe Asp Asn Pro Val Tyr Gln Lys Thr Thr
 820 825 830

Glu Asp Glu Val His Ile Cys His Asn Gln Asp Gly Tyr Ser Tyr Pro
 835 840 845

ITI-08-PCT_Sequence_Listing_ST25.txt

Ser Arg Gln Met Val Ser Leu Glu Asp Asp Val Ala
850 855 860

<210> 449

<211> 433

<212> PRT

<213> Artificial Sequence

<220>

<223> LGMN__Homo_sapiens__Q99538

<400> 449

Met Val Trp Lys Val Ala Val Phe Leu Ser Val Ala Leu Gly Ile Gly
1 5 10 15

Ala Val Pro Ile Asp Asp Pro Glu Asp Gly Gly Lys His Trp Val Val
20 25 30

Ile Val Ala Gly Ser Asn Gly Trp Tyr Asn Tyr Arg His Gln Ala Asp
35 40 45

Ala Cys His Ala Tyr Gln Ile Ile His Arg Asn Gly Ile Pro Asp Glu
50 55 60

Gln Ile Val Val Met Met Tyr Asp Asp Ile Ala Tyr Ser Glu Asp Asn
65 70 75 80

Pro Thr Pro Gly Ile Val Ile Asn Arg Pro Asn Gly Thr Asp Val Tyr
85 90 95

Gln Gly Val Pro Lys Asp Tyr Thr Gly Glu Asp Val Thr Pro Gln Asn
100 105 110

Phe Leu Ala Val Leu Arg Gly Asp Ala Glu Ala Val Lys Gly Ile Gly
115 120 125

Ser Gly Lys Val Leu Lys Ser Gly Pro Gln Asp His Val Phe Ile Tyr
130 135 140

Phe Thr Asp His Gly Ser Thr Gly Ile Leu Val Phe Pro Asn Glu Asp
145 150 155 160

Leu His Val Lys Asp Leu Asn Glu Thr Ile His Tyr Met Tyr Lys His
165 170 175

Lys Met Tyr Arg Lys Met Val Phe Tyr Ile Glu Ala Cys Glu Ser Gly
180 185 190

Ser Met Met Asn His Leu Pro Asp Asn Ile Asn Val Tyr Ala Thr Thr
195 200 205

ITI-08-PCT_Sequence_Listing_ST25.txt

Ala	Ala	Asn	Pro	Arg	Glu	Ser	Ser	Tyr	Ala	Cys	Tyr	Tyr	Asp	Glu	Lys
210						215				220					
Arg	Ser	Thr	Tyr	Leu	Gly	Asp	Trp	Tyr	Ser	Val	Asn	Trp	Met	Glu	Asp
225					230					235					240
Ser	Asp	Val	Glu	Asp	Leu	Thr	Lys	Glu	Thr	Leu	His	Lys	Gln	Tyr	His
				245					250					255	
Leu	Val	Lys	Ser	His	Thr	Asn	Thr	Ser	His	Val	Met	Gln	Tyr	Gly	Asn
			260					265					270		
Lys	Thr	Ile	Ser	Thr	Met	Lys	Val	Met	Gln	Phe	Gln	Gly	Met	Lys	Arg
		275					280					285			
Lys	Ala	Ser	Ser	Pro	Val	Pro	Leu	Pro	Pro	Val	Thr	His	Leu	Asp	Leu
	290					295					300				
Thr	Pro	Ser	Pro	Asp	Val	Pro	Leu	Thr	Ile	Met	Lys	Arg	Lys	Leu	Met
305					310					315					320
Asn	Thr	Asn	Asp	Leu	Glu	Glu	Ser	Arg	Gln	Leu	Thr	Glu	Glu	Ile	Gln
				325					330					335	
Arg	His	Leu	Asp	Ala	Arg	His	Leu	Ile	Glu	Lys	Ser	Val	Arg	Lys	Ile
			340					345					350		
Val	Ser	Leu	Leu	Ala	Ala	Ser	Glu	Ala	Glu	Val	Glu	Gln	Leu	Leu	Ser
		355					360					365			
Glu	Arg	Ala	Pro	Leu	Thr	Gly	His	Ser	Cys	Tyr	Pro	Glu	Ala	Leu	Leu
	370					375					380				
His	Phe	Arg	Thr	His	Cys	Phe	Asn	Trp	His	Ser	Pro	Thr	Tyr	Glu	Tyr
385					390					395					400
Ala	Leu	Arg	His	Leu	Tyr	Val	Leu	Val	Asn	Leu	Cys	Glu	Lys	Pro	Tyr
				405					410					415	
Pro	Leu	His	Arg	Ile	Lys	Leu	Ser	Met	Asp	His	Val	Cys	Leu	Gly	His
			420					425					430		

Tyr

<210> 450
 <211> 598
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> LIRB2__Homo_sapiens__Q8N423

ITI-08-PCT_Sequence_Listing_ST25.txt

<400> 450

```

Met Thr Pro Ile Val Thr Val Leu Ile Cys Leu Gly Leu Ser Leu Gly
1          5          10          15

Pro Arg Thr His Val Gln Thr Gly Thr Ile Pro Lys Pro Thr Leu Trp
          20          25          30

Ala Glu Pro Asp Ser Val Ile Thr Gln Gly Ser Pro Val Thr Leu Ser
          35          40          45

Cys Gln Gly Ser Leu Glu Ala Gln Glu Tyr Arg Leu Tyr Arg Glu Lys
50          55          60

Lys Ser Ala Ser Trp Ile Thr Arg Ile Arg Pro Glu Leu Val Lys Asn
65          70          75          80

Gly Gln Phe His Ile Pro Ser Ile Thr Trp Glu His Thr Gly Arg Tyr
          85          90          95

Gly Cys Gln Tyr Tyr Ser Arg Ala Arg Trp Ser Glu Leu Ser Asp Pro
          100          105          110

Leu Val Leu Val Met Thr Gly Ala Tyr Pro Lys Pro Thr Leu Ser Ala
          115          120          125

Gln Pro Ser Pro Val Val Thr Ser Gly Gly Arg Val Thr Leu Gln Cys
          130          135          140

Glu Ser Gln Val Ala Phe Gly Gly Phe Ile Leu Cys Lys Glu Gly Glu
145          150          155          160

Glu Glu His Pro Gln Cys Leu Asn Ser Gln Pro His Ala Arg Gly Ser
          165          170          175

Ser Arg Ala Ile Phe Ser Val Gly Pro Val Ser Pro Asn Arg Arg Trp
          180          185          190

Ser His Arg Cys Tyr Gly Tyr Asp Leu Asn Ser Pro Tyr Val Trp Ser
          195          200          205

Ser Pro Ser Asp Leu Leu Glu Leu Leu Val Pro Gly Val Ser Lys Lys
          210          215          220

Pro Ser Leu Ser Val Gln Pro Gly Pro Val Val Ala Pro Gly Glu Ser
225          230          235          240

Leu Thr Leu Gln Cys Val Ser Asp Val Gly Tyr Asp Arg Phe Val Leu
          245          250          255

Tyr Lys Glu Gly Glu Arg Asp Leu Arg Gln Leu Pro Gly Arg Gln Pro

```

ITI-08-PCT_Sequence_Listing_ST25.txt

```

260          265          270
Gln Ala Gly Leu Ser Gln Ala Asn Phe Thr Leu Gly Pro Val Ser Arg
275          280          285
Ser Tyr Gly Gly Gln Tyr Arg Cys Tyr Gly Ala His Asn Leu Ser Ser
290          295          300
Glu Cys Ser Ala Pro Ser Asp Pro Leu Asp Ile Leu Ile Thr Gly Gln
305          310          315          320
Ile Arg Gly Thr Pro Phe Ile Ser Val Gln Pro Gly Pro Thr Val Ala
325          330          335
Ser Gly Glu Asn Val Thr Leu Leu Cys Gln Ser Trp Arg Gln Phe His
340          345          350
Thr Phe Leu Leu Thr Lys Ala Gly Ala Ala Asp Ala Pro Leu Arg Leu
355          360          365
Arg Ser Ile His Glu Tyr Pro Lys Tyr Gln Ala Glu Phe Pro Met Ser
370          375          380
Pro Val Thr Ser Ala His Ala Gly Thr Tyr Arg Cys Tyr Gly Ser Leu
385          390          395          400
Asn Ser Asp Pro Tyr Leu Leu Ser His Pro Ser Glu Pro Leu Glu Leu
405          410          415
Val Val Ser Gly Pro Ser Met Gly Ser Ser Pro Pro Pro Thr Gly Pro
420          425          430
Ile Ser Thr Pro Ala Gly Pro Glu Asp Gln Pro Leu Thr Pro Thr Gly
435          440          445
Ser Asp Pro Gln Ser Gly Leu Gly Arg His Leu Gly Val Val Ile Gly
450          455          460
Ile Leu Val Ala Val Val Leu Leu Leu Leu Leu Leu Leu Leu Phe
465          470          475          480
Leu Ile Leu Arg His Arg Arg Gln Gly Lys His Trp Thr Ser Thr Gln
485          490          495
Arg Lys Ala Asp Phe Gln His Pro Ala Gly Ala Val Gly Pro Glu Pro
500          505          510
Thr Asp Arg Gly Leu Gln Trp Arg Ser Ser Pro Ala Ala Asp Ala Gln
515          520          525
Glu Glu Asn Leu Tyr Ala Ala Val Lys Asp Thr Gln Pro Glu Asp Gly
530          535          540

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Val Glu Met Asp Thr Arg Ala Ala Ala Ser Glu Ala Pro Gln Asp Val
545 550 555 560

Thr Tyr Ala Gln Leu His Ser Leu Thr Leu Arg Arg Lys Ala Thr Glu
565 570 575

Pro Pro Pro Ser Gln Glu Arg Glu Pro Pro Ala Glu Pro Ser Ile Tyr
580 585 590

Ala Thr Leu Ala Ile His
595

<210> 451

<211> 165

<212> PRT

<213> Artificial Sequence

<220>

<223> LY6K__Homo_sapiens__Q17RY6

<400> 451

Met Ala Leu Leu Ala Leu Leu Leu Val Val Ala Leu Pro Arg Val Trp
1 5 10 15

Thr Asp Ala Asn Leu Thr Ala Arg Gln Arg Asp Pro Glu Asp Ser Gln
20 25 30

Arg Thr Asp Glu Gly Asp Asn Arg Val Trp Cys His Val Cys Glu Arg
35 40 45

Glu Asn Thr Phe Glu Cys Gln Asn Pro Arg Arg Cys Lys Trp Thr Glu
50 55 60

Pro Tyr Cys Val Ile Ala Ala Val Lys Ile Phe Pro Arg Phe Phe Met
65 70 75 80

Val Ala Lys Gln Cys Ser Ala Gly Cys Ala Ala Met Glu Arg Pro Lys
85 90 95

Pro Glu Glu Lys Arg Phe Leu Leu Glu Glu Pro Met Pro Phe Phe Tyr
100 105 110

Leu Lys Cys Cys Lys Ile Arg Tyr Cys Asn Leu Glu Gly Pro Pro Ile
115 120 125

Asn Ser Ser Val Phe Lys Glu Tyr Ala Gly Ser Met Gly Glu Ser Cys
130 135 140

Gly Gly Leu Trp Leu Ala Ile Leu Leu Leu Leu Ala Ser Ile Ala Ala
145 150 155 160

ITI-08-PCT_Sequence_Listing_ST25.txt

Gly Leu Ser Leu Ser
165

<210> 452
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> MAGA5__Homo_sapiens__P43359

<400> 452

Met Ser Leu Glu Gln Lys Ser Gln His Cys Lys Pro Glu Glu Gly Leu
1 5 10 15

Asp Thr Gln Glu Glu Ala Leu Gly Leu Val Gly Val Gln Ala Ala Thr
20 25 30

Thr Glu Glu Gln Glu Ala Val Ser Ser Ser Ser Pro Leu Val Pro Gly
35 40 45

Thr Leu Gly Glu Val Pro Ala Ala Gly Ser Pro Gly Pro Leu Lys Ser
50 55 60

Pro Gln Gly Ala Ser Ala Ile Pro Thr Ala Ile Asp Phe Thr Leu Trp
65 70 75 80

Arg Gln Ser Ile Lys Gly Ser Ser Asn Gln Glu Glu Glu Gly Pro Ser
85 90 95

Thr Ser Pro Asp Pro Glu Ser Val Phe Arg Ala Ala Leu Ser Lys Lys
100 105 110

Val Ala Asp Leu Ile His Phe Leu Leu Leu Lys Tyr
115 120

<210> 453
<211> 318
<212> PRT
<213> Artificial Sequence

<220>
<223> MAGA8__Homo_sapiens__P43361

<400> 453

Met Leu Leu Gly Gln Lys Ser Gln Arg Tyr Lys Ala Glu Glu Gly Leu
1 5 10 15

Gln Ala Gln Gly Glu Ala Pro Gly Leu Met Asp Val Gln Ile Pro Thr

ITI-08-PCT_Sequence_Listing_ST25.txt

20	25	30															
Ala	Glu	Glu	Gln	Lys	Ala	Ala	Ser	Ser	Ser	Ser	Thr	Leu	Ile	Met	Gly		
	35						40					45					
Thr	Leu	Glu	Glu	Val	Thr	Asp	Ser	Gly	Ser	Pro	Ser	Pro	Pro	Gln	Ser		
	50					55					60						
Pro	Glu	Gly	Ala	Ser	Ser	Ser	Leu	Thr	Val	Thr	Asp	Ser	Thr	Leu	Trp		
65					70					75					80		
Ser	Gln	Ser	Asp	Glu	Gly	Ser	Ser	Ser	Asn	Glu	Glu	Glu	Gly	Pro	Ser		
			85						90					95			
Thr	Ser	Pro	Asp	Pro	Ala	His	Leu	Glu	Ser	Leu	Phe	Arg	Glu	Ala	Leu		
			100					105					110				
Asp	Glu	Lys	Val	Ala	Glu	Leu	Val	Arg	Phe	Leu	Leu	Arg	Lys	Tyr	Gln		
	115						120					125					
Ile	Lys	Glu	Pro	Val	Thr	Lys	Ala	Glu	Met	Leu	Glu	Ser	Val	Ile	Lys		
	130					135					140						
Asn	Tyr	Lys	Asn	His	Phe	Pro	Asp	Ile	Phe	Ser	Lys	Ala	Ser	Glu	Cys		
145					150					155					160		
Met	Gln	Val	Ile	Phe	Gly	Ile	Asp	Val	Lys	Glu	Val	Asp	Pro	Ala	Gly		
				165					170					175			
His	Ser	Tyr	Ile	Leu	Val	Thr	Cys	Leu	Gly	Leu	Ser	Tyr	Asp	Gly	Leu		
			180					185					190				
Leu	Gly	Asp	Asp	Gln	Ser	Thr	Pro	Lys	Thr	Gly	Leu	Leu	Ile	Ile	Val		
	195						200					205					
Leu	Gly	Met	Ile	Leu	Met	Glu	Gly	Ser	Arg	Ala	Pro	Glu	Glu	Ala	Ile		
	210					215					220						
Trp	Glu	Ala	Leu	Ser	Val	Met	Gly	Leu	Tyr	Asp	Gly	Arg	Glu	His	Ser		
225					230					235					240		
Val	Tyr	Trp	Lys	Leu	Arg	Lys	Leu	Leu	Thr	Gln	Glu	Trp	Val	Gln	Glu		
				245					250					255			
Asn	Tyr	Leu	Glu	Tyr	Arg	Gln	Ala	Pro	Gly	Ser	Asp	Pro	Val	Arg	Tyr		
		260						265					270				
Glu	Phe	Leu	Trp	Gly	Pro	Arg	Ala	Leu	Ala	Glu	Thr	Ser	Tyr	Val	Lys		
	275						280					285					
Val	Leu	Glu	His	Val	Val	Arg	Val	Asn	Ala	Arg	Val	Arg	Ile	Ser	Tyr		
	290					295					300						

ITI-08-PCT_Sequence_Listing_ST25.txt

Pro Ser Leu His Glu Glu Ala Leu Gly Glu Glu Lys Gly Val
305 310 315

<210> 454
<211> 429
<212> PRT
<213> Artificial Sequence

<220>
<223> MAGAB__Homo_sapiens__P43364

<400> 454

Met Glu Thr Gln Phe Arg Arg Gly Gly Leu Gly Cys Ser Pro Ala Ser
1 5 10 15

Ile Lys Arg Lys Lys Lys Arg Glu Asp Ser Gly Asp Phe Gly Leu Gln
20 25 30

Val Ser Thr Met Phe Ser Glu Asp Asp Phe Gln Ser Thr Glu Arg Ala
35 40 45

Pro Tyr Gly Pro Gln Leu Gln Trp Ser Gln Asp Leu Pro Arg Val Gln
50 55 60

Val Phe Arg Glu Gln Ala Asn Leu Glu Asp Arg Ser Pro Arg Arg Thr
65 70 75 80

Gln Arg Ile Thr Gly Gly Glu Gln Val Leu Trp Gly Pro Ile Thr Gln
85 90 95

Ile Phe Pro Thr Val Arg Pro Ala Asp Leu Thr Arg Val Ile Met Pro
100 105 110

Leu Glu Gln Arg Ser Gln His Cys Lys Pro Glu Glu Gly Leu Gln Ala
115 120 125

Gln Glu Glu Asp Leu Gly Leu Val Gly Ala Gln Ala Leu Gln Ala Glu
130 135 140

Glu Gln Glu Ala Ala Phe Phe Ser Ser Thr Leu Asn Val Gly Thr Leu
145 150 155 160

Glu Glu Leu Pro Ala Ala Glu Ser Pro Ser Pro Pro Gln Ser Pro Gln
165 170 175

Glu Glu Ser Phe Ser Pro Thr Ala Met Asp Ala Ile Phe Gly Ser Leu
180 185 190

Ser Asp Glu Gly Ser Gly Ser Gln Glu Lys Glu Gly Pro Ser Thr Ser
195 200 205

ITI-08-PCT_Sequence_Listing_ST25.txt

```

Pro Asp Leu Ile Asp Pro Glu Ser Phe Ser Gln Asp Ile Leu His Asp
 210                215                220

Lys Ile Ile Asp Leu Val His Leu Leu Leu Arg Lys Tyr Arg Val Lys
 225                230                235                240

Gly Leu Ile Thr Lys Ala Glu Met Leu Gly Ser Val Ile Lys Asn Tyr
                245                250                255

Glu Asp Tyr Phe Pro Glu Ile Phe Arg Glu Ala Ser Val Cys Met Gln
                260                265                270

Leu Leu Phe Gly Ile Asp Val Lys Glu Val Asp Pro Thr Ser His Ser
 275                280                285

Tyr Val Leu Val Thr Ser Leu Asn Leu Ser Tyr Asp Gly Ile Gln Cys
 290                295                300

Asn Glu Gln Ser Met Pro Lys Ser Gly Leu Leu Ile Ile Val Leu Gly
 305                310                315                320

Val Ile Phe Met Glu Gly Asn Cys Ile Pro Glu Glu Val Met Trp Glu
                325                330                335

Val Leu Ser Ile Met Gly Val Tyr Ala Gly Arg Glu His Phe Leu Phe
 340                345                350

Gly Glu Pro Lys Arg Leu Leu Thr Gln Asn Trp Val Gln Glu Lys Tyr
 355                360                365

Leu Val Tyr Arg Gln Val Pro Gly Thr Asp Pro Ala Cys Tyr Glu Phe
 370                375                380

Leu Trp Gly Pro Arg Ala His Ala Glu Thr Ser Lys Met Lys Val Leu
 385                390                395                400

Glu Tyr Ile Ala Asn Ala Asn Gly Arg Asp Pro Thr Ser Tyr Pro Ser
                405                410                415

Leu Tyr Glu Asp Ala Leu Arg Glu Glu Gly Glu Gly Val
 420                425

```

```

<210> 455
<211> 369
<212> PRT
<213> Artificial Sequence

<220>
<223> MAGE-A10__Homo_sapiens__A0A024RC14

<400> 455

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Met	Pro	Arg	Ala	Pro	Lys	Arg	Gln	Arg	Cys	Met	Pro	Glu	Glu	Asp	Leu	1	5	10	15
Gln	Ser	Gln	Ser	Glu	Thr	Gln	Gly	Leu	Glu	Gly	Ala	Gln	Ala	Pro	Leu	20	25	30	
Ala	Val	Glu	Glu	Asp	Ala	Ser	Ser	Ser	Thr	Ser	Thr	Ser	Ser	Ser	Phe	35	40	45	
Pro	Ser	Ser	Phe	Pro	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Cys	Tyr	50	55	60	
Pro	Leu	Ile	Pro	Ser	Thr	Pro	Glu	Glu	Val	Ser	Ala	Asp	Asp	Glu	Thr	65	70	75	80
Pro	Asn	Pro	Pro	Gln	Ser	Ala	Gln	Ile	Ala	Cys	Ser	Ser	Pro	Ser	Val	85	90	95	
Val	Ala	Ser	Leu	Pro	Leu	Asp	Gln	Ser	Asp	Glu	Gly	Ser	Ser	Ser	Gln	100	105	110	
Lys	Glu	Glu	Ser	Pro	Ser	Thr	Leu	Gln	Val	Leu	Pro	Asp	Ser	Glu	Ser	115	120	125	
Leu	Pro	Arg	Ser	Glu	Ile	Asp	Glu	Lys	Val	Thr	Asp	Leu	Val	Gln	Phe	130	135	140	
Leu	Leu	Phe	Lys	Tyr	Gln	Met	Lys	Glu	Pro	Ile	Thr	Lys	Ala	Glu	Ile	145	150	155	160
Leu	Glu	Ser	Val	Ile	Lys	Asn	Tyr	Glu	Asp	His	Phe	Pro	Leu	Leu	Phe	165	170	175	
Ser	Glu	Ala	Ser	Glu	Cys	Met	Leu	Leu	Val	Phe	Gly	Ile	Asp	Val	Lys	180	185	190	
Glu	Val	Asp	Pro	Thr	Gly	His	Ser	Phe	Val	Leu	Val	Thr	Ser	Leu	Gly	195	200	205	
Leu	Thr	Tyr	Asp	Gly	Met	Leu	Ser	Asp	Val	Gln	Ser	Met	Pro	Lys	Thr	210	215	220	
Gly	Ile	Leu	Ile	Leu	Ile	Leu	Ser	Ile	Ile	Phe	Ile	Glu	Gly	Tyr	Cys	225	230	235	240
Thr	Pro	Glu	Glu	Val	Ile	Trp	Glu	Ala	Leu	Asn	Met	Met	Gly	Leu	Tyr	245	250	255	
Asp	Gly	Met	Glu	His	Leu	Ile	Tyr	Gly	Glu	Pro	Arg	Lys	Leu	Leu	Thr	260	265	270	

ITI-08-PCT_Sequence_Listing_ST25.txt

Gln Asp Trp Val Gln Glu Asn Tyr Leu Glu Tyr Arg Gln Val Pro Gly
275 280 285

Ser Asp Pro Ala Arg Tyr Glu Phe Leu Trp Gly Pro Arg Ala His Ala
290 295 300

Glu Ile Arg Lys Met Ser Leu Leu Lys Phe Leu Ala Lys Val Asn Gly
305 310 315 320

Ser Asp Pro Arg Ser Phe Pro Leu Trp Tyr Glu Glu Ala Leu Lys Asp
325 330 335

Glu Glu Glu Arg Ala Gln Asp Arg Ile Ala Thr Thr Asp Asp Thr Thr
340 345 350

Ala Met Ala Ser Ala Ser Ser Ser Ala Thr Gly Ser Phe Ser Tyr Pro
355 360 365

Glu

<210> 456

<211> 314

<212> PRT

<213> Artificial Sequence

<220>

<223> MAGE-A12__Homo_sapiens__P43365

<400> 456

Met Pro Leu Glu Gln Arg Ser Gln His Cys Lys Pro Glu Glu Gly Leu
1 5 10 15

Glu Ala Gln Gly Glu Ala Leu Gly Leu Val Gly Ala Gln Ala Pro Ala
20 25 30

Thr Glu Glu Gln Glu Thr Ala Ser Ser Ser Ser Thr Leu Val Glu Val
35 40 45

Thr Leu Arg Glu Val Pro Ala Ala Glu Ser Pro Ser Pro Pro His Ser
50 55 60

Pro Gln Gly Ala Ser Thr Leu Pro Thr Thr Ile Asn Tyr Thr Leu Trp
65 70 75 80

Ser Gln Ser Asp Glu Gly Ser Ser Asn Glu Glu Gln Glu Gly Pro Ser
85 90 95

Thr Phe Pro Asp Leu Glu Thr Ser Phe Gln Val Ala Leu Ser Arg Lys
100 105 110

Met Ala Glu Leu Val His Phe Leu Leu Leu Lys Tyr Arg Ala Arg Glu

ITI-08-PCT_Sequence_Listing_ST25.txt

```

115          120          125
Pro Phe Thr Lys Ala Glu Met Leu Gly Ser Val Ile Arg Asn Phe Gln
 130          135          140
Asp Phe Phe Pro Val Ile Phe Ser Lys Ala Ser Glu Tyr Leu Gln Leu
145          150          155          160
Val Phe Gly Ile Glu Val Val Glu Val Val Arg Ile Gly His Leu Tyr
          165          170          175
Ile Leu Val Thr Cys Leu Gly Leu Ser Tyr Asp Gly Leu Leu Gly Asp
          180          185          190
Asn Gln Ile Val Pro Lys Thr Gly Leu Leu Ile Ile Val Leu Ala Ile
          195          200          205
Ile Ala Lys Glu Gly Asp Cys Ala Pro Glu Glu Lys Ile Trp Glu Glu
 210          215          220
Leu Ser Val Leu Glu Ala Ser Asp Gly Arg Glu Asp Ser Val Phe Ala
225          230          235          240
His Pro Arg Lys Leu Leu Thr Gln Asp Leu Val Gln Glu Asn Tyr Leu
          245          250          255
Glu Tyr Arg Gln Val Pro Gly Ser Asp Pro Ala Cys Tyr Glu Phe Leu
          260          265          270
Trp Gly Pro Arg Ala Leu Val Glu Thr Ser Tyr Val Lys Val Leu His
          275          280          285
His Leu Leu Lys Ile Ser Gly Gly Pro His Ile Ser Tyr Pro Pro Leu
 290          295          300
His Glu Trp Ala Phe Arg Glu Gly Glu Glu
305          310

```

<210> 457

<211> 309

<212> PRT

<213> Artificial Sequence

<220>

<223> MAGE-A1__Homo_sapiens__P43355

<400> 457

```

Met Ser Leu Glu Gln Arg Ser Leu His Cys Lys Pro Glu Glu Ala Leu
1          5          10          15

```

```

Glu Ala Gln Gln Glu Ala Leu Gly Leu Val Cys Val Gln Ala Ala Thr

```

ITI-08-PCT_Sequence_Listing_ST25.txt

```

20          25          30
Ser Ser Ser Ser Pro Leu Val Leu Gly Thr Leu Glu Glu Val Pro Thr
35          40          45
Ala Gly Ser Thr Asp Pro Pro Gln Ser Pro Gln Gly Ala Ser Ala Phe
50          55          60
Pro Thr Thr Ile Asn Phe Thr Arg Gln Arg Gln Pro Ser Glu Gly Ser
65          70          75          80
Ser Ser Arg Glu Glu Glu Gly Pro Ser Thr Ser Cys Ile Leu Glu Ser
85          90          95
Leu Phe Arg Ala Val Ile Thr Lys Lys Val Ala Asp Leu Val Gly Phe
100         105         110
Leu Leu Leu Lys Tyr Arg Ala Arg Glu Pro Val Thr Lys Ala Glu Met
115         120         125
Leu Glu Ser Val Ile Lys Asn Tyr Lys His Cys Phe Pro Glu Ile Phe
130         135         140
Gly Lys Ala Ser Glu Ser Leu Gln Leu Val Phe Gly Ile Asp Val Lys
145         150         155         160
Glu Ala Asp Pro Thr Gly His Ser Tyr Val Leu Val Thr Cys Leu Gly
165         170         175
Leu Ser Tyr Asp Gly Leu Leu Gly Asp Asn Gln Ile Met Pro Lys Thr
180         185         190
Gly Phe Leu Ile Ile Val Leu Val Met Ile Ala Met Glu Gly Gly His
195         200         205
Ala Pro Glu Glu Glu Ile Trp Glu Glu Leu Ser Val Met Glu Val Tyr
210         215         220
Asp Gly Arg Glu His Ser Ala Tyr Gly Glu Pro Arg Lys Leu Leu Thr
225         230         235         240
Gln Asp Leu Val Gln Glu Lys Tyr Leu Glu Tyr Arg Gln Val Pro Asp
245         250         255
Ser Asp Pro Ala Arg Tyr Glu Phe Leu Trp Gly Pro Arg Ala Leu Ala
260         265         270
Glu Thr Ser Tyr Val Lys Val Leu Glu Tyr Val Ile Lys Val Ser Ala
275         280         285
Arg Val Arg Phe Phe Phe Pro Ser Leu Arg Glu Ala Ala Leu Arg Glu
290         295         300

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Glu Glu Glu Gly Val
305

<210> 458

<211> 314

<212> PRT

<213> Artificial Sequence

<220>

<223> MAGE-A2__Homo_sapiens__P43356

<400> 458

Met Pro Leu Glu Gln Arg Ser Gln His Cys Lys Pro Glu Glu Gly Leu
1 5 10 15

Glu Ala Arg Gly Glu Ala Leu Gly Leu Val Gly Ala Gln Ala Pro Ala
20 25 30

Thr Glu Glu Gln Gln Thr Ala Ser Ser Ser Ser Thr Leu Val Glu Val
35 40 45

Thr Leu Gly Glu Val Pro Ala Ala Asp Ser Pro Ser Pro Pro His Ser
50 55 60

Pro Gln Gly Ala Ser Ser Phe Ser Thr Thr Ile Asn Tyr Thr Leu Trp
65 70 75 80

Arg Gln Ser Asp Glu Gly Ser Ser Asn Gln Glu Glu Glu Gly Pro Arg
85 90 95

Met Phe Pro Asp Leu Glu Ser Glu Phe Gln Ala Ala Ile Ser Arg Lys
100 105 110

Met Val Glu Leu Val His Phe Leu Leu Leu Lys Tyr Arg Ala Arg Glu
115 120 125

Pro Val Thr Lys Ala Glu Met Leu Glu Ser Val Leu Arg Asn Cys Gln
130 135 140

Asp Phe Phe Pro Val Ile Phe Ser Lys Ala Ser Glu Tyr Leu Gln Leu
145 150 155 160

Val Phe Gly Ile Glu Val Val Glu Val Val Pro Ile Ser His Leu Tyr
165 170 175

Ile Leu Val Thr Cys Leu Gly Leu Ser Tyr Asp Gly Leu Leu Gly Asp
180 185 190

Asn Gln Val Met Pro Lys Thr Gly Leu Leu Ile Ile Val Leu Ala Ile
195 200 205

ITI-08-PCT_Sequence_Listing_ST25.txt

Ile Ala Ile Glu Gly Asp Cys Ala Pro Glu Glu Lys Ile Trp Glu Glu
210 215 220

Leu Ser Met Leu Glu Val Phe Glu Gly Arg Glu Asp Ser Val Phe Ala
225 230 235 240

His Pro Arg Lys Leu Leu Met Gln Asp Leu Val Gln Glu Asn Tyr Leu
245 250 255

Glu Tyr Arg Gln Val Pro Gly Ser Asp Pro Ala Cys Tyr Glu Phe Leu
260 265 270

Trp Gly Pro Arg Ala Leu Ile Glu Thr Ser Tyr Val Lys Val Leu His
275 280 285

His Thr Leu Lys Ile Gly Gly Glu Pro His Ile Ser Tyr Pro Pro Leu
290 295 300

His Glu Arg Ala Leu Arg Glu Gly Glu Glu
305 310

<210> 459

<211> 314

<212> PRT

<213> Artificial Sequence

<220>

<223> MAGE-A3__Homo_sapiens__P43357

<400> 459

Met Pro Leu Glu Gln Arg Ser Gln His Cys Lys Pro Glu Glu Gly Leu
1 5 10 15

Glu Ala Arg Gly Glu Ala Leu Gly Leu Val Gly Ala Gln Ala Pro Ala
20 25 30

Thr Glu Glu Gln Glu Ala Ala Ser Ser Ser Thr Leu Val Glu Val
35 40 45

Thr Leu Gly Glu Val Pro Ala Ala Glu Ser Pro Asp Pro Pro Gln Ser
50 55 60

Pro Gln Gly Ala Ser Ser Leu Pro Thr Thr Met Asn Tyr Pro Leu Trp
65 70 75 80

Ser Gln Ser Tyr Glu Asp Ser Ser Asn Gln Glu Glu Glu Gly Pro Ser
85 90 95

Thr Phe Pro Asp Leu Glu Ser Glu Phe Gln Ala Ala Leu Ser Arg Lys
100 105 110

ITI-08-PCT_Sequence_Listing_ST25.txt

Val Ala Glu Leu Val His Phe Leu Leu Leu Lys Tyr Arg Ala Arg Glu
115 120 125

Pro Val Thr Lys Ala Glu Met Leu Gly Ser Val Val Gly Asn Trp Gln
130 135 140

Tyr Phe Phe Pro Val Ile Phe Ser Lys Ala Ser Ser Ser Leu Gln Leu
145 150 155 160

Val Phe Gly Ile Glu Leu Met Glu Val Asp Pro Ile Gly His Leu Tyr
165 170 175

Ile Phe Ala Thr Cys Leu Gly Leu Ser Tyr Asp Gly Leu Leu Gly Asp
180 185 190

Asn Gln Ile Met Pro Lys Ala Gly Leu Leu Ile Ile Val Leu Ala Ile
195 200 205

Ile Ala Arg Glu Gly Asp Cys Ala Pro Glu Glu Lys Ile Trp Glu Glu
210 215 220

Leu Ser Val Leu Glu Val Phe Glu Gly Arg Glu Asp Ser Ile Leu Gly
225 230 235 240

Asp Pro Lys Lys Leu Leu Thr Gln His Phe Val Gln Glu Asn Tyr Leu
245 250 255

Glu Tyr Arg Gln Val Pro Gly Ser Asp Pro Ala Cys Tyr Glu Phe Leu
260 265 270

Trp Gly Pro Arg Ala Leu Val Glu Thr Ser Tyr Val Lys Val Leu His
275 280 285

His Met Val Lys Ile Ser Gly Gly Pro His Ile Ser Tyr Pro Pro Leu
290 295 300

His Glu Trp Val Leu Arg Glu Gly Glu Glu
305 310

<210> 460

<211> 317

<212> PRT

<213> Artificial Sequence

<220>

<223> MAGE-A4__Homo_sapiens__A0A024RC12

<400> 460

Met Ser Ser Glu Gln Lys Ser Gln His Cys Lys Pro Glu Glu Gly Val
1 5 10 15

ITI-08-PCT_Sequence_Listing_ST25.txt

Glu	Ala	Gln	Glu	Glu	Ala	Leu	Gly	Leu	Val	Gly	Ala	Gln	Ala	Pro	Thr	20	25	30
Thr	Glu	Glu	Gln	Glu	Ala	Ala	Val	Ser	Ser	Ser	Ser	Pro	Leu	Val	Pro	35	40	45
Gly	Thr	Leu	Glu	Glu	Val	Pro	Ala	Ala	Glu	Ser	Ala	Gly	Pro	Pro	Gln	50	55	60
Ser	Pro	Gln	Gly	Ala	Ser	Ala	Leu	Pro	Thr	Thr	Ile	Ser	Phe	Thr	Cys	65	70	75
Trp	Arg	Gln	Pro	Asn	Glu	Gly	Ser	Ser	Ser	Gln	Glu	Glu	Glu	Gly	Pro	85	90	95
Ser	Thr	Ser	Pro	Asp	Ala	Glu	Ser	Leu	Phe	Arg	Glu	Ala	Leu	Ser	Asn	100	105	110
Lys	Val	Asp	Glu	Leu	Ala	His	Phe	Leu	Leu	Arg	Lys	Tyr	Arg	Ala	Lys	115	120	125
Glu	Leu	Val	Thr	Lys	Ala	Glu	Met	Leu	Glu	Arg	Val	Ile	Lys	Asn	Tyr	130	135	140
Lys	Arg	Cys	Phe	Pro	Val	Ile	Phe	Gly	Lys	Ala	Ser	Glu	Ser	Leu	Lys	145	150	155
Met	Ile	Phe	Gly	Ile	Asp	Val	Lys	Glu	Val	Asp	Pro	Ala	Ser	Asn	Thr	165	170	175
Tyr	Thr	Leu	Val	Thr	Cys	Leu	Gly	Leu	Ser	Tyr	Asp	Gly	Leu	Leu	Gly	180	185	190
Asn	Asn	Gln	Ile	Phe	Pro	Lys	Thr	Gly	Leu	Leu	Ile	Ile	Val	Leu	Gly	195	200	205
Thr	Ile	Ala	Met	Glu	Gly	Asp	Ser	Ala	Ser	Glu	Glu	Glu	Ile	Trp	Glu	210	215	220
Glu	Leu	Gly	Val	Met	Gly	Val	Tyr	Asp	Gly	Arg	Glu	His	Thr	Val	Tyr	225	230	235
Gly	Glu	Pro	Arg	Lys	Leu	Leu	Thr	Gln	Asp	Trp	Val	Gln	Glu	Asn	Tyr	245	250	255
Leu	Glu	Tyr	Arg	Gln	Val	Pro	Gly	Ser	Asn	Pro	Ala	Arg	Tyr	Glu	Phe	260	265	270
Leu	Trp	Gly	Pro	Arg	Ala	Leu	Ala	Glu	Thr	Ser	Tyr	Val	Lys	Val	Leu	275	280	285

ITI-08-PCT_Sequence_Listing_ST25.txt

Glu His Val Val Arg Val Asn Ala Arg Val Arg Ile Ala Tyr Pro Ser
290 295 300

Leu Arg Glu Ala Ala Leu Leu Glu Glu Glu Glu Gly Val
305 310 315

<210> 461

<211> 317

<212> PRT

<213> Artificial Sequence

<220>

<223> MAGE-A4__Homo_sapiens__P43358

<400> 461

Met Ser Ser Glu Gln Lys Ser Gln His Cys Lys Pro Glu Glu Gly Val
1 5 10 15

Glu Ala Gln Glu Glu Ala Leu Gly Leu Val Gly Ala Gln Ala Pro Thr
20 25 30

Thr Glu Glu Gln Glu Ala Ala Val Ser Ser Ser Ser Pro Leu Val Pro
35 40 45

Gly Thr Leu Glu Glu Val Pro Ala Ala Glu Ser Ala Gly Pro Pro Gln
50 55 60

Ser Pro Gln Gly Ala Ser Ala Leu Pro Thr Thr Ile Ser Phe Thr Cys
65 70 75 80

Trp Arg Gln Pro Asn Glu Gly Ser Ser Ser Gln Glu Glu Glu Gly Pro
85 90 95

Ser Thr Ser Pro Asp Ala Glu Ser Leu Phe Arg Glu Ala Leu Ser Asn
100 105 110

Lys Val Asp Glu Leu Ala His Phe Leu Leu Arg Lys Tyr Arg Ala Lys
115 120 125

Glu Leu Val Thr Lys Ala Glu Met Leu Glu Arg Val Ile Lys Asn Tyr
130 135 140

Lys Arg Cys Phe Pro Val Ile Phe Gly Lys Ala Ser Glu Ser Leu Lys
145 150 155 160

Met Ile Phe Gly Ile Asp Val Lys Glu Val Asp Pro Ala Ser Asn Thr
165 170 175

Tyr Thr Leu Val Thr Cys Leu Gly Leu Ser Tyr Asp Gly Leu Leu Gly
180 185 190

ITI-08-PCT_Sequence_Listing_ST25.txt

Asn Asn Gln Ile Phe Pro Lys Thr Gly Leu Leu Ile Ile Val Leu Gly
195 200 205

Thr Ile Ala Met Glu Gly Asp Ser Ala Ser Glu Glu Glu Ile Trp Glu
210 215 220

Glu Leu Gly Val Met Gly Val Tyr Asp Gly Arg Glu His Thr Val Tyr
225 230 235 240

Gly Glu Pro Arg Lys Leu Leu Thr Gln Asp Trp Val Gln Glu Asn Tyr
245 250 255

Leu Glu Tyr Arg Gln Val Pro Gly Ser Asn Pro Ala Arg Tyr Glu Phe
260 265 270

Leu Trp Gly Pro Arg Ala Leu Ala Glu Thr Ser Tyr Val Lys Val Leu
275 280 285

Glu His Val Val Arg Val Asn Ala Arg Val Arg Ile Ala Tyr Pro Ser
290 295 300

Leu Arg Glu Ala Ala Leu Leu Glu Glu Glu Glu Gly Val
305 310 315

<210> 462

<211> 317

<212> PRT

<213> Artificial Sequence

<220>

<223> MAGE-A4__Homo_sapiens__Q1RN33

<400> 462

Met Ser Ser Glu Gln Lys Ser Gln His Cys Lys Pro Glu Glu Gly Val
1 5 10 15

Glu Ala Gln Glu Glu Ala Leu Gly Leu Val Gly Ala Gln Ala Pro Thr
20 25 30

Thr Glu Glu Gln Glu Ala Ala Val Ser Ser Ser Ser Pro Leu Val Pro
35 40 45

Gly Thr Leu Glu Glu Val Pro Ala Ala Glu Ser Ala Gly Pro Pro Gln
50 55 60

Ser Pro Gln Gly Ala Ser Ala Leu Pro Thr Thr Ile Ser Phe Thr Cys
65 70 75 80

Trp Arg Gln Pro Asn Glu Gly Ser Ser Ser Gln Glu Glu Glu Gly Pro
85 90 95

ITI-08-PCT_Sequence_Listing_ST25.txt

Ser Thr Ser Pro Asp Ala Glu Ser Leu Phe Arg Glu Ala Leu Ser Asn
100 105 110

Lys Val Asp Glu Leu Ala His Phe Leu Leu Arg Lys Tyr Arg Ala Lys
115 120 125

Glu Leu Val Thr Lys Ala Glu Met Leu Glu Arg Val Ile Lys Asn Tyr
130 135 140

Lys Arg Cys Phe Pro Val Ile Phe Gly Lys Ala Ser Glu Ser Leu Lys
145 150 155 160

Met Ile Phe Gly Ile Asp Val Lys Glu Val Asp Pro Thr Ser Asn Thr
165 170 175

Tyr Thr Leu Val Thr Cys Leu Gly Leu Ser Tyr Asp Gly Leu Leu Gly
180 185 190

Asn Asn Gln Ile Phe Pro Lys Thr Gly Leu Leu Ile Ile Val Leu Gly
195 200 205

Thr Ile Ala Met Glu Gly Asp Ser Ala Ser Glu Glu Glu Ile Trp Glu
210 215 220

Glu Leu Gly Val Met Gly Val Tyr Asp Gly Arg Glu His Thr Val Tyr
225 230 235 240

Gly Glu Pro Arg Lys Leu Leu Thr Gln Asp Trp Val Gln Glu Asn Tyr
245 250 255

Leu Glu Tyr Arg Gln Val Pro Gly Ser Asn Pro Ala Arg Tyr Glu Phe
260 265 270

Leu Trp Gly Pro Arg Ala Leu Ala Glu Thr Ser Tyr Val Lys Val Leu
275 280 285

Glu His Val Val Arg Val Asn Ala Arg Val Arg Ile Ala Tyr Pro Ser
290 295 300

Leu Arg Glu Ala Ala Leu Leu Glu Glu Glu Glu Gly Val
305 310 315

<210> 463

<211> 314

<212> PRT

<213> Artificial Sequence

<220>

<223> MAGE-A6__Homo_sapiens__A8K072

<400> 463

ITI-08-PCT_Sequence_Listing_ST25.txt

```

Met Pro Leu Glu Gln Arg Ser Gln His Cys Lys Pro Glu Glu Gly Leu
1      5      10      15

Glu Ala Arg Gly Glu Ala Leu Gly Leu Val Gly Ala Gln Ala Pro Ala
      20      25      30

Thr Glu Glu Gln Glu Ala Ala Ser Ser Ser Thr Leu Val Glu Val
      35      40      45

Thr Leu Gly Glu Val Pro Ala Ala Glu Ser Pro Asp Pro Pro Gln Ser
      50      55      60

Pro Gln Gly Ala Ser Ser Leu Pro Thr Thr Met Asn Tyr Pro Leu Trp
65      70      75      80

Ser Gln Ser Tyr Glu Asp Ser Ser Asn Gln Glu Glu Glu Gly Pro Ser
      85      90      95

Thr Phe Pro Asp Leu Glu Ser Glu Phe Gln Ala Ala Leu Ser Arg Lys
      100      105      110

Leu Ala Lys Leu Val His Phe Leu Leu Leu Lys Tyr Arg Ala Arg Glu
      115      120      125

Pro Val Thr Lys Ala Glu Met Leu Gly Ser Val Val Gly Asn Trp Gln
      130      135      140

Tyr Phe Phe Pro Val Ile Phe Ser Lys Ala Ser Asp Ser Leu Gln Leu
145      150      155      160

Val Phe Gly Ile Glu Leu Met Glu Val Asp Pro Ile Gly His Val Tyr
      165      170      175

Ile Phe Ala Thr Cys Leu Gly Leu Ser Tyr Asp Gly Leu Leu Gly Asp
      180      185      190

Asn Gln Ile Met Pro Lys Thr Gly Phe Leu Ile Ile Ile Leu Ala Ile
      195      200      205

Ile Ala Lys Glu Gly Asp Cys Ala Pro Glu Glu Lys Ile Trp Glu Glu
      210      215      220

Leu Ser Val Leu Glu Val Phe Glu Gly Arg Glu Asp Ile Ile Phe Gly
225      230      235      240

Asp Pro Lys Lys Leu Leu Thr Gln Tyr Phe Val Gln Glu Asn Tyr Leu
      245      250      255

Glu Tyr Arg Gln Val Pro Gly Ser Asp Pro Ala Cys Tyr Glu Phe Leu
      260      265      270

Trp Gly Pro Arg Ala Leu Ile Glu Thr Ser Tyr Val Lys Val Leu His

```

ITI-08-PCT_Sequence_Listing_ST25.txt

275

280

285

His Met Val Lys Ile Ser Gly Gly Pro Arg Ile Ser Tyr Pro Leu Leu
290 295 300

His Glu Trp Ala Leu Arg Glu Gly Glu Glu
305 310

<210> 464

<211> 314

<212> PRT

<213> Artificial Sequence

<220>

<223> MAGE-A6__Homo_sapiens__P43360

<400> 464

Met Pro Leu Glu Gln Arg Ser Gln His Cys Lys Pro Glu Glu Gly Leu
1 5 10 15

Glu Ala Arg Gly Glu Ala Leu Gly Leu Val Gly Ala Gln Ala Pro Ala
20 25 30

Thr Glu Glu Gln Glu Ala Ala Ser Ser Ser Thr Leu Val Glu Val
35 40 45

Thr Leu Gly Glu Val Pro Ala Ala Glu Ser Pro Asp Pro Pro Gln Ser
50 55 60

Pro Gln Gly Ala Ser Ser Leu Pro Thr Thr Met Asn Tyr Pro Leu Trp
65 70 75 80

Ser Gln Ser Tyr Glu Asp Ser Ser Asn Gln Glu Glu Glu Gly Pro Ser
85 90 95

Thr Phe Pro Asp Leu Glu Ser Glu Phe Gln Ala Ala Leu Ser Arg Lys
100 105 110

Val Ala Lys Leu Val His Phe Leu Leu Leu Lys Tyr Arg Ala Arg Glu
115 120 125

Pro Val Thr Lys Ala Glu Met Leu Gly Ser Val Val Gly Asn Trp Gln
130 135 140

Tyr Phe Phe Pro Val Ile Phe Ser Lys Ala Ser Asp Ser Leu Gln Leu
145 150 155 160

Val Phe Gly Ile Glu Leu Met Glu Val Asp Pro Ile Gly His Val Tyr
165 170 175

Ile Phe Ala Thr Cys Leu Gly Leu Ser Tyr Asp Gly Leu Leu Gly Asp

ITI-08-PCT_Sequence_Listing_ST25.txt

180

185

190

Asn Gln Ile Met Pro Lys Thr Gly Phe Leu Ile Ile Ile Leu Ala Ile
195 200 205

Ile Ala Lys Glu Gly Asp Cys Ala Pro Glu Glu Lys Ile Trp Glu Glu
210 215 220

Leu Ser Val Leu Glu Val Phe Glu Gly Arg Glu Asp Ser Ile Phe Gly
225 230 235 240

Asp Pro Lys Lys Leu Leu Thr Gln Tyr Phe Val Gln Glu Asn Tyr Leu
245 250 255

Glu Tyr Arg Gln Val Pro Gly Ser Asp Pro Ala Cys Tyr Glu Phe Leu
260 265 270

Trp Gly Pro Arg Ala Leu Ile Glu Thr Ser Tyr Val Lys Val Leu His
275 280 285

His Met Val Lys Ile Ser Gly Gly Pro Arg Ile Ser Tyr Pro Leu Leu
290 295 300

His Glu Trp Ala Leu Arg Glu Gly Glu Glu
305 310

<210> 465

<211> 314

<212> PRT

<213> Artificial Sequence

<220>

<223> MAGE-A6__Homo_sapiens__Q6FHI5

<400> 465

Met Pro Leu Glu Gln Arg Ser Gln His Cys Lys Pro Glu Glu Gly Leu
1 5 10 15

Glu Ala Arg Gly Glu Ala Leu Gly Leu Val Gly Ala Gln Ala Pro Ala
20 25 30

Thr Glu Glu Gln Glu Ala Ala Ser Ser Ser Ser Thr Leu Val Glu Val
35 40 45

Thr Leu Gly Glu Val Pro Ala Ala Glu Ser Pro Asp Pro Pro Gln Ser
50 55 60

Pro Gln Gly Ala Ser Ser Leu Pro Thr Thr Met Asn Tyr Pro Leu Trp
65 70 75 80

Ser Gln Ser Tyr Glu Asp Ser Ser Asn Gln Glu Glu Glu Gly Pro Ser

ITI-08-PCT_Sequence_Listing_ST25.txt

85 90 95

Thr Phe Pro Asp Leu Glu Ser Glu Phe Gln Ala Ala Leu Ser Arg Lys
100 105 110

Val Ala Lys Leu Val His Phe Leu Leu Leu Lys Tyr Arg Ala Arg Glu
115 120 125

Pro Val Thr Lys Ala Glu Met Leu Gly Ser Val Val Gly Asn Trp Gln
130 135 140

Tyr Phe Phe Pro Val Ile Phe Ser Lys Ala Ser Asp Ser Leu Gln Leu
145 150 155 160

Val Phe Gly Ile Glu Leu Met Glu Val Asp Pro Ile Gly His Val Tyr
165 170 175

Ile Phe Ala Thr Cys Leu Gly Leu Ser Tyr Asp Gly Leu Leu Gly Asp
180 185 190

Asn Gln Ile Met Pro Lys Thr Gly Phe Leu Ile Ile Ile Leu Ala Ile
195 200 205

Ile Ala Lys Glu Gly Asp Cys Ala Pro Glu Glu Lys Ile Trp Glu Glu
210 215 220

Leu Ser Val Leu Glu Val Phe Glu Gly Arg Glu Asp Ser Ile Phe Gly
225 230 235 240

Asp Pro Lys Lys Leu Leu Thr Gln Tyr Phe Val Gln Glu Asn Tyr Leu
245 250 255

Glu Tyr Arg Gln Val Pro Gly Ser Asp Pro Ala Cys Tyr Glu Phe Leu
260 265 270

Trp Gly Pro Arg Ala Leu Ile Glu Thr Ser Tyr Val Lys Val Leu His
275 280 285

His Met Val Lys Ile Ser Gly Gly Pro Arg Ile Ser Tyr Pro Leu Leu
290 295 300

His Glu Trp Ala Phe Arg Glu Gly Glu Glu
305 310

<210> 466

<211> 315

<212> PRT

<213> Artificial Sequence

<220>

<223> MAGE-A9__Homo_sapiens__P43362

ITI-08-PCT_Sequence_Listing_ST25.txt

<400> 466

Met	Ser	Leu	Glu	Gln	Arg	Ser	Pro	His	Cys	Lys	Pro	Asp	Glu	Asp	Leu	1	5	10	15
Glu	Ala	Gln	Gly	Glu	Asp	Leu	Gly	Leu	Met	Gly	Ala	Gln	Glu	Pro	Thr	20	25	30	
Gly	Glu	Glu	Glu	Glu	Thr	Thr	Ser	Ser	Asp	Ser	Lys	Glu	Glu	Glu	35	40	45		
Val	Ser	Ala	Ala	Gly	Ser	Ser	Ser	Pro	Pro	Gln	Ser	Pro	Gln	Gly	Gly	50	55	60	
Ala	Ser	Ser	Ser	Ile	Ser	Val	Tyr	Tyr	Thr	Leu	Trp	Ser	Gln	Phe	Asp	65	70	75	80
Glu	Gly	Ser	Ser	Ser	Gln	Glu	Glu	Glu	Glu	Pro	Ser	Ser	Ser	Val	Asp	85	90	95	
Pro	Ala	Gln	Leu	Glu	Phe	Met	Phe	Gln	Glu	Ala	Leu	Lys	Leu	Lys	Val	100	105	110	
Ala	Glu	Leu	Val	His	Phe	Leu	Leu	His	Lys	Tyr	Arg	Val	Lys	Glu	Pro	115	120	125	
Val	Thr	Lys	Ala	Glu	Met	Leu	Glu	Ser	Val	Ile	Lys	Asn	Tyr	Lys	Arg	130	135	140	
Tyr	Phe	Pro	Val	Ile	Phe	Gly	Lys	Ala	Ser	Glu	Phe	Met	Gln	Val	Ile	145	150	155	160
Phe	Gly	Thr	Asp	Val	Lys	Glu	Val	Asp	Pro	Ala	Gly	His	Ser	Tyr	Ile	165	170	175	
Leu	Val	Thr	Ala	Leu	Gly	Leu	Ser	Cys	Asp	Ser	Met	Leu	Gly	Asp	Gly	180	185	190	
His	Ser	Met	Pro	Lys	Ala	Ala	Leu	Leu	Ile	Ile	Val	Leu	Gly	Val	Ile	195	200	205	
Leu	Thr	Lys	Asp	Asn	Cys	Ala	Pro	Glu	Glu	Val	Ile	Trp	Glu	Ala	Leu	210	215	220	
Ser	Val	Met	Gly	Val	Tyr	Val	Gly	Lys	Glu	His	Met	Phe	Tyr	Gly	Glu	225	230	235	240
Pro	Arg	Lys	Leu	Leu	Thr	Gln	Asp	Trp	Val	Gln	Glu	Asn	Tyr	Leu	Glu	245	250	255	
Tyr	Arg	Gln	Val	Pro	Gly	Ser	Asp	Pro	Ala	His	Tyr	Glu	Phe	Leu	Trp	260	265	270	

ITI-08-PCT_Sequence_Listing_ST25.txt

Gly Ser Lys Ala His Ala Glu Thr Ser Tyr Glu Lys Val Ile Asn Tyr
275 280 285

Leu Val Met Leu Asn Ala Arg Glu Pro Ile Cys Tyr Pro Ser Leu Tyr
290 295 300

Glu Glu Val Leu Gly Glu Glu Gln Glu Gly Val
305 310 315

<210> 467

<211> 347

<212> PRT

<213> Artificial Sequence

<220>

<223> MAGE-B10__Homo_sapiens__Q96LZ2

<400> 467

Met Pro Arg Gly Gln Lys Ser Lys Leu Arg Ala Arg Glu Lys Arg Arg
1 5 10 15

Gln Ala Arg Gly Gly Leu Glu Asp Leu Ile Asp Ala Leu Asp Ile Leu
20 25 30

Glu Glu Glu Glu Glu Ser Pro Pro Ser Ala Ser Ala Cys Leu Lys Asp
35 40 45

Val Phe Gln Ser Ser Leu Asp Gly Ala Ser Asn Asn Pro His Gly Leu
50 55 60

Arg Glu Ala Gln Ser Thr Ser Thr Ser Ala Thr Ala Ala Ser His Thr
65 70 75 80

Arg His Pro Glu Gly Val Asn Asp Gln Met Glu Glu Arg Pro Ile Cys
85 90 95

Thr Gln Asp Leu Glu Ala Thr Asp Ser Phe Pro Arg Gly Pro Val Asp
100 105 110

Glu Lys Val Ile Ile Leu Val His Tyr Leu Leu Tyr Lys Tyr Gln Met
115 120 125

Lys Glu Pro Ile Thr Lys Ala Asp Met Leu Arg Asn Val Thr Gln Met
130 135 140

Ser Lys Ser Gln Phe Pro Val Ile Leu Ser Arg Ala Ser Glu His Leu
145 150 155 160

Glu Leu Ile Phe Gly Leu Asp Leu Lys Glu Val Glu Pro Asn Lys His
165 170 175

ITI-08-PCT_Sequence_Listing_ST25.txt

Ile Tyr Val Leu Val Asn Lys Leu Asp Leu Gly Cys Asp Ala Lys Leu
180 185 190

Ser Asp Glu Thr Gly Val Pro Lys Thr Gly Leu Leu Met Thr Val Leu
195 200 205

Gly Ile Ile Phe Thr Asn Gly Asn Cys Val Ala Glu Glu Glu Val Trp
210 215 220

Lys Val Phe Asn Thr Met Gly Leu Tyr Asp Gly Ile Glu His Phe Met
225 230 235 240

Phe Gly Glu Pro Arg Lys Leu Leu Thr Lys Asp Leu Val Lys Glu Asn
245 250 255

Tyr Leu Glu Tyr Gln Gln Val Pro Asn Ser Asp Pro Pro Arg Tyr Gln
260 265 270

Phe Leu Trp Gly Pro Arg Ala His Ala Glu Thr Ser Lys Met Lys Val
275 280 285

Leu Glu Phe Leu Ala Lys Val Asn Asp Thr Ala Pro Ser Glu Phe Ser
290 295 300

Asn Trp Tyr Thr Glu Ala Leu Gln Asp Glu Glu Glu Arg Ala Arg Ala
305 310 315 320

Arg Val Ala Ala Lys Ala Arg Val Ser Ala Thr Ala Gly Ala Arg Ser
325 330 335

Lys Val Lys Ser Ser Lys Ser Ser Gln Leu Gln
340 345

<210> 468
<211> 324
<212> PRT
<213> Artificial Sequence

<220>
<223> MAGE-B16__Homo_sapiens__A2A368

<400> 468

Met Ser Gln Asp Gln Glu Ser Pro Arg Cys Thr His Asp Gln His Leu
1 5 10 15

Gln Thr Phe Ser Glu Thr Gln Ser Leu Glu Val Ala Gln Val Ser Lys
20 25 30

Ala Leu Glu Lys Thr Leu Leu Ser Ser Ser His Pro Leu Val Pro Gly
35 40 45

ITI-08-PCT_Sequence_Listing_ST25.txt

Lys	Leu	Lys	Glu	Ala	Pro	Ala	Ala	Lys	Ala	Glu	Ser	Pro	Leu	Glu	Val	50	55	60	
Pro	Gln	Ser	Phe	Cys	Ser	Ser	Ser	Ile	Ala	Val	Thr	Thr	Thr	Ser	Ser	65	70	75	80
Ser	Glu	Ser	Asp	Glu	Ala	Ser	Ser	Asn	Gln	Glu	Glu	Glu	Asp	Ser	Pro	85	90	95	
Ser	Ser	Ser	Glu	Asp	Thr	Ser	Asp	Pro	Arg	Asn	Val	Pro	Ala	Asp	Ala	100	105	110	
Leu	Asp	Gln	Lys	Val	Ala	Phe	Leu	Val	Asn	Phe	Met	Leu	His	Lys	Cys	115	120	125	
Gln	Met	Lys	Lys	Pro	Ile	Thr	Lys	Ala	Asp	Met	Leu	Lys	Ile	Ile	Ile	130	135	140	
Lys	Asp	Asp	Glu	Ser	His	Phe	Ser	Glu	Ile	Leu	Leu	Arg	Ala	Ser	Glu	145	150	155	160
His	Leu	Glu	Met	Ile	Phe	Gly	Leu	Asp	Val	Val	Glu	Val	Asp	Pro	Thr	165	170	175	
Thr	His	Cys	Tyr	Gly	Leu	Phe	Ile	Lys	Leu	Gly	Leu	Thr	Tyr	Asp	Gly	180	185	190	
Met	Leu	Ser	Gly	Glu	Lys	Gly	Val	Pro	Lys	Thr	Gly	Leu	Leu	Ile	Ile	195	200	205	
Val	Leu	Gly	Val	Ile	Phe	Met	Lys	Gly	Asn	Arg	Ala	Thr	Glu	Glu	Glu	210	215	220	
Val	Trp	Glu	Val	Leu	Asn	Leu	Thr	Gly	Val	Tyr	Ser	Gly	Lys	Lys	His	225	230	235	240
Phe	Ile	Phe	Gly	Glu	Pro	Arg	Met	Leu	Ile	Thr	Lys	Asp	Phe	Val	Lys	245	250	255	
Glu	Lys	Tyr	Leu	Glu	Tyr	Gln	Gln	Val	Ala	Asn	Ser	Asp	Pro	Ala	Arg	260	265	270	
Tyr	Glu	Phe	Leu	Trp	Gly	Pro	Arg	Ala	Lys	Ala	Glu	Thr	Ser	Lys	Met	275	280	285	
Lys	Val	Leu	Glu	Phe	Val	Ala	Lys	Val	His	Gly	Ser	Tyr	Pro	His	Ser	290	295	300	
Phe	Pro	Ser	Gln	Tyr	Ala	Glu	Ala	Leu	Lys	Glu	Glu	Glu	Glu	Arg	Ala	305	310	315	320

ITI-08-PCT_Sequence_Listing_ST25.txt

Arg Ala Arg Ile

<210> 469

<211> 336

<212> PRT

<213> Artificial Sequence

<220>

<223> MAGE-B17__Homo_sapiens__A8MXT2

<400> 469

Met Pro Arg Gly Gln Ala Ser Lys Arg Arg Ala Arg Glu Lys Arg Arg
1 5 10 15

Gln Ala Arg Gly Glu Asp Gln Cys Leu Gly Gly Ala Gln Ala Thr Ala
20 25 30

Ala Glu Lys Glu Lys Leu Pro Ser Ser Ser Ser Pro Ala Cys Gln Ser
35 40 45

Pro Pro Gln Ser Phe Pro Asn Ala Gly Ile Pro Gln Glu Ser Gln Arg
50 55 60

Ala Ser Tyr Pro Ser Ser Pro Ala Ser Ala Val Ser Leu Thr Ser Ser
65 70 75 80

Asp Glu Gly Ala Lys Gly Gln Lys Gly Glu Ser Pro Asn Ser Phe His
85 90 95

Gly Pro Ser Ser Ser Glu Ser Thr Gly Arg Asp Leu Leu Asn Thr Lys
100 105 110

Thr Gly Glu Leu Val Gln Phe Leu Leu Asn Lys Tyr Ile Arg Lys Glu
115 120 125

Pro Ile Thr Arg Glu Ala Met Leu Lys Val Ile Asn Arg Lys Tyr Lys
130 135 140

Gln His Phe Pro Glu Ile Leu Arg Arg Ser Thr Glu Asn Val Glu Val
145 150 155 160

Val Phe Gly Leu Tyr Leu Lys Glu Met Asp Pro Ser Arg Gln Ser Tyr
165 170 175

Val Leu Val Gly Lys Leu Asp Phe Pro Asn Gln Gly Ser Leu Ser Asp
180 185 190

Gly Gly Gly Phe Pro Leu Ser Gly Leu Leu Met Val Leu Leu Ser Thr
195 200 205

Ile Phe Met His Gly Asn Arg Ala Thr Glu Glu Glu Met Trp Glu Cys

ITI-08-PCT_Sequence_Listing_ST25.txt

210

215

220

Leu Asn Ala Leu Gly Met Tyr Lys Gly Arg Lys His Phe Ile Tyr Gly
225 230 235 240

Glu Pro Gln Glu Leu Val Thr Lys Asp Leu Val Arg Glu Gly Tyr Leu
245 250 255

Glu Tyr Gln Gln Val Pro Ser Ser Asp Pro Pro Arg Tyr Glu Phe Leu
260 265 270

Trp Gly Pro Arg Ala Arg Ala Glu Thr Ser Lys Met Lys Val Leu Glu
275 280 285

Phe Val Ala Lys Leu Asn Asp Thr Val Ala Ser Thr Tyr Lys Ser Arg
290 295 300

Tyr Glu Glu Ala Leu Arg Glu Glu Glu Glu Gln Ala Arg Ala Arg Ala
305 310 315 320

Val Ala Arg Asp Ser Ala Arg Ala Arg Ala Ser Arg Ser Phe Gln Pro
325 330 335

<210> 470

<211> 347

<212> PRT

<213> Artificial Sequence

<220>

<223> MAGE-_B1__Homo_sapiens__Q96TG1

<400> 470

Met Pro Arg Gly Gln Lys Ser Lys Leu Arg Ala Arg Glu Lys Arg Arg
1 5 10 15

Lys Ala Arg Glu Glu Thr Gln Gly Leu Lys Val Arg His Ala Thr Ala
20 25 30

Ala Glu Lys Glu Glu Cys Pro Ser Ser Pro Val Leu Gly Asp Thr
35 40 45

Pro Thr Ser Ser Pro Ala Ala Gly Ile Pro Gln Lys Pro Gln Gly Ala
50 55 60

Pro Pro Thr Thr Thr Ala Ala Ala Ala Val Ser Cys Thr Glu Ser Asp
65 70 75 80

Glu Gly Ala Lys Cys Gln Gly Glu Glu Asn Ala Ser Phe Ser Gln Ala
85 90 95

Thr Thr Ser Thr Glu Ser Ser Val Lys Asp Pro Val Ala Trp Glu Ala

ITI-08-PCT_Sequence_Listing_ST25.txt

100	105	110															
Gly	Met	Leu	Met	His	Phe	Ile	Leu	Arg	Lys	Tyr	Lys	Met	Arg	Glu	Pro		
	115						120					125					
Ile	Met	Lys	Ala	Asp	Met	Leu	Lys	Val	Val	Asp	Glu	Lys	Tyr	Lys	Asp		
	130					135					140						
His	Phe	Thr	Glu	Ile	Leu	Asn	Gly	Ala	Ser	Arg	Arg	Leu	Glu	Leu	Val		
145					150					155					160		
Phe	Gly	Leu	Asp	Leu	Lys	Glu	Asp	Asn	Pro	Ser	Ser	His	Thr	Tyr	Thr		
				165					170					175			
Leu	Val	Ser	Lys	Leu	Asn	Leu	Thr	Asn	Asp	Gly	Asn	Leu	Ser	Asn	Asp		
			180					185					190				
Trp	Asp	Phe	Pro	Arg	Asn	Gly	Leu	Leu	Met	Pro	Leu	Leu	Gly	Val	Ile		
	195						200					205					
Phe	Leu	Lys	Gly	Asn	Ser	Ala	Thr	Glu	Glu	Glu	Ile	Trp	Lys	Phe	Met		
	210					215					220						
Asn	Val	Leu	Gly	Ala	Tyr	Asp	Gly	Glu	Glu	His	Leu	Ile	Tyr	Gly	Glu		
225					230					235					240		
Pro	Arg	Lys	Phe	Ile	Thr	Gln	Asp	Leu	Val	Gln	Glu	Lys	Tyr	Leu	Lys		
				245					250					255			
Tyr	Glu	Gln	Val	Pro	Asn	Ser	Asp	Pro	Pro	Arg	Tyr	Gln	Phe	Leu	Trp		
			260					265					270				
Gly	Pro	Arg	Ala	Tyr	Ala	Glu	Thr	Thr	Lys	Met	Lys	Val	Leu	Glu	Phe		
		275					280					285					
Leu	Ala	Lys	Met	Asn	Gly	Ala	Thr	Pro	Arg	Asp	Phe	Pro	Ser	His	Tyr		
	290					295					300						
Glu	Glu	Ala	Leu	Arg	Asp	Glu	Glu	Glu	Arg	Ala	Gln	Val	Arg	Ser	Ser		
305					310					315					320		
Val	Arg	Ala	Arg	Arg	Arg	Thr	Thr	Ala	Thr	Thr	Phe	Arg	Ala	Arg	Ser		
				325				330						335			
Arg	Ala	Pro	Phe	Ser	Arg	Ser	Ser	His	Pro	Met							
			340					345									

<210> 471
 <211> 319
 <212> PRT
 <213> Artificial Sequence

ITI-08-PCT_Sequence_Listing_ST25.txt

<220>

<223> MAGE-B2__Homo_sapiens__015479

<400> 471

```

Met  Pro  Arg  Gly  Gln  Lys  Ser  Lys  Leu  Arg  Ala  Arg  Glu  Lys  Arg  Arg
1          5          10          15

Lys  Ala  Arg  Asp  Glu  Thr  Arg  Gly  Leu  Asn  Val  Pro  Gln  Val  Thr  Glu
          20          25          30

Ala  Glu  Glu  Glu  Glu  Ala  Pro  Cys  Cys  Ser  Ser  Ser  Val  Ser  Gly  Gly
          35          40          45

Ala  Ala  Ser  Ser  Ser  Pro  Ala  Ala  Gly  Ile  Pro  Gln  Glu  Pro  Gln  Arg
          50          55          60

Ala  Pro  Thr  Thr  Ala  Ala  Ala  Ala  Ala  Ala  Gly  Val  Ser  Ser  Thr  Lys
65          70          75          80

Ser  Lys  Lys  Gly  Ala  Lys  Ser  His  Gln  Gly  Glu  Lys  Asn  Ala  Ser  Ser
          85          90          95

Ser  Gln  Ala  Ser  Thr  Ser  Thr  Lys  Ser  Pro  Ser  Glu  Asp  Pro  Leu  Thr
          100          105          110

Arg  Lys  Ser  Gly  Ser  Leu  Val  Gln  Phe  Leu  Leu  Tyr  Lys  Tyr  Lys  Ile
          115          120          125

Lys  Lys  Ser  Val  Thr  Lys  Gly  Glu  Met  Leu  Lys  Ile  Val  Gly  Lys  Arg
          130          135          140

Phe  Arg  Glu  His  Phe  Pro  Glu  Ile  Leu  Lys  Lys  Ala  Ser  Glu  Gly  Leu
145          150          155          160

Ser  Val  Val  Phe  Gly  Leu  Glu  Leu  Asn  Lys  Val  Asn  Pro  Asn  Gly  His
          165          170          175

Thr  Tyr  Thr  Phe  Ile  Asp  Lys  Val  Asp  Leu  Thr  Asp  Glu  Glu  Ser  Leu
          180          185          190

Leu  Ser  Ser  Trp  Asp  Phe  Pro  Arg  Arg  Lys  Leu  Leu  Met  Pro  Leu  Leu
          195          200          205

Gly  Val  Ile  Phe  Leu  Asn  Gly  Asn  Ser  Ala  Thr  Glu  Glu  Glu  Ile  Trp
          210          215          220

Glu  Phe  Leu  Asn  Met  Leu  Gly  Val  Tyr  Asp  Gly  Glu  Glu  His  Ser  Val
225          230          235          240

Phe  Gly  Glu  Pro  Trp  Lys  Leu  Ile  Thr  Lys  Asp  Leu  Val  Gln  Glu  Lys
          245          250          255

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Tyr Leu Glu Tyr Lys Gln Val Pro Ser Ser Asp Pro Pro Arg Phe Gln
260 265 270

Phe Leu Trp Gly Pro Arg Ala Tyr Ala Glu Thr Ser Lys Met Lys Val
275 280 285

Leu Glu Phe Leu Ala Lys Val Asn Gly Thr Thr Pro Cys Ala Phe Pro
290 295 300

Thr His Tyr Glu Glu Ala Leu Lys Asp Glu Glu Lys Ala Gly Val
305 310 315

<210> 472

<211> 346

<212> PRT

<213> Artificial Sequence

<220>

<223> MAGE-B3__Homo_sapiens__015480

<400> 472

Met Pro Arg Gly Gln Lys Ser Thr Leu His Ala Arg Glu Lys Arg Gln
1 5 10 15

Gln Thr Arg Gly Gln Thr Gln Asp His Gln Gly Ala Gln Ile Thr Ala
20 25 30

Thr Asn Lys Lys Lys Val Ser Phe Ser Ser Pro Leu Ile Leu Gly Ala
35 40 45

Thr Ile Gln Lys Lys Ser Ala Gly Arg Ser Arg Ser Ala Leu Lys Lys
50 55 60

Pro Gln Arg Ala Leu Ser Thr Thr Thr Ser Val Asp Val Ser Tyr Lys
65 70 75 80

Lys Ser Tyr Lys Gly Ala Asn Ser Lys Ile Glu Lys Lys Gln Ser Phe
85 90 95

Ser Gln Gly Leu Ser Ser Thr Val Gln Ser Arg Thr Asp Pro Leu Ile
100 105 110

Met Lys Thr Asn Met Leu Val Gln Phe Leu Met Glu Met Tyr Lys Met
115 120 125

Lys Lys Pro Ile Met Lys Ala Asp Met Leu Lys Ile Val Gln Lys Ser
130 135 140

His Lys Asn Cys Phe Pro Glu Ile Leu Lys Lys Ala Ser Phe Asn Met
145 150 155 160

ITI-08-PCT_Sequence_Listing_ST25.txt

Glu Val Val Phe Gly Val Asp Leu Lys Lys Val Asp Ser Thr Lys Asp
165 170 175

Ser Tyr Val Leu Val Ser Lys Met Asp Leu Pro Asn Asn Gly Thr Val
180 185 190

Thr Arg Gly Arg Gly Phe Pro Lys Thr Gly Leu Leu Leu Asn Leu Leu
195 200 205

Gly Val Ile Phe Met Lys Gly Asn Cys Ala Thr Glu Glu Lys Ile Trp
210 215 220

Glu Phe Leu Asn Lys Met Arg Ile Tyr Asp Gly Lys Lys His Phe Ile
225 230 235 240

Phe Gly Glu Pro Arg Lys Leu Ile Thr Gln Asp Leu Val Lys Leu Lys
245 250 255

Tyr Leu Glu Tyr Arg Gln Val Pro Asn Ser Asn Pro Ala Arg Tyr Glu
260 265 270

Phe Leu Trp Gly Pro Arg Ala His Ala Glu Thr Ser Lys Met Lys Val
275 280 285

Leu Glu Phe Trp Ala Lys Val Asn Lys Thr Val Pro Ser Ala Phe Gln
290 295 300

Phe Trp Tyr Glu Glu Ala Leu Arg Asp Glu Glu Glu Arg Val Gln Ala
305 310 315 320

Ala Ala Met Leu Asn Asp Gly Ser Ser Ala Met Gly Arg Lys Cys Ser
325 330 335

Lys Ala Lys Ala Ser Ser Ser Ser His Ala
340 345

<210> 473

<211> 346

<212> PRT

<213> Artificial Sequence

<220>

<223> MAGE-B4__Homo_sapiens__015481

<400> 473

Met Pro Arg Gly Gln Lys Ser Lys Leu Arg Ala Arg Glu Lys Arg Gln
1 5 10 15

Arg Thr Arg Gly Gln Thr Gln Asp Leu Lys Val Gly Gln Pro Thr Ala
20 25 30

ITI-08-PCT_Sequence_Listing_ST25.txt

Ala	Glu	Lys	Glu	Glu	Ser	Pro	Ser	Ser	Ser	Ser	Ser	Val	Leu	Arg	Asp		
		35					40					45					
Thr	Ala	Ser	Ser	Ser	Leu	Ala	Phe	Gly	Ile	Pro	Gln	Glu	Pro	Gln	Arg		
	50					55					60						
Glu	Pro	Pro	Thr	Thr	Ser	Ala	Ala	Ala	Ala	Met	Ser	Cys	Thr	Gly	Ser		
65					70					75					80		
Asp	Lys	Gly	Asp	Glu	Ser	Gln	Asp	Glu	Glu	Asn	Ala	Ser	Ser	Ser	Gln		
			85						90					95			
Ala	Ser	Thr	Ser	Thr	Glu	Arg	Ser	Leu	Lys	Asp	Ser	Leu	Thr	Arg	Lys		
			100					105					110				
Thr	Lys	Met	Leu	Val	Gln	Phe	Leu	Leu	Tyr	Lys	Tyr	Lys	Met	Lys	Glu		
	115						120					125					
Pro	Thr	Thr	Lys	Ala	Glu	Met	Leu	Lys	Ile	Ile	Ser	Lys	Lys	Tyr	Lys		
	130					135					140						
Glu	His	Phe	Pro	Glu	Ile	Phe	Arg	Lys	Val	Ser	Gln	Arg	Thr	Glu	Leu		
145					150					155					160		
Val	Phe	Gly	Leu	Ala	Leu	Lys	Glu	Val	Asn	Pro	Thr	Thr	His	Ser	Tyr		
			165					170						175			
Ile	Leu	Val	Ser	Met	Leu	Gly	Pro	Asn	Asp	Gly	Asn	Gln	Ser	Ser	Ala		
		180						185					190				
Trp	Thr	Leu	Pro	Arg	Asn	Gly	Leu	Leu	Met	Pro	Leu	Leu	Ser	Val	Ile		
	195						200					205					
Phe	Leu	Asn	Gly	Asn	Cys	Ala	Arg	Glu	Glu	Glu	Ile	Trp	Glu	Phe	Leu		
	210					215					220						
Asn	Met	Leu	Gly	Ile	Tyr	Asp	Gly	Lys	Arg	His	Leu	Ile	Phe	Gly	Glu		
225					230					235					240		
Pro	Arg	Lys	Leu	Ile	Thr	Gln	Asp	Leu	Val	Gln	Glu	Lys	Tyr	Leu	Glu		
			245						250					255			
Tyr	Gln	Gln	Val	Pro	Asn	Ser	Asp	Pro	Pro	Arg	Tyr	Gln	Phe	Leu	Trp		
			260					265					270				
Gly	Pro	Arg	Ala	His	Ala	Glu	Thr	Ser	Lys	Met	Lys	Val	Leu	Glu	Phe		
		275					280					285					
Leu	Ala	Lys	Val	Asn	Asp	Thr	Thr	Pro	Asn	Asn	Phe	Pro	Leu	Leu	Tyr		
	290					295					300						

ITI-08-PCT_Sequence_Listing_ST25.txt

Glu Glu Ala Leu Arg Asp Glu Glu Glu Arg Ala Gly Ala Arg Pro Arg
305 310 315 320

Val Ala Ala Arg Arg Gly Thr Thr Ala Met Thr Ser Ala Tyr Ser Arg
325 330 335

Ala Thr Ser Ser Ser Ser Ser Gln Pro Met
340 345

<210> 474

<211> 275

<212> PRT

<213> Artificial Sequence

<220>

<223> MAGE-B5__Homo_sapiens__Q9BZ81

<400> 474

Met Thr Ser Ala Gly Val Phe Asn Ala Gly Ser Asp Glu Arg Ala Asn
1 5 10 15

Ser Arg Asp Glu Glu Tyr Pro Cys Ser Ser Glu Val Ser Pro Ser Thr
20 25 30

Glu Ser Ser Cys Ser Asn Phe Ile Asn Ile Lys Val Gly Leu Leu Glu
35 40 45

Gln Phe Leu Leu Tyr Lys Phe Lys Met Lys Gln Arg Ile Leu Lys Glu
50 55 60

Asp Met Leu Lys Ile Val Asn Pro Arg Tyr Gln Asn Gln Phe Ala Glu
65 70 75 80

Ile His Arg Arg Ala Ser Glu His Ile Glu Val Val Phe Ala Val Asp
85 90 95

Leu Lys Glu Val Asn Pro Thr Cys His Leu Tyr Asp Leu Val Ser Lys
100 105 110

Leu Lys Leu Pro Asn Asn Gly Arg Ile His Val Gly Lys Val Leu Pro
115 120 125

Lys Thr Gly Leu Leu Met Thr Phe Leu Val Val Ile Phe Leu Lys Gly
130 135 140

Asn Cys Ala Asn Lys Glu Asp Thr Trp Lys Phe Leu Asp Met Met Gln
145 150 155 160

Ile Tyr Asp Gly Lys Lys Tyr Tyr Ile Tyr Gly Glu Pro Arg Lys Leu
165 170 175

ITI-08-PCT_Sequence_Listing_ST25.txt

Ile Thr Gln Asp Phe Val Arg Leu Thr Tyr Leu Glu Tyr His Gln Val
180 185 190

Pro Cys Ser Tyr Pro Ala His Tyr Gln Phe Leu Trp Gly Pro Arg Ala
195 200 205

Tyr Thr Glu Thr Ser Lys Met Lys Val Leu Glu Tyr Leu Ala Lys Val
210 215 220

Asn Asp Ile Ala Pro Gly Ala Phe Ser Ser Gln Tyr Glu Glu Ala Leu
225 230 235 240

Gln Asp Glu Glu Glu Ser Pro Ser Gln Arg Cys Ser Arg Asn Trp His
245 250 255

Tyr Cys Ser Gly Gln Asp Cys Leu Arg Ala Lys Phe Ser Ser Phe Ser
260 265 270

Gln Pro Tyr
275

<210> 475
<211> 407
<212> PRT
<213> Artificial Sequence

<220>
<223> MAGE-B6__Homo_sapiens__Q8N7X4

<400> 475

Met Pro Arg Gly His Lys Ser Lys Leu Arg Thr Cys Glu Lys Arg Gln
1 5 10 15

Glu Thr Asn Gly Gln Pro Gln Gly Leu Thr Gly Pro Gln Ala Thr Ala
20 25 30

Glu Lys Gln Glu Glu Ser His Ser Ser Ser Ser Ser Arg Ala Cys
35 40 45

Leu Gly Asp Cys Arg Arg Ser Ser Asp Ala Ser Ile Pro Gln Glu Ser
50 55 60

Gln Gly Val Ser Pro Thr Gly Ser Pro Asp Ala Val Val Ser Tyr Ser
65 70 75 80

Lys Ser Asp Val Ala Ala Asn Gly Gln Asp Glu Lys Ser Pro Ser Thr
85 90 95

Ser Arg Asp Ala Ser Val Pro Gln Glu Ser Gln Gly Ala Ser Pro Thr
100 105 110

ITI-08-PCT_Sequence_Listing_ST25.txt

Gly	Ser	Pro	Asp	Ala	Gly	Val	Ser	Gly	Ser	Lys	Tyr	Asp	Val	Ala	Ala	115	120	125	
Asn	Gly	Gln	Asp	Glu	Lys	Ser	Pro	Ser	Thr	Ser	His	Asp	Val	Ser	Val	130	135	140	
Pro	Gln	Glu	Ser	Gln	Gly	Ala	Ser	Pro	Thr	Gly	Ser	Pro	Asp	Ala	Gly	145	150	155	160
Val	Ser	Gly	Ser	Lys	Tyr	Asp	Val	Ala	Ala	Glu	Gly	Glu	Asp	Glu	Glu	165	170	175	
Ser	Val	Ser	Ala	Ser	Gln	Lys	Ala	Ile	Ile	Phe	Lys	Arg	Leu	Ser	Lys	180	185	190	
Asp	Ala	Val	Lys	Lys	Lys	Ala	Cys	Thr	Leu	Ala	Gln	Phe	Leu	Gln	Lys	195	200	205	
Lys	Phe	Glu	Lys	Lys	Glu	Ser	Ile	Leu	Lys	Ala	Asp	Met	Leu	Lys	Cys	210	215	220	
Val	Arg	Arg	Glu	Tyr	Lys	Pro	Tyr	Phe	Pro	Gln	Ile	Leu	Asn	Arg	Thr	225	230	235	240
Ser	Gln	His	Leu	Val	Val	Ala	Phe	Gly	Val	Glu	Leu	Lys	Glu	Met	Asp	245	250	255	
Ser	Ser	Gly	Glu	Ser	Tyr	Thr	Leu	Val	Ser	Lys	Leu	Gly	Leu	Pro	Ser	260	265	270	
Glu	Gly	Ile	Leu	Ser	Gly	Asp	Asn	Ala	Leu	Pro	Lys	Ser	Gly	Leu	Leu	275	280	285	
Met	Ser	Leu	Leu	Val	Val	Ile	Phe	Met	Asn	Gly	Asn	Cys	Ala	Thr	Glu	290	295	300	
Glu	Glu	Val	Trp	Glu	Phe	Leu	Gly	Leu	Leu	Gly	Ile	Tyr	Asp	Gly	Ile	305	310	315	320
Leu	His	Ser	Ile	Tyr	Gly	Asp	Ala	Arg	Lys	Ile	Ile	Thr	Glu	Asp	Leu	325	330	335	
Val	Gln	Asp	Lys	Tyr	Val	Val	Tyr	Arg	Gln	Val	Cys	Asn	Ser	Asp	Pro	340	345	350	
Pro	Cys	Tyr	Glu	Phe	Leu	Trp	Gly	Pro	Arg	Ala	Tyr	Ala	Glu	Thr	Thr	355	360	365	
Lys	Met	Arg	Val	Leu	Arg	Val	Leu	Ala	Asp	Ser	Ser	Asn	Thr	Ser	Pro	370	375	380	
Gly	Leu	Tyr	Pro	His	Leu	Tyr	Glu	Asp	Ala	Leu	Ile	Asp	Glu	Val	Glu				

ITI-08-PCT_Sequence_Listing_ST25.txt

385 390 395 400

Arg Ala Leu Arg Leu Arg Ala
405

<210> 476
<211> 1142
<212> PRT
<213> Artificial Sequence

<220>
<223> MAGE-C1__Homo_sapiens__060732

<400> 476

Met Gly Asp Lys Asp Met Pro Thr Ala Gly Met Pro Ser Leu Leu Gln
1 5 10 15

Ser Ser Ser Glu Ser Pro Gln Ser Cys Pro Glu Gly Glu Asp Ser Gln
20 25 30

Ser Pro Leu Gln Ile Pro Gln Ser Ser Pro Glu Ser Asp Asp Thr Leu
35 40 45

Tyr Pro Leu Gln Ser Pro Gln Ser Arg Ser Glu Gly Glu Asp Ser Ser
50 55 60

Asp Pro Leu Gln Arg Pro Pro Glu Gly Lys Asp Ser Gln Ser Pro Leu
65 70 75 80

Gln Ile Pro Gln Ser Ser Pro Glu Gly Asp Asp Thr Gln Ser Pro Leu
85 90 95

Gln Asn Ser Gln Ser Ser Pro Glu Gly Lys Asp Ser Leu Ser Pro Leu
100 105 110

Glu Ile Ser Gln Ser Pro Pro Glu Gly Glu Asp Val Gln Ser Pro Leu
115 120 125

Gln Asn Pro Ala Ser Ser Phe Phe Ser Ser Ala Leu Leu Ser Ile Phe
130 135 140

Gln Ser Ser Pro Glu Ser Thr Gln Ser Pro Phe Glu Gly Phe Pro Gln
145 150 155 160

Ser Val Leu Gln Ile Pro Val Ser Ala Ala Ser Ser Ser Thr Leu Val
165 170 175

Ser Ile Phe Gln Ser Ser Pro Glu Ser Thr Gln Ser Pro Phe Glu Gly
180 185 190

Phe Pro Gln Ser Pro Leu Gln Ile Pro Val Ser Arg Ser Phe Ser Ser

ITI-08-PCT_Sequence_Listing_ST25.txt

```

195                200                205
Thr Leu Leu Ser Ile Phe Gln Ser Ser Pro Glu Arg Thr Gln Ser Thr
210                215                220
Phe Glu Gly Phe Ala Gln Ser Pro Leu Gln Ile Pro Val Ser Pro Ser
225                230                235                240
Ser Ser Ser Thr Leu Leu Ser Leu Phe Gln Ser Phe Ser Glu Arg Thr
245                250                255
Gln Ser Thr Phe Glu Gly Phe Ala Gln Ser Ser Leu Gln Ile Pro Val
260                265                270
Ser Pro Ser Phe Ser Ser Thr Leu Val Ser Leu Phe Gln Ser Ser Pro
275                280                285
Glu Arg Thr Gln Ser Thr Phe Glu Gly Phe Pro Gln Ser Pro Leu Gln
290                295                300
Ile Pro Val Ser Ser Ser Ser Ser Ser Thr Leu Leu Ser Leu Phe Gln
305                310                315                320
Ser Ser Pro Glu Arg Thr His Ser Thr Phe Glu Gly Phe Pro Gln Ser
325                330                335
Leu Leu Gln Ile Pro Met Thr Ser Ser Phe Ser Ser Thr Leu Leu Ser
340                345                350
Ile Phe Gln Ser Ser Pro Glu Ser Ala Gln Ser Thr Phe Glu Gly Phe
355                360                365
Pro Gln Ser Pro Leu Gln Ile Pro Gly Ser Pro Ser Phe Ser Ser Thr
370                375                380
Leu Leu Ser Leu Phe Gln Ser Ser Pro Glu Arg Thr His Ser Thr Phe
385                390                395                400
Glu Gly Phe Pro Gln Ser Pro Leu Gln Ile Pro Met Thr Ser Ser Phe
405                410                415
Ser Ser Thr Leu Leu Ser Ile Leu Gln Ser Ser Pro Glu Ser Ala Gln
420                425                430
Ser Ala Phe Glu Gly Phe Pro Gln Ser Pro Leu Gln Ile Pro Val Ser
435                440                445
Ser Ser Phe Ser Tyr Thr Leu Leu Ser Leu Phe Gln Ser Ser Pro Glu
450                455                460
Arg Thr His Ser Thr Phe Glu Gly Phe Pro Gln Ser Pro Leu Gln Ile
465                470                475                480

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Pro	Val	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Thr	Leu	Leu	Ser	Leu	Phe	Gln	485	490	495
Ser	Ser	Pro	Glu	Cys	Thr	Gln	Ser	Thr	Phe	Glu	Gly	Phe	Pro	Gln	Ser		500	505	510
Pro	Leu	Gln	Ile	Pro	Gln	Ser	Pro	Pro	Glu	Gly	Glu	Asn	Thr	His	Ser		515	520	525
Pro	Leu	Gln	Ile	Val	Pro	Ser	Leu	Pro	Glu	Trp	Glu	Asp	Ser	Leu	Ser		530	535	540
Pro	His	Tyr	Phe	Pro	Gln	Ser	Pro	Pro	Gln	Gly	Glu	Asp	Ser	Leu	Ser		545	550	555
Pro	His	Tyr	Phe	Pro	Gln	Ser	Pro	Pro	Gln	Gly	Glu	Asp	Ser	Leu	Ser		565	570	575
Pro	His	Tyr	Phe	Pro	Gln	Ser	Pro	Gln	Gly	Glu	Asp	Ser	Leu	Ser	Pro		580	585	590
His	Tyr	Phe	Pro	Gln	Ser	Pro	Pro	Gln	Gly	Glu	Asp	Ser	Met	Ser	Pro		595	600	605
Leu	Tyr	Phe	Pro	Gln	Ser	Pro	Leu	Gln	Gly	Glu	Glu	Phe	Gln	Ser	Ser		610	615	620
Leu	Gln	Ser	Pro	Val	Ser	Ile	Cys	Ser	Ser	Ser	Thr	Pro	Ser	Ser	Leu		625	630	635
Pro	Gln	Ser	Phe	Pro	Glu	Ser	Ser	Gln	Ser	Pro	Pro	Glu	Gly	Pro	Val		645	650	655
Gln	Ser	Pro	Leu	His	Ser	Pro	Gln	Ser	Pro	Pro	Glu	Gly	Met	His	Ser		660	665	670
Gln	Ser	Pro	Leu	Gln	Ser	Pro	Glu	Ser	Ala	Pro	Glu	Gly	Glu	Asp	Ser		675	680	685
Leu	Ser	Pro	Leu	Gln	Ile	Pro	Gln	Ser	Pro	Leu	Glu	Gly	Glu	Asp	Ser		690	695	700
Leu	Ser	Ser	Leu	His	Phe	Pro	Gln	Ser	Pro	Pro	Glu	Trp	Glu	Asp	Ser		705	710	715
Leu	Ser	Pro	Leu	His	Phe	Pro	Gln	Phe	Pro	Pro	Gln	Gly	Glu	Asp	Phe		725	730	735
Gln	Ser	Ser	Leu	Gln	Ser	Pro	Val	Ser	Ile	Cys	Ser	Ser	Ser	Thr	Ser		740	745	750

ITI-08-PCT_Sequence_Listing_ST25.txt

Leu Ser Leu Pro Gln Ser Phe Pro Glu Ser Pro Gln Ser Pro Pro Glu
 755 760 765
 Gly Pro Ala Gln Ser Pro Leu Gln Arg Pro Val Ser Ser Phe Phe Ser
 770 775 780
 Tyr Thr Leu Ala Ser Leu Leu Gln Ser Ser His Glu Ser Pro Gln Ser
 785 790 795 800
 Pro Pro Glu Gly Pro Ala Gln Ser Pro Leu Gln Ser Pro Val Ser Ser
 805 810 815
 Phe Pro Ser Ser Thr Ser Ser Ser Leu Ser Gln Ser Ser Pro Val Ser
 820 825 830
 Ser Phe Pro Ser Ser Thr Ser Ser Ser Leu Ser Lys Ser Ser Pro Glu
 835 840 845
 Ser Pro Leu Gln Ser Pro Val Ile Ser Phe Ser Ser Ser Thr Ser Leu
 850 855 860
 Ser Pro Phe Ser Glu Glu Ser Ser Ser Pro Val Asp Glu Tyr Thr Ser
 865 870 875 880
 Ser Ser Asp Thr Leu Leu Glu Ser Asp Ser Leu Thr Asp Ser Glu Ser
 885 890 895
 Leu Ile Glu Ser Glu Pro Leu Phe Thr Tyr Thr Leu Asp Glu Lys Val
 900 905 910
 Asp Glu Leu Ala Arg Phe Leu Leu Leu Lys Tyr Gln Val Lys Gln Pro
 915 920 925
 Ile Thr Lys Ala Glu Met Leu Thr Asn Val Ile Ser Arg Tyr Thr Gly
 930 935 940
 Tyr Phe Pro Val Ile Phe Arg Lys Ala Arg Glu Phe Ile Glu Ile Leu
 945 950 955 960
 Phe Gly Ile Ser Leu Arg Glu Val Asp Pro Asp Asp Ser Tyr Val Phe
 965 970 975
 Val Asn Thr Leu Asp Leu Thr Ser Glu Gly Cys Leu Ser Asp Glu Gln
 980 985 990
 Gly Met Ser Gln Asn Arg Leu Leu Ile Leu Ile Leu Ser Ile Ile Phe
 995 1000 1005
 Ile Lys Gly Thr Tyr Ala Ser Glu Glu Val Ile Trp Asp Val Leu
 1010 1015 1020
 Ser Gly Ile Gly Val Arg Ala Gly Arg Glu His Phe Ala Phe Gly

ITI-08-PCT_Sequence_Listing_ST25.txt

1025														
Glu	Pro	Arg	Glu	Leu	Leu	Thr	Lys	Val	Trp	Val	Gln	Glu	His	Tyr
1040						1045					1050			
Leu	Glu	Tyr	Arg	Glu	Val	Pro	Asn	Ser	Ser	Pro	Pro	Arg	Tyr	Glu
1055						1060					1065			
Phe	Leu	Trp	Gly	Pro	Arg	Ala	His	Ser	Glu	Val	Ile	Lys	Arg	Lys
1070						1075					1080			
Val	Val	Glu	Phe	Leu	Ala	Met	Leu	Lys	Asn	Thr	Val	Pro	Ile	Thr
1085						1090					1095			
Phe	Pro	Ser	Ser	Tyr	Lys	Asp	Ala	Leu	Lys	Asp	Val	Glu	Glu	Arg
1100						1105					1110			
Ala	Gln	Ala	Ile	Ile	Asp	Thr	Thr	Asp	Asp	Ser	Thr	Ala	Thr	Glu
1115						1120					1125			
Ser	Ala	Ser	Ser	Ser	Val	Met	Ser	Pro	Ser	Phe	Ser	Ser	Glu	
1130						1135					1140			

<210> 477

<211> 373

<212> PRT

<213> Artificial Sequence

<220>

<223> MAGE-C2__Homo_sapiens__Q9UBF1

<400> 477

Met	Pro	Pro	Val	Pro	Gly	Val	Pro	Phe	Arg	Asn	Val	Asp	Asn	Asp	Ser
1				5					10					15	
Pro	Thr	Ser	Val	Glu	Leu	Glu	Asp	Trp	Val	Asp	Ala	Gln	His	Pro	Thr
			20					25					30		
Asp	Glu	Glu	Glu	Glu	Glu	Ala	Ser	Ser	Ala	Ser	Ser	Thr	Leu	Tyr	Leu
		35				40						45			
Val	Phe	Ser	Pro	Ser	Ser	Phe	Ser	Thr	Ser	Ser	Ser	Leu	Ile	Leu	Gly
	50					55						60			
Gly	Pro	Glu	Glu	Glu	Glu	Val	Pro	Ser	Gly	Val	Ile	Pro	Asn	Leu	Thr
65					70				75					80	
Glu	Ser	Ile	Pro	Ser	Ser	Pro	Pro	Gln	Gly	Pro	Pro	Gln	Gly	Pro	Ser
				85				90						95	
Gln	Ser	Pro	Leu	Ser	Ser	Cys	Cys	Ser	Ser	Phe	Ser	Trp	Ser	Ser	Phe

ITI-08-PCT_Sequence_Listing_ST25.txt

100	105	110															
Ser	Glu	Glu	Ser	Ser	Ser	Gln	Lys	Gly	Glu	Asp	Thr	Gly	Thr	Cys	Gln		
	115						120					125					
Gly	Leu	Pro	Asp	Ser	Glu	Ser	Ser	Phe	Thr	Tyr	Thr	Leu	Asp	Glu	Lys		
	130						135					140					
Val	Ala	Glu	Leu	Val	Glu	Phe	Leu	Leu	Leu	Lys	Tyr	Glu	Ala	Glu	Glu		
145					150					155					160		
Pro	Val	Thr	Glu	Ala	Glu	Met	Leu	Met	Ile	Val	Ile	Lys	Tyr	Lys	Asp		
				165					170					175			
Tyr	Phe	Pro	Val	Ile	Leu	Lys	Arg	Ala	Arg	Glu	Phe	Met	Glu	Leu	Leu		
			180					185					190				
Phe	Gly	Leu	Ala	Leu	Ile	Glu	Val	Gly	Pro	Asp	His	Phe	Cys	Val	Phe		
	195						200					205					
Ala	Asn	Thr	Val	Gly	Leu	Thr	Asp	Glu	Gly	Ser	Asp	Asp	Glu	Gly	Met		
	210					215					220						
Pro	Glu	Asn	Ser	Leu	Leu	Ile	Ile	Ile	Leu	Ser	Val	Ile	Phe	Ile	Lys		
225					230					235					240		
Gly	Asn	Cys	Ala	Ser	Glu	Glu	Val	Ile	Trp	Glu	Val	Leu	Asn	Ala	Val		
				245					250					255			
Gly	Val	Tyr	Ala	Gly	Arg	Glu	His	Phe	Val	Tyr	Gly	Glu	Pro	Arg	Glu		
			260					265					270				
Leu	Leu	Thr	Lys	Val	Trp	Val	Gln	Gly	His	Tyr	Leu	Glu	Tyr	Arg	Glu		
		275					280					285					
Val	Pro	His	Ser	Ser	Pro	Pro	Tyr	Tyr	Glu	Phe	Leu	Trp	Gly	Pro	Arg		
	290					295					300						
Ala	His	Ser	Glu	Ser	Ile	Lys	Lys	Lys	Val	Leu	Glu	Phe	Leu	Ala	Lys		
305					310					315					320		
Leu	Asn	Asn	Thr	Val	Pro	Ser	Ser	Phe	Pro	Ser	Trp	Tyr	Lys	Asp	Ala		
				325					330					335			
Leu	Lys	Asp	Val	Glu	Glu	Arg	Val	Gln	Ala	Thr	Ile	Asp	Thr	Ala	Asp		
			340					345					350				
Asp	Ala	Thr	Val	Met	Ala	Ser	Glu	Ser	Leu	Ser	Val	Met	Ser	Ser	Asn		
		355					360					365					
Val	Ser	Phe	Ser	Glu													
	370																

ITI-08-PCT_Sequence_Listing_ST25.txt

```

<210> 478
<211> 643
<212> PRT
<213> Artificial Sequence

<220>
<223> MAGE-C3__Homo_sapiens__Q8TD91

<400> 478

Met Leu Leu Pro Cys His Trp Val Leu Asp Ala Thr Phe Ser Asp Gly
1          5          10          15

Ser Leu Gly Gln Trp Val Lys Asn Thr Cys Ala Thr Tyr Ala Leu Ser
          20          25          30

Pro Val Val Leu Pro Pro Gln Pro Gln Pro Arg Lys Lys Ala Thr Asp
          35          40          45

Lys Asp Tyr Ser Ala Phe His Leu Gly His Leu Arg Glu Val Arg Leu
          50          55          60

Phe Leu Arg Gly Gly Thr Ser Asp Gln Arg Met Asp Ser Leu Val Leu
65          70          75          80

Cys Pro Thr Tyr Phe Lys Leu Trp Arg Thr Leu Ser Gly Ser Pro Gly
          85          90          95

Leu Gln Leu Ser Asp Leu His Phe Gly Ser Gln Pro Glu Gly Lys Phe
          100          105          110

Ser Leu Arg Arg Ala Val Ser Val Lys Gln Arg Glu Glu Pro Gln Asp
          115          120          125

Trp Pro Leu Asn Glu Lys Arg Thr Leu Trp Lys Asp Ser Asp Leu Pro
          130          135          140

Thr Trp Arg Arg Gly Thr Gly Tyr Thr Leu Ser Leu Pro Ala Val Ser
145          150          155          160

Pro Gly Lys Arg Leu Trp Gly Glu Lys Ala Gly Ser Leu Pro Glu Ser
          165          170          175

Glu Pro Leu Phe Thr Tyr Thr Leu Asp Glu Lys Val Asp Lys Leu Val
          180          185          190

Gln Phe Leu Leu Leu Lys Tyr Gln Ala Lys Glu Pro Leu Thr Arg Ala
          195          200          205

Glu Met Gln Met Asn Val Ile Asn Thr Tyr Thr Gly Tyr Phe Pro Met
210          215          220

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Ile	Phe	Arg	Lys	Ala	Arg	Glu	Phe	Ile	Glu	Ile	Leu	Phe	Gly	Ile	Ser	225	230	235	240
Leu	Thr	Glu	Val	Asp	Pro	Asp	His	Phe	Tyr	Val	Phe	Val	Asn	Thr	Leu	245	250	255	
Asp	Leu	Thr	Cys	Glu	Gly	Ser	Leu	Ser	Asp	Glu	Gln	Gly	Met	Pro	Gln	260	265	270	
Asn	Arg	Leu	Leu	Ile	Leu	Ile	Leu	Ser	Val	Ile	Phe	Ile	Lys	Gly	Asn	275	280	285	
Cys	Ala	Ser	Glu	Glu	Val	Ile	Trp	Glu	Val	Leu	Asn	Ala	Ile	Gly	Pro	290	295	300	
Trp	Ser	Ala	Leu	Ala	Gly	Phe	Ala	Asp	Val	Leu	Ser	Arg	Leu	Ala	Leu	305	310	315	320
Trp	Glu	Ser	Glu	Gly	Pro	Glu	Ala	Phe	Cys	Glu	Glu	Ser	Gly	Leu	Arg	325	330	335	
Ser	Ala	Glu	Gly	Ser	Val	Leu	Asp	Leu	Ala	Asn	Pro	Gln	Gly	Leu	Ala	340	345	350	
Gly	His	Arg	Gln	Glu	Asp	Gly	Arg	Arg	Gly	Leu	Thr	Glu	Ala	Ser	Pro	355	360	365	
Gln	Gln	Lys	Lys	Gly	Gly	Glu	Asp	Glu	Asp	Met	Pro	Ala	Ala	Gly	Met	370	375	380	
Pro	Pro	Leu	Pro	Gln	Ser	Pro	Pro	Glu	Ile	Pro	Pro	Gln	Gly	Pro	Pro	385	390	395	400
Lys	Ile	Ser	Pro	Gln	Gly	Pro	Pro	Gln	Ser	Pro	Pro	Gln	Ser	Pro	Leu	405	410	415	
Asp	Ser	Cys	Ser	Ser	Pro	Leu	Leu	Trp	Thr	Arg	Leu	Asp	Glu	Glu	Ser	420	425	430	
Ser	Ser	Glu	Glu	Glu	Asp	Thr	Ala	Thr	Trp	His	Ala	Leu	Pro	Glu	Ser	435	440	445	
Glu	Ser	Leu	Pro	Arg	Tyr	Ala	Leu	Asp	Glu	Lys	Val	Ala	Glu	Leu	Val	450	455	460	
Gln	Phe	Leu	Leu	Leu	Lys	Tyr	Gln	Thr	Lys	Glu	Pro	Val	Thr	Lys	Ala	465	470	475	480
Glu	Met	Leu	Thr	Thr	Val	Ile	Lys	Lys	Tyr	Lys	Asp	Tyr	Phe	Pro	Met	485	490	495	

ITI-08-PCT_Sequence_Listing_ST25.txt

Ile Phe Gly Lys Ala His Glu Phe Ile Glu Leu Ile Phe Gly Ile Ala
500 505 510

Leu Thr Asp Met Asp Pro Asp Asn His Ser Tyr Phe Phe Glu Asp Thr
515 520 525

Leu Asp Leu Thr Tyr Glu Gly Ser Leu Ile Asp Asp Gln Gly Met Pro
530 535 540

Lys Asn Cys Leu Leu Ile Leu Ile Leu Ser Met Ile Phe Ile Lys Gly
545 550 555 560

Ser Cys Val Pro Glu Glu Val Ile Trp Glu Val Leu Ser Ala Ile Gly
565 570 575

Pro Ile Gln Arg Pro Ala Arg Glu Val Leu Glu Phe Leu Ser Lys Leu
580 585 590

Ser Ser Ile Ile Pro Ser Ala Phe Pro Ser Trp Tyr Met Asp Ala Leu
595 600 605

Lys Asp Met Glu Asp Arg Ala Gln Ala Ile Ile Asp Thr Thr Asp Asp
610 615 620

Ala Thr Ala Met Ala Ser Ala Ser Pro Ser Val Met Ser Thr Asn Phe
625 630 635 640

Cys Pro Glu

<210> 479

<211> 778

<212> PRT

<213> Artificial Sequence

<220>

<223> MAGE-D1__Homo_sapiens__Q9Y5V3

<400> 479

Met Ala Gln Lys Met Asp Cys Gly Ala Gly Leu Leu Gly Phe Gln Ala
1 5 10 15

Glu Ala Ser Val Glu Asp Ser Ala Leu Leu Met Gln Thr Leu Met Glu
20 25 30

Ala Ile Gln Ile Ser Glu Ala Pro Pro Thr Asn Gln Ala Thr Ala Ala
35 40 45

Ala Ser Pro Gln Ser Ser Gln Pro Pro Thr Ala Asn Glu Met Ala Asp
50 55 60

Ile Gln Val Ser Ala Ala Ala Ala Arg Pro Lys Ser Ala Phe Lys Val

ITI-08-PCT_Sequence_Listing_ST25.txt

```

65          70          75          80
Gln Asn Ala Thr Thr Lys Gly Pro Asn Gly Val Tyr Asp Phe Ser Gln
      85          90
Ala His Asn Ala Lys Asp Val Pro Asn Thr Gln Pro Lys Ala Ala Phe
      100         105         110
Lys Ser Gln Asn Ala Thr Pro Lys Gly Pro Asn Ala Ala Tyr Asp Phe
      115         120         125
Ser Gln Ala Ala Thr Thr Gly Glu Leu Ala Ala Asn Lys Ser Glu Met
      130         135         140
Ala Phe Lys Ala Gln Asn Ala Thr Thr Lys Val Gly Pro Asn Ala Thr
      145         150         155         160
Tyr Asn Phe Ser Gln Ser Leu Asn Ala Asn Asp Leu Ala Asn Ser Arg
      165         170         175
Pro Lys Thr Pro Phe Lys Ala Trp Asn Asp Thr Thr Lys Ala Pro Thr
      180         185         190
Ala Asp Thr Gln Thr Gln Asn Val Asn Gln Ala Lys Met Ala Thr Ser
      195         200         205
Gln Ala Asp Ile Glu Thr Asp Pro Gly Ile Ser Glu Pro Asp Gly Ala
      210         215         220
Thr Ala Gln Thr Ser Ala Asp Gly Ser Gln Ala Gln Asn Leu Glu Ser
      225         230         235         240
Arg Thr Ile Ile Arg Gly Lys Arg Thr Arg Lys Ile Asn Asn Leu Asn
      245         250         255
Val Glu Glu Asn Ser Ser Gly Asp Gln Arg Arg Ala Pro Leu Ala Ala
      260         265         270
Gly Thr Trp Arg Ser Ala Pro Val Pro Val Thr Thr Gln Asn Pro Pro
      275         280         285
Gly Ala Pro Pro Asn Val Leu Trp Gln Thr Pro Leu Ala Trp Gln Asn
      290         295         300
Pro Ser Gly Trp Gln Asn Gln Thr Ala Arg Gln Thr Pro Pro Ala Arg
      305         310         315         320
Gln Ser Pro Pro Ala Arg Gln Thr Pro Pro Ala Trp Gln Asn Pro Val
      325         330         335
Ala Trp Gln Asn Pro Val Ile Trp Pro Asn Pro Val Ile Trp Gln Asn
      340         345         350

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Pro	Val	Ile	Trp	Pro	Asn	Pro	Ile	Val	Trp	Pro	Gly	Pro	Val	Val	Trp
		355					360					365			
Pro	Asn	Pro	Leu	Ala	Trp	Gln	Asn	Pro	Pro	Gly	Trp	Gln	Thr	Pro	Pro
	370					375					380				
Gly	Trp	Gln	Thr	Pro	Pro	Gly	Trp	Gln	Gly	Pro	Pro	Asp	Trp	Gln	Gly
385					390					395					400
Pro	Pro	Asp	Trp	Pro	Leu	Pro	Pro	Asp	Trp	Pro	Leu	Pro	Pro	Asp	Trp
				405					410					415	
Pro	Leu	Pro	Thr	Asp	Trp	Pro	Leu	Pro	Pro	Asp	Trp	Ile	Pro	Ala	Asp
			420						425				430		
Trp	Pro	Ile	Pro	Pro	Asp	Trp	Gln	Asn	Leu	Arg	Pro	Ser	Pro	Asn	Leu
	435						440					445			
Arg	Pro	Ser	Pro	Asn	Ser	Arg	Ala	Ser	Gln	Asn	Pro	Gly	Ala	Ala	Gln
	450					455					460				
Pro	Arg	Asp	Val	Ala	Leu	Leu	Gln	Glu	Arg	Ala	Asn	Lys	Leu	Val	Lys
465					470				475						480
Tyr	Leu	Met	Leu	Lys	Asp	Tyr	Thr	Lys	Val	Pro	Ile	Lys	Arg	Ser	Glu
				485					490					495	
Met	Leu	Arg	Asp	Ile	Ile	Arg	Glu	Tyr	Thr	Asp	Val	Tyr	Pro	Glu	Ile
			500					505					510		
Ile	Glu	Arg	Ala	Cys	Phe	Val	Leu	Glu	Lys	Lys	Phe	Gly	Ile	Gln	Leu
		515					520					525			
Lys	Glu	Ile	Asp	Lys	Glu	Glu	His	Leu	Tyr	Ile	Leu	Ile	Ser	Thr	Pro
	530					535					540				
Glu	Ser	Leu	Ala	Gly	Ile	Leu	Gly	Thr	Thr	Lys	Asp	Thr	Pro	Lys	Leu
545					550					555					560
Gly	Leu	Leu	Leu	Val	Ile	Leu	Gly	Val	Ile	Phe	Met	Asn	Gly	Asn	Arg
				565					570					575	
Ala	Ser	Glu	Ala	Val	Leu	Trp	Glu	Ala	Leu	Arg	Lys	Met	Gly	Leu	Arg
			580					585					590		
Pro	Gly	Val	Arg	His	Pro	Leu	Leu	Gly	Asp	Leu	Arg	Lys	Leu	Leu	Thr
		595					600					605			
Tyr	Glu	Phe	Val	Lys	Gln	Lys	Tyr	Leu	Asp	Tyr	Arg	Arg	Val	Pro	Asn
	610					615					620				

ITI-08-PCT_Sequence_Listing_ST25.txt

Ser Asn Pro Pro Glu Tyr Glu Phe Leu Trp Gly Leu Arg Ser Tyr His
625 630 635 640

Glu Thr Ser Lys Met Lys Val Leu Arg Phe Ile Ala Glu Val Gln Lys
645 650 655

Arg Asp Pro Arg Asp Trp Thr Ala Gln Phe Met Glu Ala Ala Asp Glu
660 665 670

Ala Leu Asp Ala Leu Asp Ala Ala Ala Glu Ala Glu Ala Arg Ala
675 680 685

Glu Ala Arg Thr Arg Met Gly Ile Gly Asp Glu Ala Val Ser Gly Pro
690 695 700

Trp Ser Trp Asp Asp Ile Glu Phe Glu Leu Leu Thr Trp Asp Glu Glu
705 710 715 720

Gly Asp Phe Gly Asp Pro Trp Ser Arg Ile Pro Phe Thr Phe Trp Ala
725 730 735

Arg Tyr His Gln Asn Ala Arg Ser Arg Phe Pro Gln Thr Phe Ala Gly
740 745 750

Pro Ile Ile Gly Pro Gly Gly Thr Ala Ser Ala Asn Phe Ala Ala Asn
755 760 765

Phe Gly Ala Ile Gly Phe Phe Trp Val Glu
770 775

<210> 480

<211> 606

<212> PRT

<213> Artificial Sequence

<220>

<223> MAGE-D2__Homo_sapiens__Q9UNF1

<400> 480

Met Ser Asp Thr Ser Glu Ser Gly Ala Gly Leu Thr Arg Phe Gln Ala
1 5 10 15

Glu Ala Ser Glu Lys Asp Ser Ser Ser Met Met Gln Thr Leu Leu Thr
20 25 30

Val Thr Gln Asn Val Glu Val Pro Glu Thr Pro Lys Ala Ser Lys Ala
35 40 45

Leu Glu Val Ser Glu Asp Val Lys Val Ser Lys Ala Ser Gly Val Ser
50 55 60

ITI-08-PCT_Sequence_Listing_ST25.txt

Lys Ala Thr Glu Val Ser Lys Thr Pro Glu Ala Arg Glu Ala Pro Ala
 65 70 75 80
 Thr Gln Ala Ser Ser Thr Thr Gln Leu Thr Asp Thr Gln Val Leu Ala
 85 90 95
 Ala Glu Asn Lys Ser Leu Ala Ala Asp Thr Lys Lys Gln Asn Ala Asp
 100 105 110
 Pro Gln Ala Val Thr Met Pro Ala Thr Glu Thr Lys Lys Val Ser His
 115 120 125
 Val Ala Asp Thr Lys Val Asn Thr Lys Ala Gln Glu Thr Glu Ala Ala
 130 135 140
 Pro Ser Gln Ala Pro Ala Asp Glu Pro Glu Pro Glu Ser Ala Ala Ala
 145 150 155 160
 Gln Ser Gln Glu Asn Gln Asp Thr Arg Pro Lys Val Lys Ala Lys Lys
 165 170 175
 Ala Arg Lys Val Lys His Leu Asp Gly Glu Glu Asp Gly Ser Ser Asp
 180 185 190
 Gln Ser Gln Ala Ser Gly Thr Thr Gly Gly Arg Arg Val Ser Lys Ala
 195 200 205
 Leu Met Ala Ser Met Ala Arg Arg Ala Ser Arg Gly Pro Ile Ala Phe
 210 215 220
 Trp Ala Arg Arg Ala Ser Arg Thr Arg Leu Ala Ala Trp Ala Arg Arg
 225 230 235 240
 Ala Leu Leu Ser Leu Arg Ser Pro Lys Ala Arg Arg Gly Lys Ala Arg
 245 250 255
 Arg Arg Ala Ala Lys Leu Gln Ser Ser Gln Glu Pro Glu Ala Pro Pro
 260 265 270
 Pro Arg Asp Val Ala Leu Leu Gln Gly Arg Ala Asn Asp Leu Val Lys
 275 280 285
 Tyr Leu Leu Ala Lys Asp Gln Thr Lys Ile Pro Ile Lys Arg Ser Asp
 290 295 300
 Met Leu Lys Asp Ile Ile Lys Glu Tyr Thr Asp Val Tyr Pro Glu Ile
 305 310 315 320
 Ile Glu Arg Ala Gly Tyr Ser Leu Glu Lys Val Phe Gly Ile Gln Leu
 325 330 335
 Lys Glu Ile Asp Lys Asn Asp His Leu Tyr Ile Leu Leu Ser Thr Leu

ITI-08-PCT_Sequence_Listing_ST25.txt

340

345

350

Glu Pro Thr Asp Ala Gly Ile Leu Gly Thr Thr Lys Asp Ser Pro Lys
 355 360 365

Leu Gly Leu Leu Met Val Leu Leu Ser Ile Ile Phe Met Asn Gly Asn
 370 375 380

Arg Ser Ser Glu Ala Val Ile Trp Glu Val Leu Arg Lys Leu Gly Leu
 385 390 395 400

Arg Pro Gly Ile His His Ser Leu Phe Gly Asp Val Lys Lys Leu Ile
 405 410 415

Thr Asp Glu Phe Val Lys Gln Lys Tyr Leu Asp Tyr Ala Arg Val Pro
 420 425 430

Asn Ser Asn Pro Pro Glu Tyr Glu Phe Phe Trp Gly Leu Arg Ser Tyr
 435 440 445

Tyr Glu Thr Ser Lys Met Lys Val Leu Lys Phe Ala Cys Lys Val Gln
 450 455 460

Lys Lys Asp Pro Lys Glu Trp Ala Ala Gln Tyr Arg Glu Ala Met Glu
 465 470 475 480

Ala Asp Leu Lys Ala Ala Ala Glu Ala Ala Ala Glu Ala Lys Ala Arg
 485 490 495

Ala Glu Ile Arg Ala Arg Met Gly Ile Gly Leu Gly Ser Glu Asn Ala
 500 505 510

Ala Gly Pro Cys Asn Trp Asp Glu Ala Asp Ile Gly Pro Trp Ala Lys
 515 520 525

Ala Arg Ile Gln Ala Gly Ala Glu Ala Lys Ala Lys Ala Gln Glu Ser
 530 535 540

Gly Ser Ala Ser Thr Gly Ala Ser Thr Ser Thr Asn Asn Ser Ala Ser
 545 550 555 560

Ala Ser Ala Ser Thr Ser Gly Gly Phe Ser Ala Gly Ala Ser Leu Thr
 565 570 575

Ala Thr Leu Thr Phe Gly Leu Phe Ala Gly Leu Gly Gly Ala Gly Ala
 580 585 590

Ser Thr Ser Gly Ser Ser Gly Ala Cys Gly Phe Ser Tyr Lys
 595 600 605

<210> 481

<211> 741

ITI-08-PCT_Sequence_Listing_ST25.txt

<212> PRT

<213> Artificial Sequence

<220>

<223> MAGE-D4__Homo_sapiens__Q96JG8

<400> 481

Met Ala Glu Gly Ser Phe Ser Val Gln Ser Glu Ser Tyr Ser Val Glu
1 5 10 15

Asp Met Asp Glu Gly Ser Asp Glu Val Gly Glu Glu Glu Met Val Glu
20 25 30

Gly Asn Asp Tyr Glu Glu Phe Gly Ala Phe Gly Gly Tyr Gly Thr Leu
35 40 45

Thr Ser Phe Asp Ile His Ile Leu Arg Ala Phe Gly Ser Leu Gly Pro
50 55 60

Gly Leu Arg Ile Leu Ser Asn Glu Pro Trp Glu Leu Glu Asn Pro Val
65 70 75 80

Leu Ala Gln Thr Leu Val Glu Ala Leu Gln Leu Asp Pro Glu Thr Leu
85 90 95

Ala Asn Glu Thr Ala Ala Arg Ala Ala Asn Val Ala Arg Ala Ala Ala
100 105 110

Ser Asn Arg Ala Ala Arg Ala Ala Ala Ala Ala Arg Thr Ala Phe
115 120 125

Ser Gln Val Val Ala Ser His Arg Val Ala Thr Pro Gln Val Ser Gly
130 135 140

Glu Asp Thr Gln Pro Thr Thr Tyr Ala Ala Glu Ala Gln Gly Pro Thr
145 150 155 160

Pro Glu Pro Pro Leu Ala Ser Pro Gln Thr Ser Gln Met Leu Val Thr
165 170 175

Ser Lys Met Ala Ala Pro Glu Ala Pro Ala Thr Ser Ala Gln Ser Gln
180 185 190

Thr Gly Ser Pro Ala Gln Glu Ala Ala Thr Glu Gly Pro Ser Ser Ala
195 200 205

Cys Ala Phe Ser Gln Ala Pro Cys Ala Arg Glu Val Asp Ala Asn Arg
210 215 220

Pro Ser Thr Ala Phe Leu Gly Gln Asn Asp Val Phe Asp Phe Thr Gln
225 230 235 240

ITI-08-PCT_Sequence_Listing_ST25.txt

Pro	Ala	Gly	Val	Ser	Gly	Met	Ala	Phe	Pro	Arg	Pro	Lys	Arg	Pro	Ala	245	250	255
Pro	Ala	Gln	Glu	Ala	Ala	Thr	Glu	Gly	Pro	Ser	Ala	Ala	Ser	Gly	Val	260	265	270
Pro	Gln	Thr	Gly	Pro	Gly	Arg	Glu	Val	Ala	Ala	Thr	Arg	Pro	Lys	Thr	275	280	285
Thr	Lys	Ser	Gly	Lys	Ala	Leu	Ala	Lys	Thr	Arg	Trp	Val	Glu	Pro	Gln	290	295	300
Asn	Val	Val	Ala	Ala	Ala	Ala	Ala	Lys	Ala	Lys	Met	Ala	Thr	Ser	Ile	305	310	315
Pro	Glu	Pro	Glu	Gly	Ala	Ala	Ala	Ala	Thr	Ala	Gln	His	Ser	Ala	Glu	325	330	335
Pro	Trp	Ala	Arg	Met	Gly	Gly	Lys	Arg	Thr	Lys	Lys	Ser	Lys	His	Leu	340	345	350
Asp	Asp	Glu	Tyr	Glu	Ser	Ser	Glu	Glu	Glu	Arg	Glu	Thr	Pro	Ala	Val	355	360	365
Pro	Pro	Thr	Trp	Arg	Ala	Ser	Gln	Pro	Ser	Leu	Thr	Val	Arg	Ala	Gln	370	375	380
Leu	Ala	Pro	Arg	Pro	Pro	Met	Ala	Pro	Arg	Ser	Gln	Ile	Pro	Ser	Arg	385	390	395
His	Val	Leu	Cys	Leu	Pro	Pro	Arg	Asn	Val	Thr	Leu	Leu	Gln	Glu	Arg	405	410	415
Ala	Asn	Lys	Leu	Val	Lys	Tyr	Leu	Met	Ile	Lys	Asp	Tyr	Lys	Lys	Ile	420	425	430
Pro	Ile	Lys	Arg	Ala	Asp	Met	Leu	Lys	Asp	Val	Ile	Arg	Glu	Tyr	Asp	435	440	445
Glu	His	Phe	Pro	Glu	Ile	Ile	Glu	Arg	Ala	Thr	Tyr	Thr	Leu	Glu	Lys	450	455	460
Lys	Phe	Gly	Ile	His	Leu	Lys	Glu	Ile	Asp	Lys	Glu	Glu	His	Leu	Tyr	465	470	475
Ile	Leu	Val	Cys	Thr	Arg	Asp	Ser	Ser	Ala	Arg	Leu	Leu	Gly	Lys	Thr	485	490	495
Lys	Asp	Thr	Pro	Arg	Leu	Ser	Leu	Leu	Leu	Val	Ile	Leu	Gly	Val	Ile	500	505	510

ITI-08-PCT_Sequence_Listing_ST25.txt

Phe Met Asn Gly Asn Arg Ala Ser Glu Ala Val Leu Trp Glu Ala Leu
515 520 525

Arg Lys Met Gly Leu Arg Pro Gly Val Arg His Pro Phe Leu Gly Asp
530 535 540

Leu Arg Lys Leu Ile Thr Asp Asp Phe Val Lys Gln Lys Tyr Leu Glu
545 550 555 560

Tyr Lys Lys Ile Pro Asn Ser Asn Pro Pro Glu Tyr Glu Phe Leu Trp
565 570 575

Gly Leu Arg Ala Arg His Glu Thr Ser Lys Met Arg Val Leu Arg Phe
580 585 590

Ile Ala Gln Asn Gln Asn Arg Asp Pro Arg Glu Trp Lys Ala His Phe
595 600 605

Leu Glu Ala Val Asp Asp Ala Phe Lys Thr Met Asp Val Asp Met Ala
610 615 620

Glu Glu His Ala Arg Ala Gln Met Arg Ala Gln Met Asn Ile Gly Asp
625 630 635 640

Glu Ala Leu Ile Gly Arg Trp Ser Trp Asp Asp Ile Gln Val Glu Leu
645 650 655

Leu Thr Trp Asp Glu Asp Gly Asp Phe Gly Asp Ala Trp Ala Arg Ile
660 665 670

Pro Phe Ala Phe Trp Ala Arg Tyr His Gln Tyr Ile Leu Asn Ser Asn
675 680 685

Arg Ala Asn Arg Arg Ala Thr Trp Arg Ala Gly Val Ser Ser Gly Thr
690 695 700

Asn Gly Gly Ala Ser Thr Ser Val Leu Asp Gly Pro Ser Thr Ser Ser
705 710 715 720

Thr Ile Arg Thr Arg Asn Ala Ala Arg Ala Gly Ala Ser Phe Phe Ser
725 730 735

Trp Ile Gln His Arg
740

<210> 482
<211> 373
<212> PRT
<213> Artificial Sequence

<220>
<223> MAGE-_E1__Homo_sapiens__Q6IAI7

ITI-08-PCT_Sequence_Listing_ST25.txt

<400> 482

```

Met Pro Pro Val Pro Gly Val Pro Phe Arg Asn Val Asp Asn Asp Ser
1          5          10          15

Pro Thr Ser Val Glu Leu Glu Asp Trp Val Asp Ala Gln His Pro Thr
          20          25          30

Asp Glu Glu Glu Glu Glu Ala Ser Ser Ala Ser Ser Thr Leu Tyr Leu
          35          40          45

Val Phe Ser Pro Ser Ser Phe Ser Thr Ser Ser Ser Leu Ile Leu Gly
          50          55          60

Gly Pro Glu Glu Glu Glu Val Pro Ser Gly Val Ile Pro Asn Leu Thr
65          70          75          80

Glu Ser Ile Pro Ser Ser Pro Pro Gln Gly Pro Pro Gln Gly Pro Ser
          85          90          95

Gln Ser Pro Leu Ser Ser Cys Cys Ser Ser Phe Ser Trp Ser Ser Phe
          100          105          110

Ser Glu Glu Ser Ser Ser Gln Lys Gly Glu Asp Thr Gly Thr Cys Gln
          115          120          125

Gly Leu Pro Asp Ser Glu Ser Ser Phe Thr Tyr Thr Leu Asp Glu Lys
          130          135          140

Val Ala Glu Leu Val Glu Phe Leu Leu Leu Lys Tyr Glu Ala Glu Glu
145          150          155          160

Pro Val Thr Glu Ala Glu Met Leu Met Ile Val Ile Lys Tyr Lys Asp
          165          170          175

Tyr Phe Pro Val Ile Leu Lys Arg Ala Arg Glu Phe Met Glu Leu Leu
          180          185          190

Phe Gly Leu Ala Leu Ile Glu Val Gly Pro Asp His Phe Cys Val Phe
          195          200          205

Ala Asn Thr Val Gly Leu Thr Asp Glu Gly Ser Asp Asp Glu Gly Met
          210          215          220

Pro Glu Asn Ser Leu Leu Ile Ile Ile Leu Ser Val Ile Phe Ile Lys
225          230          235          240

Gly Asn Cys Ala Ser Glu Glu Val Ile Trp Glu Val Leu Asn Ala Val
          245          250          255

Gly Val Tyr Ala Gly Arg Glu His Phe Val Tyr Gly Glu Pro Arg Glu

```

ITI-08-PCT_Sequence_Listing_ST25.txt

260

265

270

Leu Leu Thr Lys Val Trp Val Gln Gly His Tyr Leu Glu Tyr Arg Glu
275 280 285

Val Pro His Ser Ser Pro Pro Tyr Tyr Glu Phe Leu Trp Gly Pro Arg
290 295 300

Ala His Ser Glu Ser Ile Lys Lys Lys Val Leu Glu Phe Leu Ala Lys
305 310 315 320

Leu Asn Asn Thr Val Pro Ser Ser Phe Pro Ser Trp Tyr Lys Asp Ala
325 330 335

Leu Lys Asp Val Glu Glu Arg Val Gln Ala Thr Ile Asp Thr Ala Asp
340 345 350

Asp Ala Thr Val Met Ala Ser Glu Ser Leu Ser Val Met Ser Ser Asn
355 360 365

Val Ser Phe Ser Asp
370

<210> 483

<211> 957

<212> PRT

<213> Artificial Sequence

<220>

<223> MAGE-E1_(MAGE1)___Homo_sapiens__Q9HCI5

<400> 483

Met Ser Leu Val Ser Gln Asn Ser Arg Arg Arg Arg Arg Arg Val Ala
1 5 10 15

Lys Ala Thr Ala His Asn Ser Ser Trp Gly Glu Met Gln Ala Pro Asn
20 25 30

Ala Pro Gly Leu Pro Ala Asp Val Pro Gly Ser Asp Val Pro Gln Gly
35 40 45

Pro Ser Asp Ser Gln Ile Leu Gln Gly Leu Cys Ala Ser Glu Gly Pro
50 55 60

Ser Thr Ser Val Leu Pro Thr Ser Ala Glu Gly Pro Ser Thr Phe Val
65 70 75 80

Pro Pro Thr Ile Ser Glu Ala Ser Ser Ala Ser Gly Gln Pro Thr Ile
85 90 95

Ser Glu Gly Pro Gly Thr Ser Val Leu Pro Thr Pro Ser Glu Gly Leu

ITI-08-PCT_Sequence_Listing_ST25.txt

100	105	110															
Ser	Thr	Ser	Gly	Pro	Pro	Thr	Ile	Ser	Lys	Gly	Leu	Cys	Thr	Ser	Val		
	115						120					125					
Thr	Leu	Ala	Ala	Ser	Glu	Gly	Arg	Asn	Thr	Ser	Arg	Pro	Pro	Thr	Ser		
	130					135					140						
Ser	Glu	Glu	Pro	Ser	Thr	Ser	Val	Pro	Pro	Thr	Ala	Ser	Glu	Val	Pro		
145					150					155					160		
Ser	Thr	Ser	Leu	Pro	Pro	Thr	Pro	Gly	Glu	Gly	Thr	Ser	Thr	Ser	Val		
				165					170					175			
Pro	Pro	Thr	Ala	Tyr	Glu	Gly	Pro	Ser	Thr	Ser	Val	Val	Pro	Thr	Pro		
			180					185					190				
Asp	Glu	Gly	Pro	Ser	Thr	Ser	Val	Leu	Pro	Thr	Pro	Gly	Glu	Gly	Pro		
	195						200					205					
Gly	Thr	Ser	Val	Pro	Leu	Ala	Ala	Thr	Glu	Gly	Leu	Ser	Thr	Ser	Val		
	210					215					220						
Gln	Ala	Thr	Pro	Asp	Glu	Gly	Pro	Ser	Thr	Ser	Val	Pro	Pro	Thr	Ala		
225					230					235					240		
Thr	Glu	Gly	Leu	Ser	Thr	Pro	Val	Pro	Pro	Thr	Arg	Asp	Glu	Gly	Pro		
				245					250					255			
Ser	Thr	Ser	Val	Pro	Ala	Thr	Pro	Gly	Glu	Gly	Pro	Ser	Thr	Ser	Val		
			260					265					270				
Leu	Pro	Ala	Ala	Ser	Asp	Gly	Gln	Ser	Ile	Ser	Leu	Val	Pro	Thr	Arg		
		275					280					285					
Gly	Lys	Gly	Ser	Ser	Thr	Ser	Val	Pro	Pro	Thr	Ala	Thr	Glu	Gly	Leu		
	290					295					300						
Ser	Thr	Ser	Val	Gln	Pro	Thr	Ala	Gly	Glu	Gly	Ser	Ser	Thr	Ser	Val		
305					310					315					320		
Pro	Pro	Thr	Pro	Gly	Gly	Gly	Leu	Ser	Thr	Ser	Val	Pro	Pro	Thr	Ala		
				325					330					335			
Thr	Glu	Glu	Leu	Ser	Thr	Ser	Val	Pro	Pro	Thr	Pro	Gly	Glu	Gly	Pro		
			340					345					350				
Ser	Thr	Ser	Val	Leu	Pro	Ile	Pro	Gly	Glu	Gly	Leu	Ser	Thr	Ser	Val		
			355				360					365					
Pro	Pro	Thr	Ala	Ser	Asp	Gly	Ser	Asp	Thr	Ser	Val	Pro	Pro	Thr	Pro		
	370					375					380						

ITI-08-PCT_Sequence_Listing_ST25.txt

Gly	Glu	Gly	Ala	Ser	Thr	Leu	Val	Gln	Pro	Thr	Ala	Pro	Asp	Gly	Pro	385	390	395	400
Gly	Ser	Ser	Val	Leu	Pro	Asn	Pro	Gly	Glu	Gly	Pro	Ser	Thr	Leu	Phe	405	410	415	
Ser	Ser	Ser	Ala	Ser	Val	Asp	Arg	Asn	Pro	Ser	Lys	Cys	Ser	Leu	Val	420	425	430	
Leu	Pro	Ser	Pro	Arg	Val	Thr	Lys	Ala	Ser	Val	Asp	Ser	Asp	Ser	Glu	435	440	445	
Gly	Pro	Lys	Gly	Ala	Glu	Gly	Pro	Ile	Glu	Phe	Glu	Val	Leu	Arg	Asp	450	455	460	
Cys	Glu	Ser	Pro	Asn	Ser	Ile	Ser	Ile	Met	Gly	Leu	Asn	Thr	Ser	Arg	465	470	475	480
Val	Ala	Ile	Thr	Leu	Lys	Pro	Gln	Asp	Pro	Met	Glu	Gln	Asn	Val	Ala	485	490	495	
Glu	Leu	Leu	Gln	Phe	Leu	Leu	Val	Lys	Asp	Gln	Ser	Lys	Tyr	Pro	Ile	500	505	510	
Arg	Glu	Ser	Glu	Met	Arg	Glu	Tyr	Ile	Val	Lys	Glu	Tyr	Arg	Asn	Gln	515	520	525	
Phe	Pro	Glu	Ile	Leu	Arg	Arg	Ala	Ala	Ala	His	Leu	Glu	Cys	Ile	Phe	530	535	540	
Arg	Phe	Glu	Leu	Arg	Glu	Leu	Asp	Pro	Glu	Ala	His	Thr	Tyr	Ile	Leu	545	550	555	560
Leu	Asn	Lys	Leu	Gly	Pro	Val	Pro	Phe	Glu	Gly	Leu	Glu	Glu	Ser	Pro	565	570	575	
Asn	Gly	Pro	Lys	Met	Gly	Leu	Leu	Met	Met	Ile	Leu	Gly	Gln	Ile	Phe	580	585	590	
Leu	Asn	Gly	Asn	Gln	Ala	Lys	Glu	Ala	Glu	Ile	Trp	Glu	Met	Leu	Trp	595	600	605	
Arg	Met	Gly	Val	Gln	Arg	Glu	Arg	Arg	Leu	Ser	Ile	Phe	Gly	Asn	Pro	610	615	620	
Lys	Arg	Leu	Leu	Ser	Val	Glu	Phe	Val	Trp	Gln	Arg	Tyr	Leu	Asp	Tyr	625	630	635	640
Arg	Pro	Val	Thr	Asp	Cys	Lys	Pro	Val	Glu	Tyr	Glu	Phe	Phe	Trp	Gly	645	650	655	

ITI-08-PCT_Sequence_Listing_ST25.txt

Pro	Arg	Ser	His	Leu	Glu	Thr	Thr	Lys	Met	Lys	Ile	Leu	Lys	Phe	Met	660	665	670
Ala	Lys	Ile	Tyr	Asn	Lys	Asp	Pro	Met	Asp	Trp	Pro	Glu	Lys	Tyr	Asn	675	680	685
Glu	Ala	Leu	Glu	Glu	Asp	Ala	Ala	Arg	Ala	Phe	Ala	Glu	Gly	Trp	Gln	690	695	700
Ala	Leu	Pro	His	Phe	Arg	Arg	Pro	Phe	Phe	Glu	Glu	Ala	Ala	Ala	Glu	705	710	715
Val	Pro	Ser	Pro	Asp	Ser	Glu	Val	Ser	Ser	Tyr	Ser	Ser	Lys	Tyr	Ala	725	730	735
Pro	His	Ser	Trp	Pro	Glu	Ser	Arg	Leu	Glu	Ser	Lys	Ala	Arg	Lys	Leu	740	745	750
Val	Gln	Leu	Phe	Leu	Leu	Met	Asp	Ser	Thr	Lys	Leu	Pro	Ile	Pro	Lys	755	760	765
Lys	Gly	Ile	Leu	Tyr	Tyr	Ile	Gly	Arg	Glu	Cys	Ser	Lys	Val	Phe	Pro	770	775	780
Asp	Leu	Leu	Asn	Arg	Ala	Ala	Arg	Thr	Leu	Asn	His	Val	Tyr	Gly	Thr	785	790	795
Glu	Leu	Val	Val	Leu	Asp	Pro	Arg	Asn	His	Ser	Tyr	Thr	Leu	Tyr	Asn	805	810	815
Arg	Arg	Glu	Met	Glu	Glu	Thr	Glu	Glu	Ile	Val	Asp	Ser	Pro	Asn	Arg	820	825	830
Pro	Gly	Asn	Asn	Phe	Leu	Met	Gln	Val	Leu	Ser	Phe	Ile	Phe	Ile	Met	835	840	845
Gly	Asn	His	Ala	Arg	Glu	Ser	Ala	Val	Trp	Ala	Phe	Leu	Arg	Gly	Leu	850	855	860
Gly	Val	Gln	Ala	Gly	Arg	Lys	His	Val	Ile	Thr	Cys	Arg	Tyr	Leu	Ser	865	870	875
Gln	Arg	Tyr	Ile	Asp	Ser	Leu	Arg	Val	Pro	Asp	Ser	Asp	Pro	Val	Gln	885	890	895
Tyr	Glu	Phe	Val	Trp	Gly	Pro	Arg	Ala	Arg	Leu	Glu	Thr	Ser	Lys	Met	900	905	910
Lys	Ala	Leu	Arg	Tyr	Val	Ala	Arg	Ile	His	Arg	Lys	Glu	Pro	Gln	Asp	915	920	925
Trp	Pro	Gln	Gln	Tyr	Arg	Glu	Ala	Met	Glu	Asp	Glu	Ala	Asn	Arg	Ala			

ITI-08-PCT_Sequence_Listing_ST25.txt

930

935

940

Asp Val Gly His Arg Gln Ile Phe Val His Asn Phe Arg
 945 950 955

<210> 484
 <211> 523
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MAGE-E2__Homo_sapiens__Q8TD90

<400> 484

Met Ser Leu Val Ser Gln Asn Ala Arg His Cys Ser Ala Glu Ile Thr
 1 5 10 15

Ala Asp Tyr Gly Asp Gly Arg Gly Glu Ile Gln Ala Thr Asn Ala Ser
 20 25 30

Gly Ser Pro Thr Ser Met Leu Val Val Asp Ala Pro Gln Cys Pro Gln
 35 40 45

Ala Pro Ile Asn Ser Gln Cys Val Asn Thr Ser Gln Ala Val Gln Asp
 50 55 60

Pro Asn Asp Leu Glu Val Leu Ile Asp Glu Gln Ser Arg Arg Leu Gly
 65 70 75 80

Ala Leu Arg Val His Asp Pro Leu Glu Asp Arg Ser Ile Ala Leu Val
 85 90 95

Asn Phe Met Arg Met Lys Ser Gln Thr Glu Gly Ser Ile Gln Gln Ser
 100 105 110

Glu Met Leu Glu Phe Leu Arg Glu Tyr Ser Asp Gln Phe Pro Glu Ile
 115 120 125

Leu Arg Arg Ala Ser Ala His Leu Asp Gln Val Phe Gly Leu Asn Leu
 130 135 140

Arg Val Ile Asp Pro Gln Ala Asp Thr Tyr Asn Leu Val Ser Lys Arg
 145 150 155 160

Gly Phe Gln Ile Thr Asp Arg Ile Ala Glu Ser Leu Asp Met Pro Lys
 165 170 175

Ala Ser Leu Leu Ala Leu Val Leu Gly His Ile Leu Leu Asn Gly Asn
 180 185 190

Arg Ala Arg Glu Ala Ser Ile Trp Asp Leu Leu Leu Lys Val Asp Met

ITI-08-PCT_Sequence_Listing_ST25.txt

```

195                200                205
Trp Asp Lys Pro Gln Arg Ile Asn Asn Leu Phe Gly Asn Thr Arg Asn
210                215                220
Leu Leu Thr Thr Asp Phe Val Cys Met Arg Phe Leu Glu Tyr Trp Pro
225                230                235                240
Val Tyr Gly Thr Asn Pro Leu Glu Phe Glu Phe Leu Trp Gly Ser Arg
245                250                255
Ala His Arg Glu Ile Thr Lys Met Glu Ala Leu Lys Phe Val Ser Asp
260                265                270
Ala His Asp Glu Glu Pro Trp Ser Trp Pro Glu Glu Tyr Asn Lys Ala
275                280                285
Leu Glu Gly Asp Lys Thr Lys Glu Arg Ser Leu Thr Ala Gly Leu Glu
290                295                300
Phe Trp Ser Glu Asp Thr Met Asn Asp Lys Ala Asn Asp Leu Val Gln
305                310                315                320
Leu Ala Ile Ser Val Thr Glu Glu Met Leu Pro Ile His Gln Asp Glu
325                330                335
Leu Leu Ala His Thr Gly Lys Glu Phe Glu Asp Val Phe Pro Asn Ile
340                345                350
Leu Asn Arg Ala Thr Leu Ile Leu Asp Met Phe Tyr Gly Leu Ser Leu
355                360                365
Ile Glu Val Asp Thr Ser Glu His Ile Tyr Leu Leu Val Gln Gln Pro
370                375                380
Glu Ser Glu Glu Glu Gln Val Met Leu Glu Ser Leu Gly Arg Pro Thr
385                390                395                400
Gln Glu Tyr Val Met Pro Ile Leu Gly Leu Ile Phe Leu Met Gly Asn
405                410                415
Arg Val Lys Glu Ala Asn Val Trp Asn Leu Leu Arg Arg Phe Ser Val
420                425                430
Asp Val Gly Arg Lys His Ser Ile Thr Arg Lys Leu Met Arg Gln Arg
435                440                445
Tyr Leu Glu Cys Arg Pro Leu Ser Tyr Ser Asn Pro Val Glu Tyr Glu
450                455                460
Leu Leu Trp Gly Pro Arg Ala His His Glu Thr Ile Lys Met Lys Val
465                470                475                480

```


ITI-08-PCT_Sequence_Listing_ST25.txt

Leu Glu Tyr Met Ala Arg Leu Tyr Arg Lys Arg Pro Gln Asn Trp Pro
485 490 495

Glu Gln Tyr Arg Glu Ala Val Glu Asp Glu Glu Ala Arg Ala Lys Ser
500 505 510

Glu Ala Thr Ile Met Phe Phe Leu Asp Pro Thr
515 520

<210> 485

<211> 307

<212> PRT

<213> Artificial Sequence

<220>

<223> MAGE-F1__Homo_sapiens__Q9HAY2

<400> 485

Met Leu Gln Thr Pro Glu Ser Arg Gly Leu Pro Val Pro Gln Ala Glu
1 5 10 15

Gly Glu Lys Asp Gly Gly His Asp Gly Glu Thr Arg Ala Pro Thr Ala
20 25 30

Ser Gln Glu Arg Pro Lys Glu Glu Leu Gly Ala Gly Arg Glu Glu Gly
35 40 45

Ala Ala Glu Pro Ala Leu Thr Arg Lys Gly Ala Arg Ala Leu Ala Ala
50 55 60

Lys Ala Leu Ala Arg Arg Arg Ala Tyr Arg Arg Leu Asn Arg Thr Val
65 70 75 80

Ala Glu Leu Val Gln Phe Leu Leu Val Lys Asp Lys Lys Lys Ser Pro
85 90 95

Ile Thr Arg Ser Glu Met Val Lys Tyr Val Ile Gly Asp Leu Lys Ile
100 105 110

Leu Phe Pro Asp Ile Ile Ala Arg Ala Ala Glu His Leu Arg Tyr Val
115 120 125

Phe Gly Phe Glu Leu Lys Gln Phe Asp Arg Lys His His Thr Tyr Ile
130 135 140

Leu Ile Asn Lys Leu Lys Pro Leu Glu Glu Glu Glu Glu Asp Leu
145 150 155 160

Gly Gly Asp Gly Pro Arg Leu Gly Leu Leu Met Met Ile Leu Gly Leu
165 170 175

ITI-08-PCT_Sequence_Listing_ST25.txt

Ile Tyr Met Arg Gly Asn Ser Ala Arg Glu Ala Gln Val Trp Glu Met
180 185 190

Leu Arg Arg Leu Gly Val Gln Pro Ser Lys Tyr His Phe Leu Phe Gly
195 200 205

Tyr Pro Lys Arg Leu Ile Met Glu Asp Phe Val Gln Gln Arg Tyr Leu
210 215 220

Ser Tyr Arg Arg Val Pro His Thr Asn Pro Pro Glu Tyr Glu Phe Ser
225 230 235 240

Trp Gly Pro Arg Ser Asn Leu Glu Ile Ser Lys Met Glu Val Leu Gly
245 250 255

Phe Val Ala Lys Leu His Lys Lys Glu Pro Gln His Trp Pro Val Gln
260 265 270

Tyr Arg Glu Ala Leu Ala Asp Glu Ala Asp Arg Ala Arg Ala Lys Ala
275 280 285

Arg Ala Glu Ala Ser Met Arg Ala Arg Ala Ser Ala Arg Ala Gly Ile
290 295 300

His Leu Trp
305

<210> 486

<211> 219

<212> PRT

<213> Artificial Sequence

<220>

<223> MAGE-H1__Homo_sapiens__Q9H213

<400> 486

Met Pro Arg Gly Arg Lys Ser Arg Arg Arg Arg Asn Ala Arg Ala Ala
1 5 10 15

Glu Glu Asn Arg Asn Asn Arg Lys Ile Gln Ala Ser Glu Ala Ser Glu
20 25 30

Thr Pro Met Ala Ala Ser Val Val Ala Ser Thr Pro Glu Asp Asp Leu
35 40 45

Ser Gly Pro Glu Glu Asp Pro Ser Thr Pro Glu Glu Ala Ser Thr Thr
50 55 60

Pro Glu Glu Ala Ser Ser Thr Ala Gln Ala Gln Lys Pro Ser Val Pro
65 70 75 80

ITI-08-PCT_Sequence_Listing_ST25.txt

Arg Ser Asn Phe Gln Gly Thr Lys Lys Ser Leu Leu Met Ser Ile Leu
85 90 95

Ala Leu Ile Phe Ile Met Gly Asn Ser Ala Lys Glu Ala Leu Val Trp
100 105 110

Lys Val Leu Gly Lys Leu Gly Met Gln Pro Gly Arg Gln His Ser Ile
115 120 125

Phe Gly Asp Pro Lys Lys Ile Val Thr Glu Glu Phe Val Arg Arg Gly
130 135 140

Tyr Leu Ile Tyr Lys Pro Val Pro Arg Ser Ser Pro Val Glu Tyr Glu
145 150 155 160

Phe Phe Trp Gly Pro Arg Ala His Val Glu Ser Ser Lys Leu Lys Val
165 170 175

Met His Phe Val Ala Arg Val Arg Asn Arg Cys Ser Lys Asp Trp Pro
180 185 190

Cys Asn Tyr Asp Trp Asp Ser Asp Asp Ala Glu Val Glu Ala Ile
195 200 205

Leu Asn Ser Gly Ala Arg Gly Tyr Ser Ala Pro
210 215

<210> 487

<211> 1249

<212> PRT

<213> Artificial Sequence

<220>

<223> MAGEL2__Homo_sapiens__Q9UJ55

<400> 487

Met Ser Gln Leu Ser Lys Asn Leu Gly Asp Ser Ser Pro Pro Ala Glu
1 5 10 15

Ala Pro Lys Pro Pro Val Tyr Ser Arg Pro Thr Val Leu Met Arg Ala
20 25 30

Pro Pro Ala Ser Ser Arg Ala Pro Pro Val Pro Trp Asp Pro Pro Pro
35 40 45

Ile Asp Leu Gln Ala Ser Leu Ala Ala Trp Gln Ala Pro Gln Pro Ala
50 55 60

Trp Glu Ala Pro Gln Gly Gln Leu Pro Ala Pro Val Val Pro Met Thr
65 70 75 80

ITI-08-PCT_Sequence_Listing_ST25.txt

Gln	Pro	Pro	Ala	Leu	Gly	Gly	Pro	Ile	Val	Pro	Ala	Pro	Pro	Leu	Gly	85	90	95
Gly	Pro	Met	Gly	Lys	Pro	Pro	Thr	Pro	Gly	Val	Leu	Met	Val	His	Pro	100	105	110
Pro	Pro	Pro	Gly	Ala	Pro	Met	Ala	Gln	Pro	Pro	Thr	Pro	Gly	Val	Leu	115	120	125
Met	Val	His	Pro	Ser	Ala	Pro	Gly	Ala	Pro	Met	Ala	His	Pro	Pro	Pro	130	135	140
Pro	Gly	Thr	Pro	Met	Ser	His	Pro	Pro	Pro	Pro	Gly	Thr	Pro	Met	Ala	145	150	155
His	Pro	Pro	Pro	Pro	Gly	Thr	Pro	Met	Ala	His	Pro	Pro	Pro	Pro	Gly	165	170	175
Thr	Pro	Met	Val	His	Pro	Pro	Pro	Pro	Gly	Thr	Pro	Met	Ala	His	Pro	180	185	190
Pro	Pro	Pro	Gly	Thr	Pro	Met	Ala	His	Pro	Pro	Pro	Pro	Gly	Thr	Pro	195	200	205
Met	Ala	His	Pro	Pro	Pro	Pro	Gly	Thr	Pro	Met	Ala	His	Pro	Pro	Pro	210	215	220
Pro	Gly	Thr	Pro	Met	Ala	Gln	Pro	Pro	Ala	Pro	Gly	Val	Leu	Met	Ala	225	230	235
Gln	Pro	Leu	Thr	Pro	Gly	Val	Leu	Met	Val	Gln	Pro	Ala	Ala	Pro	Gly	245	250	255
Ala	Pro	Met	Val	Gln	Pro	Pro	Pro	Ala	Ala	Met	Met	Thr	Gln	Pro	Gln	260	265	270
Pro	Ser	Gly	Ala	Pro	Met	Ala	Lys	Pro	Pro	Gly	Pro	Gly	Val	Leu	Met	275	280	285
Ile	His	Pro	Pro	Gly	Ala	Arg	Ala	Pro	Met	Thr	Gln	Pro	Pro	Ala	Ser	290	295	300
Gly	Ala	Pro	Met	Ala	Gln	Pro	Ala	Ala	Pro	Pro	Ala	Gln	Pro	Met	Ala	305	310	315
Pro	Pro	Ala	Gln	Pro	Met	Ala	Ser	Trp	Ala	Pro	Gln	Ala	Gln	Pro	Leu	325	330	335
Ile	Leu	Gln	Ile	Gln	Ser	Gln	Val	Ile	Arg	Ala	Pro	Pro	Gln	Val	Pro	340	345	350

ITI-08-PCT_Sequence_Listing_ST25.txt

Gln Gly Pro Gln Ala Pro Pro Ala Gln Leu Ala Thr Pro Pro Gly Trp
355 360 365

Gln Ala Thr Ser Pro Gly Trp Gln Ala Thr Gln Gln Gly Trp Gln Ala
370 375 380

Thr Pro Leu Thr Trp Gln Thr Thr Gln Val Thr Trp Gln Ala Pro Ala
385 390 395 400

Val Thr Trp Gln Val Pro Pro Pro Met Arg Gln Gly Pro Pro Pro Ile
405 410 415

Arg Pro Gly Pro Pro Pro Ile Arg Pro Gly Pro Pro Pro Val Arg Gln
420 425 430

Ala Pro Pro Leu Ile Arg Gln Ala Pro Pro Val Ile Arg Gln Ala Pro
435 440 445

Pro Val Ile Arg Gln Ala Pro Pro Val Ile Arg Gln Ala Pro Ala Val
450 455 460

Ile Arg Gln Ala Pro Pro Val Ile Arg Gln Ala Pro Pro Val Ile Arg
465 470 475 480

Gln Ala Pro Pro Val Ile Arg Gln Ala Pro Pro Leu Ile Arg Gln Ala
485 490 495

Pro Pro Pro Ile Arg Pro Ala Pro Gln Val Leu Ala Thr Gln Pro Pro
500 505 510

Leu Trp Gln Ala Leu Pro Pro Pro Pro Pro Leu Arg Gln Ala Pro Gln
515 520 525

Ala Arg Leu Pro Ala Pro Gln Val Gln Ala Ala Pro Gln Val Pro Thr
530 535 540

Ala Pro Pro Ala Thr Gln Val Pro Ala Ala Pro Pro Ala Gly Pro Gln
545 550 555 560

Val Pro Gln Pro Val Leu Pro Ala Pro Leu Ser Ala Pro Leu Ser Ala
565 570 575

Pro Gln Ala Val His Cys Pro Ser Ile Ile Trp Gln Ala Pro Lys Gly
580 585 590

Gln Pro Pro Val Pro His Glu Ile Pro Thr Ser Met Glu Phe Gln Glu
595 600 605

Val Gln Gln Thr Gln Ala Leu Ala Trp Gln Ala Gln Lys Ala Pro Thr
610 615 620

His Ile Trp Gln Pro Leu Pro Ala Gln Glu Ala Gln Arg Gln Ala Pro

ITI-08-PCT_Sequence_Listing_ST25.txt

```

625          630          635          640
Pro Leu Val Gln Leu Glu Gln Pro Phe Gln Gly Ala Pro Pro Ser Gln
          645          650          655

Lys Ala Val Gln Ile Gln Leu Pro Pro Gln Gln Ala Gln Ala Ser Gly
          660          665          670

Pro Gln Ala Glu Val Pro Thr Leu Pro Leu Gln Pro Ser Trp Gln Ala
          675          680          685

Pro Pro Ala Val Leu Gln Ala Gln Pro Gly Pro Pro Val Ala Ala Ala
          690          695          700

Asn Phe Pro Leu Gly Ser Ala Lys Ser Leu Met Thr Pro Ser Gly Glu
705          710          715          720

Cys Arg Ala Ser Ser Ile Asp Arg Arg Gly Ser Ser Lys Glu Arg Arg
          725          730          735

Thr Ser Ser Lys Glu Arg Arg Ala Pro Ser Lys Asp Arg Met Ile Phe
          740          745          750

Ala Ala Thr Phe Cys Ala Pro Lys Ala Val Ser Ala Ala Arg Ala His
          755          760          765

Leu Pro Ala Ala Trp Lys Asn Leu Pro Ala Thr Pro Glu Thr Phe Ala
          770          775          780

Pro Ser Ser Ser Val Phe Pro Ala Thr Ser Gln Phe Gln Pro Ala Ser
785          790          795          800

Leu Asn Ala Phe Lys Gly Pro Ser Ala Ala Ser Glu Thr Pro Lys Ser
          805          810          815

Leu Pro Tyr Ala Leu Gln Asp Pro Phe Ala Cys Val Glu Ala Leu Pro
          820          825          830

Ala Val Pro Trp Val Pro Gln Pro Asn Met Asn Ala Ser Lys Ala Ser
          835          840          845

Gln Ala Val Pro Thr Phe Leu Met Ala Thr Ala Ala Ala Pro Gln Ala
          850          855          860

Thr Ala Thr Thr Gln Glu Ala Ser Lys Thr Ser Val Glu Pro Pro Arg
865          870          875          880

Arg Ser Gly Lys Ala Thr Arg Lys Lys Lys His Leu Glu Ala Gln Glu
          885          890          895

Asp Ser Arg Gly His Thr Leu Ala Phe His Asp Trp Gln Gly Pro Arg
          900          905          910

```

ITI-08-PCT_Sequence_Listing_ST25.txt

```

Pro Trp Glu Asn Leu Asn Leu Ser Asp Trp Glu Val Gln Ser Pro Ile
  915                      920                      925

Gln Val Ser Gly Asp Trp Glu His Pro Asn Thr Pro Arg Gly Leu Ser
  930                      935                      940

Gly Trp Glu Gly Pro Ser Thr Ser Arg Ile Leu Ser Gly Trp Glu Gly
  945                      950                      955                      960

Pro Ser Ala Ser Trp Ala Leu Ser Ala Trp Glu Gly Pro Ser Thr Ser
                      965                      970                      975

Arg Ala Leu Gly Leu Ser Glu Ser Pro Gly Ser Ser Leu Pro Val Val
                      980                      985                      990

Val Ser Glu Val Ala Ser Val Ser Pro Gly Ser Ser Ala Thr Gln Asp
  995                      1000                      1005

Asn Ser Lys Val Glu Ala Gln Pro Leu Ser Pro Leu Asp Glu Arg
  1010                      1015                      1020

Ala Asn Ala Leu Val Gln Phe Leu Leu Val Lys Asp Gln Ala Lys
  1025                      1030                      1035

Val Pro Val Gln Arg Ser Glu Met Val Lys Val Ile Leu Arg Glu
  1040                      1045                      1050

Tyr Lys Asp Glu Cys Leu Asp Ile Ile Asn Arg Ala Asn Asn Lys
  1055                      1060                      1065

Leu Glu Cys Ala Phe Gly Tyr Gln Leu Lys Glu Ile Asp Thr Lys
  1070                      1075                      1080

Asn His Ala Tyr Ile Ile Ile Asn Lys Leu Gly Tyr His Thr Gly
  1085                      1090                      1095

Asn Leu Val Ala Ser Tyr Leu Asp Arg Pro Lys Phe Gly Leu Leu
  1100                      1105                      1110

Met Val Val Leu Ser Leu Ile Phe Met Lys Gly Asn Cys Val Arg
  1115                      1120                      1125

Glu Asp Leu Ile Phe Asn Phe Leu Phe Lys Leu Gly Leu Asp Val
  1130                      1135                      1140

Arg Glu Thr Asn Gly Leu Phe Gly Asn Thr Lys Lys Leu Ile Thr
  1145                      1150                      1155

Glu Val Phe Val Arg Gln Lys Tyr Leu Glu Tyr Arg Arg Ile Pro
  1160                      1165                      1170

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Tyr Thr Glu Pro Ala Glu Tyr Glu Phe Leu Trp Gly Pro Arg Ala
1175 1180 1185

Phe Leu Glu Thr Ser Lys Met Leu Val Leu Arg Phe Leu Ala Lys
1190 1195 1200

Leu His Lys Lys Asp Pro Gln Ser Trp Pro Phe His Tyr Leu Glu
1205 1210 1215

Ala Leu Ala Glu Cys Glu Trp Glu Asp Thr Asp Glu Asp Glu Pro
1220 1225 1230

Asp Thr Gly Asp Ser Ala His Gly Pro Thr Ser Arg Pro Pro Pro
1235 1240 1245

Arg

<210> 488
<211> 93
<212> PRT
<213> Artificial Sequence

<220>
<223> mammaglobin_A__Homo_sapiens__Q13296

<400> 488

Met Lys Leu Leu Met Val Leu Met Leu Ala Ala Leu Ser Gln His Cys
1 5 10 15

Tyr Ala Gly Ser Gly Cys Pro Leu Leu Glu Asn Val Ile Ser Lys Thr
20 25 30

Ile Asn Pro Gln Val Ser Lys Thr Glu Tyr Lys Glu Leu Leu Gln Glu
35 40 45

Phe Ile Asp Asp Asn Ala Thr Thr Asn Ala Ile Asp Glu Leu Lys Glu
50 55 60

Cys Phe Leu Asn Gln Thr Asp Glu Thr Leu Ser Asn Val Glu Val Phe
65 70 75 80

Met Gln Leu Ile Tyr Asp Ser Ser Leu Cys Asp Leu Phe
85 90

<210> 489
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> mammaglobin_A__Homo_sapiens__Q6NX70

ITI-08-PCT_Sequence_Listing_ST25.txt

<400> 489

Met Lys Leu Leu Met Val Leu Met Leu Ala Ala Leu Ser Gln His Cys
1 5 10 15

Tyr Ala Gly Ser Gly Cys Pro Leu Leu Glu Asn Val Ile Ser Lys Thr
20 25 30

Ile Asn Pro Gln Val Ser Lys Thr Glu Tyr Lys Glu Leu Leu Gln Glu
35 40 45

Phe Ile Asp Asp Asn Ala Thr Thr Asn Ala Ile Asp Glu Leu Lys Glu
50 55 60

Cys Phe Leu Asn Gln Thr Asp Glu Thr Leu Ser Asn Val Glu Val Phe
65 70 75 80

Met Val Ile Ser Phe Ser Ser Tyr Lys Leu Phe Lys Ser Pro Asp Gln
85 90 95

Gly Gln Val Gly Ser Ser Phe Leu Thr Asp Asn Ala Lys Ala Thr Ser
100 105 110

Glu Gln Ala Phe Ser Tyr Ile Gly
115 120

<210> 490

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> MART-1/melan-A__Homo_sapiens__Q16655

<400> 490

Met Pro Arg Glu Asp Ala His Phe Ile Tyr Gly Tyr Pro Lys Lys Gly
1 5 10 15

His Gly His Ser Tyr Thr Thr Ala Glu Glu Ala Ala Gly Ile Gly Ile
20 25 30

Leu Thr Val Ile Leu Gly Val Leu Leu Leu Ile Gly Cys Trp Tyr Cys
35 40 45

Arg Arg Arg Asn Gly Tyr Arg Ala Leu Met Asp Lys Ser Leu His Val
50 55 60

Gly Thr Gln Cys Ala Leu Thr Arg Arg Cys Pro Gln Glu Gly Phe Asp
65 70 75 80

ITI-08-PCT_Sequence_Listing_ST25.txt

His Arg Asp Ser Lys Val Ser Leu Gln Glu Lys Asn Cys Glu Pro Val
85 90 95

Val Pro Asn Ala Pro Pro Ala Tyr Glu Lys Leu Ser Ala Glu Gln Ser
100 105 110

Pro Pro Pro Tyr Ser Pro
115

<210> 491

<211> 493

<212> PRT

<213> Artificial Sequence

<220>

<223> MART-2__Homo_sapiens__Q5VTY9

<400> 491

Met Leu Pro Arg Trp Glu Leu Ala Leu Tyr Leu Leu Ala Ser Leu Gly
1 5 10 15

Phe His Phe Tyr Ser Phe Tyr Glu Val Tyr Lys Val Ser Arg Glu His
20 25 30

Glu Glu Glu Leu Asp Gln Glu Phe Glu Leu Glu Thr Asp Thr Leu Phe
35 40 45

Gly Gly Leu Lys Lys Asp Ala Thr Asp Phe Glu Trp Ser Phe Trp Met
50 55 60

Glu Trp Gly Lys Gln Trp Leu Val Trp Leu Leu Leu Gly His Met Val
65 70 75 80

Val Ser Gln Met Ala Thr Leu Leu Ala Arg Lys His Arg Pro Trp Ile
85 90 95

Leu Met Leu Tyr Gly Met Trp Ala Cys Trp Cys Val Leu Gly Thr Pro
100 105 110

Gly Val Ala Met Val Leu Leu His Thr Thr Ile Ser Phe Cys Val Ala
115 120 125

Gln Phe Arg Ser Gln Leu Leu Thr Trp Leu Cys Ser Leu Leu Leu Leu
130 135 140

Ser Thr Leu Arg Leu Gln Gly Val Glu Glu Val Lys Arg Arg Trp Tyr
145 150 155 160

Lys Thr Glu Asn Glu Tyr Tyr Leu Leu Gln Phe Thr Leu Thr Val Arg
165 170 175

ITI-08-PCT_Sequence_Listing_ST25.txt

Cys	Leu	Tyr	Tyr	Thr	Ser	Phe	Ser	Leu	Glu	Leu	Cys	Trp	Gln	Gln	Leu	180	185	190
Pro	Ala	Ala	Ser	Thr	Ser	Tyr	Ser	Phe	Pro	Trp	Met	Leu	Ala	Tyr	Val	195	200	205
Phe	Tyr	Tyr	Pro	Val	Leu	His	Asn	Gly	Pro	Ile	Leu	Ser	Phe	Ser	Glu	210	215	220
Phe	Ile	Lys	Gln	Met	Gln	Gln	Gln	Glu	His	Asp	Ser	Leu	Lys	Ala	Ser	225	230	235
Leu	Cys	Val	Leu	Ala	Leu	Gly	Leu	Gly	Arg	Leu	Leu	Cys	Trp	Trp	Trp	245	250	255
Leu	Ala	Glu	Leu	Met	Ala	His	Leu	Met	Tyr	Met	His	Ala	Ile	Tyr	Ser	260	265	270
Ser	Ile	Pro	Leu	Leu	Glu	Thr	Val	Ser	Cys	Trp	Thr	Leu	Gly	Gly	Leu	275	280	285
Ala	Leu	Ala	Gln	Val	Leu	Phe	Phe	Tyr	Val	Lys	Tyr	Leu	Val	Leu	Phe	290	295	300
Gly	Val	Pro	Ala	Leu	Leu	Met	Arg	Leu	Asp	Gly	Leu	Thr	Pro	Pro	Ala	305	310	315
Leu	Pro	Arg	Cys	Val	Ser	Thr	Met	Phe	Ser	Phe	Thr	Gly	Met	Trp	Arg	325	330	335
Tyr	Phe	Asp	Val	Gly	Leu	His	Asn	Phe	Leu	Ile	Arg	Tyr	Val	Tyr	Ile	340	345	350
Pro	Val	Gly	Gly	Ser	Gln	His	Gly	Leu	Leu	Gly	Thr	Leu	Phe	Ser	Thr	355	360	365
Ala	Met	Thr	Phe	Ala	Phe	Val	Ser	Tyr	Trp	His	Gly	Gly	Tyr	Asp	Tyr	370	375	380
Leu	Trp	Cys	Trp	Ala	Ala	Leu	Asn	Trp	Leu	Gly	Val	Thr	Val	Glu	Asn	385	390	395
Gly	Val	Arg	Arg	Leu	Val	Glu	Thr	Pro	Cys	Ile	Gln	Asp	Ser	Leu	Ala	405	410	415
Arg	Tyr	Phe	Ser	Pro	Gln	Ala	Arg	Arg	Arg	Phe	His	Ala	Ala	Leu	Ala	420	425	430
Ser	Cys	Ser	Thr	Ser	Met	Leu	Ile	Leu	Ser	Asn	Leu	Val	Phe	Leu	Gly	435	440	445
Gly	Asn	Glu	Val	Gly	Lys	Thr	Tyr	Trp	Asn	Arg	Ile	Phe	Ile	Gln	Gly			

ITI-08-PCT_Sequence_Listing_ST25.txt

450

455

460

Trp Pro Trp Val Thr Leu Ser Val Leu Gly Phe Leu Tyr Cys Tyr Ser
465 470 475 480

His Val Gly Ile Ala Trp Ala Gln Thr Tyr Ala Thr Asp
485 490

<210> 492

<211> 317

<212> PRT

<213> Artificial Sequence

<220>

<223> MC1_R__Homo_sapiens__Q01726

<400> 492

Met Ala Val Gln Gly Ser Gln Arg Arg Leu Leu Gly Ser Leu Asn Ser
1 5 10 15

Thr Pro Thr Ala Ile Pro Gln Leu Gly Leu Ala Ala Asn Gln Thr Gly
20 25 30

Ala Arg Cys Leu Glu Val Ser Ile Ser Asp Gly Leu Phe Leu Ser Leu
35 40 45

Gly Leu Val Ser Leu Val Glu Asn Ala Leu Val Val Ala Thr Ile Ala
50 55 60

Lys Asn Arg Asn Leu His Ser Pro Met Tyr Cys Phe Ile Cys Cys Leu
65 70 75 80

Ala Leu Ser Asp Leu Leu Val Ser Gly Ser Asn Val Leu Glu Thr Ala
85 90 95

Val Ile Leu Leu Leu Glu Ala Gly Ala Leu Val Ala Arg Ala Ala Val
100 105 110

Leu Gln Gln Leu Asp Asn Val Ile Asp Val Ile Thr Cys Ser Ser Met
115 120 125

Leu Ser Ser Leu Cys Phe Leu Gly Ala Ile Ala Val Asp Arg Tyr Ile
130 135 140

Ser Ile Phe Tyr Ala Leu Arg Tyr His Ser Ile Val Thr Leu Pro Arg
145 150 155 160

Ala Arg Arg Ala Val Ala Ala Ile Trp Val Ala Ser Val Val Phe Ser
165 170 175

Thr Leu Phe Ile Ala Tyr Tyr Asp His Val Ala Val Leu Leu Cys Leu

ITI-08-PCT_Sequence_Listing_ST25.txt

180

185

190

Val Val Phe Phe Leu Ala Met Leu Val Leu Met Ala Val Leu Tyr Val
195 200 205

His Met Leu Ala Arg Ala Cys Gln His Ala Gln Gly Ile Ala Arg Leu
210 215 220

His Lys Arg Gln Arg Pro Val His Gln Gly Phe Gly Leu Lys Gly Ala
225 230 235 240

Val Thr Leu Thr Ile Leu Leu Gly Ile Phe Phe Leu Cys Trp Gly Pro
245 250 255

Phe Phe Leu His Leu Thr Leu Ile Val Leu Cys Pro Glu His Pro Thr
260 265 270

Cys Gly Cys Ile Phe Lys Asn Phe Asn Leu Phe Leu Ala Leu Ile Ile
275 280 285

Cys Asn Ala Ile Ile Asp Pro Leu Ile Tyr Ala Phe His Ser Gln Glu
290 295 300

Leu Arg Arg Thr Leu Lys Glu Val Leu Thr Cys Ser Trp
305 310 315

<210> 493

<211> 317

<212> PRT

<213> Artificial Sequence

<220>

<223> MC1_R__Homo_sapiens__Q1JUL4

<400> 493

Met Ala Val Gln Gly Ser Gln Arg Arg Leu Leu Gly Ser Leu Asn Ser
1 5 10 15

Thr Pro Thr Ala Ile Pro Gln Leu Gly Leu Ala Ala Asn Gln Thr Gly
20 25 30

Ala Arg Cys Leu Glu Val Ser Ile Ser Asp Gly Leu Phe Leu Ser Leu
35 40 45

Gly Leu Val Ser Leu Val Glu Asn Ala Leu Val Val Ala Thr Ile Ala
50 55 60

Lys Asn Arg Asn Leu His Ser Pro Met Tyr Cys Phe Ile Cys Cys Leu
65 70 75 80

Ala Leu Ser Asp Leu Leu Val Ser Gly Ser Asn Val Leu Glu Thr Ala

ITI-08-PCT_Sequence_Listing_ST25.txt

85 90 95

Val Ile Leu Leu Leu Glu Ala Gly Ala Leu Val Ala Arg Ala Ala Val
100 105 110

Leu Gln Gln Leu Asp Asn Val Ile Asp Val Ile Thr Cys Ser Ser Met
115 120 125

Leu Ser Ser Leu Cys Phe Leu Gly Ala Ile Ala Val Asp Arg Tyr Ile
130 135 140

Ser Ile Phe Tyr Ala Leu Arg Tyr His Ser Ile Val Thr Leu Pro Arg
145 150 155 160

Ala Arg Arg Ala Val Ala Ala Ile Trp Val Ala Ser Val Val Phe Ser
165 170 175

Thr Leu Phe Ile Ala Tyr Tyr Asp His Val Ala Val Leu Leu Cys Leu
180 185 190

Val Val Phe Phe Leu Ala Met Leu Val Leu Met Ala Val Leu Tyr Val
195 200 205

His Met Leu Ala Arg Ala Cys Gln His Ala Gln Gly Ile Ala Arg Leu
210 215 220

His Lys Arg Gln Arg Pro Val His Gln Gly Phe Gly Leu Lys Gly Ala
225 230 235 240

Val Thr Leu Thr Ile Leu Leu Gly Ile Phe Phe Leu Cys Trp Gly Pro
245 250 255

Phe Phe Leu His Leu Thr Leu Ile Val Leu Cys Pro Glu His Pro Thr
260 265 270

Cys Gly Cys Ile Phe Lys Asn Phe Asn Leu Phe Leu Ala Leu Ile Ile
275 280 285

Cys Asn Ala Ile Ile Asp Pro Leu Ile Tyr Ala Phe His Ser Gln Glu
290 295 300

Leu Arg Arg Thr Leu Lys Glu Val Leu Thr Cys Ser Trp
305 310 315

<210> 494

<211> 317

<212> PRT

<213> Artificial Sequence

<220>

<223> MC1_R__Homo_sapiens__Q1JUL6

ITI-08-PCT_Sequence_Listing_ST25.txt

<400> 494

```

Met Ala Val Gln Gly Ser Gln Arg Arg Leu Leu Gly Ser Leu Asn Ser
1          5          10          15

Thr Pro Thr Ala Ile Pro Gln Leu Gly Leu Ala Ala Asn Gln Thr Gly
          20          25          30

Ala Arg Cys Leu Glu Val Ser Ile Ser Asp Gly Leu Phe Leu Ser Leu
          35          40          45

Gly Leu Val Ser Leu Val Glu Asn Ala Leu Val Val Ala Thr Ile Ala
50          55          60

Lys Asn Arg Asn Leu His Ser Pro Met Tyr Cys Phe Ile Cys Cys Leu
65          70          75          80

Ala Leu Ser Asp Leu Leu Val Ser Gly Ser Asn Val Leu Glu Thr Ala
          85          90          95

Val Ile Leu Leu Leu Glu Ala Gly Ala Leu Val Ala Arg Ala Ala Val
          100          105          110

Leu Gln Gln Leu Asp Asn Val Ile Asp Val Ile Thr Cys Ser Ser Met
          115          120          125

Leu Ser Ser Leu Cys Phe Leu Gly Ala Ile Ala Val Asp Arg Tyr Ile
          130          135          140

Ser Ile Phe Tyr Ala Leu Arg Tyr His Ser Ile Val Thr Leu Pro Arg
          145          150          155          160

Ala Arg Gln Ala Val Ala Ala Ile Trp Val Ala Ser Val Val Phe Ser
          165          170          175

Thr Leu Phe Ile Ala Tyr Tyr Asp His Val Ala Val Leu Leu Cys Leu
          180          185          190

Val Val Phe Phe Leu Ala Met Leu Val Leu Met Ala Val Leu Tyr Val
          195          200          205

His Met Leu Ala Arg Ala Cys Gln His Ala Gln Gly Ile Ala Arg Leu
          210          215          220

His Lys Arg Gln Arg Pro Val His Gln Gly Phe Gly Leu Lys Gly Ala
          225          230          235          240

Val Thr Leu Thr Ile Leu Leu Gly Ile Phe Phe Leu Cys Trp Gly Pro
          245          250          255

Phe Phe Leu His Leu Thr Leu Ile Val Leu Cys Pro Glu His Pro Thr
          260          265          270

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Cys Gly Cys Ile Phe Lys Asn Phe Asn Leu Phe Leu Ala Leu Ile Ile
275 280 285

Cys Asn Ala Ile Ile Asp Pro Leu Ile Tyr Ala Phe His Ser Gln Glu
290 295 300

Leu Arg Arg Thr Leu Lys Glu Val Leu Thr Cys Ser Trp
305 310 315

<210> 495

<211> 317

<212> PRT

<213> Artificial Sequence

<220>

<223> MC1_R__Homo_sapiens__Q1JUL8

<400> 495

Met Ala Val Gln Gly Ser Gln Arg Arg Leu Leu Gly Ser Leu Asn Ser
1 5 10 15

Thr Pro Thr Ala Ile Pro Gln Leu Gly Leu Ala Ala Asn Gln Thr Gly
20 25 30

Ala Arg Cys Leu Glu Val Ser Ile Ser Asp Gly Leu Phe Leu Ser Leu
35 40 45

Gly Leu Val Ser Leu Val Glu Asn Ala Leu Val Val Ala Thr Ile Ala
50 55 60

Lys Asn Arg Asn Leu His Ser Pro Met Tyr Cys Phe Ile Cys Cys Leu
65 70 75 80

Ala Leu Ser Asp Leu Leu Val Ser Gly Ser Asn Val Leu Glu Thr Ala
85 90 95

Val Ile Leu Leu Leu Glu Ala Gly Ala Leu Val Ala Arg Ala Ala Val
100 105 110

Leu Gln Gln Leu Asp Asn Val Thr Asp Val Ile Thr Cys Ser Ser Met
115 120 125

Leu Ser Ser Leu Cys Phe Leu Gly Ala Ile Ala Val Asp Arg Tyr Ile
130 135 140

Ser Ile Phe Tyr Ala Leu Arg Tyr His Ser Ile Val Thr Leu Pro Arg
145 150 155 160

Ala Arg Arg Ala Val Ala Ala Ile Trp Val Ala Ser Val Val Phe Ser
165 170 175

ITI-08-PCT_Sequence_Listing_ST25.txt

Thr Leu Phe Ile Ala Tyr Tyr Asp His Val Ala Val Leu Leu Cys Leu
180 185 190

Val Val Phe Phe Leu Ala Met Leu Val Leu Met Ala Val Leu Tyr Val
195 200 205

His Met Leu Ala Arg Ala Cys Gln His Ala Gln Gly Ile Ala Arg Leu
210 215 220

His Lys Arg Gln Arg Pro Val His Gln Gly Phe Gly Leu Lys Gly Ala
225 230 235 240

Val Thr Leu Thr Ile Leu Leu Gly Ile Phe Phe Leu Cys Trp Gly Pro
245 250 255

Phe Phe Leu His Leu Thr Leu Ile Val Leu Cys Pro Glu His Pro Thr
260 265 270

Cys Gly Cys Ile Phe Lys Asn Phe Asn Leu Phe Leu Ala Leu Ile Ile
275 280 285

Cys Asn Ala Ile Ile Asp Pro Leu Ile Tyr Ala Phe His Ser Gln Glu
290 295 300

Leu Arg Arg Thr Leu Lys Glu Val Leu Thr Cys Ser Trp
305 310 315

<210> 496

<211> 317

<212> PRT

<213> Artificial Sequence

<220>

<223> MC1_R__Homo_sapiens__Q1JUL9

<400> 496

Met Ala Val Gln Gly Ser Gln Arg Arg Leu Leu Gly Ser Leu Asn Ser
1 5 10 15

Thr Pro Thr Ala Ile Pro Gln Leu Gly Leu Ala Ala Asn Gln Thr Gly
20 25 30

Ala Arg Cys Leu Glu Val Ser Ile Ser Asp Gly Leu Phe Leu Ser Leu
35 40 45

Gly Leu Val Ser Leu Val Glu Asn Ala Leu Val Val Ala Thr Ile Ala
50 55 60

Lys Asn Arg Asn Leu His Ser Pro Met Tyr Cys Phe Ile Cys Cys Leu
65 70 75 80

ITI-08-PCT_Sequence_Listing_ST25.txt

Ala Leu Ser Asp Leu Leu Val Ser Gly Ser Asn Met Leu Glu Thr Ala
85 90 95

Val Ile Leu Leu Leu Glu Ala Gly Ala Leu Val Ala Arg Ala Ala Val
100 105 110

Leu Gln Gln Leu Asp Asn Val Ile Asp Val Ile Thr Cys Ser Ser Met
115 120 125

Leu Ser Ser Leu Cys Phe Leu Gly Ala Ile Ala Val Asp Arg Tyr Ile
130 135 140

Ser Ile Phe Tyr Ala Leu Arg Tyr His Ser Ile Val Thr Leu Pro Arg
145 150 155 160

Ala Arg Arg Ala Val Ala Ala Ile Trp Val Ala Ser Val Val Phe Ser
165 170 175

Thr Leu Phe Ile Ala Tyr Tyr Asp His Val Ala Val Leu Leu Cys Leu
180 185 190

Val Val Phe Phe Leu Ala Met Leu Val Leu Met Ala Val Leu Tyr Val
195 200 205

His Met Leu Ala Arg Ala Cys Gln His Ala Gln Gly Ile Ala Arg Leu
210 215 220

His Lys Arg Gln Arg Pro Val His Gln Gly Phe Gly Leu Lys Gly Ala
225 230 235 240

Val Thr Leu Thr Ile Leu Leu Gly Ile Phe Phe Leu Cys Trp Gly Pro
245 250 255

Phe Phe Leu His Leu Thr Leu Ile Val Leu Cys Pro Glu His Pro Thr
260 265 270

Cys Gly Cys Ile Phe Lys Asn Phe Asn Leu Phe Leu Ala Leu Ile Ile
275 280 285

Cys Asn Ala Ile Ile Asp Pro Leu Ile Tyr Ala Phe His Ser Gln Glu
290 295 300

Leu Arg Arg Thr Leu Lys Glu Val Leu Thr Cys Ser Trp
305 310 315

<210> 497
<211> 317
<212> PRT
<213> Artificial Sequence

<220>

ITI-08-PCT_Sequence_Listing_ST25.txt

<223> MC1_R__Homo_sapiens__Q1JUM0

<400> 497

```

Met Ala Val Gln Gly Ser Gln Arg Arg Leu Leu Gly Ser Leu Asn Ser
1          5          10          15

Thr Pro Thr Ala Ile Pro Gln Leu Gly Leu Ala Ala Asn Gln Thr Gly
          20          25          30

Ala Arg Cys Leu Glu Val Ser Ile Ser Asp Gly Leu Phe Leu Ser Leu
          35          40          45

Gly Leu Val Ser Leu Val Glu Asn Ala Leu Val Val Ala Thr Ile Ala
50          55          60

Lys Asn Gln Asn Leu His Ser Pro Met Tyr Cys Phe Ile Cys Cys Leu
65          70          75          80

Ala Leu Ser Asp Leu Leu Val Ser Gly Ser Asn Val Leu Glu Thr Ala
          85          90          95

Val Ile Leu Leu Leu Glu Ala Gly Ala Leu Val Ala Arg Ala Ala Val
          100          105          110

Leu Gln Gln Leu Asp Asn Val Ile Asp Val Ile Thr Cys Ser Ser Met
          115          120          125

Leu Ser Ser Leu Cys Phe Leu Gly Ala Ile Ala Val Asp Arg Tyr Ile
          130          135          140

Ser Ile Phe Tyr Ala Leu Arg Tyr His Ser Ile Val Thr Leu Pro Arg
145          150          155          160

Ala Arg Gln Ala Val Ala Ala Ile Trp Val Ala Ser Val Val Phe Ser
          165          170          175

Thr Leu Phe Ile Ala Tyr Tyr Asp His Val Ala Val Leu Leu Cys Leu
          180          185          190

Val Val Phe Phe Leu Ala Met Leu Val Leu Met Ala Val Leu Tyr Val
          195          200          205

His Met Leu Ala Arg Ala Cys Gln His Ala Gln Gly Ile Ala Arg Leu
          210          215          220

His Lys Arg Gln Arg Pro Val His Gln Gly Phe Gly Leu Lys Gly Ala
225          230          235          240

Val Thr Leu Thr Ile Leu Leu Gly Ile Phe Phe Leu Cys Trp Gly Pro
          245          250          255

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Phe Phe Leu His Leu Thr Leu Ile Val Leu Cys Pro Glu His Pro Thr
260 265 270

Cys Gly Cys Ile Phe Lys Asn Phe Asn Leu Phe Leu Ala Leu Ile Ile
275 280 285

Cys Asn Ala Ile Ile Asp Pro Leu Ile Tyr Ala Phe His Ser Gln Glu
290 295 300

Leu Arg Arg Thr Leu Lys Glu Val Leu Thr Cys Ser Trp
305 310 315

<210> 498

<211> 317

<212> PRT

<213> Artificial Sequence

<220>

<223> MC1_R__Homo_sapiens__Q1JUM2

<400> 498

Met Ala Val Gln Gly Ser Gln Arg Arg Leu Leu Gly Ser Leu Asn Ser
1 5 10 15

Thr Pro Thr Ala Ile Pro Gln Leu Gly Leu Ala Ala Asn Gln Thr Gly
20 25 30

Ala Arg Cys Leu Glu Val Ser Ile Ser Asp Gly Leu Phe Leu Ser Leu
35 40 45

Gly Leu Val Ser Leu Val Glu Asn Ala Leu Val Val Ala Thr Ile Ala
50 55 60

Lys Asn Arg Asn Leu His Ser Pro Met Tyr Cys Phe Ile Cys Cys Leu
65 70 75 80

Ala Leu Ser Asp Leu Leu Val Ser Gly Ser Asn Val Leu Glu Thr Ala
85 90 95

Val Ile Leu Leu Leu Glu Ala Gly Ala Leu Val Ala Arg Ala Ala Val
100 105 110

Leu Gln Gln Leu Asp Asn Val Ile Asp Val Ile Thr Cys Ser Ser Met
115 120 125

Leu Ser Ser Leu Cys Phe Leu Gly Ala Ile Ala Val Asp Arg Tyr Ile
130 135 140

Ser Ile Phe Tyr Ala Leu Arg Tyr His Ser Ile Val Thr Leu Pro Arg
145 150 155 160

ITI-08-PCT_Sequence_Listing_ST25.txt

Ala Arg Gln Ala Val Gly Ala Ile Trp Val Ala Ser Val Val Phe Ser
165 170 175

Thr Leu Phe Ile Ala Tyr Tyr Asp His Val Ala Val Leu Leu Cys Leu
180 185 190

Val Val Phe Phe Leu Ala Met Leu Val Leu Met Ala Val Leu Tyr Val
195 200 205

His Met Leu Ala Arg Ala Cys Gln His Ala Gln Gly Ile Ala Arg Leu
210 215 220

His Lys Arg Gln Arg Pro Val His Gln Gly Phe Gly Leu Lys Gly Ala
225 230 235 240

Val Thr Leu Thr Ile Leu Leu Gly Ile Phe Phe Leu Cys Trp Gly Pro
245 250 255

Phe Phe Leu His Leu Thr Leu Ile Val Leu Cys Pro Glu His Pro Thr
260 265 270

Cys Gly Cys Ile Phe Lys Asn Phe Asn Leu Phe Leu Ala Leu Ile Ile
275 280 285

Cys Asn Ala Ile Ile Asp Pro Leu Ile Tyr Ala Phe His Ser Gln Glu
290 295 300

Leu Arg Arg Thr Leu Lys Glu Val Leu Thr Cys Ser Trp
305 310 315

<210> 499

<211> 317

<212> PRT

<213> Artificial Sequence

<220>

<223> MC1_R__Homo_sapiens__Q1JUM3

<400> 499

Met Ala Val Gln Gly Ser Gln Arg Arg Leu Leu Gly Ser Leu Asn Ser
1 5 10 15

Thr Pro Thr Ala Ile Pro Gln Leu Gly Leu Ala Ala Asn Gln Thr Gly
20 25 30

Ala Arg Cys Leu Glu Val Ser Ile Ser Asp Gly Leu Phe Leu Ser Leu
35 40 45

Gly Leu Val Ser Leu Val Glu Asn Ala Leu Val Val Ala Thr Ile Ala
50 55 60

ITI-08-PCT_Sequence_Listing_ST25.txt

Lys	Asn	Arg	Asn	Leu	His	Ser	Pro	Met	Tyr	Cys	Phe	Ile	Cys	Cys	Leu
65					70					75					80
Ala	Leu	Ser	Asp	Leu	Leu	Val	Ser	Gly	Ser	Asn	Val	Leu	Glu	Thr	Ala
				85					90					95	
Val	Ile	Leu	Leu	Leu	Glu	Ala	Gly	Ala	Leu	Val	Ala	Arg	Ala	Ala	Val
			100					105					110		
Leu	Gln	Gln	Leu	Asp	Asn	Val	Thr	Asp	Val	Ile	Thr	Cys	Ser	Ser	Met
			115				120					125			
Leu	Ser	Ser	Leu	Cys	Phe	Leu	Gly	Ala	Ile	Ala	Val	Asp	Arg	Tyr	Ile
	130						135				140				
Ser	Ile	Phe	Tyr	Ala	Leu	Arg	Tyr	His	Ser	Ile	Val	Thr	Leu	Thr	Arg
145					150					155					160
Ala	Arg	Arg	Ala	Val	Ala	Ala	Ile	Trp	Val	Ala	Ser	Val	Val	Phe	Ser
				165					170					175	
Thr	Leu	Phe	Ile	Ala	Tyr	Tyr	Asp	His	Val	Ala	Val	Leu	Leu	Cys	Leu
			180					185					190		
Val	Val	Phe	Phe	Leu	Ala	Met	Leu	Val	Leu	Met	Ala	Val	Leu	Tyr	Val
			195				200					205			
His	Met	Leu	Ala	Arg	Ala	Cys	Gln	His	Ala	Gln	Gly	Ile	Ala	Arg	Leu
	210					215					220				
His	Lys	Arg	Gln	Arg	Pro	Val	His	Gln	Gly	Phe	Gly	Leu	Lys	Gly	Ala
225					230					235					240
Val	Thr	Leu	Thr	Ile	Leu	Leu	Gly	Ile	Phe	Phe	Leu	Cys	Trp	Gly	Pro
				245					250					255	
Phe	Phe	Leu	His	Leu	Thr	Leu	Ile	Val	Leu	Cys	Pro	Glu	His	Pro	Thr
			260					265					270		
Cys	Gly	Cys	Ile	Phe	Lys	Asn	Phe	Asn	Leu	Phe	Leu	Ala	Leu	Ile	Ile
		275					280					285			
Cys	Asn	Ala	Ile	Ile	Asp	Pro	Leu	Ile	Tyr	Ala	Phe	His	Ser	Gln	Glu
	290					295					300				
Leu	Arg	Arg	Thr	Leu	Lys	Glu	Val	Leu	Thr	Cys	Ser	Trp			
305					310					315					

<210> 500
 <211> 317
 <212> PRT
 <213> Artificial Sequence

ITI-08-PCT_Sequence_Listing_ST25.txt

<220>

<223> MC1_R__Homo_sapiens__Q1JUM4

<400> 500

Met Ala Val Gln Gly Ser Gln Arg Arg Leu Leu Gly Ser Leu Asn Ser
1 5 10 15

Thr Pro Thr Ala Ile Pro Gln Leu Gly Leu Ala Ala Asn Gln Thr Gly
20 25 30

Ala Arg Cys Leu Glu Val Ser Ile Ser Asp Gly Leu Phe Leu Ser Leu
35 40 45

Gly Leu Val Ser Leu Val Glu Asn Ala Leu Val Val Ala Thr Ile Ala
50 55 60

Lys Asn Arg Asn Leu His Ser Pro Met Tyr Cys Phe Ile Cys Cys Leu
65 70 75 80

Ala Leu Ser Asp Leu Leu Val Ser Gly Ser Asn Met Leu Glu Thr Ala
85 90 95

Val Ile Leu Leu Leu Glu Ala Gly Ala Leu Val Ala Arg Ala Ala Val
100 105 110

Leu Gln Gln Leu Asp Asn Val Ile Asp Val Ile Thr Cys Ser Ser Met
115 120 125

Leu Ser Ser Leu Cys Phe Leu Gly Ala Ile Ala Val Asp Arg Tyr Ile
130 135 140

Ser Ile Phe Tyr Ala Leu Arg Tyr His Ser Ile Val Ile Leu Pro Arg
145 150 155 160

Ala Arg Arg Ala Val Ala Ala Ile Trp Val Ala Ser Val Val Phe Ser
165 170 175

Thr Leu Phe Ile Ala Tyr Tyr Asp His Val Ala Val Leu Leu Cys Leu
180 185 190

Val Val Phe Phe Leu Ala Met Leu Val Leu Met Ala Val Leu Tyr Val
195 200 205

His Met Leu Ala Arg Ala Cys Gln His Ala Gln Gly Ile Ala Arg Leu
210 215 220

His Lys Arg Gln Arg Pro Val His Gln Gly Phe Gly Leu Lys Gly Ala
225 230 235 240

Val Thr Leu Thr Ile Leu Leu Gly Ile Phe Phe Leu Cys Trp Gly Pro

ITI-08-PCT_Sequence_Listing_ST25.txt

245 250 255

Phe Phe Leu His Leu Thr Leu Ile Val Leu Cys Pro Glu His Pro Thr
260 265 270

Cys Gly Cys Ile Phe Lys Asn Phe Asn Leu Phe Leu Ala Leu Ile Ile
275 280 285

Cys Asn Ala Ile Ile Asp Pro Leu Ile Tyr Ala Phe His Ser Gln Glu
290 295 300

Leu Arg Arg Thr Leu Lys Glu Val Leu Thr Cys Ser Trp
305 310 315

<210> 501

<211> 316

<212> PRT

<213> Artificial Sequence

<220>

<223> MC1_R__Homo_sapiens__Q1JUM5

<400> 501

Met Ala Val Gln Gly Ser Gln Arg Arg Leu Leu Gly Ser Leu Asn Ser
1 5 10 15

Thr Pro Thr Ala Ile Pro Gln Leu Gly Leu Ala Ala Asn Gln Thr Gly
20 25 30

Ala Arg Cys Leu Glu Val Ser Ile Ser Asp Gly Leu Phe Leu Ser Leu
35 40 45

Gly Leu Val Ser Leu Val Glu Asn Ala Leu Val Val Ala Thr Ile Ala
50 55 60

Lys Asn Arg Asn Leu His Ser Pro Met Tyr Cys Phe Ile Cys Cys Leu
65 70 75 80

Ala Leu Ser Asp Leu Leu Val Ser Gly Ser Asn Val Leu Glu Thr Ala
85 90 95

Val Ile Leu Leu Leu Glu Ala Gly Ala Leu Val Ala Arg Ala Ala Val
100 105 110

Leu Gln Gln Leu Asp Asn Val Ile Asp Val Ile Thr Cys Ser Ser Met
115 120 125

Leu Ser Ser Leu Cys Phe Leu Gly Ala Ile Ala Val Asp Arg Tyr Ile
130 135 140

Ser Ile Tyr Ala Leu Arg Tyr His Ser Ile Val Thr Leu Pro Arg Ala

ITI-08-PCT_Sequence_Listing_ST25.txt

```

145                150                155                160
Arg Gln Ala Val Ala Ala Ile Trp Val Ala Ser Val Val Phe Ser Thr
                165                170                175

Leu Phe Ile Ala Tyr Tyr Asp His Val Ala Val Leu Leu Cys Leu Val
                180                185                190

Val Phe Phe Leu Ala Met Leu Val Leu Met Ala Val Leu Tyr Val His
                195                200                205

Met Leu Ala Arg Ala Cys Gln His Ala Gln Gly Ile Ala Arg Leu His
 210                215                220

Lys Arg Gln Arg Pro Val His Gln Gly Phe Gly Leu Lys Gly Ala Val
225                230                235                240

Thr Leu Thr Ile Leu Leu Gly Ile Phe Phe Leu Cys Trp Gly Pro Phe
                245                250                255

Phe Leu His Leu Thr Leu Ile Val Leu Cys Pro Glu His Pro Thr Cys
                260                265                270

Gly Cys Ile Phe Lys Asn Phe Asn Leu Phe Leu Ala Leu Ile Ile Cys
 275                280                285

Asn Ala Ile Ile Asp Pro Leu Ile Tyr Ala Phe His Ser Gln Glu Leu
 290                295                300

Arg Arg Thr Leu Lys Glu Val Leu Thr Cys Ser Trp
305                310                315

```

<210> 502
 <211> 317
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MC1_R__Homo_sapiens__Q6UR92

<400> 502

```

Met Ala Val Gln Gly Ser Gln Arg Arg Leu Leu Gly Ser Leu Asn Ser
1                5                10                15

Thr Pro Thr Ala Ile Pro Gln Leu Gly Leu Ala Ala Asn Gln Thr Gly
                20                25                30

Ala Arg Cys Leu Glu Val Ser Ile Ser Asp Gly Leu Phe Leu Ser Leu
 35                40                45

Gly Leu Val Ser Leu Val Glu Asn Ala Leu Val Val Ala Thr Ile Ala

```

ITI-08-PCT_Sequence_Listing_ST25.txt

50

55

60

Lys Asn Arg Asn Leu His Ser Pro Met Tyr Cys Phe Ile Cys Cys Leu
65 70 75 80

Ala Leu Ser Asp Leu Leu Val Ser Gly Ser Asn Val Leu Glu Thr Ala
85 90 95

Val Ile Leu Leu Leu Glu Ala Gly Ala Leu Val Ala Arg Ala Ala Val
100 105 110

Leu Gln Gln Leu Asp Asn Val Ile Asp Val Ile Thr Cys Ser Ser Met
115 120 125

Leu Ser Ser Leu Cys Phe Leu Gly Ala Ile Ala Val Asp Arg Tyr Ile
130 135 140

Ser Ile Phe Tyr Ala Leu Arg Tyr His Ser Ile Val Thr Leu Pro Arg
145 150 155 160

Ala Arg Arg Ala Val Ala Ala Ile Trp Val Ala Ser Val Val Phe Ser
165 170 175

Thr Leu Phe Ile Ala Tyr Tyr Asp His Val Ala Val Leu Leu Cys Leu
180 185 190

Val Val Phe Phe Leu Ala Met Leu Val Leu Met Ala Val Leu Tyr Val
195 200 205

His Met Leu Ala Arg Ala Cys Gln His Ala Gln Gly Ile Ala Arg Leu
210 215 220

His Lys Arg Gln Arg Pro Val His Gln Gly Phe Gly Leu Lys Gly Ala
225 230 235 240

Val Thr Leu Thr Ile Leu Leu Gly Ile Phe Phe Leu Cys Trp Gly Pro
245 250 255

Phe Phe Leu His Leu Thr Leu Ile Ile Leu Cys Pro Glu His Pro Thr
260 265 270

Cys Gly Cys Ile Phe Lys Asn Phe Asn Leu Phe Leu Ala Leu Ile Ile
275 280 285

Cys Asn Ala Ile Ile Asp Pro Leu Ile Tyr Ala Phe His Ser Gln Glu
290 295 300

Leu Arg Arg Thr Leu Lys Glu Val Leu Thr Cys Ser Trp
305 310 315

<210> 503

<211> 317

ITI-08-PCT_Sequence_Listing_ST25.txt

<212> PRT

<213> Artificial Sequence

<220>

<223> MC1_R__Homo_sapiens__Q6UR94

<400> 503

Met Ala Val Gln Gly Ser Gln Arg Arg Leu Leu Gly Ser Leu Asn Ser
1 5 10 15

Thr Pro Thr Ala Ile Pro Gln Leu Gly Leu Ala Ala Asn Gln Thr Gly
20 25 30

Ala Arg Cys Leu Glu Val Ser Ile Ser Asp Gly Leu Phe Leu Ser Leu
35 40 45

Gly Leu Val Ser Leu Val Glu Asn Ala Leu Val Val Ala Thr Ile Ala
50 55 60

Lys Asn Arg Asn Leu His Ser Pro Met Tyr Cys Phe Ile Cys Cys Leu
65 70 75 80

Ala Leu Ser Asp Leu Leu Val Ser Gly Ser Asn Val Leu Glu Thr Ala
85 90 95

Val Ile Leu Leu Leu Glu Ala Gly Ala Leu Val Ala Arg Ala Val Val
100 105 110

Leu Gln Gln Leu Asp Asn Val Ile Asp Val Ile Thr Cys Ser Ser Met
115 120 125

Leu Ser Ser Leu Cys Phe Leu Gly Ala Ile Ala Val Asp Arg Tyr Ile
130 135 140

Ser Ile Phe Tyr Ala Leu Arg Tyr His Ser Ile Val Thr Leu Pro Arg
145 150 155 160

Ala Arg Arg Ala Val Ala Ala Ile Trp Val Ala Ser Val Val Phe Ser
165 170 175

Thr Leu Phe Ile Ala Tyr Tyr Asp His Val Ala Val Leu Leu Cys Leu
180 185 190

Val Val Phe Phe Leu Ala Met Leu Val Leu Met Ala Val Leu Tyr Val
195 200 205

His Met Leu Ala Arg Ala Cys Gln His Ala Gln Gly Ile Ala Arg Leu
210 215 220

His Lys Arg Gln Arg Pro Val His Gln Gly Phe Gly Leu Lys Gly Ala
225 230 235 240

ITI-08-PCT_Sequence_Listing_ST25.txt

Val Thr Leu Thr Ile Leu Leu Gly Ile Phe Phe Leu Cys Trp Gly Pro
245 250 255

Phe Phe Leu His Leu Thr Leu Ile Val Leu Cys Pro Glu His Pro Thr
260 265 270

Cys Gly Cys Ile Phe Lys Asn Phe Asn Leu Phe Leu Ala Leu Ile Ile
275 280 285

Cys Asn Ala Ile Ile Asp Pro Leu Ile Tyr Ala Phe His Ser Gln Glu
290 295 300

Leu Arg Arg Thr Leu Lys Glu Val Leu Thr Cys Ser Trp
305 310 315

<210> 504
<211> 317
<212> PRT
<213> Artificial Sequence

<220>
<223> MC1_R__Homo_sapiens__Q6UR95

<400> 504

Met Ala Val Gln Gly Ser Gln Arg Arg Leu Leu Gly Ser Leu Asn Ser
1 5 10 15

Thr Pro Thr Ala Ile Pro Gln Leu Gly Leu Ala Ala Asn Gln Thr Gly
20 25 30

Ala Arg Cys Leu Glu Val Ser Ile Ser Asp Gly Leu Phe Leu Ser Leu
35 40 45

Gly Leu Val Ser Leu Val Glu Asn Ala Leu Val Val Ala Thr Ile Ala
50 55 60

Lys Asn Arg Asn Leu His Ser Pro Met Tyr Cys Phe Ile Cys Cys Leu
65 70 75 80

Ala Leu Ser Asp Leu Leu Val Ser Gly Ser Asn Val Leu Glu Thr Ala
85 90 95

Val Ile Leu Leu Leu Glu Ala Gly Ala Leu Val Ala Arg Ala Ala Val
100 105 110

Leu Gln Gln Leu Asp Asn Val Ile Asp Val Ile Thr Cys Ser Ser Met
115 120 125

Leu Ser Ser Leu Cys Phe Leu Gly Ala Ile Ala Val Asp Arg Tyr Ile
130 135 140

ITI-08-PCT_Sequence_Listing_ST25.txt

Ser Ile Phe Tyr Ala Leu Arg Tyr His Ser Ile Val Thr Leu Pro Arg
145 150 155 160

Ala Arg Arg Ala Val Ala Ala Ile Trp Val Ala Ser Val Val Phe Ser
165 170 175

Thr Leu Phe Ile Ala Tyr Tyr Asp His Val Ala Val Leu Leu Cys Leu
180 185 190

Val Val Phe Phe Leu Ala Met Leu Val Leu Met Ala Val Leu Tyr Val
195 200 205

His Met Leu Ala Arg Ala Cys Gln His Ala Gln Gly Ile Ala Arg Leu
210 215 220

His Lys Arg Gln Arg Pro Val His Gln Gly Phe Gly Leu Lys Gly Ala
225 230 235 240

Val Thr Leu Thr Ile Leu Leu Gly Ile Phe Phe Leu Cys Trp Gly Pro
245 250 255

Phe Phe Leu His Leu Thr Leu Ile Val Leu Cys Pro Glu His Pro Thr
260 265 270

Cys Gly Cys Ile Phe Lys Asn Phe Asn Leu Phe Leu Ala Leu Ile Ile
275 280 285

Cys Asn Ala Ile Ile Asp Pro Leu Ile Tyr Ala Phe His Ser Gln Glu
290 295 300

Leu Arg Arg Thr Leu Lys Glu Val Leu Thr Arg Ser Trp
305 310 315

<210> 505

<211> 317

<212> PRT

<213> Artificial Sequence

<220>

<223> MC1_R__Homo_sapiens__Q6UR96

<400> 505

Met Ala Val Gln Gly Ser Gln Arg Arg Leu Leu Gly Ser Leu Asn Ser
1 5 10 15

Thr Pro Thr Ala Ile Pro Gln Leu Gly Leu Ala Ala Asn Gln Thr Gly
20 25 30

Ala Arg Cys Leu Glu Val Ser Ile Ser Asp Gly Leu Phe Leu Ser Leu
35 40 45

ITI-08-PCT_Sequence_Listing_ST25.txt

Gly	Leu	Val	Ser	Leu	Val	Glu	Asn	Ala	Leu	Val	Val	Ala	Thr	Ile	Ala	
50						55					60					
Lys	Asn	Arg	Asn	Leu	His	Ser	Pro	Met	Tyr	Cys	Phe	Ile	Cys	Cys	Leu	
65				70					75						80	
Ala	Leu	Ser	Asp	Leu	Leu	Val	Ser	Gly	Ser	Asn	Val	Leu	Glu	Thr	Ala	
			85					90					95			
Val	Ile	Leu	Leu	Leu	Glu	Ala	Gly	Ala	Leu	Val	Ala	Arg	Ala	Ala	Val	
		100					105					110				
Leu	Gln	Gln	Leu	Asp	Asn	Val	Ile	Asp	Val	Ile	Thr	Cys	Ser	Ser	Met	
	115					120						125				
Leu	Ser	Ser	Leu	Cys	Phe	Leu	Gly	Ala	Ile	Ala	Val	Asp	Arg	Tyr	Ile	
	130					135					140					
Ser	Ile	Phe	Tyr	Ala	Leu	Arg	Tyr	His	Ser	Ile	Val	Thr	Leu	Pro	Arg	
145				150						155					160	
Ala	Arg	Arg	Ala	Val	Ala	Ala	Ile	Trp	Val	Ala	Ser	Val	Val	Phe	Ser	
			165					170						175		
Thr	Leu	Phe	Ile	Ala	Tyr	Tyr	Asp	His	Val	Ala	Val	Leu	Leu	Cys	Leu	
		180					185						190			
Val	Val	Phe	Phe	Leu	Ala	Met	Leu	Val	Leu	Met	Ala	Val	Leu	Tyr	Val	
	195					200					205					
His	Met	Leu	Ala	Arg	Ala	Cys	Gln	His	Ala	Gln	Gly	Ile	Ala	Arg	Leu	
	210					215					220					
His	Lys	Arg	Gln	Arg	Pro	Val	His	Gln	Gly	Phe	Gly	Leu	Lys	Gly	Ala	
225				230					235						240	
Val	Thr	Leu	Thr	Ile	Leu	Leu	Gly	Ile	Phe	Phe	Leu	Cys	Trp	Gly	Pro	
			245					250					255			
Phe	Phe	Leu	His	Leu	Thr	Leu	Ile	Val	Leu	Cys	Pro	Glu	His	Pro	Thr	
		260					265						270			
Cys	Gly	Cys	Ile	Phe	Lys	Asn	Phe	Asn	Leu	Phe	Leu	Ala	Leu	Ile	Ile	
	275					280						285				
Cys	Asn	Ala	Ile	Ile	Asp	Pro	Leu	Ile	Tyr	Ala	Phe	His	Ser	Gln	Glu	
	290				295						300					
Leu	Arg	Arg	Met	Leu	Lys	Glu	Val	Leu	Thr	Cys	Ser	Trp				
305				310						315						

ITI-08-PCT_Sequence_Listing_ST25.txt

<210> 506

<211> 317

<212> PRT

<213> Artificial Sequence

<220>

<223> MC1_R__Homo_sapiens__Q6UR97

<400> 506

Met Ala Val Gln Gly Ser Gln Arg Arg Leu Leu Gly Ser Leu Asn Ser
1 5 10 15

Thr Pro Thr Ala Ile Pro Gln Leu Gly Leu Ala Ala Asn Gln Thr Gly
20 25 30

Ala Arg Cys Leu Glu Val Ser Ile Ser Asp Gly Leu Phe Leu Ser Leu
35 40 45

Gly Leu Val Ser Leu Val Glu Asn Ala Leu Val Val Ala Thr Ile Ala
50 55 60

Lys Asn Arg Asn Leu His Ser Pro Met Tyr Cys Phe Ile Cys Cys Leu
65 70 75 80

Ala Leu Ser Asp Leu Leu Val Ser Gly Ser Asn Val Leu Glu Thr Ala
85 90 95

Val Ile Leu Leu Leu Glu Ala Gly Ala Leu Val Ala Arg Ala Ala Val
100 105 110

Leu Gln Gln Leu Asp Asn Val Ile Asp Val Ile Thr Cys Ser Ser Met
115 120 125

Leu Ser Ser Leu Cys Phe Leu Gly Ala Ile Ala Val Asp Arg Tyr Ile
130 135 140

Ser Ile Phe Tyr Ala Leu Arg Tyr His Ser Ile Val Thr Leu Pro Arg
145 150 155 160

Ala Arg Arg Ala Val Ala Ala Ile Trp Val Ala Ser Val Val Phe Ser
165 170 175

Thr Leu Phe Ile Ala Tyr Tyr Asp His Val Ala Val Leu Leu Cys Leu
180 185 190

Val Val Phe Phe Leu Ala Met Leu Val Leu Met Ala Val Leu Tyr Val
195 200 205

His Met Leu Ala Trp Ala Cys Gln His Ala Gln Gly Ile Ala Arg Leu
210 215 220

ITI-08-PCT_Sequence_Listing_ST25.txt

His Lys Arg Gln Arg Pro Val His Gln Gly Phe Gly Leu Lys Gly Ala
225 230 235 240

Val Thr Leu Thr Ile Leu Leu Gly Ile Phe Phe Leu Cys Trp Gly Pro
245 250 255

Phe Phe Leu His Leu Thr Leu Ile Val Leu Cys Pro Glu His Pro Thr
260 265 270

Cys Gly Cys Ile Phe Lys Asn Phe Asn Leu Phe Leu Ala Leu Ile Ile
275 280 285

Cys Asn Ala Ile Ile Asp Pro Leu Ile Tyr Ala Phe His Ser Gln Glu
290 295 300

Leu Arg Arg Thr Leu Lys Glu Val Leu Thr Cys Ser Trp
305 310 315

<210> 507
<211> 317
<212> PRT
<213> Artificial Sequence

<220>
<223> MC1_R__Homo_sapiens__Q6UR98

<400> 507

Met Ala Val Gln Gly Ser Gln Arg Arg Leu Leu Gly Ser Leu Asn Ser
1 5 10 15

Thr Pro Thr Ala Ile Pro Gln Leu Gly Leu Ala Ala Asn Gln Thr Gly
20 25 30

Ala Arg Cys Leu Glu Val Ser Ile Ser Asp Gly Leu Phe Leu Ser Leu
35 40 45

Gly Leu Val Ser Leu Val Glu Asn Ala Leu Val Val Ala Thr Ile Ala
50 55 60

Lys Asn Arg Asn Leu His Ser Pro Met Tyr Cys Phe Ile Cys Cys Leu
65 70 75 80

Ala Leu Ser Asp Leu Leu Val Ser Gly Ser Asn Val Leu Glu Thr Ala
85 90 95

Val Ile Leu Leu Leu Glu Ala Gly Ala Leu Val Ala Arg Ala Ala Val
100 105 110

Leu Gln Gln Leu Asp Asn Val Ile Asp Val Ile Thr Cys Ser Ser Met
115 120 125

ITI-08-PCT_Sequence_Listing_ST25.txt

Leu Ser Ser Leu Cys Phe Leu Gly Ala Ile Ala Val Asp Arg Tyr Ile
130 135 140

Ser Ile Phe Tyr Ala Leu Arg Tyr His Ser Ile Val Thr Leu Pro Gln
145 150 155 160

Ala Arg Arg Ala Val Ala Ala Ile Trp Val Ala Ser Val Val Phe Ser
165 170 175

Thr Leu Phe Ile Ala Tyr Tyr Asp His Val Ala Val Leu Leu Cys Leu
180 185 190

Val Val Phe Phe Leu Ala Met Leu Val Leu Met Ala Val Leu Tyr Val
195 200 205

His Met Leu Ala Arg Ala Cys Gln His Ala Gln Gly Ile Ala Arg Leu
210 215 220

His Lys Arg Gln Arg Pro Val His Gln Gly Phe Gly Leu Lys Gly Ala
225 230 235 240

Val Thr Leu Thr Ile Leu Leu Gly Ile Phe Phe Leu Cys Trp Gly Pro
245 250 255

Phe Phe Leu His Leu Thr Leu Ile Val Leu Cys Pro Glu His Pro Thr
260 265 270

Cys Gly Cys Ile Phe Lys Asn Phe Asn Leu Phe Leu Ala Leu Ile Ile
275 280 285

Cys Asn Ala Ile Ile Asp Pro Leu Ile Tyr Ala Phe His Ser Gln Glu
290 295 300

Leu Arg Arg Thr Leu Lys Glu Val Leu Thr Cys Ser Trp
305 310 315

<210> 508

<211> 317

<212> PRT

<213> Artificial Sequence

<220>

<223> MC1_R__Homo_sapiens__Q6UR99

<400> 508

Met Ala Val Gln Gly Ser Gln Arg Arg Leu Leu Gly Ser Leu Asn Ser
1 5 10 15

Thr Pro Thr Ala Ile Pro Gln Leu Gly Leu Ala Ala Asn Gln Thr Gly
20 25 30

ITI-08-PCT_Sequence_Listing_ST25.txt

Ala	Arg	Cys	Leu	Glu	Val	Ser	Ile	Ser	Asp	Gly	Leu	Phe	Leu	Ser	Leu	35	40	45	
Gly	Leu	Val	Ser	Leu	Val	Glu	Asn	Ala	Leu	Val	Val	Ala	Thr	Ile	Ala	50	55	60	
Lys	Asn	Arg	Asn	Leu	His	Ser	Pro	Met	Tyr	Cys	Phe	Ile	Cys	Cys	Leu	65	70	75	80
Ala	Leu	Leu	Asp	Leu	Leu	Val	Ser	Gly	Ser	Asn	Val	Leu	Glu	Thr	Ala	85	90	95	
Val	Ile	Leu	Leu	Leu	Glu	Ala	Gly	Ala	Leu	Val	Ala	Arg	Ala	Ala	Val	100	105	110	
Leu	Gln	Gln	Leu	Asp	Asn	Val	Ile	Asp	Val	Ile	Thr	Cys	Ser	Ser	Met	115	120	125	
Leu	Ser	Ser	Leu	Cys	Phe	Leu	Gly	Ala	Ile	Ala	Val	Asp	Arg	Tyr	Ile	130	135	140	
Ser	Ile	Phe	Tyr	Ala	Leu	Arg	Tyr	His	Ser	Ile	Val	Thr	Leu	Pro	Arg	145	150	155	160
Ala	Arg	Arg	Ala	Val	Ala	Ala	Ile	Trp	Val	Ala	Ser	Val	Val	Phe	Ser	165	170	175	
Thr	Leu	Phe	Ile	Ala	Tyr	Tyr	Asp	His	Val	Ala	Val	Leu	Leu	Cys	Leu	180	185	190	
Val	Val	Phe	Phe	Leu	Ala	Met	Leu	Val	Leu	Met	Ala	Val	Leu	Tyr	Val	195	200	205	
His	Met	Leu	Ala	Arg	Ala	Cys	Gln	His	Ala	Gln	Gly	Ile	Ala	Arg	Leu	210	215	220	
His	Lys	Arg	Gln	Arg	Pro	Val	His	Gln	Gly	Phe	Gly	Leu	Lys	Gly	Ala	225	230	235	240
Val	Thr	Leu	Thr	Ile	Leu	Leu	Gly	Ile	Phe	Phe	Leu	Cys	Trp	Gly	Pro	245	250	255	
Phe	Phe	Leu	His	Leu	Thr	Leu	Ile	Val	Leu	Cys	Pro	Glu	His	Pro	Thr	260	265	270	
Cys	Gly	Cys	Ile	Phe	Lys	Asn	Phe	Asn	Leu	Phe	Leu	Ala	Leu	Ile	Ile	275	280	285	
Cys	Asn	Ala	Ile	Ile	Asp	Pro	Leu	Ile	Tyr	Ala	Phe	His	Ser	Gln	Glu	290	295	300	
Leu	Arg	Arg	Thr	Leu	Lys	Glu	Val	Leu	Thr	Cys	Ser	Trp							

ITI-08-PCT_Sequence_Listing_ST25.txt

305

310

315

<210> 509

<211> 317

<212> PRT

<213> Artificial Sequence

<220>

<223> MC1_R__Homo_sapiens__Q6URA0

<400> 509

Met Ala Val Gln Gly Ser Gln Arg Arg Leu Leu Gly Ser Leu Asn Ser
1 5 10 15

Thr Pro Thr Ala Ile Pro Gln Leu Gly Leu Ala Ala Asn Gln Thr Gly
20 25 30

Ala Arg Cys Leu Glu Val Ser Ile Ser Asp Gly Leu Leu Leu Ser Leu
35 40 45

Gly Leu Val Ser Leu Val Glu Asn Ala Leu Val Val Ala Thr Ile Ala
50 55 60

Lys Asn Arg Asn Leu His Ser Pro Met Tyr Cys Phe Ile Cys Cys Leu
65 70 75 80

Ala Leu Ser Asp Leu Leu Val Ser Gly Ser Asn Val Leu Glu Thr Ala
85 90 95

Val Ile Leu Leu Leu Glu Ala Gly Ala Leu Val Ala Arg Ala Ala Val
100 105 110

Leu Gln Gln Leu Asp Asn Val Ile Asp Val Ile Thr Cys Ser Ser Met
115 120 125

Leu Ser Ser Leu Cys Phe Leu Gly Ala Ile Ala Val Asp Arg Tyr Ile
130 135 140

Ser Ile Phe Tyr Ala Leu Arg Tyr His Ser Ile Val Thr Leu Pro Arg
145 150 155 160

Ala Arg Arg Ala Val Ala Ala Ile Trp Val Ala Ser Val Val Phe Ser
165 170 175

Thr Leu Phe Ile Ala Tyr Tyr Asp His Val Ala Val Leu Leu Cys Leu
180 185 190

Val Val Phe Phe Leu Ala Met Leu Val Leu Met Ala Val Leu Tyr Val
195 200 205

His Met Leu Ala Arg Ala Cys Gln His Ala Gln Gly Ile Ala Arg Leu

ITI-08-PCT_Sequence_Listing_ST25.txt

210

215

220

His Lys Arg Gln Arg Pro Val His Gln Gly Phe Gly Leu Lys Gly Ala
225 230 235 240

Val Thr Leu Thr Ile Leu Leu Gly Ile Phe Phe Leu Cys Trp Gly Pro
245 250 255

Phe Phe Leu His Leu Thr Leu Ile Val Leu Cys Pro Glu His Pro Thr
260 265 270

Cys Gly Cys Ile Phe Lys Asn Phe Asn Leu Phe Leu Ala Leu Ile Ile
275 280 285

Cys Asn Ala Ile Ile Asp Pro Leu Ile Tyr Ala Phe His Ser Gln Glu
290 295 300

Leu Arg Arg Thr Leu Lys Glu Val Leu Thr Cys Ser Trp
305 310 315

<210> 510

<211> 317

<212> PRT

<213> Artificial Sequence

<220>

<223> MC1_R__Homo_sapiens__Q86YW1

<400> 510

Met Ala Val Gln Gly Ser Gln Arg Arg Leu Leu Gly Ser Leu Asn Ser
1 5 10 15

Thr Pro Thr Ala Ile Pro Gln Leu Gly Leu Ala Ala Asn Gln Thr Gly
20 25 30

Ala Arg Cys Leu Glu Val Ser Ile Ser Asp Gly Leu Phe Leu Ser Leu
35 40 45

Gly Leu Val Ser Leu Val Glu Asn Ala Leu Val Val Ala Thr Ile Ala
50 55 60

Lys Asn Arg Asn Leu His Ser Pro Met Tyr Cys Phe Ile Cys Cys Leu
65 70 75 80

Ala Leu Ser Asp Leu Leu Val Ser Gly Ser Asn Val Arg Glu Thr Ala
85 90 95

Val Ile Leu Leu Leu Glu Ala Gly Ala Leu Val Ala Arg Ala Ala Val
100 105 110

Leu Gln Gln Leu Asp Asn Val Ile Asp Val Ile Thr Cys Ser Ser Met

ITI-08-PCT_Sequence_Listing_ST25.txt

115

120

125

Leu Ser Ser Leu Cys Phe Leu Gly Ala Ile Ala Val Asp Arg Tyr Ile
130 135 140

Ser Ile Phe Tyr Ala Leu Arg Tyr His Ser Ile Val Thr Leu Pro Arg
145 150 155 160

Ala Arg Arg Ala Val Ala Ala Ile Trp Val Ala Ser Val Val Phe Ser
165 170 175

Thr Leu Phe Ile Ala Tyr Tyr Asp His Val Ala Val Leu Leu Cys Leu
180 185 190

Val Val Phe Phe Leu Ala Met Leu Val Leu Met Ala Val Leu Tyr Val
195 200 205

His Met Leu Ala Arg Ala Cys Gln His Ala Gln Gly Ile Ala Arg Leu
210 215 220

His Lys Arg Gln Arg Pro Val His Gln Gly Phe Gly Leu Lys Gly Ala
225 230 235 240

Val Thr Leu Thr Ile Leu Leu Gly Ile Phe Phe Leu Cys Trp Gly Pro
245 250 255

Phe Phe Leu His Leu Thr Leu Ile Val Leu Cys Pro Glu His Pro Thr
260 265 270

Cys Gly Cys Ile Phe Lys Asn Phe Asn Leu Phe Leu Ala Leu Ile Ile
275 280 285

Cys Asn Ala Ile Ile Asp Pro Leu Ile Tyr Ala Phe His Ser Gln Glu
290 295 300

Leu Arg Arg Thr Leu Lys Glu Val Leu Thr Cys Ser Trp
305 310 315

<210> 511

<211> 317

<212> PRT

<213> Artificial Sequence

<220>

<223> MC1_R__Homo_sapiens__V9Q5S2

<400> 511

Met Ala Val Gln Gly Ser Gln Arg Arg Leu Leu Gly Ser Leu Asn Ser
1 5 10 15

Thr Pro Thr Ala Ile Pro Gln Leu Gly Leu Ala Ala Asn Gln Thr Gly

ITI-08-PCT_Sequence_Listing_ST25.txt

```

20      25      30
Ala Arg Cys Leu Glu Val Ser Ile Ser Asp Gly Leu Phe Leu Ser Leu
    35      40      45
Gly Leu Val Ser Leu Val Glu Asn Ala Leu Val Val Ala Thr Ile Ala
    50      55      60
Lys Asn Arg Asn Leu His Ser Pro Met Tyr Cys Phe Ile Cys Cys Leu
    65      70      75      80
Ala Leu Pro Asp Leu Leu Val Ser Gly Ser Asn Val Leu Glu Thr Ala
    85      90      95
Val Ile Leu Leu Leu Glu Ala Gly Ala Leu Val Ala Arg Ala Ala Val
    100      105      110
Leu Gln Gln Leu Asp Asn Val Ile Asp Val Ile Thr Cys Ser Ser Met
    115      120      125
Leu Ser Ser Leu Cys Phe Leu Gly Ala Ile Ala Val Asp Arg Tyr Ile
    130      135      140
Ser Ile Phe Tyr Ala Leu Arg Tyr His Ser Ile Val Thr Leu Pro Arg
    145      150      155      160
Ala Arg Arg Ala Val Ala Ala Ile Trp Val Ala Ser Val Val Phe Ser
    165      170      175
Thr Leu Phe Ile Ala Tyr Tyr Asp His Val Ala Val Leu Leu Cys Leu
    180      185      190
Val Val Phe Phe Leu Ala Met Leu Val Leu Met Ala Val Leu Tyr Val
    195      200      205
His Met Leu Ala Arg Ala Cys Gln His Ala Gln Gly Ile Ala Arg Leu
    210      215      220
His Lys Arg Gln Arg Pro Val His Gln Gly Phe Gly Leu Lys Gly Ala
    225      230      235      240
Val Thr Leu Thr Ile Leu Leu Gly Ile Phe Phe Leu Cys Trp Gly Pro
    245      250      255
Phe Phe Leu His Leu Thr Leu Ile Val Leu Cys Pro Glu His Pro Thr
    260      265      270
Cys Gly Cys Ile Phe Lys Asn Phe Asn Leu Phe Leu Ala Leu Ile Ile
    275      280      285
Cys Asn Ala Ile Ile Asp Pro Leu Ile Tyr Ala Phe His Ser Gln Glu
    290      295      300

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Leu Arg Arg Thr Leu Lys Glu Val Leu Thr Cys Ser Trp
305 310 315

<210> 512
<211> 317
<212> PRT
<213> Artificial Sequence

<220>
<223> MC1_R__Homo_sapiens__V9Q671

<400> 512

Met Ala Val Gln Gly Ser Gln Arg Arg Leu Leu Gly Ser Leu Asn Ser
1 5 10 15

Thr Pro Thr Ala Ile Pro Gln Leu Gly Leu Ala Ala Asn Gln Thr Gly
20 25 30

Ala Arg Cys Leu Glu Val Ser Ile Ser Asp Gly Leu Phe Leu Ser Leu
35 40 45

Gly Leu Val Ser Leu Val Glu Asn Ala Leu Val Val Ala Thr Ile Ala
50 55 60

Lys Asn Arg Asn Leu His Ser Pro Met Tyr Cys Phe Ile Cys Cys Leu
65 70 75 80

Ala Leu Ser Asp Leu Leu Val Ser Gly Ser Asn Val Leu Glu Thr Ala
85 90 95

Val Ile Leu Leu Leu Glu Ala Gly Ala Leu Val Ala Arg Ala Ala Val
100 105 110

Leu Gln Gln Leu Asp Asn Val Ile Asp Val Ile Thr Cys Ser Ser Met
115 120 125

Leu Ser Ser Leu Cys Phe Leu Gly Ala Ile Ala Val Asp Arg Tyr Ile
130 135 140

Ser Ile Phe Tyr Ala Leu Arg Tyr His Ser Ile Val Thr Leu Pro Arg
145 150 155 160

Ala Arg Arg Ala Val Ala Ala Ile Trp Val Ala Ser Val Val Phe Ser
165 170 175

Thr Leu Phe Ile Ala Tyr Tyr Asp His Val Ala Val Leu Leu Cys Leu
180 185 190

Met Val Phe Phe Leu Ala Met Leu Val Leu Met Ala Val Leu Tyr Val
195 200 205

ITI-08-PCT_Sequence_Listing_ST25.txt

His Met Leu Ala Arg Ala Cys Gln His Ala Gln Gly Ile Ala Arg Leu
210 215 220

His Lys Arg Gln Arg Pro Val His Gln Gly Phe Gly Leu Lys Gly Ala
225 230 235 240

Val Thr Leu Thr Ile Leu Leu Gly Ile Phe Phe Leu Cys Trp Gly Pro
245 250 255

Phe Phe Leu His Leu Thr Leu Ile Val Leu Cys Pro Glu His Pro Thr
260 265 270

Cys Gly Cys Ile Phe Lys Asn Phe Asn Leu Phe Leu Ala Leu Ile Ile
275 280 285

Cys Asn Ala Ile Ile Asp Pro Leu Ile Tyr Ala Phe His Ser Gln Glu
290 295 300

Leu Arg Arg Thr Leu Lys Glu Val Leu Thr Cys Ser Trp
305 310 315

<210> 513

<211> 317

<212> PRT

<213> Artificial Sequence

<220>

<223> MC1_R__Homo_sapiens__V9Q783

<400> 513

Met Ala Val Gln Gly Ser Gln Arg Arg Leu Leu Gly Ser Leu Asn Ser
1 5 10 15

Thr Pro Thr Ala Ile Pro Gln Leu Gly Leu Ala Ala Asn Gln Thr Gly
20 25 30

Ala Arg Cys Leu Glu Val Ser Ile Ser Asp Gly Leu Phe Leu Ser Leu
35 40 45

Gly Leu Val Ser Leu Val Glu Asn Ala Leu Val Val Ala Thr Ile Ala
50 55 60

Lys Asn Arg Asn Leu His Ser Pro Met Tyr Cys Phe Ile Cys Cys Leu
65 70 75 80

Ala Leu Ser Asp Leu Leu Val Ser Gly Ser Asn Val Leu Glu Thr Ala
85 90 95

Val Ile Leu Leu Leu Glu Ala Gly Ala Leu Val Ala Arg Ala Ala Val
100 105 110

ITI-08-PCT_Sequence_Listing_ST25.txt

Leu Gln Gln Leu Asp Asn Val Ile Asp Val Ile Thr Cys Ser Ser Met
115 120 125

Leu Ser Ser Leu Cys Phe Leu Gly Ala Ile Ala Val Asp Arg Tyr Ile
130 135 140

Ser Ile Phe Tyr Ala Leu Arg Tyr His Ser Ile Val Thr Leu Pro Arg
145 150 155 160

Ala Arg Arg Ala Val Ala Ala Ile Trp Val Ala Ser Val Val Phe Ser
165 170 175

Thr Leu Phe Ile Ala Tyr Tyr Asp His Val Ala Val Leu Leu Cys Leu
180 185 190

Val Val Phe Phe Leu Ala Met Leu Val Leu Met Ala Val Leu Tyr Val
195 200 205

His Met Leu Ala Arg Ala Cys Gln His Ala Gln Gly Thr Ala Arg Leu
210 215 220

His Lys Arg Gln Arg Pro Val His Gln Gly Phe Gly Leu Lys Gly Ala
225 230 235 240

Val Thr Leu Thr Ile Leu Leu Gly Ile Phe Phe Leu Cys Trp Gly Pro
245 250 255

Phe Phe Leu His Leu Thr Leu Ile Val Leu Cys Pro Glu His Pro Thr
260 265 270

Cys Gly Cys Ile Phe Lys Asn Phe Asn Leu Phe Leu Ala Leu Ile Ile
275 280 285

Cys Asn Ala Ile Ile Asp Pro Leu Ile Tyr Ala Phe His Ser Gln Glu
290 295 300

Leu Arg Arg Thr Leu Lys Glu Val Leu Thr Cys Ser Trp
305 310 315

<210> 514

<211> 317

<212> PRT

<213> Artificial Sequence

<220>

<223> MC1_R__Homo_sapiens__V9Q7F1

<400> 514

Met Ala Val Gln Gly Ser Gln Arg Arg Leu Leu Gly Ser Leu Asn Ser
1 5 10 15

ITI-08-PCT_Sequence_Listing_ST25.txt

Thr	Pro	Thr	Ala 20	Ile	Pro	Gln	Leu	Gly 25	Leu	Ala	Ala	Asn	Gln 30	Thr	Gly
Ala	Arg	Cys 35	Leu	Glu	Val	Ser	Ile 40	Ser	Asp	Gly	Leu	Phe 45	Leu	Ser	Leu
Gly	Leu	Val	Ser	Leu	Val	Glu 55	Asn	Ala	Leu	Val	Val 60	Ala	Thr	Ile	Ala
Lys 65	Asn	Arg	Asn	Leu	His 70	Ser	Pro	Met	Tyr	Cys 75	Phe	Ile	Cys	Cys	Leu 80
Ala	Leu	Ser	Asp	Leu 85	Leu	Val	Ser	Gly	Ser 90	Asn	Val	Leu	Glu	Thr 95	Ala
Val	Ile	Leu	Leu 100	Leu	Glu	Ala	Gly	Ala 105	Leu	Val	Ala	Arg	Ala 110	Ala	Val
Leu	Gln	Gln 115	Leu	Asp	Asn	Val	Ile 120	Asp	Val	Ile	Thr	Cys 125	Ser	Ser	Met
Leu	Ser 130	Ser	Leu	Cys	Phe	Leu 135	Gly	Ala	Ile	Ala	Val 140	Asp	Arg	Tyr	Ile
Ser 145	Ile	Phe	Tyr	Ala	Leu 150	Arg	Tyr	His	Ser	Thr 155	Val	Thr	Leu	Pro	Arg 160
Ala	Arg	Arg	Ala 165	Val	Ala	Ala	Ile	Trp	Val 170	Ala	Ser	Val	Val	Phe 175	Ser
Thr	Leu	Phe	Ile 180	Ala	Tyr	Tyr	Asp	His 185	Val	Ala	Val	Leu	Leu 190	Cys	Leu
Val	Val	Phe 195	Phe	Leu	Ala	Met	Leu 200	Val	Leu	Met	Ala	Val 205	Leu	Tyr	Val
His 210	Met	Leu	Ala	Arg	Ala	Cys 215	Gln	His	Ala	Gln	Gly 220	Ile	Ala	Arg	Leu
His 225	Lys	Arg	Gln	Arg	Pro 230	Val	His	Gln	Gly	Phe 235	Gly	Leu	Lys	Gly	Ala 240
Val	Thr	Leu	Thr	Ile 245	Leu	Leu	Gly	Ile	Phe 250	Phe	Leu	Cys	Trp	Gly 255	Pro
Phe	Phe	Leu	His 260	Leu	Thr	Leu	Ile	Val 265	Leu	Cys	Pro	Glu	His 270	Pro	Thr
Cys	Gly	Cys 275	Ile	Phe	Lys	Asn	Phe 280	Asn	Leu	Phe	Leu	Ala 285	Leu	Ile	Ile

ITI-08-PCT_Sequence_Listing_ST25.txt

Cys Asn Ala Ile Ile Asp Pro Leu Ile Tyr Ala Phe His Ser Gln Glu
290 295 300

Leu Arg Arg Thr Leu Lys Glu Val Leu Thr Cys Ser Trp
305 310 315

<210> 515
<211> 317
<212> PRT
<213> Artificial Sequence

<220>
<223> MC1_R__Homo_sapiens__V9Q8N1

<400> 515

Met Ala Val Gln Gly Ser Gln Arg Arg Leu Leu Gly Ser Leu Asn Ser
1 5 10 15

Thr Pro Thr Ala Ile Pro Gln Leu Gly Leu Ala Ala Asn Gln Thr Gly
20 25 30

Ala Arg Tyr Leu Glu Val Ser Ile Ser Asp Gly Leu Phe Leu Ser Leu
35 40 45

Gly Leu Val Ser Leu Val Glu Asn Ala Leu Val Val Ala Thr Ile Ala
50 55 60

Lys Asn Arg Asn Leu His Ser Pro Met Tyr Cys Phe Ile Cys Cys Leu
65 70 75 80

Ala Leu Ser Asp Leu Leu Val Ser Gly Ser Asn Val Leu Glu Thr Ala
85 90 95

Val Ile Leu Leu Leu Glu Ala Gly Ala Leu Val Ala Arg Ala Ala Val
100 105 110

Leu Gln Gln Leu Asp Asn Val Ile Asp Val Ile Thr Cys Ser Ser Met
115 120 125

Leu Ser Ser Leu Cys Phe Leu Gly Ala Ile Ala Val Asp Arg Tyr Ile
130 135 140

Ser Ile Phe Tyr Ala Leu Arg Tyr His Ser Ile Val Thr Leu Pro Arg
145 150 155 160

Ala Arg Arg Ala Val Ala Ala Ile Trp Val Ala Ser Val Val Phe Ser
165 170 175

Thr Leu Phe Ile Ala Tyr Tyr Asp His Val Ala Val Leu Leu Cys Leu
180 185 190

ITI-08-PCT_Sequence_Listing_ST25.txt

Val Val Phe Phe Leu Ala Met Leu Val Leu Met Ala Val Leu Tyr Val
195 200 205

His Met Leu Ala Arg Ala Cys Gln His Ala Gln Gly Ile Ala Arg Leu
210 215 220

His Lys Arg Gln Arg Pro Val His Gln Gly Phe Gly Leu Lys Gly Ala
225 230 235 240

Val Thr Leu Thr Ile Leu Leu Gly Ile Phe Phe Leu Cys Trp Gly Pro
245 250 255

Phe Phe Leu His Leu Thr Leu Ile Val Leu Cys Pro Glu His Pro Thr
260 265 270

Cys Gly Cys Ile Phe Lys Asn Phe Asn Leu Phe Leu Ala Leu Ile Ile
275 280 285

Cys Asn Ala Ile Ile Asp Pro Leu Ile Tyr Ala Phe His Ser Gln Glu
290 295 300

Leu Arg Arg Thr Leu Lys Glu Val Leu Thr Cys Ser Trp
305 310 315

<210> 516

<211> 317

<212> PRT

<213> Artificial Sequence

<220>

<223> MC1_R__Homo_sapiens__V9Q977

<400> 516

Met Ala Val Gln Gly Ser Gln Arg Arg Leu Leu Gly Ser Leu Asn Ser
1 5 10 15

Thr Pro Thr Ala Ile Pro Gln Leu Gly Leu Ala Ala Asn Gln Thr Gly
20 25 30

Ala Arg Cys Leu Glu Val Ser Ile Ser Asp Gly Leu Phe Leu Ser Leu
35 40 45

Gly Leu Val Ser Leu Val Glu Asn Ala Leu Val Leu Ala Thr Ile Ala
50 55 60

Lys Asn Arg Asn Leu His Ser Pro Met Tyr Cys Phe Ile Cys Cys Leu
65 70 75 80

Ala Leu Ser Asp Leu Leu Val Ser Gly Ser Asn Val Leu Glu Thr Ala
85 90 95

ITI-08-PCT_Sequence_Listing_ST25.txt

Val Ile Leu Leu Leu Glu Ala Gly Ala Leu Val Ala Arg Ala Ala Val
100 105 110

Leu Gln Gln Leu Asp Asn Val Ile Asp Val Ile Thr Cys Ser Ser Met
115 120 125

Leu Ser Ser Leu Cys Phe Leu Gly Ala Ile Ala Val Asp Arg Tyr Ile
130 135 140

Ser Ile Phe Tyr Ala Leu Arg Tyr His Ser Ile Val Thr Leu Pro Arg
145 150 155 160

Ala Arg Arg Ala Val Ala Ala Ile Trp Val Ala Ser Val Val Phe Ser
165 170 175

Thr Leu Phe Ile Ala Tyr Tyr Asp His Val Ala Val Leu Leu Cys Leu
180 185 190

Val Val Phe Phe Leu Ala Met Leu Val Leu Met Ala Val Leu Tyr Val
195 200 205

His Met Leu Ala Arg Ala Cys Gln His Ala Gln Gly Ile Ala Arg Leu
210 215 220

His Lys Arg Gln Arg Pro Val His Gln Gly Phe Gly Leu Lys Gly Ala
225 230 235 240

Val Thr Leu Thr Ile Leu Leu Gly Ile Phe Phe Leu Cys Trp Gly Pro
245 250 255

Phe Phe Leu His Leu Thr Leu Ile Val Leu Cys Pro Glu His Pro Thr
260 265 270

Cys Gly Cys Ile Phe Lys Asn Phe Asn Leu Phe Leu Ala Leu Ile Ile
275 280 285

Cys Asn Ala Ile Ile Asp Pro Leu Ile Tyr Ala Phe His Ser Gln Glu
290 295 300

Leu Arg Arg Thr Leu Lys Glu Val Leu Thr Cys Ser Trp
305 310 315

<210> 517

<211> 317

<212> PRT

<213> Artificial Sequence

<220>

<223> MC1_R__Homo_sapiens__V9Q9P5

<400> 517

ITI-08-PCT_Sequence_Listing_ST25.txt

```

Met Ala Val Gln Gly Ser Gln Arg Arg Leu Leu Gly Ser Leu Asn Ser
1          5          10          15

Thr Pro Thr Ala Ile Pro Gln Leu Gly Leu Ala Ala Asn Gln Thr Gly
          20          25          30

Ala Arg Cys Leu Glu Val Ser Ile Ser Asp Gly Leu Phe Leu Ser Leu
          35          40          45

Gly Leu Val Ser Leu Val Glu Asn Ala Leu Val Val Ala Thr Ile Ala
50          55          60

Lys Asn Arg Asn Leu His Ser Pro Met Tyr Cys Phe Ile Cys Cys Leu
65          70          75          80

Pro Leu Ser Asp Leu Leu Val Ser Gly Ser Asn Val Leu Glu Thr Ala
          85          90          95

Val Ile Leu Leu Leu Glu Ala Gly Ala Leu Val Ala Arg Ala Ala Val
          100          105          110

Leu Gln Gln Leu Asp Asn Val Ile Asp Val Ile Thr Cys Ser Ser Met
          115          120          125

Leu Ser Ser Leu Cys Phe Leu Gly Ala Ile Ala Val Asp Arg Tyr Ile
130          135          140

Ser Ile Phe Tyr Ala Leu Arg Tyr His Ser Ile Val Thr Leu Pro Arg
145          150          155          160

Ala Arg Arg Ala Val Ala Ala Ile Trp Val Ala Ser Val Val Phe Ser
          165          170          175

Thr Leu Phe Ile Ala Tyr Tyr Asp His Val Ala Val Leu Leu Cys Leu
          180          185          190

Val Val Phe Phe Leu Ala Met Leu Val Leu Met Ala Val Leu Tyr Val
          195          200          205

His Met Leu Ala Arg Ala Cys Gln His Ala Gln Gly Ile Ala Arg Leu
210          215          220

His Lys Arg Gln Arg Pro Val His Gln Gly Phe Gly Leu Lys Gly Ala
225          230          235          240

Val Thr Leu Thr Ile Leu Leu Gly Ile Phe Phe Leu Cys Trp Gly Pro
          245          250          255

Phe Phe Leu His Leu Thr Leu Ile Val Leu Cys Pro Glu His Pro Thr
          260          265          270

Cys Gly Cys Ile Phe Lys Asn Phe Asn Leu Phe Leu Ala Leu Ile Ile

```

ITI-08-PCT_Sequence_Listing_ST25.txt

275

280

285

Cys Asn Ala Ile Ile Asp Pro Leu Ile Tyr Ala Phe His Ser Gln Glu
290 295 300

Leu Arg Arg Thr Leu Lys Glu Val Leu Thr Cys Ser Trp
305 310 315

<210> 518

<211> 317

<212> PRT

<213> Artificial Sequence

<220>

<223> MC1_R__Homo_sapiens__V9Q9R8

<400> 518

Met Ala Val Gln Gly Ser Gln Arg Arg Leu Leu Gly Ser Leu Asn Ser
1 5 10 15

Thr Pro Thr Ala Ile Pro Gln Leu Gly Leu Ala Ala Asn Gln Thr Gly
20 25 30

Ala Arg Cys Leu Glu Val Ser Ile Ser Asp Gly Leu Phe Leu Ser Leu
35 40 45

Gly Leu Val Ser Leu Val Glu Asn Ala Leu Val Val Ala Thr Ile Ala
50 55 60

Lys Asn Arg Asn Leu His Ser Pro Met Tyr Cys Phe Ile Cys Cys Leu
65 70 75 80

Ala Leu Ser Asp Leu Leu Val Ser Gly Ser Asn Val Leu Glu Thr Ala
85 90 95

Val Ile Leu Leu Leu Glu Ala Gly Ala Leu Val Ala Arg Ala Ala Val
100 105 110

Leu Gln Gln Leu Asp Asn Val Ile Asp Val Ile Thr Cys Ser Ser Met
115 120 125

Leu Ser Ser Leu Cys Phe Leu Gly Ala Ile Ala Val Asp Arg Tyr Ile
130 135 140

Ser Ile Phe Tyr Ala Leu Arg Tyr His Ser Ile Val Thr Leu Pro Arg
145 150 155 160

Ala Arg Arg Ala Val Ala Ala Ile Trp Val Ala Ser Val Val Phe Ser
165 170 175

Thr Leu Phe Ile Ala Tyr Tyr Asp His Val Ala Val Leu Leu Cys Leu

ITI-08-PCT_Sequence_Listing_ST25.txt

180

185

190

Val Val Phe Phe Leu Ala Met Leu Val Leu Met Ala Val Leu Tyr Val
195 200 205

His Met Leu Ala Arg Ala Cys Gln His Ala Gln Gly Ile Ala Arg Leu
210 215 220

His Lys Arg Gln Arg Pro Val His Gln Gly Phe Gly Leu Lys Gly Ala
225 230 235 240

Val Thr Leu Thr Ile Leu Leu Gly Ile Phe Phe Leu Cys Trp Gly Pro
245 250 255

Phe Phe Leu His Leu Thr Leu Ile Val Leu Cys Pro Glu His Pro Thr
260 265 270

Cys Gly Cys Ile Phe Lys Asn Phe Ser Leu Phe Leu Ala Leu Ile Ile
275 280 285

Cys Asn Ala Ile Ile Asp Pro Leu Ile Tyr Ala Phe His Ser Gln Glu
290 295 300

Leu Arg Arg Thr Leu Lys Glu Val Leu Thr Cys Ser Trp
305 310 315

<210> 519

<211> 317

<212> PRT

<213> Artificial Sequence

<220>

<223> MC1_R__Homo_sapiens__V9QAE0

<400> 519

Met Ala Val Gln Gly Ser Gln Arg Arg Leu Leu Gly Ser Leu Asn Ser
1 5 10 15

Thr Pro Thr Ala Ile Pro Gln Leu Gly Leu Ala Ala Asn Gln Thr Gly
20 25 30

Ala Arg Cys Leu Glu Val Ser Ile Ser Asp Gly Leu Phe Leu Ser Leu
35 40 45

Gly Leu Val Ser Leu Val Glu Asn Ala Leu Val Val Ala Thr Ile Ala
50 55 60

Lys Asn Arg Asn Leu His Ser Pro Met Tyr Cys Phe Ile Cys Cys Leu
65 70 75 80

Ala Leu Ser Asp Leu Leu Val Ser Gly Ser Asn Val Leu Glu Thr Ala

ITI-08-PCT_Sequence_Listing_ST25.txt

85 90 95

Val Ile Leu Leu Leu Glu Ala Gly Ala Leu Val Ala Arg Ala Ala Val
100 105 110

Leu Gln Gln Leu Asp Asn Val Ile Asp Val Ile Thr Cys Ser Ser Met
115 120 125

Leu Ser Ser Leu Cys Phe Leu Gly Ala Ile Ala Val Asp Arg Tyr Ile
130 135 140

Ser Ile Phe Tyr Ala Leu Arg Tyr His Ser Ile Val Thr Leu Pro Arg
145 150 155 160

Ala Arg Arg Ala Val Ala Ala Ile Trp Val Ala Ser Val Val Phe Ser
165 170 175

Thr Leu Phe Ile Ala Tyr Tyr Asp His Val Ala Val Leu Leu Cys Leu
180 185 190

Val Val Phe Phe Leu Ala Met Leu Val Leu Met Ala Val Leu Tyr Val
195 200 205

His Met Leu Ala Arg Ala Cys Gln His Ala Gln Gly Ile Ala Arg Leu
210 215 220

His Lys Arg Gln Arg Pro Val His Gln Gly Phe Gly Leu Lys Gly Ala
225 230 235 240

Val Thr Leu Thr Ile Leu Leu Gly Ile Phe Phe Leu Cys Trp Gly Pro
245 250 255

Phe Phe Leu His Leu Thr Leu Ile Val Leu Cys Pro Glu His Pro Thr
260 265 270

Cys Gly Cys Ile Phe Lys Asn Phe Asn Leu Phe Leu Ala Leu Ile Ile
275 280 285

Cys Asn Ala Ile Ile Asp Pro Leu Ile His Ala Phe His Ser Gln Glu
290 295 300

Leu Arg Arg Thr Leu Lys Glu Val Leu Thr Cys Ser Trp
305 310 315

<210> 520

<211> 317

<212> PRT

<213> Artificial Sequence

<220>

<223> MC1_R__Homo_sapiens__V9QAR2

ITI-08-PCT_Sequence_Listing_ST25.txt

<400> 520

```

Met Ala Val Gln Gly Ser Gln Arg Arg Leu Leu Gly Ser Leu Asn Ser
1          5          10          15

Thr Pro Thr Ala Ile Pro Gln Leu Gly Leu Ala Ala Asn Gln Thr Gly
20        25        30

Ala Arg Cys Leu Glu Val Ser Ile Ser Asp Gly Leu Phe Leu Ser Leu
35        40        45

Gly Leu Val Ser Leu Val Glu Asn Ala Leu Val Val Ala Thr Ile Ala
50        55        60

Lys Asn Arg Asn Leu His Ser Pro Met Tyr Cys Phe Ile Cys Cys Leu
65        70        75        80

Ala Leu Ser Asp Leu Leu Val Ser Gly Ser Asn Val Leu Glu Thr Ala
85        90        95

Val Ile Leu Leu Leu Glu Ala Gly Ala Leu Val Ala Arg Ala Ala Val
100       105       110

Leu Gln Gln Leu Asp Asn Val Ile Asp Val Ile Thr Cys Ser Ser Met
115       120       125

Leu Ser Ser Leu Cys Phe Leu Gly Ala Ile Ala Val Asp Arg Tyr Ile
130       135       140

Ser Ile Phe Tyr Ala Leu Arg Tyr His Ser Ile Val Thr Leu Pro Arg
145       150       155       160

Ala Arg Arg Ala Val Ala Ala Ile Trp Val Ala Ser Val Val Phe Ser
165       170       175

Thr Leu Phe Ile Ala Tyr Tyr Asp His Val Ala Val Leu Leu Cys Leu
180       185       190

Val Val Phe Phe Leu Ala Met Leu Val Leu Met Ala Val Leu Tyr Val
195       200       205

His Met Leu Ala Arg Ala Cys Gln His Ala Gln Gly Ile Ala Arg Leu
210       215       220

His Lys Arg Gln Arg Pro Val His Gln Gly Phe Gly Leu Lys Gly Ala
225       230       235       240

Val Thr Leu Thr Ile Leu Leu Gly Ile Phe Phe Leu Cys Trp Gly Pro
245       250       255

Phe Phe Leu His Leu Thr Leu Ile Val Leu Cys Pro Glu His Pro Thr
260       265       270

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Cys Gly Cys Ile Phe Lys Asn Phe Asn Leu Phe Leu Ala Leu Ile Ile
275 280 285

Cys Asn Ala Ile Ile His Pro Leu Ile Tyr Ala Phe His Ser Gln Glu
290 295 300

Leu Arg Arg Thr Leu Lys Glu Val Leu Thr Cys Ser Trp
305 310 315

<210> 521

<211> 317

<212> PRT

<213> Artificial Sequence

<220>

<223> MC1_R__Homo_sapiens__V9QAW3

<400> 521

Met Ala Val Gln Gly Ser Gln Arg Arg Leu Leu Gly Ser Leu Asn Ser
1 5 10 15

Thr Pro Thr Ala Ile Pro Gln Leu Gly Leu Ala Ala Asn Gln Thr Gly
20 25 30

Ala Arg Cys Leu Glu Val Ser Ile Ser Asp Gly Leu Phe Leu Ser Leu
35 40 45

Gly Leu Val Ser Leu Val Glu Asn Ala Leu Val Val Ala Thr Ile Ala
50 55 60

Lys Asn Arg Asn Leu His Ser Pro Met Tyr Cys Phe Ile Cys Cys Leu
65 70 75 80

Ala Leu Ser Asp Leu Leu Val Ser Gly Ser Asn Val Leu Glu Thr Ala
85 90 95

Val Ile Leu Leu Leu Glu Ala Gly Ala Leu Val Ala Arg Ala Ala Val
100 105 110

Leu Gln Gln Leu Asp Asn Val Ile Asp Val Ile Thr Cys Ser Ser Met
115 120 125

Leu Ser Ser Leu Cys Phe Leu Gly Ala Ile Ala Val Asp Arg Tyr Ile
130 135 140

Ser Ile Phe Tyr Ala Leu Arg Tyr His Ser Ile Val Thr Leu Pro Arg
145 150 155 160

Ala Arg Arg Ala Val Ala Ala Ile Trp Val Ala Ser Val Val Phe Ser
165 170 175

ITI-08-PCT_Sequence_Listing_ST25.txt

Thr Leu Phe Ile Ala Tyr Tyr Asp His Val Ala Val Leu Leu Cys Leu
180 185 190

Val Val Phe Phe Leu Ala Met Leu Val Leu Met Ala Val Leu Tyr Val
195 200 205

His Met Leu Ala Arg Ala Cys Gln His Ala Gln Gly Ile Ala Arg Leu
210 215 220

His Lys Arg Gln His Pro Val His Gln Gly Phe Gly Leu Lys Gly Ala
225 230 235 240

Val Thr Leu Thr Ile Leu Leu Gly Ile Phe Phe Leu Cys Trp Gly Pro
245 250 255

Phe Phe Leu His Leu Thr Leu Ile Val Leu Cys Pro Glu His Pro Thr
260 265 270

Cys Gly Cys Ile Phe Lys Asn Phe Asn Leu Phe Leu Ala Leu Ile Ile
275 280 285

Cys Asn Ala Ile Ile Asp Pro Leu Ile Tyr Ala Phe His Ser Gln Glu
290 295 300

Leu Arg Arg Thr Leu Lys Glu Val Leu Thr Cys Ser Trp
305 310 315

<210> 522
<211> 317
<212> PRT
<213> Artificial Sequence

<220>
<223> MC1_R__Homo_sapiens__V9QB02

<400> 522

Met Ala Val Gln Gly Ser Gln Arg Arg Leu Leu Gly Ser Leu Asn Ser
1 5 10 15

Thr Pro Thr Ala Ile Pro Gln Leu Gly Leu Ala Ala Asn Gln Thr Gly
20 25 30

Ala Arg Cys Leu Glu Val Ser Ile Ser Asp Gly Leu Phe Leu Ser Leu
35 40 45

Gly Leu Val Ser Leu Val Glu Asn Ala Leu Val Val Ala Thr Ile Ala
50 55 60

Lys Asn Arg Asn Leu His Ser Pro Met Tyr Cys Phe Ile Cys Cys Leu
65 70 75 80

ITI-08-PCT_Sequence_Listing_ST25.txt

```

Ala Leu Ser Asp Leu Leu Val Ser Gly Ser Asn Val Leu Glu Thr Ala
      85                      90                      95

Val Ile Leu Leu Leu Glu Ala Gly Ala Leu Val Ala Arg Ala Ala Val
      100                    105                    110

Leu Gln Gln Leu Asp Asn Val Ile Asp Val Ile Thr Cys Ser Ser Met
      115                    120                    125

Leu Ser Ser Leu Cys Phe Leu Gly Ala Ile Ala Val Asp Arg Tyr Ile
      130                    135                    140

Ser Ile Phe Tyr Ala Leu Arg Tyr His Ser Ile Val Thr Leu Pro Arg
      145                    150                    155                    160

Ala Arg Arg Ala Val Ala Ala Ile Trp Val Ala Ser Val Val Phe Ser
      165                    170                    175

Thr Leu Phe Ile Ala Tyr Tyr Asp His Val Ala Val Leu Leu Cys Leu
      180                    185                    190

Val Val Phe Phe Leu Ala Met Leu Val Leu Met Ala Val Leu Tyr Val
      195                    200                    205

His Met Leu Ala Arg Ala Cys Gln His Ala Gln Gly Ile Ala Arg Leu
      210                    215                    220

His Lys Arg Gln Arg Pro Val His Gln Gly Phe Gly Leu Lys Gly Ala
      225                    230                    235                    240

Val Thr Leu Thr Ile Leu Leu Gly Ile Phe Phe Leu Cys Trp Gly Pro
      245                    250                    255

Phe Phe Leu His Leu Thr Leu Ile Val Leu Cys Pro Glu His Pro Thr
      260                    265                    270

Cys Gly Cys Ile Phe Lys Asn Phe Asn Leu Phe Leu Thr Leu Ile Ile
      275                    280                    285

Cys Asn Ala Ile Ile Asp Pro Leu Ile Tyr Ala Phe His Ser Gln Glu
      290                    295                    300

Leu Arg Arg Thr Leu Lys Glu Val Leu Thr Cys Ser Trp
      305                    310                    315

```

<210> 523
 <211> 317
 <212> PRT
 <213> Artificial Sequence

<220>

ITI-08-PCT_Sequence_Listing_ST25.txt

<223> MC1_R__Homo_sapiens__V9QB58

<400> 523

Met	Ala	Val	Gln	Gly	Ser	Gln	Arg	Arg	Leu	Leu	Gly	Ser	Leu	Asn	Ser	1	5	10	15
Thr	Pro	Thr	Ala	Ile	Pro	Gln	Leu	Gly	Leu	Ala	Ala	Asn	Gln	Thr	Gly	20	25	30	
Ala	Arg	Cys	Leu	Glu	Val	Ser	Ile	Ser	Asp	Gly	Leu	Phe	Leu	Ser	Leu	35	40	45	
Gly	Leu	Val	Ser	Leu	Val	Glu	Asn	Ala	Leu	Val	Val	Ala	Thr	Ile	Ala	50	55	60	
Lys	Asn	Arg	Asn	Leu	His	Ser	Pro	Met	Tyr	Cys	Phe	Ile	Cys	Cys	Leu	65	70	75	80
Ala	Leu	Ser	Asp	Leu	Leu	Val	Ser	Gly	Ser	Asn	Val	Leu	Glu	Thr	Ala	85	90	95	
Val	Ile	Leu	Leu	Leu	Glu	Ala	Gly	Ala	Leu	Val	Ala	Arg	Ala	Ala	Val	100	105	110	
Leu	Gln	Gln	Leu	Asp	Asn	Val	Ile	Asp	Val	Ile	Thr	Cys	Ser	Ser	Met	115	120	125	
Leu	Ser	Ser	Leu	Cys	Phe	Leu	Gly	Ala	Ile	Ala	Val	Asp	His	Tyr	Ile	130	135	140	
Ser	Ile	Phe	Tyr	Ala	Leu	Arg	Tyr	His	Ser	Ile	Val	Thr	Leu	Pro	Arg	145	150	155	160
Ala	Arg	Arg	Ala	Val	Ala	Ala	Ile	Trp	Val	Ala	Ser	Val	Val	Phe	Ser	165	170	175	
Thr	Leu	Phe	Ile	Ala	Tyr	Tyr	Asp	His	Val	Ala	Val	Leu	Leu	Cys	Leu	180	185	190	
Val	Val	Phe	Phe	Leu	Ala	Met	Leu	Val	Leu	Met	Ala	Val	Leu	Tyr	Val	195	200	205	
His	Met	Leu	Ala	Arg	Ala	Cys	Gln	His	Ala	Gln	Gly	Ile	Ala	Arg	Leu	210	215	220	
His	Lys	Arg	Gln	Arg	Pro	Val	His	Gln	Gly	Phe	Gly	Leu	Lys	Gly	Ala	225	230	235	240
Val	Thr	Leu	Thr	Ile	Leu	Leu	Gly	Ile	Phe	Phe	Leu	Cys	Trp	Gly	Pro	245	250	255	

ITI-08-PCT_Sequence_Listing_ST25.txt

Phe Phe Leu His Leu Thr Leu Ile Val Leu Cys Pro Glu His Pro Thr
260 265 270

Cys Gly Cys Ile Phe Lys Asn Phe Asn Leu Phe Leu Ala Leu Ile Ile
275 280 285

Cys Asn Ala Ile Ile Asp Pro Leu Ile Tyr Ala Phe His Ser Gln Glu
290 295 300

Leu Arg Arg Thr Leu Lys Glu Val Leu Thr Cys Ser Trp
305 310 315

<210> 524

<211> 317

<212> PRT

<213> Artificial Sequence

<220>

<223> MC1_R__Homo_sapiens__V9QBY6

<400> 524

Met Ala Val Gln Gly Ser Gln Arg Arg Leu Leu Gly Ser Leu Asn Ser
1 5 10 15

Thr Pro Thr Ala Ile Pro Gln Leu Gly Leu Ala Ala Asn Gln Thr Gly
20 25 30

Ala Arg Cys Leu Glu Val Ser Ile Ser Asp Gly Leu Phe Leu Ser Leu
35 40 45

Gly Leu Val Ser Leu Val Glu Asn Ala Leu Val Val Ala Thr Ile Ala
50 55 60

Lys Asn Arg Asn Leu His Ser Pro Met Tyr Cys Phe Ile Cys Cys Leu
65 70 75 80

Ala Leu Ser Asp Leu Leu Val Ser Gly Ser Asn Val Leu Glu Thr Ala
85 90 95

Val Ile Leu Leu Leu Glu Ala Gly Ala Leu Val Ala Arg Ala Ala Val
100 105 110

Leu Gln Gln Leu Asp Asn Val Ile Asp Val Ile Thr Cys Ser Ser Met
115 120 125

Leu Ser Ser Leu Cys Phe Leu Gly Ala Ile Ala Val Asp Arg Tyr Ile
130 135 140

Ser Ile Phe Tyr Ala Leu Arg Tyr His Ser Ile Val Thr Leu Pro Arg
145 150 155 160

ITI-08-PCT_Sequence_Listing_ST25.txt

Ala Arg Arg Ala Val Ala Ala Ile Trp Val Ala Ser Val Val Phe Ser
165 170 175

Thr Leu Phe Ile Ala Tyr Tyr Asp His Val Ala Val Leu Leu Cys Leu
180 185 190

Val Val Phe Phe Leu Ala Met Leu Val Leu Met Ala Val Leu Tyr Val
195 200 205

His Met Leu Ala Arg Ala Cys Gln His Ala Gln Gly Ile Ala Arg Leu
210 215 220

His Lys Arg Gln Arg Pro Val His Gln Gly Phe Gly Leu Lys Gly Ala
225 230 235 240

Val Thr Leu Thr Ile Leu Leu Gly Ile Phe Phe Leu Cys Trp Gly Pro
245 250 255

Phe Phe Leu His Leu Thr Leu Ile Val Leu Cys Pro Glu His Pro Thr
260 265 270

Cys Gly Cys Ile Phe Lys Asn Phe Asn Leu Phe Leu Ala Leu Ile Ile
275 280 285

Cys Asn Ala Ile Ile Asp Pro Leu Ile Tyr Ala Phe His Asn Gln Glu
290 295 300

Leu Arg Arg Thr Leu Lys Glu Val Leu Thr Cys Ser Trp
305 310 315

<210> 525

<211> 317

<212> PRT

<213> Artificial Sequence

<220>

<223> MC1_R__Homo_sapiens__V9QC17

<400> 525

Met Ala Val Gln Gly Ser Gln Arg Arg Leu Leu Gly Ser Leu Asn Ser
1 5 10 15

Thr Pro Thr Ala Ile Pro Gln Leu Gly Leu Ala Ala Asn Gln Thr Gly
20 25 30

Ala Arg Cys Leu Glu Val Ser Ile Ser Asp Gly Leu Phe Leu Ser Leu
35 40 45

Gly Leu Val Ser Leu Val Glu Asn Ala Leu Val Val Ala Thr Ile Ala
50 55 60

ITI-08-PCT_Sequence_Listing_ST25.txt

Lys Asn Arg Asn Leu His Ser Pro Met Tyr Cys Phe Ile Cys Cys Leu
 65 70 75 80
 Ala Leu Ser Asp Leu Leu Val Ser Gly Ser Asn Val Leu Glu Thr Ala
 85 90 95
 Val Ile Leu Leu Leu Glu Ala Gly Ala Leu Val Ala Arg Ala Ala Val
 100 105 110
 Leu Gln Gln Leu Asp Asn Val Ile Asp Met Ile Thr Cys Ser Ser Met
 115 120 125
 Leu Ser Ser Leu Cys Phe Leu Gly Ala Ile Ala Val Asp Arg Tyr Ile
 130 135 140
 Ser Ile Phe Tyr Ala Leu Arg Tyr His Ser Ile Val Thr Leu Pro Arg
 145 150 155 160
 Ala Arg Arg Ala Val Ala Ala Ile Trp Val Ala Ser Val Val Phe Ser
 165 170 175
 Thr Leu Phe Ile Ala Tyr Tyr Asp His Val Ala Val Leu Leu Cys Leu
 180 185 190
 Val Val Phe Phe Leu Ala Met Leu Val Leu Met Ala Val Leu Tyr Val
 195 200 205
 His Met Leu Ala Arg Ala Cys Gln His Ala Gln Gly Ile Ala Arg Leu
 210 215 220
 His Lys Arg Gln Arg Pro Val His Gln Gly Phe Gly Leu Lys Gly Ala
 225 230 235 240
 Val Thr Leu Thr Ile Leu Leu Gly Ile Phe Phe Leu Cys Trp Gly Pro
 245 250 255
 Phe Phe Leu His Leu Thr Leu Ile Val Leu Cys Pro Glu His Pro Thr
 260 265 270
 Cys Gly Cys Ile Phe Lys Asn Phe Asn Leu Phe Leu Ala Leu Ile Ile
 275 280 285
 Cys Asn Ala Ile Ile Asp Pro Leu Ile Tyr Ala Phe His Ser Gln Glu
 290 295 300
 Leu Arg Arg Thr Leu Lys Glu Val Leu Thr Cys Ser Trp
 305 310 315

<210> 526
 <211> 317
 <212> PRT
 <213> Artificial Sequence

ITI-08-PCT_Sequence_Listing_ST25.txt

<220>

<223> MC1_R__Homo_sapiens__V9QC66

<400> 526

Met Ala Val Gln Gly Ser Gln Arg Arg Leu Leu Gly Ser Leu Asn Ser
1 5 10 15

Thr Pro Thr Ala Ile Pro Gln Leu Gly Leu Ala Ala Asn Gln Thr Gly
20 25 30

Ala Arg Cys Leu Glu Val Ser Ile Ser Asp Gly Leu Phe Leu Ser Leu
35 40 45

Gly Leu Val Ser Leu Val Glu Asn Ala Leu Val Val Ala Thr Ile Ala
50 55 60

Lys Asn Arg Asn Leu His Ser Pro Met Tyr Cys Phe Ile Cys Cys Leu
65 70 75 80

Ala Leu Ser Asp Leu Leu Val Ser Gly Ser Asn Val Leu Glu Thr Ala
85 90 95

Val Ile Leu Leu Leu Glu Ala Gly Ala Leu Val Ala Arg Ala Ala Val
100 105 110

Leu Gln Gln Leu Asp Asn Val Ile Asp Val Ile Thr Cys Ser Ser Met
115 120 125

Leu Ser Ser Leu Cys Phe Leu Gly Ala Ile Ala Val Asp Arg Tyr Ile
130 135 140

Ser Ile Phe Tyr Ala Leu Arg Tyr His Ser Ile Val Thr Leu Pro Arg
145 150 155 160

Ala Arg Arg Ala Val Ala Ala Ile Trp Val Ala Ser Val Val Phe Ser
165 170 175

Thr Leu Phe Ile Ala Tyr Tyr Asp His Val Ala Val Leu Leu Cys Leu
180 185 190

Val Val Phe Phe Leu Ala Met Leu Val Leu Met Ala Val Leu Tyr Val
195 200 205

His Met Leu Ala Arg Ala Cys Gln His Ala Gln Gly Ile Ala Arg Leu
210 215 220

His Lys Arg Gln Arg Pro Val His Gln Gly Phe Gly Leu Lys Gly Ala
225 230 235 240

Val Thr Leu Thr Ile Leu Leu Gly Ile Phe Phe Leu Cys Trp Gly Pro

ITI-08-PCT_Sequence_Listing_ST25.txt

245 250 255

Phe Phe Leu His Leu Thr Leu Ile Val Leu Cys Pro Glu His Pro Thr
260 265 270

Cys Gly Cys Ile Phe Lys Asn Phe Asn Leu Phe Leu Ala Leu Ile Ile
275 280 285

Arg Asn Ala Ile Ile Asp Pro Leu Ile Tyr Ala Phe His Ser Gln Glu
290 295 300

Leu Arg Arg Thr Leu Lys Glu Val Leu Thr Cys Ser Trp
305 310 315

<210> 527

<211> 317

<212> PRT

<213> Artificial Sequence

<220>

<223> MC1_R__Homo_sapiens__V9QCQ4

<400> 527

Met Ala Val Gln Gly Ser Gln Arg Arg Leu Leu Gly Ser Leu Asn Ser
1 5 10 15

Thr Pro Thr Ala Ile Pro Gln Leu Gly Leu Ala Ala Asn Gln Thr Gly
20 25 30

Ala Arg Cys Leu Glu Val Ser Ile Ser Asp Gly Leu Phe Leu Ser Leu
35 40 45

Gly Leu Val Ser Leu Val Glu Asn Ala Leu Val Val Ala Thr Ile Ala
50 55 60

Lys Asn Arg Asn Leu His Ser Pro Met Tyr Cys Phe Ile Cys Cys Leu
65 70 75 80

Ala Leu Ser Asp Leu Leu Val Ser Gly Ser Asn Val Leu Glu Thr Ala
85 90 95

Val Ile Leu Leu Leu Glu Ala Gly Ala Leu Val Ala Arg Ala Ala Val
100 105 110

Leu Gln Gln Leu Asp Asn Val Ile Asp Val Ile Thr Cys Ser Ser Met
115 120 125

Leu Ser Ser Leu Cys Phe Leu Gly Ala Ile Ala Val Asp Arg Tyr Ile
130 135 140

Ser Ile Phe Tyr Ala Leu Arg Tyr His Ser Ile Val Thr Leu Pro Trp

ITI-08-PCT_Sequence_Listing_ST25.txt

```

145              150              155              160
Ala Arg Arg Ala Val Ala Ala Ile Trp Val Ala Ser Val Val Phe Ser
              165              170              175
Thr Leu Phe Ile Ala Tyr Tyr Asp His Val Ala Val Leu Leu Cys Leu
              180              185              190
Val Val Phe Phe Leu Ala Met Leu Val Leu Met Ala Val Leu Tyr Val
              195              200              205
His Met Leu Ala Arg Ala Cys Gln His Ala Gln Gly Ile Ala Arg Leu
              210              215              220
His Lys Arg Gln Arg Pro Val His Gln Gly Phe Gly Leu Lys Gly Ala
225              230              235              240
Val Thr Leu Thr Ile Leu Leu Gly Ile Phe Phe Leu Cys Trp Gly Pro
              245              250              255
Phe Phe Leu His Leu Thr Leu Ile Val Leu Cys Pro Glu His Pro Thr
              260              265              270
Cys Gly Cys Ile Phe Lys Asn Phe Asn Leu Phe Leu Ala Leu Ile Ile
              275              280              285
Cys Asn Ala Ile Ile Asp Pro Leu Ile Tyr Ala Phe His Ser Gln Glu
              290              295              300
Leu Arg Arg Thr Leu Lys Glu Val Leu Thr Cys Ser Trp
305              310              315

```

<210> 528
 <211> 317
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MC1_R__Homo_sapiens__V9QDF4

<400> 528

```

Met Ala Val Gln Gly Ser Gln Arg Arg Leu Leu Gly Ser Leu Asn Ser
1              5              10              15
Thr Pro Thr Ala Ile Pro Gln Leu Gly Leu Ala Ala Asn Gln Thr Gly
              20              25              30
Ala Arg Cys Leu Glu Val Ser Ile Ser Asp Gly Leu Phe Leu Ser Leu
              35              40              45
Gly Leu Val Ser Leu Val Glu Asn Ala Leu Val Val Ala Thr Ile Ala

```

ITI-08-PCT_Sequence_Listing_ST25.txt

50

55

60

Lys Asn Arg Asn Leu His Ser Pro Met Tyr Cys Phe Ile Cys Cys Leu
65 70 75 80

Ala Leu Ser Asp Leu Leu Val Ser Gly Ser Asn Val Leu Glu Thr Ala
85 90 95

Val Ile Leu Leu Leu Glu Ala Gly Ala Leu Val Ala Arg Ala Ala Val
100 105 110

Leu Gln Gln Leu Asp Asn Val Ile Asp Val Ile Thr Cys Ser Ser Met
115 120 125

Leu Ser Ser Leu Cys Phe Leu Gly Ala Ile Ala Val Asp Arg Tyr Ile
130 135 140

Ser Ile Phe Tyr Ala Leu Arg Tyr His Ser Ile Val Thr Leu Pro Arg
145 150 155 160

Ala Arg Arg Ala Val Ala Ala Ile Trp Val Ala Ser Val Val Phe Ser
165 170 175

Thr Leu Phe Ile Ala Tyr Tyr Asp His Val Ala Val Leu Leu Cys Leu
180 185 190

Val Val Phe Phe Leu Ala Met Leu Val Leu Met Ala Val Leu Tyr Val
195 200 205

His Met Leu Ala Arg Ala Cys Gln His Ala Gln Gly Ile Ala Arg Leu
210 215 220

His Lys Arg Gln Arg Pro Val His Gln Gly Phe Gly Leu Lys Gly Ala
225 230 235 240

Val Thr Leu Thr Ile Leu Leu Gly Ile Phe Phe Leu Cys Trp Gly Pro
245 250 255

Phe Phe Leu His Leu Thr Leu Ile Val Leu Cys Pro Glu His Pro Glu
260 265 270

Cys Gly Cys Ile Phe Lys Asn Phe Asn Leu Phe Leu Ala Leu Ile Ile
275 280 285

Cys Asn Ala Ile Ile Asp Pro Leu Ile Tyr Ala Phe His Ser Gln Glu
290 295 300

Leu Arg Arg Thr Leu Lys Glu Val Leu Thr Cys Ser Trp
305 310 315

<210> 529

<211> 317

ITI-08-PCT_Sequence_Listing_ST25.txt

<212> PRT

<213> Artificial Sequence

<220>

<223> MC1_R__Homo_sapiens__V9QDN7

<400> 529

Met Ala Val Gln Gly Ser Gln Arg Arg Leu Leu Gly Ser Leu Asn Ser
1 5 10 15

Thr Pro Thr Ala Ile Pro Gln Leu Gly Leu Ala Ala Asn Gln Thr Gly
20 25 30

Ala Arg Cys Leu Glu Val Ser Ile Ser Asp Gly Leu Phe Leu Ser Leu
35 40 45

Gly Leu Val Ser Leu Val Glu Asn Ala Leu Val Val Ala Thr Ile Ala
50 55 60

Lys Asn Arg Asn Leu His Ser Pro Met Tyr Cys Phe Ile Cys Cys Leu
65 70 75 80

Ala Leu Ser Glu Leu Leu Val Ser Gly Ser Asn Val Leu Glu Thr Ala
85 90 95

Val Ile Leu Leu Leu Glu Ala Gly Ala Leu Val Ala Arg Ala Ala Val
100 105 110

Leu Gln Gln Leu Asp Asn Val Ile Asp Val Ile Thr Cys Ser Ser Met
115 120 125

Leu Ser Ser Leu Cys Phe Leu Gly Ala Ile Ala Val Asp Arg Tyr Ile
130 135 140

Ser Ile Phe Tyr Ala Leu Arg Tyr His Ser Ile Val Thr Leu Pro Arg
145 150 155 160

Ala Arg Arg Ala Val Ala Ala Ile Trp Val Ala Ser Val Val Phe Ser
165 170 175

Thr Leu Phe Ile Ala Tyr Tyr Asp His Val Ala Val Leu Leu Cys Leu
180 185 190

Val Val Phe Phe Leu Ala Met Leu Val Leu Met Ala Val Leu Tyr Val
195 200 205

His Met Leu Ala Arg Ala Cys Gln His Ala Gln Gly Ile Ala Arg Leu
210 215 220

His Lys Arg Gln Arg Pro Val His Gln Gly Phe Gly Leu Lys Gly Ala
225 230 235 240

ITI-08-PCT_Sequence_Listing_ST25.txt

Val Thr Leu Thr Ile Leu Leu Gly Ile Phe Phe Leu Cys Trp Gly Pro
245 250 255

Phe Phe Leu His Leu Thr Leu Ile Val Leu Cys Pro Glu His Pro Thr
260 265 270

Cys Gly Cys Ile Phe Lys Asn Phe Asn Leu Phe Leu Ala Leu Ile Ile
275 280 285

Cys Asn Ala Ile Ile Asp Pro Leu Ile Tyr Ala Phe His Ser Gln Glu
290 295 300

Leu Arg Arg Thr Leu Lys Glu Val Leu Thr Cys Ser Trp
305 310 315

<210> 530

<211> 317

<212> PRT

<213> Artificial Sequence

<220>

<223> MC1_R__Homo_sapiens__V9QDQ6

<400> 530

Met Ala Val Gln Gly Ser Gln Arg Arg Leu Leu Gly Ser Leu Asn Ser
1 5 10 15

Thr Pro Thr Ala Ile Pro Gln Leu Gly Leu Ala Ala Asn Gln Thr Gly
20 25 30

Ala Arg Cys Leu Glu Val Ser Ile Ser Asp Gly Leu Phe Leu Ser Leu
35 40 45

Gly Leu Val Ser Leu Val Glu Asn Ala Leu Val Val Ala Thr Ile Ala
50 55 60

Lys Asn Arg Asn Leu His Ser Pro Met Tyr Cys Phe Ile Cys Cys Leu
65 70 75 80

Ala Leu Ser Asp Leu Leu Val Ser Gly Ser Asn Val Leu Glu Thr Ala
85 90 95

Val Ile Leu Leu Leu Glu Ala Gly Ala Leu Val Ala Arg Ala Ala Val
100 105 110

Leu Gln Gln Leu Asp Asn Val Ile Asp Val Ile Thr Cys Ser Ser Met
115 120 125

Leu Ser Ser Leu Cys Phe Leu Gly Ala Ile Ala Val Asp Arg Tyr Ile
130 135 140

ITI-08-PCT_Sequence_Listing_ST25.txt

Ser Ile Phe Tyr Ala Leu Cys Tyr His Ser Ile Val Thr Leu Pro Arg
145 150 155 160

Ala Arg Arg Ala Val Ala Ala Ile Trp Val Ala Ser Val Val Phe Ser
165 170 175

Thr Leu Phe Ile Ala Tyr Tyr Asp His Val Ala Val Leu Leu Cys Leu
180 185 190

Val Val Phe Phe Leu Ala Met Leu Val Leu Met Ala Val Leu Tyr Val
195 200 205

His Met Leu Ala Arg Ala Cys Gln His Ala Gln Gly Ile Ala Arg Leu
210 215 220

His Lys Arg Gln Arg Pro Val His Gln Gly Phe Gly Leu Lys Gly Ala
225 230 235 240

Val Thr Leu Thr Ile Leu Leu Gly Ile Phe Phe Leu Cys Trp Gly Pro
245 250 255

Phe Phe Leu His Leu Thr Leu Ile Val Leu Cys Pro Glu His Pro Thr
260 265 270

Cys Gly Cys Ile Phe Lys Asn Phe Asn Leu Phe Leu Ala Leu Ile Ile
275 280 285

Cys Asn Ala Ile Ile Asp Pro Leu Ile Tyr Ala Phe His Ser Gln Glu
290 295 300

Leu Arg Arg Thr Leu Lys Glu Val Leu Thr Cys Ser Trp
305 310 315

<210> 531

<211> 630

<212> PRT

<213> Artificial Sequence

<220>

<223> mesothelin__Homo_sapiens__Q13421

<400> 531

Met Ala Leu Pro Thr Ala Arg Pro Leu Leu Gly Ser Cys Gly Thr Pro
1 5 10 15

Ala Leu Gly Ser Leu Leu Phe Leu Leu Phe Ser Leu Gly Trp Val Gln
20 25 30

Pro Ser Arg Thr Leu Ala Gly Glu Thr Gly Gln Glu Ala Ala Pro Leu
35 40 45

ITI-08-PCT_Sequence_Listing_ST25.txt

Asp	Gly	Val	Leu	Ala	Asn	Pro	Pro	Asn	Ile	Ser	Ser	Leu	Ser	Pro	Arg	50	55	60
Gln	Leu	Leu	Gly	Phe	Pro	Cys	Ala	Glu	Val	Ser	Gly	Leu	Ser	Thr	Glu	65	70	75
Arg	Val	Arg	Glu	Leu	Ala	Val	Ala	Leu	Ala	Gln	Lys	Asn	Val	Lys	Leu	85	90	95
Ser	Thr	Glu	Gln	Leu	Arg	Cys	Leu	Ala	His	Arg	Leu	Ser	Glu	Pro	Pro	100	105	110
Glu	Asp	Leu	Asp	Ala	Leu	Pro	Leu	Asp	Leu	Leu	Leu	Phe	Leu	Asn	Pro	115	120	125
Asp	Ala	Phe	Ser	Gly	Pro	Gln	Ala	Cys	Thr	Arg	Phe	Phe	Ser	Arg	Ile	130	135	140
Thr	Lys	Ala	Asn	Val	Asp	Leu	Leu	Pro	Arg	Gly	Ala	Pro	Glu	Arg	Gln	145	150	155
Arg	Leu	Leu	Pro	Ala	Ala	Leu	Ala	Cys	Trp	Gly	Val	Arg	Gly	Ser	Leu	165	170	175
Leu	Ser	Glu	Ala	Asp	Val	Arg	Ala	Leu	Gly	Gly	Leu	Ala	Cys	Asp	Leu	180	185	190
Pro	Gly	Arg	Phe	Val	Ala	Glu	Ser	Ala	Glu	Val	Leu	Leu	Pro	Arg	Leu	195	200	205
Val	Ser	Cys	Pro	Gly	Pro	Leu	Asp	Gln	Asp	Gln	Gln	Glu	Ala	Ala	Arg	210	215	220
Ala	Ala	Leu	Gln	Gly	Gly	Gly	Pro	Pro	Tyr	Gly	Pro	Pro	Ser	Thr	Trp	225	230	235
Ser	Val	Ser	Thr	Met	Asp	Ala	Leu	Arg	Gly	Leu	Leu	Pro	Val	Leu	Gly	245	250	255
Gln	Pro	Ile	Ile	Arg	Ser	Ile	Pro	Gln	Gly	Ile	Val	Ala	Ala	Trp	Arg	260	265	270
Gln	Arg	Ser	Ser	Arg	Asp	Pro	Ser	Trp	Arg	Gln	Pro	Glu	Arg	Thr	Ile	275	280	285
Leu	Arg	Pro	Arg	Phe	Arg	Arg	Glu	Val	Glu	Lys	Thr	Ala	Cys	Pro	Ser	290	295	300
Gly	Lys	Lys	Ala	Arg	Glu	Ile	Asp	Glu	Ser	Leu	Ile	Phe	Tyr	Lys	Lys	305	310	315

ITI-08-PCT_Sequence_Listing_ST25.txt

Trp Glu Leu Glu Ala Cys Val Asp Ala Ala Leu Leu Ala Thr Gln Met
325 330 335

Asp Arg Val Asn Ala Ile Pro Phe Thr Tyr Glu Gln Leu Asp Val Leu
340 345 350

Lys His Lys Leu Asp Glu Leu Tyr Pro Gln Gly Tyr Pro Glu Ser Val
355 360 365

Ile Gln His Leu Gly Tyr Leu Phe Leu Lys Met Ser Pro Glu Asp Ile
370 375 380

Arg Lys Trp Asn Val Thr Ser Leu Glu Thr Leu Lys Ala Leu Leu Glu
385 390 395 400

Val Asn Lys Gly His Glu Met Ser Pro Gln Ala Pro Arg Arg Pro Leu
405 410 415

Pro Gln Val Ala Thr Leu Ile Asp Arg Phe Val Lys Gly Arg Gly Gln
420 425 430

Leu Asp Lys Asp Thr Leu Asp Thr Leu Thr Ala Phe Tyr Pro Gly Tyr
435 440 445

Leu Cys Ser Leu Ser Pro Glu Glu Leu Ser Ser Val Pro Pro Ser Ser
450 455 460

Ile Trp Ala Val Arg Pro Gln Asp Leu Asp Thr Cys Asp Pro Arg Gln
465 470 475 480

Leu Asp Val Leu Tyr Pro Lys Ala Arg Leu Ala Phe Gln Asn Met Asn
485 490 495

Gly Ser Glu Tyr Phe Val Lys Ile Gln Ser Phe Leu Gly Gly Ala Pro
500 505 510

Thr Glu Asp Leu Lys Ala Leu Ser Gln Gln Asn Val Ser Met Asp Leu
515 520 525

Ala Thr Phe Met Lys Leu Arg Thr Asp Ala Val Leu Pro Leu Thr Val
530 535 540

Ala Glu Val Gln Lys Leu Leu Gly Pro His Val Glu Gly Leu Lys Ala
545 550 555 560

Glu Glu Arg His Arg Pro Val Arg Asp Trp Ile Leu Arg Gln Arg Gln
565 570 575

Asp Asp Leu Asp Thr Leu Gly Leu Gly Leu Gln Gly Gly Ile Pro Asn
580 585 590

Gly Tyr Leu Val Leu Asp Leu Ser Met Gln Glu Ala Leu Ser Gly Thr

ITI-08-PCT_Sequence_Listing_ST25.txt

595

600

605

Pro Cys Leu Leu Gly Pro Gly Pro Val Leu Thr Val Leu Ala Leu Leu
610 615 620

Leu Ala Ser Thr Leu Ala
625 630

<210> 532

<211> 504

<212> PRT

<213> Artificial Sequence

<220>

<223> MITF__Homo_sapiens__075030-8

<400> 532

Met Glu Ala Leu Arg Val Gln Met Phe Met Pro Cys Ser Phe Glu Ser
1 5 10 15

Leu Tyr Leu Ser Ser Ala Glu His Pro Gly Ala Ser Lys Pro Pro Ile
20 25 30

Ser Ser Ser Ser Met Thr Ser Arg Ile Leu Leu Arg Gln Gln Leu Met
35 40 45

Arg Glu Gln Met Gln Glu Gln Glu Arg Arg Glu Gln Gln Gln Lys Leu
50 55 60

Gln Ala Ala Gln Phe Met Gln Gln Arg Val Pro Val Ser Gln Thr Pro
65 70 75 80

Ala Ile Asn Val Ser Val Pro Thr Thr Leu Pro Ser Ala Thr Gln Val
85 90 95

Pro Met Glu Val Leu Lys Val Gln Thr His Leu Glu Asn Pro Thr Lys
100 105 110

Tyr His Ile Gln Gln Ala Gln Arg Gln Gln Val Lys Gln Tyr Leu Ser
115 120 125

Thr Thr Leu Ala Asn Lys His Ala Asn Gln Val Leu Ser Leu Pro Cys
130 135 140

Pro Asn Gln Pro Gly Asp His Val Met Pro Pro Val Pro Gly Ser Ser
145 150 155 160

Ala Pro Asn Ser Pro Met Ala Met Leu Thr Leu Asn Ser Asn Cys Glu
165 170 175

Lys Glu Gly Phe Tyr Lys Phe Glu Glu Gln Asn Arg Ala Glu Ser Glu

ITI-08-PCT_Sequence_Listing_ST25.txt

180	185	190															
Cys	Pro	Gly	Met	Asn	Thr	His	Ser	Arg	Ala	Ser	Cys	Met	Gln	Met	Asp		
	195						200					205					
Asp	Val	Ile	Asp	Asp	Ile	Ile	Ser	Leu	Glu	Ser	Ser	Tyr	Asn	Glu	Glu		
	210					215					220						
Ile	Leu	Gly	Leu	Met	Asp	Pro	Ala	Leu	Gln	Met	Ala	Asn	Thr	Leu	Pro		
225					230					235					240		
Val	Ser	Gly	Asn	Leu	Ile	Asp	Leu	Tyr	Gly	Asn	Gln	Gly	Leu	Pro	Pro		
			245						250					255			
Pro	Gly	Leu	Thr	Ile	Ser	Asn	Ser	Cys	Pro	Ala	Asn	Leu	Pro	Asn	Ile		
			260					265					270				
Lys	Arg	Glu	Leu	Thr	Glu	Ser	Glu	Ala	Arg	Ala	Leu	Ala	Lys	Glu	Arg		
	275						280					285					
Gln	Lys	Lys	Asp	Asn	His	Asn	Leu	Ile	Glu	Arg	Arg	Arg	Arg	Phe	Asn		
	290					295					300						
Ile	Asn	Asp	Arg	Ile	Lys	Glu	Leu	Gly	Thr	Leu	Ile	Pro	Lys	Ser	Asn		
305					310					315					320		
Asp	Pro	Asp	Met	Arg	Trp	Asn	Lys	Gly	Thr	Ile	Leu	Lys	Ala	Ser	Val		
			325						330					335			
Asp	Tyr	Ile	Arg	Lys	Leu	Gln	Arg	Glu	Gln	Gln	Arg	Ala	Lys	Glu	Leu		
			340					345					350				
Glu	Asn	Arg	Gln	Lys	Lys	Leu	Glu	His	Ala	Asn	Arg	His	Leu	Leu	Leu		
	355						360					365					
Arg	Ile	Gln	Glu	Leu	Glu	Met	Gln	Ala	Arg	Ala	His	Gly	Leu	Ser	Leu		
	370					375					380						
Ile	Pro	Ser	Thr	Gly	Leu	Cys	Ser	Pro	Asp	Leu	Val	Asn	Arg	Ile	Ile		
385					390					395					400		
Lys	Gln	Glu	Pro	Val	Leu	Glu	Asn	Cys	Ser	Gln	Asp	Leu	Leu	Gln	His		
			405						410					415			
His	Ala	Asp	Leu	Thr	Cys	Thr	Thr	Thr	Leu	Asp	Leu	Thr	Asp	Gly	Thr		
			420					425					430				
Ile	Thr	Phe	Asn	Asn	Asn	Leu	Gly	Thr	Gly	Thr	Glu	Ala	Asn	Gln	Ala		
	435						440					445					
Tyr	Ser	Val	Pro	Thr	Lys	Met	Gly	Ser	Lys	Leu	Glu	Asp	Ile	Leu	Met		
	450					455					460						

ITI-08-PCT_Sequence_Listing_ST25.txt

Asp Asp Thr Leu Ser Pro Val Gly Val Thr Asp Pro Leu Leu Ser Ser
465 470 475 480

Val Ser Pro Gly Ala Ser Lys Thr Ser Ser Arg Arg Ser Ser Met Ser
485 490 495

Met Glu Glu Thr Glu His Thr Cys
500

<210> 533

<211> 419

<212> PRT

<213> Artificial Sequence

<220>

<223> MITF__Homo_sapiens__075030-9

<400> 533

Met Leu Glu Met Leu Glu Tyr Asn His Tyr Gln Val Gln Thr His Leu
1 5 10 15

Glu Asn Pro Thr Lys Tyr His Ile Gln Gln Ala Gln Arg Gln Gln Val
20 25 30

Lys Gln Tyr Leu Ser Thr Thr Leu Ala Asn Lys His Ala Asn Gln Val
35 40 45

Leu Ser Leu Pro Cys Pro Asn Gln Pro Gly Asp His Val Met Pro Pro
50 55 60

Val Pro Gly Ser Ser Ala Pro Asn Ser Pro Met Ala Met Leu Thr Leu
65 70 75 80

Asn Ser Asn Cys Glu Lys Glu Gly Phe Tyr Lys Phe Glu Glu Gln Asn
85 90 95

Arg Ala Glu Ser Glu Cys Pro Gly Met Asn Thr His Ser Arg Ala Ser
100 105 110

Cys Met Gln Met Asp Asp Val Ile Asp Asp Ile Ile Ser Leu Glu Ser
115 120 125

Ser Tyr Asn Glu Glu Ile Leu Gly Leu Met Asp Pro Ala Leu Gln Met
130 135 140

Ala Asn Thr Leu Pro Val Ser Gly Asn Leu Ile Asp Leu Tyr Gly Asn
145 150 155 160

Gln Gly Leu Pro Pro Pro Gly Leu Thr Ile Ser Asn Ser Cys Pro Ala
165 170 175

ITI-08-PCT_Sequence_Listing_ST25.txt

```

Asn Leu Pro Asn Ile Lys Arg Glu Leu Thr Ala Cys Ile Phe Pro Thr
      180                      185                      190

Glu Ser Glu Ala Arg Ala Leu Ala Lys Glu Arg Gln Lys Lys Asp Asn
      195                      200                      205

His Asn Leu Ile Glu Arg Arg Arg Arg Phe Asn Ile Asn Asp Arg Ile
      210                      215                      220

Lys Glu Leu Gly Thr Leu Ile Pro Lys Ser Asn Asp Pro Asp Met Arg
      225                      230                      235                      240

Trp Asn Lys Gly Thr Ile Leu Lys Ala Ser Val Asp Tyr Ile Arg Lys
      245                      250                      255

Leu Gln Arg Glu Gln Gln Arg Ala Lys Glu Leu Glu Asn Arg Gln Lys
      260                      265                      270

Lys Leu Glu His Ala Asn Arg His Leu Leu Leu Arg Ile Gln Glu Leu
      275                      280                      285

Glu Met Gln Ala Arg Ala His Gly Leu Ser Leu Ile Pro Ser Thr Gly
      290                      295                      300

Leu Cys Ser Pro Asp Leu Val Asn Arg Ile Ile Lys Gln Glu Pro Val
      305                      310                      315                      320

Leu Glu Asn Cys Ser Gln Asp Leu Leu Gln His His Ala Asp Leu Thr
      325                      330                      335

Cys Thr Thr Thr Leu Asp Leu Thr Asp Gly Thr Ile Thr Phe Asn Asn
      340                      345                      350

Asn Leu Gly Thr Gly Thr Glu Ala Asn Gln Ala Tyr Ser Val Pro Thr
      355                      360                      365

Lys Met Gly Ser Lys Leu Glu Asp Ile Leu Met Asp Asp Thr Leu Ser
      370                      375                      380

Pro Val Gly Val Thr Asp Pro Leu Leu Ser Ser Val Ser Pro Gly Ala
      385                      390                      395                      400

Ser Lys Thr Ser Ser Arg Arg Ser Ser Met Ser Met Glu Glu Thr Glu
      405                      410                      415

```

His Thr Cys

```

<210> 534
<211> 526
<212> PRT
<213> Artificial Sequence

```

ITI-08-PCT_Sequence_Listing_ST25.txt

<220>

<223> MITF__Homo_sapiens__075030

<400> 534

Met Gln Ser Glu Ser Gly Ile Val Pro Asp Phe Glu Val Gly Glu Glu
1 5 10 15

Phe His Glu Glu Pro Lys Thr Tyr Tyr Glu Leu Lys Ser Gln Pro Leu
20 25 30

Lys Ser Ser Ser Ser Ala Glu His Pro Gly Ala Ser Lys Pro Pro Ile
35 40 45

Ser Ser Ser Ser Met Thr Ser Arg Ile Leu Leu Arg Gln Gln Leu Met
50 55 60

Arg Glu Gln Met Gln Glu Gln Glu Arg Arg Glu Gln Gln Gln Lys Leu
65 70 75 80

Gln Ala Ala Gln Phe Met Gln Gln Arg Val Pro Val Ser Gln Thr Pro
85 90 95

Ala Ile Asn Val Ser Val Pro Thr Thr Leu Pro Ser Ala Thr Gln Val
100 105 110

Pro Met Glu Val Leu Lys Val Gln Thr His Leu Glu Asn Pro Thr Lys
115 120 125

Tyr His Ile Gln Gln Ala Gln Arg Gln Gln Val Lys Gln Tyr Leu Ser
130 135 140

Thr Thr Leu Ala Asn Lys His Ala Asn Gln Val Leu Ser Leu Pro Cys
145 150 155 160

Pro Asn Gln Pro Gly Asp His Val Met Pro Pro Val Pro Gly Ser Ser
165 170 175

Ala Pro Asn Ser Pro Met Ala Met Leu Thr Leu Asn Ser Asn Cys Glu
180 185 190

Lys Glu Gly Phe Tyr Lys Phe Glu Glu Gln Asn Arg Ala Glu Ser Glu
195 200 205

Cys Pro Gly Met Asn Thr His Ser Arg Ala Ser Cys Met Gln Met Asp
210 215 220

Asp Val Ile Asp Asp Ile Ile Ser Leu Glu Ser Ser Tyr Asn Glu Glu
225 230 235 240

Ile Leu Gly Leu Met Asp Pro Ala Leu Gln Met Ala Asn Thr Leu Pro

ITI-08-PCT_Sequence_Listing_ST25.txt

245 250 255

Val Ser Gly Asn Leu Ile Asp Leu Tyr Gly Asn Gln Gly Leu Pro Pro
260 265 270

Pro Gly Leu Thr Ile Ser Asn Ser Cys Pro Ala Asn Leu Pro Asn Ile
275 280 285

Lys Arg Glu Leu Thr Ala Cys Ile Phe Pro Thr Glu Ser Glu Ala Arg
290 295 300

Ala Leu Ala Lys Glu Arg Gln Lys Lys Asp Asn His Asn Leu Ile Glu
305 310 315 320

Arg Arg Arg Arg Phe Asn Ile Asn Asp Arg Ile Lys Glu Leu Gly Thr
325 330 335

Leu Ile Pro Lys Ser Asn Asp Pro Asp Met Arg Trp Asn Lys Gly Thr
340 345 350

Ile Leu Lys Ala Ser Val Asp Tyr Ile Arg Lys Leu Gln Arg Glu Gln
355 360 365

Gln Arg Ala Lys Glu Leu Glu Asn Arg Gln Lys Lys Leu Glu His Ala
370 375 380

Asn Arg His Leu Leu Leu Arg Ile Gln Glu Leu Glu Met Gln Ala Arg
385 390 395 400

Ala His Gly Leu Ser Leu Ile Pro Ser Thr Gly Leu Cys Ser Pro Asp
405 410 415

Leu Val Asn Arg Ile Ile Lys Gln Glu Pro Val Leu Glu Asn Cys Ser
420 425 430

Gln Asp Leu Leu Gln His His Ala Asp Leu Thr Cys Thr Thr Thr Leu
435 440 445

Asp Leu Thr Asp Gly Thr Ile Thr Phe Asn Asn Asn Leu Gly Thr Gly
450 455 460

Thr Glu Ala Asn Gln Ala Tyr Ser Val Pro Thr Lys Met Gly Ser Lys
465 470 475 480

Leu Glu Asp Ile Leu Met Asp Asp Thr Leu Ser Pro Val Gly Val Thr
485 490 495

Asp Pro Leu Leu Ser Ser Val Ser Pro Gly Ala Ser Lys Thr Ser Ser
500 505 510

Arg Arg Ser Ser Met Ser Met Glu Glu Thr Glu His Thr Cys
515 520 525

ITI-08-PCT_Sequence_Listing_ST25.txt

```

<210> 535
<211> 354
<212> PRT
<213> Artificial Sequence

<220>
<223> MMP1_1__Homo_sapiens__B3KQS8

<400> 535

Met Ala Pro Ala Ala Trp Leu Arg Ser Ala Ala Ala Arg Ala Leu Leu
1          5          10          15

Pro Pro Met Leu Leu Leu Leu Leu Gln Pro Pro Pro Leu Leu Ala Arg
20          25          30

Ala Leu Pro Pro Asp Val His His Leu His Ala Glu Arg Arg Gly Pro
35          40          45

Gln Pro Trp His Ala Ala Leu Pro Ser Ser Pro Ala Pro Ala Pro Ala
50          55          60

Thr Gln Glu Ala Pro Arg Pro Ala Ser Ser Leu Arg Pro Pro Arg Cys
65          70          75          80

Gly Val Pro Asp Pro Ser Asp Gly Leu Ser Ala Arg Asn Arg Gln Lys
85          90          95

Arg Ile Leu Arg Phe Pro Trp Gln Leu Val Gln Glu Gln Val Arg Gln
100         105         110

Thr Met Ala Glu Ala Leu Lys Val Trp Ser Asp Val Thr Pro Leu Thr
115         120         125

Phe Thr Glu Val His Glu Gly Arg Ala Asp Ile Met Ile Asp Phe Ala
130         135         140

Arg Tyr Trp His Gly Asp Asp Leu Pro Phe Asp Gly Pro Gly Gly Ile
145         150         155         160

Leu Ala His Ala Phe Phe Pro Lys Thr His Arg Glu Gly Asp Val His
165         170         175

Phe Asp Tyr Asp Glu Thr Trp Thr Ile Gly Asp Asp Gln Gly Thr Asp
180         185         190

Leu Leu Gln Val Ala Ala His Glu Phe Gly His Val Leu Gly Leu Gln
195         200         205

His Thr Thr Ala Ala Lys Ala Leu Met Ser Ala Phe Tyr Thr Phe Arg
210         215         220

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Tyr Pro Leu Ser Leu Ser Pro Asp Asp Cys Arg Gly Val Gln His Leu
225 230 235 240

Tyr Gly Gln Pro Trp Pro Thr Val Thr Ser Arg Thr Pro Ala Leu Gly
245 250 255

Pro Gln Ala Gly Ile Asp Thr Asn Glu Ile Ala Pro Leu Glu Pro Asp
260 265 270

Ala Pro Pro Asp Ala Cys Glu Ala Ser Phe Asp Ala Val Ser Thr Ile
275 280 285

Arg Gly Glu Leu Phe Phe Phe Lys Ala Gly Phe Val Trp Arg Leu Arg
290 295 300

Gly Gly Gln Leu Gln Pro Gly Tyr Pro Ala Leu Ala Ser Arg His Trp
305 310 315 320

Gln Gly Leu Pro Ser Pro Val Asp Ala Ala Phe Glu Asp Ala Gln Gly
325 330 335

His Ile Trp Phe Phe Gln Gly Thr Thr Gly Val Ser Thr Pro Ala Pro
340 345 350

Gly Val

<210> 536

<211> 267

<212> PRT

<213> Artificial Sequence

<220>

<223> MMP7__Homo_sapiens__P09237

<400> 536

Met Arg Leu Thr Val Leu Cys Ala Val Cys Leu Leu Pro Gly Ser Leu
1 5 10 15

Ala Leu Pro Leu Pro Gln Glu Ala Gly Gly Met Ser Glu Leu Gln Trp
20 25 30

Glu Gln Ala Gln Asp Tyr Leu Lys Arg Phe Tyr Leu Tyr Asp Ser Glu
35 40 45

Thr Lys Asn Ala Asn Ser Leu Glu Ala Lys Leu Lys Glu Met Gln Lys
50 55 60

Phe Phe Gly Leu Pro Ile Thr Gly Met Leu Asn Ser Arg Val Ile Glu
65 70 75 80

ITI-08-PCT_Sequence_Listing_ST25.txt

Ile Met Gln Lys Pro Arg Cys Gly Val Pro Asp Val Ala Glu Tyr Ser
85 90 95

Leu Phe Pro Asn Ser Pro Lys Trp Thr Ser Lys Val Val Thr Tyr Arg
100 105 110

Ile Val Ser Tyr Thr Arg Asp Leu Pro His Ile Thr Val Asp Arg Leu
115 120 125

Val Ser Lys Ala Leu Asn Met Trp Gly Lys Glu Ile Pro Leu His Phe
130 135 140

Arg Lys Val Val Trp Gly Thr Ala Asp Ile Met Ile Gly Phe Ala Arg
145 150 155 160

Gly Ala His Gly Asp Ser Tyr Pro Phe Asp Gly Pro Gly Asn Thr Leu
165 170 175

Ala His Ala Phe Ala Pro Gly Thr Gly Leu Gly Gly Asp Ala His Phe
180 185 190

Asp Glu Asp Glu Arg Trp Thr Asp Gly Ser Ser Leu Gly Ile Asn Phe
195 200 205

Leu Tyr Ala Ala Thr His Glu Leu Gly His Ser Leu Gly Met Gly His
210 215 220

Ser Ser Asp Pro Asn Ala Val Met Tyr Pro Thr Tyr Gly Asn Gly Asp
225 230 235 240

Pro Gln Asn Phe Lys Leu Ser Gln Asp Asp Ile Lys Gly Ile Gln Lys
245 250 255

Leu Tyr Gly Lys Arg Ser Asn Ser Arg Lys Lys
260 265

<210> 537
<211> 1255
<212> PRT
<213> Artificial Sequence

<220>
<223> MUC-1__Homo_sapiens__AAA60019

<400> 537

Met Thr Pro Gly Thr Gln Ser Pro Phe Phe Leu Leu Leu Leu Thr
1 5 10 15

Val Leu Thr Val Val Thr Gly Ser Gly His Ala Ser Ser Thr Pro Gly
20 25 30

ITI-08-PCT_Sequence_Listing_ST25.txt

Gly	Glu	Lys	Glu	Thr	Ser	Ala	Thr	Gln	Arg	Ser	Ser	Val	Pro	Ser	Ser		
		35					40					45					
Thr	Glu	Lys	Asn	Ala	Val	Ser	Met	Thr	Ser	Ser	Val	Leu	Ser	Ser	His		
	50					55					60						
Ser	Pro	Gly	Ser	Gly	Ser	Ser	Thr	Thr	Gln	Gly	Gln	Asp	Val	Thr	Leu		
65					70					75					80		
Ala	Pro	Ala	Thr	Glu	Pro	Ala	Ser	Gly	Ser	Ala	Ala	Thr	Trp	Gly	Gln		
				85					90					95			
Asp	Val	Thr	Ser	Val	Pro	Val	Thr	Arg	Pro	Ala	Leu	Gly	Ser	Thr	Thr		
			100					105					110				
Pro	Pro	Ala	His	Asp	Val	Thr	Ser	Ala	Pro	Asp	Asn	Lys	Pro	Ala	Pro		
		115					120					125					
Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr		
	130					135					140						
Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr	Ser		
145					150					155					160		
Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala	Pro	Pro	Ala	His		
				165					170					175			
Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala		
			180					185					190				
Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro		
		195					200					205					
Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr		
	210					215					220						
Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr	Ser		
225					230					235					240		
Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala	Pro	Pro	Ala	His		
				245					250					255			
Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala		
			260					265					270				
Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro		
		275					280					285					
Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr		
	290					295					300						
Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr	Ser		

ITI-08-PCT_Sequence_Listing_ST25.txt

```

305          310          315          320
Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His
          325          330          335
Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala
          340          345          350
Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro
          355          360          365
Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr
          370          375          380
Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser
385          390          395          400
Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His
          405          410          415
Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala
          420          425          430
Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro
          435          440          445
Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr
          450          455          460
Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser
465          470          475          480
Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His
          485          490          495
Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala
          500          505          510
Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro
          515          520          525
Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr
          530          535          540
Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser
545          550          555          560
Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His
          565          570          575
Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala
          580          585          590

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro	595	600	605	
Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr	610	615	620	
Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr	Ser	625	630	635	640
Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	645	650	655	
Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala	660	665	670	
Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro	675	680	685	
Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr	690	695	700	
Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr	Ser	705	710	715	720
Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	725	730	735	
Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala	740	745	750	
Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro	755	760	765	
Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr	770	775	780	
Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr	Ser	785	790	795	800
Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	805	810	815	
Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala	820	825	830	
Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro	835	840	845	
Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr	850	855	860	

ITI-08-PCT_Sequence_Listing_ST25.txt

Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser
865 870 875 880

Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His
885 890 895

Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala
900 905 910

Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro
915 920 925

Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Asn
930 935 940

Arg Pro Ala Leu Gly Ser Thr Ala Pro Pro Val His Asn Val Thr Ser
945 950 955 960

Ala Ser Gly Ser Ala Ser Gly Ser Ala Ser Thr Leu Val His Asn Gly
965 970 975

Thr Ser Ala Arg Ala Thr Thr Thr Pro Ala Ser Lys Ser Thr Pro Phe
980 985 990

Ser Ile Pro Ser His His Ser Asp Thr Pro Thr Thr Leu Ala Ser His
995 1000 1005

Ser Thr Lys Thr Asp Ala Ser Ser Thr His His Ser Ser Val Pro
1010 1015 1020

Pro Leu Thr Ser Ser Asn His Ser Thr Ser Pro Gln Leu Ser Thr
1025 1030 1035

Gly Val Ser Phe Phe Phe Leu Ser Phe His Ile Ser Asn Leu Gln
1040 1045 1050

Phe Asn Ser Ser Leu Glu Asp Pro Ser Thr Asp Tyr Tyr Gln Glu
1055 1060 1065

Leu Gln Arg Asp Ile Ser Glu Met Phe Leu Gln Ile Tyr Lys Gln
1070 1075 1080

Gly Gly Phe Leu Gly Leu Ser Asn Ile Lys Phe Arg Pro Gly Ser
1085 1090 1095

Val Val Val Gln Leu Thr Leu Ala Phe Arg Glu Gly Thr Ile Asn
1100 1105 1110

Val His Asp Val Glu Thr Gln Phe Asn Gln Tyr Lys Thr Glu Ala
1115 1120 1125

Ala Ser Arg Tyr Asn Leu Thr Ile Ser Asp Val Ser Val Ser Asp

ITI-08-PCT_Sequence_Listing_ST25.txt

```

1130                      1135                      1140
Val Pro  Phe Pro Phe Ser Ala  Gln Ser Gly Ala Gly  Val Pro Gly
1145                      1150                      1155

Trp Gly  Ile Ala Leu Leu Val  Leu Val Cys Val Leu  Val Ala Leu
1160                      1165                      1170

Ala Ile  Val Tyr Leu Ile Ala  Leu Ala Val Cys Gln  Cys Arg Arg
1175                      1180                      1185

Lys Asn  Tyr Gly Gln Leu Asp  Ile Phe Pro Ala Arg  Asp Thr Tyr
1190                      1195                      1200

His Pro  Met Ser Glu Tyr Pro  Thr Tyr His Thr His  Gly Arg Tyr
1205                      1210                      1215

Val Pro  Pro Ser Ser Thr Asp  Arg Ser Pro Tyr Glu  Lys Val Ser
1220                      1225                      1230

Ala Gly  Asn Gly Gly Ser Ser  Leu Ser Tyr Thr Asn  Pro Ala Val
1235                      1240                      1245

Ala Ala  Ala Ser Ala Asn Leu
1250                      1255

<210>  538
<211>  711
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  MUM-1/m__Homo_sapiens__NP_116242

<400>  538

Met Met Ala Asp Ala Lys Tyr Val Leu Cys Arg Trp Glu Lys Arg Leu
1      5      10      15

Trp Pro Ala Lys Val Leu Ala Arg Thr Ala Thr Ser Thr Lys Asn Lys
20      25      30

Arg Arg Lys Glu Tyr Phe Leu Ala Val Gln Ile Leu Ser Leu Glu Glu
35      40      45

Lys Ile Lys Val Lys Ser Thr Glu Val Glu Ile Leu Glu Lys Ser Gln
50      55      60

Ile Glu Ala Ile Ala Ser Ser Leu Ala Ser Gln Asn Glu Val Pro Ala
65      70      75      80

Ala Pro Leu Glu Glu Leu Ala Tyr Arg Arg Ser Leu Arg Val Ala Leu

```


ITI-08-PCT_Sequence_Listing_ST25.txt

85

90

95

Asp Val Leu Ser Glu Gly Ser Ile Trp Ser Gln Glu Ser Ser Ala Gly
 100 105 110

Thr Gly Arg Ala Asp Arg Ser Leu Arg Gly Lys Pro Met Glu His Val
 115 120 125

Ser Ser Pro Cys Asp Ser Asn Ser Ser Ser Leu Pro Arg Gly Asp Val
 130 135 140

Leu Gly Ser Ser Arg Pro His Arg Arg Arg Pro Cys Val Gln Gln Ser
 145 150 155 160

Leu Ser Ser Ser Phe Thr Cys Glu Lys Asp Pro Glu Cys Lys Val Asp
 165 170 175

His Lys Lys Gly Leu Arg Lys Ser Glu Asn Pro Arg Gly Pro Leu Val
 180 185 190

Leu Pro Ala Gly Gly Gly Ala Gln Asp Glu Ser Gly Ser Arg Ile His
 195 200 205

His Lys Asn Trp Thr Leu Ala Ser Lys Arg Gly Gly Asn Ser Ala Gln
 210 215 220

Lys Ala Ser Leu Cys Leu Asn Gly Ser Ser Leu Ser Glu Asp Asp Thr
 225 230 235 240

Glu Arg Asp Met Gly Ser Lys Gly Gly Ser Trp Ala Ala Pro Ser Leu
 245 250 255

Pro Ser Gly Val Arg Glu Asp Asp Pro Cys Ala Asn Ala Glu Gly His
 260 265 270

Asp Pro Gly Leu Pro Leu Gly Ser Leu Thr Ala Pro Pro Ala Pro Glu
 275 280 285

Pro Ser Ala Cys Ser Glu Pro Gly Glu Cys Pro Ala Lys Lys Arg Pro
 290 295 300

Arg Leu Asp Gly Ser Gln Arg Pro Pro Ala Val Gln Leu Glu Pro Met
 305 310 315 320

Ala Ala Gly Ala Ala Pro Ser Pro Gly Pro Gly Pro Gly Pro Arg Glu
 325 330 335

Ser Val Thr Pro Arg Ser Thr Ala Arg Leu Gly Pro Pro Pro Ser His
 340 345 350

Ala Ser Ala Asp Ala Thr Arg Cys Leu Pro Cys Pro Asp Ser Gln Lys
 355 360 365

ITI-08-PCT_Sequence_Listing_ST25.txt

Leu	Glu	Lys	Glu	Cys	Gln	Ser	Ser	Glu	Glu	Ser	Met	Gly	Ser	Asn	Ser		
	370					375					380						
Met	Arg	Ser	Ile	Leu	Glu	Glu	Asp	Glu	Glu	Asp	Glu	Glu	Pro	Pro	Arg		
385					390					395					400		
Val	Leu	Leu	Tyr	His	Glu	Pro	Arg	Ser	Phe	Glu	Val	Gly	Met	Leu	Val		
				405					410					415			
Trp	His	Lys	His	Lys	Lys	Tyr	Pro	Phe	Trp	Pro	Ala	Val	Val	Lys	Ser		
			420					425					430				
Val	Arg	Gln	Arg	Asp	Lys	Lys	Ala	Ser	Val	Leu	Tyr	Ile	Glu	Gly	His		
		435					440					445					
Met	Asn	Pro	Lys	Met	Lys	Gly	Phe	Thr	Val	Ser	Leu	Lys	Ser	Leu	Lys		
	450					455					460						
His	Phe	Asp	Cys	Lys	Glu	Lys	Gln	Thr	Leu	Leu	Asn	Gln	Ala	Arg	Glu		
465					470					475					480		
Asp	Phe	Asn	Gln	Asp	Ile	Gly	Trp	Cys	Val	Ser	Leu	Ile	Thr	Asp	Tyr		
				485					490					495			
Arg	Val	Arg	Leu	Gly	Cys	Gly	Ser	Phe	Ala	Gly	Ser	Phe	Leu	Glu	Tyr		
			500					505					510				
Tyr	Ala	Ala	Asp	Ile	Ser	Tyr	Pro	Val	Arg	Lys	Ser	Ile	Gln	Gln	Asp		
		515					520					525					
Val	Leu	Gly	Thr	Lys	Leu	Pro	Gln	Leu	Ser	Lys	Gly	Ser	Pro	Glu	Glu		
	530					535					540						
Pro	Val	Val	Gly	Cys	Pro	Leu	Gly	Gln	Arg	Gln	Pro	Cys	Arg	Lys	Met		
545					550					555					560		
Leu	Pro	Asp	Arg	Ser	Arg	Ala	Ala	Arg	Asp	Arg	Ala	Asn	Gln	Lys	Leu		
				565					570					575			
Val	Glu	Tyr	Ile	Val	Lys	Ala	Lys	Gly	Ala	Glu	Ser	His	Leu	Arg	Ala		
			580					585					590				
Ile	Leu	Lys	Ser	Arg	Lys	Pro	Ser	Arg	Trp	Leu	Gln	Thr	Phe	Leu	Ser		
		595					600					605					
Ser	Ser	Gln	Tyr	Val	Thr	Cys	Val	Glu	Thr	Tyr	Leu	Glu	Asp	Glu	Gly		
	610					615					620						
Gln	Leu	Asp	Leu	Val	Val	Lys	Tyr	Leu	Gln	Gly	Val	Tyr	Gln	Glu	Val		
625					630					635					640		

ITI-08-PCT_Sequence_Listing_ST25.txt

Gly Ala Lys Val Leu Gln Arg Thr Asn Gly Asp Arg Ile Arg Phe Ile
645 650 655

Leu Asp Val Leu Leu Pro Glu Ala Ile Ile Cys Ala Ile Ser Ala Val
660 665 670

Asp Glu Val Asp Tyr Lys Thr Ala Glu Glu Lys Tyr Ile Lys Gly Pro
675 680 685

Ser Leu Ser Tyr Arg Glu Lys Glu Ile Phe Asp Asn Gln Leu Leu Glu
690 695 700

Glu Arg Asn Arg Arg Arg Arg
705 710

<210> 539

<211> 145

<212> PRT

<213> Artificial Sequence

<220>

<223> MUM-2/m__Homo_sapiens__Q9Y5R8

<400> 539

Met Thr Val His Asn Leu Tyr Leu Phe Asp Arg Asn Gly Val Cys Leu
1 5 10 15

His Tyr Ser Glu Trp His Arg Lys Lys Gln Ala Gly Ile Pro Lys Glu
20 25 30

Glu Glu Tyr Lys Leu Met Tyr Gly Met Leu Phe Ser Ile Arg Ser Phe
35 40 45

Val Ser Lys Met Ser Pro Leu Asp Met Lys Asp Gly Phe Leu Ala Phe
50 55 60

Gln Thr Ser Arg Tyr Lys Leu His Tyr Tyr Glu Thr Pro Thr Gly Ile
65 70 75 80

Lys Val Val Met Asn Thr Asp Leu Gly Val Gly Pro Ile Arg Asp Val
85 90 95

Leu His His Ile Tyr Ser Ala Leu Tyr Val Glu Leu Val Val Lys Asn
100 105 110

Pro Leu Cys Pro Leu Gly Gln Thr Val Gln Ser Glu Leu Phe Arg Ser
115 120 125

Arg Leu Asp Ser Tyr Val Arg Ser Leu Pro Phe Phe Ser Ala Arg Ala
130 135 140

ITI-08-PCT_Sequence_Listing_ST25.txt

Gly
145

<210> 540
<211> 1043
<212> PRT
<213> Artificial Sequence

<220>
<223> MY01A__Homo_sapiens__Q9UBC5

<400> 540

Met Pro Leu Leu Glu Gly Ser Val Gly Val Glu Asp Leu Val Leu Leu
1 5 10 15

Glu Pro Leu Val Glu Glu Ser Leu Leu Lys Asn Leu Gln Leu Arg Tyr
20 25 30

Glu Asn Lys Glu Ile Tyr Thr Tyr Ile Gly Asn Val Val Ile Ser Val
35 40 45

Asn Pro Tyr Gln Gln Leu Pro Ile Tyr Gly Pro Glu Phe Ile Ala Lys
50 55 60

Tyr Gln Asp Tyr Thr Phe Tyr Glu Leu Lys Pro His Ile Tyr Ala Leu
65 70 75 80

Ala Asn Val Ala Tyr Gln Ser Leu Arg Asp Arg Asp Arg Asp Gln Cys
85 90 95

Ile Leu Ile Thr Gly Glu Ser Gly Ser Gly Lys Thr Glu Ala Ser Lys
100 105 110

Leu Val Met Ser Tyr Val Ala Ala Val Cys Gly Lys Gly Glu Gln Val
115 120 125

Asn Ser Val Lys Glu Gln Leu Leu Gln Ser Asn Pro Val Leu Glu Ala
130 135 140

Phe Gly Asn Ala Lys Thr Ile Arg Asn Asn Asn Ser Ser Arg Phe Gly
145 150 155 160

Lys Tyr Met Asp Ile Glu Phe Asp Phe Lys Gly Ser Pro Leu Gly Gly
165 170 175

Val Ile Thr Asn Tyr Leu Leu Glu Lys Ser Arg Leu Val Lys Gln Leu
180 185 190

Lys Gly Glu Arg Asn Phe His Ile Phe Tyr Gln Leu Leu Ala Gly Ala
195 200 205

ITI-08-PCT_Sequence_Listing_ST25.txt

Asp	Glu	Gln	Leu	Leu	Lys	Ala	Leu	Lys	Leu	Glu	Arg	Asp	Thr	Thr	Gly
210						215					220				
Tyr	Ala	Tyr	Leu	Asn	His	Glu	Val	Ser	Arg	Val	Asp	Gly	Met	Asp	Asp
225					230					235					240
Ala	Ser	Ser	Phe	Arg	Ala	Val	Gln	Ser	Ala	Met	Ala	Val	Ile	Gly	Phe
				245					250					255	
Ser	Glu	Glu	Glu	Ile	Arg	Gln	Val	Leu	Glu	Val	Thr	Ser	Met	Val	Leu
			260					265					270		
Lys	Leu	Gly	Asn	Val	Leu	Val	Ala	Asp	Glu	Phe	Gln	Ala	Ser	Gly	Ile
		275					280					285			
Pro	Ala	Ser	Gly	Ile	Arg	Asp	Gly	Arg	Gly	Val	Arg	Glu	Ile	Gly	Glu
	290					295					300				
Met	Val	Gly	Leu	Asn	Ser	Glu	Glu	Val	Glu	Arg	Ala	Leu	Cys	Ser	Arg
305					310					315					320
Thr	Met	Glu	Thr	Ala	Lys	Glu	Lys	Val	Val	Thr	Ala	Leu	Asn	Val	Met
				325					330					335	
Gln	Ala	Gln	Tyr	Ala	Arg	Asp	Ala	Leu	Ala	Lys	Asn	Ile	Tyr	Ser	Arg
			340					345					350		
Leu	Phe	Asp	Trp	Ile	Val	Asn	Arg	Ile	Asn	Glu	Ser	Ile	Lys	Val	Gly
		355					360					365			
Ile	Gly	Glu	Lys	Lys	Lys	Val	Met	Gly	Val	Leu	Asp	Ile	Tyr	Gly	Phe
	370					375					380				
Glu	Ile	Leu	Glu	Asp	Asn	Ser	Phe	Glu	Gln	Phe	Val	Ile	Asn	Tyr	Cys
385					390					395					400
Asn	Glu	Lys	Leu	Gln	Gln	Val	Phe	Ile	Glu	Met	Thr	Leu	Lys	Glu	Glu
				405					410					415	
Gln	Glu	Glu	Tyr	Lys	Arg	Glu	Gly	Ile	Pro	Trp	Thr	Lys	Val	Asp	Tyr
			420					425					430		
Phe	Asp	Asn	Gly	Ile	Ile	Cys	Lys	Leu	Ile	Glu	His	Asn	Gln	Arg	Gly
	435						440					445			
Ile	Leu	Ala	Met	Leu	Asp	Glu	Glu	Cys	Leu	Arg	Pro	Gly	Val	Val	Ser
	450					455					460				
Asp	Ser	Thr	Phe	Leu	Ala	Lys	Leu	Asn	Gln	Leu	Phe	Ser	Lys	His	Gly
465					470					475					480
His	Tyr	Glu	Ser	Lys	Val	Thr	Gln	Asn	Ala	Gln	Arg	Gln	Tyr	Asp	His

ITI-08-PCT_Sequence_Listing_ST25.txt

485

490

495

Thr Met Gly Leu Ser Cys Phe Arg Ile Cys His Tyr Ala Gly Lys Val
 500 505 510

Thr Tyr Asn Val Thr Ser Phe Ile Asp Lys Asn Asn Asp Leu Leu Phe
 515 520 525

Arg Asp Leu Leu Gln Ala Met Trp Lys Ala Gln His Pro Leu Leu Arg
 530 535 540

Ser Leu Phe Pro Glu Gly Asn Pro Lys Gln Ala Ser Leu Lys Arg Pro
 545 550 555 560

Pro Thr Ala Gly Ala Gln Phe Lys Ser Ser Val Ala Ile Leu Met Lys
 565 570 575

Asn Leu Tyr Ser Lys Ser Pro Asn Tyr Ile Arg Cys Ile Lys Pro Asn
 580 585 590

Glu His Gln Gln Arg Gly Gln Phe Ser Ser Asp Leu Val Ala Thr Gln
 595 600 605

Ala Arg Tyr Leu Gly Leu Leu Glu Asn Val Arg Val Arg Arg Ala Gly
 610 615 620

Tyr Ala His Arg Gln Gly Tyr Gly Pro Phe Leu Glu Arg Tyr Arg Leu
 625 630 635 640

Leu Ser Arg Ser Thr Trp Pro His Trp Asn Gly Gly Asp Arg Glu Gly
 645 650 655

Val Glu Lys Val Leu Gly Glu Leu Ser Met Ser Ser Gly Glu Leu Ala
 660 665 670

Phe Gly Lys Thr Lys Ile Phe Ile Arg Ser Pro Lys Thr Leu Phe Tyr
 675 680 685

Leu Glu Glu Gln Arg Arg Leu Arg Leu Gln Gln Leu Ala Thr Leu Ile
 690 695 700

Gln Lys Ile Tyr Arg Gly Trp Arg Cys Arg Thr His Tyr Gln Leu Met
 705 710 715 720

Arg Lys Ser Gln Ile Leu Ile Ser Ser Trp Phe Arg Gly Asn Met Gln
 725 730 735

Lys Lys Cys Tyr Gly Lys Ile Lys Ala Ser Val Leu Leu Ile Gln Ala
 740 745 750

Phe Val Arg Gly Trp Lys Ala Arg Lys Asn Tyr Arg Lys Tyr Phe Arg
 755 760 765

ITI-08-PCT_Sequence_Listing_ST25.txt

```

Ser Glu Ala Ala Leu Thr Leu Ala Asp Phe Ile Tyr Lys Ser Met Val
 770                775                780

Gln Lys Phe Leu Leu Gly Leu Lys Asn Asn Leu Pro Ser Thr Asn Val
 785                790                795                800

Leu Asp Lys Thr Trp Pro Ala Ala Pro Tyr Lys Cys Leu Ser Thr Ala
                805                810                815

Asn Gln Glu Leu Gln Gln Leu Phe Tyr Gln Trp Lys Cys Lys Arg Phe
                820                825                830

Arg Asp Gln Leu Ser Pro Lys Gln Val Glu Ile Leu Arg Glu Lys Leu
 835                840                845

Cys Ala Ser Glu Leu Phe Lys Gly Lys Lys Ala Ser Tyr Pro Gln Ser
 850                855                860

Val Pro Ile Pro Phe Cys Gly Asp Tyr Ile Gly Leu Gln Gly Asn Pro
 865                870                875                880

Lys Leu Gln Lys Leu Lys Gly Gly Glu Glu Gly Pro Val Leu Met Ala
                885                890                895

Glu Ala Val Lys Lys Val Asn Arg Gly Asn Gly Lys Thr Ser Ser Arg
 900                905                910

Ile Leu Leu Leu Thr Lys Gly His Val Ile Leu Thr Asp Thr Lys Lys
 915                920                925

Ser Gln Ala Lys Ile Val Ile Gly Leu Asp Asn Val Ala Gly Val Ser
 930                935                940

Val Thr Ser Leu Lys Asp Gly Leu Phe Ser Leu His Leu Ser Glu Met
 945                950                955                960

Ser Ser Val Gly Ser Lys Gly Asp Phe Leu Leu Val Ser Glu His Val
                965                970                975

Ile Glu Leu Leu Thr Lys Met Tyr Arg Ala Val Leu Asp Ala Thr Gln
 980                985                990

Arg Gln Leu Thr Val Thr Val Thr Glu Lys Phe Ser Val Arg Phe Lys
 995                1000                1005

Glu Asn Ser Val Ala Val Lys Val Val Gln Gly Pro Ala Gly Gly
 1010                1015                1020

Asp Asn Ser Lys Leu Arg Tyr Lys Lys Lys Gly Ser His Cys Leu
 1025                1030                1035

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Glu Val Thr Val Gln
1040

<210> 541
<211> 1136
<212> PRT
<213> Artificial Sequence

<220>
<223> MY01B__Homo_sapiens__043795

<400> 541

Met Ala Lys Met Glu Val Lys Thr Ser Leu Leu Asp Asn Met Ile Gly
1 5 10 15

Val Gly Asp Met Val Leu Leu Glu Pro Leu Asn Glu Glu Thr Phe Ile
20 25 30

Asn Asn Leu Lys Lys Arg Phe Asp His Ser Glu Ile Tyr Thr Tyr Ile
35 40 45

Gly Ser Val Val Ile Ser Val Asn Pro Tyr Arg Ser Leu Pro Ile Tyr
50 55 60

Ser Pro Glu Lys Val Glu Glu Tyr Arg Asn Arg Asn Phe Tyr Glu Leu
65 70 75 80

Ser Pro His Ile Phe Ala Leu Ser Asp Glu Ala Tyr Arg Ser Leu Arg
85 90 95

Asp Gln Asp Lys Asp Gln Cys Ile Leu Ile Thr Gly Glu Ser Gly Ala
100 105 110

Gly Lys Thr Glu Ala Ser Lys Leu Val Met Ser Tyr Val Ala Ala Val
115 120 125

Cys Gly Lys Gly Ala Glu Val Asn Gln Val Lys Glu Gln Leu Leu Gln
130 135 140

Ser Asn Pro Val Leu Glu Ala Phe Gly Asn Ala Lys Thr Val Arg Asn
145 150 155 160

Asp Asn Ser Ser Arg Phe Gly Lys Tyr Met Asp Ile Glu Phe Asp Phe
165 170 175

Lys Gly Asp Pro Leu Gly Gly Val Ile Ser Asn Tyr Leu Leu Glu Lys
180 185 190

Ser Arg Val Val Lys Gln Pro Arg Gly Glu Arg Asn Phe His Val Phe
195 200 205

ITI-08-PCT_Sequence_Listing_ST25.txt

Tyr	Gln	Leu	Leu	Ser	Gly	Ala	Ser	Glu	Glu	Leu	Leu	Asn	Lys	Leu	Lys	210	215	220	
Leu	Glu	Arg	Asp	Phe	Ser	Arg	Tyr	Asn	Tyr	Leu	Ser	Leu	Asp	Ser	Ala	225	230	235	240
Lys	Val	Asn	Gly	Val	Asp	Asp	Ala	Ala	Asn	Phe	Arg	Thr	Val	Arg	Asn	245	250	255	
Ala	Met	Gln	Ile	Val	Gly	Phe	Met	Asp	His	Glu	Ala	Glu	Ser	Val	Leu	260	265	270	
Ala	Val	Val	Ala	Ala	Val	Leu	Lys	Leu	Gly	Asn	Ile	Glu	Phe	Lys	Pro	275	280	285	
Glu	Ser	Arg	Val	Asn	Gly	Leu	Asp	Glu	Ser	Lys	Ile	Lys	Asp	Lys	Asn	290	295	300	
Glu	Leu	Lys	Glu	Ile	Cys	Glu	Leu	Thr	Gly	Ile	Asp	Gln	Ser	Val	Leu	305	310	315	320
Glu	Arg	Ala	Phe	Ser	Phe	Arg	Thr	Val	Glu	Ala	Lys	Gln	Glu	Lys	Val	325	330	335	
Ser	Thr	Thr	Leu	Asn	Val	Ala	Gln	Ala	Tyr	Tyr	Ala	Arg	Asp	Ala	Leu	340	345	350	
Ala	Lys	Asn	Leu	Tyr	Ser	Arg	Leu	Phe	Ser	Trp	Leu	Val	Asn	Arg	Ile	355	360	365	
Asn	Glu	Ser	Ile	Lys	Ala	Gln	Thr	Lys	Val	Arg	Lys	Lys	Val	Met	Gly	370	375	380	
Val	Leu	Asp	Ile	Tyr	Gly	Phe	Glu	Ile	Phe	Glu	Asp	Asn	Ser	Phe	Glu	385	390	395	400
Gln	Phe	Ile	Ile	Asn	Tyr	Cys	Asn	Glu	Lys	Leu	Gln	Gln	Ile	Phe	Ile	405	410	415	
Glu	Leu	Thr	Leu	Lys	Glu	Glu	Gln	Glu	Glu	Tyr	Ile	Arg	Glu	Asp	Ile	420	425	430	
Glu	Trp	Thr	His	Ile	Asp	Tyr	Phe	Asn	Asn	Ala	Ile	Ile	Cys	Asp	Leu	435	440	445	
Ile	Glu	Asn	Asn	Thr	Asn	Gly	Ile	Leu	Ala	Met	Leu	Asp	Glu	Glu	Cys	450	455	460	
Leu	Arg	Pro	Gly	Thr	Val	Thr	Asp	Glu	Thr	Phe	Leu	Glu	Lys	Leu	Asn	465	470	475	480
Gln	Val	Cys	Ala	Thr	His	Gln	His	Phe	Glu	Ser	Arg	Met	Ser	Lys	Cys				

ITI-08-PCT_Sequence_Listing_ST25.txt

485

490

495

Ser Arg Phe Leu Asn Asp Thr Ser Leu Pro His Ser Cys Phe Arg Ile
500 505 510

Gln His Tyr Ala Gly Lys Val Leu Tyr Gln Val Glu Gly Phe Val Asp
515 520 525

Lys Asn Asn Asp Leu Leu Tyr Arg Asp Leu Ser Gln Ala Met Trp Lys
530 535 540

Ala Ser His Ala Leu Ile Lys Ser Leu Phe Pro Glu Gly Asn Pro Ala
545 550 555 560

Lys Ile Asn Leu Lys Arg Pro Pro Thr Ala Gly Ser Gln Phe Lys Ala
565 570 575

Ser Val Ala Thr Leu Met Lys Asn Leu Gln Thr Lys Asn Pro Asn Tyr
580 585 590

Ile Arg Cys Ile Lys Pro Asn Asp Lys Lys Ala Ala His Ile Phe Asn
595 600 605

Glu Ala Leu Val Cys His Gln Ile Arg Tyr Leu Gly Leu Leu Glu Asn
610 615 620

Val Arg Val Arg Arg Ala Gly Tyr Ala Phe Arg Gln Ala Tyr Glu Pro
625 630 635 640

Cys Leu Glu Arg Tyr Lys Met Leu Cys Lys Gln Thr Trp Pro His Trp
645 650 655

Lys Gly Pro Ala Arg Ser Gly Val Glu Val Leu Phe Asn Glu Leu Glu
660 665 670

Ile Pro Val Glu Glu Tyr Ser Phe Gly Arg Ser Lys Ile Phe Ile Arg
675 680 685

Asn Pro Arg Thr Leu Phe Lys Leu Glu Asp Leu Arg Lys Gln Arg Leu
690 695 700

Glu Asp Leu Ala Thr Leu Ile Gln Lys Ile Tyr Arg Gly Trp Lys Cys
705 710 715 720

Arg Thr His Phe Leu Leu Met Lys Lys Ser Gln Ile Val Ile Ala Ala
725 730 735

Trp Tyr Arg Arg Tyr Ala Gln Gln Lys Arg Tyr Gln Gln Thr Lys Ser
740 745 750

Ser Ala Leu Val Ile Gln Ser Tyr Ile Arg Gly Trp Lys Ala Arg Lys
755 760 765

ITI-08-PCT_Sequence_Listing_ST25.txt

```

Ile Leu Arg Glu Leu Lys His Gln Lys Arg Cys Lys Glu Ala Val Thr
 770                      775                      780

Thr Ile Ala Ala Tyr Trp His Gly Thr Gln Ala Arg Arg Glu Leu Arg
785                      790                      795                      800

Arg Leu Lys Glu Glu Ala Arg Asn Lys His Ala Ile Ala Val Ile Trp
                        805                      810                      815

Ala Tyr Trp Leu Gly Ser Lys Ala Arg Arg Glu Leu Lys Arg Leu Lys
                        820                      825                      830

Glu Glu Ala Arg Arg Lys His Ala Val Ala Val Ile Trp Ala Tyr Trp
      835                      840                      845

Leu Gly Leu Lys Val Arg Arg Glu Tyr Arg Lys Phe Phe Arg Ala Asn
      850                      855                      860

Ala Gly Lys Lys Ile Tyr Glu Phe Thr Leu Gln Arg Ile Val Gln Lys
865                      870                      875                      880

Tyr Phe Leu Glu Met Lys Asn Lys Met Pro Ser Leu Ser Pro Ile Asp
                        885                      890                      895

Lys Asn Trp Pro Ser Arg Pro Tyr Leu Phe Leu Asp Ser Thr His Lys
                        900                      905                      910

Glu Leu Lys Arg Ile Phe His Leu Trp Arg Cys Lys Lys Tyr Arg Asp
      915                      920                      925

Gln Phe Thr Asp Gln Gln Lys Leu Ile Tyr Glu Glu Lys Leu Glu Ala
      930                      935                      940

Ser Glu Leu Phe Lys Asp Lys Lys Ala Leu Tyr Pro Ser Ser Val Gly
945                      950                      955                      960

Gln Pro Phe Gln Gly Ala Tyr Leu Glu Ile Asn Lys Asn Pro Lys Tyr
                        965                      970                      975

Lys Lys Leu Lys Asp Ala Ile Glu Glu Lys Ile Ile Ile Ala Glu Val
      980                      985                      990

Val Asn Lys Ile Asn Arg Ala Asn Gly Lys Ser Thr Ser Arg Ile Phe
      995                      1000                      1005

Leu Leu Thr Asn Asn Asn Leu Leu Leu Ala Asp Gln Lys Ser Gly
1010                      1015                      1020

Gln Ile Lys Ser Glu Val Pro Leu Val Asp Val Thr Lys Val Ser
1025                      1030                      1035

```

ITI-08-PCT_Sequence_Listing_ST25.txt

```

Met Ser  Ser Gln Asn Asp Gly  Phe Phe Ala Val His  Leu Lys Glu
 1040                      1045                      1050

Gly Ser  Glu Ala Ala Ser Lys  Gly Asp Phe Leu Phe  Ser Ser Asp
 1055                      1060                      1065

His Leu  Ile Glu Met Ala Thr  Lys Leu Tyr Arg Thr  Thr Leu Ser
 1070                      1075                      1080

Gln Thr  Lys Gln Lys Leu Asn  Ile Glu Ile Ser Asp  Glu Phe Leu
 1085                      1090                      1095

Val Gln  Phe Arg Gln Asp Lys  Val Cys Val Lys Phe  Ile Gln Gly
 1100                      1105                      1110

Asn Gln  Lys Asn Gly Ser Val  Pro Thr Cys Lys Arg  Lys Asn Asn
 1115                      1120                      1125

Arg Leu  Leu Glu Val Ala Val  Pro
 1130                      1135

<210>  542
<211>  1063
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  MY01C__Homo_sapiens__000159

<400>  542

Met Ala Leu Gln Val Glu Leu Val Pro Thr Gly Glu Ile Ile Arg Val
1                      5                      10                      15

Val His Pro His Arg Pro Cys Lys Leu Ala Leu Gly Ser Asp Gly Val
                20                      25                      30

Arg Val Thr Met Glu Ser Ala Leu Thr Ala Arg Asp Arg Val Gly Val
        35                      40                      45

Gln Asp Phe Val Leu Leu Glu Asn Phe Thr Ser Glu Ala Ala Phe Ile
50                      55                      60

Glu Asn Leu Arg Arg Arg Phe Arg Glu Asn Leu Ile Tyr Thr Tyr Ile
65                      70                      75                      80

Gly Pro Val Leu Val Ser Val Asn Pro Tyr Arg Asp Leu Gln Ile Tyr
                85                      90                      95

Ser Arg Gln His Met Glu Arg Tyr Arg Gly Val Ser Phe Tyr Glu Val
        100                      105                      110

```

Pro	Pro	His	Leu	Phe	Ala	Val	Ala	Asp	Thr	Val	Tyr	Arg	Ala	Leu	Arg
		115					120					125			
Thr	Glu	Arg	Arg	Asp	Gln	Ala	Val	Met	Ile	Ser	Gly	Glu	Ser	Gly	Ala
	130					135					140				
Gly	Lys	Thr	Glu	Ala	Thr	Lys	Arg	Leu	Leu	Gln	Phe	Tyr	Ala	Glu	Thr
145					150					155					160
Cys	Pro	Ala	Pro	Glu	Arg	Gly	Gly	Ala	Val	Arg	Asp	Arg	Leu	Leu	Gln
				165					170					175	
Ser	Asn	Pro	Val	Leu	Glu	Ala	Phe	Gly	Asn	Ala	Lys	Thr	Leu	Arg	Asn
			180					185					190		
Asp	Asn	Ser	Ser	Arg	Phe	Gly	Lys	Tyr	Met	Asp	Val	Gln	Phe	Asp	Phe
	195						200					205			
Lys	Gly	Ala	Pro	Val	Gly	Gly	His	Ile	Leu	Ser	Tyr	Leu	Leu	Glu	Lys
	210					215					220				
Ser	Arg	Val	Val	His	Gln	Asn	His	Gly	Glu	Arg	Asn	Phe	His	Ile	Phe
225					230					235					240
Tyr	Gln	Leu	Leu	Glu	Gly	Gly	Glu	Glu	Glu	Thr	Leu	Arg	Arg	Leu	Gly
				245					250					255	
Leu	Glu	Arg	Asn	Pro	Gln	Ser	Tyr	Leu	Tyr	Leu	Val	Lys	Gly	Gln	Cys
			260					265					270		
Ala	Lys	Val	Ser	Ser	Ile	Asn	Asp	Lys	Ser	Asp	Trp	Lys	Val	Val	Arg
	275						280					285			
Lys	Ala	Leu	Thr	Val	Ile	Asp	Phe	Thr	Glu	Asp	Glu	Val	Glu	Asp	Leu
	290					295					300				
Leu	Ser	Ile	Val	Ala	Ser	Val	Leu	His	Leu	Gly	Asn	Ile	His	Phe	Ala
305					310					315					320
Ala	Asn	Glu	Glu	Ser	Asn	Ala	Gln	Val	Thr	Thr	Glu	Asn	Gln	Leu	Lys
				325					330					335	
Tyr	Leu	Thr	Arg	Leu	Leu	Ser	Val	Glu	Gly	Ser	Thr	Leu	Arg	Glu	Ala
			340					345					350		
Leu	Thr	His	Arg	Lys	Ile	Ile	Ala	Lys	Gly	Glu	Glu	Leu	Leu	Ser	Pro
		355					360					365			
Leu	Asn	Leu	Glu	Gln	Ala	Ala	Tyr	Ala	Arg	Asp	Ala	Leu	Ala	Lys	Ala
	370					375					380				
Val	Tyr	Ser	Arg	Thr	Phe	Thr	Trp	Leu	Val	Gly	Lys	Ile	Asn	Arg	Ser

ITI-08-PCT_Sequence_Listing_ST25.txt

```

385          390          395          400
Leu Ala Ser Lys Asp Val Glu Ser Pro Ser Trp Arg Ser Thr Thr Val
          405          410          415
Leu Gly Leu Leu Asp Ile Tyr Gly Phe Glu Val Phe Gln His Asn Ser
          420          425          430
Phe Glu Gln Phe Cys Ile Asn Tyr Cys Asn Glu Lys Leu Gln Gln Leu
          435          440          445
Phe Ile Glu Leu Thr Leu Lys Ser Glu Gln Glu Glu Tyr Glu Ala Glu
          450          455          460
Gly Ile Ala Trp Glu Pro Val Gln Tyr Phe Asn Asn Lys Ile Ile Cys
465          470          475          480
Asp Leu Val Glu Glu Lys Phe Lys Gly Ile Ile Ser Ile Leu Asp Glu
          485          490          495
Glu Cys Leu Arg Pro Gly Glu Ala Thr Asp Leu Thr Phe Leu Glu Lys
          500          505          510
Leu Glu Asp Thr Val Lys His His Pro His Phe Leu Thr His Lys Leu
          515          520          525
Ala Asp Gln Arg Thr Arg Lys Ser Leu Gly Arg Gly Glu Phe Arg Leu
          530          535          540
Leu His Tyr Ala Gly Glu Val Thr Tyr Ser Val Thr Gly Phe Leu Asp
545          550          555          560
Lys Asn Asn Asp Leu Leu Phe Arg Asn Leu Lys Glu Thr Met Cys Ser
          565          570          575
Ser Lys Asn Pro Ile Met Ser Gln Cys Phe Asp Arg Ser Glu Leu Ser
          580          585          590
Asp Lys Lys Arg Pro Glu Thr Val Ala Thr Gln Phe Lys Met Ser Leu
          595          600          605
Leu Gln Leu Val Glu Ile Leu Gln Ser Lys Glu Pro Ala Tyr Val Arg
          610          615          620
Cys Ile Lys Pro Asn Asp Ala Lys Gln Pro Gly Arg Phe Asp Glu Val
625          630          635          640
Leu Ile Arg His Gln Val Lys Tyr Leu Gly Leu Leu Glu Asn Leu Arg
          645          650          655
Val Arg Arg Ala Gly Phe Ala Tyr Arg Arg Lys Tyr Glu Ala Phe Leu
          660          665          670

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Gln	Arg	Tyr	Lys	Ser	Leu	Cys	Pro	Glu	Thr	Trp	Pro	Thr	Trp	Ala	Gly
675						680						685			
Arg	Pro	Gln	Asp	Gly	Val	Ala	Val	Leu	Val	Arg	His	Leu	Gly	Tyr	Lys
690						695				700					
Pro	Glu	Glu	Tyr	Lys	Met	Gly	Arg	Thr	Lys	Ile	Phe	Ile	Arg	Phe	Pro
705				710						715				720	
Lys	Thr	Leu	Phe	Ala	Thr	Glu	Asp	Ala	Leu	Glu	Val	Arg	Arg	Gln	Ser
				725				730						735	
Leu	Ala	Thr	Lys	Ile	Gln	Ala	Ala	Trp	Arg	Gly	Phe	His	Trp	Arg	Gln
		740						745				750			
Lys	Phe	Leu	Arg	Val	Lys	Arg	Ser	Ala	Ile	Cys	Ile	Gln	Ser	Trp	Trp
755						760						765			
Arg	Gly	Thr	Leu	Gly	Arg	Arg	Lys	Ala	Ala	Lys	Arg	Lys	Trp	Ala	Ala
770						775				780					
Gln	Thr	Ile	Arg	Arg	Leu	Ile	Arg	Gly	Phe	Val	Leu	Arg	His	Ala	Pro
785				790						795				800	
Arg	Cys	Pro	Glu	Asn	Ala	Phe	Phe	Leu	Asp	His	Val	Arg	Thr	Ser	Phe
				805				810						815	
Leu	Leu	Asn	Leu	Arg	Arg	Gln	Leu	Pro	Gln	Asn	Val	Leu	Asp	Thr	Ser
		820						825				830			
Trp	Pro	Thr	Pro	Pro	Pro	Ala	Leu	Arg	Glu	Ala	Ser	Glu	Leu	Leu	Arg
		835				840						845			
Glu	Leu	Cys	Ile	Lys	Asn	Met	Val	Trp	Lys	Tyr	Cys	Arg	Ser	Ile	Ser
850						855				860					
Pro	Glu	Trp	Lys	Gln	Gln	Leu	Gln	Gln	Lys	Ala	Val	Ala	Ser	Glu	Ile
865				870						875				880	
Phe	Lys	Gly	Lys	Lys	Asp	Asn	Tyr	Pro	Gln	Ser	Val	Pro	Arg	Leu	Phe
				885				890						895	
Ile	Ser	Thr	Arg	Leu	Gly	Thr	Asp	Glu	Ile	Ser	Pro	Arg	Val	Leu	Gln
		900						905				910			
Ala	Leu	Gly	Ser	Glu	Pro	Ile	Gln	Tyr	Ala	Val	Pro	Val	Val	Lys	Tyr
		915				920						925			
Asp	Arg	Lys	Gly	Tyr	Lys	Pro	Arg	Ser	Arg	Gln	Leu	Leu	Leu	Thr	Pro
930						935				940					

ITI-08-PCT_Sequence_Listing_ST25.txt

Asn Ala Val Val Ile Val Glu Asp Ala Lys Val Lys Gln Arg Ile Asp
945 950 955 960

Tyr Ala Asn Leu Thr Gly Ile Ser Val Ser Ser Leu Ser Asp Ser Leu
965 970 975

Phe Val Leu His Val Gln Arg Ala Asp Asn Lys Gln Lys Gly Asp Val
980 985 990

Val Leu Gln Ser Asp His Val Ile Glu Thr Leu Thr Lys Thr Ala Leu
995 1000 1005

Ser Ala Asn Arg Val Asn Ser Ile Asn Ile Asn Gln Gly Ser Ile
1010 1015 1020

Thr Phe Ala Gly Gly Pro Gly Arg Asp Gly Thr Ile Asp Phe Thr
1025 1030 1035

Pro Gly Ser Glu Leu Leu Ile Thr Lys Ala Lys Asn Gly His Leu
1040 1045 1050

Ala Val Val Ala Pro Arg Leu Asn Ser Arg
1055 1060

<210> 543

<211> 1006

<212> PRT

<213> Artificial Sequence

<220>

<223> MY01D__Homo_sapiens__094832

<400> 543

Met Ala Glu Gln Glu Ser Leu Glu Phe Gly Lys Ala Asp Phe Val Leu
1 5 10 15

Met Asp Thr Val Ser Met Pro Glu Phe Met Ala Asn Leu Arg Leu Arg
20 25 30

Phe Glu Lys Gly Arg Ile Tyr Thr Phe Ile Gly Glu Val Val Val Ser
35 40 45

Val Asn Pro Tyr Lys Leu Leu Asn Ile Tyr Gly Arg Asp Thr Ile Glu
50 55 60

Gln Tyr Lys Gly Arg Glu Leu Tyr Glu Arg Pro Pro His Leu Phe Ala
65 70 75 80

Ile Ala Asp Ala Ala Tyr Lys Ala Met Lys Arg Arg Ser Lys Asp Thr
85 90 95

ITI-08-PCT_Sequence_Listing_ST25.txt

Cys Ile Val Ile Ser Gly Glu Ser Gly Ala Gly Lys Thr Glu Ala Ser
 100 105 110
 Lys Tyr Ile Met Gln Tyr Ile Ala Ala Ile Thr Asn Pro Ser Gln Arg
 115 120 125
 Ala Glu Val Glu Arg Val Lys Asn Met Leu Leu Lys Ser Asn Cys Val
 130 135 140
 Leu Glu Ala Phe Gly Asn Ala Lys Thr Asn Arg Asn Asp Asn Ser Ser
 145 150 155 160
 Arg Phe Gly Lys Tyr Met Asp Ile Asn Phe Asp Phe Lys Gly Asp Pro
 165 170 175
 Ile Gly Gly His Ile Asn Asn Tyr Leu Leu Glu Lys Ser Arg Val Ile
 180 185 190
 Val Gln Gln Pro Gly Glu Arg Ser Phe His Ser Phe Tyr Gln Leu Leu
 195 200 205
 Gln Gly Gly Ser Glu Gln Met Leu Arg Ser Leu His Leu Gln Lys Ser
 210 215 220
 Leu Ser Ser Tyr Asn Tyr Ile His Val Gly Ala Gln Leu Lys Ser Ser
 225 230 235 240
 Ile Asn Asp Ala Ala Glu Phe Arg Val Val Ala Asp Ala Met Lys Val
 245 250 255
 Ile Gly Phe Lys Pro Glu Glu Ile Gln Thr Val Tyr Lys Ile Leu Ala
 260 265 270
 Ala Ile Leu His Leu Gly Asn Leu Lys Phe Val Val Asp Gly Asp Thr
 275 280 285
 Pro Leu Ile Glu Asn Gly Lys Val Val Ser Ile Ile Ala Glu Leu Leu
 290 295 300
 Ser Thr Lys Thr Asp Met Val Glu Lys Ala Leu Leu Tyr Arg Thr Val
 305 310 315 320
 Ala Thr Gly Arg Asp Ile Ile Asp Lys Gln His Thr Glu Gln Glu Ala
 325 330 335
 Ser Tyr Gly Arg Asp Ala Phe Ala Lys Ala Ile Tyr Glu Arg Leu Phe
 340 345 350
 Cys Trp Ile Val Thr Arg Ile Asn Asp Ile Ile Glu Val Lys Asn Tyr
 355 360 365
 Asp Thr Thr Ile His Gly Lys Asn Thr Val Ile Gly Val Leu Asp Ile

ITI-08-PCT_Sequence_Listing_ST25.txt

```

370          375          380
Tyr Gly Phe Glu Ile Phe Asp Asn Asn Ser Phe Glu Gln Phe Cys Ile
385          390          395          400
Asn Tyr Cys Asn Glu Lys Leu Gln Gln Leu Phe Ile Gln Leu Val Leu
          405          410          415
Lys Gln Glu Gln Glu Glu Tyr Gln Arg Glu Gly Ile Pro Trp Lys His
          420          425          430
Ile Asp Tyr Phe Asn Asn Gln Ile Ile Val Asp Leu Val Glu Gln Gln
          435          440          445
His Lys Gly Ile Ile Ala Ile Leu Asp Asp Ala Cys Met Asn Val Gly
          450          455          460
Lys Val Thr Asp Glu Met Phe Leu Glu Ala Leu Asn Ser Lys Leu Gly
465          470          475          480
Lys His Ala His Phe Ser Ser Arg Lys Leu Cys Ala Ser Asp Lys Ile
          485          490          495
Leu Glu Phe Asp Arg Asp Phe Arg Ile Arg His Tyr Ala Gly Asp Val
          500          505          510
Val Tyr Ser Val Ile Gly Phe Ile Asp Lys Asn Lys Asp Thr Leu Phe
          515          520          525
Gln Asp Phe Lys Arg Leu Met Tyr Asn Ser Ser Asn Pro Val Leu Lys
          530          535          540
Asn Met Trp Pro Glu Gly Lys Leu Ser Ile Thr Glu Val Thr Lys Arg
545          550          555          560
Pro Leu Thr Ala Ala Thr Leu Phe Lys Asn Ser Met Ile Ala Leu Val
          565          570          575
Asp Asn Leu Ala Ser Lys Glu Pro Tyr Tyr Val Arg Cys Ile Lys Pro
          580          585          590
Asn Asp Lys Lys Ser Pro Gln Ile Phe Asp Asp Glu Arg Cys Arg His
          595          600          605
Gln Val Glu Tyr Leu Gly Leu Leu Glu Asn Val Arg Val Arg Arg Ala
          610          615          620
Gly Phe Ala Phe Arg Gln Thr Tyr Glu Lys Phe Leu His Arg Tyr Lys
625          630          635          640
Met Ile Ser Glu Phe Thr Trp Pro Asn His Asp Leu Pro Ser Asp Lys
          645          650          655

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Glu	Ala	Val	Lys	Lys	Leu	Ile	Glu	Arg	Cys	Gly	Phe	Gln	Asp	Asp	Val	660	665	670
Ala	Tyr	Gly	Lys	Thr	Lys	Ile	Phe	Ile	Arg	Thr	Pro	Arg	Thr	Leu	Phe	675	680	685
Thr	Leu	Glu	Glu	Leu	Arg	Ala	Gln	Met	Leu	Ile	Arg	Ile	Val	Leu	Phe	690	695	700
Leu	Gln	Lys	Val	Trp	Arg	Gly	Thr	Leu	Ala	Arg	Met	Arg	Tyr	Lys	Arg	705	710	715
Thr	Lys	Ala	Ala	Leu	Thr	Ile	Ile	Arg	Tyr	Tyr	Arg	Arg	Tyr	Lys	Val	725	730	735
Lys	Ser	Tyr	Ile	His	Glu	Val	Ala	Arg	Arg	Phe	His	Gly	Val	Lys	Thr	740	745	750
Met	Arg	Asp	Tyr	Gly	Lys	His	Val	Lys	Trp	Pro	Ser	Pro	Pro	Lys	Val	755	760	765
Leu	Arg	Arg	Phe	Glu	Glu	Ala	Leu	Gln	Thr	Ile	Phe	Asn	Arg	Trp	Arg	770	775	780
Ala	Ser	Gln	Leu	Ile	Lys	Ser	Ile	Pro	Ala	Ser	Asp	Leu	Pro	Gln	Val	785	790	795
Arg	Ala	Lys	Val	Ala	Ala	Val	Glu	Met	Leu	Lys	Gly	Gln	Arg	Ala	Asp	805	810	815
Leu	Gly	Leu	Gln	Arg	Ala	Trp	Glu	Gly	Asn	Tyr	Leu	Ala	Ser	Lys	Pro	820	825	830
Asp	Thr	Pro	Gln	Thr	Ser	Gly	Thr	Phe	Val	Pro	Val	Ala	Asn	Glu	Leu	835	840	845
Lys	Arg	Lys	Asp	Lys	Tyr	Met	Asn	Val	Leu	Phe	Ser	Cys	His	Val	Arg	850	855	860
Lys	Val	Asn	Arg	Phe	Ser	Lys	Val	Glu	Asp	Arg	Ala	Ile	Phe	Val	Thr	865	870	875
Asp	Arg	His	Leu	Tyr	Lys	Met	Asp	Pro	Thr	Lys	Gln	Tyr	Lys	Val	Met	885	890	895
Lys	Thr	Ile	Pro	Leu	Tyr	Asn	Leu	Thr	Gly	Leu	Ser	Val	Ser	Asn	Gly	900	905	910
Lys	Asp	Gln	Leu	Val	Val	Phe	His	Thr	Lys	Asp	Asn	Lys	Asp	Leu	Ile	915	920	925

ITI-08-PCT_Sequence_Listing_ST25.txt

Val Cys Leu Phe Ser Lys Gln Pro Thr His Glu Ser Arg Ile Gly Glu
930 935 940

Leu Val Gly Val Leu Val Asn His Phe Lys Ser Glu Lys Arg His Leu
945 950 955 960

Gln Val Asn Val Thr Asn Pro Val Gln Cys Ser Leu His Gly Lys Lys
965 970 975

Cys Thr Val Ser Val Glu Thr Arg Leu Asn Gln Pro Gln Pro Asp Phe
980 985 990

Thr Lys Asn Arg Ser Gly Phe Ile Leu Ser Val Pro Gly Asn
995 1000 1005

<210> 544

<211> 1108

<212> PRT

<213> Artificial Sequence

<220>

<223> MY01E__Homo_sapiens__Q12965

<400> 544

Met Gly Ser Lys Gly Val Tyr Gln Tyr His Trp Gln Ser His Asn Val
1 5 10 15

Lys His Ser Gly Val Asp Asp Met Val Leu Leu Ser Lys Ile Thr Glu
20 25 30

Asn Ser Ile Val Glu Asn Leu Lys Lys Arg Tyr Met Asp Asp Tyr Ile
35 40 45

Phe Thr Tyr Ile Gly Ser Val Leu Ile Ser Val Asn Pro Phe Lys Gln
50 55 60

Met Pro Tyr Phe Gly Glu Lys Glu Ile Glu Met Tyr Gln Gly Ala Ala
65 70 75 80

Gln Tyr Glu Asn Pro Pro His Ile Tyr Ala Leu Ala Asp Asn Met Tyr
85 90 95

Arg Asn Met Ile Ile Asp Arg Glu Asn Gln Cys Val Ile Ile Ser Gly
100 105 110

Glu Ser Gly Ala Gly Lys Thr Val Ala Ala Lys Tyr Ile Met Ser Tyr
115 120 125

Ile Ser Arg Val Ser Gly Gly Gly Thr Lys Val Gln His Val Lys Asp
130 135 140

ITI-08-PCT_Sequence_Listing_ST25.txt

Ile	Ile	Leu	Gln	Ser	Asn	Pro	Leu	Leu	Glu	Ala	Phe	Gly	Asn	Ala	Lys	145	150	155	160
Thr	Val	Arg	Asn	Asn	Asn	Ser	Ser	Arg	Phe	Gly	Lys	Tyr	Phe	Glu	Ile	165	170	175	
Gln	Phe	Ser	Pro	Gly	Gly	Glu	Pro	Asp	Gly	Gly	Lys	Ile	Ser	Asn	Phe	180	185	190	
Leu	Leu	Glu	Lys	Ser	Arg	Val	Val	Met	Arg	Asn	Pro	Gly	Glu	Arg	Ser	195	200	205	
Phe	His	Ile	Phe	Tyr	Gln	Leu	Ile	Glu	Gly	Ala	Ser	Ala	Glu	Gln	Lys	210	215	220	
His	Ser	Leu	Gly	Ile	Thr	Ser	Met	Asp	Tyr	Tyr	Tyr	Tyr	Leu	Ser	Leu	225	230	235	240
Ser	Gly	Ser	Tyr	Lys	Val	Asp	Asp	Ile	Asp	Asp	Arg	Arg	Glu	Phe	Gln	245	250	255	
Glu	Thr	Leu	His	Ala	Met	Asn	Val	Ile	Gly	Ile	Phe	Ala	Glu	Glu	Gln	260	265	270	
Thr	Leu	Val	Leu	Gln	Ile	Val	Ala	Gly	Ile	Leu	His	Leu	Gly	Asn	Ile	275	280	285	
Ser	Phe	Lys	Glu	Val	Gly	Asn	Tyr	Ala	Ala	Val	Glu	Ser	Glu	Glu	Phe	290	295	300	
Leu	Ala	Phe	Pro	Ala	Tyr	Leu	Leu	Gly	Ile	Asn	Gln	Asp	Arg	Leu	Lys	305	310	315	320
Glu	Lys	Leu	Thr	Ser	Arg	Gln	Met	Asp	Ser	Lys	Trp	Gly	Gly	Lys	Ser	325	330	335	
Glu	Ser	Ile	His	Val	Thr	Leu	Asn	Val	Glu	Gln	Ala	Cys	Tyr	Thr	Arg	340	345	350	
Asp	Ala	Leu	Ala	Lys	Ala	Leu	His	Ala	Arg	Val	Phe	Asp	Phe	Leu	Val	355	360	365	
Asp	Ser	Ile	Asn	Lys	Ala	Met	Glu	Lys	Asp	His	Glu	Glu	Tyr	Asn	Ile	370	375	380	
Gly	Val	Leu	Asp	Ile	Tyr	Gly	Phe	Glu	Ile	Phe	Gln	Lys	Asn	Gly	Phe	385	390	395	400
Glu	Gln	Phe	Cys	Ile	Asn	Phe	Val	Asn	Glu	Lys	Leu	Gln	Gln	Ile	Phe	405	410	415	
Ile	Glu	Leu	Thr	Leu	Lys	Ala	Glu	Gln	Glu	Glu	Tyr	Val	Gln	Glu	Gly				

ITI-08-PCT_Sequence_Listing_ST25.txt

```

420
Ile Arg Trp Thr Pro Ile Glu Tyr Phe Asn Asn Lys Ile Val Cys Asp
435
Leu Ile Glu Asn Lys Val Asn Pro Pro Gly Ile Met Ser Ile Leu Asp
450
Asp Val Cys Ala Thr Met His Ala Val Gly Glu Gly Ala Asp Gln Thr
465
Leu Leu Gln Lys Leu Gln Met Gln Ile Gly Ser His Glu His Phe Asn
485
Ser Trp Asn Gln Gly Phe Ile Ile His His Tyr Ala Gly Lys Val Ser
500
Tyr Asp Met Asp Gly Phe Cys Glu Arg Asn Arg Asp Val Leu Phe Met
515
Asp Leu Ile Glu Leu Met Gln Ser Ser Glu Leu Pro Phe Ile Lys Ser
530
Leu Phe Pro Glu Asn Leu Gln Ala Asp Lys Lys Gly Arg Pro Thr Thr
545
Ala Gly Ser Lys Ile Lys Lys Gln Ala Asn Asp Leu Val Ser Thr Leu
565
Met Lys Cys Thr Pro His Tyr Ile Arg Cys Ile Lys Pro Asn Glu Thr
580
Lys Lys Pro Arg Asp Trp Glu Glu Ser Arg Val Lys His Gln Val Glu
595
Tyr Leu Gly Leu Lys Glu Asn Ile Arg Val Arg Arg Ala Gly Tyr Ala
610
Tyr Arg Arg Ile Phe Gln Lys Phe Leu Gln Arg Tyr Ala Ile Leu Thr
625
Lys Ala Thr Trp Pro Ser Trp Gln Gly Glu Glu Lys Gln Gly Val Leu
645
His Leu Leu Gln Ser Val Asn Met Asp Ser Asp Gln Phe Gln Leu Gly
660
Arg Ser Lys Val Phe Ile Lys Ala Pro Glu Ser Leu Phe Leu Leu Glu
675
Glu Met Arg Glu Arg Lys Tyr Asp Gly Tyr Ala Arg Val Ile Gln Lys
690

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Ser	Trp	Arg	Lys	Phe	Val	Ala	Arg	Lys	Lys	Tyr	Val	Gln	Met	Arg	Glu	705	710	715	720
Glu	Ala	Ser	Asp	Leu	Leu	Leu	Asn	Lys	Lys	Glu	Arg	Arg	Arg	Asn	Ser	725	730	735	
Ile	Asn	Arg	Asn	Phe	Ile	Gly	Asp	Tyr	Ile	Gly	Met	Glu	Glu	His	Pro	740	745	750	
Glu	Leu	Gln	Gln	Phe	Val	Gly	Lys	Arg	Glu	Lys	Ile	Asp	Phe	Ala	Asp	755	760	765	
Thr	Val	Thr	Lys	Tyr	Asp	Arg	Arg	Phe	Lys	Gly	Val	Lys	Arg	Asp	Leu	770	775	780	
Leu	Leu	Thr	Pro	Lys	Cys	Leu	Tyr	Leu	Ile	Gly	Arg	Glu	Lys	Val	Lys	785	790	795	800
Gln	Gly	Pro	Asp	Lys	Gly	Leu	Val	Lys	Glu	Val	Leu	Lys	Arg	Lys	Ile	805	810	815	
Glu	Ile	Glu	Arg	Ile	Leu	Ser	Val	Ser	Leu	Ser	Thr	Met	Gln	Asp	Asp	820	825	830	
Ile	Phe	Ile	Leu	His	Glu	Gln	Glu	Tyr	Asp	Ser	Leu	Leu	Glu	Ser	Val	835	840	845	
Phe	Lys	Thr	Glu	Phe	Leu	Ser	Leu	Leu	Ala	Lys	Arg	Tyr	Glu	Glu	Lys	850	855	860	
Thr	Gln	Lys	Gln	Leu	Pro	Leu	Lys	Phe	Ser	Asn	Thr	Leu	Glu	Leu	Lys	865	870	875	880
Leu	Lys	Lys	Glu	Asn	Trp	Gly	Pro	Trp	Ser	Ala	Gly	Gly	Ser	Arg	Gln	885	890	895	
Val	Gln	Phe	His	Gln	Gly	Phe	Gly	Asp	Leu	Ala	Val	Leu	Lys	Pro	Ser	900	905	910	
Asn	Lys	Val	Leu	Gln	Val	Ser	Ile	Gly	Pro	Gly	Leu	Pro	Lys	Asn	Ser	915	920	925	
Arg	Pro	Thr	Arg	Arg	Asn	Thr	Thr	Gln	Asn	Thr	Gly	Tyr	Ser	Ser	Gly	930	935	940	
Thr	Gln	Asn	Ala	Asn	Tyr	Pro	Val	Arg	Ala	Ala	Pro	Pro	Pro	Pro	Gly	945	950	955	960
Tyr	His	Gln	Asn	Gly	Val	Ile	Arg	Asn	Gln	Tyr	Val	Pro	Tyr	Pro	His	965	970	975	

ITI-08-PCT_Sequence_Listing_ST25.txt

Ala Pro Gly Ser Gln Arg Ser Asn Gln Lys Ser Leu Tyr Thr Ser Met
980 985 990

Ala Arg Pro Pro Leu Pro Arg Gln Gln Ser Thr Ser Ser Asp Arg Val
995 1000 1005

Ser Gln Thr Pro Glu Ser Leu Asp Phe Leu Lys Val Pro Asp Gln
1010 1015 1020

Gly Ala Ala Gly Val Arg Arg Gln Thr Thr Ser Arg Pro Pro Pro
1025 1030 1035

Ala Gly Gly Arg Pro Lys Pro Gln Pro Lys Pro Lys Pro Gln Val
1040 1045 1050

Pro Gln Cys Lys Ala Leu Tyr Ala Tyr Asp Ala Gln Asp Thr Asp
1055 1060 1065

Glu Leu Ser Phe Asn Ala Asn Asp Ile Ile Asp Ile Ile Lys Glu
1070 1075 1080

Asp Pro Ser Gly Trp Trp Thr Gly Arg Leu Arg Gly Lys Gln Gly
1085 1090 1095

Leu Phe Pro Asn Asn Tyr Val Thr Lys Ile
1100 1105

<210> 545
<211> 1098
<212> PRT
<213> Artificial Sequence

<220>
<223> MY01F__Homo_sapiens__000160

<400> 545

Met Gly Ser Lys Glu Arg Phe His Trp Gln Ser His Asn Val Lys Gln
1 5 10 15

Ser Gly Val Asp Asp Met Val Leu Leu Pro Gln Ile Thr Glu Asp Ala
20 25 30

Ile Ala Ala Asn Leu Arg Lys Arg Phe Met Asp Asp Tyr Ile Phe Thr
35 40 45

Tyr Ile Gly Ser Val Leu Ile Ser Val Asn Pro Phe Lys Gln Met Pro
50 55 60

Tyr Phe Thr Asp Arg Glu Ile Asp Leu Tyr Gln Gly Ala Ala Gln Tyr
65 70 75 80

ITI-08-PCT_Sequence_Listing_ST25.txt

Glu	Asn	Pro	Pro	His	Ile	Tyr	Ala	Leu	Thr	Asp	Asn	Met	Tyr	Arg	Asn		
				85					90					95			
Met	Leu	Ile	Asp	Cys	Glu	Asn	Gln	Cys	Val	Ile	Ile	Ser	Gly	Glu	Ser		
			100					105					110				
Gly	Ala	Gly	Lys	Thr	Val	Ala	Ala	Lys	Tyr	Ile	Met	Gly	Tyr	Ile	Ser		
		115					120					125					
Lys	Val	Ser	Gly	Gly	Gly	Glu	Lys	Val	Gln	His	Val	Lys	Asp	Ile	Ile		
	130					135					140						
Leu	Gln	Ser	Asn	Pro	Leu	Leu	Glu	Ala	Phe	Gly	Asn	Ala	Lys	Thr	Val		
145					150					155					160		
Arg	Asn	Asn	Asn	Ser	Ser	Arg	Phe	Gly	Lys	Tyr	Phe	Glu	Ile	Gln	Phe		
				165					170					175			
Ser	Arg	Gly	Gly	Glu	Pro	Asp	Gly	Gly	Lys	Ile	Ser	Asn	Phe	Leu	Leu		
			180					185					190				
Glu	Lys	Ser	Arg	Val	Val	Met	Gln	Asn	Glu	Asn	Glu	Arg	Asn	Phe	His		
		195					200					205					
Ile	Tyr	Tyr	Gln	Leu	Leu	Glu	Gly	Ala	Ser	Gln	Glu	Gln	Arg	Gln	Asn		
	210					215					220						
Leu	Gly	Leu	Met	Thr	Pro	Asp	Tyr	Tyr	Tyr	Tyr	Leu	Asn	Gln	Ser	Asp		
225					230				235						240		
Thr	Tyr	Gln	Val	Asp	Gly	Thr	Asp	Asp	Arg	Ser	Asp	Phe	Gly	Glu	Thr		
				245					250					255			
Leu	Ser	Ala	Met	Gln	Val	Ile	Gly	Ile	Pro	Pro	Ser	Ile	Gln	Gln	Leu		
			260					265					270				
Val	Leu	Gln	Leu	Val	Ala	Gly	Ile	Leu	His	Leu	Gly	Asn	Ile	Ser	Phe		
		275					280					285					
Cys	Glu	Asp	Gly	Asn	Tyr	Ala	Arg	Val	Glu	Ser	Val	Asp	Leu	Leu	Ala		
	290					295					300						
Phe	Pro	Ala	Tyr	Leu	Leu	Gly	Ile	Asp	Ser	Gly	Arg	Leu	Gln	Glu	Lys		
305					310					315					320		
Leu	Thr	Ser	Arg	Lys	Met	Asp	Ser	Arg	Trp	Gly	Gly	Arg	Ser	Glu	Ser		
				325					330					335			
Ile	Asn	Val	Thr	Leu	Asn	Val	Glu	Gln	Ala	Ala	Tyr	Thr	Arg	Asp	Ala		
			340				345						350				
Leu	Ala	Lys	Gly	Leu	Tyr	Ala	Arg	Leu	Phe	Asp	Phe	Leu	Val	Glu	Ala		

ITI-08-PCT_Sequence_Listing_ST25.txt

```

355                               360                               365
Ile Asn Arg Ala Met Gln Lys Pro Gln Glu Glu Tyr Ser Ile Gly Val
370                               375                               380
Leu Asp Ile Tyr Gly Phe Glu Ile Phe Gln Lys Asn Gly Phe Glu Gln
385                               390                               395                               400
Phe Cys Ile Asn Phe Val Asn Glu Lys Leu Gln Gln Ile Phe Ile Glu
405                               410                               415
Leu Thr Leu Lys Ala Glu Gln Glu Glu Tyr Val Gln Glu Gly Ile Arg
420                               425                               430
Trp Thr Pro Ile Gln Tyr Phe Asn Asn Lys Val Val Cys Asp Leu Ile
435                               440                               445
Glu Asn Lys Leu Ser Pro Pro Gly Ile Met Ser Val Leu Asp Asp Val
450                               455                               460
Cys Ala Thr Met His Ala Thr Gly Gly Gly Ala Asp Gln Thr Leu Leu
465                               470                               475                               480
Gln Lys Leu Gln Ala Ala Val Gly Thr His Glu His Phe Asn Ser Trp
485                               490                               495
Ser Ala Gly Phe Val Ile His His Tyr Ala Gly Lys Val Ser Tyr Asp
500                               505                               510
Val Ser Gly Phe Cys Glu Arg Asn Arg Asp Val Leu Phe Ser Asp Leu
515                               520                               525
Ile Glu Leu Met Gln Thr Ser Glu Gln Ala Phe Leu Arg Met Leu Phe
530                               535                               540
Pro Glu Lys Leu Asp Gly Asp Lys Lys Gly Arg Pro Ser Thr Ala Gly
545                               550                               555                               560
Ser Lys Ile Lys Lys Gln Ala Asn Asp Leu Val Ala Thr Leu Met Arg
565                               570                               575
Cys Thr Pro His Tyr Ile Arg Cys Ile Lys Pro Asn Glu Thr Lys Arg
580                               585                               590
Pro Arg Asp Trp Glu Glu Asn Arg Val Lys His Gln Val Glu Tyr Leu
595                               600                               605
Gly Leu Lys Glu Asn Ile Arg Val Arg Arg Ala Gly Phe Ala Tyr Arg
610                               615                               620
Arg Gln Phe Ala Lys Phe Leu Gln Arg Tyr Ala Ile Leu Thr Pro Glu
625                               630                               635                               640

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Thr	Trp	Pro	Arg	Trp	Arg	Gly	Asp	Glu	Arg	Gln	Gly	Val	Gln	His	Leu	
				645					650					655		
Leu	Arg	Ala	Val	Asn	Met	Glu	Pro	Asp	Gln	Tyr	Gln	Met	Gly	Ser	Thr	
				660					665					670		
Lys	Val	Phe	Val	Lys	Asn	Pro	Glu	Ser	Leu	Phe	Leu	Leu	Glu	Glu	Val	
				675					680					685		
Arg	Glu	Arg	Lys	Phe	Asp	Gly	Phe	Ala	Arg	Thr	Ile	Gln	Lys	Ala	Trp	
				690					695					700		
Arg	Arg	His	Val	Ala	Val	Arg	Lys	Tyr	Glu	Glu	Met	Arg	Glu	Glu	Ala	
				705					710					715		
Ser	Asn	Ile	Leu	Leu	Asn	Lys	Lys	Glu	Arg	Arg	Arg	Asn	Ser	Ile	Asn	
				725					730					735		
Arg	Asn	Phe	Val	Gly	Asp	Tyr	Leu	Gly	Leu	Glu	Glu	Arg	Pro	Glu	Leu	
				740					745					750		
Arg	Gln	Phe	Leu	Gly	Lys	Arg	Glu	Arg	Val	Asp	Phe	Ala	Asp	Ser	Val	
				755					760					765		
Thr	Lys	Tyr	Asp	Arg	Arg	Phe	Lys	Pro	Ile	Lys	Arg	Asp	Leu	Ile	Leu	
				770					775					780		
Thr	Pro	Lys	Cys	Val	Tyr	Val	Ile	Gly	Arg	Glu	Lys	Val	Lys	Lys	Gly	
				785					790					795		
Pro	Glu	Lys	Gly	Gln	Val	Cys	Glu	Val	Leu	Lys	Lys	Lys	Val	Asp	Ile	
				805					810					815		
Gln	Ala	Leu	Arg	Gly	Val	Ser	Leu	Ser	Thr	Arg	Gln	Asp	Asp	Phe	Phe	
				820					825					830		
Ile	Leu	Gln	Glu	Asp	Ala	Ala	Asp	Ser	Phe	Leu	Glu	Ser	Val	Phe	Lys	
				835					840					845		
Thr	Glu	Phe	Val	Ser	Leu	Leu	Cys	Lys	Arg	Phe	Glu	Glu	Ala	Thr	Arg	
				850					855					860		
Arg	Pro	Leu	Pro	Leu	Thr	Phe	Ser	Asp	Thr	Leu	Gln	Phe	Arg	Val	Lys	
				865					870					875		
Lys	Glu	Gly	Trp	Gly	Gly	Gly	Gly	Thr	Arg	Ser	Val	Thr	Phe	Ser	Arg	
				885					890					895		
Gly	Phe	Gly	Asp	Leu	Ala	Val	Leu	Lys	Val	Gly	Gly	Arg	Thr	Leu	Thr	
				900					905					910		

ITI-08-PCT_Sequence_Listing_ST25.txt

Val Ser Val Gly Asp Gly Leu Pro Lys Ser Ser Lys Pro Thr Arg Lys
915 920 925

Gly Met Ala Lys Gly Lys Pro Arg Arg Ser Ser Gln Ala Pro Thr Arg
930 935 940

Ala Ala Pro Ala Pro Pro Arg Gly Met Asp Arg Asn Gly Val Pro Pro
945 950 955 960

Ser Ala Arg Gly Gly Pro Leu Pro Leu Glu Ile Met Ser Gly Gly Gly
965 970 975

Thr His Arg Pro Pro Arg Gly Pro Pro Ser Thr Ser Leu Gly Ala Ser
980 985 990

Arg Arg Pro Arg Ala Arg Pro Pro Ser Glu His Asn Thr Glu Phe Leu
995 1000 1005

Asn Val Pro Asp Gln Gly Met Ala Gly Met Gln Arg Lys Arg Ser
1010 1015 1020

Val Gly Gln Arg Pro Val Pro Gly Val Gly Arg Pro Lys Pro Gln
1025 1030 1035

Pro Arg Thr His Gly Pro Arg Cys Arg Ala Leu Tyr Gln Tyr Val
1040 1045 1050

Gly Gln Asp Val Asp Glu Leu Ser Phe Asn Val Asn Glu Val Ile
1055 1060 1065

Glu Ile Leu Met Glu Asp Pro Ser Gly Trp Trp Lys Gly Arg Leu
1070 1075 1080

His Gly Gln Glu Gly Leu Phe Pro Gly Asn Tyr Val Glu Lys Ile
1085 1090 1095

<210> 546
<211> 1018
<212> PRT
<213> Artificial Sequence

<220>
<223> MY01G__Homo_sapiens__B0I1T2

<400> 546

Met Glu Asp Glu Glu Gly Pro Glu Tyr Gly Lys Pro Asp Phe Val Leu
1 5 10 15

Leu Asp Gln Val Thr Met Glu Asp Phe Met Arg Asn Leu Gln Leu Arg
20 25 30

ITI-08-PCT_Sequence_Listing_ST25.txt

Phe Glu Lys Gly Arg Ile Tyr Thr Tyr Ile Gly Glu Val Leu Val Ser
 35 40 45
 Val Asn Pro Tyr Gln Glu Leu Pro Leu Tyr Gly Pro Glu Ala Ile Ala
 50 55 60
 Arg Tyr Gln Gly Arg Glu Leu Tyr Glu Arg Pro Pro His Leu Tyr Ala
 65 70 75 80
 Val Ala Asn Ala Ala Tyr Lys Ala Met Lys His Arg Ser Arg Asp Thr
 85 90 95
 Cys Ile Val Ile Ser Gly Glu Ser Gly Ala Gly Lys Thr Glu Ala Ser
 100 105 110
 Lys His Ile Met Gln Tyr Ile Ala Ala Val Thr Asn Pro Ser Gln Arg
 115 120 125
 Ala Glu Val Glu Arg Val Lys Asp Val Leu Leu Lys Ser Thr Cys Val
 130 135 140
 Leu Glu Ala Phe Gly Asn Ala Arg Thr Asn Arg Asn His Asn Ser Ser
 145 150 155 160
 Arg Phe Gly Lys Tyr Met Asp Ile Asn Phe Asp Phe Lys Gly Asp Pro
 165 170 175
 Ile Gly Gly His Ile His Ser Tyr Leu Leu Glu Lys Ser Arg Val Leu
 180 185 190
 Lys Gln His Val Gly Glu Arg Asn Phe His Ala Phe Tyr Gln Leu Leu
 195 200 205
 Arg Gly Ser Glu Asp Lys Gln Leu His Glu Leu His Leu Glu Arg Asn
 210 215 220
 Pro Ala Val Tyr Asn Phe Thr His Gln Gly Ala Gly Leu Asn Met Thr
 225 230 235 240
 Val His Ser Ala Leu Asp Ser Asp Glu Gln Ser His Gln Ala Val Thr
 245 250 255
 Glu Ala Met Arg Val Ile Gly Phe Ser Pro Glu Glu Val Glu Ser Val
 260 265 270
 His Arg Ile Leu Ala Ala Ile Leu His Leu Gly Asn Ile Glu Phe Val
 275 280 285
 Glu Thr Glu Glu Gly Gly Leu Gln Lys Glu Gly Leu Ala Val Ala Glu
 290 295 300
 Glu Ala Leu Val Asp His Val Ala Glu Leu Thr Ala Thr Pro Arg Asp

ITI-08-PCT_Sequence_Listing_ST25.txt

```

305          310          315          320
Leu Val Leu Arg Ser Leu Leu Ala Arg Thr Val Ala Ser Gly Gly Arg
          325          330          335
Glu Leu Ile Glu Lys Gly His Thr Ala Ala Glu Ala Ser Tyr Ala Arg
          340          345          350
Asp Ala Cys Ala Lys Ala Val Tyr Gln Arg Leu Phe Glu Trp Val Val
          355          360          365
Asn Arg Ile Asn Ser Val Met Glu Pro Arg Gly Arg Asp Pro Arg Arg
          370          375          380
Asp Gly Lys Asp Thr Val Ile Gly Val Leu Asp Ile Tyr Gly Phe Glu
385          390          395          400
Val Phe Pro Val Asn Ser Phe Glu Gln Phe Cys Ile Asn Tyr Cys Asn
          405          410          415
Glu Lys Leu Gln Gln Leu Phe Ile Gln Leu Ile Leu Lys Gln Glu Gln
          420          425          430
Glu Glu Tyr Glu Arg Glu Gly Ile Thr Trp Gln Ser Val Glu Tyr Phe
          435          440          445
Asn Asn Ala Thr Ile Val Asp Leu Val Glu Arg Pro His Arg Gly Ile
          450          455          460
Leu Ala Val Leu Asp Glu Ala Cys Ser Ser Ala Gly Thr Ile Thr Asp
465          470          475          480
Arg Ile Phe Leu Gln Thr Leu Asp Met His His Arg His His Leu His
          485          490          495
Tyr Thr Ser Arg Gln Leu Cys Pro Thr Asp Lys Thr Met Glu Phe Gly
          500          505          510
Arg Asp Phe Arg Ile Lys His Tyr Ala Gly Asp Val Thr Tyr Ser Val
          515          520          525
Glu Gly Phe Ile Asp Lys Asn Arg Asp Phe Leu Phe Gln Asp Phe Lys
          530          535          540
Arg Leu Leu Tyr Asn Ser Thr Asp Pro Thr Leu Arg Ala Met Trp Pro
545          550          555          560
Asp Gly Gln Gln Asp Ile Thr Glu Val Thr Lys Arg Pro Leu Thr Ala
          565          570          575
Gly Thr Leu Phe Lys Asn Ser Met Val Ala Leu Val Glu Asn Leu Ala
          580          585          590

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Ser	Lys	Glu	Pro	Phe	Tyr	Val	Arg	Cys	Ile	Lys	Pro	Asn	Glu	Asp	Lys	595	600	605
Val	Ala	Gly	Lys	Leu	Asp	Glu	Asn	His	Cys	Arg	His	Gln	Val	Ala	Tyr	610	615	620
Leu	Gly	Leu	Leu	Glu	Asn	Val	Arg	Val	Arg	Arg	Ala	Gly	Phe	Ala	Ser	625	630	635
Arg	Gln	Pro	Tyr	Ser	Arg	Phe	Leu	Leu	Arg	Tyr	Lys	Met	Thr	Cys	Glu	645	650	655
Tyr	Thr	Trp	Pro	Asn	His	Leu	Leu	Gly	Ser	Asp	Lys	Ala	Ala	Val	Ser	660	665	670
Ala	Leu	Leu	Glu	Gln	His	Gly	Leu	Gln	Gly	Asp	Val	Ala	Phe	Gly	His	675	680	685
Ser	Lys	Leu	Phe	Ile	Arg	Ser	Pro	Arg	Thr	Leu	Val	Thr	Leu	Glu	Gln	690	695	700
Ser	Arg	Ala	Arg	Leu	Ile	Pro	Ile	Ile	Val	Leu	Leu	Leu	Gln	Lys	Ala	705	710	715
Trp	Arg	Gly	Thr	Leu	Ala	Arg	Trp	Arg	Cys	Arg	Arg	Leu	Arg	Ala	Ile	725	730	735
Tyr	Thr	Ile	Met	Arg	Trp	Phe	Arg	Arg	His	Lys	Val	Arg	Ala	His	Leu	740	745	750
Ala	Glu	Leu	Gln	Arg	Arg	Phe	Gln	Ala	Ala	Arg	Gln	Pro	Pro	Leu	Tyr	755	760	765
Gly	Arg	Asp	Leu	Val	Trp	Pro	Leu	Pro	Pro	Ala	Val	Leu	Gln	Pro	Phe	770	775	780
Gln	Asp	Thr	Cys	His	Ala	Leu	Phe	Cys	Arg	Trp	Arg	Ala	Arg	Gln	Leu	785	790	795
Val	Lys	Asn	Ile	Pro	Pro	Ser	Asp	Met	Pro	Gln	Ile	Lys	Ala	Lys	Val	805	810	815
Ala	Ala	Met	Gly	Ala	Leu	Gln	Gly	Leu	Arg	Gln	Asp	Trp	Gly	Cys	Arg	820	825	830
Arg	Ala	Trp	Ala	Arg	Asp	Tyr	Leu	Ser	Ser	Ala	Thr	Asp	Asn	Pro	Thr	835	840	845
Ala	Ser	Ser	Leu	Phe	Ala	Gln	Arg	Leu	Lys	Thr	Leu	Gln	Asp	Lys	Asp	850	855	860

ITI-08-PCT_Sequence_Listing_ST25.txt

Gly Phe Gly Ala Val Leu Phe Ser Ser His Val Arg Lys Val Asn Arg
865 870 875 880

Phe His Lys Ile Arg Asn Arg Ala Leu Leu Leu Thr Asp Gln His Leu
885 890 895

Tyr Lys Leu Asp Pro Asp Arg Gln Tyr Arg Val Met Arg Ala Val Pro
900 905 910

Leu Glu Ala Val Thr Gly Leu Ser Val Thr Ser Gly Gly Asp Gln Leu
915 920 925

Val Val Leu His Ala Arg Gly Gln Asp Asp Leu Val Val Cys Leu His
930 935 940

Arg Ser Arg Pro Pro Leu Asp Asn Arg Val Gly Glu Leu Val Gly Val
945 950 955 960

Leu Ala Ala His Cys Gln Gly Glu Gly Arg Thr Leu Glu Val Arg Val
965 970 975

Ser Asp Cys Ile Pro Leu Ser His Arg Gly Val Arg Arg Leu Ile Ser
980 985 990

Val Glu Pro Arg Pro Glu Gln Pro Glu Pro Asp Phe Arg Cys Ala Arg
995 1000 1005

Gly Ser Phe Thr Leu Leu Trp Pro Ser Arg
1010 1015

<210> 547

<211> 1022

<212> PRT

<213> Artificial Sequence

<220>

<223> MY01H__Homo_sapiens__NP_001094891

<400> 547

Met Glu Gly Ala Leu Thr Ala Arg Asp Lys Val Gly Val Gln Asp Phe
1 5 10 15

Val Leu Leu Asp Ala Tyr Thr Ser Glu Ser Ala Phe Val Asp Asn Leu
20 25 30

Arg Lys Arg Phe Ser Glu Asn Leu Ile Tyr Thr Tyr Ile Gly Thr Leu
35 40 45

Leu Val Ser Val Asn Pro Tyr Gln Glu Leu Gly Ile Tyr Thr Val Ser
50 55 60

ITI-08-PCT_Sequence_Listing_ST25.txt

Gln	Met	Glu	Leu	Tyr	Gln	Gly	Val	Asn	Phe	Phe	Glu	Leu	Pro	Pro	His	65	70	75	80
Val	Tyr	Ala	Ile	Ala	Asp	Asn	Ala	Tyr	Arg	Met	Met	Cys	Ala	Glu	Leu	85	90	95	
Asn	Asn	His	Phe	Ile	Leu	Ile	Ser	Gly	Glu	Ser	Gly	Ala	Gly	Lys	Thr	100	105	110	
Glu	Ala	Ser	Lys	Lys	Ile	Leu	Glu	Tyr	Phe	Ala	Val	Thr	Cys	Pro	Met	115	120	125	
Thr	Gln	Ser	Leu	Gln	Ile	Ala	Arg	Asp	Arg	Leu	Leu	Phe	Ser	Asn	Pro	130	135	140	
Val	Leu	Glu	Ala	Phe	Gly	Asn	Ala	Arg	Thr	Leu	Arg	Asn	Asp	Asn	Ser	145	150	155	160
Ser	Arg	Phe	Gly	Lys	Tyr	Met	Asp	Ile	Gln	Phe	Asp	Phe	Gln	Gly	Ile	165	170	175	
Pro	Val	Gly	Gly	His	Ile	Ile	Ser	Tyr	Leu	Ile	Glu	Lys	Ser	Arg	Val	180	185	190	
Val	Tyr	Gln	Asn	Glu	Gly	Glu	Arg	Asn	Phe	His	Ile	Phe	Tyr	Gln	Leu	195	200	205	
Leu	Ala	Gly	Gly	Glu	Glu	Glu	Arg	Leu	Ser	Tyr	Leu	Gly	Leu	Glu	Arg	210	215	220	
Asp	Pro	Gln	Leu	Tyr	Lys	Tyr	Leu	Ser	Gln	Gly	His	Cys	Ala	Lys	Glu	225	230	235	240
Ser	Ser	Ile	Ser	Asp	Lys	Asn	Asp	Trp	Lys	Thr	Val	Ser	Asn	Ala	Phe	245	250	255	
Ser	Val	Ile	Asp	Phe	Thr	Glu	Ala	Asp	Leu	Glu	Asn	Leu	Phe	Gly	Ile	260	265	270	
Ile	Ala	Ser	Val	Leu	His	Leu	Gly	Asn	Ile	Gly	Phe	Glu	Glu	Asp	Asp	275	280	285	
Gln	Gly	Cys	Ala	Thr	Ile	Pro	Asp	Thr	His	Glu	Ile	Lys	Trp	Ile	Ala	290	295	300	
Lys	Leu	Leu	Gly	Val	His	Pro	Ser	Val	Leu	Leu	Glu	Ala	Leu	Thr	His	305	310	315	320
Arg	Lys	Ile	Glu	Ala	Lys	Thr	Glu	Glu	Val	Ile	Cys	Pro	Leu	Thr	Leu	325	330	335	
Glu	Leu	Ser	Val	Tyr	Ala	Arg	Asp	Ala	Met	Ala	Lys	Ala	Val	Tyr	Gly				

ITI-08-PCT_Sequence_Listing_ST25.txt

340

345

350

Arg Thr Phe Thr Trp Leu Val Asn Lys Ile Asn Ser Ser Leu Val Asn
 355 360 365

Lys Asp Phe Thr Arg Lys Thr Val Ile Gly Leu Leu Asp Ile Tyr Gly
 370 375 380

Phe Glu Val Phe Asp Lys Asn Gly Phe Glu Gln Phe Cys Ile Asn Tyr
 385 390 395 400

Cys Asn Glu Lys Leu Gln Gln Leu Leu Ile Glu Arg Thr Leu Lys Ala
 405 410 415

Glu Gln Ala Glu Tyr Glu Met Glu Gly Ile Glu Trp Glu Pro Ile Lys
 420 425 430

Tyr Phe Asn Asn Lys Ile Ile Cys Asp Leu Val Glu Glu Arg His Lys
 435 440 445

Gly Ile Ile Ser Ile Leu Asp Glu Glu Cys Ile Arg Pro Gly Pro Ala
 450 455 460

Thr Asp Leu Ser Phe Leu Glu Lys Leu Glu Glu Lys Val Gly Lys His
 465 470 475 480

Ala His Phe Glu Thr Arg Lys Leu Ala Gly Pro Lys Gly Arg Lys Arg
 485 490 495

Ile Gly Trp Met Glu Phe Arg Leu Leu His Tyr Ala Gly Glu Val Thr
 500 505 510

Tyr Cys Thr Lys Gly Phe Leu Glu Lys Asn Asn Asp Leu Leu Tyr Arg
 515 520 525

His Leu Lys Glu Val Leu Cys Lys Ser Lys Asn Ile Ile Leu Arg Glu
 530 535 540

Cys Phe Leu Leu Ala Glu Leu Glu Asn Arg Arg Arg Pro Pro Thr Val
 545 550 555 560

Gly Thr Gln Phe Lys Asn Ser Leu Ser Ser Leu Leu Glu Thr Leu Ile
 565 570 575

Ser Lys Glu Pro Ser Tyr Ile Arg Cys Ile Lys Pro Asn Asp Arg Lys
 580 585 590

Glu Pro Ser Lys Phe Asp Asp Phe Leu Ile Arg His Gln Ile Lys Tyr
 595 600 605

Leu Gly Leu Met Glu His Leu Arg Val Arg Arg Ala Gly Phe Ala Tyr
 610 615 620

ITI-08-PCT_Sequence_Listing_ST25.txt

Arg	Arg	Lys	Tyr	Glu	His	Phe	Leu	Gln	Arg	Tyr	Lys	Ser	Leu	Cys	Pro	625	630	635	640
Asp	Thr	Trp	Pro	His	Trp	His	Gly	Pro	Pro	Ala	Glu	Gly	Val	Glu	Arg	645	650	655	
Leu	Ile	Lys	Tyr	Ile	Gly	Tyr	Lys	Pro	Glu	Glu	Tyr	Lys	Leu	Gly	Lys	660	665	670	
Thr	Lys	Ile	Phe	Ile	Arg	Phe	Pro	Arg	Thr	Leu	Phe	Ala	Thr	Glu	Asp	675	680	685	
Ala	Phe	Glu	Phe	Ser	Lys	His	Gln	Leu	Val	Ala	Arg	Ile	Gln	Ala	Thr	690	695	700	
Tyr	Lys	Arg	Cys	Leu	Gly	Arg	Arg	Glu	Tyr	Val	Lys	Lys	Arg	Gln	Ala	705	710	715	720
Ala	Ile	Lys	Leu	Glu	Ala	His	Trp	Arg	Gly	Ala	Leu	Ala	Arg	Lys	Ala	725	730	735	
Ile	Gln	Arg	Arg	Lys	Trp	Ala	Val	Arg	Ile	Ile	Arg	Lys	Phe	Ile	Lys	740	745	750	
Gly	Phe	Ile	Ser	Arg	Asn	Lys	Pro	Leu	Cys	Pro	Asp	Asn	Glu	Glu	Phe	755	760	765	
Ile	Val	Phe	Val	Arg	Lys	Asn	Tyr	Ile	Leu	Asn	Leu	Arg	Tyr	His	Leu	770	775	780	
Pro	Lys	Thr	Val	Leu	Asp	Lys	Ser	Trp	Leu	Arg	Pro	Pro	Gly	Ile	Leu	785	790	795	800
Glu	Asn	Ala	Ser	Asp	Leu	Leu	Arg	Lys	Met	Cys	Val	Arg	Asn	Leu	Val	805	810	815	
Gln	Lys	Tyr	Cys	Arg	Gly	Ile	Thr	Ala	Glu	Arg	Lys	Ala	Met	Met	Gln	820	825	830	
Gln	Lys	Val	Val	Thr	Ser	Glu	Ile	Phe	Arg	Gly	Arg	Lys	Asp	Gly	Tyr	835	840	845	
Thr	Glu	Ser	Leu	Asn	Gln	Pro	Phe	Val	Asn	Ser	Arg	Ile	Asp	Glu	Gly	850	855	860	
Asp	Ile	Asn	Pro	Lys	Val	Leu	Gln	Leu	Ile	Ser	His	Glu	Lys	Ile	Gln	865	870	875	880
Tyr	Gly	Val	Pro	Val	Ile	Lys	Tyr	Asp	Arg	Lys	Gly	Phe	Lys	Ala	Arg	885	890	895	

ITI-08-PCT_Sequence_Listing_ST25.txt

Gln Arg Gln Leu Ile Leu Thr Gln Lys Ala Ala Tyr Val Val Glu Leu
900 905 910

Ala Lys Ile Lys Gln Lys Ile Glu Tyr Ser Ala Leu Lys Gly Val Ser
915 920 925

Thr Ser Asn Leu Ser Asp Gly Ile Leu Val Ile His Val Ser Pro Glu
930 935 940

Asp Ser Lys Gln Lys Gly Asp Ala Val Leu Gln Cys Gly His Val Phe
945 950 955 960

Glu Ala Val Thr Lys Leu Val Met Leu Val Lys Lys Glu Asn Ile Val
965 970 975

Asn Val Val Gln Gly Ser Leu Gln Phe Phe Ile Ser Pro Gly Lys Glu
980 985 990

Gly Thr Ile Val Phe Asp Thr Gly Leu Glu Glu Gln Val Tyr Lys Asn
995 1000 1005

Lys Asn Gly Gln Leu Thr Val Val Ser Val Arg Arg Lys Ser
1010 1015 1020

<210> 548
<211> 792
<212> PRT
<213> Artificial Sequence

<220>
<223> NA17__Homo_sapiens__Q3V5L5

<400> 548

Met Ile Thr Val Asn Pro Asp Gly Lys Ile Met Val Arg Arg Cys Leu
1 5 10 15

Val Thr Leu Arg Pro Phe Arg Leu Phe Val Leu Gly Ile Gly Phe Phe
20 25 30

Thr Leu Cys Phe Leu Met Thr Ser Leu Gly Gly Gln Phe Ser Ala Arg
35 40 45

Arg Leu Gly Asp Ser Pro Phe Thr Ile Arg Thr Glu Val Met Gly Gly
50 55 60

Pro Glu Ser Arg Gly Val Leu Arg Lys Met Ser Asp Leu Leu Glu Leu
65 70 75 80

Met Val Lys Arg Met Asp Ala Leu Ala Arg Leu Glu Asn Ser Ser Glu
85 90 95

ITI-08-PCT_Sequence_Listing_ST25.txt

Leu His Arg Ala Gly Gly Asp Leu His Phe Pro Ala Asp Arg Met Pro
 100 105 110
 Pro Gly Ala Gly Leu Met Glu Arg Ile Gln Ala Ile Ala Gln Asn Val
 115 120 125
 Ser Asp Ile Ala Val Lys Val Asp Gln Ile Leu Arg His Ser Leu Leu
 130 135 140
 Leu His Ser Lys Val Ser Glu Gly Arg Arg Asp Gln Cys Glu Ala Pro
 145 150 155 160
 Ser Asp Pro Lys Phe Pro Asp Cys Ser Gly Lys Val Glu Trp Met Arg
 165 170 175
 Ala Arg Trp Thr Ser Asp Pro Cys Tyr Ala Phe Phe Gly Val Asp Gly
 180 185 190
 Thr Glu Cys Ser Phe Leu Ile Tyr Leu Ser Glu Val Glu Trp Phe Cys
 195 200 205
 Pro Pro Leu Pro Trp Arg Asn Gln Thr Ala Ala Gln Arg Ala Pro Lys
 210 215 220
 Pro Leu Pro Lys Val Gln Ala Val Phe Arg Ser Asn Leu Ser His Leu
 225 230 235 240
 Leu Asp Leu Met Gly Ser Gly Lys Glu Ser Leu Ile Phe Met Lys Lys
 245 250 255
 Arg Thr Lys Arg Leu Thr Ala Gln Trp Ala Leu Ala Ala Gln Arg Leu
 260 265 270
 Ala Gln Lys Leu Gly Ala Thr Gln Arg Asp Gln Lys Gln Ile Leu Val
 275 280 285
 His Ile Gly Phe Leu Thr Glu Glu Ser Gly Asp Val Phe Ser Pro Arg
 290 295 300
 Val Leu Lys Gly Gly Pro Leu Gly Glu Met Val Gln Trp Ala Asp Ile
 305 310 315 320
 Leu Thr Ala Leu Tyr Val Leu Gly His Gly Leu Arg Val Thr Val Ser
 325 330 335
 Leu Lys Glu Leu Gln Ser Asn Leu Gly Val Pro Pro Gly Arg Gly Ser
 340 345 350
 Cys Pro Leu Thr Met Pro Leu Pro Phe Asp Leu Ile Tyr Thr Asp Tyr
 355 360 365
 His Gly Leu Gln Gln Met Lys Arg His Met Gly Leu Ser Phe Lys Lys

ITI-08-PCT_Sequence_Listing_ST25.txt

```

370          375          380
Tyr Arg Cys Arg Ile Arg Val Ile Asp Thr Phe Gly Thr Glu Pro Ala
385          390          395          400
Tyr Asn His Glu Glu Tyr Ala Thr Leu His Gly Tyr Arg Thr Asn Trp
          405          410          415
Gly Tyr Trp Asn Leu Asn Pro Lys Gln Phe Met Thr Met Phe Pro His
          420          425          430
Thr Pro Asp Asn Ser Phe Met Gly Phe Val Ser Glu Glu Leu Asn Glu
          435          440          445
Thr Glu Lys Arg Leu Ile Lys Gly Gly Lys Ala Ser Asn Met Ala Val
          450          455          460
Val Tyr Gly Lys Glu Ala Ser Ile Trp Lys Leu Gln Gly Lys Glu Lys
465          470          475          480
Phe Leu Gly Ile Leu Asn Lys Tyr Met Glu Ile His Gly Thr Val Tyr
          485          490          495
Tyr Glu Ser Gln Arg Pro Pro Glu Val Pro Ala Phe Val Lys Asn His
          500          505          510
Gly Leu Leu Pro Gln Pro Glu Phe Gln Gln Leu Leu Arg Lys Ala Lys
          515          520          525
Leu Phe Ile Gly Phe Gly Phe Pro Tyr Glu Gly Pro Ala Pro Leu Glu
          530          535          540
Ala Ile Ala Asn Gly Cys Ile Phe Leu Gln Ser Arg Phe Ser Pro Pro
545          550          555          560
His Ser Ser Leu Asn His Glu Phe Phe Arg Gly Lys Pro Thr Ser Arg
          565          570          575
Glu Val Phe Ser Gln His Pro Tyr Ala Glu Asn Phe Ile Gly Lys Pro
          580          585          590
His Val Trp Thr Val Asp Tyr Asn Asn Ser Glu Glu Phe Glu Ala Ala
          595          600          605
Ile Lys Ala Ile Met Arg Thr Gln Val Asp Pro Tyr Leu Pro Tyr Glu
          610          615          620
Tyr Thr Cys Glu Gly Met Leu Glu Arg Ile His Ala Tyr Ile Gln His
625          630          635          640
Gln Asp Phe Cys Arg Ala Pro Asp Pro Ala Leu Pro Glu Ala His Ala
          645          650          655

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Pro Gln Ser Pro Phe Val Leu Ala Pro Asn Ala Thr His Leu Glu Trp
660 665 670

Ala Arg Asn Thr Ser Leu Ala Pro Gly Ala Trp Pro Pro Ala His Ala
675 680 685

Leu Arg Ala Trp Leu Ala Val Pro Gly Arg Ala Cys Thr Asp Thr Cys
690 695 700

Leu Asp His Gly Leu Ile Cys Glu Pro Ser Phe Phe Pro Phe Leu Asn
705 710 715 720

Ser Gln Asp Ala Phe Leu Lys Leu Gln Val Pro Cys Asp Ser Thr Glu
725 730 735

Ser Glu Met Asn His Leu Tyr Pro Ala Phe Ala Gln Pro Gly Gln Glu
740 745 750

Cys Tyr Leu Gln Lys Glu Pro Leu Leu Phe Ser Cys Ala Gly Ser Asn
755 760 765

Thr Lys Tyr Arg Arg Leu Cys Pro Cys Arg Asp Phe Arg Lys Gly Gln
770 775 780

Val Ala Leu Cys Gln Gly Cys Leu
785 790

<210> 549
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> NA88-A__Homo_sapiens__10790436

<400> 549

Met Thr Gln Gly Gln His Phe Leu Gln Lys Val
1 5 10

<210> 550
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Neo-PAP__Homo_sapiens__Q9BWT3

<400> 550

Met Lys Glu Met Ser Ala Asn Thr Val Leu Asp Ser Gln Arg Gln Gln

ITI-08-PCT_Sequence_Listing_ST25.txt

```

1           5           10           15
Lys His Tyr Gly Ile Thr Ser Pro Ile Ser Leu Ala Ser Pro Lys Glu
      20                25                30
Ile Asp His Ile Tyr Thr Gln Lys Leu Ile Asp Ala Met Lys Pro Phe
      35                40                45
Gly Val Phe Glu Asp Glu Glu Glu Leu Asn His Arg Leu Val Val Leu
      50                55                60
Gly Lys Leu Asn Asn Leu Val Lys Glu Trp Ile Ser Asp Val Ser Glu
65                70                75                80
Ser Lys Asn Leu Pro Pro Ser Val Val Ala Thr Val Gly Gly Lys Ile
      85                90                95
Phe Thr Phe Gly Ser Tyr Arg Leu Gly Val His Thr Lys Gly Ala Asp
      100               105               110
Ile Asp Ala Leu Cys Val Ala Pro Arg His Val Glu Arg Ser Asp Phe
      115               120               125
Phe Gln Ser Phe Phe Glu Lys Leu Lys His Gln Asp Gly Ile Arg Asn
      130               135               140
Leu Arg Ala Val Glu Asp Ala Phe Val Pro Val Ile Lys Phe Glu Phe
145               150               155               160
Asp Gly Ile Glu Ile Asp Leu Val Phe Ala Arg Leu Ala Ile Gln Thr
      165               170               175
Ile Ser Asp Asn Leu Asp Leu Arg Asp Asp Ser Arg Leu Arg Ser Leu
      180               185               190
Asp Ile Arg Cys Ile Arg Ser Leu Asn Gly Cys Arg Val Thr Asp Glu
      195               200               205
Ile Leu His Leu Val Pro Asn Lys Glu Thr Phe Arg Leu Thr Leu Arg
      210               215               220
Ala Val Lys Leu Trp Ala Lys Arg Arg Gly Ile Tyr Ser Asn Met Leu
225               230               235               240
Gly Phe Leu Gly Gly Val Ser Trp Ala Met Leu Val Ala Arg Thr Cys
      245               250               255
Gln Leu Tyr Pro Asn Ala Ala Ala Ser Thr Leu Val His Lys Phe Phe
      260               265               270
Leu Val Phe Ser Lys Trp Glu Trp Pro Asn Pro Val Leu Leu Lys Gln
      275               280               285

```


ITI-08-PCT_Sequence_Listing_ST25.txt

Pro	Glu	Glu	Ser	Asn	Leu	Asn	Leu	Pro	Val	Trp	Asp	Pro	Arg	Val	Asn	290	295	300	
Pro	Ser	Asp	Arg	Tyr	His	Leu	Met	Pro	Ile	Ile	Thr	Pro	Ala	Tyr	Pro	305	310	315	320
Gln	Gln	Asn	Ser	Thr	Tyr	Asn	Val	Ser	Thr	Ser	Thr	Arg	Thr	Val	Met	325	330	335	
Val	Glu	Glu	Phe	Lys	Gln	Gly	Leu	Ala	Val	Thr	Asp	Glu	Ile	Leu	Gln	340	345	350	
Gly	Lys	Ser	Asp	Trp	Ser	Lys	Leu	Leu	Glu	Pro	Pro	Asn	Phe	Phe	Gln	355	360	365	
Lys	Tyr	Arg	His	Tyr	Ile	Val	Leu	Thr	Ala	Ser	Ala	Ser	Thr	Glu	Glu	370	375	380	
Asn	His	Leu	Glu	Trp	Val	Gly	Leu	Val	Glu	Ser	Lys	Ile	Arg	Val	Leu	385	390	395	400
Val	Gly	Asn	Leu	Glu	Arg	Asn	Glu	Phe	Ile	Thr	Leu	Ala	His	Val	Asn	405	410	415	
Pro	Gln	Ser	Phe	Pro	Gly	Asn	Lys	Glu	His	His	Lys	Asp	Asn	Asn	Tyr	420	425	430	
Val	Ser	Met	Trp	Phe	Leu	Gly	Ile	Ile	Phe	Arg	Arg	Val	Glu	Asn	Ala	435	440	445	
Glu	Ser	Val	Asn	Ile	Asp	Leu	Thr	Tyr	Asp	Ile	Gln	Ser	Phe	Thr	Asp	450	455	460	
Thr	Val	Tyr	Arg	Gln	Ala	Asn	Asn	Ile	Asn	Met	Leu	Lys	Glu	Gly	Met	465	470	475	480
Lys	Ile	Glu	Ala	Thr	His	Val	Lys	Lys	Lys	Gln	Leu	His	His	Tyr	Leu	485	490	495	
Pro	Ala	Glu	Ile	Leu	Gln	Lys	Lys	Lys	Lys	Gln	Ser	Leu	Ser	Asp	Val	500	505	510	
Asn	Arg	Ser	Ser	Gly	Gly	Leu	Gln	Ser	Lys	Arg	Leu	Ser	Leu	Asp	Ser	515	520	525	
Ser	Cys	Leu	Asp	Ser	Ser	Arg	Asp	Thr	Asp	Asn	Gly	Thr	Pro	Phe	Asn	530	535	540	
Ser	Pro	Ala	Ser	Lys	Ser	Asp	Ser	Pro	Ser	Val	Gly	Glu	Thr	Glu	Arg	545	550	555	560

ITI-08-PCT_Sequence_Listing_ST25.txt

Asn Ser Ala Glu Pro Ala Ala Val Ile Val Glu Lys Pro Leu Ser Val
565 570 575

Pro Pro Ala Gln Gly Leu Ser Ile Pro Val Ile Gly Ala Lys Val Asp
580 585 590

Ser Thr Val Lys Thr Val Ser Pro Pro Thr Val Cys Thr Ile Pro Thr
595 600 605

Val Val Gly Arg Asn Val Ile Pro Arg Ile Thr Thr Pro His Asn Pro
610 615 620

Ala Gln Gly Gln Pro His Leu Asn Gly Met Ser Asn Ile Thr Lys Thr
625 630 635 640

Val Thr Pro Lys Arg Ser His Ser Pro Ser Ile Asp Gly Thr Pro Lys
645 650 655

Arg Leu Lys Asp Val Glu Lys Phe Ile Arg Leu Glu Ser Thr Phe Lys
660 665 670

Asp Pro Arg Thr Ala Glu Glu Arg Lys Arg Lys Ser Val Asp Ala Ile
675 680 685

Gly Gly Glu Ser Met Pro Ile Pro Thr Ile Asp Thr Ser Arg Lys Lys
690 695 700

Arg Leu Pro Ser Lys Glu Leu Pro Asp Ser Ser Ser Pro Val Pro Ala
705 710 715 720

Asn Asn Ile Arg Val Ile Lys Asn Ser Ile Arg Leu Thr Leu Asn Arg
725 730 735

<210> 551

<211> 458

<212> PRT

<213> Artificial Sequence

<220>

<223> NFYC/m__Homo_sapiens__Q13952

<400> 551

Met Ser Thr Glu Gly Gly Phe Gly Gly Thr Ser Ser Ser Asp Ala Gln
1 5 10 15

Gln Ser Leu Gln Ser Phe Trp Pro Arg Val Met Glu Glu Ile Arg Asn
20 25 30

Leu Thr Val Lys Asp Phe Arg Val Gln Glu Leu Pro Leu Ala Arg Ile
35 40 45

ITI-08-PCT_Sequence_Listing_ST25.txt

Lys Lys Ile Met Lys Leu Asp Glu Asp Val Lys Met Ile Ser Ala Glu
 50 55 60
 Ala Pro Val Leu Phe Ala Lys Ala Ala Gln Ile Phe Ile Thr Glu Leu
 65 70 75 80
 Thr Leu Arg Ala Trp Ile His Thr Glu Asp Asn Lys Arg Arg Thr Leu
 85 90 95
 Gln Arg Asn Asp Ile Ala Met Ala Ile Thr Lys Phe Asp Gln Phe Asp
 100 105 110
 Phe Leu Ile Asp Ile Val Pro Arg Asp Glu Leu Lys Pro Pro Lys Arg
 115 120 125
 Gln Glu Glu Val Arg Gln Ser Val Thr Pro Ala Glu Pro Val Gln Tyr
 130 135 140
 Tyr Phe Thr Leu Ala Gln Gln Pro Thr Ala Val Gln Val Gln Gly Gln
 145 150 155 160
 Gln Gln Gly Gln Gln Thr Thr Ser Ser Thr Thr Thr Ile Gln Pro Gly
 165 170 175
 Gln Ile Ile Ile Ala Gln Pro Gln Gln Gly Gln Thr Thr Pro Val Thr
 180 185 190
 Met Gln Val Gly Glu Gly Gln Gln Val Gln Ile Val Gln Ala Gln Pro
 195 200 205
 Gln Gly Gln Ala Gln Gln Ala Gln Ser Gly Thr Gly Gln Thr Met Gln
 210 215 220
 Val Met Gln Gln Ile Ile Thr Asn Thr Gly Glu Ile Gln Gln Ile Pro
 225 230 235 240
 Val Gln Leu Asn Ala Gly Gln Leu Gln Tyr Ile Arg Leu Ala Gln Pro
 245 250 255
 Val Ser Gly Thr Gln Val Val Gln Gly Gln Ile Gln Thr Leu Ala Thr
 260 265 270
 Asn Ala Gln Gln Gly Gln Arg Asn Ala Ser Gln Gly Lys Pro Arg Arg
 275 280 285
 Cys Leu Lys Glu Thr Leu Gln Ile Thr Gln Thr Glu Val Gln Gln Gly
 290 295 300
 Gln Gln Gln Phe Ser Gln Phe Thr Asp Gly Gln Arg Asn Ser Val Gln
 305 310 315 320
 Gln Ala Arg Val Ser Glu Leu Thr Gly Glu Ala Glu Pro Arg Glu Val

ITI-08-PCT_Sequence_Listing_ST25.txt

325 330 335

Lys Ala Thr Gly Asn Ser Thr Pro Cys Thr Ser Ser Leu Pro Thr Thr
340 345 350

His Pro Pro Ser His Arg Ala Gly Ala Ser Cys Val Cys Cys Ser Gln
355 360 365

Pro Gln Gln Ser Ser Thr Ser Pro Pro Pro Ser Asp Ala Leu Gln Trp
370 375 380

Val Val Val Glu Val Ser Gly Thr Pro Asn Gln Leu Glu Thr His Arg
385 390 395 400

Glu Leu His Ala Pro Leu Pro Gly Met Thr Ser Leu Ser Pro Leu His
405 410 415

Pro Ser Gln Gln Leu Tyr Gln Ile Gln Gln Val Thr Met Pro Ala Gly
420 425 430

Gln Asp Leu Ala Gln Pro Met Phe Ile Gln Ser Ala Asn Gln Pro Ser
435 440 445

Asp Gly Gln Ala Pro Gln Val Thr Gly Asp
450 455

<210> 552

<211> 933

<212> PRT

<213> Artificial Sequence

<220>

<223> NGEP__Homo_sapiens__Q6IWH7

<400> 552

Met Arg Met Ala Ala Thr Ala Trp Ala Gly Leu Gln Gly Pro Pro Leu
1 5 10 15

Pro Thr Leu Cys Pro Ala Val Arg Thr Gly Leu Tyr Cys Arg Asp Gln
20 25 30

Ala His Ala Glu Arg Trp Ala Met Thr Ser Glu Thr Ser Ser Gly Ser
35 40 45

His Cys Ala Arg Ser Arg Met Leu Arg Arg Arg Ala Gln Glu Glu Asp
50 55 60

Ser Thr Val Leu Ile Asp Val Ser Pro Pro Glu Ala Glu Lys Arg Gly
65 70 75 80

Ser Tyr Gly Ser Thr Ala His Ala Ser Glu Pro Gly Gly Gln Gln Ala

ITI-08-PCT_Sequence_Listing_ST25.txt

85

90

95

Ala Ala Cys Arg Ala Gly Ser Pro Ala Lys Pro Arg Ile Ala Asp Phe
 100 105 110

Val Leu Val Trp Glu Glu Asp Leu Lys Leu Asp Arg Gln Gln Asp Ser
 115 120 125

Ala Ala Arg Asp Arg Thr Asp Met His Arg Thr Trp Arg Glu Thr Phe
 130 135 140

Leu Asp Asn Leu Arg Ala Ala Gly Leu Cys Val Asp Gln Gln Asp Val
 145 150 155 160

Gln Asp Gly Asn Thr Thr Val His Tyr Ala Leu Leu Ser Ala Ser Trp
 165 170 175

Ala Val Leu Cys Tyr Tyr Ala Glu Asp Leu Arg Leu Lys Leu Pro Leu
 180 185 190

Gln Glu Leu Pro Asn Gln Ala Ser Asn Trp Ser Ala Gly Leu Leu Ala
 195 200 205

Trp Leu Gly Ile Pro Asn Val Leu Leu Glu Val Val Pro Asp Val Pro
 210 215 220

Pro Glu Tyr Tyr Ser Cys Arg Phe Arg Val Asn Lys Leu Pro Arg Phe
 225 230 235 240

Leu Gly Ser Asp Asn Gln Asp Thr Phe Phe Thr Ser Thr Lys Arg His
 245 250 255

Gln Ile Leu Phe Glu Ile Leu Ala Lys Thr Pro Tyr Gly His Glu Lys
 260 265 270

Lys Asn Leu Leu Gly Ile His Gln Leu Leu Ala Glu Gly Val Leu Ser
 275 280 285

Ala Ala Phe Pro Leu His Asp Gly Pro Phe Lys Thr Pro Pro Glu Gly
 290 295 300

Pro Gln Ala Pro Arg Leu Asn Gln Arg Gln Val Leu Phe Gln His Trp
 305 310 315 320

Ala Arg Trp Gly Lys Trp Asn Lys Tyr Gln Pro Leu Asp His Val Arg
 325 330 335

Arg Tyr Phe Gly Glu Lys Val Ala Leu Tyr Phe Ala Trp Leu Gly Phe
 340 345 350

Tyr Thr Gly Trp Leu Leu Pro Ala Ala Val Val Gly Thr Leu Val Phe
 355 360 365

ITI-08-PCT_Sequence_Listing_ST25.txt

```

Leu Val Gly Cys Phe Leu Val Phe Ser Asp Ile Pro Thr Gln Glu Leu
 370                      375                      380

Cys Gly Ser Lys Asp Ser Phe Glu Met Cys Pro Leu Cys Leu Asp Cys
385                      390                      395                      400

Pro Phe Trp Leu Leu Ser Ser Ala Cys Ala Leu Ala Gln Ala Gly Arg
                      405                      410                      415

Leu Phe Asp His Gly Gly Thr Val Phe Phe Ser Leu Phe Met Ala Leu
                      420                      425                      430

Trp Ala Val Leu Leu Leu Glu Tyr Trp Lys Arg Lys Ser Ala Thr Leu
                      435                      440                      445

Ala Tyr Arg Trp Asp Cys Ser Asp Tyr Glu Asp Thr Glu Glu Arg Pro
450                      455                      460

Arg Pro Gln Phe Ala Ala Ser Ala Pro Met Thr Ala Pro Asn Pro Ile
465                      470                      475                      480

Thr Gly Glu Asp Glu Pro Tyr Phe Pro Glu Arg Ser Arg Ala Arg Arg
                      485                      490                      495

Met Leu Ala Gly Ser Val Val Ile Val Val Met Val Ala Val Val Val
500                      505                      510

Met Cys Leu Val Ser Ile Ile Leu Tyr Arg Ala Ile Met Ala Ile Val
515                      520                      525

Val Ser Arg Ser Gly Asn Thr Leu Leu Ala Ala Trp Ala Ser Arg Ile
530                      535                      540

Ala Ser Leu Thr Gly Ser Val Val Asn Leu Val Phe Ile Leu Ile Leu
545                      550                      555                      560

Ser Lys Ile Tyr Val Ser Leu Ala His Val Leu Thr Arg Trp Glu Met
                      565                      570                      575

His Arg Thr Gln Thr Lys Phe Glu Asp Ala Phe Thr Leu Lys Val Phe
580                      585                      590

Ile Phe Gln Phe Val Asn Phe Tyr Ser Ser Pro Val Tyr Ile Ala Phe
595                      600                      605

Phe Lys Gly Arg Phe Val Gly Tyr Pro Gly Asn Tyr His Thr Leu Phe
610                      615                      620

Gly Val Arg Asn Glu Glu Cys Ala Ala Gly Gly Cys Leu Ile Glu Leu
625                      630                      635                      640

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Ala Gln Glu Leu Leu Val Ile Met Val Gly Lys Gln Val Ile Asn Asn
645 650 655

Met Gln Glu Val Leu Ile Pro Lys Leu Lys Gly Trp Trp Gln Lys Phe
660 665 670

Arg Leu Arg Ser Lys Lys Arg Lys Ala Gly Ala Ser Ala Gly Ala Ser
675 680 685

Gln Gly Pro Trp Glu Asp Asp Tyr Glu Leu Val Pro Cys Glu Gly Leu
690 695 700

Phe Asp Glu Tyr Leu Glu Met Val Leu Gln Phe Gly Phe Val Thr Ile
705 710 715 720

Phe Val Ala Ala Cys Pro Leu Ala Pro Leu Phe Ala Leu Leu Asn Asn
725 730 735

Trp Val Glu Ile Arg Leu Asp Ala Arg Lys Phe Val Cys Glu Tyr Arg
740 745 750

Arg Pro Val Ala Glu Arg Ala Gln Asp Ile Gly Ile Trp Phe His Ile
755 760 765

Leu Ala Gly Leu Thr His Leu Ala Val Ile Ser Asn Ala Phe Leu Leu
770 775 780

Ala Phe Ser Ser Asp Phe Leu Pro Arg Ala Tyr Tyr Arg Trp Thr Arg
785 790 795 800

Ala His Asp Leu Arg Gly Phe Leu Asn Phe Thr Leu Ala Arg Ala Pro
805 810 815

Ser Ser Phe Ala Ala Ala His Asn Arg Thr Cys Arg Tyr Arg Ala Phe
820 825 830

Arg Asp Asp Asp Gly His Tyr Ser Gln Thr Tyr Trp Asn Leu Leu Ala
835 840 845

Ile Arg Leu Ala Phe Val Ile Val Phe Glu His Val Val Phe Ser Val
850 855 860

Gly Arg Leu Leu Asp Leu Leu Val Pro Asp Ile Pro Glu Ser Val Glu
865 870 875 880

Ile Lys Val Lys Arg Glu Tyr Tyr Leu Ala Lys Gln Ala Leu Ala Glu
885 890 895

Asn Glu Val Leu Phe Gly Thr Asn Gly Thr Lys Asp Glu Gln Pro Glu
900 905 910

Gly Ser Glu Leu Ser Ser His Trp Thr Pro Phe Thr Val Pro Lys Ala

ITI-08-PCT_Sequence_Listing_ST25.txt

915

920

925

Ser Gln Leu Gln Gln
930

<210> 553

<211> 294

<212> PRT

<213> Artificial Sequence

<220>

<223> NPM__Homo_sapiens__P06748

<400> 553

Met Glu Asp Ser Met Asp Met Asp Met Ser Pro Leu Arg Pro Gln Asn
1 5 10 15

Tyr Leu Phe Gly Cys Glu Leu Lys Ala Asp Lys Asp Tyr His Phe Lys
20 25 30

Val Asp Asn Asp Glu Asn Glu His Gln Leu Ser Leu Arg Thr Val Ser
35 40 45

Leu Gly Ala Gly Ala Lys Asp Glu Leu His Ile Val Glu Ala Glu Ala
50 55 60

Met Asn Tyr Glu Gly Ser Pro Ile Lys Val Thr Leu Ala Thr Leu Lys
65 70 75 80

Met Ser Val Gln Pro Thr Val Ser Leu Gly Gly Phe Glu Ile Thr Pro
85 90 95

Pro Val Val Leu Arg Leu Lys Cys Gly Ser Gly Pro Val His Ile Ser
100 105 110

Gly Gln His Leu Val Ala Val Glu Glu Asp Ala Glu Ser Glu Asp Glu
115 120 125

Glu Glu Glu Asp Val Lys Leu Leu Ser Ile Ser Gly Lys Arg Ser Ala
130 135 140

Pro Gly Gly Gly Ser Lys Val Pro Gln Lys Lys Val Lys Leu Ala Ala
145 150 155 160

Asp Glu Asp Asp Asp Asp Asp Asp Glu Glu Asp Asp Asp Glu Asp Asp
165 170 175

Asp Asp Asp Asp Phe Asp Asp Glu Glu Ala Glu Glu Lys Ala Pro Val
180 185 190

Lys Lys Ser Ile Arg Asp Thr Pro Ala Lys Asn Ala Gln Lys Ser Asn

ITI-08-PCT_Sequence_Listing_ST25.txt

195

200

205

Gln Asn Gly Lys Asp Ser Lys Pro Ser Ser Thr Pro Arg Ser Lys Gly
210 215 220

Gln Glu Ser Phe Lys Lys Gln Glu Lys Thr Pro Lys Thr Pro Lys Gly
225 230 235 240

Pro Ser Ser Val Glu Asp Ile Lys Ala Lys Met Gln Ala Ser Ile Glu
245 250 255

Lys Gly Gly Ser Leu Pro Lys Val Glu Ala Lys Phe Ile Asn Tyr Val
260 265 270

Lys Asn Cys Phe Arg Met Thr Asp Gln Glu Ala Ile Gln Asp Leu Trp
275 280 285

Gln Trp Arg Lys Ser Leu
290

<210> 554
<211> 1304
<212> PRT
<213> Artificial Sequence

<220>
<223> NRCAM__Homo_sapiens__Q92823

<400> 554

Met Gln Leu Lys Ile Met Pro Lys Lys Lys Arg Leu Ser Ala Gly Arg
1 5 10 15

Val Pro Leu Ile Leu Phe Leu Cys Gln Met Ile Ser Ala Leu Glu Val
20 25 30

Pro Leu Asp Pro Lys Leu Leu Glu Asp Leu Val Gln Pro Pro Thr Ile
35 40 45

Thr Gln Gln Ser Pro Lys Asp Tyr Ile Ile Asp Pro Arg Glu Asn Ile
50 55 60

Val Ile Gln Cys Glu Ala Lys Gly Lys Pro Pro Pro Ser Phe Ser Trp
65 70 75 80

Thr Arg Asn Gly Thr His Phe Asp Ile Asp Lys Asp Pro Leu Val Thr
85 90 95

Met Lys Pro Gly Thr Gly Thr Leu Ile Ile Asn Ile Met Ser Glu Gly
100 105 110

Lys Ala Glu Thr Tyr Glu Gly Val Tyr Gln Cys Thr Ala Arg Asn Glu

ITI-08-PCT_Sequence_Listing_ST25.txt

```

115              120              125
Arg Gly Ala Ala Val Ser Asn Asn Ile Val Val Arg Pro Ser Arg Ser
130              135              140
Pro Leu Trp Thr Lys Glu Lys Leu Glu Pro Ile Thr Leu Gln Ser Gly
145              150              155              160
Gln Ser Leu Val Leu Pro Cys Arg Pro Pro Ile Gly Leu Pro Pro Pro
165              170              175
Ile Ile Phe Trp Met Asp Asn Ser Phe Gln Arg Leu Pro Gln Ser Glu
180              185              190
Arg Val Ser Gln Gly Leu Asn Gly Asp Leu Tyr Phe Ser Asn Val Leu
195              200              205
Pro Glu Asp Thr Arg Glu Asp Tyr Ile Cys Tyr Ala Arg Phe Asn His
210              215              220
Thr Gln Thr Ile Gln Gln Lys Gln Pro Ile Ser Val Lys Val Ile Ser
225              230              235              240
Val Asp Glu Leu Asn Asp Thr Ile Ala Ala Asn Leu Ser Asp Thr Glu
245              250              255
Phe Tyr Gly Ala Lys Ser Ser Arg Glu Arg Pro Pro Thr Phe Leu Thr
260              265              270
Pro Glu Gly Asn Ala Ser Asn Lys Glu Glu Leu Arg Gly Asn Val Leu
275              280              285
Ser Leu Glu Cys Ile Ala Glu Gly Leu Pro Thr Pro Ile Ile Tyr Trp
290              295              300
Ala Lys Glu Asp Gly Met Leu Pro Lys Asn Arg Thr Val Tyr Lys Asn
305              310              315              320
Phe Glu Lys Thr Leu Gln Ile Ile His Val Ser Glu Ala Asp Ser Gly
325              330              335
Asn Tyr Gln Cys Ile Ala Lys Asn Ala Leu Gly Ala Ile His His Thr
340              345              350
Ile Ser Val Arg Val Lys Ala Ala Pro Tyr Trp Ile Thr Ala Pro Gln
355              360              365
Asn Leu Val Leu Ser Pro Gly Glu Asp Gly Thr Leu Ile Cys Arg Ala
370              375              380
Asn Gly Asn Pro Lys Pro Arg Ile Ser Trp Leu Thr Asn Gly Val Pro
385              390              395              400

```

ITI-08-PCT_Sequence_Listing_ST25.txt

```

Ile Glu Ile Ala Pro Asp Asp Pro Ser Arg Lys Ile Asp Gly Asp Thr
      405                      410                      415

Ile Ile Phe Ser Asn Val Gln Glu Arg Ser Ser Ala Val Tyr Gln Cys
      420                      425                      430

Asn Ala Ser Asn Glu Tyr Gly Tyr Leu Leu Ala Asn Ala Phe Val Asn
      435                      440                      445

Val Leu Ala Glu Pro Pro Arg Ile Leu Thr Pro Ala Asn Thr Leu Tyr
      450                      455                      460

Gln Val Ile Ala Asn Arg Pro Ala Leu Leu Asp Cys Ala Phe Phe Gly
465                      470                      475                      480

Ser Pro Leu Pro Thr Ile Glu Trp Phe Lys Gly Ala Lys Gly Ser Ala
      485                      490                      495

Leu His Glu Asp Ile Tyr Val Leu His Glu Asn Gly Thr Leu Glu Ile
      500                      505                      510

Pro Val Ala Gln Lys Asp Ser Thr Gly Thr Tyr Thr Cys Val Ala Arg
      515                      520                      525

Asn Lys Leu Gly Met Ala Lys Asn Glu Val His Leu Glu Ile Lys Asp
      530                      535                      540

Pro Thr Trp Ile Val Lys Gln Pro Glu Tyr Ala Val Val Gln Arg Gly
545                      550                      555                      560

Ser Met Val Ser Phe Glu Cys Lys Val Lys His Asp His Thr Leu Ser
      565                      570                      575

Leu Thr Val Leu Trp Leu Lys Asp Asn Arg Glu Leu Pro Ser Asp Glu
      580                      585                      590

Arg Phe Thr Val Asp Lys Asp His Leu Val Val Ala Asp Val Ser Asp
      595                      600                      605

Asp Asp Ser Gly Thr Tyr Thr Cys Val Ala Asn Thr Thr Leu Asp Ser
      610                      615                      620

Val Ser Ala Ser Ala Val Leu Ser Val Val Ala Pro Thr Pro Thr Pro
625                      630                      635                      640

Ala Pro Val Tyr Asp Val Pro Asn Pro Pro Phe Asp Leu Glu Leu Thr
      645                      650                      655

Asp Gln Leu Asp Lys Ser Val Gln Leu Ser Trp Thr Pro Gly Asp Asp
      660                      665                      670

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Asn Asn Ser Pro Ile Thr Lys Phe Ile Ile Glu Tyr Glu Asp Ala Met
 675 680 685
 His Lys Pro Gly Leu Trp His His Gln Thr Glu Val Ser Gly Thr Gln
 690 695 700
 Thr Thr Ala Gln Leu Lys Leu Ser Pro Tyr Val Asn Tyr Ser Phe Arg
 705 710 715 720
 Val Met Ala Val Asn Ser Ile Gly Lys Ser Leu Pro Ser Glu Ala Ser
 725 730 735
 Glu Gln Tyr Leu Thr Lys Ala Ser Glu Pro Asp Lys Asn Pro Thr Ala
 740 745 750
 Val Glu Gly Leu Gly Ser Glu Pro Asp Asn Leu Val Ile Thr Trp Lys
 755 760 765
 Pro Leu Asn Gly Phe Glu Ser Asn Gly Pro Gly Leu Gln Tyr Lys Val
 770 775 780
 Ser Trp Arg Gln Lys Asp Gly Asp Asp Glu Trp Thr Ser Val Val Val
 785 790 795 800
 Ala Asn Val Ser Lys Tyr Ile Val Ser Gly Thr Pro Thr Phe Val Pro
 805 810 815
 Tyr Leu Ile Lys Val Gln Ala Leu Asn Asp Met Gly Phe Ala Pro Glu
 820 825 830
 Pro Ala Val Val Met Gly His Ser Gly Glu Asp Leu Pro Met Val Ala
 835 840 845
 Pro Gly Asn Val Arg Val Asn Val Val Asn Ser Thr Leu Ala Glu Val
 850 855 860
 His Trp Asp Pro Val Pro Leu Lys Ser Ile Arg Gly His Leu Gln Gly
 865 870 875 880
 Tyr Arg Ile Tyr Tyr Trp Lys Thr Gln Ser Ser Ser Lys Arg Asn Arg
 885 890 895
 Arg His Ile Glu Lys Lys Ile Leu Thr Phe Gln Gly Ser Lys Thr His
 900 905 910
 Gly Met Leu Pro Gly Leu Glu Pro Phe Ser His Tyr Thr Leu Asn Val
 915 920 925
 Arg Val Val Asn Gly Lys Gly Glu Gly Pro Ala Ser Pro Asp Arg Val
 930 935 940
 Phe Asn Thr Pro Glu Gly Val Pro Ser Ala Pro Ser Ser Leu Lys Ile

ITI-08-PCT_Sequence_Listing_ST25.txt

```

945                               950                               955                               960
Val Asn Pro Thr Leu Asp Ser Leu Thr Leu Glu Trp Asp Pro Pro Ser
                               965                               970                               975

His Pro Asn Gly Ile Leu Thr Glu Tyr Thr Leu Lys Tyr Gln Pro Ile
                               980                               985                               990

Asn Ser Thr His Glu Leu Gly Pro Leu Val Asp Leu Lys Ile Pro Ala
                               995                               1000                               1005

Asn Lys Thr Arg Trp Thr Leu Lys Asn Leu Asn Phe Ser Thr Arg
   1010                               1015                               1020

Tyr Lys Phe Tyr Phe Tyr Ala Gln Thr Ser Ala Gly Ser Gly Ser
   1025                               1030                               1035

Gln Ile Thr Glu Glu Ala Val Thr Thr Val Asp Glu Ala Gly Ile
   1040                               1045                               1050

Leu Pro Pro Asp Val Gly Ala Gly Lys Val Gln Ala Val Asn Pro
   1055                               1060                               1065

Arg Ile Ser Asn Leu Thr Ala Ala Ala Ala Glu Thr Tyr Ala Asn
   1070                               1075                               1080

Ile Ser Trp Glu Tyr Glu Gly Pro Glu His Val Asn Phe Tyr Val
   1085                               1090                               1095

Glu Tyr Gly Val Ala Gly Ser Lys Glu Glu Trp Arg Lys Glu Ile
   1100                               1105                               1110

Val Asn Gly Ser Arg Ser Phe Phe Gly Leu Lys Gly Leu Met Pro
   1115                               1120                               1125

Gly Thr Ala Tyr Lys Val Arg Val Gly Ala Val Gly Asp Ser Gly
   1130                               1135                               1140

Phe Val Ser Ser Glu Asp Val Phe Glu Thr Gly Pro Ala Met Ala
   1145                               1150                               1155

Ser Arg Gln Val Asp Ile Ala Thr Gln Gly Trp Phe Ile Gly Leu
   1160                               1165                               1170

Met Cys Ala Val Ala Leu Leu Ile Leu Ile Leu Leu Ile Val Cys
   1175                               1180                               1185

Phe Ile Arg Arg Asn Lys Gly Gly Lys Tyr Pro Val Lys Glu Lys
   1190                               1195                               1200

Glu Asp Ala His Ala Asp Pro Glu Ile Gln Pro Met Lys Glu Asp
   1205                               1210                               1215

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Asp	Gly	Thr	Phe	Gly	Glu	Tyr	Ser	Asp	Ala	Glu	Asp	His	Lys	Pro	
1220						1225					1230				
Leu	Lys	Lys	Gly	Ser	Arg	Thr	Pro	Ser	Asp	Arg	Thr	Val	Lys	Lys	
1235						1240					1245				
Glu	Asp	Ser	Asp	Asp	Ser	Leu	Val	Asp	Tyr	Gly	Glu	Gly	Val	Asn	
1250						1255					1260				
Gly	Gln	Phe	Asn	Glu	Asp	Gly	Ser	Phe	Ile	Gly	Gln	Tyr	Ser	Gly	
1265						1270					1275				
Lys	Lys	Glu	Lys	Glu	Pro	Ala	Glu	Gly	Asn	Glu	Ser	Ser	Glu	Ala	
1280						1285					1290				
Pro	Ser	Pro	Val	Asn	Ala	Met	Asn	Ser	Phe	Val					
1295						1300									
<210> 555															
<211> 434															
<212> PRT															
<213> Artificial Sequence															
<220>															
<223> NSE__Homo_sapiens__P09104															
<400> 555															
Met	Ser	Ile	Glu	Lys	Ile	Trp	Ala	Arg	Glu	Ile	Leu	Asp	Ser	Arg	Gly
1				5					10					15	
Asn	Pro	Thr	Val	Glu	Val	Asp	Leu	Tyr	Thr	Ala	Lys	Gly	Leu	Phe	Arg
			20					25					30		
Ala	Ala	Val	Pro	Ser	Gly	Ala	Ser	Thr	Gly	Ile	Tyr	Glu	Ala	Leu	Glu
			35				40					45			
Leu	Arg	Asp	Gly	Asp	Lys	Gln	Arg	Tyr	Leu	Gly	Lys	Gly	Val	Leu	Lys
	50					55					60				
Ala	Val	Asp	His	Ile	Asn	Ser	Thr	Ile	Ala	Pro	Ala	Leu	Ile	Ser	Ser
65					70				75					80	
Gly	Leu	Ser	Val	Val	Glu	Gln	Glu	Lys	Leu	Asp	Asn	Leu	Met	Leu	Glu
			85					90					95		
Leu	Asp	Gly	Thr	Glu	Asn	Lys	Ser	Lys	Phe	Gly	Ala	Asn	Ala	Ile	Leu
			100					105					110		
Gly	Val	Ser	Leu	Ala	Val	Cys	Lys	Ala	Gly	Ala	Ala	Glu	Arg	Glu	Leu
			115				120					125			

ITI-08-PCT_Sequence_Listing_ST25.txt

Pro	Leu	Tyr	Arg	His	Ile	Ala	Gln	Leu	Ala	Gly	Asn	Ser	Asp	Leu	Ile	130	135	140	
Leu	Pro	Val	Pro	Ala	Phe	Asn	Val	Ile	Asn	Gly	Gly	Ser	His	Ala	Gly	145	150	155	160
Asn	Lys	Leu	Ala	Met	Gln	Glu	Phe	Met	Ile	Leu	Pro	Val	Gly	Ala	Glu	165	170	175	
Ser	Phe	Arg	Asp	Ala	Met	Arg	Leu	Gly	Ala	Glu	Val	Tyr	His	Thr	Leu	180	185	190	
Lys	Gly	Val	Ile	Lys	Asp	Lys	Tyr	Gly	Lys	Asp	Ala	Thr	Asn	Val	Gly	195	200	205	
Asp	Glu	Gly	Gly	Phe	Ala	Pro	Asn	Ile	Leu	Glu	Asn	Ser	Glu	Ala	Leu	210	215	220	
Glu	Leu	Val	Lys	Glu	Ala	Ile	Asp	Lys	Ala	Gly	Tyr	Thr	Glu	Lys	Ile	225	230	235	240
Val	Ile	Gly	Met	Asp	Val	Ala	Ala	Ser	Glu	Phe	Tyr	Arg	Asp	Gly	Lys	245	250	255	
Tyr	Asp	Leu	Asp	Phe	Lys	Ser	Pro	Thr	Asp	Pro	Ser	Arg	Tyr	Ile	Thr	260	265	270	
Gly	Asp	Gln	Leu	Gly	Ala	Leu	Tyr	Gln	Asp	Phe	Val	Arg	Asp	Tyr	Pro	275	280	285	
Val	Val	Ser	Ile	Glu	Asp	Pro	Phe	Asp	Gln	Asp	Asp	Trp	Ala	Ala	Trp	290	295	300	
Ser	Lys	Phe	Thr	Ala	Asn	Val	Gly	Ile	Gln	Ile	Val	Gly	Asp	Asp	Leu	305	310	315	320
Thr	Val	Thr	Asn	Pro	Lys	Arg	Ile	Glu	Arg	Ala	Val	Glu	Glu	Lys	Ala	325	330	335	
Cys	Asn	Cys	Leu	Leu	Leu	Lys	Val	Asn	Gln	Ile	Gly	Ser	Val	Thr	Glu	340	345	350	
Ala	Ile	Gln	Ala	Cys	Lys	Leu	Ala	Gln	Glu	Asn	Gly	Trp	Gly	Val	Met	355	360	365	
Val	Ser	His	Arg	Ser	Gly	Glu	Thr	Glu	Asp	Thr	Phe	Ile	Ala	Asp	Leu	370	375	380	
Val	Val	Gly	Leu	Cys	Thr	Gly	Gln	Ile	Lys	Thr	Gly	Ala	Pro	Cys	Arg	385	390	395	400

ITI-08-PCT_Sequence_Listing_ST25.txt

Ser Glu Arg Leu Ala Lys Tyr Asn Gln Leu Met Arg Ile Glu Glu Glu
405 410 415

Leu Gly Asp Glu Ala Arg Phe Ala Gly His Asn Phe Arg Asn Pro Ser
420 425 430

Val Leu

<210> 556
<211> 464
<212> PRT
<213> Artificial Sequence

<220>
<223> NUF2__Homo_sapiens__Q9BZD4

<400> 556

Met Glu Thr Leu Ser Phe Pro Arg Tyr Asn Val Ala Glu Ile Val Ile
1 5 10 15

His Ile Arg Asn Lys Ile Leu Thr Gly Ala Asp Gly Lys Asn Leu Thr
20 25 30

Lys Asn Asp Leu Tyr Pro Asn Pro Lys Pro Glu Val Leu His Met Ile
35 40 45

Tyr Met Arg Ala Leu Gln Ile Val Tyr Gly Ile Arg Leu Glu His Phe
50 55 60

Tyr Met Met Pro Val Asn Ser Glu Val Met Tyr Pro His Leu Met Glu
65 70 75 80

Gly Phe Leu Pro Phe Ser Asn Leu Val Thr His Leu Asp Ser Phe Leu
85 90 95

Pro Ile Cys Arg Val Asn Asp Phe Glu Thr Ala Asp Ile Leu Cys Pro
100 105 110

Lys Ala Lys Arg Thr Ser Arg Phe Leu Ser Gly Ile Ile Asn Phe Ile
115 120 125

His Phe Arg Glu Ala Cys Arg Glu Thr Tyr Met Glu Phe Leu Trp Gln
130 135 140

Tyr Lys Ser Ser Ala Asp Lys Met Gln Gln Leu Asn Ala Ala His Gln
145 150 155 160

Glu Ala Leu Met Lys Leu Glu Arg Leu Asp Ser Val Pro Val Glu Glu
165 170 175

Gln Glu Glu Phe Lys Gln Leu Ser Asp Gly Ile Gln Glu Leu Gln Gln

ITI-08-PCT_Sequence_Listing_ST25.txt

```

180          185          190
Ser  Leu  Asn  Gln  Asp  Phe  His  Gln  Lys  Thr  Ile  Val  Leu  Gln  Glu  Gly
195          200          205

Asn  Ser  Gln  Lys  Lys  Ser  Asn  Ile  Ser  Glu  Lys  Thr  Lys  Arg  Leu  Asn
210          215          220

Glu  Leu  Lys  Leu  Ser  Val  Val  Ser  Leu  Lys  Glu  Ile  Gln  Glu  Ser  Leu
225          230          235

Lys  Thr  Lys  Ile  Val  Asp  Ser  Pro  Glu  Lys  Leu  Lys  Asn  Tyr  Lys  Glu
245          250          255

Lys  Met  Lys  Asp  Thr  Val  Gln  Lys  Leu  Lys  Asn  Ala  Arg  Gln  Glu  Val
260          265          270

Val  Glu  Lys  Tyr  Glu  Ile  Tyr  Gly  Asp  Ser  Val  Asp  Cys  Leu  Pro  Ser
275          280          285

Cys  Gln  Leu  Glu  Val  Gln  Leu  Tyr  Gln  Lys  Lys  Ile  Gln  Asp  Leu  Ser
290          295          300

Asp  Asn  Arg  Glu  Lys  Leu  Ala  Ser  Ile  Leu  Lys  Glu  Ser  Leu  Asn  Leu
305          310          315

Glu  Asp  Gln  Ile  Glu  Ser  Asp  Glu  Ser  Glu  Leu  Lys  Lys  Leu  Lys  Thr
325          330          335

Glu  Glu  Asn  Ser  Phe  Lys  Arg  Leu  Met  Ile  Val  Lys  Lys  Glu  Lys  Leu
340          345          350

Ala  Thr  Ala  Gln  Phe  Lys  Ile  Asn  Lys  Lys  His  Glu  Asp  Val  Lys  Gln
355          360          365

Tyr  Lys  Arg  Thr  Val  Ile  Glu  Asp  Cys  Asn  Lys  Val  Gln  Glu  Lys  Arg
370          375          380

Gly  Ala  Val  Tyr  Glu  Arg  Val  Thr  Thr  Ile  Asn  Gln  Glu  Ile  Gln  Lys
385          390          395

Ile  Lys  Leu  Gly  Ile  Gln  Gln  Leu  Lys  Asp  Ala  Ala  Glu  Arg  Glu  Lys
405          410          415

Leu  Lys  Ser  Gln  Glu  Ile  Phe  Leu  Asn  Leu  Lys  Thr  Ala  Leu  Glu  Lys
420          425          430

Tyr  His  Asp  Gly  Ile  Glu  Lys  Ala  Ala  Glu  Asp  Ser  Tyr  Ala  Lys  Ile
435          440          445

Asp  Glu  Lys  Thr  Ala  Glu  Leu  Lys  Arg  Lys  Met  Phe  Lys  Met  Ser  Thr
450          455          460

```

ITI-08-PCT_Sequence_Listing_ST25.txt

<210> 557
 <211> 180
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> NY-ESO-1__Homo_sapiens__P78358

<400> 557

Met Gln Ala Glu Gly Arg Gly Thr Gly Gly Ser Thr Gly Asp Ala Asp
 1 5 10 15

Gly Pro Gly Gly Pro Gly Ile Pro Asp Gly Pro Gly Gly Asn Ala Gly
 20 25 30

Gly Pro Gly Glu Ala Gly Ala Thr Gly Gly Arg Gly Pro Arg Gly Ala
 35 40 45

Gly Ala Ala Arg Ala Ser Gly Pro Gly Gly Gly Ala Pro Arg Gly Pro
 50 55 60

His Gly Gly Ala Ala Ser Gly Leu Asn Gly Cys Cys Arg Cys Gly Ala
 65 70 75 80

Arg Gly Pro Glu Ser Arg Leu Leu Glu Phe Tyr Leu Ala Met Pro Phe
 85 90 95

Ala Thr Pro Met Glu Ala Glu Leu Ala Arg Arg Ser Leu Ala Gln Asp
 100 105 110

Ala Pro Pro Leu Pro Val Pro Gly Val Leu Leu Lys Glu Phe Thr Val
 115 120 125

Ser Gly Asn Ile Leu Thr Ile Arg Leu Thr Ala Ala Asp His Arg Gln
 130 135 140

Leu Gln Leu Ser Ile Ser Ser Cys Leu Gln Gln Leu Ser Leu Leu Met
 145 150 155 160

Trp Ile Thr Gln Cys Phe Leu Pro Val Phe Leu Ala Gln Pro Pro Ser
 165 170 175

Gly Gln Arg Arg
 180

<210> 558
 <211> 404
 <212> PRT
 <213> Artificial Sequence

ITI-08-PCT_Sequence_Listing_ST25.txt

<220>

<223> OA1__Homo_sapiens__P51810

<400> 558

Met	Ala	Ser	Pro	Arg	Leu	Gly	Thr	Phe	Cys	Cys	Pro	Thr	Arg	Asp	Ala	1	5	10	15
Ala	Thr	Gln	Leu	Val	Leu	Ser	Phe	Gln	Pro	Arg	Ala	Phe	His	Ala	Leu	20	25	30	
Cys	Leu	Gly	Ser	Gly	Gly	Leu	Arg	Leu	Ala	Leu	Gly	Leu	Leu	Gln	Leu	35	40	45	
Leu	Pro	Gly	Arg	Arg	Pro	Ala	Gly	Pro	Gly	Ser	Pro	Ala	Thr	Ser	Pro	50	55	60	
Pro	Ala	Ser	Val	Arg	Ile	Leu	Arg	Ala	Ala	Ala	Ala	Cys	Asp	Leu	Leu	65	70	75	80
Gly	Cys	Leu	Gly	Met	Val	Ile	Arg	Ser	Thr	Val	Trp	Leu	Gly	Phe	Pro	85	90	95	
Asn	Phe	Val	Asp	Ser	Val	Ser	Asp	Met	Asn	His	Thr	Glu	Ile	Trp	Pro	100	105	110	
Ala	Ala	Phe	Cys	Val	Gly	Ser	Ala	Met	Trp	Ile	Gln	Leu	Leu	Tyr	Ser	115	120	125	
Ala	Cys	Phe	Trp	Trp	Leu	Phe	Cys	Tyr	Ala	Val	Asp	Ala	Tyr	Leu	Val	130	135	140	
Ile	Arg	Arg	Ser	Ala	Gly	Leu	Ser	Thr	Ile	Leu	Leu	Tyr	His	Ile	Met	145	150	155	160
Ala	Trp	Gly	Leu	Ala	Thr	Leu	Leu	Cys	Val	Glu	Gly	Ala	Ala	Met	Leu	165	170	175	
Tyr	Tyr	Pro	Ser	Val	Ser	Arg	Cys	Glu	Arg	Gly	Leu	Asp	His	Ala	Ile	180	185	190	
Pro	His	Tyr	Val	Thr	Met	Tyr	Leu	Pro	Leu	Leu	Leu	Val	Leu	Val	Ala	195	200	205	
Asn	Pro	Ile	Leu	Phe	Gln	Lys	Thr	Val	Thr	Ala	Val	Ala	Ser	Leu	Leu	210	215	220	
Lys	Gly	Arg	Gln	Gly	Ile	Tyr	Thr	Glu	Asn	Glu	Arg	Arg	Met	Gly	Ala	225	230	235	240
Val	Ile	Lys	Ile	Arg	Phe	Phe	Lys	Ile	Met	Leu	Val	Leu	Ile	Ile	Cys	245	250	255	

ITI-08-PCT_Sequence_Listing_ST25.txt

Trp Leu Ser Asn Ile Ile Asn Glu Ser Leu Leu Phe Tyr Leu Glu Met
260 265 270

Gln Thr Asp Ile Asn Gly Gly Ser Leu Lys Pro Val Arg Thr Ala Ala
275 280 285

Lys Thr Thr Trp Phe Ile Met Gly Ile Leu Asn Pro Ala Gln Gly Phe
290 295 300

Leu Leu Ser Leu Ala Phe Tyr Gly Trp Thr Gly Cys Ser Leu Gly Phe
305 310 315 320

Gln Ser Pro Arg Lys Glu Ile Gln Trp Glu Ser Leu Thr Thr Ser Ala
325 330 335

Ala Glu Gly Ala His Pro Ser Pro Leu Met Pro His Glu Asn Pro Ala
340 345 350

Ser Gly Lys Val Ser Gln Val Gly Gly Gln Thr Ser Asp Glu Ala Leu
355 360 365

Ser Met Leu Ser Glu Gly Ser Asp Ala Ser Thr Ile Glu Ile His Thr
370 375 380

Ala Ser Glu Ser Cys Asn Lys Asn Glu Gly Asp Pro Ala Leu Pro Thr
385 390 395 400

His Gly Asp Leu

<210> 559
<211> 1046
<212> PRT
<213> Artificial Sequence

<220>
<223> OGT__Homo_sapiens__015294

<400> 559

Met Ala Ser Ser Val Gly Asn Val Ala Asp Ser Thr Glu Pro Thr Lys
1 5 10 15

Arg Met Leu Ser Phe Gln Gly Leu Ala Glu Leu Ala His Arg Glu Tyr
20 25 30

Gln Ala Gly Asp Phe Glu Ala Ala Glu Arg His Cys Met Gln Leu Trp
35 40 45

Arg Gln Glu Pro Asp Asn Thr Gly Val Leu Leu Leu Leu Ser Ser Ile
50 55 60

ITI-08-PCT_Sequence_Listing_ST25.txt

His	Phe	Gln	Cys	Arg	Arg	Leu	Asp	Arg	Ser	Ala	His	Phe	Ser	Thr	Leu
65					70					75					80
Ala	Ile	Lys	Gln	Asn	Pro	Leu	Leu	Ala	Glu	Ala	Tyr	Ser	Asn	Leu	Gly
				85					90					95	
Asn	Val	Tyr	Lys	Glu	Arg	Gly	Gln	Leu	Gln	Glu	Ala	Ile	Glu	His	Tyr
			100					105					110		
Arg	His	Ala	Leu	Arg	Leu	Lys	Pro	Asp	Phe	Ile	Asp	Gly	Tyr	Ile	Asn
		115					120					125			
Leu	Ala	Ala	Ala	Leu	Val	Ala	Ala	Gly	Asp	Met	Glu	Gly	Ala	Val	Gln
	130					135					140				
Ala	Tyr	Val	Ser	Ala	Leu	Gln	Tyr	Asn	Pro	Asp	Leu	Tyr	Cys	Val	Arg
145					150					155					160
Ser	Asp	Leu	Gly	Asn	Leu	Leu	Lys	Ala	Leu	Gly	Arg	Leu	Glu	Glu	Ala
				165					170					175	
Lys	Ala	Cys	Tyr	Leu	Lys	Ala	Ile	Glu	Thr	Gln	Pro	Asn	Phe	Ala	Val
			180					185					190		
Ala	Trp	Ser	Asn	Leu	Gly	Cys	Val	Phe	Asn	Ala	Gln	Gly	Glu	Ile	Trp
		195					200					205			
Leu	Ala	Ile	His	His	Phe	Glu	Lys	Ala	Val	Thr	Leu	Asp	Pro	Asn	Phe
	210					215					220				
Leu	Asp	Ala	Tyr	Ile	Asn	Leu	Gly	Asn	Val	Leu	Lys	Glu	Ala	Arg	Ile
225					230					235					240
Phe	Asp	Arg	Ala	Val	Ala	Ala	Tyr	Leu	Arg	Ala	Leu	Ser	Leu	Ser	Pro
				245					250					255	
Asn	His	Ala	Val	Val	His	Gly	Asn	Leu	Ala	Cys	Val	Tyr	Tyr	Glu	Gln
			260					265					270		
Gly	Leu	Ile	Asp	Leu	Ala	Ile	Asp	Thr	Tyr	Arg	Arg	Ala	Ile	Glu	Leu
		275					280					285			
Gln	Pro	His	Phe	Pro	Asp	Ala	Tyr	Cys	Asn	Leu	Ala	Asn	Ala	Leu	Lys
	290					295					300				
Glu	Lys	Gly	Ser	Val	Ala	Glu	Ala	Glu	Asp	Cys	Tyr	Asn	Thr	Ala	Leu
305					310					315					320
Arg	Leu	Cys	Pro	Thr	His	Ala	Asp	Ser	Leu	Asn	Asn	Leu	Ala	Asn	Ile
				325					330					335	
Lys	Arg	Glu	Gln	Gly	Asn	Ile	Glu	Glu	Ala	Val	Arg	Leu	Tyr	Arg	Lys

ITI-08-PCT_Sequence_Listing_ST25.txt

```

340          345          350
Ala Leu Glu Val Phe Pro Glu Phe Ala Ala Ala His Ser Asn Leu Ala
355          360          365
Ser Val Leu Gln Gln Gln Gly Lys Leu Gln Glu Ala Leu Met His Tyr
370          375          380
Lys Glu Ala Ile Arg Ile Ser Pro Thr Phe Ala Asp Ala Tyr Ser Asn
385          390          395          400
Met Gly Asn Thr Leu Lys Glu Met Gln Asp Val Gln Gly Ala Leu Gln
405          410          415
Cys Tyr Thr Arg Ala Ile Gln Ile Asn Pro Ala Phe Ala Asp Ala His
420          425          430
Ser Asn Leu Ala Ser Ile His Lys Asp Ser Gly Asn Ile Pro Glu Ala
435          440          445
Ile Ala Ser Tyr Arg Thr Ala Leu Lys Leu Lys Pro Asp Phe Pro Asp
450          455          460
Ala Tyr Cys Asn Leu Ala His Cys Leu Gln Ile Val Cys Asp Trp Thr
465          470          475          480
Asp Tyr Asp Glu Arg Met Lys Lys Leu Val Ser Ile Val Ala Asp Gln
485          490          495
Leu Glu Lys Asn Arg Leu Pro Ser Val His Pro His His Ser Met Leu
500          505          510
Tyr Pro Leu Ser His Gly Phe Arg Lys Ala Ile Ala Glu Arg His Gly
515          520          525
Asn Leu Cys Leu Asp Lys Ile Asn Val Leu His Lys Pro Pro Tyr Glu
530          535          540
His Pro Lys Asp Leu Lys Leu Ser Asp Gly Arg Leu Arg Val Gly Tyr
545          550          555          560
Val Ser Ser Asp Phe Gly Asn His Pro Thr Ser His Leu Met Gln Ser
565          570          575
Ile Pro Gly Met His Asn Pro Asp Lys Phe Glu Val Phe Cys Tyr Ala
580          585          590
Leu Ser Pro Asp Asp Gly Thr Asn Phe Arg Val Lys Val Met Ala Glu
595          600          605
Ala Asn His Phe Ile Asp Leu Ser Gln Ile Pro Cys Asn Gly Lys Ala
610          615          620

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Ala	Asp	Arg	Ile	His	Gln	Asp	Gly	Ile	His	Ile	Leu	Val	Asn	Met	Asn	625	630	635	640
Gly	Tyr	Thr	Lys	Gly	Ala	Arg	Asn	Glu	Leu	Phe	Ala	Leu	Arg	Pro	Ala	645	650	655	
Pro	Ile	Gln	Ala	Met	Trp	Leu	Gly	Tyr	Pro	Gly	Thr	Ser	Gly	Ala	Leu	660	665	670	
Phe	Met	Asp	Tyr	Ile	Ile	Thr	Asp	Gln	Glu	Thr	Ser	Pro	Ala	Glu	Val	675	680	685	
Ala	Glu	Gln	Tyr	Ser	Glu	Lys	Leu	Ala	Tyr	Met	Pro	His	Thr	Phe	Phe	690	695	700	
Ile	Gly	Asp	His	Ala	Asn	Met	Phe	Pro	His	Leu	Lys	Lys	Lys	Ala	Val	705	710	715	720
Ile	Asp	Phe	Lys	Ser	Asn	Gly	His	Ile	Tyr	Asp	Asn	Arg	Ile	Val	Leu	725	730	735	
Asn	Gly	Ile	Asp	Leu	Lys	Ala	Phe	Leu	Asp	Ser	Leu	Pro	Asp	Val	Lys	740	745	750	
Ile	Val	Lys	Met	Lys	Cys	Pro	Asp	Gly	Gly	Asp	Asn	Ala	Asp	Ser	Ser	755	760	765	
Asn	Thr	Ala	Leu	Asn	Met	Pro	Val	Ile	Pro	Met	Asn	Thr	Ile	Ala	Glu	770	775	780	
Ala	Val	Ile	Glu	Met	Ile	Asn	Arg	Gly	Gln	Ile	Gln	Ile	Thr	Ile	Asn	785	790	795	800
Gly	Phe	Ser	Ile	Ser	Asn	Gly	Leu	Ala	Thr	Thr	Gln	Ile	Asn	Asn	Lys	805	810	815	
Ala	Ala	Thr	Gly	Glu	Glu	Val	Pro	Arg	Thr	Ile	Ile	Val	Thr	Thr	Arg	820	825	830	
Ser	Gln	Tyr	Gly	Leu	Pro	Glu	Asp	Ala	Ile	Val	Tyr	Cys	Asn	Phe	Asn	835	840	845	
Gln	Leu	Tyr	Lys	Ile	Asp	Pro	Ser	Thr	Leu	Gln	Met	Trp	Ala	Asn	Ile	850	855	860	
Leu	Lys	Arg	Val	Pro	Asn	Ser	Val	Leu	Trp	Leu	Leu	Arg	Phe	Pro	Ala	865	870	875	880
Val	Gly	Glu	Pro	Asn	Ile	Gln	Gln	Tyr	Ala	Gln	Asn	Met	Gly	Leu	Pro	885	890	895	

ITI-08-PCT_Sequence_Listing_ST25.txt

Gln Asn Arg Ile Ile Phe Ser Pro Val Ala Pro Lys Glu Glu His Val
900 905 910

Arg Arg Gly Gln Leu Ala Asp Val Cys Leu Asp Thr Pro Leu Cys Asn
915 920 925

Gly His Thr Thr Gly Met Asp Val Leu Trp Ala Gly Thr Pro Met Val
930 935 940

Thr Met Pro Gly Glu Thr Leu Ala Ser Arg Val Ala Ala Ser Gln Leu
945 950 955 960

Thr Cys Leu Gly Cys Leu Glu Leu Ile Ala Lys Asn Arg Gln Glu Tyr
965 970 975

Glu Asp Ile Ala Val Lys Leu Gly Thr Asp Leu Glu Tyr Leu Lys Lys
980 985 990

Val Arg Gly Lys Val Trp Lys Gln Arg Ile Ser Ser Pro Leu Phe Asn
995 1000 1005

Thr Lys Gln Tyr Thr Met Glu Leu Glu Arg Leu Tyr Leu Gln Met
1010 1015 1020

Trp Glu His Tyr Ala Ala Gly Asn Lys Pro Asp His Met Ile Lys
1025 1030 1035

Pro Val Glu Val Thr Glu Ser Ala
1040 1045

<210> 560

<211> 146

<212> PRT

<213> Artificial Sequence

<220>

<223> OS-9__Homo_sapiens__B4DH11

<400> 560

Met Ala Ala Glu Thr Leu Leu Ser Ser Leu Leu Gly Leu Leu Leu Leu
1 5 10 15

Gly Leu Leu Leu Pro Ala Ser Leu Thr Gly Gly Val Gly Ser Leu Asn
20 25 30

Leu Glu Glu Leu Ser Glu Met Arg Tyr Gly Ile Glu Ile Leu Pro Leu
35 40 45

Pro Val Met Gly Gly Gln Ser Gln Ser Ser Asp Val Val Ile Val Ser
50 55 60

ITI-08-PCT_Sequence_Listing_ST25.txt

Ser Lys Tyr Lys Gln Arg Tyr Glu Cys Arg Leu Pro Val Gly Ala Ile
65 70 75 80

His Phe Gln Arg Glu Arg Glu Glu Glu Thr Pro Ala Tyr Gln Gly Pro
85 90 95

Gly Ile Pro Glu Leu Leu Ser Pro Met Arg Asp Ala Pro Cys Leu Leu
100 105 110

Lys Thr Lys Asp Trp Trp Thr Tyr Glu Phe Cys Tyr Gly Arg His Ile
115 120 125

Gln Gln Tyr His Met Glu Asp Ser Glu Ile Lys Gly Leu Gln Ala Ala
130 135 140

Ser Ser
145

<210> 561
<211> 406
<212> PRT
<213> Artificial Sequence

<220>
<223> OS-9__Homo_sapiens__B4E321

<400> 561

Met Ala Ala Glu Thr Leu Leu Ser Ser Leu Leu Gly Leu Leu Leu Leu
1 5 10 15

Gly Leu Leu Leu Pro Ala Ser Leu Thr Gly Gly Val Gly Ser Leu Asn
20 25 30

Leu Glu Glu Leu Ser Glu Met Arg Tyr Gly Ile Glu Ile Leu Pro Leu
35 40 45

Pro Val Met Gly Gly Gln Ser Gln Ser Ser Asp Val Val Ile Val Ser
50 55 60

Ser Lys Tyr Lys Gln Arg Tyr Glu Cys Arg Leu Pro Ala Gly Ala Ile
65 70 75 80

His Phe Gln Arg Glu Arg Glu Glu Glu Thr Pro Ala Tyr Gln Gly Pro
85 90 95

Gly Ile Pro Glu Leu Leu Ser Pro Met Arg Asp Ala Pro Cys Leu Leu
100 105 110

Lys Thr Lys Asp Trp Trp Thr Tyr Glu Phe Cys Tyr Gly Arg His Ile
115 120 125

ITI-08-PCT_Sequence_Listing_ST25.txt

Gln Gln Tyr His Met Glu Asp Ser Ala Ser Gly Ala Pro Asn Asp Phe
130 135 140

Gln Asn Asn Val Gln Val Lys Val Ile Arg Ser Pro Ala Asp Leu Ile
145 150 155 160

Arg Phe Ile Glu Glu Leu Lys Gly Gly Thr Lys Lys Gly Lys Pro Asn
165 170 175

Ile Gly Gln Glu Gln Pro Val Asp Asp Ala Ala Glu Val Pro Gln Arg
180 185 190

Glu Pro Glu Lys Glu Arg Gly Asp Pro Glu Arg Gln Arg Glu Met Glu
195 200 205

Glu Glu Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp Glu Arg
210 215 220

Gln Leu Leu Gly Glu Phe Glu Lys Glu Leu Glu Gly Ile Leu Leu Pro
225 230 235 240

Ser Asp Arg Asp Arg Leu Arg Ser Glu Val Lys Ala Gly Met Glu Arg
245 250 255

Glu Leu Glu Asn Ile Ile Gln Glu Thr Glu Lys Glu Leu Asp Pro Asp
260 265 270

Gly Leu Lys Lys Glu Ser Glu Arg Asp Arg Ala Met Leu Ala Leu Thr
275 280 285

Ser Thr Leu Asn Lys Leu Ile Lys Arg Leu Glu Glu Lys Gln Ser Pro
290 295 300

Glu Leu Val Lys Lys His Lys Lys Lys Arg Val Val Pro Lys Lys Pro
305 310 315 320

Pro Pro Ser Pro Gln Pro Thr Gly Lys Ile Glu Ile Lys Ile Val Arg
325 330 335

Pro Trp Ala Glu Gly Thr Glu Glu Gly Ala Arg Trp Leu Thr Asp Glu
340 345 350

Asp Thr Arg Asn Leu Lys Glu Ile Phe Phe Asn Ile Leu Val Pro Gly
355 360 365

Ala Glu Glu Ala Gln Lys Glu Arg Gln Arg Gln Lys Glu Leu Glu Ser
370 375 380

Asn Tyr Arg Arg Val Trp Gly Ser Pro Gly Gly Glu Gly Thr Gly Asp
385 390 395 400

Leu Asp Glu Phe Asp Phe

<210> 562
 <211> 740
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> OS-9__Homo_sapiens__B7Z8E7

<400> 562

Met Ala Val Glu Thr Leu Leu Ser Ser Leu Leu Gly Leu Leu Leu Leu
 1 5 10 15

Gly Leu Leu Leu Pro Ala Ser Leu Thr Gly Gly Val Gly Ser Leu Asn
 20 25 30

Leu Glu Glu Leu Ser Glu Met Arg Tyr Gly Ile Glu Ile Leu Pro Leu
 35 40 45

Pro Val Met Gly Gly Gln Ser Gln Ser Ser Asp Val Val Ile Val Ser
 50 55 60

Ser Lys Tyr Lys Gln Arg Tyr Glu Cys Arg Leu Pro Ala Gly Ala Ile
 65 70 75 80

His Phe Gln Arg Glu Arg Glu Glu Glu Thr Pro Ala Tyr Gln Gly Pro
 85 90 95

Gly Ile Pro Glu Leu Leu Ser Pro Met Arg Asp Ala Pro Cys Leu Leu
 100 105 110

Lys Thr Lys Asp Trp Trp Thr Tyr Glu Phe Cys Tyr Gly Arg His Ile
 115 120 125

Gln Gln Tyr His Met Glu Asp Ser Glu Ile Lys Gly Glu Val Leu Tyr
 130 135 140

Leu Gly Tyr Tyr Gln Ser Ala Phe Asp Trp Asp Asp Glu Thr Ala Lys
 145 150 155 160

Ala Ser Lys Gln His Arg Leu Lys Arg Tyr His Ser Gln Thr Tyr Gly
 165 170 175

Asn Gly Ser Lys Cys Asp Leu Asn Gly Arg Pro Arg Glu Ala Glu Val
 180 185 190

Arg Phe Leu Cys Asp Glu Gly Ala Gly Ile Ser Gly Asp Tyr Ile Asp
 195 200 205

Arg Val Asp Glu Pro Leu Ser Cys Ser Tyr Val Leu Thr Ile Arg Thr

ITI-08-PCT_Sequence_Listing_ST25.txt

```

210                215                220
Pro Arg Leu Cys Pro His Pro Leu Leu Arg Pro Pro Pro Ser Ala Ala
225                230                235                240

Pro Gln Ala Ile Leu Cys His Pro Ser Leu Gln Pro Glu Glu Tyr Met
                245                250                255

Ala Tyr Val Gln Arg Gln Ala Asp Ser Lys Gln Tyr Gly Asp Lys Ile
                260                265                270

Ile Glu Glu Leu Gln Asp Leu Gly Pro Gln Val Trp Ser Glu Thr Lys
                275                280                285

Ser Gly Val Ala Pro Gln Lys Met Ala Gly Arg Thr Leu Phe His Leu
                290                295                300

Phe Arg Glu Ile His Phe His Phe Phe Pro Ser Pro Asp Leu Thr Val
305                310                315                320

Leu Thr Asp Trp Trp Gly Gly Gly Gly Val Glu Lys Tyr His Gly Pro
                325                330                335

Ser Ser Leu Gly Asp Arg Gly Gly Glu Gly Thr Pro Ser Tyr Leu Leu
                340                345                350

Pro Ser Val Ser Pro Leu Leu Ser Asp Gln Ser Leu Pro Val Leu Cys
                355                360                365

Thr Leu Gly Ala Ser Pro Thr Lys Asp Asp Ser Lys Asp Ser Asp Phe
                370                375                380

Trp Lys Met Leu Asn Glu Pro Glu Asp Gln Ala Pro Gly Gly Glu Glu
385                390                395                400

Val Pro Ala Glu Glu Gln Asp Pro Ser Pro Glu Ala Ala Asp Ser Ala
                405                410                415

Ser Gly Ala Pro Asn Asp Phe Gln Asn Asn Val Gln Val Lys Val Ile
                420                425                430

Arg Ser Pro Ala Asp Leu Ile Arg Phe Ile Glu Glu Leu Lys Gly Gly
                435                440                445

Thr Lys Lys Gly Lys Pro Asn Ile Gly Gln Glu Gln Pro Val Asp Asp
                450                455                460

Ala Ala Glu Val Pro Gln Arg Glu Pro Glu Lys Glu Arg Gly Asp Pro
465                470                475                480

Glu Arg Gln Arg Glu Met Glu Glu Glu Glu Asp Glu Asp Glu Asp Glu
                485                490                495

```

ITI-08-PCT_Sequence_Listing_ST25.txt

```

Asp Glu Asp Glu Asp Glu Arg Gln Leu Leu Gly Glu Phe Glu Lys Glu
      500                      505                      510

Leu Glu Gly Ile Leu Leu Pro Ser Asp Arg Asp Arg Leu Arg Ser Glu
      515                      520                      525

Val Lys Ala Gly Met Glu Arg Glu Leu Glu Asn Ile Ile Gln Glu Thr
      530                      535                      540

Glu Lys Glu Leu Asp Pro Asp Gly Leu Lys Lys Glu Ser Glu Arg Asp
545                      550                      555                      560

Arg Ala Met Leu Ala Leu Thr Ser Thr Leu Asn Lys Leu Ile Lys Arg
      565                      570                      575

Leu Glu Glu Lys Gln Ser Pro Glu Leu Val Lys Lys His Lys Lys Lys
      580                      585                      590

Arg Val Val Pro Lys Lys Pro Pro Pro Ser Pro Gln Pro Thr Glu Glu
      595                      600                      605

Asp Pro Glu His Arg Val Arg Val Arg Val Thr Lys Leu Arg Leu Gly
      610                      615                      620

Gly Pro Asn Gln Asp Leu Thr Val Leu Glu Met Lys Arg Glu Asn Pro
625                      630                      635                      640

Gln Leu Lys Gln Ile Glu Gly Leu Val Lys Glu Leu Leu Glu Arg Glu
      645                      650                      655

Gly Leu Thr Ala Ala Gly Lys Ile Glu Ile Lys Ile Val Arg Pro Trp
      660                      665                      670

Ala Glu Gly Thr Glu Glu Gly Ala Arg Trp Leu Thr Asp Glu Asp Thr
      675                      680                      685

Arg Asn Leu Lys Glu Ile Phe Phe Asn Ile Leu Val Pro Gly Ala Glu
      690                      695                      700

Glu Ala Gln Lys Glu Arg Gln Arg Gln Lys Glu Leu Glu Ser Asn Tyr
705                      710                      715                      720

Arg Arg Val Trp Gly Ser Pro Gly Gly Glu Gly Thr Gly Asp Leu Asp
      725                      730                      735

Glu Phe Asp Phe
      740

```

<210> 563

<211> 667

<212> PRT

ITI-08-PCT_Sequence_Listing_ST25.txt

<213> Artificial Sequence

<220>

<223> OS-9__Homo_sapiens__Q13438

<400> 563

Met Ala Ala Glu Thr Leu Leu Ser Ser Leu Leu Gly Leu Leu Leu Leu
1 5 10 15

Gly Leu Leu Leu Pro Ala Ser Leu Thr Gly Gly Val Gly Ser Leu Asn
20 25 30

Leu Glu Glu Leu Ser Glu Met Arg Tyr Gly Ile Glu Ile Leu Pro Leu
35 40 45

Pro Val Met Gly Gly Gln Ser Gln Ser Ser Asp Val Val Ile Val Ser
50 55 60

Ser Lys Tyr Lys Gln Arg Tyr Glu Cys Arg Leu Pro Ala Gly Ala Ile
65 70 75 80

His Phe Gln Arg Glu Arg Glu Glu Glu Thr Pro Ala Tyr Gln Gly Pro
85 90 95

Gly Ile Pro Glu Leu Leu Ser Pro Met Arg Asp Ala Pro Cys Leu Leu
100 105 110

Lys Thr Lys Asp Trp Trp Thr Tyr Glu Phe Cys Tyr Gly Arg His Ile
115 120 125

Gln Gln Tyr His Met Glu Asp Ser Glu Ile Lys Gly Glu Val Leu Tyr
130 135 140

Leu Gly Tyr Tyr Gln Ser Ala Phe Asp Trp Asp Asp Glu Thr Ala Lys
145 150 155 160

Ala Ser Lys Gln His Arg Leu Lys Arg Tyr His Ser Gln Thr Tyr Gly
165 170 175

Asn Gly Ser Lys Cys Asp Leu Asn Gly Arg Pro Arg Glu Ala Glu Val
180 185 190

Arg Phe Leu Cys Asp Glu Gly Ala Gly Ile Ser Gly Asp Tyr Ile Asp
195 200 205

Arg Val Asp Glu Pro Leu Ser Cys Ser Tyr Val Leu Thr Ile Arg Thr
210 215 220

Pro Arg Leu Cys Pro His Pro Leu Leu Arg Pro Pro Pro Ser Ala Ala
225 230 235 240

ITI-08-PCT_Sequence_Listing_ST25.txt

Pro	Gln	Ala	Ile	Leu	Cys	His	Pro	Ser	Leu	Gln	Pro	Glu	Glu	Tyr	Met	245	250	255
Ala	Tyr	Val	Gln	Arg	Gln	Ala	Asp	Ser	Lys	Gln	Tyr	Gly	Asp	Lys	Ile	260	265	270
Ile	Glu	Glu	Leu	Gln	Asp	Leu	Gly	Pro	Gln	Val	Trp	Ser	Glu	Thr	Lys	275	280	285
Ser	Gly	Val	Ala	Pro	Gln	Lys	Met	Ala	Gly	Ala	Ser	Pro	Thr	Lys	Asp	290	295	300
Asp	Ser	Lys	Asp	Ser	Asp	Phe	Trp	Lys	Met	Leu	Asn	Glu	Pro	Glu	Asp	305	310	315
Gln	Ala	Pro	Gly	Gly	Glu	Glu	Val	Pro	Ala	Glu	Glu	Gln	Asp	Pro	Ser	325	330	335
Pro	Glu	Ala	Ala	Asp	Ser	Ala	Ser	Gly	Ala	Pro	Asn	Asp	Phe	Gln	Asn	340	345	350
Asn	Val	Gln	Val	Lys	Val	Ile	Arg	Ser	Pro	Ala	Asp	Leu	Ile	Arg	Phe	355	360	365
Ile	Glu	Glu	Leu	Lys	Gly	Gly	Thr	Lys	Lys	Gly	Lys	Pro	Asn	Ile	Gly	370	375	380
Gln	Glu	Gln	Pro	Val	Asp	Asp	Ala	Ala	Glu	Val	Pro	Gln	Arg	Glu	Pro	385	390	395
Glu	Lys	Glu	Arg	Gly	Asp	Pro	Glu	Arg	Gln	Arg	Glu	Met	Glu	Glu	Glu	405	410	415
Glu	Asp	Glu	Asp	Glu	Asp	Glu	Asp	Glu	Asp	Glu	Asp	Glu	Arg	Gln	Leu	420	425	430
Leu	Gly	Glu	Phe	Glu	Lys	Glu	Leu	Glu	Gly	Ile	Leu	Leu	Pro	Ser	Asp	435	440	445
Arg	Asp	Arg	Leu	Arg	Ser	Glu	Val	Lys	Ala	Gly	Met	Glu	Arg	Glu	Leu	450	455	460
Glu	Asn	Ile	Ile	Gln	Glu	Thr	Glu	Lys	Glu	Leu	Asp	Pro	Asp	Gly	Leu	465	470	475
Lys	Lys	Glu	Ser	Glu	Arg	Asp	Arg	Ala	Met	Leu	Ala	Leu	Thr	Ser	Thr	485	490	495
Leu	Asn	Lys	Leu	Ile	Lys	Arg	Leu	Glu	Glu	Lys	Gln	Ser	Pro	Glu	Leu	500	505	510
Val	Lys	Lys	His	Lys	Lys	Lys	Arg	Val	Val	Pro	Lys	Lys	Pro	Pro	Pro			

ITI-08-PCT_Sequence_Listing_ST25.txt

```

515                               520                               525
Ser Pro Gln Pro Thr Glu Glu Asp Pro Glu His Arg Val Arg Val Arg
530                               535                               540

Val Thr Lys Leu Arg Leu Gly Gly Pro Asn Gln Asp Leu Thr Val Leu
545                               550                               555                               560

Glu Met Lys Arg Glu Asn Pro Gln Leu Lys Gln Ile Glu Gly Leu Val
565                               570                               575

Lys Glu Leu Leu Glu Arg Glu Gly Leu Thr Ala Ala Gly Lys Ile Glu
580                               585                               590

Ile Lys Ile Val Arg Pro Trp Ala Glu Gly Thr Glu Glu Gly Ala Arg
595                               600                               605

Trp Leu Thr Asp Glu Asp Thr Arg Asn Leu Lys Glu Ile Phe Phe Asn
610                               615                               620

Ile Leu Val Pro Gly Ala Glu Glu Ala Gln Lys Glu Arg Gln Arg Gln
625                               630                               635                               640

Lys Glu Leu Glu Ser Asn Tyr Arg Arg Val Trp Gly Ser Pro Gly Gly
645                               650                               655

Glu Gly Thr Gly Asp Leu Asp Glu Phe Asp Phe
660                               665

```

<210> 564
 <211> 100
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> osteocalcin__Homo_sapiens__P02818

<400> 564

```

Met Arg Ala Leu Thr Leu Leu Ala Leu Leu Ala Leu Ala Ala Leu Cys
1                               5                               10                               15

Ile Ala Gly Gln Ala Gly Ala Lys Pro Ser Gly Ala Glu Ser Ser Lys
20                               25                               30

Gly Ala Ala Phe Val Ser Lys Gln Glu Gly Ser Glu Val Val Lys Arg
35                               40                               45

Pro Arg Arg Tyr Leu Tyr Gln Trp Leu Gly Ala Pro Val Pro Tyr Pro
50                               55                               60

Asp Pro Leu Glu Pro Arg Arg Glu Val Cys Glu Leu Asn Pro Asp Cys

```


65 70 75 80

Asp Glu Leu Ala Asp His Ile Gly Phe Gln Glu Ala Tyr Arg Arg Phe
 85 90 95

$\langle 210 \rangle$	565
$\langle 211 \rangle$	314
$\langle 212 \rangle$	PRT
$\langle 213 \rangle$	Artificial Sequence

<400> 565

Pro Asp Ile Gln Tyr Pro Asp Ala Thr Asp Glu Asp Ile Thr Ser His

ITI-08-PCT_Sequence_Listing_ST25.txt

180

185

190

Met Glu Ser Glu Glu Leu Asn Gly Ala Tyr Lys Ala Ile Pro Val Ala
195 200 205

Gln Asp Leu Asn Ala Pro Ser Asp Trp Asp Ser Arg Gly Lys Asp Ser
210 215 220

Tyr Glu Thr Ser Gln Leu Asp Asp Gln Ser Ala Glu Thr His Ser His
225 230 235 240

Lys Gln Ser Arg Leu Tyr Lys Arg Lys Ala Asn Asp Glu Ser Asn Glu
245 250 255

His Ser Asp Val Ile Asp Ser Gln Glu Leu Ser Lys Val Ser Arg Glu
260 265 270

Phe His Ser His Glu Phe His Ser His Glu Asp Met Leu Val Val Asp
275 280 285

Pro Lys Ser Lys Glu Glu Asp Lys His Leu Lys Phe Arg Ile Ser His
290 295 300

Glu Leu Asp Ser Ala Ser Ser Glu Val Asn
305 310

<210> 566

<211> 300

<212> PRT

<213> Artificial Sequence

<220>

<223> osteopontin__Homo_sapiens__A0A024RDE6

<400> 566

Met Arg Ile Ala Val Ile Cys Phe Cys Leu Leu Gly Ile Thr Cys Ala
1 5 10 15

Ile Pro Val Lys Gln Ala Asp Ser Gly Ser Ser Glu Glu Lys Gln Leu
20 25 30

Tyr Asn Lys Tyr Pro Asp Ala Val Ala Thr Trp Leu Asn Pro Asp Pro
35 40 45

Ser Gln Lys Gln Asn Leu Leu Ala Pro Gln Thr Leu Pro Ser Lys Ser
50 55 60

Asn Glu Ser His Asp His Met Asp Asp Met Asp Asp Glu Asp Asp Asp
65 70 75 80

Asp His Val Asp Ser Gln Asp Ser Ile Asp Ser Asn Asp Ser Asp Asp

ITI-08-PCT_Sequence_Listing_ST25.txt

85 90 95

Val Asp Asp Thr Asp Asp Ser His Gln Ser Asp Glu Ser His His Ser
100 105 110

Asp Glu Ser Asp Glu Leu Val Thr Asp Phe Pro Thr Asp Leu Pro Ala
115 120 125

Thr Glu Val Phe Thr Pro Val Val Pro Thr Val Asp Thr Tyr Asp Gly
130 135 140

Arg Gly Asp Ser Val Val Tyr Gly Leu Arg Ser Lys Ser Lys Lys Phe
145 150 155 160

Arg Arg Pro Asp Ile Gln Tyr Pro Asp Ala Thr Asp Glu Asp Ile Thr
165 170 175

Ser His Met Glu Ser Glu Glu Leu Asn Gly Ala Tyr Lys Ala Ile Pro
180 185 190

Val Ala Gln Asp Leu Asn Ala Pro Ser Asp Trp Asp Ser Arg Gly Lys
195 200 205

Asp Ser Tyr Glu Thr Ser Gln Leu Asp Asp Gln Ser Ala Glu Thr His
210 215 220

Ser His Lys Gln Ser Arg Leu Tyr Lys Arg Lys Ala Asn Asp Glu Ser
225 230 235 240

Asn Glu His Ser Asp Val Ile Asp Ser Gln Glu Leu Ser Lys Val Ser
245 250 255

Arg Glu Phe His Ser His Glu Phe His Ser His Glu Asp Met Leu Val
260 265 270

Val Asp Pro Lys Ser Lys Glu Glu Asp Lys His Leu Lys Phe Arg Ile
275 280 285

Ser His Glu Leu Asp Ser Ala Ser Ser Glu Val Asn
290 295 300

<210> 567

<211> 287

<212> PRT

<213> Artificial Sequence

<220>

<223> osteopontin__Homo_sapiens__A0A024RDJ0

<400> 567

Met Arg Ile Ala Val Ile Cys Phe Cys Leu Leu Gly Ile Thr Cys Ala

ITI-08-PCT_Sequence_Listing_ST25.txt

1		5		10		15										
Ile	Pro	Val	Lys	Gln	Ala	Asp	Ser	Gly	Ser	Ser	Glu	Glu	Lys	Gln	Asn	
			20					25					30			
Ala	Val	Ser	Ser	Glu	Glu	Thr	Asn	Asp	Phe	Lys	Gln	Glu	Thr	Leu	Pro	
		35					40					45				
Ser	Lys	Ser	Asn	Glu	Ser	His	Asp	His	Met	Asp	Asp	Met	Asp	Asp	Glu	
	50					55					60					
Asp	Asp	Asp	Asp	His	Val	Asp	Ser	Gln	Asp	Ser	Ile	Asp	Ser	Asn	Asp	
65					70					75					80	
Ser	Asp	Asp	Val	Asp	Asp	Thr	Asp	Asp	Ser	His	Gln	Ser	Asp	Glu	Ser	
				85					90					95		
His	His	Ser	Asp	Glu	Ser	Asp	Glu	Leu	Val	Thr	Asp	Phe	Pro	Thr	Asp	
			100					105					110			
Leu	Pro	Ala	Thr	Glu	Val	Phe	Thr	Pro	Val	Val	Pro	Thr	Val	Asp	Thr	
		115					120					125				
Tyr	Asp	Gly	Arg	Gly	Asp	Ser	Val	Val	Tyr	Gly	Leu	Arg	Ser	Lys	Ser	
	130					135					140					
Lys	Lys	Phe	Arg	Arg	Pro	Asp	Ile	Gln	Tyr	Pro	Asp	Ala	Thr	Asp	Glu	
145					150					155					160	
Asp	Ile	Thr	Ser	His	Met	Glu	Ser	Glu	Glu	Leu	Asn	Gly	Ala	Tyr	Lys	
				165					170					175		
Ala	Ile	Pro	Val	Ala	Gln	Asp	Leu	Asn	Ala	Pro	Ser	Asp	Trp	Asp	Ser	
			180					185					190			
Arg	Gly	Lys	Asp	Ser	Tyr	Glu	Thr	Ser	Gln	Leu	Asp	Asp	Gln	Ser	Ala	
		195					200					205				
Glu	Thr	His	Ser	His	Lys	Gln	Ser	Arg	Leu	Tyr	Lys	Arg	Lys	Ala	Asn	
	210					215					220					
Asp	Glu	Ser	Asn	Glu	His	Ser	Asp	Val	Ile	Asp	Ser	Gln	Glu	Leu	Ser	
225					230					235					240	
Lys	Val	Ser	Arg	Glu	Phe	His	Ser	His	Glu	Phe	His	Ser	His	Glu	Asp	
				245					250					255		
Met	Leu	Val	Val	Asp	Pro	Lys	Ser	Lys	Glu	Glu	Asp	Lys	His	Leu	Lys	
			260					265					270			
Phe	Arg	Ile	Ser	His	Glu	Leu	Asp	Ser	Ala	Ser	Ser	Glu	Val	Asn		
		275					280					285				

ITI-08-PCT_Sequence_Listing_ST25.txt

<210> 568
 <211> 327
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> osteopontin__Homo_sapiens__B7Z351

<400> 568

```

Met Gly Ile Val Pro Arg Ser Leu Asp Lys Lys Ala His Arg Val Gln
1          5          10          15

Phe Gln Leu Asn Arg Ile Lys Ala Lys Ile Glu Leu Pro Trp Gly Ser
      20          25          30

Leu Gln Leu Asp Cys Leu Met Lys Thr Leu Lys Glu Leu Tyr Asn Lys
      35          40          45

Tyr Pro Asp Ala Val Ala Thr Trp Leu Asn Pro Asp Pro Ser Gln Lys
      50          55          60

Gln Asn Leu Leu Ala Pro Gln Asn Ala Val Ser Ser Glu Glu Thr Asn
65          70          75          80

Asp Phe Lys Gln Glu Thr Leu Pro Ser Lys Ser Asn Glu Ser His Asp
      85          90          95

His Met Asp Asp Met Asp Asp Glu Asp Asp Asp Asp His Val Asp Ser
      100          105          110

Gln Asp Ser Ile Asp Ser Asn Asp Ser Asp Asp Val Asp Asp Thr Asp
      115          120          125

Asp Ser His Gln Ser Asp Glu Ser His His Ser Asp Glu Ser Asp Glu
      130          135          140

Leu Val Thr Asp Phe Pro Thr Asp Leu Pro Ala Thr Glu Val Phe Thr
145          150          155          160

Pro Val Val Pro Thr Val Asp Thr Tyr Asp Gly Arg Gly Asp Ser Val
      165          170          175

Val Tyr Gly Leu Arg Ser Lys Ser Lys Lys Phe Arg Arg Pro Asp Ile
      180          185          190

Gln Tyr Pro Asp Ala Thr Asp Glu Asp Ile Thr Ser His Met Glu Ser
      195          200          205

Glu Glu Leu Asn Gly Ala Tyr Lys Ala Ile Pro Val Ala Gln Asp Leu
210          215          220
    
```

ITI-08-PCT_Sequence_Listing_ST25.txt

Asn Ala Pro Ser Asp Trp Asp Ser Arg Gly Lys Asp Ser Tyr Glu Thr
225 230 235 240

Ser Gln Leu Asp Asp Gln Ser Ala Glu Thr His Ser His Lys Gln Ser
245 250 255

Arg Leu Tyr Lys Arg Lys Ala Asn Asp Glu Ser Asn Glu His Ser Asp
260 265 270

Val Ile Asp Ser Gln Glu Leu Ser Lys Val Ser Arg Glu Phe His Ser
275 280 285

His Glu Phe His Ser His Glu Asp Met Leu Val Val Asp Pro Lys Ser
290 295 300

Lys Glu Glu Asp Lys His Leu Lys Phe Arg Ile Ser His Glu Leu Asp
305 310 315 320

Ser Ala Ser Ser Glu Val Asn
325

<210> 569

<211> 292

<212> PRT

<213> Artificial Sequence

<220>

<223> osteopontin__Homo_sapiens__F2YQ21

<400> 569

Met Arg Ile Ala Val Ile Cys Phe Cys Leu Leu Gly Ile Thr Cys Ala
1 5 10 15

Ile Pro Val Lys Gln Ala Asp Ser Gly Ser Ser Glu Glu Lys Gln Leu
20 25 30

Tyr Asn Lys Tyr Pro Asp Ala Val Ala Thr Trp Leu Asn Pro Asp Pro
35 40 45

Ser Gln Lys Gln Asn Leu Leu Ala Pro Gln Asn Ala Val Ser Ser Glu
50 55 60

Glu Thr Asn Asp Phe Lys Gln Glu Thr Leu Pro Ser Lys Ser Asn Glu
65 70 75 80

Ser His Asp His Met Asp Asp Met Asp Asp Glu Asp Asp Asp Ser His
85 90 95

Gln Ser Asp Glu Ser His His Ser Asp Glu Ser Asp Glu Leu Val Thr
100 105 110

ITI-08-PCT_Sequence_Listing_ST25.txt

Asp Phe Pro Thr Asp Leu Pro Ala Thr Glu Val Phe Thr Pro Val Val
115 120 125

Pro Thr Val Asp Thr Tyr Asp Gly Arg Gly Asp Ser Val Val Tyr Gly
130 135 140

Leu Arg Ser Lys Ser Lys Lys Phe Arg Arg Pro Asp Ile Gln Tyr Pro
145 150 155 160

Asp Ala Thr Asp Glu Asp Ile Thr Ser His Met Glu Ser Glu Glu Leu
165 170 175

Asn Gly Ala Tyr Lys Ala Ile Pro Val Ala Gln Asp Leu Asn Ala Pro
180 185 190

Ser Asp Trp Asp Ser Arg Gly Lys Asp Ser Tyr Glu Thr Ser Gln Leu
195 200 205

Asp Asp Gln Ser Ala Glu Thr His Ser His Lys Gln Ser Arg Leu Tyr
210 215 220

Lys Arg Lys Ala Asn Asp Glu Ser Asn Glu His Ser Asp Val Ile Asp
225 230 235 240

Ser Gln Glu Leu Ser Lys Val Ser Arg Glu Phe His Ser His Glu Phe
245 250 255

His Ser His Glu Asp Met Leu Val Val Asp Pro Lys Ser Lys Glu Glu
260 265 270

Asp Lys His Leu Lys Phe Arg Ile Ser His Glu Leu Asp Ser Ala Ser
275 280 285

Ser Glu Val Asn
290

<210> 570
<211> 314
<212> PRT
<213> Artificial Sequence

<220>
<223> osteopontin__Homo_sapiens__P10451

<400> 570

Met Arg Ile Ala Val Ile Cys Phe Cys Leu Leu Gly Ile Thr Cys Ala
1 5 10 15

Ile Pro Val Lys Gln Ala Asp Ser Gly Ser Ser Glu Glu Lys Gln Leu
20 25 30

ITI-08-PCT_Sequence_Listing_ST25.txt

Tyr	Asn	Lys	Tyr	Pro	Asp	Ala	Val	Ala	Thr	Trp	Leu	Asn	Pro	Asp	Pro	35	40	45	
Ser	Gln	Lys	Gln	Asn	Leu	Leu	Ala	Pro	Gln	Asn	Ala	Val	Ser	Ser	Glu	50	55	60	
Glu	Thr	Asn	Asp	Phe	Lys	Gln	Glu	Thr	Leu	Pro	Ser	Lys	Ser	Asn	Glu	65	70	75	80
Ser	His	Asp	His	Met	Asp	Asp	Met	Asp	Asp	Glu	Asp	Asp	Asp	Asp	His	85	90	95	
Val	Asp	Ser	Gln	Asp	Ser	Ile	Asp	Ser	Asn	Asp	Ser	Asp	Asp	Val	Asp	100	105	110	
Asp	Thr	Asp	Asp	Ser	His	Gln	Ser	Asp	Glu	Ser	His	His	Ser	Asp	Glu	115	120	125	
Ser	Asp	Glu	Leu	Val	Thr	Asp	Phe	Pro	Thr	Asp	Leu	Pro	Ala	Thr	Glu	130	135	140	
Val	Phe	Thr	Pro	Val	Val	Pro	Thr	Val	Asp	Thr	Tyr	Asp	Gly	Arg	Gly	145	150	155	160
Asp	Ser	Val	Val	Tyr	Gly	Leu	Arg	Ser	Lys	Ser	Lys	Lys	Phe	Arg	Arg	165	170	175	
Pro	Asp	Ile	Gln	Tyr	Pro	Asp	Ala	Thr	Asp	Glu	Asp	Ile	Thr	Ser	His	180	185	190	
Met	Glu	Ser	Glu	Glu	Leu	Asn	Gly	Ala	Tyr	Lys	Ala	Ile	Pro	Val	Ala	195	200	205	
Gln	Asp	Leu	Asn	Ala	Pro	Ser	Asp	Trp	Asp	Ser	Arg	Gly	Lys	Asp	Ser	210	215	220	
Tyr	Glu	Thr	Ser	Gln	Leu	Asp	Asp	Gln	Ser	Ala	Glu	Thr	His	Ser	His	225	230	235	240
Lys	Gln	Ser	Arg	Leu	Tyr	Lys	Arg	Lys	Ala	Asn	Asp	Glu	Ser	Asn	Glu	245	250	255	
His	Ser	Asp	Val	Ile	Asp	Ser	Gln	Glu	Leu	Ser	Lys	Val	Ser	Arg	Glu	260	265	270	
Phe	His	Ser	His	Glu	Phe	His	Ser	His	Glu	Asp	Met	Leu	Val	Val	Asp	275	280	285	
Pro	Lys	Ser	Lys	Glu	Glu	Asp	Lys	His	Leu	Lys	Phe	Arg	Ile	Ser	His	290	295	300	

ITI-08-PCT_Sequence_Listing_ST25.txt

Glu Leu Asp Ser Ala Ser Ser Glu Val Asn
305 310

<210> 571
<211> 393
<212> PRT
<213> Artificial Sequence

<220>
<223> p53__Homo_sapiens__P04637

<400> 571

Met Glu Glu Pro Gln Ser Asp Pro Ser Val Glu Pro Pro Leu Ser Gln
1 5 10 15

Glu Thr Phe Ser Asp Leu Trp Lys Leu Leu Pro Glu Asn Asn Val Leu
20 25 30

Ser Pro Leu Pro Ser Gln Ala Met Asp Asp Leu Met Leu Ser Pro Asp
35 40 45

Asp Ile Glu Gln Trp Phe Thr Glu Asp Pro Gly Pro Asp Glu Ala Pro
50 55 60

Arg Met Pro Glu Ala Ala Pro Pro Val Ala Pro Ala Pro Ala Ala Pro
65 70 75 80

Thr Pro Ala Ala Pro Ala Pro Ala Pro Ser Trp Pro Leu Ser Ser Ser
85 90 95

Val Pro Ser Gln Lys Thr Tyr Gln Gly Ser Tyr Gly Phe Arg Leu Gly
100 105 110

Phe Leu His Ser Gly Thr Ala Lys Ser Val Thr Cys Thr Tyr Ser Pro
115 120 125

Ala Leu Asn Lys Met Phe Cys Gln Leu Ala Lys Thr Cys Pro Val Gln
130 135 140

Leu Trp Val Asp Ser Thr Pro Pro Pro Gly Thr Arg Val Arg Ala Met
145 150 155 160

Ala Ile Tyr Lys Gln Ser Gln His Met Thr Glu Val Val Arg Arg Cys
165 170 175

Pro His His Glu Arg Cys Ser Asp Ser Asp Gly Leu Ala Pro Pro Gln
180 185 190

His Leu Ile Arg Val Glu Gly Asn Leu Arg Val Glu Tyr Leu Asp Asp
195 200 205

ITI-08-PCT_Sequence_Listing_ST25.txt

Arg Asn Thr Phe Arg His Ser Val Val Val Pro Tyr Glu Pro Pro Glu
210 215 220

Val Gly Ser Asp Cys Thr Thr Ile His Tyr Asn Tyr Met Cys Asn Ser
225 230 235 240

Ser Cys Met Gly Gly Met Asn Arg Arg Pro Ile Leu Thr Ile Ile Thr
245 250 255

Leu Glu Asp Ser Ser Gly Asn Leu Leu Gly Arg Asn Ser Phe Glu Val
260 265 270

Arg Val Cys Ala Cys Pro Gly Arg Asp Arg Arg Thr Glu Glu Glu Asn
275 280 285

Leu Arg Lys Lys Gly Glu Pro His His Glu Leu Pro Pro Gly Ser Thr
290 295 300

Lys Arg Ala Leu Pro Asn Asn Thr Ser Ser Ser Pro Gln Pro Lys Lys
305 310 315 320

Lys Pro Leu Asp Gly Glu Tyr Phe Thr Leu Gln Ile Arg Gly Arg Glu
325 330 335

Arg Phe Glu Met Phe Arg Glu Leu Asn Glu Ala Leu Glu Leu Lys Asp
340 345 350

Ala Gln Ala Gly Lys Glu Pro Gly Gly Ser Arg Ala His Ser Ser His
355 360 365

Leu Lys Ser Lys Lys Gly Gln Ser Thr Ser Arg His Lys Lys Leu Met
370 375 380

Phe Lys Thr Glu Gly Pro Asp Ser Asp
385 390

<210> 572

<211> 102

<212> PRT

<213> Artificial Sequence

<220>

<223> PAGE-4__Homo_sapiens__060829

<400> 572

Met Ser Ala Arg Val Arg Ser Arg Ser Arg Gly Arg Gly Asp Gly Gln
1 5 10 15

Glu Ala Pro Asp Val Val Ala Phe Val Ala Pro Gly Glu Ser Gln Gln
20 25 30

ITI-08-PCT_Sequence_Listing_ST25.txt

Glu Glu Pro Pro Thr Asp Asn Gln Asp Ile Glu Pro Gly Gln Glu Arg
35 40 45

Glu Gly Thr Pro Pro Ile Glu Glu Arg Lys Val Glu Gly Asp Cys Gln
50 55 60

Glu Met Asp Leu Glu Lys Thr Arg Ser Glu Arg Gly Asp Gly Ser Asp
65 70 75 80

Val Lys Glu Lys Thr Pro Pro Asn Pro Lys His Ala Lys Thr Lys Glu
85 90 95

Ala Gly Asp Gly Gln Pro
100

<210> 573

<211> 402

<212> PRT

<213> Artificial Sequence

<220>

<223> PAI-1__Homo_sapiens__P05121

<400> 573

Met Gln Met Ser Pro Ala Leu Thr Cys Leu Val Leu Gly Leu Ala Leu
1 5 10 15

Val Phe Gly Glu Gly Ser Ala Val His His Pro Pro Ser Tyr Val Ala
20 25 30

His Leu Ala Ser Asp Phe Gly Val Arg Val Phe Gln Gln Val Ala Gln
35 40 45

Ala Ser Lys Asp Arg Asn Val Val Phe Ser Pro Tyr Gly Val Ala Ser
50 55 60

Val Leu Ala Met Leu Gln Leu Thr Thr Gly Gly Glu Thr Gln Gln Gln
65 70 75 80

Ile Gln Ala Ala Met Gly Phe Lys Ile Asp Asp Lys Gly Met Ala Pro
85 90 95

Ala Leu Arg His Leu Tyr Lys Glu Leu Met Gly Pro Trp Asn Lys Asp
100 105 110

Glu Ile Ser Thr Thr Asp Ala Ile Phe Val Gln Arg Asp Leu Lys Leu
115 120 125

Val Gln Gly Phe Met Pro His Phe Phe Arg Leu Phe Arg Ser Thr Val
130 135 140

ITI-08-PCT_Sequence_Listing_ST25.txt

Lys	Gln	Val	Asp	Phe	Ser	Glu	Val	Glu	Arg	Ala	Arg	Phe	Ile	Ile	Asn	145	150	155	160
Asp	Trp	Val	Lys	Thr	His	Thr	Lys	Gly	Met	Ile	Ser	Asn	Leu	Leu	Gly	165	170	175	
Lys	Gly	Ala	Val	Asp	Gln	Leu	Thr	Arg	Leu	Val	Leu	Val	Asn	Ala	Leu	180	185	190	
Tyr	Phe	Asn	Gly	Gln	Trp	Lys	Thr	Pro	Phe	Pro	Asp	Ser	Ser	Thr	His	195	200	205	
Arg	Arg	Leu	Phe	His	Lys	Ser	Asp	Gly	Ser	Thr	Val	Ser	Val	Pro	Met	210	215	220	
Met	Ala	Gln	Thr	Asn	Lys	Phe	Asn	Tyr	Thr	Glu	Phe	Thr	Thr	Pro	Asp	225	230	235	240
Gly	His	Tyr	Tyr	Asp	Ile	Leu	Glu	Leu	Pro	Tyr	His	Gly	Asp	Thr	Leu	245	250	255	
Ser	Met	Phe	Ile	Ala	Ala	Pro	Tyr	Glu	Lys	Glu	Val	Pro	Leu	Ser	Ala	260	265	270	
Leu	Thr	Asn	Ile	Leu	Ser	Ala	Gln	Leu	Ile	Ser	His	Trp	Lys	Gly	Asn	275	280	285	
Met	Thr	Arg	Leu	Pro	Arg	Leu	Leu	Val	Leu	Pro	Lys	Phe	Ser	Leu	Glu	290	295	300	
Thr	Glu	Val	Asp	Leu	Arg	Lys	Pro	Leu	Glu	Asn	Leu	Gly	Met	Thr	Asp	305	310	315	320
Met	Phe	Arg	Gln	Phe	Gln	Ala	Asp	Phe	Thr	Ser	Leu	Ser	Asp	Gln	Glu	325	330	335	
Pro	Leu	His	Val	Ala	Gln	Ala	Leu	Gln	Lys	Val	Lys	Ile	Glu	Val	Asn	340	345	350	
Glu	Ser	Gly	Thr	Val	Ala	Ser	Ser	Ser	Thr	Ala	Val	Ile	Val	Ser	Ala	355	360	365	
Arg	Met	Ala	Pro	Glu	Glu	Ile	Ile	Met	Asp	Arg	Pro	Phe	Leu	Phe	Val	370	375	380	
Val	Arg	His	Asn	Pro	Thr	Gly	Thr	Val	Leu	Phe	Met	Gly	Gln	Val	Met	385	390	395	400

Glu Pro

<210> 574

<211> 415

ITI-08-PCT_Sequence_Listing_ST25.txt

<212> PRT

<213> Artificial Sequence

<220>

<223> PAI-2__Homo_sapiens__P05120

<400> 574

Met Glu Asp Leu Cys Val Ala Asn Thr Leu Phe Ala Leu Asn Leu Phe
1 5 10 15

Lys His Leu Ala Lys Ala Ser Pro Thr Gln Asn Leu Phe Leu Ser Pro
20 25 30

Trp Ser Ile Ser Ser Thr Met Ala Met Val Tyr Met Gly Ser Arg Gly
35 40 45

Ser Thr Glu Asp Gln Met Ala Lys Val Leu Gln Phe Asn Glu Val Gly
50 55 60

Ala Asn Ala Val Thr Pro Met Thr Pro Glu Asn Phe Thr Ser Cys Gly
65 70 75 80

Phe Met Gln Gln Ile Gln Lys Gly Ser Tyr Pro Asp Ala Ile Leu Gln
85 90 95

Ala Gln Ala Ala Asp Lys Ile His Ser Ser Phe Arg Ser Leu Ser Ser
100 105 110

Ala Ile Asn Ala Ser Thr Gly Asn Tyr Leu Leu Glu Ser Val Asn Lys
115 120 125

Leu Phe Gly Glu Lys Ser Ala Ser Phe Arg Glu Glu Tyr Ile Arg Leu
130 135 140

Cys Gln Lys Tyr Tyr Ser Ser Glu Pro Gln Ala Val Asp Phe Leu Glu
145 150 155 160

Cys Ala Glu Glu Ala Arg Lys Lys Ile Asn Ser Trp Val Lys Thr Gln
165 170 175

Thr Lys Gly Lys Ile Pro Asn Leu Leu Pro Glu Gly Ser Val Asp Gly
180 185 190

Asp Thr Arg Met Val Leu Val Asn Ala Val Tyr Phe Lys Gly Lys Trp
195 200 205

Lys Thr Pro Phe Glu Lys Lys Leu Asn Gly Leu Tyr Pro Phe Arg Val
210 215 220

Asn Ser Ala Gln Arg Thr Pro Val Gln Met Met Tyr Leu Arg Glu Lys
225 230 235 240

ITI-08-PCT_Sequence_Listing_ST25.txt

Leu Asn Ile Gly Tyr Ile Glu Asp Leu Lys Ala Gln Ile Leu Glu Leu
245 250 255

Pro Tyr Ala Gly Asp Val Ser Met Phe Leu Leu Leu Pro Asp Glu Ile
260 265 270

Ala Asp Val Ser Thr Gly Leu Glu Leu Leu Glu Ser Glu Ile Thr Tyr
275 280 285

Asp Lys Leu Asn Lys Trp Thr Ser Lys Asp Lys Met Ala Glu Asp Glu
290 295 300

Val Glu Val Tyr Ile Pro Gln Phe Lys Leu Glu Glu His Tyr Glu Leu
305 310 315 320

Arg Ser Ile Leu Arg Ser Met Gly Met Glu Asp Ala Phe Asn Lys Gly
325 330 335

Arg Ala Asn Phe Ser Gly Met Ser Glu Arg Asn Asp Leu Phe Leu Ser
340 345 350

Glu Val Phe His Gln Ala Met Val Asp Val Asn Glu Glu Gly Thr Glu
355 360 365

Ala Ala Ala Gly Thr Gly Gly Val Met Thr Gly Arg Thr Gly His Gly
370 375 380

Gly Pro Gln Phe Val Ala Asp His Pro Phe Leu Phe Leu Ile Met His
385 390 395 400

Lys Ile Thr Asn Cys Ile Leu Phe Phe Gly Arg Phe Ser Ser Pro
405 410 415

<210> 575

<211> 175

<212> PRT

<213> Artificial Sequence

<220>

<223> PAP__Homo_sapiens__Q06141

<400> 575

Met Leu Pro Pro Met Ala Leu Pro Ser Val Ser Trp Met Leu Leu Ser
1 5 10 15

Cys Leu Met Leu Leu Ser Gln Val Gln Gly Glu Glu Pro Gln Arg Glu
20 25 30

Leu Pro Ser Ala Arg Ile Arg Cys Pro Lys Gly Ser Lys Ala Tyr Gly
35 40 45

ITI-08-PCT_Sequence_Listing_ST25.txt

Ser His Cys Tyr Ala Leu Phe Leu Ser Pro Lys Ser Trp Thr Asp Ala
50 55 60

Asp Leu Ala Cys Gln Lys Arg Pro Ser Gly Asn Leu Val Ser Val Leu
65 70 75 80

Ser Gly Ala Glu Gly Ser Phe Val Ser Ser Leu Val Lys Ser Ile Gly
85 90 95

Asn Ser Tyr Ser Tyr Val Trp Ile Gly Leu His Asp Pro Thr Gln Gly
100 105 110

Thr Glu Pro Asn Gly Glu Gly Trp Glu Trp Ser Ser Ser Asp Val Met
115 120 125

Asn Tyr Phe Ala Trp Glu Arg Asn Pro Ser Thr Ile Ser Ser Pro Gly
130 135 140

His Cys Ala Ser Leu Ser Arg Ser Thr Ala Phe Leu Arg Trp Lys Asp
145 150 155 160

Tyr Asn Cys Asn Val Arg Leu Pro Tyr Val Cys Lys Phe Thr Asp
165 170 175

<210> 576

<211> 175

<212> PRT

<213> Artificial Sequence

<220>

<223> PAP__Homo_sapiens__Q53S56

<400> 576

Met Leu Pro Pro Met Ala Leu Pro Ser Val Ser Trp Met Leu Leu Ser
1 5 10 15

Cys Leu Met Leu Leu Ser Gln Val Gln Gly Glu Glu Pro Gln Arg Glu
20 25 30

Leu Pro Ser Ala Arg Ile Arg Cys Pro Lys Gly Ser Lys Ala Tyr Gly
35 40 45

Ser His Cys Tyr Ala Leu Phe Leu Ser Pro Lys Ser Trp Thr Asp Ala
50 55 60

Asp Leu Ala Cys Gln Lys Arg Pro Ser Gly Asn Leu Val Ser Val Leu
65 70 75 80

Ser Gly Ala Glu Gly Ser Phe Val Ser Ser Leu Val Lys Ser Ile Gly
85 90 95

ITI-08-PCT_Sequence_Listing_ST25.txt

Asn Ser Tyr Ser Tyr Val Trp Ile Gly Leu His Asp Pro Thr Gln Gly
100 105 110

Thr Glu Pro Asn Gly Glu Gly Trp Glu Trp Ser Ser Ser Asp Val Met
115 120 125

Asn Tyr Phe Ala Trp Glu Arg Asn Pro Ser Thr Ile Ser Ser Pro Gly
130 135 140

His Cys Ala Ser Leu Ser Arg Ser Thr Ala Phe Leu Arg Trp Lys Asp
145 150 155 160

Tyr Asn Cys Asn Val Arg Leu Pro Tyr Val Cys Lys Phe Thr Asp
165 170 175

<210> 577

<211> 126

<212> PRT

<213> Artificial Sequence

<220>

<223> PATE__Homo_sapiens__Q8WXA2

<400> 577

Met Asp Lys Ser Leu Leu Leu Glu Leu Pro Ile Leu Leu Cys Cys Phe
1 5 10 15

Arg Ala Leu Ser Gly Ser Leu Ser Met Arg Asn Asp Ala Val Asn Glu
20 25 30

Ile Val Ala Val Lys Asn Asn Phe Pro Val Ile Glu Ile Val Gln Cys
35 40 45

Arg Met Cys His Leu Gln Phe Pro Gly Glu Lys Cys Ser Arg Gly Arg
50 55 60

Gly Ile Cys Thr Ala Thr Thr Glu Glu Ala Cys Met Val Gly Arg Met
65 70 75 80

Phe Lys Arg Asp Gly Asn Pro Trp Leu Thr Phe Met Gly Cys Leu Lys
85 90 95

Asn Cys Ala Asp Val Lys Gly Ile Arg Trp Ser Val Tyr Leu Val Asn
100 105 110

Phe Arg Cys Cys Arg Ser His Asp Leu Cys Asn Glu Asp Leu
115 120 125

<210> 578

<211> 479

ITI-08-PCT_Sequence_Listing_ST25.txt

<212> PRT

<213> Artificial Sequence

<220>

<223> PAX3__Homo_sapiens__P23760

<400> 578

Met Thr Thr Leu Ala Gly Ala Val Pro Arg Met Met Arg Pro Gly Pro
1 5 10 15

Gly Gln Asn Tyr Pro Arg Ser Gly Phe Pro Leu Glu Val Ser Thr Pro
20 25 30

Leu Gly Gln Gly Arg Val Asn Gln Leu Gly Gly Val Phe Ile Asn Gly
35 40 45

Arg Pro Leu Pro Asn His Ile Arg His Lys Ile Val Glu Met Ala His
50 55 60

His Gly Ile Arg Pro Cys Val Ile Ser Arg Gln Leu Arg Val Ser His
65 70 75 80

Gly Cys Val Ser Lys Ile Leu Cys Arg Tyr Gln Glu Thr Gly Ser Ile
85 90 95

Arg Pro Gly Ala Ile Gly Gly Ser Lys Pro Lys Gln Val Thr Thr Pro
100 105 110

Asp Val Glu Lys Lys Ile Glu Glu Tyr Lys Arg Glu Asn Pro Gly Met
115 120 125

Phe Ser Trp Glu Ile Arg Asp Lys Leu Leu Lys Asp Ala Val Cys Asp
130 135 140

Arg Asn Thr Val Pro Ser Val Ser Ser Ile Ser Arg Ile Leu Arg Ser
145 150 155 160

Lys Phe Gly Lys Gly Glu Glu Glu Glu Ala Asp Leu Glu Arg Lys Glu
165 170 175

Ala Glu Glu Ser Glu Lys Lys Ala Lys His Ser Ile Asp Gly Ile Leu
180 185 190

Ser Glu Arg Ala Ser Ala Pro Gln Ser Asp Glu Gly Ser Asp Ile Asp
195 200 205

Ser Glu Pro Asp Leu Pro Leu Lys Arg Lys Gln Arg Arg Ser Arg Thr
210 215 220

Thr Phe Thr Ala Glu Gln Leu Glu Glu Leu Glu Arg Ala Phe Glu Arg
225 230 235 240

ITI-08-PCT_Sequence_Listing_ST25.txt

```

Thr His Tyr Pro Asp Ile Tyr Thr Arg Glu Glu Leu Ala Gln Arg Ala
      245                      250                      255

Lys Leu Thr Glu Ala Arg Val Gln Val Trp Phe Ser Asn Arg Arg Ala
      260                      265                      270

Arg Trp Arg Lys Gln Ala Gly Ala Asn Gln Leu Met Ala Phe Asn His
      275                      280                      285

Leu Ile Pro Gly Gly Phe Pro Pro Thr Ala Met Pro Thr Leu Pro Thr
      290                      295                      300

Tyr Gln Leu Ser Glu Thr Ser Tyr Gln Pro Thr Ser Ile Pro Gln Ala
305                      310                      315                      320

Val Ser Asp Pro Ser Ser Thr Val His Arg Pro Gln Pro Leu Pro Pro
      325                      330                      335

Ser Thr Val His Gln Ser Thr Ile Pro Ser Asn Pro Asp Ser Ser Ser
      340                      345                      350

Ala Tyr Cys Leu Pro Ser Thr Arg His Gly Phe Ser Ser Tyr Thr Asp
      355                      360                      365

Ser Phe Val Pro Pro Ser Gly Pro Ser Asn Pro Met Asn Pro Thr Ile
      370                      375                      380

Gly Asn Gly Leu Ser Pro Gln Val Met Gly Leu Leu Thr Asn His Gly
385                      390                      395                      400

Gly Val Pro His Gln Pro Gln Thr Asp Tyr Ala Leu Ser Pro Leu Thr
      405                      410                      415

Gly Gly Leu Glu Pro Thr Thr Thr Val Ser Ala Ser Cys Ser Gln Arg
      420                      425                      430

Leu Asp His Met Lys Ser Leu Asp Ser Leu Pro Thr Ser Gln Ser Tyr
      435                      440                      445

Cys Pro Pro Thr Tyr Ser Thr Thr Gly Tyr Ser Met Asp Pro Val Thr
      450                      455                      460

Gly Tyr Gln Tyr Gly Gln Tyr Gly Gln Ser Lys Pro Trp Thr Phe
465                      470                      475

```

```

<210> 579
<211> 391
<212> PRT
<213> Artificial Sequence

```

```

<220>

```

ITI-08-PCT_Sequence_Listing_ST25.txt

<223> PAX5__Homo_sapiens__Q02548

<400> 579

Met	Asp	Leu	Glu	Lys	Asn	Tyr	Pro	Thr	Pro	Arg	Thr	Ser	Arg	Thr	Gly	1	5	10	15
His	Gly	Gly	Val	Asn	Gln	Leu	Gly	Gly	Val	Phe	Val	Asn	Gly	Arg	Pro	20	25	30	
Leu	Pro	Asp	Val	Val	Arg	Gln	Arg	Ile	Val	Glu	Leu	Ala	His	Gln	Gly	35	40	45	
Val	Arg	Pro	Cys	Asp	Ile	Ser	Arg	Gln	Leu	Arg	Val	Ser	His	Gly	Cys	50	55	60	
Val	Ser	Lys	Ile	Leu	Gly	Arg	Tyr	Tyr	Glu	Thr	Gly	Ser	Ile	Lys	Pro	65	70	75	80
Gly	Val	Ile	Gly	Gly	Ser	Lys	Pro	Lys	Val	Ala	Thr	Pro	Lys	Val	Val	85	90	95	
Glu	Lys	Ile	Ala	Glu	Tyr	Lys	Arg	Gln	Asn	Pro	Thr	Met	Phe	Ala	Trp	100	105	110	
Glu	Ile	Arg	Asp	Arg	Leu	Leu	Ala	Glu	Arg	Val	Cys	Asp	Asn	Asp	Thr	115	120	125	
Val	Pro	Ser	Val	Ser	Ser	Ile	Asn	Arg	Ile	Ile	Arg	Thr	Lys	Val	Gln	130	135	140	
Gln	Pro	Pro	Asn	Gln	Pro	Val	Pro	Ala	Ser	Ser	His	Ser	Ile	Val	Ser	145	150	155	160
Thr	Gly	Ser	Val	Thr	Gln	Val	Ser	Ser	Val	Ser	Thr	Asp	Ser	Ala	Gly	165	170	175	
Ser	Ser	Tyr	Ser	Ile	Ser	Gly	Ile	Leu	Gly	Ile	Thr	Ser	Pro	Ser	Ala	180	185	190	
Asp	Thr	Asn	Lys	Arg	Lys	Arg	Asp	Glu	Gly	Ile	Gln	Glu	Ser	Pro	Val	195	200	205	
Pro	Asn	Gly	His	Ser	Leu	Pro	Gly	Arg	Asp	Phe	Leu	Arg	Lys	Gln	Met	210	215	220	
Arg	Gly	Asp	Leu	Phe	Thr	Gln	Gln	Gln	Leu	Glu	Val	Leu	Asp	Arg	Val	225	230	235	240
Phe	Glu	Arg	Gln	His	Tyr	Ser	Asp	Ile	Phe	Thr	Thr	Thr	Glu	Pro	Ile	245	250	255	

ITI-08-PCT_Sequence_Listing_ST25.txt

Lys Pro Glu Gln Thr Thr Glu Tyr Ser Ala Met Ala Ser Leu Ala Gly
260 265 270

Gly Leu Asp Asp Met Lys Ala Asn Leu Ala Ser Pro Thr Pro Ala Asp
275 280 285

Ile Gly Ser Ser Val Pro Gly Pro Gln Ser Tyr Pro Ile Val Thr Gly
290 295 300

Arg Asp Leu Ala Ser Thr Thr Leu Pro Gly Tyr Pro Pro His Val Pro
305 310 315 320

Pro Ala Gly Gln Gly Ser Tyr Ser Ala Pro Thr Leu Thr Gly Met Val
325 330 335

Pro Gly Ser Glu Phe Ser Gly Ser Pro Tyr Ser His Pro Gln Tyr Ser
340 345 350

Ser Tyr Asn Asp Ser Trp Arg Phe Pro Asn Pro Gly Leu Leu Gly Ser
355 360 365

Pro Tyr Tyr Tyr Ser Ala Ala Ala Arg Gly Ala Ala Pro Pro Ala Ala
370 375 380

Ala Thr Ala Tyr Asp Arg His
385 390

<210> 580

<211> 290

<212> PRT

<213> Artificial Sequence

<220>

<223> PD1L1__Homo_sapiens__Q9NZQ7

<400> 580

Met Arg Ile Phe Ala Val Phe Ile Phe Met Thr Tyr Trp His Leu Leu
1 5 10 15

Asn Ala Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr
20 25 30

Gly Ser Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu
35 40 45

Asp Leu Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile
50 55 60

Ile Gln Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser
65 70 75 80

ITI-08-PCT_Sequence_Listing_ST25.txt

Tyr Arg Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn
85 90 95

Ala Ala Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr
100 105 110

Arg Cys Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val
115 120 125

Lys Val Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val
130 135 140

Asp Pro Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr
145 150 155 160

Pro Lys Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser
165 170 175

Gly Lys Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn
180 185 190

Val Thr Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr
195 200 205

Cys Thr Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu
210 215 220

Val Ile Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr His
225 230 235 240

Leu Val Ile Leu Gly Ala Ile Leu Leu Cys Leu Gly Val Ala Leu Thr
245 250 255

Phe Ile Phe Arg Leu Arg Lys Gly Arg Met Met Asp Val Lys Lys Cys
260 265 270

Gly Ile Gln Asp Thr Asn Ser Lys Lys Gln Ser Asp Thr His Leu Glu
275 280 285

Glu Thr
290

<210> 581

<211> 288

<212> PRT

<213> Artificial Sequence

<220>

<223> PDCD1__Homo_sapiens__Q15116

<400> 581

ITI-08-PCT_Sequence_Listing_ST25.txt

```

Met Gln Ile Pro Gln Ala Pro Trp Pro Val Val Trp Ala Val Leu Gln
1          5          10          15

Leu Gly Trp Arg Pro Gly Trp Phe Leu Asp Ser Pro Asp Arg Pro Trp
          20          25          30

Asn Pro Pro Thr Phe Ser Pro Ala Leu Leu Val Val Thr Glu Gly Asp
          35          40          45

Asn Ala Thr Phe Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser Phe Val
          50          55          60

Leu Asn Trp Tyr Arg Met Ser Pro Ser Asn Gln Thr Asp Lys Leu Ala
65          70          75          80

Ala Phe Pro Glu Asp Arg Ser Gln Pro Gly Gln Asp Cys Arg Phe Arg
          85          90          95

Val Thr Gln Leu Pro Asn Gly Arg Asp Phe His Met Ser Val Val Arg
          100          105          110

Ala Arg Arg Asn Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile Ser Leu
          115          120          125

Ala Pro Lys Ala Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu Arg Val
          130          135          140

Thr Glu Arg Arg Ala Glu Val Pro Thr Ala His Pro Ser Pro Ser Pro
145          150          155          160

Arg Pro Ala Gly Gln Phe Gln Thr Leu Val Val Gly Val Val Gly Gly
          165          170          175

Leu Leu Gly Ser Leu Val Leu Leu Val Trp Val Leu Ala Val Ile Cys
          180          185          190

Ser Arg Ala Ala Arg Gly Thr Ile Gly Ala Arg Arg Thr Gly Gln Pro
          195          200          205

Leu Lys Glu Asp Pro Ser Ala Val Pro Val Phe Ser Val Asp Tyr Gly
          210          215          220

Glu Leu Asp Phe Gln Trp Arg Glu Lys Thr Pro Glu Pro Pro Val Pro
225          230          235          240

Cys Val Pro Glu Gln Thr Glu Tyr Ala Thr Ile Val Phe Pro Ser Gly
          245          250          255

Met Gly Thr Ser Ser Pro Ala Arg Arg Gly Ser Ala Asp Gly Pro Arg
          260          265          270

Ser Ala Gln Pro Leu Arg Pro Glu Asp Gly His Cys Ser Trp Pro Leu

```

ITI-08-PCT_Sequence_Listing_ST25.txt

275

280

285

<210> 582
<211> 335
<212> PRT
<213> Artificial Sequence

<220>
<223> PDEF__Homo_sapiens__095238

<400> 582

Met Gly Ser Ala Ser Pro Gly Leu Ser Ser Val Ser Pro Ser His Leu
1 5 10 15

Leu Leu Pro Pro Asp Thr Val Ser Arg Thr Gly Leu Glu Lys Ala Ala
20 25 30

Ala Gly Ala Val Gly Leu Glu Arg Arg Asp Trp Ser Pro Ser Pro Pro
35 40 45

Ala Thr Pro Glu Gln Gly Leu Ser Ala Phe Tyr Leu Ser Tyr Phe Asp
50 55 60

Met Leu Tyr Pro Glu Asp Ser Ser Trp Ala Ala Lys Ala Pro Gly Ala
65 70 75 80

Ser Ser Arg Glu Glu Pro Pro Glu Glu Pro Glu Gln Cys Pro Val Ile
85 90 95

Asp Ser Gln Ala Pro Ala Gly Ser Leu Asp Leu Val Pro Gly Gly Leu
100 105 110

Thr Leu Glu Glu His Ser Leu Glu Gln Val Gln Ser Met Val Val Gly
115 120 125

Glu Val Leu Lys Asp Ile Glu Thr Ala Cys Lys Leu Leu Asn Ile Thr
130 135 140

Ala Asp Pro Met Asp Trp Ser Pro Ser Asn Val Gln Lys Trp Leu Leu
145 150 155 160

Trp Thr Glu His Gln Tyr Arg Leu Pro Pro Met Gly Lys Ala Phe Gln
165 170 175

Glu Leu Ala Gly Lys Glu Leu Cys Ala Met Ser Glu Glu Gln Phe Arg
180 185 190

Gln Arg Ser Pro Leu Gly Gly Asp Val Leu His Ala His Leu Asp Ile
195 200 205

Trp Lys Ser Ala Ala Trp Met Lys Glu Arg Thr Ser Pro Gly Ala Ile

ITI-08-PCT_Sequence_Listing_ST25.txt

210

215

220

His Tyr Cys Ala Ser Thr Ser Glu Glu Ser Trp Thr Asp Ser Glu Val
225 230 235 240

Asp Ser Ser Cys Ser Gly Gln Pro Ile His Leu Trp Gln Phe Leu Lys
245 250 255

Glu Leu Leu Leu Lys Pro His Ser Tyr Gly Arg Phe Ile Arg Trp Leu
260 265 270

Asn Lys Glu Lys Gly Ile Phe Lys Ile Glu Asp Ser Ala Gln Val Ala
275 280 285

Arg Leu Trp Gly Ile Arg Lys Asn Arg Pro Ala Met Asn Tyr Asp Lys
290 295 300

Leu Ser Arg Ser Ile Arg Gln Tyr Tyr Lys Lys Gly Ile Ile Arg Lys
305 310 315 320

Pro Asp Ile Ser Gln Arg Leu Val Tyr Gln Phe Val His Pro Ile
325 330 335

<210> 583

<211> 738

<212> PRT

<213> Artificial Sequence

<220>

<223> PECA1__Homo_sapiens__P16284

<400> 583

Met Gln Pro Arg Trp Ala Gln Gly Ala Thr Met Trp Leu Gly Val Leu
1 5 10 15

Leu Thr Leu Leu Leu Cys Ser Ser Leu Glu Gly Gln Glu Asn Ser Phe
20 25 30

Thr Ile Asn Ser Val Asp Met Lys Ser Leu Pro Asp Trp Thr Val Gln
35 40 45

Asn Gly Lys Asn Leu Thr Leu Gln Cys Phe Ala Asp Val Ser Thr Thr
50 55 60

Ser His Val Lys Pro Gln His Gln Met Leu Phe Tyr Lys Asp Asp Val
65 70 75 80

Leu Phe Tyr Asn Ile Ser Ser Met Lys Ser Thr Glu Ser Tyr Phe Ile
85 90 95

Pro Glu Val Arg Ile Tyr Asp Ser Gly Thr Tyr Lys Cys Thr Val Ile

ITI-08-PCT_Sequence_Listing_ST25.txt

100	105	110															
Val	Asn	Asn	Lys	Glu	Lys	Thr	Thr	Ala	Glu	Tyr	Gln	Leu	Leu	Val	Glu		
	115						120					125					
Gly	Val	Pro	Ser	Pro	Arg	Val	Thr	Leu	Asp	Lys	Lys	Glu	Ala	Ile	Gln		
	130					135					140						
Gly	Gly	Ile	Val	Arg	Val	Asn	Cys	Ser	Val	Pro	Glu	Glu	Lys	Ala	Pro		
145					150					155					160		
Ile	His	Phe	Thr	Ile	Glu	Lys	Leu	Glu	Leu	Asn	Glu	Lys	Met	Val	Lys		
				165					170					175			
Leu	Lys	Arg	Glu	Lys	Asn	Ser	Arg	Asp	Gln	Asn	Phe	Val	Ile	Leu	Glu		
			180					185					190				
Phe	Pro	Val	Glu	Glu	Gln	Asp	Arg	Val	Leu	Ser	Phe	Arg	Cys	Gln	Ala		
		195					200					205					
Arg	Ile	Ile	Ser	Gly	Ile	His	Met	Gln	Thr	Ser	Glu	Ser	Thr	Lys	Ser		
	210					215					220						
Glu	Leu	Val	Thr	Val	Thr	Glu	Ser	Phe	Ser	Thr	Pro	Lys	Phe	His	Ile		
225					230					235					240		
Ser	Pro	Thr	Gly	Met	Ile	Met	Glu	Gly	Ala	Gln	Leu	His	Ile	Lys	Cys		
				245					250					255			
Thr	Ile	Gln	Val	Thr	His	Leu	Ala	Gln	Glu	Phe	Pro	Glu	Ile	Ile	Ile		
			260					265					270				
Gln	Lys	Asp	Lys	Ala	Ile	Val	Ala	His	Asn	Arg	His	Gly	Asn	Lys	Ala		
		275					280					285					
Val	Tyr	Ser	Val	Met	Ala	Met	Val	Glu	His	Ser	Gly	Asn	Tyr	Thr	Cys		
	290					295					300						
Lys	Val	Glu	Ser	Ser	Arg	Ile	Ser	Lys	Val	Ser	Ser	Ile	Val	Val	Asn		
305					310					315					320		
Ile	Thr	Glu	Leu	Phe	Ser	Lys	Pro	Glu	Leu	Glu	Ser	Ser	Phe	Thr	His		
				325					330					335			
Leu	Asp	Gln	Gly	Glu	Arg	Leu	Asn	Leu	Ser	Cys	Ser	Ile	Pro	Gly	Ala		
			340					345					350				
Pro	Pro	Ala	Asn	Phe	Thr	Ile	Gln	Lys	Glu	Asp	Thr	Ile	Val	Ser	Gln		
		355					360					365					
Thr	Gln	Asp	Phe	Thr	Lys	Ile	Ala	Ser	Lys	Ser	Asp	Ser	Gly	Thr	Tyr		
	370					375					380						

ITI-08-PCT_Sequence_Listing_ST25.txt

Ile	Cys	Thr	Ala	Gly	Ile	Asp	Lys	Val	Val	Lys	Lys	Ser	Asn	Thr	Val	385	390	395	400
Gln	Ile	Val	Val	Cys	Glu	Met	Leu	Ser	Gln	Pro	Arg	Ile	Ser	Tyr	Asp	405	410	415	
Ala	Gln	Phe	Glu	Val	Ile	Lys	Gly	Gln	Thr	Ile	Glu	Val	Arg	Cys	Glu	420	425	430	
Ser	Ile	Ser	Gly	Thr	Leu	Pro	Ile	Ser	Tyr	Gln	Leu	Leu	Lys	Thr	Ser	435	440	445	
Lys	Val	Leu	Glu	Asn	Ser	Thr	Lys	Asn	Ser	Asn	Asp	Pro	Ala	Val	Phe	450	455	460	
Lys	Asp	Asn	Pro	Thr	Glu	Asp	Val	Glu	Tyr	Gln	Cys	Val	Ala	Asp	Asn	465	470	475	480
Cys	His	Ser	His	Ala	Lys	Met	Leu	Ser	Glu	Val	Leu	Arg	Val	Lys	Val	485	490	495	
Ile	Ala	Pro	Val	Asp	Glu	Val	Gln	Ile	Ser	Ile	Leu	Ser	Ser	Lys	Val	500	505	510	
Val	Glu	Ser	Gly	Glu	Asp	Ile	Val	Leu	Gln	Cys	Ala	Val	Asn	Glu	Gly	515	520	525	
Ser	Gly	Pro	Ile	Thr	Tyr	Lys	Phe	Tyr	Arg	Glu	Lys	Glu	Gly	Lys	Pro	530	535	540	
Phe	Tyr	Gln	Met	Thr	Ser	Asn	Ala	Thr	Gln	Ala	Phe	Trp	Thr	Lys	Gln	545	550	555	560
Lys	Ala	Ser	Lys	Glu	Gln	Glu	Gly	Glu	Tyr	Tyr	Cys	Thr	Ala	Phe	Asn	565	570	575	
Arg	Ala	Asn	His	Ala	Ser	Ser	Val	Pro	Arg	Ser	Lys	Ile	Leu	Thr	Val	580	585	590	
Arg	Val	Ile	Leu	Ala	Pro	Trp	Lys	Lys	Gly	Leu	Ile	Ala	Val	Val	Ile	595	600	605	
Ile	Gly	Val	Ile	Ile	Ala	Leu	Leu	Ile	Ile	Ala	Ala	Lys	Cys	Tyr	Phe	610	615	620	
Leu	Arg	Lys	Ala	Lys	Ala	Lys	Gln	Met	Pro	Val	Glu	Met	Ser	Arg	Pro	625	630	635	640
Ala	Val	Pro	Leu	Leu	Asn	Ser	Asn	Asn	Glu	Lys	Met	Ser	Asp	Pro	Asn	645	650	655	

ITI-08-PCT_Sequence_Listing_ST25.txt

Met Glu Ala Asn Ser His Tyr Gly His Asn Asp Asp Val Arg Asn His
660 665 670

Ala Met Lys Pro Ile Asn Asp Asn Lys Glu Pro Leu Asn Ser Asp Val
675 680 685

Gln Tyr Thr Glu Val Gln Val Ser Ser Ala Glu Ser His Lys Asp Leu
690 695 700

Gly Lys Lys Asp Thr Glu Thr Val Tyr Ser Glu Val Arg Lys Ala Val
705 710 715 720

Pro Asp Ala Val Glu Ser Arg Tyr Ser Arg Thr Glu Gly Ser Leu Asp
725 730 735

Gly Thr

<210> 584
<211> 911
<212> PRT
<213> Artificial Sequence

<220>
<223> PGCB__Homo_sapiens__Q96GW7

<400> 584

Met Ala Gln Leu Phe Leu Pro Leu Leu Ala Ala Leu Val Leu Ala Gln
1 5 10 15

Ala Pro Ala Ala Leu Ala Asp Val Leu Glu Gly Asp Ser Ser Glu Asp
20 25 30

Arg Ala Phe Arg Val Arg Ile Ala Gly Asp Ala Pro Leu Gln Gly Val
35 40 45

Leu Gly Gly Ala Leu Thr Ile Pro Cys His Val His Tyr Leu Arg Pro
50 55 60

Pro Pro Ser Arg Arg Ala Val Leu Gly Ser Pro Arg Val Lys Trp Thr
65 70 75 80

Phe Leu Ser Arg Gly Arg Glu Ala Glu Val Leu Val Ala Arg Gly Val
85 90 95

Arg Val Lys Val Asn Glu Ala Tyr Arg Phe Arg Val Ala Leu Pro Ala
100 105 110

Tyr Pro Ala Ser Leu Thr Asp Val Ser Leu Ala Leu Ser Glu Leu Arg
115 120 125

Pro Asn Asp Ser Gly Ile Tyr Arg Cys Glu Val Gln His Gly Ile Asp

ITI-08-PCT_Sequence_Listing_ST25.txt

```

130          135          140
Asp Ser Ser Asp Ala Val Glu Val Lys Val Lys Gly Val Val Phe Leu
145          150          155          160
Tyr Arg Glu Gly Ser Ala Arg Tyr Ala Phe Ser Phe Ser Gly Ala Gln
          165          170          175
Glu Ala Cys Ala Arg Ile Gly Ala His Ile Ala Thr Pro Glu Gln Leu
          180          185          190
Tyr Ala Ala Tyr Leu Gly Gly Tyr Glu Gln Cys Asp Ala Gly Trp Leu
          195          200          205
Ser Asp Gln Thr Val Arg Tyr Pro Ile Gln Thr Pro Arg Glu Ala Cys
          210          215          220
Tyr Gly Asp Met Asp Gly Phe Pro Gly Val Arg Asn Tyr Gly Val Val
225          230          235          240
Asp Pro Asp Asp Leu Tyr Asp Val Tyr Cys Tyr Ala Glu Asp Leu Asn
          245          250          255
Gly Glu Leu Phe Leu Gly Asp Pro Pro Glu Lys Leu Thr Leu Glu Glu
          260          265          270
Ala Arg Ala Tyr Cys Gln Glu Arg Gly Ala Glu Ile Ala Thr Thr Gly
          275          280          285
Gln Leu Tyr Ala Ala Trp Asp Gly Gly Leu Asp His Cys Ser Pro Gly
          290          295          300
Trp Leu Ala Asp Gly Ser Val Arg Tyr Pro Ile Val Thr Pro Ser Gln
305          310          315          320
Arg Cys Gly Gly Gly Leu Pro Gly Val Lys Thr Leu Phe Leu Phe Pro
          325          330          335
Asn Gln Thr Gly Phe Pro Asn Lys His Ser Arg Phe Asn Val Tyr Cys
          340          345          350
Phe Arg Asp Ser Ala Gln Pro Ser Ala Ile Pro Glu Ala Ser Asn Pro
          355          360          365
Ala Ser Asn Pro Ala Ser Asp Gly Leu Glu Ala Ile Val Thr Val Thr
          370          375          380
Glu Thr Leu Glu Glu Leu Gln Leu Pro Gln Glu Ala Thr Glu Ser Glu
385          390          395          400
Ser Arg Gly Ala Ile Tyr Ser Ile Pro Ile Met Glu Asp Gly Gly Gly
          405          410          415

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Gly	Ser	Ser	Thr	Pro	Glu	Asp	Pro	Ala	Glu	Ala	Pro	Arg	Thr	Leu	Leu	420	425	430
Glu	Phe	Glu	Thr	Gln	Ser	Met	Val	Pro	Pro	Thr	Gly	Phe	Ser	Glu	Glu	435	440	445
Glu	Gly	Lys	Ala	Leu	Glu	Glu	Glu	Glu	Lys	Tyr	Glu	Asp	Glu	Glu	Glu	450	455	460
Lys	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Val	Glu	Asp	Glu	Ala	Leu	Trp	465	470	475
Ala	Trp	Pro	Ser	Glu	Leu	Ser	Ser	Pro	Gly	Pro	Glu	Ala	Ser	Leu	Pro	485	490	495
Thr	Glu	Pro	Ala	Ala	Gln	Glu	Glu	Ser	Leu	Ser	Gln	Ala	Pro	Ala	Arg	500	505	510
Ala	Val	Leu	Gln	Pro	Gly	Ala	Ser	Pro	Leu	Pro	Asp	Gly	Glu	Ser	Glu	515	520	525
Ala	Ser	Arg	Pro	Pro	Arg	Val	His	Gly	Pro	Pro	Thr	Glu	Thr	Leu	Pro	530	535	540
Thr	Pro	Arg	Glu	Arg	Asn	Leu	Ala	Ser	Pro	Ser	Pro	Ser	Thr	Leu	Val	545	550	555
Glu	Ala	Arg	Glu	Val	Gly	Glu	Ala	Thr	Gly	Gly	Pro	Glu	Leu	Ser	Gly	565	570	575
Val	Pro	Arg	Gly	Glu	Ser	Glu	Glu	Thr	Gly	Ser	Ser	Glu	Gly	Ala	Pro	580	585	590
Ser	Leu	Leu	Pro	Ala	Thr	Arg	Ala	Pro	Glu	Gly	Thr	Arg	Glu	Leu	Glu	595	600	605
Ala	Pro	Ser	Glu	Asp	Asn	Ser	Gly	Arg	Thr	Ala	Pro	Ala	Gly	Thr	Ser	610	615	620
Val	Gln	Ala	Gln	Pro	Val	Leu	Pro	Thr	Asp	Ser	Ala	Ser	Arg	Gly	Gly	625	630	635
Val	Ala	Val	Val	Pro	Ala	Ser	Gly	Asp	Cys	Val	Pro	Ser	Pro	Cys	His	645	650	655
Asn	Gly	Gly	Thr	Cys	Leu	Glu	Glu	Glu	Glu	Gly	Val	Arg	Cys	Leu	Cys	660	665	670
Leu	Pro	Gly	Tyr	Gly	Gly	Asp	Leu	Cys	Asp	Val	Gly	Leu	Arg	Phe	Cys	675	680	685

ITI-08-PCT_Sequence_Listing_ST25.txt

Asn Pro Gly Trp Asp Ala Phe Gln Gly Ala Cys Tyr Lys His Phe Ser
690 695 700

Thr Arg Arg Ser Trp Glu Glu Ala Glu Thr Gln Cys Arg Met Tyr Gly
705 710 715 720

Ala His Leu Ala Ser Ile Ser Thr Pro Glu Glu Gln Asp Phe Ile Asn
725 730 735

Asn Arg Tyr Arg Glu Tyr Gln Trp Ile Gly Leu Asn Asp Arg Thr Ile
740 745 750

Glu Gly Asp Phe Leu Trp Ser Asp Gly Val Pro Leu Leu Tyr Glu Asn
755 760 765

Trp Asn Pro Gly Gln Pro Asp Ser Tyr Phe Leu Ser Gly Glu Asn Cys
770 775 780

Val Val Met Val Trp His Asp Gln Gly Gln Trp Ser Asp Val Pro Cys
785 790 795 800

Asn Tyr His Leu Ser Tyr Thr Cys Lys Met Gly Leu Val Ser Cys Gly
805 810 815

Pro Pro Pro Glu Leu Pro Leu Ala Gln Val Phe Gly Arg Pro Arg Leu
820 825 830

Arg Tyr Glu Val Asp Thr Val Leu Arg Tyr Arg Cys Arg Glu Gly Leu
835 840 845

Ala Gln Arg Asn Leu Pro Leu Ile Arg Cys Gln Glu Asn Gly Arg Trp
850 855 860

Glu Ala Pro Gln Ile Ser Cys Val Pro Arg Arg Pro Ala Arg Ala Leu
865 870 875 880

His Pro Glu Glu Asp Pro Glu Gly Arg Gln Gly Arg Leu Leu Gly Arg
885 890 895

Trp Lys Ala Leu Leu Ile Pro Pro Ser Ser Pro Met Pro Gly Pro
900 905 910

<210> 585

<211> 1106

<212> PRT

<213> Artificial Sequence

<220>

<223> PGFRB__Homo_sapiens__P09619

<400> 585

ITI-08-PCT_Sequence_Listing_ST25.txt

```

Met Arg Leu Pro Gly Ala Met Pro Ala Leu Ala Leu Lys Gly Glu Leu
1      5      10      15

Leu Leu Leu Ser Leu Leu Leu Leu Leu Glu Pro Gln Ile Ser Gln Gly
20      25      30

Leu Val Val Thr Pro Pro Gly Pro Glu Leu Val Leu Asn Val Ser Ser
35      40      45

Thr Phe Val Leu Thr Cys Ser Gly Ser Ala Pro Val Val Trp Glu Arg
50      55      60

Met Ser Gln Glu Pro Pro Gln Glu Met Ala Lys Ala Gln Asp Gly Thr
65      70      75      80

Phe Ser Ser Val Leu Thr Leu Thr Asn Leu Thr Gly Leu Asp Thr Gly
85      90      95

Glu Tyr Phe Cys Thr His Asn Asp Ser Arg Gly Leu Glu Thr Asp Glu
100     105     110

Arg Lys Arg Leu Tyr Ile Phe Val Pro Asp Pro Thr Val Gly Phe Leu
115     120     125

Pro Asn Asp Ala Glu Glu Leu Phe Ile Phe Leu Thr Glu Ile Thr Glu
130     135     140

Ile Thr Ile Pro Cys Arg Val Thr Asp Pro Gln Leu Val Val Thr Leu
145     150     155     160

His Glu Lys Lys Gly Asp Val Ala Leu Pro Val Pro Tyr Asp His Gln
165     170     175

Arg Gly Phe Ser Gly Ile Phe Glu Asp Arg Ser Tyr Ile Cys Lys Thr
180     185     190

Thr Ile Gly Asp Arg Glu Val Asp Ser Asp Ala Tyr Tyr Val Tyr Arg
195     200     205

Leu Gln Val Ser Ser Ile Asn Val Ser Val Asn Ala Val Gln Thr Val
210     215     220

Val Arg Gln Gly Glu Asn Ile Thr Leu Met Cys Ile Val Ile Gly Asn
225     230     235     240

Glu Val Val Asn Phe Glu Trp Thr Tyr Pro Arg Lys Glu Ser Gly Arg
245     250     255

Leu Val Glu Pro Val Thr Asp Phe Leu Leu Asp Met Pro Tyr His Ile
260     265     270

Arg Ser Ile Leu His Ile Pro Ser Ala Glu Leu Glu Asp Ser Gly Thr

```

ITI-08-PCT_Sequence_Listing_ST25.txt

```

275                280                285
Tyr Thr Cys Asn Val Thr Glu Ser Val Asn Asp His Gln Asp Glu Lys
290                295                300
Ala Ile Asn Ile Thr Val Val Glu Ser Gly Tyr Val Arg Leu Leu Gly
305                310                315                320
Glu Val Gly Thr Leu Gln Phe Ala Glu Leu His Arg Ser Arg Thr Leu
325                330                335
Gln Val Val Phe Glu Ala Tyr Pro Pro Pro Thr Val Leu Trp Phe Lys
340                345                350
Asp Asn Arg Thr Leu Gly Asp Ser Ser Ala Gly Glu Ile Ala Leu Ser
355                360                365
Thr Arg Asn Val Ser Glu Thr Arg Tyr Val Ser Glu Leu Thr Leu Val
370                375                380
Arg Val Lys Val Ala Glu Ala Gly His Tyr Thr Met Arg Ala Phe His
385                390                395                400
Glu Asp Ala Glu Val Gln Leu Ser Phe Gln Leu Gln Ile Asn Val Pro
405                410                415
Val Arg Val Leu Glu Leu Ser Glu Ser His Pro Asp Ser Gly Glu Gln
420                425                430
Thr Val Arg Cys Arg Gly Arg Gly Met Pro Gln Pro Asn Ile Ile Trp
435                440                445
Ser Ala Cys Arg Asp Leu Lys Arg Cys Pro Arg Glu Leu Pro Pro Thr
450                455                460
Leu Leu Gly Asn Ser Ser Glu Glu Glu Ser Gln Leu Glu Thr Asn Val
465                470                475                480
Thr Tyr Trp Glu Glu Glu Gln Glu Phe Glu Val Val Ser Thr Leu Arg
485                490                495
Leu Gln His Val Asp Arg Pro Leu Ser Val Arg Cys Thr Leu Arg Asn
500                505                510
Ala Val Gly Gln Asp Thr Gln Glu Val Ile Val Val Pro His Ser Leu
515                520                525
Pro Phe Lys Val Val Val Ile Ser Ala Ile Leu Ala Leu Val Val Leu
530                535                540
Thr Ile Ile Ser Leu Ile Ile Leu Ile Met Leu Trp Gln Lys Lys Pro
545                550                555                560

```


ITI-08-PCT_Sequence_Listing_ST25.txt

Arg	Tyr	Glu	Ile	Arg	Trp	Lys	Val	Ile	Glu	Ser	Val	Ser	Ser	Asp	Gly	565	570	575
His	Glu	Tyr	Ile	Tyr	Val	Asp	Pro	Met	Gln	Leu	Pro	Tyr	Asp	Ser	Thr	580	585	590
Trp	Glu	Leu	Pro	Arg	Asp	Gln	Leu	Val	Leu	Gly	Arg	Thr	Leu	Gly	Ser	595	600	605
Gly	Ala	Phe	Gly	Gln	Val	Val	Glu	Ala	Thr	Ala	His	Gly	Leu	Ser	His	610	615	620
Ser	Gln	Ala	Thr	Met	Lys	Val	Ala	Val	Lys	Met	Leu	Lys	Ser	Thr	Ala	625	630	635
Arg	Ser	Ser	Glu	Lys	Gln	Ala	Leu	Met	Ser	Glu	Leu	Lys	Ile	Met	Ser	645	650	655
His	Leu	Gly	Pro	His	Leu	Asn	Val	Val	Asn	Leu	Leu	Gly	Ala	Cys	Thr	660	665	670
Lys	Gly	Gly	Pro	Ile	Tyr	Ile	Ile	Thr	Glu	Tyr	Cys	Arg	Tyr	Gly	Asp	675	680	685
Leu	Val	Asp	Tyr	Leu	His	Arg	Asn	Lys	His	Thr	Phe	Leu	Gln	His	His	690	695	700
Ser	Asp	Lys	Arg	Arg	Pro	Pro	Ser	Ala	Glu	Leu	Tyr	Ser	Asn	Ala	Leu	705	710	715
Pro	Val	Gly	Leu	Pro	Leu	Pro	Ser	His	Val	Ser	Leu	Thr	Gly	Glu	Ser	725	730	735
Asp	Gly	Gly	Tyr	Met	Asp	Met	Ser	Lys	Asp	Glu	Ser	Val	Asp	Tyr	Val	740	745	750
Pro	Met	Leu	Asp	Met	Lys	Gly	Asp	Val	Lys	Tyr	Ala	Asp	Ile	Glu	Ser	755	760	765
Ser	Asn	Tyr	Met	Ala	Pro	Tyr	Asp	Asn	Tyr	Val	Pro	Ser	Ala	Pro	Glu	770	775	780
Arg	Thr	Cys	Arg	Ala	Thr	Leu	Ile	Asn	Glu	Ser	Pro	Val	Leu	Ser	Tyr	785	790	795
Met	Asp	Leu	Val	Gly	Phe	Ser	Tyr	Gln	Val	Ala	Asn	Gly	Met	Glu	Phe	805	810	815
Leu	Ala	Ser	Lys	Asn	Cys	Val	His	Arg	Asp	Leu	Ala	Ala	Arg	Asn	Val	820	825	830

ITI-08-PCT_Sequence_Listing_ST25.txt

Leu Ile Cys Glu Gly Lys Leu Val Lys Ile Cys Asp Phe Gly Leu Ala
 835 840 845
 Arg Asp Ile Met Arg Asp Ser Asn Tyr Ile Ser Lys Gly Ser Thr Phe
 850 855 860
 Leu Pro Leu Lys Trp Met Ala Pro Glu Ser Ile Phe Asn Ser Leu Tyr
 865 870 875 880
 Thr Thr Leu Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Trp Glu Ile
 885 890 895
 Phe Thr Leu Gly Gly Thr Pro Tyr Pro Glu Leu Pro Met Asn Glu Gln
 900 905 910
 Phe Tyr Asn Ala Ile Lys Arg Gly Tyr Arg Met Ala Gln Pro Ala His
 915 920 925
 Ala Ser Asp Glu Ile Tyr Glu Ile Met Gln Lys Cys Trp Glu Glu Lys
 930 935 940
 Phe Glu Ile Arg Pro Pro Phe Ser Gln Leu Val Leu Leu Leu Glu Arg
 945 950 955 960
 Leu Leu Gly Glu Gly Tyr Lys Lys Lys Tyr Gln Gln Val Asp Glu Glu
 965 970 975
 Phe Leu Arg Ser Asp His Pro Ala Ile Leu Arg Ser Gln Ala Arg Leu
 980 985 990
 Pro Gly Phe His Gly Leu Arg Ser Pro Leu Asp Thr Ser Ser Val Leu
 995 1000 1005
 Tyr Thr Ala Val Gln Pro Asn Glu Gly Asp Asn Asp Tyr Ile Ile
 1010 1015 1020
 Pro Leu Pro Asp Pro Lys Pro Glu Val Ala Asp Glu Gly Pro Leu
 1025 1030 1035
 Glu Gly Ser Pro Ser Leu Ala Ser Ser Thr Leu Asn Glu Val Asn
 1040 1045 1050
 Thr Ser Ser Thr Ile Ser Cys Asp Ser Pro Leu Glu Pro Gln Asp
 1055 1060 1065
 Glu Pro Glu Pro Glu Pro Gln Leu Glu Leu Gln Val Glu Pro Glu
 1070 1075 1080
 Pro Glu Leu Glu Gln Leu Pro Asp Ser Gly Cys Pro Ala Pro Arg
 1085 1090 1095
 Ala Glu Ala Glu Asp Ser Phe Leu

ITI-08-PCT_Sequence_Listing_ST25.txt

1100

1105

<210> 586

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> Pim-1_Kinase__Homo_sapiens__A0A024RD25

<400> 586

Met Leu Leu Ser Lys Ile Asn Ser Leu Ala His Leu Arg Ala Ala Pro
1 5 10 15

Cys Asn Asp Leu His Ala Thr Lys Leu Ala Pro Gly Lys Glu Lys Glu
20 25 30

Pro Leu Glu Ser Gln Tyr Gln Val Gly Pro Leu Leu Gly Ser Gly Gly
35 40 45

Phe Gly Ser Val Tyr Ser Gly Ile Arg Val Ser Asp Asn Leu Pro Val
50 55 60

Ala Ile Lys His Val Glu Lys Asp Arg Ile Ser Asp Trp Gly Glu Leu
65 70 75 80

Pro Asn Gly Thr Arg Val Pro Met Glu Val Val Leu Leu Lys Lys Val
85 90 95

Ser Ser Gly Phe Ser Gly Val Ile Arg Leu Leu Asp Trp Phe Glu Arg
100 105 110

Pro Asp Ser Phe Val Leu Ile Leu Glu Arg Pro Glu Pro Val Gln Asp
115 120 125

Leu Phe Asp Phe Ile Thr Glu Arg Gly Ala Leu Gln Glu Glu Leu Ala
130 135 140

Arg Ser Phe Phe Trp Gln Val Leu Glu Ala Val Arg His Cys His Asn
145 150 155 160

Cys Gly Val Leu His Arg Asp Ile Lys Asp Glu Asn Ile Leu Ile Asp
165 170 175

Leu Asn Arg Gly Glu Leu Lys Leu Ile Asp Phe Gly Ser Gly Ala Leu
180 185 190

Leu Lys Asp Thr Val Tyr Thr Asp Phe Asp Gly Thr Arg Val Tyr Ser
195 200 205

Pro Pro Glu Trp Ile Arg Tyr His Arg Tyr His Gly Arg Ser Ala Ala

ITI-08-PCT_Sequence_Listing_ST25.txt

210

215

220

Val Trp Ser Leu Gly Ile Leu Leu Tyr Asp Met Val Cys Gly Asp Ile
225 230 235 240

Pro Phe Glu His Asp Glu Glu Ile Ile Arg Gly Gln Val Phe Phe Arg
245 250 255

Gln Arg Val Ser Ser Glu Cys Gln His Leu Ile Arg Trp Cys Leu Ala
260 265 270

Leu Arg Pro Ser Asp Arg Pro Thr Phe Glu Glu Ile Gln Asn His Pro
275 280 285

Trp Met Gln Asp Val Leu Leu Pro Gln Glu Thr Ala Glu Ile His Leu
290 295 300

His Ser Leu Ser Pro Gly Pro Ser Lys
305 310

<210> 587

<211> 100

<212> PRT

<213> Artificial Sequence

<220>

<223> Pin-1__Homo_sapiens__015428

<400> 587

Met Ala Asp Glu Glu Lys Leu Pro Pro Gly Trp Glu Lys Arg Met Ser
1 5 10 15

Arg Pro Ser Gly Arg Gly Tyr Tyr Phe Asn His Ile Thr Asn Pro Ser
20 25 30

Gln Trp Glu Arg Pro Ser Gly Asn Ser Ser Ser Gly Gly Lys Ile Trp
35 40 45

Gln Gly Glu Pro Ala Arg Val Arg Arg Ser His Leu Leu Val Lys Pro
50 55 60

Val Lys Ala Ala Leu Asp Leu Ala Ala Gly Asn His Pro Asp Gln Gly
65 70 75 80

Gly Gly Pro Gly Ala Asp Gln Arg Leu His Pro Glu Asp Gln Gly Arg
85 90 95

Arg Glu Gly Leu
100

<210> 588

ITI-08-PCT_Sequence_Listing_ST25.txt

<211> 163
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Pin-1__Homo_sapiens__Q13526

<400> 588

Met Ala Asp Glu Glu Lys Leu Pro Pro Gly Trp Glu Lys Arg Met Ser
 1 5 10 15

Arg Ser Ser Gly Arg Val Tyr Tyr Phe Asn His Ile Thr Asn Ala Ser
 20 25 30

Gln Trp Glu Arg Pro Ser Gly Asn Ser Ser Ser Gly Gly Lys Asn Gly
 35 40 45

Gln Gly Glu Pro Ala Arg Val Arg Cys Ser His Leu Leu Val Lys His
 50 55 60

Ser Gln Ser Arg Arg Pro Ser Ser Trp Arg Gln Glu Lys Ile Thr Arg
 65 70 75 80

Thr Lys Glu Glu Ala Leu Glu Leu Ile Asn Gly Tyr Ile Gln Lys Ile
 85 90 95

Lys Ser Gly Glu Glu Asp Phe Glu Ser Leu Ala Ser Gln Phe Ser Asp
 100 105 110

Cys Ser Ser Ala Lys Ala Arg Gly Asp Leu Gly Ala Phe Ser Arg Gly
 115 120 125

Gln Met Gln Lys Pro Phe Glu Asp Ala Ser Phe Ala Leu Arg Thr Gly
 130 135 140

Glu Met Ser Gly Pro Val Phe Thr Asp Ser Gly Ile His Ile Ile Leu
 145 150 155 160

Arg Thr Glu

<210> 589
 <211> 45
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Pin-1__Homo_sapiens__Q49AR7

<400> 589

Met Gln Lys Pro Phe Glu Asp Ala Ser Phe Ala Leu Arg Thr Gly Glu

ITI-08-PCT_Sequence_Listing_ST25.txt

```

1           5           10           15
Met Ser Gly Pro Val Phe Thr Asp Ser Gly Ile His Ile Ile Leu Arg
    20           25           30

Thr Glu Cys Trp Arg Gln Thr Arg Gly Pro Asn Cys Phe
    35           40           45

<210> 590
<211> 212
<212> PRT
<213> Artificial Sequence

<220>
<223> PLAC1__Homo_sapiens__Q9HBJ0

<400> 590

Met Lys Val Phe Lys Phe Ile Gly Leu Met Ile Leu Leu Thr Ser Ala
1           5           10           15

Phe Ser Ala Gly Ser Gly Gln Ser Pro Met Thr Val Leu Cys Ser Ile
    20           25           30

Asp Trp Phe Met Val Thr Val His Pro Phe Met Leu Asn Asn Asp Val
    35           40           45

Cys Val His Phe His Glu Leu His Leu Gly Leu Gly Cys Pro Pro Asn
    50           55           60

His Val Gln Pro His Ala Tyr Gln Phe Thr Tyr Arg Val Thr Glu Cys
65           70           75           80

Gly Ile Arg Ala Lys Ala Val Ser Gln Asp Met Val Ile Tyr Ser Thr
    85           90           95

Glu Ile His Tyr Ser Ser Lys Gly Thr Pro Ser Lys Phe Val Ile Pro
    100          105          110

Val Ser Cys Ala Ala Pro Gln Lys Ser Pro Trp Leu Thr Lys Pro Cys
    115          120          125

Ser Met Arg Val Ala Ser Lys Ser Arg Ala Thr Ala Gln Lys Asp Glu
    130          135          140

Lys Cys Tyr Glu Val Phe Ser Leu Ser Gln Ser Ser Gln Arg Pro Asn
145          150          155          160

Cys Asp Cys Pro Pro Cys Val Phe Ser Glu Glu Glu His Thr Gln Val
    165          170          175

Pro Cys His Gln Ala Gly Ala Gln Glu Ala Gln Pro Leu Gln Pro Ser

```

ITI-08-PCT_Sequence_Listing_ST25.txt

180

185

190

His Phe Leu Asp Ile Ser Glu Asp Trp Ser Leu His Thr Asp Asp Met
195 200 205

Ile Gly Ser Met
210

<210> 591

<211> 661

<212> PRT

<213> Artificial Sequence

<220>

<223> PMEL__Homo_sapiens__P40967

<400> 591

Met Asp Leu Val Leu Lys Arg Cys Leu Leu His Leu Ala Val Ile Gly
1 5 10 15

Ala Leu Leu Ala Val Gly Ala Thr Lys Val Pro Arg Asn Gln Asp Trp
20 25 30

Leu Gly Val Ser Arg Gln Leu Arg Thr Lys Ala Trp Asn Arg Gln Leu
35 40 45

Tyr Pro Glu Trp Thr Glu Ala Gln Arg Leu Asp Cys Trp Arg Gly Gly
50 55 60

Gln Val Ser Leu Lys Val Ser Asn Asp Gly Pro Thr Leu Ile Gly Ala
65 70 75 80

Asn Ala Ser Phe Ser Ile Ala Leu Asn Phe Pro Gly Ser Gln Lys Val
85 90 95

Leu Pro Asp Gly Gln Val Ile Trp Val Asn Asn Thr Ile Ile Asn Gly
100 105 110

Ser Gln Val Trp Gly Gly Gln Pro Val Tyr Pro Gln Glu Thr Asp Asp
115 120 125

Ala Cys Ile Phe Pro Asp Gly Gly Pro Cys Pro Ser Gly Ser Trp Ser
130 135 140

Gln Lys Arg Ser Phe Val Tyr Val Trp Lys Thr Trp Gly Gln Tyr Trp
145 150 155 160

Gln Val Leu Gly Gly Pro Val Ser Gly Leu Ser Ile Gly Thr Gly Arg
165 170 175

Ala Met Leu Gly Thr His Thr Met Glu Val Thr Val Tyr His Arg Arg

180 185 190

Page 1005

ITI-08-PCT_Sequence_Listing_ST25.txt

Arg Leu Val Lys Arg Gln Val Pro Leu Asp Cys Val Leu Tyr Arg Tyr
465 470 475 480

Gly Ser Phe Ser Val Thr Leu Asp Ile Val Gln Gly Ile Glu Ser Ala
485 490 495

Glu Ile Leu Gln Ala Val Pro Ser Gly Glu Gly Asp Ala Phe Glu Leu
500 505 510

Thr Val Ser Cys Gln Gly Gly Leu Pro Lys Glu Ala Cys Met Glu Ile
515 520 525

Ser Ser Pro Gly Cys Gln Pro Pro Ala Gln Arg Leu Cys Gln Pro Val
530 535 540

Leu Pro Ser Pro Ala Cys Gln Leu Val Leu His Gln Ile Leu Lys Gly
545 550 555 560

Gly Ser Gly Thr Tyr Cys Leu Asn Val Ser Leu Ala Asp Thr Asn Ser
565 570 575

Leu Ala Val Val Ser Thr Gln Leu Ile Met Pro Gly Gln Glu Ala Gly
580 585 590

Leu Gly Gln Val Pro Leu Ile Val Gly Ile Leu Leu Val Leu Met Ala
595 600 605

Val Val Leu Ala Ser Leu Ile Tyr Arg Arg Arg Leu Met Lys Gln Asp
610 615 620

Phe Ser Val Pro Gln Leu Pro His Ser Ser Ser His Trp Leu Arg Leu
625 630 635 640

Pro Arg Ile Phe Cys Ser Cys Pro Ile Gly Glu Asn Ser Pro Leu Leu
645 650 655

Ser Gly Gln Gln Val
660

<210> 592
<211> 882
<212> PRT
<213> Artificial Sequence

<220>
<223> PML__Homo_sapiens__P29590

<400> 592

Met Glu Pro Ala Pro Ala Arg Ser Pro Arg Pro Gln Gln Asp Pro Ala
1 5 10 15

ITI-08-PCT_Sequence_Listing_ST25.txt

Arg	Pro	Gln	Glu 20	Pro	Thr	Met	Pro	Pro 25	Pro	Glu	Thr	Pro	Ser 30	Glu	Gly
Arg	Gln	Pro 35	Ser	Pro	Ser	Pro	Ser 40	Pro	Thr	Glu	Arg	Ala 45	Pro	Ala	Ser
Glu	Glu 50	Glu	Phe	Gln	Phe	Leu 55	Arg	Cys	Gln	Gln	Cys 60	Gln	Ala	Glu	Ala
Lys 65	Cys	Pro	Lys	Leu	Leu 70	Pro	Cys	Leu	His	Thr 75	Leu	Cys	Ser	Gly	Cys 80
Leu	Glu	Ala	Ser	Gly 85	Met	Gln	Cys	Pro	Ile 90	Cys	Gln	Ala	Pro	Trp 95	Pro
Leu	Gly	Ala	Asp 100	Thr	Pro	Ala	Leu	Asp 105	Asn	Val	Phe	Phe	Glu 110	Ser	Leu
Gln	Arg	Arg 115	Leu	Ser	Val	Tyr	Arg 120	Gln	Ile	Val	Asp	Ala 125	Gln	Ala	Val
Cys	Thr 130	Arg	Cys	Lys	Glu	Ser 135	Ala	Asp	Phe	Trp	Cys 140	Phe	Glu	Cys	Glu
Gln 145	Leu	Leu	Cys	Ala	Lys 150	Cys	Phe	Glu	Ala	His 155	Gln	Trp	Phe	Leu	Lys 160
His	Glu	Ala	Arg	Pro 165	Leu	Ala	Glu	Leu	Arg 170	Asn	Gln	Ser	Val	Arg 175	Glu
Phe	Leu	Asp	Gly 180	Thr	Arg	Lys	Thr	Asn 185	Asn	Ile	Phe	Cys	Ser 190	Asn	Pro
Asn	His 195	Arg	Thr	Pro	Thr	Leu 200	Thr	Ser	Ile	Tyr	Cys 205	Arg	Gly	Cys	Ser
Lys	Pro 210	Leu	Cys	Cys	Ser	Cys 215	Ala	Leu	Leu	Asp	Ser 220	Ser	His	Ser	Glu
Leu 225	Lys	Cys	Asp	Ile	Ser 230	Ala	Glu	Ile	Gln	Gln 235	Arg	Gln	Glu	Glu	Leu 240
Asp	Ala	Met	Thr	Gln 245	Ala	Leu	Gln	Glu	Gln	Asp 250	Ser	Ala	Phe	Gly 255	Ala
Val	His	Ala	Gln 260	Met	His	Ala	Ala	Val	Gly	Gln	Leu	Gly	Arg 270	Ala	Arg
Ala	Glu	Thr 275	Glu	Glu	Leu	Ile	Arg 280	Glu	Arg	Val	Arg	Gln 285	Val	Val	Ala

ITI-08-PCT_Sequence_Listing_ST25.txt

His Val Arg Ala Gln Glu Arg Glu Leu Leu Glu Ala Val Asp Ala Arg
 290 295 300
 Tyr Gln Arg Asp Tyr Glu Glu Met Ala Ser Arg Leu Gly Arg Leu Asp
 305 310 315 320
 Ala Val Leu Gln Arg Ile Arg Thr Gly Ser Ala Leu Val Gln Arg Met
 325 330 335
 Lys Cys Tyr Ala Ser Asp Gln Glu Val Leu Asp Met His Gly Phe Leu
 340 345 350
 Arg Gln Ala Leu Cys Arg Leu Arg Gln Glu Glu Pro Gln Ser Leu Gln
 355 360 365
 Ala Ala Val Arg Thr Asp Gly Phe Asp Glu Phe Lys Val Arg Leu Gln
 370 375 380
 Asp Leu Ser Ser Cys Ile Thr Gln Gly Lys Asp Ala Ala Val Ser Lys
 385 390 395 400
 Lys Ala Ser Pro Glu Ala Ala Ser Thr Pro Arg Asp Pro Ile Asp Val
 405 410 415
 Asp Leu Pro Glu Glu Ala Glu Arg Val Lys Ala Gln Val Gln Ala Leu
 420 425 430
 Gly Leu Ala Glu Ala Gln Pro Met Ala Val Val Gln Ser Val Pro Gly
 435 440 445
 Ala His Pro Val Pro Val Tyr Ala Phe Ser Ile Lys Gly Pro Ser Tyr
 450 455 460
 Gly Glu Asp Val Ser Asn Thr Thr Thr Ala Gln Lys Arg Lys Cys Ser
 465 470 475 480
 Gln Thr Gln Cys Pro Arg Lys Val Ile Lys Met Glu Ser Glu Glu Gly
 485 490 495
 Lys Glu Ala Arg Leu Ala Arg Ser Ser Pro Glu Gln Pro Arg Pro Ser
 500 505 510
 Thr Ser Lys Ala Val Ser Pro Pro His Leu Asp Gly Pro Pro Ser Pro
 515 520 525
 Arg Ser Pro Val Ile Gly Ser Glu Val Phe Leu Pro Asn Ser Asn His
 530 535 540
 Val Ala Ser Gly Ala Gly Glu Ala Glu Glu Arg Val Val Val Ile Ser
 545 550 555 560
 Ser Ser Glu Asp Ser Asp Ala Glu Asn Ser Ser Ser Arg Glu Leu Asp

ITI-08-PCT_Sequence_Listing_ST25.txt

565

570

575

Asp Ser Ser Ser Glu Ser Ser Asp Leu Gln Leu Glu Gly Pro Ser Thr
580 585 590

Leu Arg Val Leu Asp Glu Asn Leu Ala Asp Pro Gln Ala Glu Asp Arg
595 600 605

Pro Leu Val Phe Phe Asp Leu Lys Ile Asp Asn Glu Thr Gln Lys Ile
610 615 620

Ser Gln Leu Ala Ala Val Asn Arg Glu Ser Lys Phe Arg Val Val Ile
625 630 635 640

Gln Pro Glu Ala Phe Phe Ser Ile Tyr Ser Lys Ala Val Ser Leu Glu
645 650 655

Val Gly Leu Gln His Phe Leu Ser Phe Leu Ser Ser Met Arg Arg Pro
660 665 670

Ile Leu Ala Cys Tyr Lys Leu Trp Gly Pro Gly Leu Pro Asn Phe Phe
675 680 685

Arg Ala Leu Glu Asp Ile Asn Arg Leu Trp Glu Phe Gln Glu Ala Ile
690 695 700

Ser Gly Phe Leu Ala Ala Leu Pro Leu Ile Arg Glu Arg Val Pro Gly
705 710 715 720

Ala Ser Ser Phe Lys Leu Lys Asn Leu Ala Gln Thr Tyr Leu Ala Arg
725 730 735

Asn Met Ser Glu Arg Ser Ala Met Ala Ala Val Leu Ala Met Arg Asp
740 745 750

Leu Cys Arg Leu Leu Glu Val Ser Pro Gly Pro Gln Leu Ala Gln His
755 760 765

Val Tyr Pro Phe Ser Ser Leu Gln Cys Phe Ala Ser Leu Gln Pro Leu
770 775 780

Val Gln Ala Ala Val Leu Pro Arg Ala Glu Ala Arg Leu Leu Ala Leu
785 790 795 800

His Asn Val Ser Phe Met Glu Leu Leu Ser Ala His Arg Arg Asp Arg
805 810 815

Gln Gly Gly Leu Lys Lys Tyr Ser Arg Tyr Leu Ser Leu Gln Thr Thr
820 825 830

Thr Leu Pro Pro Ala Gln Pro Ala Phe Asn Leu Gln Ala Leu Gly Thr
835 840 845

ITI-08-PCT_Sequence_Listing_ST25.txt

Tyr Phe Glu Gly Leu Leu Glu Gly Pro Ala Leu Ala Arg Ala Glu Gly
850 855 860

Val Ser Thr Pro Leu Ala Gly Arg Gly Leu Ala Glu Arg Ala Ser Gln
865 870 875 880

Gln Ser

<210> 593

<211> 1075

<212> PRT

<213> Artificial Sequence

<220>

<223> POTEF__Homo_sapiens__A5A3E0

<400> 593

Met Val Val Glu Val Asp Ser Met Pro Ala Ala Ser Ser Val Lys Lys
1 5 10 15

Pro Phe Gly Leu Arg Ser Lys Met Gly Lys Trp Cys Cys Arg Cys Phe
20 25 30

Pro Cys Cys Arg Glu Ser Gly Lys Ser Asn Val Gly Thr Ser Gly Asp
35 40 45

His Asp Asp Ser Ala Met Lys Thr Leu Arg Ser Lys Met Gly Lys Trp
50 55 60

Cys Arg His Cys Phe Pro Cys Cys Arg Gly Ser Gly Lys Ser Asn Val
65 70 75 80

Gly Ala Ser Gly Asp His Asp Asp Ser Ala Met Lys Thr Leu Arg Asn
85 90 95

Lys Met Gly Lys Trp Cys Cys His Cys Phe Pro Cys Cys Arg Gly Ser
100 105 110

Ser Lys Ser Lys Val Gly Ala Trp Gly Asp Tyr Asp Asp Ser Ala Phe
115 120 125

Met Glu Pro Arg Tyr His Val Arg Gly Glu Asp Leu Asp Lys Leu His
130 135 140

Arg Ala Ala Trp Trp Gly Lys Val Pro Arg Lys Asp Leu Ile Val Met
145 150 155 160

Leu Arg Asp Thr Asp Val Asn Lys Gln Asp Lys Gln Lys Arg Thr Ala
165 170 175

ITI-08-PCT_Sequence_Listing_ST25.txt

Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu Val Val Lys Leu Leu
 180 185 190
 Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp Asn Lys Lys Arg Thr
 195 200 205
 Ala Leu Ile Lys Ala Val Gln Cys Gln Glu Asp Glu Cys Ala Leu Met
 210 215 220
 Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro Asp Glu Tyr Gly Asn
 225 230 235 240
 Thr Thr Leu His Tyr Ala Ile Tyr Asn Glu Asp Lys Leu Met Ala Lys
 245 250 255
 Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu Ser Lys Asn Lys His Gly
 260 265 270
 Leu Thr Pro Leu Leu Leu Gly Val His Glu Gln Lys Gln Gln Val Val
 275 280 285
 Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu Asn Ala Leu Asp Arg Tyr
 290 295 300
 Gly Arg Thr Ala Leu Ile Leu Ala Val Cys Cys Gly Ser Ala Ser Ile
 305 310 315 320
 Val Ser Leu Leu Leu Glu Gln Asn Ile Asp Val Ser Ser Gln Asp Leu
 325 330 335
 Ser Gly Gln Thr Ala Arg Glu Tyr Ala Val Ser Ser His His His Val
 340 345 350
 Ile Cys Gln Leu Leu Ser Asp Tyr Lys Glu Lys Gln Met Leu Lys Ile
 355 360 365
 Ser Ser Glu Asn Ser Asn Pro Glu Gln Asp Leu Lys Leu Thr Ser Glu
 370 375 380
 Glu Glu Ser Gln Arg Phe Lys Gly Ser Glu Asn Ser Gln Pro Glu Lys
 385 390 395 400
 Met Ser Gln Glu Pro Glu Ile Asn Lys Asp Gly Asp Arg Glu Val Glu
 405 410 415
 Glu Glu Met Lys Lys His Glu Ser Asn Asn Val Gly Leu Leu Glu Asn
 420 425 430
 Leu Thr Asn Gly Val Thr Ala Gly Asn Gly Asp Asn Gly Leu Ile Pro
 435 440 445
 Gln Arg Lys Ser Arg Thr Pro Glu Asn Gln Gln Phe Pro Asp Asn Glu

ITI-08-PCT_Sequence_Listing_ST25.txt

```

450                               455                               460
Ser Glu Glu Tyr His Arg Ile Cys Glu Leu Leu Ser Asp Tyr Lys Glu
465                               470                               475                               480
Lys Gln Met Pro Lys Tyr Ser Ser Glu Asn Ser Asn Pro Glu Gln Asp
485                               490                               495
Leu Lys Leu Thr Ser Glu Glu Glu Ser Gln Arg Leu Lys Gly Ser Glu
500                               505                               510
Asn Gly Gln Pro Glu Lys Arg Ser Gln Glu Pro Glu Ile Asn Lys Asp
515                               520                               525
Gly Asp Arg Glu Leu Glu Asn Phe Met Ala Ile Glu Glu Met Lys Lys
530                               535                               540
His Arg Ser Thr His Val Gly Phe Pro Glu Asn Leu Thr Asn Gly Ala
545                               550                               555                               560
Thr Ala Gly Asn Gly Asp Asp Gly Leu Ile Pro Pro Arg Lys Ser Arg
565                               570                               575
Thr Pro Glu Ser Gln Gln Phe Pro Asp Thr Glu Asn Glu Glu Tyr His
580                               585                               590
Ser Asp Glu Gln Asn Asp Thr Gln Lys Gln Phe Cys Glu Glu Gln Asn
595                               600                               605
Thr Gly Ile Leu His Asp Glu Ile Leu Ile His Glu Glu Lys Gln Ile
610                               615                               620
Glu Val Val Glu Lys Met Asn Ser Glu Leu Ser Leu Ser Cys Lys Lys
625                               630                               635                               640
Glu Lys Asp Ile Leu His Glu Asn Ser Thr Leu Arg Glu Glu Ile Ala
645                               650                               655
Met Leu Arg Leu Glu Leu Asp Thr Met Lys His Gln Ser Gln Leu Arg
660                               665                               670
Glu Lys Lys Tyr Leu Glu Asp Ile Glu Ser Val Lys Lys Arg Asn Asp
675                               680                               685
Asn Leu Leu Lys Ala Leu Gln Leu Asn Glu Leu Thr Met Asp Asp Asp
690                               695                               700
Thr Ala Val Leu Val Ile Asp Asn Gly Ser Gly Met Cys Lys Ala Gly
705                               710                               715                               720
Phe Ala Gly Asp Asp Ala Pro Arg Ala Val Phe Pro Ser Ile Val Gly
725                               730                               735

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Arg	Pro	Arg	Gln	Gln	Gly	Met	Met	Gly	Gly	Met	His	Gln	Lys	Glu	Ser	740	745	750
Tyr	Val	Gly	Lys	Glu	Ala	Gln	Ser	Lys	Arg	Gly	Ile	Leu	Thr	Leu	Lys	755	760	765
Tyr	Pro	Met	Glu	His	Gly	Ile	Ile	Thr	Asn	Trp	Asp	Asp	Met	Glu	Lys	770	775	780
Ile	Trp	His	His	Thr	Phe	Tyr	Asn	Glu	Leu	Arg	Val	Ala	Pro	Glu	Glu	785	790	795
His	Pro	Val	Leu	Leu	Thr	Glu	Ala	Thr	Leu	Asn	Pro	Lys	Ala	Asn	Arg	805	810	815
Glu	Lys	Met	Thr	Gln	Ile	Met	Phe	Glu	Thr	Phe	Asn	Thr	Pro	Ala	Met	820	825	830
Tyr	Val	Ala	Ile	Gln	Ala	Val	Leu	Ser	Leu	Tyr	Thr	Ser	Gly	Arg	Thr	835	840	845
Thr	Gly	Ile	Val	Met	Asp	Ser	Gly	Asp	Gly	Val	Thr	His	Thr	Val	Pro	850	855	860
Ile	Tyr	Glu	Gly	Asn	Ala	Leu	Pro	His	Ala	Thr	Leu	Arg	Leu	Asp	Leu	865	870	875
Ala	Gly	Arg	Glu	Leu	Pro	Asp	Tyr	Leu	Met	Lys	Ile	Leu	Thr	Glu	His	885	890	895
Gly	Tyr	Arg	Phe	Thr	Thr	Met	Ala	Glu	Arg	Glu	Ile	Val	Arg	Asp	Ile	900	905	910
Lys	Glu	Lys	Leu	Cys	Tyr	Val	Ala	Leu	Asp	Phe	Glu	Gln	Glu	Met	Ala	915	920	925
Thr	Val	Ala	Ser	Ser	Ser	Ser	Leu	Glu	Lys	Ser	Tyr	Glu	Leu	Pro	Asp	930	935	940
Gly	Gln	Val	Ile	Thr	Ile	Gly	Asn	Glu	Arg	Phe	Arg	Cys	Pro	Glu	Ala	945	950	955
Leu	Phe	Gln	Pro	Cys	Phe	Leu	Gly	Met	Glu	Ser	Cys	Gly	Ile	His	Glu	965	970	975
Thr	Thr	Phe	Asn	Ser	Ile	Met	Lys	Ser	Asp	Val	Asp	Ile	Arg	Lys	Asp	980	985	990
Leu	Tyr	Thr	Asn	Thr	Val	Leu	Ser	Gly	Gly	Thr	Thr	Met	Tyr	Pro	Gly	995	1000	1005

ITI-08-PCT_Sequence_Listing_ST25.txt

Met Ala His Arg Met Gln Lys Glu Ile Ala Ala Leu Ala Pro Ser
1010 1015 1020

Met Met Lys Ile Arg Ile Ile Ala Pro Pro Lys Arg Lys Tyr Ser
1025 1030 1035

Val Trp Val Gly Gly Ser Ile Leu Ala Ser Leu Ser Thr Phe Gln
1040 1045 1050

Gln Met Trp Ile Ser Lys Gln Glu Tyr Asp Glu Ser Gly Pro Ser
1055 1060 1065

Ile Val His Arg Lys Cys Leu
1070 1075

<210> 594

<211> 584

<212> PRT

<213> Artificial Sequence

<220>

<223> POTE__Homo_sapiens__Q86YR6

<400> 594

Met Val Ala Glu Val Cys Ser Met Pro Thr Ala Ser Thr Val Lys Lys
1 5 10 15

Pro Phe Asp Leu Arg Ser Lys Met Gly Lys Trp Cys His His Arg Phe
20 25 30

Pro Cys Cys Arg Gly Ser Gly Lys Ser Asn Met Gly Thr Ser Gly Asp
35 40 45

His Asp Asp Ser Phe Met Lys Met Leu Arg Ser Lys Met Gly Lys Cys
50 55 60

Cys Arg His Cys Phe Pro Cys Cys Arg Gly Ser Gly Thr Ser Asn Val
65 70 75 80

Gly Thr Ser Gly Asp His Glu Asn Ser Phe Met Lys Met Leu Arg Ser
85 90 95

Lys Met Gly Lys Trp Cys Cys His Cys Phe Pro Cys Cys Arg Gly Ser
100 105 110

Gly Lys Ser Asn Val Gly Ala Trp Gly Asp Tyr Asp His Ser Ala Phe
115 120 125

Met Glu Pro Arg Tyr His Ile Arg Arg Glu Asp Leu Asp Lys Leu His
130 135 140

ITI-08-PCT_Sequence_Listing_ST25.txt

Arg	Ala	Ala	Trp	Trp	Gly	Lys	Val	Pro	Arg	Lys	Asp	Leu	Ile	Val	Met
145					150					155					160
Leu	Arg	Asp	Thr	Asp	Met	Asn	Lys	Arg	Asp	Lys	Glu	Lys	Arg	Thr	Ala
				165					170					175	
Leu	His	Leu	Ala	Ser	Ala	Asn	Gly	Asn	Ser	Glu	Val	Val	Gln	Leu	Leu
			180					185					190		
Leu	Asp	Arg	Arg	Cys	Gln	Leu	Asn	Val	Leu	Asp	Asn	Lys	Lys	Arg	Thr
		195					200					205			
Ala	Leu	Ile	Lys	Ala	Ile	Gln	Cys	Gln	Glu	Asp	Glu	Cys	Val	Leu	Met
	210					215					220				
Leu	Leu	Glu	His	Gly	Ala	Asp	Arg	Asn	Ile	Pro	Asp	Glu	Tyr	Gly	Asn
225					230					235					240
Thr	Ala	Leu	His	Tyr	Ala	Ile	Tyr	Asn	Glu	Asp	Lys	Leu	Met	Ala	Lys
				245					250					255	
Ala	Leu	Leu	Leu	Tyr	Gly	Ala	Asp	Ile	Glu	Ser	Lys	Asn	Lys	Cys	Gly
			260					265					270		
Leu	Thr	Pro	Leu	Leu	Leu	Gly	Val	His	Glu	Gln	Lys	Gln	Gln	Val	Val
		275					280					285			
Lys	Phe	Leu	Ile	Lys	Lys	Lys	Ala	Asn	Leu	Asn	Val	Leu	Asp	Arg	Tyr
	290					295					300				
Gly	Arg	Thr	Ala	Leu	Ile	Leu	Ala	Val	Cys	Cys	Gly	Ser	Ala	Ser	Ile
305					310					315					320
Val	Asn	Leu	Leu	Leu	Glu	Gln	Asn	Val	Asp	Val	Ser	Ser	Gln	Asp	Leu
			325						330					335	
Ser	Gly	Gln	Thr	Ala	Arg	Glu	Tyr	Ala	Val	Ser	Ser	His	His	His	Val
			340					345					350		
Ile	Cys	Glu	Leu	Leu	Ser	Asp	Tyr	Lys	Glu	Lys	Gln	Met	Leu	Lys	Ile
		355					360					365			
Ser	Ser	Glu	Asn	Ser	Asn	Pro	Glu	Gln	Asp	Leu	Lys	Leu	Thr	Ser	Glu
	370					375					380				
Glu	Glu	Ser	Gln	Arg	Leu	Lys	Val	Ser	Glu	Asn	Ser	Gln	Pro	Glu	Lys
385					390					395					400
Met	Ser	Gln	Glu	Pro	Glu	Ile	Asn	Lys	Asp	Cys	Asp	Arg	Glu	Val	Glu
				405					410					415	
Glu	Glu	Ile	Lys	Lys	His	Gly	Ser	Asn	Pro	Val	Gly	Leu	Pro	Glu	Asn

ITI-08-PCT_Sequence_Listing_ST25.txt

420

425

430

Leu Thr Asn Gly Ala Ser Ala Gly Asn Gly Asp Asp Gly Leu Ile Pro
435 440 445

Gln Arg Arg Ser Arg Lys Pro Glu Asn Gln Gln Phe Pro Asp Thr Glu
450 455 460

Asn Glu Glu Tyr His Ser Asp Glu Gln Asn Asp Thr Arg Lys Gln Leu
465 470 475 480

Ser Glu Glu Gln Asn Thr Gly Ile Ser Gln Asp Glu Ile Leu Thr Asn
485 490 495

Lys Gln Lys Gln Ile Glu Val Ala Glu Gln Lys Met Asn Ser Glu Leu
500 505 510

Ser Leu Ser His Lys Lys Glu Glu Asp Leu Leu Arg Glu Asn Ser Val
515 520 525

Leu Gln Glu Glu Ile Ala Met Leu Arg Leu Glu Leu Asp Glu Thr Lys
530 535 540

His Gln Asn Gln Leu Arg Glu Asn Lys Ile Leu Glu Glu Ile Glu Ser
545 550 555 560

Val Lys Glu Lys Thr Asp Lys Leu Leu Arg Ala Met Gln Leu Asn Glu
565 570 575

Glu Ala Leu Thr Lys Thr Asn Ile
580

<210> 595

<211> 509

<212> PRT

<213> Artificial Sequence

<220>

<223> PRAME__Homo_sapiens__A0A024R1E6

<400> 595

Met Glu Arg Arg Arg Leu Trp Gly Ser Ile Gln Ser Arg Tyr Ile Ser
1 5 10 15

Met Ser Val Trp Thr Ser Pro Arg Arg Leu Val Glu Leu Ala Gly Gln
20 25 30

Ser Leu Leu Lys Asp Glu Ala Leu Ala Ile Ala Ala Leu Glu Leu Leu
35 40 45

Pro Arg Glu Leu Phe Pro Pro Leu Phe Met Ala Ala Phe Asp Gly Arg

ITI-08-PCT_Sequence_Listing_ST25.txt

50						55						60					
His	Ser	Gln	Thr	Leu	Lys	Ala	Met	Val	Gln	Ala	Trp	Pro	Phe	Thr	Cys		
65					70					75					80		
Leu	Pro	Leu	Gly	Val	Leu	Met	Lys	Gly	Gln	His	Leu	His	Leu	Glu	Thr		
				85					90					95			
Phe	Lys	Ala	Val	Leu	Asp	Gly	Leu	Asp	Val	Leu	Leu	Ala	Gln	Glu	Val		
			100					105					110				
Arg	Pro	Arg	Arg	Trp	Lys	Leu	Gln	Val	Leu	Asp	Leu	Arg	Lys	Asn	Ser		
		115					120					125					
His	Gln	Asp	Phe	Trp	Thr	Val	Trp	Ser	Gly	Asn	Arg	Ala	Ser	Leu	Tyr		
	130					135					140						
Ser	Phe	Pro	Glu	Pro	Glu	Ala	Ala	Gln	Pro	Met	Thr	Lys	Lys	Arg	Lys		
145					150					155					160		
Val	Asp	Gly	Leu	Ser	Thr	Glu	Ala	Glu	Gln	Pro	Phe	Ile	Pro	Val	Glu		
				165					170					175			
Val	Leu	Val	Asp	Leu	Phe	Leu	Lys	Glu	Gly	Ala	Cys	Asp	Glu	Leu	Phe		
			180					185					190				
Ser	Tyr	Leu	Ile	Glu	Lys	Val	Lys	Arg	Lys	Lys	Asn	Val	Leu	Arg	Leu		
		195					200					205					
Cys	Cys	Lys	Lys	Leu	Lys	Ile	Phe	Ala	Met	Pro	Met	Gln	Asp	Ile	Lys		
	210					215					220						
Met	Ile	Leu	Lys	Met	Val	Gln	Leu	Asp	Ser	Ile	Glu	Asp	Leu	Glu	Val		
225					230					235					240		
Thr	Cys	Thr	Trp	Lys	Leu	Pro	Thr	Leu	Ala	Lys	Phe	Ser	Pro	Tyr	Leu		
				245					250					255			
Gly	Gln	Met	Ile	Asn	Leu	Arg	Arg	Leu	Leu	Leu	Ser	His	Ile	His	Ala		
			260					265					270				
Ser	Ser	Tyr	Ile	Ser	Pro	Glu	Lys	Glu	Glu	Gln	Tyr	Ile	Ala	Gln	Phe		
		275					280					285					
Thr	Ser	Gln	Phe	Leu	Ser	Leu	Gln	Cys	Leu	Gln	Ala	Leu	Tyr	Val	Asp		
	290					295					300						
Ser	Leu	Phe	Phe	Leu	Arg	Gly	Arg	Leu	Asp	Gln	Leu	Leu	Arg	His	Val		
305					310					315					320		
Met	Asn	Pro	Leu	Glu	Thr	Leu	Ser	Ile	Thr	Asn	Cys	Arg	Leu	Ser	Glu		
				325					330					335			

ITI-08-PCT_Sequence_Listing_ST25.txt

Gly Asp Val Met His Leu Ser Gln Ser Pro Ser Val Ser Gln Leu Ser
340 345 350

Val Leu Ser Leu Ser Gly Val Met Leu Thr Asp Val Ser Pro Glu Pro
355 360 365

Leu Gln Ala Leu Leu Glu Arg Ala Ser Ala Thr Leu Gln Asp Leu Val
370 375 380

Phe Asp Glu Cys Gly Ile Thr Asp Asp Gln Leu Leu Ala Leu Leu Pro
385 390 395 400

Ser Leu Ser His Cys Ser Gln Leu Thr Thr Leu Ser Phe Tyr Gly Asn
405 410 415

Ser Ile Ser Ile Ser Ala Leu Gln Ser Leu Leu Gln His Leu Ile Gly
420 425 430

Leu Ser Asn Leu Thr His Val Leu Tyr Pro Val Pro Leu Glu Ser Tyr
435 440 445

Glu Asp Ile His Gly Thr Leu His Leu Glu Arg Leu Ala Tyr Leu His
450 455 460

Ala Arg Leu Arg Glu Leu Leu Cys Glu Leu Gly Arg Pro Ser Met Val
465 470 475 480

Trp Leu Ser Ala Asn Pro Cys Pro His Cys Gly Asp Arg Thr Phe Tyr
485 490 495

Asp Pro Glu Pro Ile Leu Cys Pro Cys Phe Met Pro Asn
500 505

<210> 596
<211> 509
<212> PRT
<213> Artificial Sequence

<220>
<223> PRAME__Homo_sapiens__P78395

<400> 596

Met Glu Arg Arg Arg Leu Trp Gly Ser Ile Gln Ser Arg Tyr Ile Ser
1 5 10 15

Met Ser Val Trp Thr Ser Pro Arg Arg Leu Val Glu Leu Ala Gly Gln
20 25 30

Ser Leu Leu Lys Asp Glu Ala Leu Ala Ile Ala Ala Leu Glu Leu Leu
35 40 45

ITI-08-PCT_Sequence_Listing_ST25.txt

Pro	Arg	Glu	Leu	Phe	Pro	Pro	Leu	Phe	Met	Ala	Ala	Phe	Asp	Gly	Arg	50	55	60
His	Ser	Gln	Thr	Leu	Lys	Ala	Met	Val	Gln	Ala	Trp	Pro	Phe	Thr	Cys	65	70	75
Leu	Pro	Leu	Gly	Val	Leu	Met	Lys	Gly	Gln	His	Leu	His	Leu	Glu	Thr	85	90	95
Phe	Lys	Ala	Val	Leu	Asp	Gly	Leu	Asp	Val	Leu	Leu	Ala	Gln	Glu	Val	100	105	110
Arg	Pro	Arg	Arg	Trp	Lys	Leu	Gln	Val	Leu	Asp	Leu	Arg	Lys	Asn	Ser	115	120	125
His	Gln	Asp	Phe	Trp	Thr	Val	Trp	Ser	Gly	Asn	Arg	Ala	Ser	Leu	Tyr	130	135	140
Ser	Phe	Pro	Glu	Pro	Glu	Ala	Ala	Gln	Pro	Met	Thr	Lys	Lys	Arg	Lys	145	150	155
Val	Asp	Gly	Leu	Ser	Thr	Glu	Ala	Glu	Gln	Pro	Phe	Ile	Pro	Val	Glu	165	170	175
Val	Leu	Val	Asp	Leu	Phe	Leu	Lys	Glu	Gly	Ala	Cys	Asp	Glu	Leu	Phe	180	185	190
Ser	Tyr	Leu	Ile	Glu	Lys	Val	Lys	Arg	Lys	Lys	Asn	Val	Leu	Arg	Leu	195	200	205
Cys	Cys	Lys	Lys	Leu	Lys	Ile	Phe	Ala	Met	Pro	Met	Gln	Asp	Ile	Lys	210	215	220
Met	Ile	Leu	Lys	Met	Val	Gln	Leu	Asp	Ser	Ile	Glu	Asp	Leu	Glu	Val	225	230	235
Thr	Cys	Thr	Trp	Lys	Leu	Pro	Thr	Leu	Ala	Lys	Phe	Ser	Pro	Tyr	Leu	245	250	255
Gly	Gln	Met	Ile	Asn	Leu	Arg	Arg	Leu	Leu	Leu	Ser	His	Ile	His	Ala	260	265	270
Ser	Ser	Tyr	Ile	Ser	Pro	Glu	Lys	Glu	Glu	Gln	Tyr	Ile	Ala	Gln	Phe	275	280	285
Thr	Ser	Gln	Phe	Leu	Ser	Leu	Gln	Cys	Leu	Gln	Ala	Leu	Tyr	Val	Asp	290	295	300
Ser	Leu	Phe	Phe	Leu	Arg	Gly	Arg	Leu	Asp	Gln	Leu	Leu	Arg	His	Val	305	310	315

ITI-08-PCT_Sequence_Listing_ST25.txt

Met Asn Pro Leu Glu Thr Leu Ser Ile Thr Asn Cys Arg Leu Ser Glu
325 330 335

Gly Asp Val Met His Leu Ser Gln Ser Pro Ser Val Ser Gln Leu Ser
340 345 350

Val Leu Ser Leu Ser Gly Val Met Leu Thr Asp Val Ser Pro Glu Pro
355 360 365

Leu Gln Ala Leu Leu Glu Arg Ala Ser Ala Thr Leu Gln Asp Leu Val
370 375 380

Phe Asp Glu Cys Gly Ile Thr Asp Asp Gln Leu Leu Ala Leu Leu Pro
385 390 395 400

Ser Leu Ser His Cys Ser Gln Leu Thr Thr Leu Ser Phe Tyr Gly Asn
405 410 415

Ser Ile Ser Ile Ser Ala Leu Gln Ser Leu Leu Gln His Leu Ile Gly
420 425 430

Leu Ser Asn Leu Thr His Val Leu Tyr Pro Val Pro Leu Glu Ser Tyr
435 440 445

Glu Asp Ile His Gly Thr Leu His Leu Glu Arg Leu Ala Tyr Leu His
450 455 460

Ala Arg Leu Arg Glu Leu Leu Cys Glu Leu Gly Arg Pro Ser Met Val
465 470 475 480

Trp Leu Ser Ala Asn Pro Cys Pro His Cys Gly Asp Arg Thr Phe Tyr
485 490 495

Asp Pro Glu Pro Ile Leu Cys Pro Cys Phe Met Pro Asn
500 505

<210> 597

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> PRDX5/m__Homo_sapiens__P30044

<400> 597

Met Gly Leu Ala Gly Val Cys Ala Leu Arg Arg Ser Ala Gly Tyr Ile
1 5 10 15

Leu Val Gly Gly Ala Gly Gly Gln Ser Ala Ala Ala Ala Ala Arg Arg
20 25 30

ITI-08-PCT_Sequence_Listing_ST25.txt

Tyr Ser Glu Gly Glu Trp Ala Ser Gly Gly Val Arg Ser Phe Ser Arg
35 40 45

Ala Ala Ala Ala Met Ala Pro Ile Lys Val Gly Asp Ala Ile Pro Ala
50 55 60

Val Glu Val Phe Glu Gly Glu Pro Gly Asn Lys Val Asn Leu Ala Glu
65 70 75 80

Leu Phe Lys Gly Lys Lys Gly Val Leu Phe Gly Val Pro Gly Ala Phe
85 90 95

Thr Pro Gly Cys Ser Lys Thr His Leu Pro Gly Phe Val Glu Gln Ala
100 105 110

Glu Ala Leu Lys Ala Lys Gly Val Gln Val Val Ala Cys Leu Ser Val
115 120 125

Asn Asp Ala Phe Val Thr Gly Glu Trp Gly Arg Ala His Lys Ala Glu
130 135 140

Gly Lys Val Arg Leu Leu Ala Asp Pro Thr Gly Ala Phe Gly Lys Glu
145 150 155 160

Thr Asp Leu Leu Leu Asp Asp Ser Leu Val Ser Ile Phe Gly Asn Arg
165 170 175

Arg Leu Lys Arg Phe Ser Met Val Val Gln Asp Gly Ile Val Lys Ala
180 185 190

Leu Asn Val Glu Pro Asp Gly Thr Gly Leu Thr Cys Ser Leu Ala Pro
195 200 205

Asn Ile Ile Ser Gln Leu
210

<210> 598

<211> 102

<212> PRT

<213> Artificial Sequence

<220>

<223> PRM2__Homo_sapiens__P04554

<400> 598

Met Val Arg Tyr Arg Val Arg Ser Leu Ser Glu Arg Ser His Glu Val
1 5 10 15

Tyr Arg Gln Gln Leu His Gly Gln Glu Gln Gly His His Gly Gln Glu
20 25 30

ITI-08-PCT_Sequence_Listing_ST25.txt

Glu Gln Gly Leu Ser Pro Glu His Val Glu Val Tyr Glu Arg Thr His
35 40 45

Gly Gln Ser His Tyr Arg Arg Arg His Cys Ser Arg Arg Arg Leu His
50 55 60

Arg Ile His Arg Arg Gln His Arg Ser Cys Arg Arg Arg Lys Arg Arg
65 70 75 80

Ser Cys Arg His Arg Arg Arg His Arg Arg Gly Cys Arg Thr Arg Lys
85 90 95

Arg Thr Cys Arg Arg His
100

<210> 599

<211> 553

<212> PRT

<213> Artificial Sequence

<220>

<223> prostein__Homo_sapiens__Q96JT2

<400> 599

Met Val Gln Arg Leu Trp Val Ser Arg Leu Leu Arg His Arg Lys Ala
1 5 10 15

Gln Leu Leu Leu Val Asn Leu Leu Thr Phe Gly Leu Glu Val Cys Leu
20 25 30

Ala Ala Gly Ile Thr Tyr Val Pro Pro Leu Leu Leu Glu Val Gly Val
35 40 45

Glu Glu Lys Phe Met Thr Met Val Leu Gly Ile Gly Pro Val Leu Gly
50 55 60

Leu Val Cys Val Pro Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly
65 70 75 80

Arg Tyr Gly Arg Arg Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile
85 90 95

Leu Leu Ser Leu Phe Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu
100 105 110

Leu Cys Pro Asp Pro Arg Pro Leu Glu Leu Ala Leu Leu Ile Leu Gly
115 120 125

Val Gly Leu Leu Asp Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu
130 135 140

ITI-08-PCT_Sequence_Listing_ST25.txt

Ala	Leu	Leu	Ser	Asp	Leu	Phe	Arg	Asp	Pro	Asp	His	Cys	Arg	Gln	Ala	145	150	155	160
Tyr	Ser	Val	Tyr	Ala	Phe	Met	Ile	Ser	Leu	Gly	Gly	Cys	Leu	Gly	Tyr	165	170	175	
Leu	Leu	Pro	Ala	Ile	Asp	Trp	Asp	Thr	Ser	Ala	Leu	Ala	Pro	Tyr	Leu	180	185	190	
Gly	Thr	Gln	Glu	Glu	Cys	Leu	Phe	Gly	Leu	Leu	Thr	Leu	Ile	Phe	Leu	195	200	205	
Thr	Cys	Val	Ala	Ala	Thr	Leu	Leu	Val	Ala	Glu	Glu	Ala	Ala	Leu	Gly	210	215	220	
Pro	Thr	Glu	Pro	Ala	Glu	Gly	Leu	Ser	Ala	Pro	Ser	Leu	Ser	Pro	His	225	230	235	240
Cys	Cys	Pro	Cys	Arg	Ala	Arg	Leu	Ala	Phe	Arg	Asn	Leu	Gly	Ala	Leu	245	250	255	
Leu	Pro	Arg	Leu	His	Gln	Leu	Cys	Cys	Arg	Met	Pro	Arg	Thr	Leu	Arg	260	265	270	
Arg	Leu	Phe	Val	Ala	Glu	Leu	Cys	Ser	Trp	Met	Ala	Leu	Met	Thr	Phe	275	280	285	
Thr	Leu	Phe	Tyr	Thr	Asp	Phe	Val	Gly	Glu	Gly	Leu	Tyr	Gln	Gly	Val	290	295	300	
Pro	Arg	Ala	Glu	Pro	Gly	Thr	Glu	Ala	Arg	Arg	His	Tyr	Asp	Glu	Gly	305	310	315	320
Val	Arg	Met	Gly	Ser	Leu	Gly	Leu	Phe	Leu	Gln	Cys	Ala	Ile	Ser	Leu	325	330	335	
Val	Phe	Ser	Leu	Val	Met	Asp	Arg	Leu	Val	Gln	Arg	Phe	Gly	Thr	Arg	340	345	350	
Ala	Val	Tyr	Leu	Ala	Ser	Val	Ala	Ala	Phe	Pro	Val	Ala	Ala	Gly	Ala	355	360	365	
Thr	Cys	Leu	Ser	His	Ser	Val	Ala	Val	Val	Thr	Ala	Ser	Ala	Ala	Leu	370	375	380	
Thr	Gly	Phe	Thr	Phe	Ser	Ala	Leu	Gln	Ile	Leu	Pro	Tyr	Thr	Leu	Ala	385	390	395	400
Ser	Leu	Tyr	His	Arg	Glu	Lys	Gln	Val	Phe	Leu	Pro	Lys	Tyr	Arg	Gly	405	410	415	
Asp	Thr	Gly	Gly	Ala	Ser	Ser	Glu	Asp	Ser	Leu	Met	Thr	Ser	Phe	Leu				

ITI-08-PCT_Sequence_Listing_ST25.txt

420

425

430

Pro Gly Pro Lys Pro Gly Ala Pro Phe Pro Asn Gly His Val Gly Ala
435 440 445

Gly Gly Ser Gly Leu Leu Pro Pro Pro Pro Ala Leu Cys Gly Ala Ser
450 455 460

Ala Cys Asp Val Ser Val Arg Val Val Val Gly Glu Pro Thr Glu Ala
465 470 475 480

Arg Val Val Pro Gly Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp
485 490 495

Ser Ala Phe Leu Leu Ser Gln Val Ala Pro Ser Leu Phe Met Gly Ser
500 505 510

Ile Val Gln Leu Ser Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala
515 520 525

Gly Leu Gly Leu Val Ala Ile Tyr Phe Ala Thr Gln Val Val Phe Asp
530 535 540

Lys Ser Asp Leu Ala Lys Tyr Ser Ala
545 550

<210> 600

<211> 215

<212> PRT

<213> Artificial Sequence

<220>

<223> proteinase-3__Homo_sapiens__D6CHE9

<400> 600

Met Ala Ser Leu Gln Met Arg Gly Asn Pro Gly Ser His Phe Cys Gly
1 5 10 15

Gly Thr Leu Ile His Pro Ser Phe Val Leu Thr Ala Ala His Cys Leu
20 25 30

Arg Asp Ile Pro Gln Arg Leu Val Asn Val Val Leu Gly Ala His Asn
35 40 45

Val Arg Thr Gln Glu Pro Thr Gln Gln His Phe Ser Val Ala Gln Val
50 55 60

Phe Leu Asn Asn Tyr Asp Ala Glu Asn Lys Leu Asn Asp Ile Leu Leu
65 70 75 80

Ile Gln Leu Ser Ser Pro Ala Asn Leu Ser Ala Ser Val Ala Thr Val

ITI-08-PCT_Sequence_Listing_ST25.txt

85 90 95

Gln Leu Pro Gln Gln Asp Gln Pro Val Pro His Gly Thr Gln Cys Leu
100 105 110

Ala Met Gly Trp Gly Arg Val Gly Ala His Asp Pro Pro Ala Gln Val
115 120 125

Leu Gln Glu Leu Asn Val Thr Val Val Thr Phe Phe Cys Arg Pro His
130 135 140

Asn Ile Cys Thr Phe Val Pro Arg Arg Lys Ala Gly Ile Cys Phe Gly
145 150 155 160

Asp Ser Gly Gly Pro Leu Ile Cys Asp Gly Ile Ile Gln Gly Ile Asp
165 170 175

Ser Phe Val Ile Trp Gly Cys Ala Thr Arg Leu Phe Pro Asp Phe Phe
180 185 190

Thr Arg Val Ala Leu Tyr Val Asp Trp Ile Arg Ser Thr Leu Arg Arg
195 200 205

Val Glu Ala Lys Gly Arg Pro
210 215

<210> 601

<211> 256

<212> PRT

<213> Artificial Sequence

<220>

<223> proteinase-3__Homo_sapiens__P24158

<400> 601

Met Ala His Arg Pro Pro Ser Pro Ala Leu Ala Ser Val Leu Leu Ala
1 5 10 15

Leu Leu Leu Ser Gly Ala Ala Arg Ala Ala Glu Ile Val Gly Gly His
20 25 30

Glu Ala Gln Pro His Ser Arg Pro Tyr Met Ala Ser Leu Gln Met Arg
35 40 45

Gly Asn Pro Gly Ser His Phe Cys Gly Gly Thr Leu Ile His Pro Ser
50 55 60

Phe Val Leu Thr Ala Ala His Cys Leu Arg Asp Ile Pro Gln Arg Leu
65 70 75 80

Val Asn Val Val Leu Gly Ala His Asn Val Arg Thr Gln Glu Pro Thr

ITI-08-PCT_Sequence_Listing_ST25.txt

85 90 95

Gln Gln His Phe Ser Val Ala Gln Val Phe Leu Asn Asn Tyr Asp Ala
100 105 110

Glu Asn Lys Leu Asn Asp Val Leu Leu Ile Gln Leu Ser Ser Pro Ala
115 120 125

Asn Leu Ser Ala Ser Val Ala Thr Val Gln Leu Pro Gln Gln Asp Gln
130 135 140

Pro Val Pro His Gly Thr Gln Cys Leu Ala Met Gly Trp Gly Arg Val
145 150 155 160

Gly Ala His Asp Pro Pro Ala Gln Val Leu Gln Glu Leu Asn Val Thr
165 170 175

Val Val Thr Phe Phe Cys Arg Pro His Asn Ile Cys Thr Phe Val Pro
180 185 190

Arg Arg Lys Ala Gly Ile Cys Phe Gly Asp Ser Gly Gly Pro Leu Ile
195 200 205

Cys Asp Gly Ile Ile Gln Gly Ile Asp Ser Phe Val Ile Trp Gly Cys
210 215 220

Ala Thr Arg Leu Phe Pro Asp Phe Phe Thr Arg Val Ala Leu Tyr Val
225 230 235 240

Asp Trp Ile Arg Ser Thr Leu Arg Arg Val Glu Ala Lys Gly Arg Pro
245 250 255

<210> 602
<211> 919
<212> PRT
<213> Artificial Sequence

<220>
<223> PSA__Homo_sapiens__P55786

<400> 602

Met Trp Leu Ala Ala Ala Ala Pro Ser Leu Ala Arg Arg Leu Leu Phe
1 5 10 15

Leu Gly Pro Pro Pro Pro Pro Leu Leu Leu Leu Val Phe Ser Arg Ser
20 25 30

Ser Arg Arg Arg Leu His Ser Leu Gly Leu Ala Ala Met Pro Glu Lys
35 40 45

Arg Pro Phe Glu Arg Leu Pro Ala Asp Val Ser Pro Ile Asn Tyr Ser

ITI-08-PCT_Sequence_Listing_ST25.txt

50	55	60													
Leu	Cys	Leu	Lys	Pro	Asp	Leu	Leu	Asp	Phe	Thr	Phe	Glu	Gly	Lys	Leu
65					70					75					80
Glu	Ala	Ala	Ala	Gln	Val	Arg	Gln	Ala	Thr	Asn	Gln	Ile	Val	Met	Asn
				85					90					95	
Cys	Ala	Asp	Ile	Asp	Ile	Ile	Thr	Ala	Ser	Tyr	Ala	Pro	Glu	Gly	Asp
			100					105					110		
Glu	Glu	Ile	His	Ala	Thr	Gly	Phe	Asn	Tyr	Gln	Asn	Glu	Asp	Glu	Lys
		115					120					125			
Val	Thr	Leu	Ser	Phe	Pro	Ser	Thr	Leu	Gln	Thr	Gly	Thr	Gly	Thr	Leu
	130					135					140				
Lys	Ile	Asp	Phe	Val	Gly	Glu	Leu	Asn	Asp	Lys	Met	Lys	Gly	Phe	Tyr
145					150					155					160
Arg	Ser	Lys	Tyr	Thr	Thr	Pro	Ser	Gly	Glu	Val	Arg	Tyr	Ala	Ala	Val
				165					170					175	
Thr	Gln	Phe	Glu	Ala	Thr	Asp	Ala	Arg	Arg	Ala	Phe	Pro	Cys	Trp	Asp
			180					185					190		
Glu	Pro	Ala	Ile	Lys	Ala	Thr	Phe	Asp	Ile	Ser	Leu	Val	Val	Pro	Lys
		195						200				205			
Asp	Arg	Val	Ala	Leu	Ser	Asn	Met	Asn	Val	Ile	Asp	Arg	Lys	Pro	Tyr
	210					215					220				
Pro	Asp	Asp	Glu	Asn	Leu	Val	Glu	Val	Lys	Phe	Ala	Arg	Thr	Pro	Val
225					230					235					240
Met	Ser	Thr	Tyr	Leu	Val	Ala	Phe	Val	Val	Gly	Glu	Tyr	Asp	Phe	Val
				245					250					255	
Glu	Thr	Arg	Ser	Lys	Asp	Gly	Val	Cys	Val	Arg	Val	Tyr	Thr	Pro	Val
			260					265					270		
Gly	Lys	Ala	Glu	Gln	Gly	Lys	Phe	Ala	Leu	Glu	Val	Ala	Ala	Lys	Thr
		275					280					285			
Leu	Pro	Phe	Tyr	Lys	Asp	Tyr	Phe	Asn	Val	Pro	Tyr	Pro	Leu	Pro	Lys
	290					295					300				
Ile	Asp	Leu	Ile	Ala	Ile	Ala	Asp	Phe	Ala	Ala	Gly	Ala	Met	Glu	Asn
305					310					315					320
Trp	Gly	Leu	Val	Thr	Tyr	Arg	Glu	Thr	Ala	Leu	Leu	Ile	Asp	Pro	Lys
				325					330					335	

ITI-08-PCT_Sequence_Listing_ST25.txt

Asn	Ser	Cys	Ser	Ser	Ser	Arg	Gln	Trp	Val	Ala	Leu	Val	Val	Gly	His
340						345						350			
Glu	Leu	Ala	His	Gln	Trp	Phe	Gly	Asn	Leu	Val	Thr	Met	Glu	Trp	Trp
355						360						365			
Thr	His	Leu	Trp	Leu	Asn	Glu	Gly	Phe	Ala	Ser	Trp	Ile	Glu	Tyr	Leu
370						375						380			
Cys	Val	Asp	His	Cys	Phe	Pro	Glu	Tyr	Asp	Ile	Trp	Thr	Gln	Phe	Val
385						390						395			
Ser	Ala	Asp	Tyr	Thr	Arg	Ala	Gln	Glu	Leu	Asp	Ala	Leu	Asp	Asn	Ser
			405						410			415			
His	Pro	Ile	Glu	Val	Ser	Val	Gly	His	Pro	Ser	Glu	Val	Asp	Glu	Ile
			420						425			430			
Phe	Asp	Ala	Ile	Ser	Tyr	Ser	Lys	Gly	Ala	Ser	Val	Ile	Arg	Met	Leu
435						440						445			
His	Asp	Tyr	Ile	Gly	Asp	Lys	Asp	Phe	Lys	Lys	Gly	Met	Asn	Met	Tyr
450						455						460			
Leu	Thr	Lys	Phe	Gln	Gln	Lys	Asn	Ala	Ala	Thr	Glu	Asp	Leu	Trp	Glu
465						470						475			
Ser	Leu	Glu	Asn	Ala	Ser	Gly	Lys	Pro	Ile	Ala	Ala	Val	Met	Asn	Thr
			485						490			495			
Trp	Thr	Lys	Gln	Met	Gly	Phe	Pro	Leu	Ile	Tyr	Val	Glu	Ala	Glu	Gln
			500						505			510			
Val	Glu	Asp	Asp	Arg	Leu	Leu	Arg	Leu	Ser	Gln	Lys	Lys	Phe	Cys	Ala
515						520						525			
Gly	Gly	Ser	Tyr	Val	Gly	Glu	Asp	Cys	Pro	Gln	Trp	Met	Val	Pro	Ile
530						535						540			
Thr	Ile	Ser	Thr	Ser	Glu	Asp	Pro	Asn	Gln	Ala	Lys	Leu	Lys	Ile	Leu
545						550						555			
Met	Asp	Lys	Pro	Glu	Met	Asn	Val	Val	Leu	Lys	Asn	Val	Lys	Pro	Asp
			565						570			575			
Gln	Trp	Val	Lys	Leu	Asn	Leu	Gly	Thr	Val	Gly	Phe	Tyr	Arg	Thr	Gln
			580						585			590			
Tyr	Ser	Ser	Ala	Met	Leu	Glu	Ser	Leu	Leu	Pro	Gly	Ile	Arg	Asp	Leu
595						600						605			

Ser 610	Leu	Pro	Pro	Val	Asp	Arg 615	Leu	Gly	Leu	Gln	Asn 620	Asp	Leu	Phe	Ser
Leu 625	Ala	Arg	Ala	Gly	Ile 630	Ile	Ser	Thr	Val	Glu 635	Val	Leu	Lys	Val	Met 640
Glu	Ala	Phe	Val	Asn 645	Glu	Pro	Asn	Tyr	Thr 650	Val	Trp	Ser	Asp	Leu 655	Ser
Cys	Asn	Leu	Gly 660	Ile	Leu	Ser	Thr	Leu 665	Leu	Ser	His	Thr	Asp 670	Phe	Tyr
Glu	Glu	Ile 675	Gln	Glu	Phe	Val	Lys 680	Asp	Val	Phe	Ser	Pro 685	Ile	Gly	Glu
Arg 690	Leu	Gly	Trp	Asp	Pro	Lys 695	Pro	Gly	Glu	Gly	His 700	Leu	Asp	Ala	Leu
Leu 705	Arg	Gly	Leu	Val	Leu 710	Gly	Lys	Leu	Gly	Lys 715	Ala	Gly	His	Lys	Ala 720
Thr	Leu	Glu	Glu	Ala 725	Arg	Arg	Arg	Phe	Lys 730	Asp	His	Val	Glu	Gly 735	Lys
Gln	Ile	Leu	Ser 740	Ala	Asp	Leu	Arg 745	Ser	Pro	Val	Tyr	Leu 750	Thr	Val	Leu
Lys	His	Gly 755	Asp	Gly	Thr	Thr 760	Leu	Asp	Ile	Met	Leu 765	Lys	Leu	His	Lys
Gln	Ala 770	Asp	Met	Gln	Glu	Glu 775	Lys	Asn	Arg	Ile	Glu 780	Arg	Val	Leu	Gly
Ala 785	Thr	Leu	Leu	Pro	Asp 790	Leu	Ile	Gln	Lys	Val 795	Leu	Thr	Phe	Ala	Leu 800
Ser	Glu	Glu	Val	Arg 805	Pro	Gln	Asp	Thr	Val 810	Ser	Val	Ile	Gly	Gly 815	Val
Ala	Gly	Gly	Ser 820	Lys	His	Gly	Arg	Lys 825	Ala	Ala	Trp	Lys	Phe 830	Ile	Lys
Asp	Asn	Trp 835	Glu	Glu	Leu	Tyr	Asn 840	Arg	Tyr	Gln	Gly	Gly 845	Phe	Leu	Ile
Ser 850	Arg	Leu	Ile	Lys	Leu	Ser 855	Val	Glu	Gly	Phe	Ala 860	Val	Asp	Lys	Met
Ala 865	Gly	Glu	Val	Lys	Ala 870	Phe	Phe	Glu	Ser	His 875	Pro	Ala	Pro	Ser	Ala 880
Glu	Arg	Thr	Ile	Gln	Gln	Cys	Cys	Glu	Asn	Ile	Leu	Leu	Asn	Ala	Ala

ITI-08-PCT_Sequence_Listing_ST25.txt

885

890

895

Trp Leu Lys Arg Asp Ala Glu Ser Ile His Gln Tyr Leu Leu Gln Arg
 900 905 910

Lys Ala Ser Pro Pro Thr Val
 915

<210> 603

<211> 219

<212> PRT

<213> Artificial Sequence

<220>

<223> PSB9__Homo_sapiens__P28065

<400> 603

Met Leu Arg Ala Gly Ala Pro Thr Gly Asp Leu Pro Arg Ala Gly Glu
 1 5 10 15

Val His Thr Gly Thr Thr Ile Met Ala Val Glu Phe Asp Gly Gly Val
 20 25 30

Val Met Gly Ser Asp Ser Arg Val Ser Ala Gly Glu Ala Val Val Asn
 35 40 45

Arg Val Phe Asp Lys Leu Ser Pro Leu His Glu Arg Ile Tyr Cys Ala
 50 55 60

Leu Ser Gly Ser Ala Ala Asp Ala Gln Ala Val Ala Asp Met Ala Ala
 65 70 75 80

Tyr Gln Leu Glu Leu His Gly Ile Glu Leu Glu Glu Pro Pro Leu Val
 85 90 95

Leu Ala Ala Ala Asn Val Val Arg Asn Ile Ser Tyr Lys Tyr Arg Glu
 100 105 110

Asp Leu Ser Ala His Leu Met Val Ala Gly Trp Asp Gln Arg Glu Gly
 115 120 125

Gly Gln Val Tyr Gly Thr Leu Gly Gly Met Leu Thr Arg Gln Pro Phe
 130 135 140

Ala Ile Gly Gly Ser Gly Ser Thr Phe Ile Tyr Gly Tyr Val Asp Ala
 145 150 155 160

Ala Tyr Lys Pro Gly Met Ser Pro Glu Glu Cys Arg Arg Phe Thr Thr
 165 170 175

Asp Ala Ile Ala Leu Ala Met Ser Arg Asp Gly Ser Ser Gly Gly Val

ITI-08-PCT_Sequence_Listing_ST25.txt

180

185

190

Ile Tyr Leu Val Thr Ile Thr Ala Ala Gly Val Asp His Arg Val Ile
195 200 205

Leu Gly Asn Glu Leu Pro Lys Phe Tyr Asp Glu
210 215

<210> 604

<211> 114

<212> PRT

<213> Artificial Sequence

<220>

<223> PSCA__Homo_sapiens__D3DWI6

<400> 604

Met Ala Gly Leu Ala Leu Gln Pro Gly Thr Ala Leu Leu Cys Tyr Ser
1 5 10 15

Cys Lys Ala Gln Val Ser Asn Glu Asp Cys Leu Gln Val Glu Asn Cys
20 25 30

Thr Gln Leu Gly Glu Gln Cys Trp Thr Ala Arg Ile Arg Ala Val Gly
35 40 45

Leu Leu Thr Val Ile Ser Lys Gly Cys Ser Leu Asn Cys Val Asp Asp
50 55 60

Ser Gln Asp Tyr Tyr Val Gly Lys Lys Asn Ile Thr Cys Cys Asp Thr
65 70 75 80

Asp Leu Cys Asn Ala Ser Gly Ala His Ala Leu Gln Pro Ala Ala Ala
85 90 95

Ile Leu Ala Leu Leu Pro Ala Leu Gly Leu Leu Leu Trp Gly Pro Gly
100 105 110

Gln Leu

<210> 605

<211> 123

<212> PRT

<213> Artificial Sequence

<220>

<223> PSCA__Homo_sapiens__043653

<400> 605

Met Lys Ala Val Leu Leu Ala Leu Leu Met Ala Gly Leu Ala Leu Gln

ITI-08-PCT_Sequence_Listing_ST25.txt

```

1             5             10             15
Pro Gly Thr Ala Leu Leu Cys Tyr Ser Cys Lys Ala Gln Val Ser Asn
      20             25             30
Glu Asp Cys Leu Gln Val Glu Asn Cys Thr Gln Leu Gly Glu Gln Cys
      35             40             45
Trp Thr Ala Arg Ile Arg Ala Val Gly Leu Leu Thr Val Ile Ser Lys
      50             55             60
Gly Cys Ser Leu Asn Cys Val Asp Asp Ser Gln Asp Tyr Tyr Val Gly
65             70             75             80
Lys Lys Asn Ile Thr Cys Cys Asp Thr Asp Leu Cys Asn Ala Ser Gly
      85             90             95
Ala His Ala Leu Gln Pro Ala Ala Ala Ile Leu Ala Leu Leu Pro Ala
      100            105            110
Leu Gly Leu Leu Leu Trp Gly Pro Gly Gln Leu
      115            120

```

<210> 606

<211> 320

<212> PRT

<213> Artificial Sequence

<220>

<223> PSGR__Homo_sapiens__Q9H255

<400> 606

```

Met Ser Ser Cys Asn Phe Thr His Ala Thr Phe Val Leu Ile Gly Ile
1             5             10             15
Pro Gly Leu Glu Lys Ala His Phe Trp Val Gly Phe Pro Leu Leu Ser
      20             25             30
Met Tyr Val Val Ala Met Phe Gly Asn Cys Ile Val Val Phe Ile Val
      35             40             45
Arg Thr Glu Arg Ser Leu His Ala Pro Met Tyr Leu Phe Leu Cys Met
      50             55             60
Leu Ala Ala Ile Asp Leu Ala Leu Ser Thr Ser Thr Met Pro Lys Ile
65             70             75             80
Leu Ala Leu Phe Trp Phe Asp Ser Arg Glu Ile Ser Phe Glu Ala Cys
      85             90             95
Leu Thr Gln Met Phe Phe Ile His Ala Leu Ser Ala Ile Glu Ser Thr

```

ITI-08-PCT_Sequence_Listing_ST25.txt

100

105

110

Ile Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys His Pro
115 120 125

Leu Arg His Ala Ala Val Leu Asn Asn Thr Val Thr Ala Gln Ile Gly
130 135 140

Ile Val Ala Val Val Arg Gly Ser Leu Phe Phe Phe Pro Leu Pro Leu
145 150 155 160

Leu Ile Lys Arg Leu Ala Phe Cys His Ser Asn Val Leu Ser His Ser
165 170 175

Tyr Cys Val His Gln Asp Val Met Lys Leu Ala Tyr Ala Asp Thr Leu
180 185 190

Pro Asn Val Val Tyr Gly Leu Thr Ala Ile Leu Leu Val Met Gly Val
195 200 205

Asp Val Met Phe Ile Ser Leu Ser Tyr Phe Leu Ile Ile Arg Thr Val
210 215 220

Leu Gln Leu Pro Ser Lys Ser Glu Arg Ala Lys Ala Phe Gly Thr Cys
225 230 235 240

Val Ser His Ile Gly Val Val Leu Ala Phe Tyr Val Pro Leu Ile Gly
245 250 255

Leu Ser Val Val His Arg Phe Gly Asn Ser Leu His Pro Ile Val Arg
260 265 270

Val Val Met Gly Asp Ile Tyr Leu Leu Leu Pro Pro Val Ile Asn Pro
275 280 285

Ile Ile Tyr Gly Ala Lys Thr Lys Gln Ile Arg Thr Arg Val Leu Ala
290 295 300

Met Phe Lys Ile Ser Cys Asp Lys Asp Leu Gln Ala Val Gly Gly Lys
305 310 315 320

<210> 607

<211> 750

<212> PRT

<213> Artificial Sequence

<220>

<223> PSM__Homo_sapiens__Q04609

<400> 607

Met Trp Asn Leu Leu His Glu Thr Asp Ser Ala Val Ala Thr Ala Arg

ITI-08-PCT_Sequence_Listing_ST25.txt

```

1           5           10           15
Arg Pro Arg Trp Leu Cys Ala Gly Ala Leu Val Leu Ala Gly Gly Phe
      20      25      30
Phe Leu Leu Gly Phe Leu Phe Gly Trp Phe Ile Lys Ser Ser Asn Glu
      35      40      45
Ala Thr Asn Ile Thr Pro Lys His Asn Met Lys Ala Phe Leu Asp Glu
      50      55      60
Leu Lys Ala Glu Asn Ile Lys Lys Phe Leu Tyr Asn Phe Thr Gln Ile
65      70      75      80
Pro His Leu Ala Gly Thr Glu Gln Asn Phe Gln Leu Ala Lys Gln Ile
      85      90      95
Gln Ser Gln Trp Lys Glu Phe Gly Leu Asp Ser Val Glu Leu Ala His
      100     105     110
Tyr Asp Val Leu Leu Ser Tyr Pro Asn Lys Thr His Pro Asn Tyr Ile
      115     120     125
Ser Ile Ile Asn Glu Asp Gly Asn Glu Ile Phe Asn Thr Ser Leu Phe
      130     135     140
Glu Pro Pro Pro Pro Gly Tyr Glu Asn Val Ser Asp Ile Val Pro Pro
145     150     155     160
Phe Ser Ala Phe Ser Pro Gln Gly Met Pro Glu Gly Asp Leu Val Tyr
      165     170     175
Val Asn Tyr Ala Arg Thr Glu Asp Phe Phe Lys Leu Glu Arg Asp Met
      180     185     190
Lys Ile Asn Cys Ser Gly Lys Ile Val Ile Ala Arg Tyr Gly Lys Val
      195     200     205
Phe Arg Gly Asn Lys Val Lys Asn Ala Gln Leu Ala Gly Ala Lys Gly
      210     215     220
Val Ile Leu Tyr Ser Asp Pro Ala Asp Tyr Phe Ala Pro Gly Val Lys
225     230     235     240
Ser Tyr Pro Asp Gly Trp Asn Leu Pro Gly Gly Gly Val Gln Arg Gly
      245     250     255
Asn Ile Leu Asn Leu Asn Gly Ala Gly Asp Pro Leu Thr Pro Gly Tyr
      260     265     270
Pro Ala Asn Glu Tyr Ala Tyr Arg Arg Gly Ile Ala Glu Ala Val Gly
      275     280     285

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Leu	Pro	Ser	Ile	Pro	Val	His	Pro	Ile	Gly	Tyr	Tyr	Asp	Ala	Gln	Lys	290	295	300
Leu	Leu	Glu	Lys	Met	Gly	Gly	Ser	Ala	Pro	Pro	Asp	Ser	Ser	Trp	Arg	305	310	315
Gly	Ser	Leu	Lys	Val	Pro	Tyr	Asn	Val	Gly	Pro	Gly	Phe	Thr	Gly	Asn	325	330	335
Phe	Ser	Thr	Gln	Lys	Val	Lys	Met	His	Ile	His	Ser	Thr	Asn	Glu	Val	340	345	350
Thr	Arg	Ile	Tyr	Asn	Val	Ile	Gly	Thr	Leu	Arg	Gly	Ala	Val	Glu	Pro	355	360	365
Asp	Arg	Tyr	Val	Ile	Leu	Gly	Gly	His	Arg	Asp	Ser	Trp	Val	Phe	Gly	370	375	380
Gly	Ile	Asp	Pro	Gln	Ser	Gly	Ala	Ala	Val	Val	His	Glu	Ile	Val	Arg	385	390	395
Ser	Phe	Gly	Thr	Leu	Lys	Lys	Glu	Gly	Trp	Arg	Pro	Arg	Arg	Thr	Ile	405	410	415
Leu	Phe	Ala	Ser	Trp	Asp	Ala	Glu	Glu	Phe	Gly	Leu	Leu	Gly	Ser	Thr	420	425	430
Glu	Trp	Ala	Glu	Glu	Asn	Ser	Arg	Leu	Leu	Gln	Glu	Arg	Gly	Val	Ala	435	440	445
Tyr	Ile	Asn	Ala	Asp	Ser	Ser	Ile	Glu	Gly	Asn	Tyr	Thr	Leu	Arg	Val	450	455	460
Asp	Cys	Thr	Pro	Leu	Met	Tyr	Ser	Leu	Val	His	Asn	Leu	Thr	Lys	Glu	465	470	475
Leu	Lys	Ser	Pro	Asp	Glu	Gly	Phe	Glu	Gly	Lys	Ser	Leu	Tyr	Glu	Ser	485	490	495
Trp	Thr	Lys	Lys	Ser	Pro	Ser	Pro	Glu	Phe	Ser	Gly	Met	Pro	Arg	Ile	500	505	510
Ser	Lys	Leu	Gly	Ser	Gly	Asn	Asp	Phe	Glu	Val	Phe	Phe	Gln	Arg	Leu	515	520	525
Gly	Ile	Ala	Ser	Gly	Arg	Ala	Arg	Tyr	Thr	Lys	Asn	Trp	Glu	Thr	Asn	530	535	540
Lys	Phe	Ser	Gly	Tyr	Pro	Leu	Tyr	His	Ser	Val	Tyr	Glu	Thr	Tyr	Glu	545	550	555

ITI-08-PCT_Sequence_Listing_ST25.txt

Leu Val Glu Lys Phe Tyr Asp Pro Met Phe Lys Tyr His Leu Thr Val
565 570 575

Ala Gln Val Arg Gly Gly Met Val Phe Glu Leu Ala Asn Ser Ile Val
580 585 590

Leu Pro Phe Asp Cys Arg Asp Tyr Ala Val Val Leu Arg Lys Tyr Ala
595 600 605

Asp Lys Ile Tyr Ser Ile Ser Met Lys His Pro Gln Glu Met Lys Thr
610 615 620

Tyr Ser Val Ser Phe Asp Ser Leu Phe Ser Ala Val Lys Asn Phe Thr
625 630 635 640

Glu Ile Ala Ser Lys Phe Ser Glu Arg Leu Gln Asp Phe Asp Lys Ser
645 650 655

Asn Pro Ile Val Leu Arg Met Met Asn Asp Gln Leu Met Phe Leu Glu
660 665 670

Arg Ala Phe Ile Asp Pro Leu Gly Leu Pro Asp Arg Pro Phe Tyr Arg
675 680 685

His Val Ile Tyr Ala Pro Ser Ser His Asn Lys Tyr Ala Gly Glu Ser
690 695 700

Phe Pro Gly Ile Tyr Asp Ala Leu Phe Asp Ile Glu Ser Lys Val Asp
705 710 715 720

Pro Ser Lys Ala Trp Gly Glu Val Lys Arg Gln Ile Tyr Val Ala Ala
725 730 735

Phe Thr Val Gln Ala Ala Ala Glu Thr Leu Ser Glu Val Ala
740 745 750

<210> 608

<211> 1306

<212> PRT

<213> Artificial Sequence

<220>

<223> PTPRC__Homo_sapiens__NP_002829

<400> 608

Met Thr Met Tyr Leu Trp Leu Lys Leu Leu Ala Phe Gly Phe Ala Phe
1 5 10 15

Leu Asp Thr Glu Val Phe Val Thr Gly Gln Ser Pro Thr Pro Ser Pro
20 25 30

ITI-08-PCT_Sequence_Listing_ST25.txt

Thr Gly Leu Thr Thr Ala Lys Met Pro Ser Val Pro Leu Ser Ser Asp
35 40 45

Pro Leu Pro Thr His Thr Thr Ala Phe Ser Pro Ala Ser Thr Phe Glu
50 55 60

Arg Glu Asn Asp Phe Ser Glu Thr Thr Thr Ser Leu Ser Pro Asp Asn
65 70 75 80

Thr Ser Thr Gln Val Ser Pro Asp Ser Leu Asp Asn Ala Ser Ala Phe
85 90 95

Asn Thr Thr Gly Val Ser Ser Val Gln Thr Pro His Leu Pro Thr His
100 105 110

Ala Asp Ser Gln Thr Pro Ser Ala Gly Thr Asp Thr Gln Thr Phe Ser
115 120 125

Gly Ser Ala Ala Asn Ala Lys Leu Asn Pro Thr Pro Gly Ser Asn Ala
130 135 140

Ile Ser Asp Val Pro Gly Glu Arg Ser Thr Ala Ser Thr Phe Pro Thr
145 150 155 160

Asp Pro Val Ser Pro Leu Thr Thr Thr Leu Ser Leu Ala His His Ser
165 170 175

Ser Ala Ala Leu Pro Ala Arg Thr Ser Asn Thr Thr Ile Thr Ala Asn
180 185 190

Thr Ser Asp Ala Tyr Leu Asn Ala Ser Glu Thr Thr Thr Leu Ser Pro
195 200 205

Ser Gly Ser Ala Val Ile Ser Thr Thr Thr Ile Ala Thr Thr Pro Ser
210 215 220

Lys Pro Thr Cys Asp Glu Lys Tyr Ala Asn Ile Thr Val Asp Tyr Leu
225 230 235 240

Tyr Asn Lys Glu Thr Lys Leu Phe Thr Ala Lys Leu Asn Val Asn Glu
245 250 255

Asn Val Glu Cys Gly Asn Asn Thr Cys Thr Asn Asn Glu Val His Asn
260 265 270

Leu Thr Glu Cys Lys Asn Ala Ser Val Ser Ile Ser His Asn Ser Cys
275 280 285

Thr Ala Pro Asp Lys Thr Leu Ile Leu Asp Val Pro Pro Gly Val Glu
290 295 300

Lys Phe Gln Leu His Asp Cys Thr Gln Val Glu Lys Ala Asp Thr Thr

ITI-08-PCT_Sequence_Listing_ST25.txt

```

305          310          315          320
Ile Cys Leu Lys Trp Lys Asn Ile Glu Thr Phe Thr Cys Asp Thr Gln
          325          330          335
Asn Ile Thr Tyr Arg Phe Gln Cys Gly Asn Met Ile Phe Asp Asn Lys
          340          345          350
Glu Ile Lys Leu Glu Asn Leu Glu Pro Glu His Glu Tyr Lys Cys Asp
          355          360          365
Ser Glu Ile Leu Tyr Asn Asn His Lys Phe Thr Asn Ala Ser Lys Ile
          370          375          380
Ile Lys Thr Asp Phe Gly Ser Pro Gly Glu Pro Gln Ile Ile Phe Cys
385          390          395          400
Arg Ser Glu Ala Ala His Gln Gly Val Ile Thr Trp Asn Pro Pro Gln
          405          410          415
Arg Ser Phe His Asn Phe Thr Leu Cys Tyr Ile Lys Glu Thr Glu Lys
          420          425          430
Asp Cys Leu Asn Leu Asp Lys Asn Leu Ile Lys Tyr Asp Leu Gln Asn
          435          440          445
Leu Lys Pro Tyr Thr Lys Tyr Val Leu Ser Leu His Ala Tyr Ile Ile
          450          455          460
Ala Lys Val Gln Arg Asn Gly Ser Ala Ala Met Cys His Phe Thr Thr
465          470          475          480
Lys Ser Ala Pro Pro Ser Gln Val Trp Asn Met Thr Val Ser Met Thr
          485          490          495
Ser Asp Asn Ser Met His Val Lys Cys Arg Pro Pro Arg Asp Arg Asn
          500          505          510
Gly Pro His Glu Arg Tyr His Leu Glu Val Glu Ala Gly Asn Thr Leu
          515          520          525
Val Arg Asn Glu Ser His Lys Asn Cys Asp Phe Arg Val Lys Asp Leu
          530          535          540
Gln Tyr Ser Thr Asp Tyr Thr Phe Lys Ala Tyr Phe His Asn Gly Asp
545          550          555          560
Tyr Pro Gly Glu Pro Phe Ile Leu His His Ser Thr Ser Tyr Asn Ser
          565          570          575
Lys Ala Leu Ile Ala Phe Leu Ala Phe Leu Ile Ile Val Thr Ser Ile
          580          585          590

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Ala	Leu	Leu	Val	Val	Leu	Tyr	Lys	Ile	Tyr	Asp	Leu	His	Lys	Lys	Arg	595	600	605
Ser	Cys	Asn	Leu	Asp	Glu	Gln	Gln	Glu	Leu	Val	Glu	Arg	Asp	Asp	Glu	610	615	620
Lys	Gln	Leu	Met	Asn	Val	Glu	Pro	Ile	His	Ala	Asp	Ile	Leu	Leu	Glu	625	630	635
Thr	Tyr	Lys	Arg	Lys	Ile	Ala	Asp	Glu	Gly	Arg	Leu	Phe	Leu	Ala	Glu	645	650	655
Phe	Gln	Ser	Ile	Pro	Arg	Val	Phe	Ser	Lys	Phe	Pro	Ile	Lys	Glu	Ala	660	665	670
Arg	Lys	Pro	Phe	Asn	Gln	Asn	Lys	Asn	Arg	Tyr	Val	Asp	Ile	Leu	Pro	675	680	685
Tyr	Asp	Tyr	Asn	Arg	Val	Glu	Leu	Ser	Glu	Ile	Asn	Gly	Asp	Ala	Gly	690	695	700
Ser	Asn	Tyr	Ile	Asn	Ala	Ser	Tyr	Ile	Asp	Gly	Phe	Lys	Glu	Pro	Arg	705	710	715
Lys	Tyr	Ile	Ala	Ala	Gln	Gly	Pro	Arg	Asp	Glu	Thr	Val	Asp	Asp	Phe	725	730	735
Trp	Arg	Met	Ile	Trp	Glu	Gln	Lys	Ala	Thr	Val	Ile	Val	Met	Val	Thr	740	745	750
Arg	Cys	Glu	Glu	Gly	Asn	Arg	Asn	Lys	Cys	Ala	Glu	Tyr	Trp	Pro	Ser	755	760	765
Met	Glu	Glu	Gly	Thr	Arg	Ala	Phe	Gly	Asp	Val	Val	Val	Lys	Ile	Asn	770	775	780
Gln	His	Lys	Arg	Cys	Pro	Asp	Tyr	Ile	Ile	Gln	Lys	Leu	Asn	Ile	Val	785	790	795
Asn	Lys	Lys	Glu	Lys	Ala	Thr	Gly	Arg	Glu	Val	Thr	His	Ile	Gln	Phe	805	810	815
Thr	Ser	Trp	Pro	Asp	His	Gly	Val	Pro	Glu	Asp	Pro	His	Leu	Leu	Leu	820	825	830
Lys	Leu	Arg	Arg	Arg	Val	Asn	Ala	Phe	Ser	Asn	Phe	Phe	Ser	Gly	Pro	835	840	845
Ile	Val	Val	His	Cys	Ser	Ala	Gly	Val	Gly	Arg	Thr	Gly	Thr	Tyr	Ile	850	855	860

ITI-08-PCT_Sequence_Listing_ST25.txt

Gly Ile Asp Ala Met Leu Glu Gly Leu Glu Ala Glu Asn Lys Val Asp
865 870 875 880

Val Tyr Gly Tyr Val Val Lys Leu Arg Arg Gln Arg Cys Leu Met Val
885 890 895

Gln Val Glu Ala Gln Tyr Ile Leu Ile His Gln Ala Leu Val Glu Tyr
900 905 910

Asn Gln Phe Gly Glu Thr Glu Val Asn Leu Ser Glu Leu His Pro Tyr
915 920 925

Leu His Asn Met Lys Lys Arg Asp Pro Pro Ser Glu Pro Ser Pro Leu
930 935 940

Glu Ala Glu Phe Gln Arg Leu Pro Ser Tyr Arg Ser Trp Arg Thr Gln
945 950 955 960

His Ile Gly Asn Gln Glu Glu Asn Lys Ser Lys Asn Arg Asn Ser Asn
965 970 975

Val Ile Pro Tyr Asp Tyr Asn Arg Val Pro Leu Lys His Glu Leu Glu
980 985 990

Met Ser Lys Glu Ser Glu His Asp Ser Asp Glu Ser Ser Asp Asp Asp
995 1000 1005

Ser Asp Ser Glu Glu Pro Ser Lys Tyr Ile Asn Ala Ser Phe Ile
1010 1015 1020

Met Ser Tyr Trp Lys Pro Glu Val Met Ile Ala Ala Gln Gly Pro
1025 1030 1035

Leu Lys Glu Thr Ile Gly Asp Phe Trp Gln Met Ile Phe Gln Arg
1040 1045 1050

Lys Val Lys Val Ile Val Met Leu Thr Glu Leu Lys His Gly Asp
1055 1060 1065

Gln Glu Ile Cys Ala Gln Tyr Trp Gly Glu Gly Lys Gln Thr Tyr
1070 1075 1080

Gly Asp Ile Glu Val Asp Leu Lys Asp Thr Asp Lys Ser Ser Thr
1085 1090 1095

Tyr Thr Leu Arg Val Phe Glu Leu Arg His Ser Lys Arg Lys Asp
1100 1105 1110

Ser Arg Thr Val Tyr Gln Tyr Gln Tyr Thr Asn Trp Ser Val Glu
1115 1120 1125

Gln Leu Pro Ala Glu Pro Lys Glu Leu Ile Ser Met Ile Gln Val

ITI-08-PCT_Sequence_Listing_ST25.txt

1130														
						1135						1140		
Val	Lys	Gln	Lys	Leu	Pro	Gln	Lys	Asn	Ser	Ser	Glu	Gly	Asn	Lys
1145						1150					1155			
His	His	Lys	Ser	Thr	Pro	Leu	Leu	Ile	His	Cys	Arg	Asp	Gly	Ser
1160						1165					1170			
Gln	Gln	Thr	Gly	Ile	Phe	Cys	Ala	Leu	Leu	Asn	Leu	Leu	Glu	Ser
1175						1180					1185			
Ala	Glu	Thr	Glu	Glu	Val	Val	Asp	Ile	Phe	Gln	Val	Val	Lys	Ala
1190						1195					1200			
Leu	Arg	Lys	Ala	Arg	Pro	Gly	Met	Val	Ser	Thr	Phe	Glu	Gln	Tyr
1205						1210					1215			
Gln	Phe	Leu	Tyr	Asp	Val	Ile	Ala	Ser	Thr	Tyr	Pro	Ala	Gln	Asn
1220						1225					1230			
Gly	Gln	Val	Lys	Lys	Asn	Asn	His	Gln	Glu	Asp	Lys	Ile	Glu	Phe
1235						1240					1245			
Asp	Asn	Glu	Val	Asp	Lys	Val	Lys	Gln	Asp	Ala	Asn	Cys	Val	Asn
1250						1255					1260			
Pro	Leu	Gly	Ala	Pro	Glu	Lys	Leu	Pro	Glu	Ala	Lys	Glu	Gln	Ala
1265						1270					1275			
Glu	Gly	Ser	Glu	Pro	Thr	Ser	Gly	Thr	Glu	Gly	Pro	Glu	His	Ser
1280						1285					1290			
Val	Asn	Gly	Pro	Ala	Ser	Pro	Ala	Leu	Asn	Gln	Gly	Ser		
1295						1300					1305			

<210> 609
 <211> 207
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> RAB8A__Homo_sapiens__P61006

<400> 609

Met	Ala	Lys	Thr	Tyr	Asp	Tyr	Leu	Phe	Lys	Leu	Leu	Leu	Ile	Gly	Asp
1				5					10					15	
Ser	Gly	Val	Gly	Lys	Thr	Cys	Val	Leu	Phe	Arg	Phe	Ser	Glu	Asp	Ala
			20					25					30		
Phe	Asn	Ser	Thr	Phe	Ile	Ser	Thr	Ile	Gly	Ile	Asp	Phe	Lys	Ile	Arg

ITI-08-PCT_Sequence_Listing_ST25.txt

```

35          40          45
Thr Ile Glu Leu Asp Gly Lys Arg Ile Lys Leu Gln Ile Trp Asp Thr
50          55          60
Ala Gly Gln Glu Arg Phe Arg Thr Ile Thr Thr Ala Tyr Tyr Arg Gly
65          70          75          80
Ala Met Gly Ile Met Leu Val Tyr Asp Ile Thr Asn Glu Lys Ser Phe
85          90          95
Asp Asn Ile Arg Asn Trp Ile Arg Asn Ile Glu Glu His Ala Ser Ala
100         105         110
Asp Val Glu Lys Met Ile Leu Gly Asn Lys Cys Asp Val Asn Asp Lys
115         120         125
Arg Gln Val Ser Lys Glu Arg Gly Glu Lys Leu Ala Leu Asp Tyr Gly
130         135         140
Ile Lys Phe Met Glu Thr Ser Ala Lys Ala Asn Ile Asn Val Glu Asn
145         150         155         160
Ala Phe Phe Thr Leu Ala Arg Asp Ile Lys Ala Lys Met Asp Lys Lys
165         170         175
Leu Glu Gly Asn Ser Pro Gln Gly Ser Asn Gln Gly Val Lys Ile Thr
180         185         190
Pro Asp Gln Gln Lys Arg Ser Ser Phe Phe Arg Cys Val Leu Leu
195         200         205

```

<210> 610

<211> 419

<212> PRT

<213> Artificial Sequence

<220>

<223> RAGE-1__Homo_sapiens__Q9UQ07

<400> 610

```

Met Lys Asn Tyr Lys Ala Ile Gly Lys Ile Gly Glu Gly Thr Phe Ser
1          5          10          15
Glu Val Met Lys Met Gln Ser Leu Arg Asp Gly Asn Tyr Tyr Ala Cys
20         25         30
Lys Gln Met Lys Gln Arg Phe Glu Ser Ile Glu Gln Val Asn Asn Leu
35         40         45
Arg Glu Ile Gln Ala Leu Arg Arg Leu Asn Pro His Pro Asn Ile Leu

```

ITI-08-PCT_Sequence_Listing_ST25.txt

50	55	60														
Met	Leu	His	Glu	Val	Val	Phe	Asp	Arg	Lys	Ser	Gly	Ser	Leu	Ala	Leu	
65					70					75					80	
Ile	Cys	Glu	Leu	Met	Asp	Met	Asn	Ile	Tyr	Glu	Leu	Ile	Arg	Gly	Arg	
				85					90					95		
Arg	Tyr	Pro	Leu	Ser	Glu	Lys	Lys	Ile	Met	His	Tyr	Met	Tyr	Gln	Leu	
			100					105					110			
Cys	Lys	Ser	Leu	Asp	His	Ile	His	Arg	Asn	Gly	Ile	Phe	His	Arg	Asp	
		115					120					125				
Val	Lys	Pro	Glu	Asn	Ile	Leu	Ile	Lys	Gln	Asp	Val	Leu	Lys	Leu	Gly	
	130					135					140					
Asp	Phe	Gly	Ser	Cys	Arg	Ser	Val	Tyr	Ser	Lys	Gln	Pro	Tyr	Thr	Glu	
145					150					155					160	
Tyr	Ile	Ser	Thr	Arg	Trp	Tyr	Arg	Ala	Pro	Glu	Cys	Leu	Leu	Thr	Asp	
				165					170					175		
Gly	Phe	Tyr	Thr	Tyr	Lys	Met	Asp	Leu	Trp	Ser	Ala	Gly	Cys	Val	Phe	
			180					185					190			
Tyr	Glu	Ile	Ala	Ser	Leu	Gln	Pro	Leu	Phe	Pro	Gly	Val	Asn	Glu	Leu	
		195					200					205				
Asp	Gln	Ile	Ser	Lys	Ile	His	Asp	Val	Ile	Gly	Thr	Pro	Ala	Gln	Lys	
	210					215					220					
Ile	Leu	Thr	Lys	Phe	Lys	Gln	Ser	Arg	Ala	Met	Asn	Phe	Asp	Phe	Pro	
225					230					235					240	
Phe	Lys	Lys	Gly	Ser	Gly	Ile	Pro	Leu	Leu	Thr	Thr	Asn	Leu	Ser	Pro	
				245					250					255		
Gln	Cys	Leu	Ser	Leu	Leu	His	Ala	Met	Val	Ala	Tyr	Asp	Pro	Asp	Glu	
			260					265					270			
Arg	Ile	Ala	Ala	His	Gln	Ala	Leu	Gln	His	Pro	Tyr	Phe	Gln	Glu	Gln	
		275					280					285				
Arg	Lys	Thr	Glu	Lys	Arg	Ala	Leu	Gly	Ser	His	Arg	Lys	Ala	Gly	Phe	
	290					295					300					
Pro	Glu	His	Pro	Val	Ala	Pro	Glu	Pro	Leu	Ser	Asn	Ser	Cys	Gln	Ile	
305					310					315					320	
Ser	Lys	Glu	Gly	Arg	Lys	Gln	Lys	Gln	Ser	Leu	Lys	Gln	Glu	Glu	Asp	
				325					330					335		

ITI-08-PCT_Sequence_Listing_ST25.txt

Arg Pro Lys Arg Arg Gly Pro Ala Tyr Val Met Glu Leu Pro Lys Leu
340 345 350

Lys Leu Ser Gly Val Val Arg Leu Ser Ser Tyr Ser Ser Pro Thr Leu
355 360 365

Gln Ser Val Leu Gly Ser Gly Thr Asn Gly Arg Val Pro Val Leu Arg
370 375 380

Pro Leu Lys Cys Ile Pro Ala Ser Lys Lys Thr Asp Pro Gln Lys Asp
385 390 395 400

Leu Lys Pro Ala Pro Gln Gln Cys Arg Leu Pro Thr Ile Val Arg Lys
405 410 415

Gly Gly Arg

<210> 611

<211> 462

<212> PRT

<213> Artificial Sequence

<220>

<223> RARA__Homo_sapiens__P10276

<400> 611

Met Ala Ser Asn Ser Ser Ser Cys Pro Thr Pro Gly Gly Gly His Leu
1 5 10 15

Asn Gly Tyr Pro Val Pro Pro Tyr Ala Phe Phe Phe Pro Pro Met Leu
20 25 30

Gly Gly Leu Ser Pro Pro Gly Ala Leu Thr Thr Leu Gln His Gln Leu
35 40 45

Pro Val Ser Gly Tyr Ser Thr Pro Ser Pro Ala Thr Ile Glu Thr Gln
50 55 60

Ser Ser Ser Ser Glu Glu Ile Val Pro Ser Pro Pro Ser Pro Pro Pro
65 70 75 80

Leu Pro Arg Ile Tyr Lys Pro Cys Phe Val Cys Gln Asp Lys Ser Ser
85 90 95

Gly Tyr His Tyr Gly Val Ser Ala Cys Glu Gly Cys Lys Gly Phe Phe
100 105 110

Arg Arg Ser Ile Gln Lys Asn Met Val Tyr Thr Cys His Arg Asp Lys
115 120 125

ITI-08-PCT_Sequence_Listing_ST25.txt

Asn	Cys	Ile	Ile	Asn	Lys	Val	Thr	Arg	Asn	Arg	Cys	Gln	Tyr	Cys	Arg	130	135	140	
Leu	Gln	Lys	Cys	Phe	Glu	Val	Gly	Met	Ser	Lys	Glu	Ser	Val	Arg	Asn	145	150	155	160
Asp	Arg	Asn	Lys	Lys	Lys	Lys	Glu	Val	Pro	Lys	Pro	Glu	Cys	Ser	Glu	165	170	175	
Ser	Tyr	Thr	Leu	Thr	Pro	Glu	Val	Gly	Glu	Leu	Ile	Glu	Lys	Val	Arg	180	185	190	
Lys	Ala	His	Gln	Glu	Thr	Phe	Pro	Ala	Leu	Cys	Gln	Leu	Gly	Lys	Tyr	195	200	205	
Thr	Thr	Asn	Asn	Ser	Ser	Glu	Gln	Arg	Val	Ser	Leu	Asp	Ile	Asp	Leu	210	215	220	
Trp	Asp	Lys	Phe	Ser	Glu	Leu	Ser	Thr	Lys	Cys	Ile	Ile	Lys	Thr	Val	225	230	235	240
Glu	Phe	Ala	Lys	Gln	Leu	Pro	Gly	Phe	Thr	Thr	Leu	Thr	Ile	Ala	Asp	245	250	255	
Gln	Ile	Thr	Leu	Leu	Lys	Ala	Ala	Cys	Leu	Asp	Ile	Leu	Ile	Leu	Arg	260	265	270	
Ile	Cys	Thr	Arg	Tyr	Thr	Pro	Glu	Gln	Asp	Thr	Met	Thr	Phe	Ser	Asp	275	280	285	
Gly	Leu	Thr	Leu	Asn	Arg	Thr	Gln	Met	His	Asn	Ala	Gly	Phe	Gly	Pro	290	295	300	
Leu	Thr	Asp	Leu	Val	Phe	Ala	Phe	Ala	Asn	Gln	Leu	Leu	Pro	Leu	Glu	305	310	315	320
Met	Asp	Asp	Ala	Glu	Thr	Gly	Leu	Leu	Ser	Ala	Ile	Cys	Leu	Ile	Cys	325	330	335	
Gly	Asp	Arg	Gln	Asp	Leu	Glu	Gln	Pro	Asp	Arg	Val	Asp	Met	Leu	Gln	340	345	350	
Glu	Pro	Leu	Leu	Glu	Ala	Leu	Lys	Val	Tyr	Val	Arg	Lys	Arg	Arg	Pro	355	360	365	
Ser	Arg	Pro	His	Met	Phe	Pro	Lys	Met	Leu	Met	Lys	Ile	Thr	Asp	Leu	370	375	380	
Arg	Ser	Ile	Ser	Ala	Lys	Gly	Ala	Glu	Arg	Val	Ile	Thr	Leu	Lys	Met	385	390	395	400
Glu	Ile	Pro	Gly	Ser	Met	Pro	Pro	Leu	Ile	Gln	Glu	Met	Leu	Glu	Asn				

ITI-08-PCT_Sequence_Listing_ST25.txt

405 410 415

Ser Glu Gly Leu Asp Thr Leu Ser Gly Gln Pro Gly Gly Gly Gly Arg
420 425 430

Asp Gly Gly Gly Leu Ala Pro Pro Pro Gly Ser Cys Ser Pro Ser Leu
435 440 445

Ser Pro Ser Ser Asn Arg Ser Ser Pro Ala Thr His Ser Pro
450 455 460

<210> 612
<211> 189
<212> PRT
<213> Artificial Sequence

<220>
<223> RASH__Homo_sapiens__P01112

<400> 612

Met Thr Glu Tyr Lys Leu Val Val Val Gly Ala Gly Gly Val Gly Lys
1 5 10 15

Ser Ala Leu Thr Ile Gln Leu Ile Gln Asn His Phe Val Asp Glu Tyr
20 25 30

Asp Pro Thr Ile Glu Asp Ser Tyr Arg Lys Gln Val Val Ile Asp Gly
35 40 45

Glu Thr Cys Leu Leu Asp Ile Leu Asp Thr Ala Gly Gln Glu Glu Tyr
50 55 60

Ser Ala Met Arg Asp Gln Tyr Met Arg Thr Gly Glu Gly Phe Leu Cys
65 70 75 80

Val Phe Ala Ile Asn Asn Thr Lys Ser Phe Glu Asp Ile His Gln Tyr
85 90 95

Arg Glu Gln Ile Lys Arg Val Lys Asp Ser Asp Asp Val Pro Met Val
100 105 110

Leu Val Gly Asn Lys Cys Asp Leu Ala Ala Arg Thr Val Glu Ser Arg
115 120 125

Gln Ala Gln Asp Leu Ala Arg Ser Tyr Gly Ile Pro Tyr Ile Glu Thr
130 135 140

Ser Ala Lys Thr Arg Gln Gly Val Glu Asp Ala Phe Tyr Thr Leu Val
145 150 155 160

Arg Glu Ile Arg Gln His Lys Leu Arg Lys Leu Asn Pro Pro Asp Glu

ITI-08-PCT_Sequence_Listing_ST25.txt

165 170 175

Ser Gly Pro Gly Cys Met Ser Cys Lys Cys Val Leu Ser
180 185

<210> 613
<211> 189
<212> PRT
<213> Artificial Sequence

<220>
<223> RASK__Homo_sapiens__P01116

<400> 613

Met Thr Glu Tyr Lys Leu Val Val Val Gly Ala Gly Gly Val Gly Lys
1 5 10 15

Ser Ala Leu Thr Ile Gln Leu Ile Gln Asn His Phe Val Asp Glu Tyr
20 25 30

Asp Pro Thr Ile Glu Asp Ser Tyr Arg Lys Gln Val Val Ile Asp Gly
35 40 45

Glu Thr Cys Leu Leu Asp Ile Leu Asp Thr Ala Gly Gln Glu Glu Tyr
50 55 60

Ser Ala Met Arg Asp Gln Tyr Met Arg Thr Gly Glu Gly Phe Leu Cys
65 70 75 80

Val Phe Ala Ile Asn Asn Thr Lys Ser Phe Glu Asp Ile His His Tyr
85 90 95

Arg Glu Gln Ile Lys Arg Val Lys Asp Ser Glu Asp Val Pro Met Val
100 105 110

Leu Val Gly Asn Lys Cys Asp Leu Pro Ser Arg Thr Val Asp Thr Lys
115 120 125

Gln Ala Gln Asp Leu Ala Arg Ser Tyr Gly Ile Pro Phe Ile Glu Thr
130 135 140

Ser Ala Lys Thr Arg Gln Arg Val Glu Asp Ala Phe Tyr Thr Leu Val
145 150 155 160

Arg Glu Ile Arg Gln Tyr Arg Leu Lys Lys Ile Ser Lys Glu Glu Lys
165 170 175

Thr Pro Gly Cys Val Lys Ile Lys Lys Cys Ile Ile Met
180 185

<210> 614

ITI-08-PCT_Sequence_Listing_ST25.txt

```

<211> 189
<212> PRT
<213> Artificial Sequence

<220>
<223> RASN__Homo_sapiens__P01111

<400> 614

Met Thr Glu Tyr Lys Leu Val Val Val Gly Ala Gly Gly Val Gly Lys
1          5          10          15

Ser Ala Leu Thr Ile Gln Leu Ile Gln Asn His Phe Val Asp Glu Tyr
          20          25          30

Asp Pro Thr Ile Glu Asp Ser Tyr Arg Lys Gln Val Val Ile Asp Gly
          35          40          45

Glu Thr Cys Leu Leu Asp Ile Leu Asp Thr Ala Gly Gln Glu Glu Tyr
          50          55          60

Ser Ala Met Arg Asp Gln Tyr Met Arg Thr Gly Glu Gly Phe Leu Cys
65          70          75          80

Val Phe Ala Ile Asn Asn Ser Lys Ser Phe Ala Asp Ile Asn Leu Tyr
          85          90          95

Arg Glu Gln Ile Lys Arg Val Lys Asp Ser Asp Asp Val Pro Met Val
          100          105          110

Leu Val Gly Asn Lys Cys Asp Leu Pro Thr Arg Thr Val Asp Thr Lys
          115          120          125

Gln Ala His Glu Leu Ala Lys Ser Tyr Gly Ile Pro Phe Ile Glu Thr
          130          135          140

Ser Ala Lys Thr Arg Gln Gly Val Glu Asp Ala Phe Tyr Thr Leu Val
145          150          155          160

Arg Glu Ile Arg Gln Tyr Arg Met Lys Lys Leu Asn Ser Ser Asp Asp
          165          170          175

Gly Thr Gln Gly Cys Met Gly Leu Pro Cys Val Val Met
          180          185

```

```

<210> 615
<211> 181
<212> PRT
<213> Artificial Sequence

<220>
<223> RGS5__Homo_sapiens__015539

```

ITI-08-PCT_Sequence_Listing_ST25.txt

<400> 615

Met Cys Lys Gly Leu Ala Ala Leu Pro His Ser Cys Leu Glu Arg Ala
1 5 10 15

Lys Glu Ile Lys Ile Lys Leu Gly Ile Leu Leu Gln Lys Pro Asp Ser
20 25 30

Val Gly Asp Leu Val Ile Pro Tyr Asn Glu Lys Pro Glu Lys Pro Ala
35 40 45

Lys Thr Gln Lys Thr Ser Leu Asp Glu Ala Leu Gln Trp Arg Asp Ser
50 55 60

Leu Asp Lys Leu Leu Gln Asn Asn Tyr Gly Leu Ala Ser Phe Lys Ser
65 70 75 80

Phe Leu Lys Ser Glu Phe Ser Glu Glu Asn Leu Glu Phe Trp Ile Ala
85 90 95

Cys Glu Asp Tyr Lys Lys Ile Lys Ser Pro Ala Lys Met Ala Glu Lys
100 105 110

Ala Lys Gln Ile Tyr Glu Glu Phe Ile Gln Thr Glu Ala Pro Lys Glu
115 120 125

Val Asn Ile Asp His Phe Thr Lys Asp Ile Thr Met Lys Asn Leu Val
130 135 140

Glu Pro Ser Leu Ser Ser Phe Asp Met Ala Gln Lys Arg Ile His Ala
145 150 155 160

Leu Met Glu Lys Asp Ser Leu Pro Arg Phe Val Arg Ser Glu Phe Tyr
165 170 175

Gln Glu Leu Ile Lys
180

<210> 616

<211> 724

<212> PRT

<213> Artificial Sequence

<220>

<223> RHAMM/CD168__Homo_sapiens__075330

<400> 616

Met Ser Phe Pro Lys Ala Pro Leu Lys Arg Phe Asn Asp Pro Ser Gly
1 5 10 15

ITI-08-PCT_Sequence_Listing_ST25.txt

Cys Ala Pro Ser Pro Gly Ala Tyr Asp Val Lys Thr Leu Glu Val Leu
 20 25 30
 Lys Gly Pro Val Ser Phe Gln Lys Ser Gln Arg Phe Lys Gln Gln Lys
 35 40 45
 Glu Ser Lys Gln Asn Leu Asn Val Asp Lys Asp Thr Thr Leu Pro Ala
 50 55 60
 Ser Ala Arg Lys Val Lys Ser Ser Glu Ser Lys Glu Ser Gln Lys Asn
 65 70 75 80
 Asp Lys Asp Leu Lys Ile Leu Glu Lys Glu Ile Arg Val Leu Leu Gln
 85 90 95
 Glu Arg Gly Ala Gln Asp Arg Arg Ile Gln Asp Leu Glu Thr Glu Leu
 100 105 110
 Glu Lys Met Glu Ala Arg Leu Asn Ala Ala Leu Arg Glu Lys Thr Ser
 115 120 125
 Leu Ser Ala Asn Asn Ala Thr Leu Glu Lys Gln Leu Ile Glu Leu Thr
 130 135 140
 Arg Thr Asn Glu Leu Leu Lys Ser Lys Phe Ser Glu Asn Gly Asn Gln
 145 150 155 160
 Lys Asn Leu Arg Ile Leu Ser Leu Glu Leu Met Lys Leu Arg Asn Lys
 165 170 175
 Arg Glu Thr Lys Met Arg Gly Met Met Ala Lys Gln Glu Gly Met Glu
 180 185 190
 Met Lys Leu Gln Val Thr Gln Arg Ser Leu Glu Glu Ser Gln Gly Lys
 195 200 205
 Ile Ala Gln Leu Glu Gly Lys Leu Val Ser Ile Glu Lys Glu Lys Ile
 210 215 220
 Asp Glu Lys Ser Glu Thr Glu Lys Leu Leu Glu Tyr Ile Glu Glu Ile
 225 230 235 240
 Ser Cys Ala Ser Asp Gln Val Glu Lys Tyr Lys Leu Asp Ile Ala Gln
 245 250 255
 Leu Glu Glu Asn Leu Lys Glu Lys Asn Asp Glu Ile Leu Ser Leu Lys
 260 265 270
 Gln Ser Leu Glu Glu Asn Ile Val Ile Leu Ser Lys Gln Val Glu Asp
 275 280 285
 Leu Asn Val Lys Cys Gln Leu Leu Glu Lys Glu Lys Glu Asp His Val

ITI-08-PCT_Sequence_Listing_ST25.txt

290		295		300													
Asn	Arg	Asn	Arg	Glu	His	Asn	Glu	Asn	Leu	Asn	Ala	Glu	Met	Gln	Asn		
305					310					315					320		
Leu	Lys	Gln	Lys	Phe	Ile	Leu	Glu	Gln	Gln	Glu	Arg	Glu	Lys	Leu	Gln		
				325					330					335			
Gln	Lys	Glu	Leu	Gln	Ile	Asp	Ser	Leu	Leu	Gln	Gln	Glu	Lys	Glu	Leu		
			340					345					350				
Ser	Ser	Ser	Leu	His	Gln	Lys	Leu	Cys	Ser	Phe	Gln	Glu	Glu	Met	Val		
		355					360					365					
Lys	Glu	Lys	Asn	Leu	Phe	Glu	Glu	Glu	Leu	Lys	Gln	Thr	Leu	Asp	Glu		
	370					375					380						
Leu	Asp	Lys	Leu	Gln	Gln	Lys	Glu	Glu	Gln	Ala	Glu	Arg	Leu	Val	Lys		
385					390					395					400		
Gln	Leu	Glu	Glu	Glu	Ala	Lys	Ser	Arg	Ala	Glu	Glu	Leu	Lys	Leu	Leu		
				405					410					415			
Glu	Glu	Lys	Leu	Lys	Gly	Lys	Glu	Ala	Glu	Leu	Glu	Lys	Ser	Ser	Ala		
			420				425						430				
Ala	His	Thr	Gln	Ala	Thr	Leu	Leu	Leu	Gln	Glu	Lys	Tyr	Asp	Ser	Met		
		435				440						445					
Val	Gln	Ser	Leu	Glu	Asp	Val	Thr	Ala	Gln	Phe	Glu	Ser	Tyr	Lys	Ala		
	450					455					460						
Leu	Thr	Ala	Ser	Glu	Ile	Glu	Asp	Leu	Lys	Leu	Glu	Asn	Ser	Ser	Leu		
465					470					475					480		
Gln	Glu	Lys	Ala	Ala	Lys	Ala	Gly	Lys	Asn	Ala	Glu	Asp	Val	Gln	His		
			485						490					495			
Gln	Ile	Leu	Ala	Thr	Glu	Ser	Ser	Asn	Gln	Glu	Tyr	Val	Arg	Met	Leu		
			500					505					510				
Leu	Asp	Leu	Gln	Thr	Lys	Ser	Ala	Leu	Lys	Glu	Thr	Glu	Ile	Lys	Glu		
		515					520					525					
Ile	Thr	Val	Ser	Phe	Leu	Gln	Lys	Ile	Thr	Asp	Leu	Gln	Asn	Gln	Leu		
	530					535					540						
Lys	Gln	Gln	Glu	Glu	Asp	Phe	Arg	Lys	Gln	Leu	Glu	Asp	Glu	Glu	Gly		
545					550					555					560		
Arg	Lys	Ala	Glu	Lys	Glu	Asn	Thr	Thr	Ala	Glu	Leu	Thr	Glu	Glu	Ile		
				565					570					575			

ITI-08-PCT_Sequence_Listing_ST25.txt

Asn Lys Trp Arg Leu Leu Tyr Glu Glu Leu Tyr Asn Lys Thr Lys Pro
580 585 590

Phe Gln Leu Gln Leu Asp Ala Phe Glu Val Glu Lys Gln Ala Leu Leu
595 600 605

Asn Glu His Gly Ala Ala Gln Glu Gln Leu Asn Lys Ile Arg Asp Ser
610 615 620

Tyr Ala Lys Leu Leu Gly His Gln Asn Leu Lys Gln Lys Ile Lys His
625 630 635 640

Val Val Lys Leu Lys Asp Glu Asn Ser Gln Leu Lys Ser Glu Val Ser
645 650 655

Lys Leu Arg Cys Gln Leu Ala Lys Lys Lys Gln Ser Glu Thr Lys Leu
660 665 670

Gln Glu Glu Leu Asn Lys Val Leu Gly Ile Lys His Phe Asp Pro Ser
675 680 685

Lys Ala Phe His His Glu Ser Lys Glu Asn Phe Ala Leu Lys Thr Pro
690 695 700

Leu Lys Glu Gly Asn Thr Asn Cys Tyr Arg Ala Pro Met Glu Cys Gln
705 710 715 720

Glu Ser Trp Lys

<210> 617
<211> 193
<212> PRT
<213> Artificial Sequence

<220>
<223> RHOC__Homo_sapiens__P08134

<400> 617

Met Ala Ala Ile Arg Lys Lys Leu Val Ile Val Gly Asp Gly Ala Cys
1 5 10 15

Gly Lys Thr Cys Leu Leu Ile Val Phe Ser Lys Asp Gln Phe Pro Glu
20 25 30

Val Tyr Val Pro Thr Val Phe Glu Asn Tyr Ile Ala Asp Ile Glu Val
35 40 45

Asp Gly Lys Gln Val Glu Leu Ala Leu Trp Asp Thr Ala Gly Gln Glu
50 55 60

ITI-08-PCT_Sequence_Listing_ST25.txt

Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr Pro Asp Thr Asp Val Ile
65 70 75 80

Leu Met Cys Phe Ser Ile Asp Ser Pro Asp Ser Leu Glu Asn Ile Pro
85 90 95

Glu Lys Trp Thr Pro Glu Val Lys His Phe Cys Pro Asn Val Pro Ile
100 105 110

Ile Leu Val Gly Asn Lys Lys Asp Leu Arg Gln Asp Glu His Thr Arg
115 120 125

Arg Glu Leu Ala Lys Met Lys Gln Glu Pro Val Arg Ser Glu Glu Gly
130 135 140

Arg Asp Met Ala Asn Arg Ile Ser Ala Phe Gly Tyr Leu Glu Cys Ser
145 150 155 160

Ala Lys Thr Lys Glu Gly Val Arg Glu Val Phe Glu Met Ala Thr Arg
165 170 175

Ala Gly Leu Gln Val Arg Lys Asn Lys Arg Arg Arg Gly Cys Pro Ile
180 185 190

Leu

<210> 618

<211> 295

<212> PRT

<213> Artificial Sequence

<220>

<223> RSSA__Homo_sapiens__P08865

<400> 618

Met Ser Gly Ala Leu Asp Val Leu Gln Met Lys Glu Glu Asp Val Leu
1 5 10 15

Lys Phe Leu Ala Ala Gly Thr His Leu Gly Gly Thr Asn Leu Asp Phe
20 25 30

Gln Met Glu Gln Tyr Ile Tyr Lys Arg Lys Ser Asp Gly Ile Tyr Ile
35 40 45

Ile Asn Leu Lys Arg Thr Trp Glu Lys Leu Leu Leu Ala Ala Arg Ala
50 55 60

Ile Val Ala Ile Glu Asn Pro Ala Asp Val Ser Val Ile Ser Ser Arg
65 70 75 80

Asn Thr Gly Gln Arg Ala Val Leu Lys Phe Ala Ala Ala Thr Gly Ala

ITI-08-PCT_Sequence_Listing_ST25.txt

85 90 95

Thr Pro Ile Ala Gly Arg Phe Thr Pro Gly Thr Phe Thr Asn Gln Ile
100 105 110

Gln Ala Ala Phe Arg Glu Pro Arg Leu Leu Val Val Thr Asp Pro Arg
115 120 125

Ala Asp His Gln Pro Leu Thr Glu Ala Ser Tyr Val Asn Leu Pro Thr
130 135 140

Ile Ala Leu Cys Asn Thr Asp Ser Pro Leu Arg Tyr Val Asp Ile Ala
145 150 155 160

Ile Pro Cys Asn Asn Lys Gly Ala His Ser Val Gly Leu Met Trp Trp
165 170 175

Met Leu Ala Arg Glu Val Leu Arg Met Arg Gly Thr Ile Ser Arg Glu
180 185 190

His Pro Trp Glu Val Met Pro Asp Leu Tyr Phe Tyr Arg Asp Pro Glu
195 200 205

Glu Ile Glu Lys Glu Glu Gln Ala Ala Ala Glu Lys Ala Val Thr Lys
210 215 220

Glu Glu Phe Gln Gly Glu Trp Thr Ala Pro Ala Pro Glu Phe Thr Ala
225 230 235 240

Thr Gln Pro Glu Val Ala Asp Trp Ser Glu Gly Val Gln Val Pro Ser
245 250 255

Val Pro Ile Gln Gln Phe Pro Thr Glu Asp Trp Ser Ala Gln Pro Ala
260 265 270

Thr Glu Asp Trp Ser Ala Ala Pro Thr Ala Gln Ala Thr Glu Trp Val
275 280 285

Gly Ala Thr Thr Asp Trp Ser
290 295

<210> 619

<211> 866

<212> PRT

<213> Artificial Sequence

<220>

<223> RU1__Homo_sapiens__Q9UHH3

<400> 619

Met Asn Gly Glu Gln Gln Leu Asp Ala Asp Ala Gly Ser Gly Met Glu

ITI-08-PCT_Sequence_Listing_ST25.txt

```

1           5           10           15
Glu Val Glu Leu Ser Trp Glu Asp Tyr Leu Glu Glu Thr Gly Ser Thr
      20                25                30
Ala Val Pro Tyr Gly Ser Phe Lys His Val Asp Thr Arg Leu Gln Asn
      35                40                45
Gly Phe Ala Pro Gly Met Lys Leu Glu Val Ala Val Arg Thr Asp Pro
      50                55                60
Glu Thr Tyr Trp Val Ala Thr Val Ile Thr Thr Cys Glu Gln Leu Leu
65                70                75                80
Leu Leu Arg Tyr Asp Gly Tyr Gly Glu Asp Arg Arg Ala Asp Phe Trp
      85                90                95
Cys Asp Ile Arg Lys Ala Asp Leu Tyr Pro Ile Gly Trp Cys Glu Gln
      100               105               110
Asn Lys Lys Thr Leu Glu Ala Pro Glu Gly Ile Arg Asp Lys Val Ser
      115               120               125
Asp Trp Asp Glu Phe Leu Arg Gln Thr Leu Ile Gly Ala Cys Ser Pro
      130               135               140
Pro Val Pro Leu Leu Glu Gly Leu Arg Asn Gly Arg Asn Pro Leu Asp
145                150                155                160
Leu Ile Ala Pro Gly Ser Arg Leu Glu Cys Gln Ala Phe Gln Asp Ser
      165               170               175
Leu Ser Thr Trp Ile Val Thr Val Val Glu Asn Ile Gly Gly Arg Leu
      180               185               190
Lys Leu Arg Tyr Glu Gly Leu Glu Ser Ser Asp Asn Tyr Glu His Trp
      195               200               205
Leu Tyr Tyr Leu Asp Pro Phe Leu His His Val Gly Trp Ala Ala Gln
      210               215               220
Gln Gly Tyr Glu Leu Gln Pro Pro Ser Ala Ile Arg His Leu Lys Asn
225                230                235                240
Glu Ala Glu Trp Gln Glu Ile Leu Ala Lys Val Lys Glu Glu Glu Glu
      245                250                255
Glu Pro Leu Pro Ser Tyr Leu Phe Lys Asp Lys Gln Val Ile Gly Ile
      260               265               270
His Thr Phe Ser Val Asn Met Lys Leu Glu Ala Val Asp Pro Trp Ser
      275               280               285

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Pro	Phe	Gly	Ile	Ser	Pro	Ala	Thr	Val	Val	Lys	Val	Phe	Asp	Glu	Lys	290	295	300	
Tyr	Phe	Leu	Val	Glu	Met	Asp	Asp	Leu	Arg	Pro	Glu	Asn	His	Ala	Arg	305	310	315	320
Arg	Ser	Phe	Val	Cys	His	Ala	Asp	Ser	Pro	Gly	Ile	Phe	Pro	Val	Gln	325	330	335	
Trp	Ser	Leu	Lys	Asn	Gly	Leu	His	Ile	Ser	Pro	Pro	Pro	Gly	Tyr	Pro	340	345	350	
Ser	Gln	Asp	Phe	Asp	Trp	Ala	Asp	Tyr	Leu	Lys	Gln	Cys	Gly	Ala	Glu	355	360	365	
Ala	Ala	Pro	Gln	Arg	Cys	Phe	Pro	Pro	Leu	Ile	Ser	Glu	His	Glu	Phe	370	375	380	
Lys	Glu	Asn	Met	Lys	Leu	Glu	Ala	Val	Asn	Pro	Ile	Leu	Pro	Glu	Glu	385	390	395	400
Val	Cys	Val	Ala	Thr	Ile	Thr	Ala	Val	Arg	Gly	Ser	Tyr	Leu	Trp	Leu	405	410	415	
Gln	Leu	Glu	Gly	Ser	Lys	Lys	Pro	Ile	Pro	Glu	Cys	Ile	Val	Ser	Val	420	425	430	
Glu	Ser	Met	Asp	Ile	Phe	Pro	Leu	Gly	Trp	Cys	Glu	Thr	Asn	Gly	His	435	440	445	
Pro	Leu	Ser	Thr	Pro	Arg	Arg	Ala	Arg	Val	Tyr	Lys	Gln	Arg	Lys	Ile	450	455	460	
Ala	Val	Val	Gln	Pro	Glu	Lys	Gln	Val	Pro	Ser	Ser	Arg	Thr	Val	His	465	470	475	480
Glu	Gly	Leu	Arg	Asn	Gln	Glu	Leu	Asn	Ser	Thr	Glu	Ser	Val	Met	Ile	485	490	495	
Asn	Gly	Lys	Tyr	Cys	Cys	Pro	Lys	Ile	Tyr	Phe	Asn	His	Arg	Cys	Phe	500	505	510	
Ser	Gly	Pro	Tyr	Leu	Asn	Lys	Gly	Arg	Ile	Ala	Glu	Leu	Pro	Gln	Cys	515	520	525	
Val	Gly	Pro	Gly	Asn	Cys	Val	Leu	Val	Leu	Arg	Glu	Val	Leu	Thr	Leu	530	535	540	
Leu	Ile	Asn	Ala	Ala	Tyr	Lys	Pro	Ser	Arg	Val	Leu	Arg	Glu	Leu	Gln	545	550	555	560

ITI-08-PCT_Sequence_Listing_ST25.txt

Leu Asp Lys Asp Ser Val Trp His Gly Cys Gly Glu Val Leu Lys Ala
 565 570 575
 Lys Tyr Lys Gly Lys Ser Tyr Arg Ala Thr Val Glu Ile Val Lys Thr
 580 585 590
 Ala Asp Arg Val Thr Glu Phe Cys Arg Gln Thr Cys Ile Lys Leu Glu
 595 600 605
 Cys Cys Pro Asn Leu Phe Gly Pro Arg Met Val Leu Asp Lys Cys Ser
 610 615 620
 Glu Asn Cys Ser Val Leu Thr Lys Thr Lys Tyr Thr His Tyr Tyr Gly
 625 630 635 640
 Lys Lys Lys Asn Lys Arg Ile Gly Arg Pro Pro Gly Gly His Ser Asn
 645 650 655
 Leu Ala Cys Ala Leu Lys Lys Ala Ser Lys Arg Arg Lys Arg Arg Lys
 660 665 670
 Asn Val Phe Val His Lys Lys Lys Arg Ser Ser Ala Ser Val Asp Asn
 675 680 685
 Thr Pro Ala Gly Ser Pro Gln Gly Ser Gly Gly Glu Asp Glu Asp Asp
 690 695 700
 Pro Asp Glu Gly Asp Asp Asp Ser Leu Ser Glu Gly Ser Thr Ser Glu
 705 710 715 720
 Gln Gln Asp Glu Leu Gln Glu Glu Ser Glu Met Ser Glu Lys Lys Ser
 725 730 735
 Cys Ser Ser Ser Pro Thr Gln Ser Glu Ile Ser Thr Ser Leu Pro Pro
 740 745 750
 Asp Arg Gln Arg Arg Lys Arg Glu Leu Arg Thr Phe Ser Phe Ser Asp
 755 760 765
 Asp Glu Asn Lys Pro Pro Ser Pro Lys Glu Ile Arg Ile Glu Val Ala
 770 775 780
 Glu Arg Leu His Leu Asp Ser Asn Pro Leu Lys Trp Ser Val Ala Asp
 785 790 795 800
 Val Val Arg Phe Ile Arg Ser Thr Asp Cys Ala Pro Leu Ala Arg Ile
 805 810 815
 Phe Leu Asp Gln Glu Ile Asp Gly Gln Ala Leu Leu Leu Leu Thr Leu
 820 825 830
 Pro Thr Val Gln Glu Cys Met Asp Leu Lys Leu Gly Pro Ala Ile Lys

ITI-08-PCT_Sequence_Listing_ST25.txt

835

840

845

Leu Cys His His Ile Glu Arg Ile Lys Phe Ala Phe Tyr Glu Gln Phe
850 855 860

Ala Asn
865

<210> 620
<211> 476
<212> PRT
<213> Artificial Sequence

<220>
<223> RU2__Homo_sapiens__Q9UHG0

<400> 620

Met Ser Gly Ser Ser Ala Arg Ser Ser His Leu Ser Gln Pro Val Val
1 5 10 15

Lys Ser Val Leu Val Tyr Arg Asn Gly Asp Pro Phe Tyr Ala Gly Arg
20 25 30

Arg Val Val Ile His Glu Lys Lys Val Ser Ser Phe Glu Val Phe Leu
35 40 45

Lys Glu Val Thr Gly Gly Val Gln Ala Pro Phe Gly Ala Val Arg Asn
50 55 60

Ile Tyr Thr Pro Arg Thr Gly His Arg Ile Arg Lys Leu Asp Gln Ile
65 70 75 80

Gln Ser Gly Gly Asn Tyr Val Ala Gly Gly Gln Glu Ala Phe Lys Lys
85 90 95

Leu Asn Tyr Leu Asp Ile Gly Glu Ile Lys Lys Arg Pro Met Glu Val
100 105 110

Val Asn Thr Glu Val Lys Pro Val Ile His Ser Arg Ile Asn Val Ser
115 120 125

Ala Arg Phe Arg Lys Pro Leu Gln Glu Pro Cys Thr Ile Phe Leu Ile
130 135 140

Ala Asn Gly Asp Leu Ile Asn Pro Ala Ser Arg Leu Leu Ile Pro Arg
145 150 155 160

Lys Thr Leu Asn Gln Trp Asp His Val Leu Gln Met Val Thr Glu Lys
165 170 175

Ile Thr Leu Arg Ser Gly Ala Val His Arg Leu Tyr Thr Leu Glu Gly

ITI-08-PCT_Sequence_Listing_ST25.txt

180	185	190															
Lys	Leu	Val	Glu	Ser	Gly	Ala	Glu	Leu	Glu	Asn	Gly	Gln	Phe	Tyr	Val		
	195						200					205					
Ala	Val	Gly	Arg	Asp	Lys	Phe	Lys	Lys	Leu	Pro	Tyr	Ser	Glu	Leu	Leu		
	210					215					220						
Phe	Asp	Lys	Ser	Thr	Met	Arg	Arg	Pro	Phe	Gly	Gln	Lys	Ala	Ser	Ser		
225					230					235					240		
Leu	Pro	Pro	Ile	Val	Gly	Ser	Arg	Lys	Ser	Lys	Gly	Ser	Gly	Asn	Asp		
			245						250					255			
Arg	His	Ser	Lys	Ser	Thr	Val	Gly	Ser	Ser	Asp	Asn	Ser	Ser	Pro	Gln		
			260					265					270				
Pro	Leu	Lys	Arg	Lys	Gly	Lys	Lys	Glu	Asp	Val	Asn	Ser	Glu	Lys	Leu		
		275					280					285					
Thr	Lys	Leu	Lys	Gln	Asn	Val	Lys	Leu	Lys	Asn	Ser	Gln	Glu	Thr	Ile		
	290					295					300						
Pro	Asn	Ser	Asp	Glu	Gly	Ile	Phe	Lys	Ala	Gly	Ala	Glu	Arg	Ser	Glu		
305					310					315					320		
Thr	Arg	Gly	Ala	Ala	Glu	Val	Gln	Glu	Asp	Glu	Asp	Thr	Gln	Val	Glu		
			325						330					335			
Val	Pro	Val	Asp	Gln	Arg	Pro	Ala	Glu	Ile	Val	Asp	Glu	Glu	Glu	Asp		
			340					345					350				
Gly	Glu	Lys	Ala	Asn	Lys	Asp	Ala	Glu	Gln	Lys	Glu	Asp	Phe	Ser	Gly		
		355					360					365					
Met	Asn	Gly	Asp	Leu	Glu	Glu	Glu	Gly	Gly	Arg	Glu	Ala	Thr	Asp	Ala		
	370					375					380						
Pro	Glu	Gln	Val	Glu	Glu	Ile	Leu	Asp	His	Ser	Glu	Gln	Gln	Ala	Arg		
385					390					395					400		
Pro	Ala	Arg	Val	Asn	Gly	Gly	Thr	Asp	Glu	Glu	Asn	Gly	Glu	Glu	Leu		
				405					410					415			
Gln	Gln	Val	Asn	Asn	Glu	Leu	Gln	Leu	Val	Leu	Asp	Lys	Glu	Arg	Lys		
			420					425					430				
Ser	Gln	Gly	Ala	Gly	Ser	Gly	Gln	Asp	Glu	Ala	Asp	Val	Asp	Pro	Gln		
		435					440					445					
Arg	Pro	Pro	Arg	Pro	Glu	Val	Lys	Ile	Thr	Ser	Pro	Glu	Glu	Asn	Glu		
	450					455					460						

ITI-08-PCT_Sequence_Listing_ST25.txt

Asn Asn Gln Gln Asn Lys Asp Tyr Ala Ala Val Ala
465 470 475

<210> 621
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> RUNX1__Homo_sapiens__Q01196

<400> 621

Met Arg Ile Pro Val Asp Ala Ser Thr Ser Arg Arg Phe Thr Pro Pro
1 5 10 15

Ser Thr Ala Leu Ser Pro Gly Lys Met Ser Glu Ala Leu Pro Leu Gly
20 25 30

Ala Pro Asp Ala Gly Ala Ala Leu Ala Gly Lys Leu Arg Ser Gly Asp
35 40 45

Arg Ser Met Val Glu Val Leu Ala Asp His Pro Gly Glu Leu Val Arg
50 55 60

Thr Asp Ser Pro Asn Phe Leu Cys Ser Val Leu Pro Thr His Trp Arg
65 70 75 80

Cys Asn Lys Thr Leu Pro Ile Ala Phe Lys Val Val Ala Leu Gly Asp
85 90 95

Val Pro Asp Gly Thr Leu Val Thr Val Met Ala Gly Asn Asp Glu Asn
100 105 110

Tyr Ser Ala Glu Leu Arg Asn Ala Thr Ala Ala Met Lys Asn Gln Val
115 120 125

Ala Arg Phe Asn Asp Leu Arg Phe Val Gly Arg Ser Gly Arg Gly Lys
130 135 140

Ser Phe Thr Leu Thr Ile Thr Val Phe Thr Asn Pro Pro Gln Val Ala
145 150 155 160

Thr Tyr His Arg Ala Ile Lys Ile Thr Val Asp Gly Pro Arg Glu Pro
165 170 175

Arg Arg His Arg Gln Lys Leu Asp Asp Gln Thr Lys Pro Gly Ser Leu
180 185 190

Ser Phe Ser Glu Arg Leu Ser Glu Leu Glu Gln Leu Arg Arg Thr Ala
195 200 205

ITI-08-PCT_Sequence_Listing_ST25.txt

```

Met Arg Val Ser Pro His His Pro Ala Pro Thr Pro Asn Pro Arg Ala
 210                215                220

Ser Leu Asn His Ser Thr Ala Phe Asn Pro Gln Pro Gln Ser Gln Met
225                230                235                240

Gln Asp Thr Arg Gln Ile Gln Pro Ser Pro Pro Trp Ser Tyr Asp Gln
                245                250                255

Ser Tyr Gln Tyr Leu Gly Ser Ile Ala Ser Pro Ser Val His Pro Ala
                260                265                270

Thr Pro Ile Ser Pro Gly Arg Ala Ser Gly Met Thr Thr Leu Ser Ala
                275                280                285

Glu Leu Ser Ser Arg Leu Ser Thr Ala Pro Asp Leu Thr Ala Phe Ser
290                295                300

Asp Pro Arg Gln Phe Pro Ala Leu Pro Ser Ile Ser Asp Pro Arg Met
305                310                315                320

His Tyr Pro Gly Ala Phe Thr Tyr Ser Pro Thr Pro Val Thr Ser Gly
                325                330                335

Ile Gly Ile Gly Met Ser Ala Met Gly Ser Ala Thr Arg Tyr His Thr
                340                345                350

Tyr Leu Pro Pro Pro Tyr Pro Gly Ser Ser Gln Ala Gln Gly Gly Pro
                355                360                365

Phe Gln Ala Ser Ser Pro Ser Tyr His Leu Tyr Tyr Gly Ala Ser Ala
370                375                380

Gly Ser Tyr Gln Phe Ser Met Val Gly Gly Glu Arg Ser Pro Pro Arg
385                390                395                400

Ile Leu Pro Pro Cys Thr Asn Ala Ser Thr Gly Ser Ala Leu Leu Asn
                405                410                415

Pro Ser Leu Pro Asn Gln Ser Asp Val Val Glu Ala Glu Gly Ser His
                420                425                430

Ser Asn Ser Pro Thr Asn Met Ala Pro Ser Ala Arg Leu Glu Glu Ala
435                440                445

Val Trp Arg Pro Tyr
450

```

<210> 622

<211> 359

<212> PRT

ITI-08-PCT_Sequence_Listing_ST25.txt

<213> Artificial Sequence

<220>

<223> S-100__Homo_sapiens__V9HW39

<400> 622

Met Pro Leu Glu Leu Glu Leu Cys Pro Gly Arg Trp Val Gly Gly Gln
1 5 10 15

His Pro Cys Phe Ile Ile Ala Glu Ile Gly Gln Asn His Gln Gly Asp
20 25 30

Leu Asp Val Ala Lys Arg Met Ile Arg Met Ala Lys Glu Cys Gly Ala
35 40 45

Asp Cys Ala Lys Phe Gln Lys Ser Glu Leu Glu Phe Lys Phe Asn Arg
50 55 60

Lys Ala Leu Glu Arg Pro Tyr Thr Ser Lys His Ser Trp Gly Lys Thr
65 70 75 80

Tyr Gly Glu His Lys Arg His Leu Glu Phe Ser His Asp Gln Tyr Arg
85 90 95

Glu Leu Gln Arg Tyr Ala Glu Glu Val Gly Ile Phe Phe Thr Ala Ser
100 105 110

Gly Met Asp Glu Met Ala Val Glu Phe Leu His Glu Leu Asn Val Pro
115 120 125

Phe Phe Lys Val Gly Ser Gly Asp Thr Asn Asn Phe Pro Tyr Leu Glu
130 135 140

Lys Thr Ala Lys Lys Gly Arg Pro Met Val Ile Ser Ser Gly Met Gln
145 150 155 160

Ser Met Asp Thr Met Lys Gln Val Tyr Gln Ile Val Lys Pro Leu Asn
165 170 175

Pro Asn Phe Cys Phe Leu Gln Cys Thr Ser Ala Tyr Pro Leu Gln Pro
180 185 190

Glu Asp Val Asn Leu Arg Val Ile Ser Glu Tyr Gln Lys Leu Phe Pro
195 200 205

Asp Ile Pro Ile Gly Tyr Ser Gly His Glu Thr Gly Ile Ala Ile Ser
210 215 220

Val Ala Ala Val Ala Leu Gly Ala Lys Val Leu Glu Arg His Ile Thr
225 230 235 240

ITI-08-PCT_Sequence_Listing_ST25.txt

Leu Asp Lys Thr Trp Lys Gly Ser Asp His Ser Ala Ser Leu Glu Pro
245 250 255

Gly Glu Leu Ala Glu Leu Val Arg Ser Val Arg Leu Val Glu Arg Ala
260 265 270

Leu Gly Ser Pro Thr Lys Gln Leu Leu Pro Cys Glu Met Ala Cys Asn
275 280 285

Glu Lys Leu Gly Lys Ser Val Val Ala Lys Val Lys Ile Pro Glu Gly
290 295 300

Thr Ile Leu Thr Met Asp Met Leu Thr Val Lys Val Gly Glu Pro Lys
305 310 315 320

Ala Tyr Pro Pro Glu Asp Ile Phe Asn Leu Val Gly Lys Lys Val Leu
325 330 335

Val Thr Val Glu Glu Asp Asp Thr Ile Met Glu Glu Leu Val Asp Asn
340 345 350

His Gly Lys Lys Ile Lys Ser
355

<210> 623

<211> 904

<212> PRT

<213> Artificial Sequence

<220>

<223> SAGE__Homo_sapiens__Q9NXZ1

<400> 623

Met Gln Ala Ser Pro Leu Gln Thr Ser Gln Pro Thr Pro Pro Glu Glu
1 5 10 15

Leu His Ala Ala Ala Tyr Val Phe Thr Asn Asp Gly Gln Gln Met Arg
20 25 30

Ser Asp Glu Val Asn Leu Val Ala Thr Gly His Gln Ser Lys Lys Lys
35 40 45

His Ser Arg Lys Ser Lys Arg His Ser Ser Ser Lys Arg Arg Lys Ser
50 55 60

Met Ser Ser Trp Leu Asp Lys Gln Glu Asp Ala Ala Val Thr His Ser
65 70 75 80

Ile Cys Glu Glu Arg Ile Asn Asn Gly Gln Pro Val Ala Asp Asn Val
85 90 95

ITI-08-PCT_Sequence_Listing_ST25.txt

```

Leu Ser Thr Ala Pro Pro Trp Pro Asp Ala Thr Ile Ala His Asn Ile
    100                      105                      110

Arg Glu Glu Arg Met Glu Asn Gly Gln Ser Arg Thr Asp Lys Val Leu
    115                      120                      125

Ser Thr Ala Pro Pro Gln Leu Val His Met Ala Ala Ala Gly Ile Pro
    130                      135                      140

Ser Met Ser Thr Arg Asp Leu His Ser Thr Val Thr His Asn Ile Arg
    145                      150                      155                      160

Glu Glu Arg Met Glu Asn Gly Gln Pro Gln Pro Asp Asn Val Leu Ser
    165                      170                      175

Thr Gly Pro Thr Gly Leu Ile Asn Met Ala Ala Thr Pro Ile Pro Ala
    180                      185                      190

Met Ser Ala Arg Asp Leu Tyr Ala Thr Val Thr His Asn Val Cys Glu
    195                      200                      205

Gln Lys Met Glu Asn Val Gln Pro Ala Pro Asp Asn Val Leu Leu Thr
    210                      215                      220

Leu Arg Pro Arg Arg Ile Asn Met Thr Asp Thr Gly Ile Ser Pro Met
    225                      230                      235                      240

Ser Thr Arg Asp Pro Tyr Ala Thr Ile Thr Tyr Asn Val Pro Glu Glu
    245                      250                      255

Lys Met Glu Lys Gly Gln Pro Gln Pro Asp Asn Ile Leu Ser Thr Ala
    260                      265                      270

Ser Thr Gly Leu Ile Asn Val Ala Gly Ala Gly Thr Pro Ala Ile Ser
    275                      280                      285

Thr Asn Gly Leu Tyr Ser Thr Val Pro His Asn Val Cys Glu Glu Lys
    290                      295                      300

Met Glu Asn Asp Gln Pro Gln Pro Asn Asn Val Leu Ser Thr Val Gln
    305                      310                      315                      320

Pro Val Ile Ile Tyr Leu Thr Ala Thr Gly Ile Pro Gly Met Asn Thr
    325                      330                      335

Arg Asp Gln Tyr Ala Thr Ile Thr His Asn Val Cys Glu Glu Arg Val
    340                      345                      350

Val Asn Asn Gln Pro Leu Pro Ser Asn Ala Leu Ser Thr Val Leu Pro
    355                      360                      365

Gly Leu Ala Tyr Leu Ala Thr Ala Asp Met Pro Ala Met Ser Thr Arg

```

ITI-08-PCT_Sequence_Listing_ST25.txt

```

370          375          380
Asp Gln His Ala Thr Ile Ile His Asn Leu Arg Glu Glu Lys Lys Asp
385          390          395          400

Asn Ser Gln Pro Thr Pro Asp Asn Val Leu Ser Ala Val Thr Pro Glu
          405          410          415

Leu Ile Asn Leu Ala Gly Ala Gly Ile Pro Pro Met Ser Thr Arg Asp
          420          425          430

Gln Tyr Ala Thr Val Asn His His Val His Glu Ala Arg Met Glu Asn
          435          440          445

Gly Gln Arg Lys Gln Asp Asn Val Leu Ser Asn Val Leu Ser Gly Leu
          450          455          460

Ile Asn Met Ala Gly Ala Ser Ile Pro Ala Met Ser Ser Arg Asp Leu
465          470          475          480

Tyr Ala Thr Ile Thr His Ser Val Arg Glu Glu Lys Met Glu Ser Gly
          485          490          495

Lys Pro Gln Thr Asp Lys Val Ile Ser Asn Asp Ala Pro Gln Leu Gly
          500          505          510

His Met Ala Ala Gly Gly Ile Pro Ser Met Ser Thr Lys Asp Leu Tyr
          515          520          525

Ala Thr Val Thr Gln Asn Val His Glu Glu Arg Met Glu Asn Asn Gln
          530          535          540

Pro Gln Pro Ser Tyr Asp Leu Ser Thr Val Leu Pro Gly Leu Thr Tyr
545          550          555          560

Leu Thr Val Ala Gly Ile Pro Ala Met Ser Thr Arg Asp Gln Tyr Ala
          565          570          575

Thr Val Thr His Asn Val His Glu Glu Lys Ile Lys Asn Gly Gln Ala
          580          585          590

Ala Ser Asp Asn Val Phe Ser Thr Val Pro Pro Ala Phe Ile Asn Met
          595          600          605

Ala Ala Thr Gly Val Ser Ser Met Ser Thr Arg Asp Gln Tyr Ala Ala
          610          615          620

Val Thr His Asn Ile Arg Glu Glu Lys Ile Asn Asn Ser Gln Pro Ala
625          630          635          640

Pro Gly Asn Ile Leu Ser Thr Ala Pro Pro Trp Leu Arg His Met Ala
          645          650          655

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Ala Ala Gly Ile Ser Ser Thr Ile Thr Arg Asp Leu Tyr Val Thr Ala
660 665 670

Thr His Ser Val His Glu Glu Lys Met Thr Asn Gly Gln Gln Ala Pro
675 680 685

Asp Asn Ser Leu Ser Thr Val Pro Pro Gly Cys Ile Asn Leu Ser Gly
690 695 700

Ala Gly Ile Ser Cys Arg Ser Thr Arg Asp Leu Tyr Ala Thr Val Ile
705 710 715 720

His Asp Ile Gln Glu Glu Glu Met Glu Asn Asp Gln Thr Pro Pro Asp
725 730 735

Gly Phe Leu Ser Asn Ser Asp Ser Pro Glu Leu Ile Asn Met Thr Gly
740 745 750

His Cys Met Pro Pro Asn Ala Leu Asp Ser Phe Ser His Asp Phe Thr
755 760 765

Ser Leu Ser Lys Asp Glu Leu Leu Tyr Lys Pro Asp Ser Asn Glu Phe
770 775 780

Ala Val Gly Thr Lys Asn Tyr Ser Val Ser Ala Gly Asp Pro Pro Val
785 790 795 800

Thr Val Met Ser Leu Val Glu Thr Val Pro Asn Thr Pro Gln Ile Ser
805 810 815

Pro Ala Met Ala Lys Lys Ile Asn Asp Asp Ile Lys Tyr Gln Leu Met
820 825 830

Lys Glu Val Arg Arg Phe Gly Gln Asn Tyr Glu Arg Ile Phe Ile Leu
835 840 845

Leu Glu Glu Val Gln Gly Ser Met Lys Val Lys Arg Gln Phe Val Glu
850 855 860

Phe Thr Ile Lys Glu Ala Ala Arg Phe Lys Lys Val Val Leu Ile Gln
865 870 875 880

Gln Leu Glu Lys Ala Leu Lys Glu Ile Asp Ser His Cys His Leu Arg
885 890 895

Lys Val Lys His Met Arg Lys Arg
900

<210> 624

<211> 800

<212> PRT

ITI-08-PCT_Sequence_Listing_ST25.txt

<213> Artificial Sequence

<220>

<223> SART-_1__Homo_sapiens__043290

<400> 624

```

Met Gly Ser Ser Lys Lys His Arg Gly Glu Lys Glu Ala Ala Gly Thr
1          5          10          15

Thr Ala Ala Ala Gly Thr Gly Gly Ala Thr Glu Gln Pro Pro Arg His
          20          25          30

Arg Glu His Lys Lys His Lys His Arg Ser Gly Gly Ser Gly Gly Ser
          35          40          45

Gly Gly Glu Arg Arg Lys Arg Ser Arg Glu Arg Gly Gly Glu Arg Gly
50          55          60

Ser Gly Arg Arg Gly Ala Glu Ala Glu Ala Arg Ser Ser Thr His Gly
65          70          75          80

Arg Glu Arg Ser Gln Ala Glu Pro Ser Glu Arg Arg Val Lys Arg Glu
          85          90          95

Lys Arg Asp Asp Gly Tyr Glu Ala Ala Ala Ser Ser Lys Thr Ser Ser
          100          105          110

Gly Asp Ala Ser Ser Leu Ser Ile Glu Glu Thr Asn Lys Leu Arg Ala
          115          120          125

Lys Leu Gly Leu Lys Pro Leu Glu Val Asn Ala Ile Lys Lys Glu Ala
          130          135          140

Gly Thr Lys Glu Glu Pro Val Thr Ala Asp Val Ile Asn Pro Met Ala
          145          150          155          160

Leu Arg Gln Arg Glu Glu Leu Arg Glu Lys Leu Ala Ala Ala Lys Glu
          165          170          175

Lys Arg Leu Leu Asn Gln Lys Leu Gly Lys Ile Lys Thr Leu Gly Glu
          180          185          190

Asp Asp Pro Trp Leu Asp Asp Thr Ala Ala Trp Ile Glu Arg Ser Arg
          195          200          205

Gln Leu Gln Lys Glu Lys Asp Leu Ala Glu Lys Arg Ala Lys Leu Leu
          210          215          220

Glu Glu Met Asp Gln Glu Phe Gly Val Ser Thr Leu Val Glu Glu Glu
          225          230          235          240

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Phe Gly Gln Arg Arg Gln Asp Leu Tyr Ser Ala Arg Asp Leu Gln Gly
 245 250 255
 Leu Thr Val Glu His Ala Ile Asp Ser Phe Arg Glu Gly Glu Thr Met
 260 265 270
 Ile Leu Thr Leu Lys Asp Lys Gly Val Leu Gln Glu Glu Glu Asp Val
 275 280 285
 Leu Val Asn Val Asn Leu Val Asp Lys Glu Arg Ala Glu Lys Asn Val
 290 295 300
 Glu Leu Arg Lys Lys Lys Pro Asp Tyr Leu Pro Tyr Ala Glu Asp Glu
 305 310 315 320
 Ser Val Asp Asp Leu Ala Gln Gln Lys Pro Arg Ser Ile Leu Ser Lys
 325 330 335
 Tyr Asp Glu Glu Leu Glu Gly Glu Arg Pro His Ser Phe Arg Leu Glu
 340 345 350
 Gln Gly Gly Thr Ala Asp Gly Leu Arg Glu Arg Glu Leu Glu Glu Ile
 355 360 365
 Arg Ala Lys Leu Arg Leu Gln Ala Gln Ser Leu Ser Thr Val Gly Pro
 370 375 380
 Arg Leu Ala Ser Glu Tyr Leu Thr Pro Glu Glu Met Val Thr Phe Lys
 385 390 395 400
 Lys Thr Lys Arg Arg Val Lys Lys Ile Arg Lys Lys Glu Lys Glu Val
 405 410 415
 Val Val Arg Ala Asp Asp Leu Leu Pro Leu Gly Asp Gln Thr Gln Asp
 420 425 430
 Gly Asp Phe Gly Ser Arg Leu Arg Gly Arg Gly Arg Arg Arg Val Ser
 435 440 445
 Glu Val Glu Glu Glu Lys Glu Pro Val Pro Gln Pro Leu Pro Ser Asp
 450 455 460
 Asp Thr Arg Val Glu Asn Met Asp Ile Ser Asp Glu Glu Glu Gly Gly
 465 470 475 480
 Ala Pro Pro Pro Gly Ser Pro Gln Val Leu Glu Glu Asp Glu Ala Glu
 485 490 495
 Leu Glu Leu Gln Lys Gln Leu Glu Lys Gly Arg Arg Leu Arg Gln Leu
 500 505 510
 Gln Gln Leu Gln Gln Leu Arg Asp Ser Gly Glu Lys Val Val Glu Ile

ITI-08-PCT_Sequence_Listing_ST25.txt

```

515                               520                               525
Val Lys Lys Leu Glu Ser Arg Gln Arg Gly Trp Glu Glu Asp Glu Asp
530                               535                               540

Pro Glu Arg Lys Gly Ala Ile Val Phe Asn Ala Thr Ser Glu Phe Cys
545                               550                               555                               560

Arg Thr Leu Gly Glu Ile Pro Thr Tyr Gly Leu Ala Gly Asn Arg Glu
565                               570                               575

Glu Gln Glu Glu Leu Met Asp Phe Glu Arg Asp Glu Glu Arg Ser Ala
580                               585                               590

Asn Gly Gly Ser Glu Ser Asp Gly Glu Glu Asn Ile Gly Trp Ser Thr
595                               600                               605

Val Asn Leu Asp Glu Glu Lys Gln Gln Gln Asp Phe Ser Ala Ser Ser
610                               615                               620

Thr Thr Ile Leu Asp Glu Glu Pro Ile Val Asn Arg Gly Leu Ala Ala
625                               630                               635                               640

Ala Leu Leu Leu Cys Gln Asn Lys Gly Leu Leu Glu Thr Thr Val Gln
645                               650                               655

Lys Val Ala Arg Val Lys Ala Pro Asn Lys Ser Leu Pro Ser Ala Val
660                               665                               670

Tyr Cys Ile Glu Asp Lys Met Ala Ile Asp Asp Lys Tyr Ser Arg Arg
675                               680                               685

Glu Glu Tyr Arg Gly Phe Thr Gln Asp Phe Lys Glu Lys Asp Gly Tyr
690                               695                               700

Lys Pro Asp Val Lys Ile Glu Tyr Val Asp Glu Thr Gly Arg Lys Leu
705                               710                               715                               720

Thr Pro Lys Glu Ala Phe Arg Gln Leu Ser His Arg Phe His Gly Lys
725                               730                               735

Gly Ser Gly Lys Met Lys Thr Glu Arg Arg Met Lys Lys Leu Asp Glu
740                               745                               750

Glu Ala Leu Leu Lys Lys Met Ser Ser Ser Asp Thr Pro Leu Gly Thr
755                               760                               765

Val Ala Leu Leu Gln Glu Lys Gln Lys Ala Gln Lys Thr Pro Tyr Ile
770                               775                               780

Val Leu Ser Gly Ser Gly Lys Ser Met Asn Ala Asn Thr Ile Thr Lys
785                               790                               795                               800

```


ITI-08-PCT_Sequence_Listing_ST25.txt

```

<210> 625
<211> 958
<212> PRT
<213> Artificial Sequence

<220>
<223> SART-2__Homo_sapiens__Q9UL01

<400> 625

Met Arg Thr His Thr Arg Gly Ala Pro Ser Val Phe Phe Ile Tyr Leu
1          5          10          15

Leu Cys Phe Val Ser Ala Tyr Ile Thr Asp Glu Asn Pro Glu Val Met
          20          25          30

Ile Pro Phe Thr Asn Ala Asn Tyr Asp Ser His Pro Met Leu Tyr Phe
          35          40          45

Ser Arg Ala Glu Val Ala Glu Leu Gln Leu Arg Ala Ala Ser Ser His
          50          55          60

Glu His Ile Ala Ala Arg Leu Thr Glu Ala Val His Thr Met Leu Ser
65          70          75          80

Ser Pro Leu Glu Tyr Leu Pro Pro Trp Asp Pro Lys Asp Tyr Ser Ala
          85          90          95

Arg Trp Asn Glu Ile Phe Gly Asn Asn Leu Gly Ala Leu Ala Met Phe
          100          105          110

Cys Val Leu Tyr Pro Glu Asn Ile Glu Ala Arg Asp Met Ala Lys Asp
          115          120          125

Tyr Met Glu Arg Met Ala Ala Gln Pro Ser Trp Leu Val Lys Asp Ala
          130          135          140

Pro Trp Asp Glu Val Pro Leu Ala His Ser Leu Val Gly Phe Ala Thr
145          150          155          160

Ala Tyr Asp Phe Leu Tyr Asn Tyr Leu Ser Lys Thr Gln Gln Glu Lys
          165          170          175

Phe Leu Glu Val Ile Ala Asn Ala Ser Gly Tyr Met Tyr Glu Thr Ser
          180          185          190

Tyr Arg Arg Gly Trp Gly Phe Gln Tyr Leu His Asn His Gln Pro Thr
          195          200          205

Asn Cys Met Ala Leu Leu Thr Gly Ser Leu Val Leu Met Asn Gln Gly
          210          215          220

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Tyr	Leu	Gln	Glu	Ala	Tyr	Leu	Trp	Thr	Lys	Gln	Val	Leu	Thr	Ile	Met	225	230	235	240
Glu	Lys	Ser	Leu	Val	Leu	Leu	Arg	Glu	Val	Thr	Asp	Gly	Ser	Leu	Tyr	245	250	255	
Glu	Gly	Val	Ala	Tyr	Gly	Ser	Tyr	Thr	Thr	Arg	Ser	Leu	Phe	Gln	Tyr	260	265	270	
Met	Phe	Leu	Val	Gln	Arg	His	Phe	Asn	Ile	Asn	His	Phe	Gly	His	Pro	275	280	285	
Trp	Leu	Lys	Gln	His	Phe	Ala	Phe	Met	Tyr	Arg	Thr	Ile	Leu	Pro	Gly	290	295	300	
Phe	Gln	Arg	Thr	Val	Ala	Ile	Ala	Asp	Ser	Asn	Tyr	Asn	Trp	Phe	Tyr	305	310	315	320
Gly	Pro	Glu	Ser	Gln	Leu	Val	Phe	Leu	Asp	Lys	Phe	Val	Met	Arg	Asn	325	330	335	
Gly	Ser	Gly	Asn	Trp	Leu	Ala	Asp	Gln	Ile	Arg	Arg	Asn	Arg	Val	Val	340	345	350	
Glu	Gly	Pro	Gly	Thr	Pro	Ser	Lys	Gly	Gln	Arg	Trp	Cys	Thr	Leu	His	355	360	365	
Thr	Glu	Phe	Leu	Trp	Tyr	Asp	Gly	Ser	Leu	Lys	Ser	Val	Pro	Pro	Pro	370	375	380	
Asp	Phe	Gly	Thr	Pro	Thr	Leu	His	Tyr	Phe	Glu	Asp	Trp	Gly	Val	Val	385	390	395	400
Thr	Tyr	Gly	Ser	Ala	Leu	Pro	Ala	Glu	Ile	Asn	Arg	Ser	Phe	Leu	Ser	405	410	415	
Phe	Lys	Ser	Gly	Lys	Leu	Gly	Gly	Arg	Ala	Ile	Tyr	Asp	Ile	Val	His	420	425	430	
Arg	Asn	Lys	Tyr	Lys	Asp	Trp	Ile	Lys	Gly	Trp	Arg	Asn	Phe	Asn	Ala	435	440	445	
Gly	His	Glu	His	Pro	Asp	Gln	Asn	Ser	Phe	Thr	Phe	Ala	Pro	Asn	Gly	450	455	460	
Val	Pro	Phe	Ile	Thr	Glu	Ala	Leu	Tyr	Gly	Pro	Lys	Tyr	Thr	Phe	Phe	465	470	475	480
Asn	Asn	Val	Leu	Met	Phe	Ser	Pro	Ala	Val	Ser	Lys	Ser	Cys	Phe	Ser	485	490	495	

ITI-08-PCT_Sequence_Listing_ST25.txt

Pro Trp Val Gly Gln Val Thr Glu Asp Cys Ser Ser Lys Trp Ser Lys
500 505 510

Tyr Lys His Asp Leu Ala Ala Ser Cys Gln Gly Arg Val Val Ala Ala
515 520 525

Glu Glu Lys Asn Gly Val Val Phe Ile Arg Gly Glu Gly Val Gly Ala
530 535 540

Tyr Asn Pro Gln Leu Asn Leu Lys Asn Val Gln Arg Asn Leu Ile Leu
545 550 555 560

Leu His Pro Gln Leu Leu Leu Leu Val Asp Gln Ile His Leu Gly Glu
565 570 575

Glu Ser Pro Leu Glu Thr Ala Ala Ser Phe Phe His Asn Val Asp Val
580 585 590

Pro Phe Glu Glu Thr Val Val Asp Gly Val His Gly Ala Phe Ile Arg
595 600 605

Gln Arg Asp Gly Leu Tyr Lys Met Tyr Trp Met Asp Asp Thr Gly Tyr
610 615 620

Ser Glu Lys Ala Thr Phe Ala Ser Val Thr Tyr Pro Arg Gly Tyr Pro
625 630 635 640

Tyr Asn Gly Thr Asn Tyr Val Asn Val Thr Met His Leu Arg Ser Pro
645 650 655

Ile Thr Arg Ala Ala Tyr Leu Phe Ile Gly Pro Ser Ile Asp Val Gln
660 665 670

Ser Phe Thr Val His Gly Asp Ser Gln Gln Leu Asp Val Phe Ile Ala
675 680 685

Thr Ser Lys His Ala Tyr Ala Thr Tyr Leu Trp Thr Gly Glu Ala Thr
690 695 700

Gly Gln Ser Ala Phe Ala Gln Val Ile Ala Asp Arg His Lys Ile Leu
705 710 715 720

Phe Asp Arg Asn Ser Ala Ile Lys Ser Ser Ile Val Pro Glu Val Lys
725 730 735

Asp Tyr Ala Ala Ile Val Glu Gln Asn Leu Gln His Phe Lys Pro Val
740 745 750

Phe Gln Leu Leu Glu Lys Gln Ile Leu Ser Arg Val Arg Asn Thr Ala
755 760 765

Ser Phe Arg Lys Thr Ala Glu Arg Leu Leu Arg Phe Ser Asp Lys Arg

ITI-08-PCT_Sequence_Listing_ST25.txt

770

775

780

Gln Thr Glu Glu Ala Ile Asp Arg Ile Phe Ala Ile Ser Gln Gln Gln
785 790 795 800

Gln Gln Gln Ser Lys Ser Lys Lys Asn Arg Arg Ala Gly Lys Arg Tyr
805 810 815

Lys Phe Val Asp Ala Val Pro Asp Ile Phe Ala Gln Ile Glu Val Asn
820 825 830

Glu Lys Lys Ile Arg Gln Lys Ala Gln Ile Leu Ala Gln Lys Glu Leu
835 840 845

Pro Ile Asp Glu Asp Glu Glu Met Lys Asp Leu Leu Asp Phe Ala Asp
850 855 860

Val Thr Tyr Glu Lys His Lys Asn Gly Gly Leu Ile Lys Gly Arg Phe
865 870 875 880

Gly Gln Ala Arg Met Val Thr Thr Thr His Ser Arg Ala Pro Ser Leu
885 890 895

Ser Ala Ser Tyr Thr Arg Leu Phe Leu Ile Leu Asn Ile Ala Ile Phe
900 905 910

Phe Val Met Leu Ala Met Gln Leu Thr Tyr Phe Gln Arg Ala Gln Ser
915 920 925

Leu His Gly Gln Arg Cys Leu Tyr Ala Val Leu Leu Ile Asp Ser Cys
930 935 940

Ile Leu Leu Trp Leu Tyr Ser Ser Cys Ser Gln Ser Gln Cys
945 950 955

<210> 626

<211> 963

<212> PRT

<213> Artificial Sequence

<220>

<223> SART-3__Homo_sapiens__Q15020

<400> 626

Met Ala Thr Ala Ala Glu Thr Ser Ala Ser Glu Pro Glu Ala Glu Ser
1 5 10 15

Lys Ala Gly Pro Lys Ala Asp Gly Glu Glu Asp Glu Val Lys Ala Ala
20 25 30

Arg Thr Arg Arg Lys Val Leu Ser Arg Ala Val Ala Ala Ala Thr Tyr

35 40 45

Page 1074

ITI-08-PCT_Sequence_Listing_ST25.txt

```

Met Lys Ile Gly Asp Pro Ala Arg Ile Gln Leu Ile Phe Glu Arg Ala
    325                      330                      335

Leu Val Glu Asn Cys Leu Val Pro Asp Leu Trp Ile Arg Tyr Ser Gln
    340                      345                      350

Tyr Leu Asp Arg Gln Leu Lys Val Lys Asp Leu Val Leu Ser Val His
    355                      360                      365

Asn Arg Ala Ile Arg Asn Cys Pro Trp Thr Val Ala Leu Trp Ser Arg
    370                      375                      380

Tyr Leu Leu Ala Met Glu Arg His Gly Val Asp His Gln Val Ile Ser
385                      390                      395                      400

Val Thr Phe Glu Lys Ala Leu Asn Ala Gly Phe Ile Gln Ala Thr Asp
    405                      410                      415

Tyr Val Glu Ile Trp Gln Ala Tyr Leu Asp Tyr Leu Arg Arg Arg Val
    420                      425                      430

Asp Phe Lys Gln Asp Ser Ser Lys Glu Leu Glu Glu Leu Arg Ala Ala
    435                      440                      445

Phe Thr Arg Ala Leu Glu Tyr Leu Lys Gln Glu Val Glu Glu Arg Phe
    450                      455                      460

Asn Glu Ser Gly Asp Pro Ser Cys Val Ile Met Gln Asn Trp Ala Arg
465                      470                      475                      480

Ile Glu Ala Arg Leu Cys Asn Asn Met Gln Lys Ala Arg Glu Leu Trp
    485                      490                      495

Asp Ser Ile Met Thr Arg Gly Asn Ala Lys Tyr Ala Asn Met Trp Leu
    500                      505                      510

Glu Tyr Tyr Asn Leu Glu Arg Ala His Gly Asp Thr Gln His Cys Arg
    515                      520                      525

Lys Ala Leu His Arg Ala Val Gln Cys Thr Ser Asp Tyr Pro Glu His
    530                      535                      540

Val Cys Glu Val Leu Leu Thr Met Glu Arg Thr Glu Gly Ser Leu Glu
545                      550                      555                      560

Asp Trp Asp Ile Ala Val Gln Lys Thr Glu Thr Arg Leu Ala Arg Val
    565                      570                      575

Asn Glu Gln Arg Met Lys Ala Ala Glu Lys Glu Ala Ala Leu Val Gln
    580                      585                      590

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Gln Glu Glu Glu Lys Ala Glu Gln Arg Lys Arg Ala Arg Ala Glu Lys
595 600 605

Lys Ala Leu Lys Lys Lys Lys Lys Ile Arg Gly Pro Glu Lys Arg Gly
610 615 620

Ala Asp Glu Asp Asp Glu Lys Glu Trp Gly Asp Asp Glu Glu Glu Gln
625 630 635 640

Pro Ser Lys Arg Arg Arg Val Glu Asn Ser Ile Pro Ala Ala Gly Glu
645 650 655

Thr Gln Asn Val Glu Val Ala Ala Gly Pro Ala Gly Lys Cys Ala Ala
660 665 670

Val Asp Val Glu Pro Pro Ser Lys Gln Lys Glu Lys Ala Ala Ser Leu
675 680 685

Lys Arg Asp Met Pro Lys Val Leu His Asp Ser Ser Lys Asp Ser Ile
690 695 700

Thr Val Phe Val Ser Asn Leu Pro Tyr Ser Met Gln Glu Pro Asp Thr
705 710 715 720

Lys Leu Arg Pro Leu Phe Glu Ala Cys Gly Glu Val Val Gln Ile Arg
725 730 735

Pro Ile Phe Ser Asn Arg Gly Asp Phe Arg Gly Tyr Cys Tyr Val Glu
740 745 750

Phe Lys Glu Glu Lys Ser Ala Leu Gln Ala Leu Glu Met Asp Arg Lys
755 760 765

Ser Val Glu Gly Arg Pro Met Phe Val Ser Pro Cys Val Asp Lys Ser
770 775 780

Lys Asn Pro Asp Phe Lys Val Phe Arg Tyr Ser Thr Ser Leu Glu Lys
785 790 795 800

His Lys Leu Phe Ile Ser Gly Leu Pro Phe Ser Cys Thr Lys Glu Glu
805 810 815

Leu Glu Glu Ile Cys Lys Ala His Gly Thr Val Lys Asp Leu Arg Leu
820 825 830

Val Thr Asn Arg Ala Gly Lys Pro Lys Gly Leu Ala Tyr Val Glu Tyr
835 840 845

Glu Asn Glu Ser Gln Ala Ser Gln Ala Val Met Lys Met Asp Gly Met
850 855 860

Thr Ile Lys Glu Asn Ile Ile Lys Val Ala Ile Ser Asn Pro Pro Gln

ITI-08-PCT Sequence Listing ST25.txt

865 870 875 880

Arg Lys Val Pro Glu Lys Pro Glu Thr Arg Lys Ala Pro Gly Gly Pro
885 890 895

Met Leu Leu Pro Gln Thr Tyr Gly Ala Arg Gly Lys Gly Arg Thr Gln
900 905 910

Leu Ser Leu Leu Pro Arg Ala Leu Gln Arg Pro Ser Ala Ala Ala Pro
915 920 925

Gln Ala Glu Asn Gly Pro Ala Ala Ala Pro Ala Val Ala Ala Pro Ala
930 935 940

Ala Thr Glu Ala Pro Lys Met Ser Asn Ala Asp Phe Ala Lys Leu Phe
945 950 955 960

Leu Arg Lys

<210> 627

<211> 760

<212> PRT

<213> Artificial Sequence

$\langle 220 \rangle$

<223> SEPR Homo sapiens Q12884

<400> 627

Met Lys Thr Trp Val Lys Ile Val Phe Gly Val Ala Thr Ser Ala Val
1 5 10 15

Leu Ala Leu Leu Val Met Cys Ile Val Leu Arg Pro Ser Arg Val His
20 25 30

Asn Ser Glu Glu Asn Thr Met Arg Ala Leu Thr Leu Lys Asp Ile Leu
35 40 45

Asn Gly Thr Phe Ser Tyr Lys Thr Phe Phe Pro Asn Trp Ile Ser Gly
50 55 60

Gln Glu Tyr Leu His Gln Ser Ala Asp Asn Asn Ile Val Leu Tyr Asn
65 70 75 80

Ile Glu Thr Gly Gln Ser Tyr Thr Ile Leu Ser Asn Arg Thr Met Lys
85 90 95

Ser Val Asn Ala Ser Asn Tyr Gly Leu Ser Pro Asp Arg Gln Phe Val
100 105 110

Tyr Leu Glu Ser Asp Tyr Ser Lys Leu Trp Arg Tyr Ser Tyr Thr Ala
115 120 125

ITI-08-PCT_Sequence_Listing_ST25.txt

Thr	Tyr	Tyr	Ile	Tyr	Asp	Leu	Ser	Asn	Gly	Glu	Phe	Val	Arg	Gly	Asn	130	135	140	
Glu	Leu	Pro	Arg	Pro	Ile	Gln	Tyr	Leu	Cys	Trp	Ser	Pro	Val	Gly	Ser	145	150	155	160
Lys	Leu	Ala	Tyr	Val	Tyr	Gln	Asn	Asn	Ile	Tyr	Leu	Lys	Gln	Arg	Pro	165	170	175	
Gly	Asp	Pro	Pro	Phe	Gln	Ile	Thr	Phe	Asn	Gly	Arg	Glu	Asn	Lys	Ile	180	185	190	
Phe	Asn	Gly	Ile	Pro	Asp	Trp	Val	Tyr	Glu	Glu	Glu	Met	Leu	Ala	Thr	195	200	205	
Lys	Tyr	Ala	Leu	Trp	Trp	Ser	Pro	Asn	Gly	Lys	Phe	Leu	Ala	Tyr	Ala	210	215	220	
Glu	Phe	Asn	Asp	Thr	Asp	Ile	Pro	Val	Ile	Ala	Tyr	Ser	Tyr	Tyr	Gly	225	230	235	240
Asp	Glu	Gln	Tyr	Pro	Arg	Thr	Ile	Asn	Ile	Pro	Tyr	Pro	Lys	Ala	Gly	245	250	255	
Ala	Lys	Asn	Pro	Val	Val	Arg	Ile	Phe	Ile	Ile	Asp	Thr	Thr	Tyr	Pro	260	265	270	
Ala	Tyr	Val	Gly	Pro	Gln	Glu	Val	Pro	Val	Pro	Ala	Met	Ile	Ala	Ser	275	280	285	
Ser	Asp	Tyr	Tyr	Phe	Ser	Trp	Leu	Thr	Trp	Val	Thr	Asp	Glu	Arg	Val	290	295	300	
Cys	Leu	Gln	Trp	Leu	Lys	Arg	Val	Gln	Asn	Val	Ser	Val	Leu	Ser	Ile	305	310	315	320
Cys	Asp	Phe	Arg	Glu	Asp	Trp	Gln	Thr	Trp	Asp	Cys	Pro	Lys	Thr	Gln	325	330	335	
Glu	His	Ile	Glu	Glu	Ser	Arg	Thr	Gly	Trp	Ala	Gly	Gly	Phe	Phe	Val	340	345	350	
Ser	Thr	Pro	Val	Phe	Ser	Tyr	Asp	Ala	Ile	Ser	Tyr	Tyr	Lys	Ile	Phe	355	360	365	
Ser	Asp	Lys	Asp	Gly	Tyr	Lys	His	Ile	His	Tyr	Ile	Lys	Asp	Thr	Val	370	375	380	
Glu	Asn	Ala	Ile	Gln	Ile	Thr	Ser	Gly	Lys	Trp	Glu	Ala	Ile	Asn	Ile	385	390	395	400

ITI-08-PCT_Sequence_Listing_ST25.txt

Phe Arg Val Thr Gln Asp Ser Leu Phe Tyr Ser Ser Asn Glu Phe Glu
 405 410 415
 Glu Tyr Pro Gly Arg Arg Asn Ile Tyr Arg Ile Ser Ile Gly Ser Tyr
 420 425 430
 Pro Pro Ser Lys Lys Cys Val Thr Cys His Leu Arg Lys Glu Arg Cys
 435 440 445
 Gln Tyr Tyr Thr Ala Ser Phe Ser Asp Tyr Ala Lys Tyr Tyr Ala Leu
 450 455 460
 Val Cys Tyr Gly Pro Gly Ile Pro Ile Ser Thr Leu His Asp Gly Arg
 465 470 475 480
 Thr Asp Gln Glu Ile Lys Ile Leu Glu Glu Asn Lys Glu Leu Glu Asn
 485 490 495
 Ala Leu Lys Asn Ile Gln Leu Pro Lys Glu Glu Ile Lys Lys Leu Glu
 500 505 510
 Val Asp Glu Ile Thr Leu Trp Tyr Lys Met Ile Leu Pro Pro Gln Phe
 515 520 525
 Asp Arg Ser Lys Lys Tyr Pro Leu Leu Ile Gln Val Tyr Gly Gly Pro
 530 535 540
 Cys Ser Gln Ser Val Arg Ser Val Phe Ala Val Asn Trp Ile Ser Tyr
 545 550 555 560
 Leu Ala Ser Lys Glu Gly Met Val Ile Ala Leu Val Asp Gly Arg Gly
 565 570 575
 Thr Ala Phe Gln Gly Asp Lys Leu Leu Tyr Ala Val Tyr Arg Lys Leu
 580 585 590
 Gly Val Tyr Glu Val Glu Asp Gln Ile Thr Ala Val Arg Lys Phe Ile
 595 600 605
 Glu Met Gly Phe Ile Asp Glu Lys Arg Ile Ala Ile Trp Gly Trp Ser
 610 615 620
 Tyr Gly Gly Tyr Val Ser Ser Leu Ala Leu Ala Ser Gly Thr Gly Leu
 625 630 635 640
 Phe Lys Cys Gly Ile Ala Val Ala Pro Val Ser Ser Trp Glu Tyr Tyr
 645 650 655
 Ala Ser Val Tyr Thr Glu Arg Phe Met Gly Leu Pro Thr Lys Asp Asp
 660 665 670
 Asn Leu Glu His Tyr Lys Asn Ser Thr Val Met Ala Arg Ala Glu Tyr

ITI-08-PCT_Sequence_Listing_ST25.txt

675

680

685

Phe Arg Asn Val Asp Tyr Leu Leu Ile His Gly Thr Ala Asp Asp Asn
690 695 700

Val His Phe Gln Asn Ser Ala Gln Ile Ala Lys Ala Leu Val Asn Ala
705 710 715 720

Gln Val Asp Phe Gln Ala Met Trp Tyr Ser Asp Gln Asn His Gly Leu
725 730 735

Ser Gly Leu Ser Thr Asn His Leu Tyr Thr His Met Thr His Phe Leu
740 745 750

Lys Gln Cys Phe Ser Leu Ser Asp
755 760

<210> 628

<211> 333

<212> PRT

<213> Artificial Sequence

<220>

<223> SIA7F__Homo_sapiens__Q969X2

<400> 628

Met Ala Cys Ser Arg Pro Pro Ser Gln Cys Glu Pro Thr Ser Leu Pro
1 5 10 15

Pro Gly Pro Pro Ala Gly Arg Arg His Leu Pro Leu Ser Arg Arg Arg
20 25 30

Arg Glu Met Ser Ser Asn Lys Glu Gln Arg Ser Ala Val Phe Val Ile
35 40 45

Leu Phe Ala Leu Ile Thr Ile Leu Ile Leu Tyr Ser Ser Asn Ser Ala
50 55 60

Asn Glu Val Phe His Tyr Gly Ser Leu Arg Gly Arg Ser Arg Arg Pro
65 70 75 80

Val Asn Leu Lys Lys Trp Ser Ile Thr Asp Gly Tyr Val Pro Ile Leu
85 90 95

Gly Asn Lys Thr Leu Pro Ser Arg Cys His Gln Cys Val Ile Val Ser
100 105 110

Ser Ser Ser His Leu Leu Gly Thr Lys Leu Gly Pro Glu Ile Glu Arg
115 120 125

Ala Glu Cys Thr Ile Arg Met Asn Asp Ala Pro Thr Thr Gly Tyr Ser

ITI-08-PCT_Sequence_Listing_ST25.txt

130

135

140

Ala Asp Val Gly Asn Lys Thr Thr Tyr Arg Val Val Ala His Ser Ser
145 150 155 160

Val Phe Arg Val Leu Arg Arg Pro Gln Glu Phe Val Asn Arg Thr Pro
165 170 175

Glu Thr Val Phe Ile Phe Trp Gly Pro Pro Ser Lys Met Gln Lys Pro
180 185 190

Gln Gly Ser Leu Val Arg Val Ile Gln Arg Ala Gly Leu Val Phe Pro
195 200 205

Asn Met Glu Ala Tyr Ala Val Ser Pro Gly Arg Met Arg Gln Phe Asp
210 215 220

Asp Leu Phe Arg Gly Glu Thr Gly Lys Asp Arg Glu Lys Ser His Ser
225 230 235 240

Trp Leu Ser Thr Gly Trp Phe Thr Met Val Ile Ala Val Glu Leu Cys
245 250 255

Asp His Val His Val Tyr Gly Met Val Pro Pro Asn Tyr Cys Ser Gln
260 265 270

Arg Pro Arg Leu Gln Arg Met Pro Tyr His Tyr Tyr Glu Pro Lys Gly
275 280 285

Pro Asp Glu Cys Val Thr Tyr Ile Gln Asn Glu His Ser Arg Lys Gly
290 295 300

Asn His His Arg Phe Ile Thr Glu Lys Arg Val Phe Ser Ser Trp Ala
305 310 315 320

Gln Leu Tyr Gly Ile Thr Phe Ser His Pro Ser Trp Thr
325 330

<210> 629

<211> 356

<212> PRT

<213> Artificial Sequence

<220>

<223> SIA8A__Homo_sapiens__Q92185

<400> 629

Met Ser Pro Cys Gly Arg Ala Arg Arg Gln Thr Ser Arg Gly Ala Met
1 5 10 15

Ala Val Leu Ala Trp Lys Phe Pro Arg Thr Arg Leu Pro Met Gly Ala

ITI-08-PCT_Sequence_Listing_ST25.txt

```

20          25          30
Ser  Ala  Leu  Cys  Val  Val  Val  Leu  Cys  Trp  Leu  Tyr  Ile  Phe  Pro  Val
35          40          45

Tyr  Arg  Leu  Pro  Asn  Glu  Lys  Glu  Ile  Val  Gln  Gly  Val  Leu  Gln  Gln
50          55          60

Gly  Thr  Ala  Trp  Arg  Arg  Asn  Gln  Thr  Ala  Ala  Arg  Ala  Phe  Arg  Lys
65          70          75          80

Gln  Met  Glu  Asp  Cys  Cys  Asp  Pro  Ala  His  Leu  Phe  Ala  Met  Thr  Lys
85          90          95

Met  Asn  Ser  Pro  Met  Gly  Lys  Ser  Met  Trp  Tyr  Asp  Gly  Glu  Phe  Leu
100         105         110

Tyr  Ser  Phe  Thr  Ile  Asp  Asn  Ser  Thr  Tyr  Ser  Leu  Phe  Pro  Gln  Ala
115         120         125

Thr  Pro  Phe  Gln  Leu  Pro  Leu  Lys  Lys  Cys  Ala  Val  Val  Gly  Asn  Gly
130         135         140

Gly  Ile  Leu  Lys  Lys  Ser  Gly  Cys  Gly  Arg  Gln  Ile  Asp  Glu  Ala  Asn
145         150         155         160

Phe  Val  Met  Arg  Cys  Asn  Leu  Pro  Pro  Leu  Ser  Ser  Glu  Tyr  Thr  Lys
165         170         175

Asp  Val  Gly  Ser  Lys  Ser  Gln  Leu  Val  Thr  Ala  Asn  Pro  Ser  Ile  Ile
180         185         190

Arg  Gln  Arg  Phe  Gln  Asn  Leu  Leu  Trp  Ser  Arg  Lys  Thr  Phe  Val  Asp
195         200         205

Asn  Met  Lys  Ile  Tyr  Asn  His  Ser  Tyr  Ile  Tyr  Met  Pro  Ala  Phe  Ser
210         215         220

Met  Lys  Thr  Gly  Thr  Glu  Pro  Ser  Leu  Arg  Val  Tyr  Tyr  Thr  Leu  Ser
225         230         235         240

Asp  Val  Gly  Ala  Asn  Gln  Thr  Val  Leu  Phe  Ala  Asn  Pro  Asn  Phe  Leu
245         250         255

Arg  Ser  Ile  Gly  Lys  Phe  Trp  Lys  Ser  Arg  Gly  Ile  His  Ala  Lys  Arg
260         265         270

Leu  Ser  Thr  Gly  Leu  Phe  Leu  Val  Ser  Ala  Ala  Leu  Gly  Leu  Cys  Glu
275         280         285

Glu  Val  Ala  Ile  Tyr  Gly  Phe  Trp  Pro  Phe  Ser  Val  Asn  Met  His  Glu
290         295         300

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Gln Pro Ile Ser His His Tyr Tyr Asp Asn Val Leu Pro Phe Ser Gly
305 310 315 320

Phe His Ala Met Pro Glu Glu Phe Leu Gln Leu Trp Tyr Leu His Lys
325 330 335

Ile Gly Ala Leu Arg Met Gln Leu Asp Pro Cys Glu Asp Thr Ser Leu
340 345 350

Gln Pro Thr Ser
355

<210> 630

<211> 418

<212> PRT

<213> Artificial Sequence

<220>

<223> SIAT9__Homo_sapiens__Q9UNP4

<400> 630

Met Arg Thr Lys Ala Ala Gly Cys Ala Glu Arg Arg Pro Leu Gln Pro
1 5 10 15

Arg Thr Glu Ala Ala Ala Ala Pro Ala Gly Arg Ala Met Pro Ser Glu
20 25 30

Tyr Thr Tyr Val Lys Leu Arg Ser Asp Cys Ser Arg Pro Ser Leu Gln
35 40 45

Trp Tyr Thr Arg Ala Gln Ser Lys Met Arg Arg Pro Ser Leu Leu Leu
50 55 60

Lys Asp Ile Leu Lys Cys Thr Leu Leu Val Phe Gly Val Trp Ile Leu
65 70 75 80

Tyr Ile Leu Lys Leu Asn Tyr Thr Thr Glu Glu Cys Asp Met Lys Lys
85 90 95

Met His Tyr Val Asp Pro Asp His Val Lys Arg Ala Gln Lys Tyr Ala
100 105 110

Gln Gln Val Leu Gln Lys Glu Cys Arg Pro Lys Phe Ala Lys Thr Ser
115 120 125

Met Ala Leu Leu Phe Glu His Arg Tyr Ser Val Asp Leu Leu Pro Phe
130 135 140

Val Gln Lys Ala Pro Lys Asp Ser Glu Ala Glu Ser Lys Tyr Asp Pro
145 150 155 160

ITI-08-PCT_Sequence_Listing_ST25.txt

```

Pro Phe Gly Phe Arg Lys Phe Ser Ser Lys Val Gln Thr Leu Leu Glu
      165                      170                      175

Leu Leu Pro Glu His Asp Leu Pro Glu His Leu Lys Ala Lys Thr Cys
      180                      185                      190

Arg Arg Cys Val Val Ile Gly Ser Gly Gly Ile Leu His Gly Leu Glu
      195                      200                      205

Leu Gly His Thr Leu Asn Gln Phe Asp Val Val Ile Arg Leu Asn Ser
      210                      215                      220

Ala Pro Val Glu Gly Tyr Ser Glu His Val Gly Asn Lys Thr Thr Ile
225                      230                      235                      240

Arg Met Thr Tyr Pro Glu Gly Ala Pro Leu Ser Asp Leu Glu Tyr Tyr
      245                      250                      255

Ser Asn Asp Leu Phe Val Ala Val Leu Phe Lys Ser Val Asp Phe Asn
      260                      265                      270

Trp Leu Gln Ala Met Val Lys Lys Glu Thr Leu Pro Phe Trp Val Arg
      275                      280                      285

Leu Phe Phe Trp Lys Gln Val Ala Glu Lys Ile Pro Leu Gln Pro Lys
      290                      295                      300

His Phe Arg Ile Leu Asn Pro Val Ile Ile Lys Glu Thr Ala Phe Asp
305                      310                      315                      320

Ile Leu Gln Tyr Ser Glu Pro Gln Ser Arg Phe Trp Gly Arg Asp Lys
      325                      330                      335

Asn Val Pro Thr Ile Gly Val Ile Ala Val Val Leu Ala Thr His Leu
      340                      345                      350

Cys Asp Glu Val Ser Leu Ala Gly Phe Gly Tyr Asp Leu Asn Gln Pro
      355                      360                      365

Arg Thr Pro Leu His Tyr Phe Asp Ser Gln Cys Met Ala Ala Met Asn
      370                      375                      380

Phe Gln Thr Met His Asn Val Thr Thr Glu Thr Lys Phe Leu Leu Lys
385                      390                      395                      400

Leu Val Lys Glu Gly Val Val Lys Asp Leu Ser Gly Gly Ile Asp Arg
      405                      410                      415

Glu Phe

```

<210> 631

ITI-08-PCT_Sequence_Listing_ST25.txt

<211> 352

<212> PRT

<213> Artificial Sequence

<220>

<223> SIRT2/m__Homo_sapiens__A0A024R0G8

<400> 631

Met Asp Phe Leu Arg Asn Leu Phe Ser Gln Thr Leu Ser Leu Gly Ser
1 5 10 15

Gln Lys Glu Arg Leu Leu Asp Glu Leu Thr Leu Glu Gly Val Ala Arg
20 25 30

Tyr Met Gln Ser Glu Arg Cys Arg Arg Val Ile Cys Leu Val Gly Ala
35 40 45

Gly Ile Ser Thr Ser Ala Gly Ile Pro Asp Phe Arg Ser Pro Ser Thr
50 55 60

Gly Leu Tyr Asp Asn Leu Glu Lys Tyr His Leu Pro Tyr Pro Glu Ala
65 70 75 80

Ile Phe Glu Ile Ser Tyr Phe Lys Lys His Pro Glu Pro Phe Phe Ala
85 90 95

Leu Ala Lys Glu Leu Tyr Pro Gly Gln Phe Lys Pro Thr Ile Cys His
100 105 110

Tyr Phe Met Arg Leu Leu Lys Asp Lys Gly Leu Leu Leu Arg Cys Tyr
115 120 125

Thr Gln Asn Ile Asp Thr Leu Glu Arg Ile Ala Gly Leu Glu Gln Glu
130 135 140

Asp Leu Val Glu Ala His Gly Thr Phe Tyr Thr Ser His Cys Val Ser
145 150 155 160

Ala Ser Cys Arg His Glu Tyr Pro Leu Ser Trp Met Lys Glu Lys Ile
165 170 175

Phe Ser Glu Val Thr Pro Lys Cys Glu Asp Cys Gln Ser Leu Val Lys
180 185 190

Pro Asp Ile Val Phe Phe Gly Glu Ser Leu Pro Ala Arg Phe Phe Ser
195 200 205

Cys Met Gln Ser Asp Phe Leu Lys Val Asp Leu Leu Leu Val Met Gly
210 215 220

Thr Ser Leu Gln Val Gln Pro Phe Ala Ser Leu Ile Ser Lys Ala Pro

ITI-08-PCT_Sequence_Listing_ST25.txt

225 230 235 240
 Leu Ser Thr Pro Arg Leu Leu Ile Asn Lys Glu Lys Ala Gly Gln Ser
 245 250 255
 Asp Pro Phe Leu Gly Met Ile Met Gly Leu Gly Gly Gly Met Asp Phe
 260 265 270
 Asp Ser Lys Lys Ala Tyr Arg Asp Val Ala Trp Leu Gly Glu Cys Asp
 275 280 285
 Gln Gly Cys Leu Ala Leu Ala Glu Leu Leu Gly Trp Lys Lys Glu Leu
 290 295 300
 Glu Asp Leu Val Arg Arg Glu His Ala Ser Ile Asp Ala Gln Ser Gly
 305 310 315 320
 Ala Gly Val Pro Asn Pro Ser Thr Ser Ala Ser Pro Lys Lys Ser Pro
 325 330 335
 Pro Pro Ala Lys Asp Glu Ala Arg Thr Thr Glu Arg Glu Lys Pro Gln
 340 345 350

<210> 632

<211> 389

<212> PRT

<213> Artificial Sequence

<220>

<223> SIRT2/m__Homo_sapiens__Q8IXJ6

<400> 632

Met Ala Glu Pro Asp Pro Ser His Pro Leu Glu Thr Gln Ala Gly Lys
 1 5 10 15
 Val Gln Glu Ala Gln Asp Ser Asp Ser Asp Ser Glu Gly Gly Ala Ala
 20 25 30
 Gly Gly Glu Ala Asp Met Asp Phe Leu Arg Asn Leu Phe Ser Gln Thr
 35 40 45
 Leu Ser Leu Gly Ser Gln Lys Glu Arg Leu Leu Asp Glu Leu Thr Leu
 50 55 60
 Glu Gly Val Ala Arg Tyr Met Gln Ser Glu Arg Cys Arg Arg Val Ile
 65 70 75 80
 Cys Leu Val Gly Ala Gly Ile Ser Thr Ser Ala Gly Ile Pro Asp Phe
 85 90 95
 Arg Ser Pro Ser Thr Gly Leu Tyr Asp Asn Leu Glu Lys Tyr His Leu

ITI-08-PCT_Sequence_Listing_ST25.txt

```

100          105          110
Pro Tyr Pro Glu Ala Ile Phe Glu Ile Ser Tyr Phe Lys Lys His Pro
115          120          125

Glu Pro Phe Phe Ala Leu Ala Lys Glu Leu Tyr Pro Gly Gln Phe Lys
130          135          140

Pro Thr Ile Cys His Tyr Phe Met Arg Leu Leu Lys Asp Lys Gly Leu
145          150          155

Leu Leu Arg Cys Tyr Thr Gln Asn Ile Asp Thr Leu Glu Arg Ile Ala
165          170          175

Gly Leu Glu Gln Glu Asp Leu Val Glu Ala His Gly Thr Phe Tyr Thr
180          185          190

Ser His Cys Val Ser Ala Ser Cys Arg His Glu Tyr Pro Leu Ser Trp
195          200          205

Met Lys Glu Lys Ile Phe Ser Glu Val Thr Pro Lys Cys Glu Asp Cys
210          215          220

Gln Ser Leu Val Lys Pro Asp Ile Val Phe Phe Gly Glu Ser Leu Pro
225          230          235

Ala Arg Phe Phe Ser Cys Met Gln Ser Asp Phe Leu Lys Val Asp Leu
245          250          255

Leu Leu Val Met Gly Thr Ser Leu Gln Val Gln Pro Phe Ala Ser Leu
260          265          270

Ile Ser Lys Ala Pro Leu Ser Thr Pro Arg Leu Leu Ile Asn Lys Glu
275          280          285

Lys Ala Gly Gln Ser Asp Pro Phe Leu Gly Met Ile Met Gly Leu Gly
290          295          300

Gly Gly Met Asp Phe Asp Ser Lys Lys Ala Tyr Arg Asp Val Ala Trp
305          310          315

Leu Gly Glu Cys Asp Gln Gly Cys Leu Ala Leu Ala Glu Leu Leu Gly
325          330          335

Trp Lys Lys Glu Leu Glu Asp Leu Val Arg Arg Glu His Ala Ser Ile
340          345          350

Asp Ala Gln Ser Gly Ala Gly Val Pro Asn Pro Ser Thr Ser Ala Ser
355          360          365

Pro Lys Lys Ser Pro Pro Pro Ala Lys Asp Glu Ala Arg Thr Thr Glu
370          375          380

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Arg Glu Lys Pro Gln
385

<210> 633
<211> 466
<212> PRT
<213> Artificial Sequence

<220>
<223> SOX10__Homo_sapiens__P56693

<400> 633

Met Ala Glu Glu Gln Asp Leu Ser Glu Val Glu Leu Ser Pro Val Gly
1 5 10 15

Ser Glu Glu Pro Arg Cys Leu Ser Pro Gly Ser Ala Pro Ser Leu Gly
20 25 30

Pro Asp Gly Gly Gly Gly Ser Gly Leu Arg Ala Ser Pro Gly Pro
35 40 45

Gly Glu Leu Gly Lys Val Lys Lys Glu Gln Gln Asp Gly Glu Ala Asp
50 55 60

Asp Asp Lys Phe Pro Val Cys Ile Arg Glu Ala Val Ser Gln Val Leu
65 70 75 80

Ser Gly Tyr Asp Trp Thr Leu Val Pro Met Pro Val Arg Val Asn Gly
85 90 95

Ala Ser Lys Ser Lys Pro His Val Lys Arg Pro Met Asn Ala Phe Met
100 105 110

Val Trp Ala Gln Ala Ala Arg Arg Lys Leu Ala Asp Gln Tyr Pro His
115 120 125

Leu His Asn Ala Glu Leu Ser Lys Thr Leu Gly Lys Leu Trp Arg Leu
130 135 140

Leu Asn Glu Ser Asp Lys Arg Pro Phe Ile Glu Glu Ala Glu Arg Leu
145 150 155 160

Arg Met Gln His Lys Lys Asp His Pro Asp Tyr Lys Tyr Gln Pro Arg
165 170 175

Arg Arg Lys Asn Gly Lys Ala Ala Gln Gly Glu Ala Glu Cys Pro Gly
180 185 190

Gly Glu Ala Glu Gln Gly Gly Thr Ala Ala Ile Gln Ala His Tyr Lys
195 200 205

ITI-08-PCT_Sequence_Listing_ST25.txt

Ser Ala His Leu Asp His Arg His Pro Gly Glu Gly Ser Pro Met Ser
210 215 220

Asp Gly Asn Pro Glu His Pro Ser Gly Gln Ser His Gly Pro Pro Thr
225 230 235 240

Pro Pro Thr Thr Pro Lys Thr Glu Leu Gln Ser Gly Lys Ala Asp Pro
245 250 255

Lys Arg Asp Gly Arg Ser Met Gly Glu Gly Gly Lys Pro His Ile Asp
260 265 270

Phe Gly Asn Val Asp Ile Gly Glu Ile Ser His Glu Val Met Ser Asn
275 280 285

Met Glu Thr Phe Asp Val Ala Glu Leu Asp Gln Tyr Leu Pro Pro Asn
290 295 300

Gly His Pro Gly His Val Ser Ser Tyr Ser Ala Ala Gly Tyr Gly Leu
305 310 315 320

Gly Ser Ala Leu Ala Val Ala Ser Gly His Ser Ala Trp Ile Ser Lys
325 330 335

Pro Pro Gly Val Ala Leu Pro Thr Val Ser Pro Pro Gly Val Asp Ala
340 345 350

Lys Ala Gln Val Lys Thr Glu Thr Ala Gly Pro Gln Gly Pro Pro His
355 360 365

Tyr Thr Asp Gln Pro Ser Thr Ser Gln Ile Ala Tyr Thr Ser Leu Ser
370 375 380

Leu Pro His Tyr Gly Ser Ala Phe Pro Ser Ile Ser Arg Pro Gln Phe
385 390 395 400

Asp Tyr Ser Asp His Gln Pro Ser Gly Pro Tyr Tyr Gly His Ser Gly
405 410 415

Gln Ala Ser Gly Leu Tyr Ser Ala Phe Ser Tyr Met Gly Pro Ser Gln
420 425 430

Arg Pro Leu Tyr Thr Ala Ile Ser Asp Pro Ser Pro Ser Gly Pro Gln
435 440 445

Ser His Ser Pro Thr His Trp Glu Gln Pro Val Tyr Thr Thr Leu Ser
450 455 460

Arg Pro
465

ITI-08-PCT_Sequence_Listing_ST25.txt

<210> 634
 <211> 151
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> SP17__Homo_sapiens__Q15506

 <400> 634

```

Met Ser Ile Pro Phe Ser Asn Thr His Tyr Arg Ile Pro Gln Gly Phe
1           5           10          15

Gly Asn Leu Leu Glu Gly Leu Thr Arg Glu Ile Leu Arg Glu Gln Pro
          20          25          30

Asp Asn Ile Pro Ala Phe Ala Ala Ala Tyr Phe Glu Ser Leu Leu Glu
          35          40          45

Lys Arg Glu Lys Thr Asn Phe Asp Pro Ala Glu Trp Gly Ser Lys Val
          50          55          60

Glu Asp Arg Phe Tyr Asn Asn His Ala Phe Glu Glu Gln Glu Pro Pro
65          70          75          80

Glu Lys Ser Asp Pro Lys Gln Glu Glu Ser Gln Ile Ser Gly Lys Glu
          85          90          95

Glu Glu Thr Ser Val Thr Ile Leu Asp Ser Ser Glu Glu Asp Lys Glu
          100         105         110

Lys Glu Glu Val Ala Ala Val Lys Ile Gln Ala Ala Phe Arg Gly His
          115         120         125

Ile Ala Arg Glu Glu Ala Lys Lys Met Lys Thr Asn Ser Leu Gln Asn
          130         135         140

Glu Glu Lys Glu Glu Asn Lys
145          150
    
```

<210> 635
 <211> 97
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> SPNXA__Homo_sapiens__Q9NS26

 <400> 635

```

Met Asp Lys Gln Ser Ser Ala Gly Gly Val Lys Arg Ser Val Pro Cys
1           5           10          15
    
```

ITI-08-PCT_Sequence_Listing_ST25.txt

Asp Ser Asn Glu Ala Asn Glu Met Met Pro Glu Thr Pro Thr Gly Asp
20 25 30

Ser Asp Pro Gln Pro Ala Pro Lys Lys Met Lys Thr Ser Glu Ser Ser
35 40 45

Thr Ile Leu Val Val Arg Tyr Arg Arg Asn Phe Lys Arg Thr Ser Pro
50 55 60

Glu Glu Leu Leu Asn Asp His Ala Arg Glu Asn Arg Ile Asn Pro Leu
65 70 75 80

Gln Met Glu Glu Glu Glu Phe Met Glu Ile Met Val Glu Ile Pro Ala
85 90 95

Lys

<210> 636

<211> 141

<212> PRT

<213> Artificial Sequence

<220>

<223> SPXN3__Homo_sapiens__Q5MJ09

<400> 636

Met Glu Gln Pro Thr Ser Ser Thr Asn Gly Glu Lys Thr Lys Ser Pro
1 5 10 15

Cys Glu Ser Asn Asn Lys Lys Asn Asp Glu Met Gln Glu Val Pro Asn
20 25 30

Arg Val Leu Ala Pro Glu Gln Ser Leu Lys Lys Thr Lys Thr Ser Glu
35 40 45

Tyr Pro Ile Ile Phe Val Tyr Tyr Leu Arg Lys Gly Lys Lys Ile Asn
50 55 60

Ser Asn Gln Leu Glu Asn Glu Gln Ser Gln Glu Asn Ser Ile Asn Pro
65 70 75 80

Ile Gln Lys Glu Glu Asp Glu Gly Val Asp Leu Ser Glu Gly Ser Ser
85 90 95

Asn Glu Asp Glu Asp Leu Gly Pro Cys Glu Gly Pro Ser Lys Glu Asp
100 105 110

Lys Asp Leu Asp Ser Ser Glu Gly Ser Ser Gln Glu Asp Glu Asp Leu
115 120 125

ITI-08-PCT_Sequence_Listing_ST25.txt

Gly Leu Ser Glu Gly Ser Ser Gln Asp Ser Gly Glu Asp
130 135 140

<210> 637
<211> 188
<212> PRT
<213> Artificial Sequence

<220>
<223> SSX-1__Homo_sapiens__Q16384

<400> 637

Met Asn Gly Asp Asp Thr Phe Ala Lys Arg Pro Arg Asp Asp Ala Lys
1 5 10 15

Ala Ser Glu Lys Arg Ser Lys Ala Phe Asp Asp Ile Ala Thr Tyr Phe
20 25 30

Ser Lys Lys Glu Trp Lys Lys Met Lys Tyr Ser Glu Lys Ile Ser Tyr
35 40 45

Val Tyr Met Lys Arg Asn Tyr Lys Ala Met Thr Lys Leu Gly Phe Lys
50 55 60

Val Thr Leu Pro Pro Phe Met Cys Asn Lys Gln Ala Thr Asp Phe Gln
65 70 75 80

Gly Asn Asp Phe Asp Asn Asp His Asn Arg Arg Ile Gln Val Glu His
85 90 95

Pro Gln Met Thr Phe Gly Arg Leu His Arg Ile Ile Pro Lys Ile Met
100 105 110

Pro Lys Lys Pro Ala Glu Asp Glu Asn Asp Ser Lys Gly Val Ser Glu
115 120 125

Ala Ser Gly Pro Gln Asn Asp Gly Lys Gln Leu His Pro Pro Gly Lys
130 135 140

Ala Asn Ile Ser Glu Lys Ile Asn Lys Arg Ser Gly Pro Lys Arg Gly
145 150 155 160

Lys His Ala Trp Thr His Arg Leu Arg Glu Arg Lys Gln Leu Val Ile
165 170 175

Tyr Glu Glu Ile Ser Asp Pro Glu Glu Asp Asp Glu
180 185

<210> 638
<211> 188
<212> PRT

ITI-08-PCT_Sequence_Listing_ST25.txt

<213> Artificial Sequence

<220>

<223> SSX-2__Homo_sapiens__Q16385

<400> 638

Met Asn Gly Asp Asp Ala Phe Ala Arg Arg Pro Thr Val Gly Ala Gln
1 5 10 15

Ile Pro Glu Lys Ile Gln Lys Ala Phe Asp Asp Ile Ala Lys Tyr Phe
20 25 30

Ser Lys Glu Glu Trp Glu Lys Met Lys Ala Ser Glu Lys Ile Phe Tyr
35 40 45

Val Tyr Met Lys Arg Lys Tyr Glu Ala Met Thr Lys Leu Gly Phe Lys
50 55 60

Ala Thr Leu Pro Pro Phe Met Cys Asn Lys Arg Ala Glu Asp Phe Gln
65 70 75 80

Gly Asn Asp Leu Asp Asn Asp Pro Asn Arg Gly Asn Gln Val Glu Arg
85 90 95

Pro Gln Met Thr Phe Gly Arg Leu Gln Gly Ile Ser Pro Lys Ile Met
100 105 110

Pro Lys Lys Pro Ala Glu Glu Gly Asn Asp Ser Glu Glu Val Pro Glu
115 120 125

Ala Ser Gly Pro Gln Asn Asp Gly Lys Glu Leu Cys Pro Pro Gly Lys
130 135 140

Pro Thr Thr Ser Glu Lys Ile His Glu Arg Ser Gly Pro Lys Arg Gly
145 150 155 160

Glu His Ala Trp Thr His Arg Leu Arg Glu Arg Lys Gln Leu Val Ile
165 170 175

Tyr Glu Glu Ile Ser Asp Pro Glu Glu Asp Asp Glu
180 185

<210> 639

<211> 188

<212> PRT

<213> Artificial Sequence

<220>

<223> SSX3__Homo_sapiens__Q99909

<400> 639

ITI-08-PCT_Sequence_Listing_ST25.txt

```

Met Asn Gly Asp Asp Thr Phe Ala Arg Arg Pro Thr Val Gly Ala Gln
1          5          10          15

Ile Pro Glu Lys Ile Gln Lys Ala Phe Asp Asp Ile Ala Lys Tyr Phe
          20          25          30

Ser Lys Glu Glu Trp Glu Lys Met Lys Val Ser Glu Lys Ile Val Tyr
          35          40          45

Val Tyr Met Lys Arg Lys Tyr Glu Ala Met Thr Lys Leu Gly Phe Lys
          50          55          60

Ala Ile Leu Pro Ser Phe Met Arg Asn Lys Arg Val Thr Asp Phe Gln
65          70          75          80

Gly Asn Asp Phe Asp Asn Asp Pro Asn Arg Gly Asn Gln Val Gln Arg
          85          90          95

Pro Gln Met Thr Phe Gly Arg Leu Gln Gly Ile Phe Pro Lys Ile Met
          100          105          110

Pro Lys Lys Pro Ala Glu Glu Gly Asn Val Ser Lys Glu Val Pro Glu
          115          120          125

Ala Ser Gly Pro Gln Asn Asp Gly Lys Gln Leu Cys Pro Pro Gly Lys
          130          135          140

Pro Thr Thr Ser Glu Lys Ile Asn Met Ile Ser Gly Pro Lys Arg Gly
145          150          155          160

Glu His Ala Trp Thr His Arg Leu Arg Glu Arg Lys Gln Leu Val Ile
          165          170          175

Tyr Glu Glu Ile Ser Asp Pro Glu Glu Asp Asp Glu
          180          185

```

<210> 640

<211> 188

<212> PRT

<213> Artificial Sequence

<220>

<223> SSX-4__Homo_sapiens__060224

<400> 640

```

Met Asn Gly Asp Asp Ala Phe Ala Arg Arg Pro Arg Asp Asp Ala Gln
1          5          10          15

Ile Ser Glu Lys Leu Arg Lys Ala Phe Asp Asp Ile Ala Lys Tyr Phe
          20          25          30

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Ser Lys Lys Glu Trp Glu Lys Met Lys Ser Ser Glu Lys Ile Val Tyr
35 40 45

Val Tyr Met Lys Leu Asn Tyr Glu Val Met Thr Lys Leu Gly Phe Lys
50 55 60

Val Thr Leu Pro Pro Phe Met Arg Ser Lys Arg Ala Ala Asp Phe His
65 70 75 80

Gly Asn Asp Phe Gly Asn Asp Arg Asn His Arg Asn Gln Val Glu Arg
85 90 95

Pro Gln Met Thr Phe Gly Ser Leu Gln Arg Ile Phe Pro Lys Ile Met
100 105 110

Pro Lys Lys Pro Ala Glu Glu Glu Asn Gly Leu Lys Glu Val Pro Glu
115 120 125

Ala Ser Gly Pro Gln Asn Asp Gly Lys Gln Leu Cys Pro Pro Gly Asn
130 135 140

Pro Ser Thr Leu Glu Lys Ile Asn Lys Thr Ser Gly Pro Lys Arg Gly
145 150 155 160

Lys His Ala Trp Thr His Arg Leu Arg Glu Arg Lys Gln Leu Val Val
165 170 175

Tyr Glu Glu Ile Ser Asp Pro Glu Glu Asp Asp Glu
180 185

<210> 641

<211> 295

<212> PRT

<213> Artificial Sequence

<220>

<223> ST1A1__Homo_sapiens__P50225

<400> 641

Met Glu Leu Ile Gln Asp Thr Ser Arg Pro Pro Leu Glu Tyr Val Lys
1 5 10 15

Gly Val Pro Leu Ile Lys Tyr Phe Ala Glu Ala Leu Gly Pro Leu Gln
20 25 30

Ser Phe Gln Ala Arg Pro Asp Asp Leu Leu Ile Ser Thr Tyr Pro Lys
35 40 45

Ser Gly Thr Thr Trp Val Ser Gln Ile Leu Asp Met Ile Tyr Gln Gly
50 55 60

ITI-08-PCT_Sequence_Listing_ST25.txt

Gly	Asp	Leu	Glu	Lys	Cys	His	Arg	Ala	Pro	Ile	Phe	Met	Arg	Val	Pro	65	70	75	80
Phe	Leu	Glu	Phe	Lys	Ala	Pro	Gly	Ile	Pro	Ser	Gly	Met	Glu	Thr	Leu	85	90	95	
Lys	Asp	Thr	Pro	Ala	Pro	Arg	Leu	Leu	Lys	Thr	His	Leu	Pro	Leu	Ala	100	105	110	
Leu	Leu	Pro	Gln	Thr	Leu	Leu	Asp	Gln	Lys	Val	Lys	Val	Val	Tyr	Val	115	120	125	
Ala	Arg	Asn	Ala	Lys	Asp	Val	Ala	Val	Ser	Tyr	Tyr	His	Phe	Tyr	His	130	135	140	
Met	Ala	Lys	Val	His	Pro	Glu	Pro	Gly	Thr	Trp	Asp	Ser	Phe	Leu	Glu	145	150	155	160
Lys	Phe	Met	Val	Gly	Glu	Val	Ser	Tyr	Gly	Ser	Trp	Tyr	Gln	His	Val	165	170	175	
Gln	Glu	Trp	Trp	Glu	Leu	Ser	Arg	Thr	His	Pro	Val	Leu	Tyr	Leu	Phe	180	185	190	
Tyr	Glu	Asp	Met	Lys	Glu	Asn	Pro	Lys	Arg	Glu	Ile	Gln	Lys	Ile	Leu	195	200	205	
Glu	Phe	Val	Gly	Arg	Ser	Leu	Pro	Glu	Glu	Thr	Val	Asp	Phe	Val	Val	210	215	220	
Gln	His	Thr	Ser	Phe	Lys	Glu	Met	Lys	Lys	Asn	Pro	Met	Thr	Asn	Tyr	225	230	235	240
Thr	Thr	Val	Pro	Gln	Glu	Phe	Met	Asp	His	Ser	Ile	Ser	Pro	Phe	Met	245	250	255	
Arg	Lys	Gly	Met	Ala	Gly	Asp	Trp	Lys	Thr	Thr	Phe	Thr	Val	Ala	Gln	260	265	270	
Asn	Glu	Arg	Phe	Asp	Ala	Asp	Tyr	Ala	Glu	Lys	Met	Ala	Gly	Cys	Ser	275	280	285	
Leu	Ser	Phe	Arg	Ser	Glu	Leu										290	295		

<210> 642
 <211> 1268
 <212> PRT
 <213> Artificial Sequence

<220>

ITI-08-PCT_Sequence_Listing_ST25.txt

<223> STAG2__Homo_sapiens__Q8N3U4-2

<400> 642

```

Met Ile Ala Ala Pro Glu Ile Pro Thr Asp Phe Asn Leu Leu Gln Glu
1           5           10           15

Ser Glu Thr His Phe Ser Ser Asp Thr Asp Phe Glu Asp Ile Glu Gly
          20           25           30

Lys Asn Gln Lys Gln Gly Lys Gly Lys Thr Cys Lys Lys Gly Lys Lys
          35           40           45

Gly Pro Ala Glu Lys Gly Lys Gly Gly Asn Gly Gly Gly Lys Pro Pro
          50           55           60

Ser Gly Pro Asn Arg Met Asn Gly His His Gln Gln Asn Gly Val Glu
65           70           75           80

Asn Met Met Leu Phe Glu Val Val Lys Met Gly Lys Ser Ala Met Gln
          85           90           95

Ser Val Val Asp Asp Trp Ile Glu Ser Tyr Lys His Asp Arg Asp Ile
          100          105          110

Ala Leu Leu Asp Leu Ile Asn Phe Phe Ile Gln Cys Ser Gly Cys Lys
          115          120          125

Gly Val Val Thr Ala Glu Met Phe Arg His Met Gln Asn Ser Glu Ile
          130          135          140

Ile Arg Lys Met Thr Glu Glu Phe Asp Glu Asp Ser Gly Asp Tyr Pro
145          150          155          160

Leu Thr Met Ala Gly Pro Gln Trp Lys Lys Phe Lys Ser Ser Phe Cys
          165          170          175

Glu Phe Ile Gly Val Leu Val Arg Gln Cys Gln Tyr Ser Ile Ile Tyr
          180          185          190

Asp Glu Tyr Met Met Asp Thr Val Ile Ser Leu Leu Thr Gly Leu Ser
          195          200          205

Asp Ser Gln Val Arg Ala Phe Arg His Thr Ser Thr Leu Ala Ala Met
          210          215          220

Lys Leu Met Thr Ala Leu Val Asn Val Ala Leu Asn Leu Ser Ile Asn
225          230          235          240

Met Asp Asn Thr Gln Arg Gln Tyr Glu Ala Glu Arg Asn Lys Met Ile
          245          250          255

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Gly Lys Arg Ala Asn Glu Arg Leu Glu Leu Leu Leu Gln Lys Arg Lys
260 265 270

Glu Leu Gln Glu Asn Gln Asp Glu Ile Glu Asn Met Met Asn Ala Ile
275 280 285

Phe Lys Gly Val Phe Val His Arg Tyr Arg Asp Ala Ile Ala Glu Ile
290 295 300

Arg Ala Ile Cys Ile Glu Glu Ile Gly Ile Trp Met Lys Met Tyr Ser
305 310 315 320

Asp Ala Phe Leu Asn Asp Ser Tyr Leu Lys Tyr Val Gly Trp Thr Met
325 330 335

His Asp Lys Gln Gly Glu Val Arg Leu Lys Cys Leu Thr Ala Leu Gln
340 345 350

Gly Leu Tyr Tyr Asn Lys Glu Leu Asn Ser Lys Leu Glu Leu Phe Thr
355 360 365

Ser Arg Phe Lys Asp Arg Ile Val Ser Met Thr Leu Asp Lys Glu Tyr
370 375 380

Asp Val Ala Val Gln Ala Ile Lys Leu Leu Thr Leu Val Leu Gln Ser
385 390 395 400

Ser Glu Glu Val Leu Thr Ala Glu Asp Cys Glu Asn Val Tyr His Leu
405 410 415

Val Tyr Ser Ala His Arg Pro Val Ala Val Ala Ala Gly Glu Phe Leu
420 425 430

Tyr Lys Lys Leu Phe Ser Arg Arg Asp Pro Glu Glu Asp Gly Met Met
435 440 445

Lys Arg Arg Gly Arg Gln Gly Pro Asn Ala Asn Leu Val Lys Thr Leu
450 455 460

Val Phe Phe Phe Leu Glu Ser Glu Leu His Glu His Ala Ala Tyr Leu
465 470 475 480

Val Asp Ser Met Trp Asp Cys Ala Thr Glu Leu Leu Lys Asp Trp Glu
485 490 495

Cys Met Asn Ser Leu Leu Leu Glu Glu Pro Leu Ser Gly Glu Glu Ala
500 505 510

Leu Thr Asp Arg Gln Glu Ser Ala Leu Ile Glu Ile Met Leu Cys Thr
515 520 525

Ile Arg Gln Ala Ala Glu Cys His Pro Pro Val Gly Arg Gly Thr Gly

ITI-08-PCT_Sequence_Listing_ST25.txt

```

530          535          540
Lys Arg Val Leu Thr Ala Lys Glu Lys Lys Thr Gln Leu Asp Asp Arg
545          550          555          560
Thr Lys Ile Thr Glu Leu Phe Ala Val Ala Leu Pro Gln Leu Leu Ala
565          570          575
Lys Tyr Ser Val Asp Ala Glu Lys Val Thr Asn Leu Leu Gln Leu Pro
580          585          590
Gln Tyr Phe Asp Leu Glu Ile Tyr Thr Thr Gly Arg Leu Glu Lys His
595          600          605
Leu Asp Ala Leu Leu Arg Gln Ile Arg Asn Ile Val Glu Lys His Thr
610          615          620
Asp Thr Asp Val Leu Glu Ala Cys Ser Lys Thr Tyr His Ala Leu Cys
625          630          635          640
Asn Glu Glu Phe Thr Ile Phe Asn Arg Val Asp Ile Ser Arg Ser Gln
645          650          655
Leu Ile Asp Glu Leu Ala Asp Lys Phe Asn Arg Leu Leu Glu Asp Phe
660          665          670
Leu Gln Glu Gly Glu Glu Pro Asp Glu Asp Asp Ala Tyr Gln Val Leu
675          680          685
Ser Thr Leu Lys Arg Ile Thr Ala Phe His Asn Ala His Asp Leu Ser
690          695          700
Lys Trp Asp Leu Phe Ala Cys Asn Tyr Lys Leu Leu Lys Thr Gly Ile
705          710          715          720
Glu Asn Gly Asp Met Pro Glu Gln Ile Val Ile His Ala Leu Gln Cys
725          730          735
Thr His Tyr Val Ile Leu Trp Gln Leu Ala Lys Ile Thr Glu Ser Ser
740          745          750
Ser Thr Lys Glu Asp Leu Leu Arg Leu Lys Lys Gln Met Arg Val Phe
755          760          765
Cys Gln Ile Cys Gln His Tyr Leu Thr Asn Val Asn Thr Thr Val Lys
770          775          780
Glu Gln Ala Phe Thr Ile Leu Cys Asp Ile Leu Met Ile Phe Ser His
785          790          795          800
Gln Ile Met Ser Gly Gly Arg Asp Met Leu Glu Pro Leu Val Tyr Thr
805          810          815

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Pro	Asp	Ser	820			Leu	Gln	Ser	Glu	Leu	Ser	Phe	Ile	Leu	Asp	His
										825				830		
Val	Phe	Ile	Glu	Gln	Asp	Asp	Asp	Asn	Asn	Ser	Ala	Asp	Gly	Gln	Gln	
		835					840					845				
Glu	Asp	Glu	Ala	Ser	Lys	Ile	Glu	Ala	Leu	His	Lys	Arg	Arg	Asn	Leu	
		850				855					860					
Leu	Ala	Ala	Phe	Cys	Lys	Leu	Ile	Val	Tyr	Thr	Val	Val	Glu	Met	Asn	
865					870					875					880	
Thr	Ala	Ala	Asp	Ile	Phe	Lys	Gln	Tyr	Met	Lys	Tyr	Tyr	Asn	Asp	Tyr	
				885					890					895		
Gly	Asp	Ile	Ile	Lys	Glu	Thr	Met	Ser	Lys	Thr	Arg	Gln	Ile	Asp	Lys	
			900					905					910			
Ile	Gln	Cys	Ala	Lys	Thr	Leu	Ile	Leu	Ser	Leu	Gln	Gln	Leu	Phe	Asn	
		915					920					925				
Glu	Met	Ile	Gln	Glu	Asn	Gly	Tyr	Asn	Phe	Asp	Arg	Ser	Ser	Ser	Thr	
		930				935					940					
Phe	Ser	Gly	Ile	Lys	Glu	Leu	Ala	Arg	Arg	Phe	Ala	Leu	Thr	Phe	Gly	
945					950					955					960	
Leu	Asp	Gln	Leu	Lys	Thr	Arg	Glu	Ala	Ile	Ala	Met	Leu	His	Lys	Asp	
				965					970					975		
Gly	Ile	Glu	Phe	Ala	Phe	Lys	Glu	Pro	Asn	Pro	Gln	Gly	Glu	Ser	His	
			980					985					990			
Pro	Pro	Leu	Asn	Leu	Ala	Phe	Leu	Asp	Ile	Leu	Ser	Glu	Phe	Ser	Ser	
		995					1000					1005				
Lys	Leu	Leu	Arg	Gln	Asp	Lys	Arg	Thr	Val	Tyr	Val	Tyr	Leu	Glu		
	1010					1015					1020					
Lys	Phe	Met	Thr	Phe	Gln	Met	Ser	Leu	Arg	Arg	Glu	Asp	Val	Trp		
	1025					1030					1035					
Leu	Pro	Leu	Met	Ser	Tyr	Arg	Asn	Ser	Leu	Leu	Ala	Gly	Gly	Asp		
	1040					1045					1050					
Asp	Asp	Thr	Met	Ser	Val	Ile	Ser	Gly	Ile	Ser	Ser	Arg	Gly	Ser		
	1055					1060					1065					
Thr	Val	Arg	Ser	Lys	Lys	Ser	Lys	Pro	Ser	Thr	Gly	Lys	Arg	Lys		
	1070					1075					1080					

ITI-08-PCT_Sequence_Listing_ST25.txt

Val	Val	Glu	Gly	Met	Gln	Leu	Ser	Leu	Thr	Glu	Glu	Ser	Ser	Ser
1085						1090					1095			
Ser	Asp	Ser	Met	Trp	Leu	Ser	Arg	Glu	Gln	Thr	Leu	His	Thr	Pro
1100						1105					1110			
Val	Met	Met	Gln	Thr	Pro	Gln	Leu	Thr	Ser	Thr	Ile	Met	Arg	Glu
1115						1120					1125			
Pro	Lys	Arg	Leu	Arg	Pro	Glu	Asp	Ser	Phe	Met	Ser	Val	Tyr	Pro
1130						1135					1140			
Met	Gln	Thr	Glu	His	His	Gln	Thr	Pro	Leu	Asp	Tyr	Asn	Thr	Gln
1145						1150					1155			
Val	Thr	Trp	Met	Leu	Ala	Gln	Arg	Gln	Gln	Glu	Glu	Ala	Arg	Gln
1160						1165					1170			
Gln	Gln	Glu	Arg	Ala	Ala	Met	Ser	Tyr	Val	Lys	Leu	Arg	Thr	Asn
1175						1180					1185			
Leu	Gln	His	Ala	Ile	Arg	Arg	Gly	Thr	Ser	Leu	Met	Glu	Asp	Asp
1190						1195					1200			
Glu	Glu	Pro	Ile	Val	Glu	Asp	Val	Met	Met	Ser	Ser	Glu	Gly	Arg
1205						1210					1215			
Ile	Glu	Asp	Leu	Asn	Glu	Gly	Met	Asp	Phe	Asp	Thr	Met	Asp	Ile
1220						1225					1230			
Asp	Leu	Pro	Pro	Ser	Lys	Asn	Arg	Arg	Glu	Arg	Thr	Glu	Leu	Lys
1235						1240					1245			
Pro	Asp	Phe	Phe	Asp	Pro	Ala	Ser	Ile	Met	Asp	Glu	Ser	Val	Leu
1250						1255					1260			
Gly	Val	Ser	Met	Phe										
1265														

<210> 643

<211> 490

<212> PRT

<213> Artificial Sequence

<220>

<223> STAMP-1__Homo_sapiens__Q8NFT2

<400> 643

Met	Glu	Ser	Ile	Ser	Met	Met	Gly	Ser	Pro	Lys	Ser	Leu	Ser	Glu	Thr
1				5				10						15	

ITI-08-PCT_Sequence_Listing_ST25.txt

Phe Leu Pro Asn Gly Ile Asn Gly Ile Lys Asp Ala Arg Lys Val Thr
 20 25 30
 Val Gly Val Ile Gly Ser Gly Asp Phe Ala Lys Ser Leu Thr Ile Arg
 35 40 45
 Leu Ile Arg Cys Gly Tyr His Val Val Ile Gly Ser Arg Asn Pro Lys
 50 55 60
 Phe Ala Ser Glu Phe Phe Pro His Val Val Asp Val Thr His His Glu
 65 70 75 80
 Asp Ala Leu Thr Lys Thr Asn Ile Ile Phe Val Ala Ile His Arg Glu
 85 90 95
 His Tyr Thr Ser Leu Trp Asp Leu Arg His Leu Leu Val Gly Lys Ile
 100 105 110
 Leu Ile Asp Val Ser Asn Asn Met Arg Ile Asn Gln Tyr Pro Glu Ser
 115 120 125
 Asn Ala Glu Tyr Leu Ala Ser Leu Phe Pro Asp Ser Leu Ile Val Lys
 130 135 140
 Gly Phe Asn Val Val Ser Ala Trp Ala Leu Gln Leu Gly Pro Lys Asp
 145 150 155 160
 Ala Ser Arg Gln Val Tyr Ile Cys Ser Asn Asn Ile Gln Ala Arg Gln
 165 170 175
 Gln Val Ile Glu Leu Ala Arg Gln Leu Asn Phe Ile Pro Ile Asp Leu
 180 185 190
 Gly Ser Leu Ser Ser Ala Arg Glu Ile Glu Asn Leu Pro Leu Arg Leu
 195 200 205
 Phe Thr Leu Trp Arg Gly Pro Val Val Val Ala Ile Ser Leu Ala Thr
 210 215 220
 Phe Phe Phe Leu Tyr Ser Phe Val Arg Asp Val Ile His Pro Tyr Ala
 225 230 235 240
 Arg Asn Gln Gln Ser Asp Phe Tyr Lys Ile Pro Ile Glu Ile Val Asn
 245 250 255
 Lys Thr Leu Pro Ile Val Ala Ile Thr Leu Leu Ser Leu Val Tyr Leu
 260 265 270
 Ala Gly Leu Leu Ala Ala Ala Tyr Gln Leu Tyr Tyr Gly Thr Lys Tyr
 275 280 285
 Arg Arg Phe Pro Pro Trp Leu Glu Thr Trp Leu Gln Cys Arg Lys Gln

ITI-08-PCT_Sequence_Listing_ST25.txt

290

295

300

Leu Gly Leu Leu Ser Phe Phe Phe Ala Met Val His Val Ala Tyr Ser
305 310 315 320

Leu Cys Leu Pro Met Arg Arg Ser Glu Arg Tyr Leu Phe Leu Asn Met
325 330 335

Ala Tyr Gln Gln Val His Ala Asn Ile Glu Asn Ser Trp Asn Glu Glu
340 345 350

Glu Val Trp Arg Ile Glu Met Tyr Ile Ser Phe Gly Ile Met Ser Leu
355 360 365

Gly Leu Leu Ser Leu Leu Ala Val Thr Ser Ile Pro Ser Val Ser Asn
370 375 380

Ala Leu Asn Trp Arg Glu Phe Ser Phe Ile Gln Ser Thr Leu Gly Tyr
385 390 395 400

Val Ala Leu Leu Ile Ser Thr Phe His Val Leu Ile Tyr Gly Trp Lys
405 410 415

Arg Ala Phe Glu Glu Glu Tyr Tyr Arg Phe Tyr Thr Pro Pro Asn Phe
420 425 430

Val Leu Ala Leu Val Leu Pro Ser Ile Val Ile Leu Gly Lys Ile Ile
435 440 445

Leu Phe Leu Pro Cys Ile Ser Arg Lys Leu Lys Arg Ile Lys Lys Gly
450 455 460

Trp Glu Lys Ser Gln Phe Leu Glu Glu Gly Met Gly Gly Thr Ile Pro
465 470 475 480

His Val Ser Pro Glu Arg Val Thr Val Met
485 490

<210> 644

<211> 258

<212> PRT

<213> Artificial Sequence

<220>

<223> STEAP-1__Homo_sapiens__A0A024RA63

<400> 644

Met Glu Ser Arg Lys Asp Ile Thr Asn Gln Glu Glu Ile Trp Lys Met
1 5 10 15

Lys Pro Arg Arg Asn Leu Glu Asp Asn Asp Tyr Leu His Lys Asp Thr

ITI-08-PCT_Sequence_Listing_ST25.txt

```

      20      25      30
Gly Glu Thr Ser Met Leu Lys Arg Pro Val Leu Leu His Leu Gln Gln
      35      40      45
Thr Ala His Ala Asp Glu Phe Asp Cys Pro Ser Glu Leu Gln His Ala
      50      55      60
Gln Glu Leu Phe Pro Gln Trp His Leu Pro Ile Lys Ile Ala Ala Val
      65      70      75      80
Met Ala Ser Leu Thr Phe Leu Tyr Thr Leu Leu Arg Glu Val Ile His
      85      90      95
Pro Leu Ala Thr Ser His Gln Gln Tyr Phe Tyr Lys Ile Pro Ile Leu
      100      105      110
Val Ile Asn Lys Val Leu Pro Met Val Ser Ile Thr Leu Leu Ala Leu
      115      120      125
Val Tyr Leu Pro Gly Val Ile Ala Ala Ile Val Gln Val His Asn Gly
      130      135      140
Thr Lys Tyr Lys Lys Phe Pro His Trp Leu Asp Lys Trp Met Leu Thr
      145      150      155      160
Arg Lys Gln Phe Gly Leu Leu Ser Leu Phe Phe Ala Val Leu His Ala
      165      170      175
Ile Tyr Thr Leu Ser Tyr Ala Met Arg Arg Ser Tyr Arg Tyr Lys Leu
      180      185      190
Leu Asn Trp Ala Tyr Gln Gln Val Gln Gln Asn Lys Glu Asp Ala Trp
      195      200      205
Ile Glu His Asp Val Trp Arg Met Glu Ile Tyr Val Ser Leu Gly Ile
      210      215      220
Val Gly Leu Ala Ile Leu Ala Leu Leu Ala Val Thr Ser Ile Pro Ser
      225      230      235      240
Val Ser Asp Ser Leu Thr Trp Arg Glu Phe His Tyr Ile Gln Val Asn
      245      250      255

```

Asn Ile

<210> 645
 <211> 339
 <212> PRT
 <213> Artificial Sequence

<220>

ITI-08-PCT_Sequence_Listing_ST25.txt

<223> STEAP-1__Homo_sapiens__Q9UHE8

<400> 645

```

Met Glu Ser Arg Lys Asp Ile Thr Asn Gln Glu Glu Leu Trp Lys Met
1          5          10          15

Lys Pro Arg Arg Asn Leu Glu Glu Asp Asp Tyr Leu His Lys Asp Thr
          20          25          30

Gly Glu Thr Ser Met Leu Lys Arg Pro Val Leu Leu His Leu His Gln
          35          40          45

Thr Ala His Ala Asp Glu Phe Asp Cys Pro Ser Glu Leu Gln His Thr
          50          55          60

Gln Glu Leu Phe Pro Gln Trp His Leu Pro Ile Lys Ile Ala Ala Ile
65          70          75          80

Ile Ala Ser Leu Thr Phe Leu Tyr Thr Leu Leu Arg Glu Val Ile His
          85          90          95

Pro Leu Ala Thr Ser His Gln Gln Tyr Phe Tyr Lys Ile Pro Ile Leu
          100          105          110

Val Ile Asn Lys Val Leu Pro Met Val Ser Ile Thr Leu Leu Ala Leu
          115          120          125

Val Tyr Leu Pro Gly Val Ile Ala Ala Ile Val Gln Leu His Asn Gly
          130          135          140

Thr Lys Tyr Lys Lys Phe Pro His Trp Leu Asp Lys Trp Met Leu Thr
145          150          155          160

Arg Lys Gln Phe Gly Leu Leu Ser Phe Phe Phe Ala Val Leu His Ala
          165          170          175

Ile Tyr Ser Leu Ser Tyr Pro Met Arg Arg Ser Tyr Arg Tyr Lys Leu
          180          185          190

Leu Asn Trp Ala Tyr Gln Gln Val Gln Gln Asn Lys Glu Asp Ala Trp
          195          200          205

Ile Glu His Asp Val Trp Arg Met Glu Ile Tyr Val Ser Leu Gly Ile
          210          215          220

Val Gly Leu Ala Ile Leu Ala Leu Leu Ala Val Thr Ser Ile Pro Ser
225          230          235          240

Val Ser Asp Ser Leu Thr Trp Arg Glu Phe His Tyr Ile Gln Ser Lys
          245          250          255

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Leu Gly Ile Val Ser Leu Leu Leu Gly Thr Ile His Ala Leu Ile Phe
260 265 270

Ala Trp Asn Lys Trp Ile Asp Ile Lys Gln Phe Val Trp Tyr Thr Pro
275 280 285

Pro Thr Phe Met Ile Ala Val Phe Leu Pro Ile Val Val Leu Ile Phe
290 295 300

Lys Ser Ile Leu Phe Leu Pro Cys Leu Arg Lys Lys Ile Leu Lys Ile
305 310 315 320

Arg His Gly Trp Glu Asp Val Thr Lys Ile Asn Lys Thr Glu Ile Cys
325 330 335

Ser Gln Leu

<210> 646

<211> 165

<212> PRT

<213> Artificial Sequence

<220>

<223> Survivin-2B__Homo_sapiens__015392-2

<400> 646

Met Gly Ala Pro Thr Leu Pro Pro Ala Trp Gln Pro Phe Leu Lys Asp
1 5 10 15

His Arg Ile Ser Thr Phe Lys Asn Trp Pro Phe Leu Glu Gly Cys Ala
20 25 30

Cys Thr Pro Glu Arg Met Ala Glu Ala Gly Phe Ile His Cys Pro Thr
35 40 45

Glu Asn Glu Pro Asp Leu Ala Gln Cys Phe Phe Cys Phe Lys Glu Leu
50 55 60

Glu Gly Trp Glu Pro Asp Asp Asp Pro Ile Gly Pro Gly Thr Val Ala
65 70 75 80

Tyr Ala Cys Asn Thr Ser Thr Leu Gly Gly Arg Gly Gly Arg Ile Thr
85 90 95

Arg Glu Glu His Lys Lys His Ser Ser Gly Cys Ala Phe Leu Ser Val
100 105 110

Lys Lys Gln Phe Glu Glu Leu Thr Leu Gly Glu Phe Leu Lys Leu Asp
115 120 125

Arg Glu Arg Ala Lys Asn Lys Ile Ala Lys Glu Thr Asn Asn Lys Lys

ITI-08-PCT_Sequence_Listing_ST25.txt

130

135

140

Lys Glu Phe Glu Glu Thr Ala Glu Lys Val Arg Arg Ala Ile Glu Gln
145 150 155 160

Leu Ala Ala Met Asp
165

<210> 647

<211> 142

<212> PRT

<213> Artificial Sequence

<220>

<223> survivin__Homo_sapiens__015392

<400> 647

Met Gly Ala Pro Thr Leu Pro Pro Ala Trp Gln Pro Phe Leu Lys Asp
1 5 10 15

His Arg Ile Ser Thr Phe Lys Asn Trp Pro Phe Leu Glu Gly Cys Ala
20 25 30

Cys Thr Pro Glu Arg Met Ala Glu Ala Gly Phe Ile His Cys Pro Thr
35 40 45

Glu Asn Glu Pro Asp Leu Ala Gln Cys Phe Phe Cys Phe Lys Glu Leu
50 55 60

Glu Gly Trp Glu Pro Asp Asp Asp Pro Ile Glu Glu His Lys Lys His
65 70 75 80

Ser Ser Gly Cys Ala Phe Leu Ser Val Lys Lys Gln Phe Glu Glu Leu
85 90 95

Thr Leu Gly Glu Phe Leu Lys Leu Asp Arg Glu Arg Ala Lys Asn Lys
100 105 110

Ile Ala Lys Glu Thr Asn Asn Lys Lys Lys Glu Phe Glu Glu Thr Ala
115 120 125

Lys Lys Val Arg Arg Ala Ile Glu Gln Leu Ala Ala Met Asp
130 135 140

<210> 648

<211> 976

<212> PRT

<213> Artificial Sequence

<220>

<223> SYCP1__Homo_sapiens__A0A024R0I2

ITI-08-PCT_Sequence_Listing_ST25.txt

<400> 648

```

Met Glu Lys Gln Lys Pro Phe Ala Leu Phe Val Pro Pro Arg Ser Ser
1          5          10          15

Ser Ser Gln Val Ser Ala Val Lys Pro Gln Thr Leu Gly Gly Asp Ser
          20          25          30

Thr Phe Phe Lys Ser Phe Asn Lys Cys Thr Glu Asp Asp Phe Glu Phe
          35          40          45

Pro Phe Ala Lys Thr Asn Leu Ser Lys Asn Gly Glu Asn Ile Asp Ser
          50          55          60

Asp Pro Ala Leu Gln Lys Val Asn Phe Leu Pro Val Leu Glu Gln Val
65          70          75          80

Gly Asn Ser Asp Cys His Tyr Gln Glu Gly Leu Lys Asp Ser Asp Leu
          85          90          95

Glu Asn Ser Glu Gly Leu Ser Arg Val Tyr Ser Lys Leu Tyr Lys Glu
          100          105          110

Ala Glu Lys Ile Lys Lys Trp Lys Val Ser Thr Glu Ala Glu Leu Arg
          115          120          125

Gln Lys Glu Ser Lys Leu Gln Glu Asn Arg Lys Ile Ile Glu Ala Gln
          130          135          140

Arg Lys Ala Ile Gln Glu Leu Gln Phe Gly Asn Glu Lys Val Ser Leu
145          150          155          160

Lys Leu Glu Glu Gly Ile Gln Glu Asn Lys Asp Leu Ile Lys Glu Asn
          165          170          175

Asn Ala Thr Arg His Leu Cys Asn Leu Leu Lys Glu Thr Cys Ala Arg
          180          185          190

Ser Ala Glu Lys Thr Lys Lys Tyr Glu Tyr Glu Arg Glu Glu Thr Arg
          195          200          205

Gln Val Tyr Met Asp Leu Asn Asn Asn Ile Glu Lys Met Ile Thr Ala
          210          215          220

Phe Glu Glu Leu Arg Val Gln Ala Glu Asn Ser Arg Leu Glu Met His
225          230          235          240

Phe Lys Leu Lys Glu Asp Tyr Glu Lys Ile Gln His Leu Glu Gln Glu
          245          250          255

Tyr Lys Lys Glu Ile Asn Asp Lys Glu Lys Gln Val Ser Leu Leu Leu

```

260 265 270

Page 1109

ITI-08-PCT_Sequence_Listing_ST25.txt

Gln	Glu	Asp	Ile	Asn	Asn	Asn	Lys	Lys	Gln	Glu	Glu	Arg	Met	Leu	Lys	545	550	555	560
Gln	Ile	Glu	Asn	Leu	Gln	Glu	Thr	Glu	Thr	Gln	Leu	Arg	Asn	Glu	Leu	565	570	575	
Glu	Tyr	Val	Arg	Glu	Glu	Leu	Lys	Gln	Lys	Arg	Asp	Glu	Val	Lys	Cys	580	585	590	
Lys	Leu	Asp	Lys	Ser	Glu	Glu	Asn	Cys	Asn	Asn	Leu	Arg	Lys	Gln	Val	595	600	605	
Glu	Asn	Lys	Asn	Lys	Tyr	Ile	Glu	Glu	Leu	Gln	Gln	Glu	Asn	Lys	Ala	610	615	620	
Leu	Lys	Lys	Lys	Gly	Thr	Ala	Glu	Ser	Lys	Gln	Leu	Asn	Val	Tyr	Glu	625	630	635	640
Ile	Lys	Val	Asn	Lys	Leu	Glu	Leu	Glu	Leu	Glu	Ser	Ala	Lys	Gln	Lys	645	650	655	
Phe	Gly	Glu	Ile	Thr	Asp	Thr	Tyr	Gln	Lys	Glu	Ile	Glu	Asp	Lys	Lys	660	665	670	
Ile	Ser	Glu	Glu	Asn	Leu	Leu	Glu	Glu	Val	Glu	Lys	Ala	Lys	Val	Ile	675	680	685	
Ala	Asp	Glu	Ala	Val	Lys	Leu	Gln	Lys	Glu	Ile	Asp	Lys	Arg	Cys	Gln	690	695	700	
His	Lys	Ile	Ala	Glu	Met	Val	Ala	Leu	Met	Glu	Lys	His	Lys	His	Gln	705	710	715	720
Tyr	Asp	Lys	Ile	Ile	Glu	Glu	Arg	Asp	Ser	Glu	Leu	Gly	Leu	Tyr	Lys	725	730	735	
Ser	Lys	Glu	Gln	Glu	Gln	Ser	Ser	Leu	Arg	Ala	Ser	Leu	Glu	Ile	Glu	740	745	750	
Leu	Ser	Asn	Leu	Lys	Ala	Glu	Leu	Leu	Ser	Val	Lys	Lys	Gln	Leu	Glu	755	760	765	
Ile	Glu	Arg	Glu	Glu	Lys	Glu	Lys	Leu	Lys	Arg	Glu	Ala	Lys	Glu	Asn	770	775	780	
Thr	Ala	Thr	Leu	Lys	Glu	Lys	Lys	Asp	Lys	Lys	Thr	Gln	Thr	Phe	Leu	785	790	795	800
Leu	Glu	Thr	Pro	Glu	Ile	Tyr	Trp	Lys	Leu	Asp	Ser	Lys	Ala	Val	Pro	805	810	815	

ITI-08-PCT_Sequence_Listing_ST25.txt

Ser Gln Thr Val Ser Arg Asn Phe Thr Ser Val Asp His Gly Ile Ser
820 825 830

Lys Asp Lys Arg Asp Tyr Leu Trp Thr Ser Ala Lys Asn Thr Leu Ser
835 840 845

Thr Pro Leu Pro Lys Ala Tyr Thr Val Lys Thr Pro Thr Lys Pro Lys
850 855 860

Leu Gln Gln Arg Glu Asn Leu Asn Ile Pro Ile Glu Glu Ser Lys Lys
865 870 875 880

Lys Arg Lys Met Ala Phe Glu Phe Asp Ile Asn Ser Asp Ser Ser Glu
885 890 895

Thr Thr Asp Leu Leu Ser Met Val Ser Glu Glu Glu Thr Leu Lys Thr
900 905 910

Leu Tyr Arg Asn Asn Asn Pro Pro Ala Ser His Leu Cys Val Lys Thr
915 920 925

Pro Lys Lys Ala Pro Ser Ser Leu Thr Thr Pro Gly Ser Thr Leu Lys
930 935 940

Phe Gly Ala Ile Arg Lys Met Arg Glu Asp Arg Trp Ala Val Ile Ala
945 950 955 960

Lys Met Asp Arg Lys Lys Lys Leu Lys Glu Ala Glu Lys Leu Phe Val
965 970 975

<210> 649

<211> 976

<212> PRT

<213> Artificial Sequence

<220>

<223> SYCP1__Homo_sapiens__B7ZLS9

<400> 649

Met Glu Lys Gln Lys Pro Phe Ala Leu Phe Val Pro Pro Arg Ser Ser
1 5 10 15

Ser Ser Gln Val Ser Ala Val Lys Pro Gln Thr Leu Gly Gly Asp Ser
20 25 30

Thr Phe Phe Lys Ser Phe Asn Lys Cys Thr Glu Asp Asp Phe Glu Phe
35 40 45

Pro Phe Ala Lys Thr Asn Leu Ser Lys Asn Gly Glu Asn Ile Asp Ser
50 55 60

ITI-08-PCT_Sequence_Listing_ST25.txt

Asp	Pro	Ala	Leu	Gln	Lys	Val	Asn	Phe	Leu	Pro	Val	Phe	Glu	Gln	Val	65	70	75	80
Gly	Asn	Ser	Asp	Cys	His	Tyr	Gln	Glu	Gly	Leu	Lys	Asp	Ser	Asp	Leu		85	90	95
Glu	Asn	Ser	Glu	Gly	Leu	Ser	Arg	Val	Tyr	Ser	Lys	Leu	Tyr	Lys	Glu	100	105	110	
Ala	Glu	Lys	Ile	Lys	Lys	Trp	Lys	Val	Ser	Thr	Glu	Ala	Glu	Leu	Arg	115	120	125	
Gln	Lys	Glu	Ser	Lys	Leu	Gln	Glu	Asn	Arg	Lys	Ile	Ile	Glu	Ala	Gln	130	135	140	
Arg	Lys	Ala	Ile	Gln	Glu	Leu	Gln	Phe	Gly	Asn	Glu	Lys	Val	Ser	Leu	145	150	155	160
Lys	Leu	Glu	Glu	Gly	Ile	Gln	Glu	Asn	Lys	Asp	Leu	Ile	Lys	Glu	Asn		165	170	175
Asn	Ala	Thr	Arg	His	Leu	Cys	Asn	Leu	Leu	Lys	Glu	Thr	Cys	Ala	Arg	180	185	190	
Ser	Ala	Glu	Lys	Thr	Lys	Lys	Tyr	Glu	Tyr	Glu	Arg	Glu	Glu	Thr	Arg	195	200	205	
Gln	Val	Tyr	Met	Asp	Leu	Asn	Ser	Asn	Ile	Glu	Lys	Met	Ile	Thr	Ala	210	215	220	
Phe	Glu	Glu	Leu	Arg	Val	Gln	Ala	Glu	Asn	Ser	Arg	Leu	Glu	Met	His	225	230	235	240
Phe	Lys	Leu	Lys	Glu	Asp	Tyr	Glu	Lys	Ile	Gln	His	Leu	Glu	Gln	Glu		245	250	255
Tyr	Lys	Lys	Glu	Ile	Asn	Asp	Lys	Glu	Lys	Gln	Val	Ser	Leu	Leu	Leu	260	265	270	
Ile	Gln	Ile	Thr	Glu	Lys	Glu	Asn	Lys	Met	Lys	Asp	Leu	Thr	Phe	Leu	275	280	285	
Leu	Glu	Glu	Ser	Arg	Asp	Lys	Val	Asn	Gln	Leu	Glu	Glu	Lys	Thr	Lys	290	295	300	
Leu	Gln	Ser	Glu	Asn	Leu	Lys	Gln	Ser	Ile	Glu	Lys	Gln	His	His	Leu	305	310	315	320
Thr	Lys	Glu	Leu	Glu	Asp	Ile	Lys	Val	Ser	Leu	Gln	Arg	Ser	Val	Ser		325	330	335
Thr	Gln	Lys	Ala	Leu	Glu	Glu	Asp	Leu	Gln	Ile	Ala	Thr	Lys	Thr	Ile				

340 345 350

Page 1113

ITI-08-PCT_Sequence_Listing_ST25.txt

Leu	Lys	Lys	Lys	Gly	Thr	Ala	Glu	Ser	Lys	Gln	Leu	Asn	Val	Tyr	Glu	625	630	635	640
Ile	Lys	Val	Asn	Lys	Leu	Glu	Leu	Glu	Leu	Glu	Ser	Ala	Lys	Gln	Lys	645	650	655	
Phe	Gly	Glu	Ile	Thr	Asp	Thr	Tyr	Gln	Lys	Glu	Ile	Glu	Asp	Lys	Lys	660	665	670	
Ile	Ser	Glu	Glu	Asn	Leu	Leu	Glu	Glu	Val	Glu	Lys	Ala	Lys	Val	Ile	675	680	685	
Ala	Asp	Glu	Ala	Val	Lys	Leu	Gln	Lys	Glu	Ile	Asp	Lys	Arg	Cys	Gln	690	695	700	
His	Lys	Ile	Ala	Glu	Met	Val	Ala	Leu	Met	Glu	Lys	His	Lys	His	Gln	705	710	715	720
Tyr	Asp	Lys	Ile	Ile	Glu	Glu	Arg	Asp	Ser	Glu	Leu	Gly	Leu	Tyr	Lys	725	730	735	
Ser	Lys	Glu	Gln	Glu	Gln	Ser	Ser	Leu	Arg	Ala	Ser	Leu	Glu	Ile	Glu	740	745	750	
Leu	Ser	Asn	Leu	Lys	Ala	Glu	Leu	Leu	Ser	Val	Lys	Lys	Gln	Leu	Glu	755	760	765	
Ile	Glu	Arg	Glu	Glu	Lys	Glu	Lys	Leu	Lys	Arg	Glu	Ala	Lys	Glu	Asn	770	775	780	
Thr	Ala	Thr	Leu	Lys	Glu	Lys	Lys	Asp	Lys	Lys	Thr	Gln	Thr	Phe	Leu	785	790	795	800
Leu	Glu	Thr	Pro	Glu	Ile	Tyr	Trp	Lys	Leu	Asp	Ser	Lys	Ala	Val	Pro	805	810	815	
Ser	Gln	Thr	Val	Ser	Arg	Asn	Phe	Thr	Ser	Val	Asp	His	Gly	Ile	Ser	820	825	830	
Lys	Asp	Lys	Arg	Asp	Tyr	Leu	Trp	Thr	Ser	Ala	Lys	Asn	Thr	Leu	Ser	835	840	845	
Thr	Pro	Leu	Pro	Lys	Ala	Tyr	Thr	Val	Lys	Thr	Pro	Thr	Lys	Pro	Lys	850	855	860	
Leu	Gln	Gln	Arg	Glu	Asn	Leu	Asn	Ile	Pro	Ile	Glu	Glu	Ser	Lys	Lys	865	870	875	880
Lys	Arg	Lys	Met	Ala	Phe	Glu	Phe	Asp	Ile	Asn	Ser	Asp	Ser	Ser	Glu	885	890	895	

ITI-08-PCT_Sequence_Listing_ST25.txt

Thr Thr Asp Leu Leu Ser Met Val Ser Glu Glu Glu Thr Leu Lys Thr
900 905 910

Leu Tyr Arg Asn Asn Asn Pro Pro Ala Ser His Leu Cys Val Lys Thr
915 920 925

Pro Lys Lys Ala Pro Ser Ser Leu Thr Thr Pro Gly Ser Thr Leu Lys
930 935 940

Phe Gly Ala Ile Arg Lys Met Arg Glu Asp Arg Trp Ala Val Ile Ala
945 950 955 960

Lys Met Asp Arg Lys Lys Lys Leu Lys Glu Ala Glu Lys Leu Phe Val
965 970 975

<210> 650

<211> 976

<212> PRT

<213> Artificial Sequence

<220>

<223> SYCP1__Homo_sapiens__Q15431

<400> 650

Met Glu Lys Gln Lys Pro Phe Ala Leu Phe Val Pro Pro Arg Ser Ser
1 5 10 15

Ser Ser Gln Val Ser Ala Val Lys Pro Gln Thr Leu Gly Gly Asp Ser
20 25 30

Thr Phe Phe Lys Ser Phe Asn Lys Cys Thr Glu Asp Asp Phe Glu Phe
35 40 45

Pro Phe Ala Lys Thr Asn Leu Ser Lys Asn Gly Glu Asn Ile Asp Ser
50 55 60

Asp Pro Ala Leu Gln Lys Val Asn Phe Leu Pro Val Leu Glu Gln Val
65 70 75 80

Gly Asn Ser Asp Cys His Tyr Gln Glu Gly Leu Lys Asp Ser Asp Leu
85 90 95

Glu Asn Ser Glu Gly Leu Ser Arg Val Tyr Ser Lys Leu Tyr Lys Glu
100 105 110

Ala Glu Lys Ile Lys Lys Trp Lys Val Ser Thr Glu Ala Glu Leu Arg
115 120 125

Gln Lys Glu Ser Lys Leu Gln Glu Asn Arg Lys Ile Ile Glu Ala Gln
130 135 140

ITI-08-PCT_Sequence_Listing_ST25.txt

Arg Lys Ala Ile Gln Glu Leu Gln Phe Gly Asn Glu Lys Val Ser Leu
 145 150 155 160
 Lys Leu Glu Glu Gly Ile Gln Glu Asn Lys Asp Leu Ile Lys Glu Asn
 165 170 175
 Asn Ala Thr Arg His Leu Cys Asn Leu Leu Lys Glu Thr Cys Ala Arg
 180 185 190
 Ser Ala Glu Lys Thr Lys Lys Tyr Glu Tyr Glu Arg Glu Glu Thr Arg
 195 200 205
 Gln Val Tyr Met Asp Leu Asn Asn Asn Ile Glu Lys Met Ile Thr Ala
 210 215 220
 Phe Glu Glu Leu Arg Val Gln Ala Glu Asn Ser Arg Leu Glu Met His
 225 230 235 240
 Phe Lys Leu Lys Glu Asp Tyr Glu Lys Ile Gln His Leu Glu Gln Glu
 245 250 255
 Tyr Lys Lys Glu Ile Asn Asp Lys Glu Lys Gln Val Ser Leu Leu Leu
 260 265 270
 Ile Gln Ile Thr Glu Lys Glu Asn Lys Met Lys Asp Leu Thr Phe Leu
 275 280 285
 Leu Glu Glu Ser Arg Asp Lys Val Asn Gln Leu Glu Glu Lys Thr Lys
 290 295 300
 Leu Gln Ser Glu Asn Leu Lys Gln Ser Ile Glu Lys Gln His His Leu
 305 310 315 320
 Thr Lys Glu Leu Glu Asp Ile Lys Val Ser Leu Gln Arg Ser Val Ser
 325 330 335
 Thr Gln Lys Ala Leu Glu Glu Asp Leu Gln Ile Ala Thr Lys Thr Ile
 340 345 350
 Cys Gln Leu Thr Glu Glu Lys Glu Thr Gln Met Glu Glu Ser Asn Lys
 355 360 365
 Ala Arg Ala Ala His Ser Phe Val Val Thr Glu Phe Glu Thr Thr Val
 370 375 380
 Cys Ser Leu Glu Glu Leu Leu Arg Thr Glu Gln Gln Arg Leu Glu Lys
 385 390 395 400
 Asn Glu Asp Gln Leu Lys Ile Leu Thr Met Glu Leu Gln Lys Lys Ser
 405 410 415
 Ser Glu Leu Glu Glu Met Thr Lys Leu Thr Asn Asn Lys Glu Val Glu

ITI-08-PCT_Sequence_Listing_ST25.txt

```

420                               425                               430
Leu Glu Glu Leu Lys Lys Val Leu Gly Glu Lys Glu Thr Leu Leu Tyr
435                               440                               445
Glu Asn Lys Gln Phe Glu Lys Ile Ala Glu Glu Leu Lys Gly Thr Glu
450                               455                               460
Gln Glu Leu Ile Gly Leu Leu Gln Ala Arg Glu Lys Glu Val His Asp
465                               470                               475                               480
Leu Glu Ile Gln Leu Thr Ala Ile Thr Thr Ser Glu Gln Tyr Tyr Ser
485                               490                               495
Lys Glu Val Lys Asp Leu Lys Thr Glu Leu Glu Asn Glu Lys Leu Lys
500                               505                               510
Asn Thr Glu Leu Thr Ser His Cys Asn Lys Leu Ser Leu Glu Asn Lys
515                               520                               525
Glu Leu Thr Gln Glu Thr Ser Asp Met Thr Leu Glu Leu Lys Asn Gln
530                               535                               540
Gln Glu Asp Ile Asn Asn Asn Lys Lys Gln Glu Glu Arg Met Leu Lys
545                               550                               555                               560
Gln Ile Glu Asn Leu Gln Glu Thr Glu Thr Gln Leu Arg Asn Glu Leu
565                               570                               575
Glu Tyr Val Arg Glu Glu Leu Lys Gln Lys Arg Asp Glu Val Lys Cys
580                               585                               590
Lys Leu Asp Lys Ser Glu Glu Asn Cys Asn Asn Leu Arg Lys Gln Val
595                               600                               605
Glu Asn Lys Asn Lys Tyr Ile Glu Glu Leu Gln Gln Glu Asn Lys Ala
610                               615                               620
Leu Lys Lys Lys Gly Thr Ala Glu Ser Lys Gln Leu Asn Val Tyr Glu
625                               630                               635                               640
Ile Lys Val Asn Lys Leu Glu Leu Glu Leu Glu Ser Ala Lys Gln Lys
645                               650                               655
Phe Gly Glu Ile Thr Asp Thr Tyr Gln Lys Glu Ile Glu Asp Lys Lys
660                               665                               670
Ile Ser Glu Glu Asn Leu Leu Glu Glu Val Glu Lys Ala Lys Val Ile
675                               680                               685
Ala Asp Glu Ala Val Lys Leu Gln Lys Glu Ile Asp Lys Arg Cys Gln
690                               695                               700

```


ITI-08-PCT_Sequence_Listing_ST25.txt

His	Lys	Ile	Ala	Glu	Met	Val	Ala	Leu	Met	Glu	Lys	His	Lys	His	Gln
705					710					715					720
Tyr	Asp	Lys	Ile	Ile	Glu	Glu	Arg	Asp	Ser	Glu	Leu	Gly	Leu	Tyr	Lys
			725						730					735	
Ser	Lys	Glu	Gln	Glu	Gln	Ser	Ser	Leu	Arg	Ala	Ser	Leu	Glu	Ile	Glu
		740						745					750		
Leu	Ser	Asn	Leu	Lys	Ala	Glu	Leu	Leu	Ser	Val	Lys	Lys	Gln	Leu	Glu
		755					760					765			
Ile	Glu	Arg	Glu	Glu	Lys	Glu	Lys	Leu	Lys	Arg	Glu	Ala	Lys	Glu	Asn
	770					775					780				
Thr	Ala	Thr	Leu	Lys	Glu	Lys	Lys	Asp	Lys	Lys	Thr	Gln	Thr	Phe	Leu
785					790					795					800
Leu	Glu	Thr	Pro	Glu	Ile	Tyr	Trp	Lys	Leu	Asp	Ser	Lys	Ala	Val	Pro
				805					810					815	
Ser	Gln	Thr	Val	Ser	Arg	Asn	Phe	Thr	Ser	Val	Asp	His	Gly	Ile	Ser
			820					825					830		
Lys	Asp	Lys	Arg	Asp	Tyr	Leu	Trp	Thr	Ser	Ala	Lys	Asn	Thr	Leu	Ser
		835					840					845			
Thr	Pro	Leu	Pro	Lys	Ala	Tyr	Thr	Val	Lys	Thr	Pro	Thr	Lys	Pro	Lys
	850					855					860				
Leu	Gln	Gln	Arg	Glu	Asn	Leu	Asn	Ile	Pro	Ile	Glu	Glu	Ser	Lys	Lys
865					870					875					880
Lys	Arg	Lys	Met	Ala	Phe	Glu	Phe	Asp	Ile	Asn	Ser	Asp	Ser	Ser	Glu
				885					890					895	
Thr	Thr	Asp	Leu	Leu	Ser	Met	Val	Ser	Glu	Glu	Glu	Thr	Leu	Lys	Thr
			900					905					910		
Leu	Tyr	Arg	Asn	Asn	Asn	Pro	Pro	Ala	Ser	His	Leu	Cys	Val	Lys	Thr
		915					920					925			
Pro	Lys	Lys	Ala	Pro	Ser	Ser	Leu	Thr	Thr	Pro	Gly	Ser	Thr	Leu	Lys
	930					935					940				
Phe	Gly	Ala	Ile	Arg	Lys	Met	Arg	Glu	Asp	Arg	Trp	Ala	Val	Ile	Ala
945					950					955					960
Lys	Met	Asp	Arg	Lys	Lys	Lys	Leu	Lys	Glu	Ala	Glu	Lys	Leu	Phe	Val
				965					970					975	

ITI-08-PCT_Sequence_Listing_ST25.txt

<210> 651
 <211> 109
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> SYCP1__Homo_sapiens__Q3MHC4

<400> 651

Met Glu Lys Gln Lys Pro Phe Ala Leu Phe Val Pro Pro Arg Ser Ser
 1 5 10 15

Ser Ser Gln Val Ser Ala Val Lys Pro Gln Thr Leu Gly Gly Asp Ser
 20 25 30

Thr Phe Phe Lys Ser Phe Asn Lys Cys Thr Glu Asp Asp Phe Glu Phe
 35 40 45

Pro Phe Ala Lys Thr Asn Leu Ser Lys Asn Gly Glu Asn Ile Asp Ser
 50 55 60

Asp Pro Ala Leu Gln Asn Val Asn Phe Leu Pro Val Leu Glu Gln Val
 65 70 75 80

Gly Asn Ser Asp Cys His Tyr Gln Glu Gly Leu Lys Asp Ser Asp Leu
 85 90 95

Glu Asn Ser Glu Gly Leu Ser Arg Val Tyr Ser Lys Leu
 100 105

<210> 652
 <211> 488
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> SYT-SSX-1__Homo_sapiens__A4PIV7

<400> 652

Met Ser Val Ala Phe Ala Ala Pro Arg Gln Arg Gly Lys Gly Glu Ile
 1 5 10 15

Thr Pro Ala Ala Ile Gln Lys Met Leu Asp Asp Asn Asn His Leu Ile
 20 25 30

Gln Cys Ile Met Asp Ser Gln Asn Lys Gly Lys Thr Ser Glu Cys Ser
 35 40 45

Gln Tyr Gln Gln Met Leu His Thr Asn Leu Val Tyr Leu Ala Thr Ile
 50 55 60

ITI-08-PCT_Sequence_Listing_ST25.txt

Ala	Asp	Ser	Asn	Gln	Asn	Met	Gln	Ser	Leu	Leu	Pro	Ala	Pro	Pro	Thr	65	70	75	80
Gln	Asn	Met	Pro	Met	Gly	Pro	Gly	Gly	Met	Asn	Gln	Ser	Gly	Pro	Pro	85	90	95	
Pro	Pro	Pro	Arg	Ser	His	Asn	Met	Pro	Ser	Asp	Gly	Met	Val	Gly	Gly	100	105	110	
Gly	Pro	Pro	Ala	Pro	His	Met	Gln	Asn	Gln	Met	Asn	Gly	Gln	Met	Pro	115	120	125	
Gly	Pro	Asn	His	Met	Pro	Met	Gln	Gly	Pro	Gly	Pro	Asn	Gln	Leu	Asn	130	135	140	
Met	Thr	Asn	Ser	Ser	Met	Asn	Met	Pro	Ser	Ser	Ser	His	Gly	Ser	Met	145	150	155	160
Gly	Gly	Tyr	Asn	His	Ser	Val	Pro	Ser	Ser	Gln	Ser	Met	Pro	Val	Gln	165	170	175	
Asn	Gln	Met	Thr	Met	Ser	Gln	Gly	Gln	Pro	Met	Gly	Asn	Tyr	Gly	Pro	180	185	190	
Arg	Pro	Asn	Met	Ser	Met	Gln	Pro	Asn	Gln	Gly	Pro	Met	Met	His	Gln	195	200	205	
Gln	Pro	Pro	Ser	Gln	Gln	Tyr	Asn	Met	Pro	Gln	Gly	Gly	Gly	Gln	His	210	215	220	
Tyr	Gln	Gly	Gln	Gln	Pro	Pro	Met	Gly	Met	Met	Gly	Gln	Val	Asn	Gln	225	230	235	240
Gly	Asn	His	Met	Met	Gly	Gln	Arg	Gln	Ile	Pro	Pro	Tyr	Arg	Pro	Pro	245	250	255	
Gln	Gln	Gly	Pro	Pro	Gln	Gln	Tyr	Ser	Gly	Gln	Glu	Asp	Tyr	Tyr	Gly	260	265	270	
Asp	Gln	Tyr	Ser	His	Gly	Gly	Gln	Gly	Pro	Pro	Glu	Gly	Met	Asn	Gln	275	280	285	
Gln	Tyr	Tyr	Pro	Asp	Gly	His	Asn	Asp	Tyr	Gly	Tyr	Gln	Gln	Pro	Ser	290	295	300	
Tyr	Pro	Glu	Gln	Gly	Tyr	Asp	Arg	Pro	Tyr	Glu	Asp	Ser	Ser	Gln	His	305	310	315	320
Tyr	Tyr	Glu	Gly	Gly	Asn	Ser	Gln	Tyr	Gly	Gln	Gln	Gln	Asp	Ala	Tyr	325	330	335	

ITI-08-PCT_Sequence_Listing_ST25.txt

Gln Gly Pro Pro Pro Gln Gln Gly Tyr Pro Pro Gln Gln Gln Gln Tyr
340 345 350

Pro Gly Gln Gln Gly Tyr Pro Gly Gln Gln Gln Gly Tyr Gly Pro Ser
355 360 365

Gln Gly Gly Pro Gly Pro Gln Tyr Pro Asn Tyr Pro Gln Gly Gln Gly
370 375 380

Gln Gln Tyr Gly Gly Tyr Arg Pro Thr Gln Pro Gly Pro Pro Gln Pro
385 390 395 400

Pro Gln Gln Arg Pro Tyr Gly Tyr Asp Gln Ile Met Pro Lys Lys Pro
405 410 415

Ala Glu Asp Glu Asn Asp Ser Lys Gly Val Ser Glu Ala Ser Gly Pro
420 425 430

Gln Asn Asp Gly Lys Gln Leu His Pro Pro Gly Lys Ala Asn Ile Ser
435 440 445

Glu Lys Ile Asn Lys Arg Ser Gly Pro Lys Arg Gly Lys His Ala Trp
450 455 460

Thr His Arg Leu Arg Glu Arg Lys Gln Leu Val Ile Tyr Glu Glu Ile
465 470 475 480

Ser Asp Pro Glu Glu Asp Asp Glu
485

<210> 653

<211> 457

<212> PRT

<213> Artificial Sequence

<220>

<223> SYT-SSX-1__Homo_sapiens__A4PIV8

<400> 653

Met Ser Val Ala Phe Ala Ala Pro Arg Gln Arg Gly Lys Gly Glu Ile
1 5 10 15

Thr Pro Ala Ala Ile Gln Lys Met Leu Asp Asp Asn Asn His Leu Ile
20 25 30

Gln Cys Ile Met Asp Ser Gln Asn Lys Gly Lys Thr Ser Glu Cys Ser
35 40 45

Gln Tyr Gln Gln Met Leu His Thr Asn Leu Val Tyr Leu Ala Thr Ile
50 55 60

ITI-08-PCT_Sequence_Listing_ST25.txt

Ala	Asp	Ser	Asn	Gln	Asn	Met	Gln	Ser	Leu	Leu	Pro	Ala	Pro	Pro	Thr	65	70	75	80
Gln	Asn	Met	Pro	Met	Gly	Pro	Gly	Gly	Met	Asn	Gln	Ser	Gly	Pro	Pro	85	90	95	
Pro	Pro	Pro	Arg	Ser	His	Asn	Met	Pro	Ser	Asp	Gly	Met	Val	Gly	Gly	100	105	110	
Gly	Pro	Pro	Ala	Pro	His	Met	Gln	Asn	Gln	Met	Asn	Gly	Gln	Met	Pro	115	120	125	
Gly	Pro	Asn	His	Met	Pro	Met	Gln	Gly	Pro	Gly	Pro	Asn	Gln	Leu	Asn	130	135	140	
Met	Thr	Asn	Ser	Ser	Met	Asn	Met	Pro	Ser	Ser	Ser	His	Gly	Ser	Met	145	150	155	160
Gly	Gly	Tyr	Asn	His	Ser	Val	Pro	Ser	Ser	Gln	Ser	Met	Pro	Val	Gln	165	170	175	
Asn	Gln	Met	Thr	Met	Ser	Gln	Gly	Gln	Pro	Met	Gly	Asn	Tyr	Gly	Pro	180	185	190	
Arg	Pro	Asn	Met	Ser	Met	Gln	Pro	Asn	Gln	Gly	Pro	Met	Met	His	Gln	195	200	205	
Gln	Pro	Pro	Ser	Gln	Gln	Tyr	Asn	Met	Pro	Gln	Gly	Gly	Gly	Gln	His	210	215	220	
Tyr	Gln	Gly	Gln	Gln	Pro	Pro	Met	Gly	Met	Met	Gly	Gln	Val	Asn	Gln	225	230	235	240
Gly	Asn	His	Met	Met	Gly	Gln	Arg	Gln	Ile	Pro	Pro	Tyr	Arg	Pro	Pro	245	250	255	
Gln	Gln	Gly	Pro	Pro	Gln	Gln	Tyr	Ser	Gly	Gln	Glu	Asp	Tyr	Tyr	Gly	260	265	270	
Asp	Gln	Tyr	Ser	His	Gly	Gly	Gln	Gly	Pro	Pro	Glu	Gly	Met	Asn	Gln	275	280	285	
Gln	Tyr	Tyr	Pro	Asp	Gly	Asn	Ser	Gln	Tyr	Gly	Gln	Gln	Gln	Asp	Ala	290	295	300	
Tyr	Gln	Gly	Pro	Pro	Pro	Gln	Gln	Gly	Tyr	Pro	Pro	Gln	Gln	Gln	Gln	305	310	315	320
Tyr	Pro	Gly	Gln	Gln	Gly	Tyr	Pro	Gly	Gln	Gln	Gln	Gly	Tyr	Gly	Pro	325	330	335	
Ser	Gln	Gly	Gly	Pro	Gly	Pro	Gln	Tyr	Pro	Asn	Tyr	Pro	Gln	Gly	Gln				

ITI-08-PCT_Sequence_Listing_ST25.txt

340

345

350

Gly Gln Gln Tyr Gly Gly Tyr Arg Pro Thr Gln Pro Gly Pro Pro Gln
355 360 365

Pro Pro Gln Gln Arg Pro Tyr Gly Tyr Asp Gln Ile Met Pro Lys Lys
370 375 380

Pro Ala Glu Asp Glu Asn Asp Ser Lys Gly Val Ser Glu Ala Ser Gly
385 390 395 400

Pro Gln Asn Asp Gly Lys Gln Leu His Pro Pro Gly Lys Ala Asn Ile
405 410 415

Ser Glu Lys Ile Asn Lys Arg Ser Gly Pro Lys Arg Gly Lys His Ala
420 425 430

Trp Thr His Arg Leu Arg Glu Arg Lys Gln Leu Val Ile Tyr Glu Glu
435 440 445

Ile Ser Asp Pro Glu Glu Asp Asp Glu
450 455

<210> 654

<211> 488

<212> PRT

<213> Artificial Sequence

<220>

<223> SYT-SSX-2__Homo_sapiens__A4PIV9

<400> 654

Met Ser Val Ala Phe Ala Ala Pro Arg Gln Arg Gly Lys Gly Glu Ile
1 5 10 15

Thr Pro Ala Ala Ile Gln Lys Met Leu Asp Asp Asn Asn His Leu Ile
20 25 30

Gln Cys Ile Met Asp Ser Gln Asn Lys Gly Lys Thr Ser Glu Cys Ser
35 40 45

Gln Tyr Gln Gln Met Leu His Thr Asn Leu Val Tyr Leu Ala Thr Ile
50 55 60

Ala Asp Ser Asn Gln Asn Met Gln Ser Leu Leu Pro Ala Pro Pro Thr
65 70 75 80

Gln Asn Met Pro Met Gly Pro Gly Gly Met Asn Gln Ser Gly Pro Pro
85 90 95

Pro Pro Pro Arg Ser His Asn Met Pro Ser Asp Gly Met Val Gly Gly

ITI-08-PCT_Sequence_Listing_ST25.txt

100	105	110																	
Gly	Pro	Pro	Ala	Pro	His	Met	Gln	Asn	Gln	Met	Asn	Gly	Gln	Met	Pro				
	115						120					125							
Gly	Pro	Asn	His	Met	Pro	Met	Gln	Gly	Pro	Gly	Pro	Asn	Gln	Leu	Asn				
	130					135					140								
Met	Thr	Asn	Ser	Ser	Met	Asn	Met	Pro	Ser	Ser	Ser	His	Gly	Ser	Met				
145					150					155					160				
Gly	Gly	Tyr	Asn	His	Ser	Val	Pro	Ser	Ser	Gln	Ser	Met	Pro	Val	Gln				
			165					170						175					
Asn	Gln	Met	Thr	Met	Ser	Gln	Gly	Gln	Pro	Met	Gly	Asn	Tyr	Gly	Pro				
			180					185					190						
Arg	Pro	Asn	Met	Ser	Met	Gln	Pro	Asn	Gln	Gly	Pro	Met	Met	His	Gln				
	195						200					205							
Gln	Pro	Pro	Ser	Gln	Gln	Tyr	Asn	Met	Pro	Gln	Gly	Gly	Gly	Gln	His				
	210					215					220								
Tyr	Gln	Gly	Gln	Gln	Pro	Pro	Met	Gly	Met	Met	Gly	Gln	Val	Asn	Gln				
225					230				235						240				
Gly	Asn	His	Met	Met	Gly	Gln	Arg	Gln	Ile	Pro	Pro	Tyr	Arg	Pro	Pro				
			245					250						255					
Gln	Gln	Gly	Pro	Pro	Gln	Gln	Tyr	Ser	Gly	Gln	Glu	Asp	Tyr	Tyr	Gly				
		260						265					270						
Asp	Gln	Tyr	Ser	His	Gly	Gly	Gln	Gly	Pro	Pro	Glu	Gly	Met	Asn	Gln				
	275						280					285							
Gln	Tyr	Tyr	Pro	Asp	Gly	His	Asn	Asp	Tyr	Gly	Tyr	Gln	Gln	Pro	Ser				
	290					295					300								
Tyr	Pro	Glu	Gln	Gly	Tyr	Asp	Arg	Pro	Tyr	Glu	Asp	Ser	Ser	Gln	His				
305					310					315					320				
Tyr	Tyr	Glu	Gly	Gly	Asn	Ser	Gln	Tyr	Gly	Gln	Gln	Gln	Asp	Ala	Tyr				
			325						330					335					
Gln	Gly	Pro	Pro	Pro	Gln	Gln	Gly	Tyr	Pro	Pro	Gln	Gln	Gln	Gln	Tyr				
		340						345					350						
Pro	Gly	Gln	Gln	Gly	Tyr	Pro	Gly	Gln	Gln	Gln	Gly	Tyr	Gly	Pro	Ser				
	355						360					365							
Gln	Gly	Gly	Pro	Gly	Pro	Gln	Tyr	Pro	Asn	Tyr	Pro	Gln	Gly	Gln	Gly				
	370					375					380								

ITI-08-PCT_Sequence_Listing_ST25.txt

Gln Gln Tyr Gly Gly Tyr Arg Pro Thr Gln Pro Gly Pro Pro Gln Pro
385 390 395 400

Pro Gln Gln Arg Pro Tyr Gly Tyr Asp Gln Ile Met Pro Lys Lys Pro
405 410 415

Ala Glu Glu Gly Asn Asp Ser Glu Glu Val Pro Glu Ala Ser Gly Pro
420 425 430

Gln Asn Asp Gly Lys Glu Leu Cys Pro Pro Gly Lys Pro Thr Thr Ser
435 440 445

Glu Lys Ile His Glu Arg Ser Gly Pro Lys Arg Gly Glu His Ala Trp
450 455 460

Thr His Arg Leu Arg Glu Arg Lys Gln Leu Val Ile Tyr Glu Glu Ile
465 470 475 480

Ser Asp Pro Glu Glu Asp Asp Glu
485

<210> 655

<211> 457

<212> PRT

<213> Artificial Sequence

<220>

<223> SYT-SSX-2__Homo_sapiens__A4PIW0

<400> 655

Met Ser Val Ala Phe Ala Ala Pro Arg Gln Arg Gly Lys Gly Glu Ile
1 5 10 15

Thr Pro Ala Ala Ile Gln Lys Met Leu Asp Asp Asn Asn His Leu Ile
20 25 30

Gln Cys Ile Met Asp Ser Gln Asn Lys Gly Lys Thr Ser Glu Cys Ser
35 40 45

Gln Tyr Gln Gln Met Leu His Thr Asn Leu Val Tyr Leu Ala Thr Ile
50 55 60

Ala Asp Ser Asn Gln Asn Met Gln Ser Leu Leu Pro Ala Pro Pro Thr
65 70 75 80

Gln Asn Met Pro Met Gly Pro Gly Gly Met Asn Gln Ser Gly Pro Pro
85 90 95

Pro Pro Pro Arg Ser His Asn Met Pro Ser Asp Gly Met Val Gly Gly
100 105 110

ITI-08-PCT_Sequence_Listing_ST25.txt

Gly	Pro	Pro	Ala	Pro	His	Met	Gln	Asn	Gln	Met	Asn	Gly	Gln	Met	Pro	115	120	125
Gly	Pro	Asn	His	Met	Pro	Met	Gln	Gly	Pro	Gly	Pro	Asn	Gln	Leu	Asn	130	135	140
Met	Thr	Asn	Ser	Ser	Met	Asn	Met	Pro	Ser	Ser	Ser	His	Gly	Ser	Met	145	150	155
Gly	Gly	Tyr	Asn	His	Ser	Val	Pro	Ser	Ser	Gln	Ser	Met	Pro	Val	Gln	165	170	175
Asn	Gln	Met	Thr	Met	Ser	Gln	Gly	Gln	Pro	Met	Gly	Asn	Tyr	Gly	Pro	180	185	190
Arg	Pro	Asn	Met	Ser	Met	Gln	Pro	Asn	Gln	Gly	Pro	Met	Met	His	Gln	195	200	205
Gln	Pro	Pro	Ser	Gln	Gln	Tyr	Asn	Met	Pro	Gln	Gly	Gly	Gly	Gln	His	210	215	220
Tyr	Gln	Gly	Gln	Gln	Pro	Pro	Met	Gly	Met	Met	Gly	Gln	Val	Asn	Gln	225	230	235
Gly	Asn	His	Met	Met	Gly	Gln	Arg	Gln	Ile	Pro	Pro	Tyr	Arg	Pro	Pro	245	250	255
Gln	Gln	Gly	Pro	Pro	Gln	Gln	Tyr	Ser	Gly	Gln	Glu	Asp	Tyr	Tyr	Gly	260	265	270
Asp	Gln	Tyr	Ser	His	Gly	Gly	Gln	Gly	Pro	Pro	Glu	Gly	Met	Asn	Gln	275	280	285
Gln	Tyr	Tyr	Pro	Asp	Gly	Asn	Ser	Gln	Tyr	Gly	Gln	Gln	Gln	Asp	Ala	290	295	300
Tyr	Gln	Gly	Pro	Pro	Pro	Gln	Gln	Gly	Tyr	Pro	Pro	Gln	Gln	Gln	Gln	305	310	315
Tyr	Pro	Gly	Gln	Gln	Gly	Tyr	Pro	Gly	Gln	Gln	Gln	Gly	Tyr	Gly	Pro	325	330	335
Ser	Gln	Gly	Gly	Pro	Gly	Pro	Gln	Tyr	Pro	Asn	Tyr	Pro	Gln	Gly	Gln	340	345	350
Gly	Gln	Gln	Tyr	Gly	Gly	Tyr	Arg	Pro	Thr	Gln	Pro	Gly	Pro	Pro	Gln	355	360	365
Pro	Pro	Gln	Gln	Arg	Pro	Tyr	Gly	Tyr	Asp	Gln	Ile	Met	Pro	Lys	Lys	370	375	380

ITI-08-PCT_Sequence_Listing_ST25.txt

Pro Ala Glu Glu Gly Asn Asp Ser Glu Glu Val Pro Glu Ala Ser Gly
385 390 395 400

Pro Gln Asn Asp Gly Lys Glu Leu Cys Pro Pro Gly Lys Pro Thr Thr
405 410 415

Ser Glu Lys Ile His Glu Arg Ser Gly Pro Lys Arg Gly Glu His Ala
420 425 430

Trp Thr His Arg Leu Arg Glu Arg Lys Gln Leu Val Ile Tyr Glu Glu
435 440 445

Ile Ser Asp Pro Glu Glu Asp Asp Glu
450 455

<210> 656

<211> 111

<212> PRT

<213> Artificial Sequence

<220>

<223> TARP__Homo_sapiens__Q0VGM3

<400> 656

Met Lys Thr Asn Asp Thr Tyr Met Lys Phe Ser Trp Leu Thr Val Pro
1 5 10 15

Glu Lys Ser Leu Asp Lys Glu His Arg Cys Ile Val Arg His Glu Asn
20 25 30

Asn Lys Asn Gly Val Asp Gln Glu Ile Ile Phe Pro Pro Ile Lys Thr
35 40 45

Asp Val Ile Thr Met Asp Pro Lys Asp Asn Cys Ser Lys Asp Ala Asn
50 55 60

Asp Thr Leu Leu Leu Gln Leu Thr Asn Thr Ser Ala Tyr Tyr Met Tyr
65 70 75 80

Leu Leu Leu Leu Leu Lys Ser Val Val Tyr Phe Ala Ile Ile Thr Cys
85 90 95

Cys Leu Leu Arg Arg Thr Ala Phe Cys Cys Asn Gly Glu Lys Ser
100 105 110

<210> 657

<211> 58

<212> PRT

<213> Artificial Sequence

<220>

ITI-08-PCT_Sequence_Listing_ST25.txt

<223> TCRg__Homo_sapiens__A2JGV3

<400> 657

Met Gln Met Phe Pro Pro Ser Pro Leu Phe Phe Phe Leu Gln Leu Leu
1 5 10 15

Lys Gln Ser Ser Arg Arg Leu Glu His Thr Phe Val Phe Leu Arg Asn
20 25 30

Phe Ser Leu Met Leu Leu Arg Tyr Ile Gly Lys Lys Arg Arg Ala Thr
35 40 45

Arg Phe Trp Asp Pro Arg Arg Gly Thr Pro
50 55

<210> 658

<211> 376

<212> PRT

<213> Artificial Sequence

<220>

<223> TF2AA__Homo_sapiens__P52655

<400> 658

Met Ala Asn Ser Ala Asn Thr Asn Thr Val Pro Lys Leu Tyr Arg Ser
1 5 10 15

Val Ile Glu Asp Val Ile Asn Asp Val Arg Asp Ile Phe Leu Asp Asp
20 25 30

Gly Val Asp Glu Gln Val Leu Met Glu Leu Lys Thr Leu Trp Glu Asn
35 40 45

Lys Leu Met Gln Ser Arg Ala Val Asp Gly Phe His Ser Glu Glu Gln
50 55 60

Gln Leu Leu Leu Gln Val Gln Gln Gln His Gln Pro Gln Gln Gln Gln
65 70 75 80

His His His His His His His Gln Gln Ala Gln Pro Gln Gln Thr Val
85 90 95

Pro Gln Gln Ala Gln Thr Gln Gln Val Leu Ile Pro Ala Ser Gln Gln
100 105 110

Ala Thr Ala Pro Gln Val Ile Val Pro Asp Ser Lys Leu Ile Gln His
115 120 125

Met Asn Ala Ser Asn Met Ser Ala Ala Ala Thr Ala Ala Thr Leu Ala
130 135 140

ITI-08-PCT_Sequence_Listing_ST25.txt

```

Leu Pro Ala Gly Val Thr Pro Val Gln Gln Ile Leu Thr Asn Ser Gly
145                      150                      155                      160

Gln Leu Leu Gln Val Val Arg Ala Ala Asn Gly Ala Gln Tyr Ile Phe
                      165                      170                      175

Gln Pro Gln Gln Ser Val Val Leu Gln Gln Gln Val Ile Pro Gln Met
                      180                      185                      190

Gln Pro Gly Gly Val Gln Ala Pro Val Ile Gln Gln Val Leu Ala Pro
195                      200                      205

Leu Pro Gly Gly Ile Ser Pro Gln Thr Gly Val Ile Ile Gln Pro Gln
210                      215                      220

Gln Ile Leu Phe Thr Gly Asn Lys Thr Gln Val Ile Pro Thr Thr Val
225                      230                      235                      240

Ala Ala Pro Thr Pro Ala Gln Ala Gln Ile Thr Ala Thr Gly Gln Gln
                      245                      250                      255

Gln Pro Gln Ala Gln Pro Ala Gln Thr Gln Ala Pro Leu Val Leu Gln
                      260                      265                      270

Val Asp Gly Thr Gly Asp Thr Ser Ser Glu Glu Asp Glu Asp Glu Glu
275                      280                      285

Glu Asp Tyr Asp Asp Asp Glu Glu Glu Asp Lys Glu Lys Asp Gly Ala
290                      295                      300

Glu Asp Gly Gln Val Glu Glu Glu Pro Leu Asn Ser Glu Asp Asp Val
305                      310                      315                      320

Ser Asp Glu Glu Gly Gln Glu Leu Phe Asp Thr Glu Asn Val Val Val
                      325                      330                      335

Cys Gln Tyr Asp Lys Ile His Arg Ser Lys Asn Lys Trp Lys Phe His
                      340                      345                      350

Leu Lys Asp Gly Ile Met Asn Leu Asn Gly Arg Asp Tyr Ile Phe Ser
355                      360                      365

Lys Ala Ile Gly Asp Ala Glu Trp
370                      375

```

<210> 659
 <211> 567
 <212> PRT
 <213> Artificial Sequence

<220>

ITI-08-PCT_Sequence_Listing_ST25.txt

<223> TGFR2__Homo_sapiens__P37173

<400> 659

```

Met Gly Arg Gly Leu Leu Arg Gly Leu Trp Pro Leu His Ile Val Leu
1          5          10          15

Trp Thr Arg Ile Ala Ser Thr Ile Pro Pro His Val Gln Lys Ser Val
          20          25          30

Asn Asn Asp Met Ile Val Thr Asp Asn Asn Gly Ala Val Lys Phe Pro
          35          40          45

Gln Leu Cys Lys Phe Cys Asp Val Arg Phe Ser Thr Cys Asp Asn Gln
          50          55          60

Lys Ser Cys Met Ser Asn Cys Ser Ile Thr Ser Ile Cys Glu Lys Pro
65          70          75          80

Gln Glu Val Cys Val Ala Val Trp Arg Lys Asn Asp Glu Asn Ile Thr
          85          90          95

Leu Glu Thr Val Cys His Asp Pro Lys Leu Pro Tyr His Asp Phe Ile
          100          105          110

Leu Glu Asp Ala Ala Ser Pro Lys Cys Ile Met Lys Glu Lys Lys Lys
          115          120          125

Pro Gly Glu Thr Phe Phe Met Cys Ser Cys Ser Ser Asp Glu Cys Asn
          130          135          140

Asp Asn Ile Ile Phe Ser Glu Glu Tyr Asn Thr Ser Asn Pro Asp Leu
145          150          155          160

Leu Leu Val Ile Phe Gln Val Thr Gly Ile Ser Leu Leu Pro Pro Leu
          165          170          175

Gly Val Ala Ile Ser Val Ile Ile Ile Phe Tyr Cys Tyr Arg Val Asn
          180          185          190

Arg Gln Gln Lys Leu Ser Ser Thr Trp Glu Thr Gly Lys Thr Arg Lys
          195          200          205

Leu Met Glu Phe Ser Glu His Cys Ala Ile Ile Leu Glu Asp Asp Arg
          210          215          220

Ser Asp Ile Ser Ser Thr Cys Ala Asn Asn Ile Asn His Asn Thr Glu
225          230          235          240

Leu Leu Pro Ile Glu Leu Asp Thr Leu Val Gly Lys Gly Arg Phe Ala
          245          250          255

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Glu Val Tyr Lys Ala Lys Leu Lys Gln Asn Thr Ser Glu Gln Phe Glu
 260 265 270
 Thr Val Ala Val Lys Ile Phe Pro Tyr Glu Glu Tyr Ala Ser Trp Lys
 275 280 285
 Thr Glu Lys Asp Ile Phe Ser Asp Ile Asn Leu Lys His Glu Asn Ile
 290 295 300
 Leu Gln Phe Leu Thr Ala Glu Glu Arg Lys Thr Glu Leu Gly Lys Gln
 305 310 315 320
 Tyr Trp Leu Ile Thr Ala Phe His Ala Lys Gly Asn Leu Gln Glu Tyr
 325 330 335
 Leu Thr Arg His Val Ile Ser Trp Glu Asp Leu Arg Lys Leu Gly Ser
 340 345 350
 Ser Leu Ala Arg Gly Ile Ala His Leu His Ser Asp His Thr Pro Cys
 355 360 365
 Gly Arg Pro Lys Met Pro Ile Val His Arg Asp Leu Lys Ser Ser Asn
 370 375 380
 Ile Leu Val Lys Asn Asp Leu Thr Cys Cys Leu Cys Asp Phe Gly Leu
 385 390 395 400
 Ser Leu Arg Leu Asp Pro Thr Leu Ser Val Asp Asp Leu Ala Asn Ser
 405 410 415
 Gly Gln Val Gly Thr Ala Arg Tyr Met Ala Pro Glu Val Leu Glu Ser
 420 425 430
 Arg Met Asn Leu Glu Asn Val Glu Ser Phe Lys Gln Thr Asp Val Tyr
 435 440 445
 Ser Met Ala Leu Val Leu Trp Glu Met Thr Ser Arg Cys Asn Ala Val
 450 455 460
 Gly Glu Val Lys Asp Tyr Glu Pro Pro Phe Gly Ser Lys Val Arg Glu
 465 470 475 480
 His Pro Cys Val Glu Ser Met Lys Asp Asn Val Leu Arg Asp Arg Gly
 485 490 495
 Arg Pro Glu Ile Pro Ser Phe Trp Leu Asn His Gln Gly Ile Gln Met
 500 505 510
 Val Cys Glu Thr Leu Thr Glu Cys Trp Asp His Asp Pro Glu Ala Arg
 515 520 525
 Leu Thr Ala Gln Cys Val Ala Glu Arg Phe Ser Glu Leu Glu His Leu

ITI-08-PCT_Sequence_Listing_ST25.txt

530

535

540

Asp Arg Leu Ser Gly Arg Ser Cys Ser Glu Glu Lys Ile Pro Glu Asp
 545 550 555 560

Gly Ser Leu Asn Thr Thr Lys
 565

<210> 660

<211> 684

<212> PRT

<213> Artificial Sequence

<220>

<223> TGM-4__Homo_sapiens__B2R7D1

<400> 660

Met Met Asp Ala Ser Lys Glu Leu Gln Val Leu His Ile Asp Phe Leu
 1 5 10 15

Asn Gln Asp Asn Ala Val Ser His His Thr Trp Glu Phe Gln Thr Ser
 20 25 30

Ser Pro Val Phe Arg Arg Gly Gln Val Phe His Leu Arg Leu Val Leu
 35 40 45

Asn Gln Pro Pro Gln Ser Tyr His Gln Leu Lys Leu Glu Phe Ser Thr
 50 55 60

Gly Pro Asn Pro Ser Ile Ala Lys His Thr Leu Val Val Leu Asp Pro
 65 70 75 80

Arg Thr Pro Ser Asp His Tyr Asn Trp Gln Ala Thr Leu Gln Asn Glu
 85 90 95

Ser Gly Lys Glu Val Thr Val Ala Val Thr Ser Ser Pro Asn Ala Ile
 100 105 110

Leu Gly Lys Tyr Gln Leu Asn Val Lys Thr Gly Asn His Ile Leu Lys
 115 120 125

Ser Glu Glu Asn Ile Leu Tyr Leu Leu Phe Asn Pro Trp Cys Lys Glu
 130 135 140

Asp Met Val Phe Met Pro Asp Glu Asp Glu Arg Lys Glu Tyr Ile Leu
 145 150 155 160

Asn Asp Thr Gly Cys His Tyr Val Gly Ala Ala Arg Ser Ile Lys Cys
 165 170 175

Lys Pro Trp Asn Phe Gly Gln Phe Glu Lys Asn Val Leu Asp Cys Cys

180 185 190

Page 1133

ITI-08-PCT_Sequence_Listing_ST25.txt

Arg Arg Pro Val Lys Glu Asn Phe Leu His Met Ser Val Gln Ser Asp
465 470 475 480

Asp Val Leu Leu Gly Asn Ser Val Asn Phe Thr Val Ile Leu Lys Arg
485 490 495

Lys Thr Ala Ala Leu Gln Asn Val Asn Ile Leu Gly Ser Phe Glu Leu
500 505 510

Gln Leu Tyr Thr Gly Lys Lys Met Ala Lys Leu Cys Asp Leu Asn Lys
515 520 525

Thr Ser Gln Ile Gln Gly Gln Val Ser Glu Val Thr Leu Thr Leu Asp
530 535 540

Ser Lys Thr Tyr Ile Asn Ser Leu Ala Ile Leu Asp Asp Glu Pro Val
545 550 555 560

Ile Arg Gly Phe Ile Ile Ala Glu Ile Val Glu Ser Lys Glu Ile Met
565 570 575

Ala Ser Glu Val Phe Thr Ser Phe Gln Tyr Pro Glu Phe Ser Ile Glu
580 585 590

Leu Pro Asn Thr Gly Arg Ile Gly Gln Leu Leu Val Cys Asn Cys Ile
595 600 605

Phe Lys Asn Thr Leu Ala Ile Pro Leu Thr Asp Val Lys Phe Ser Leu
610 615 620

Glu Ser Leu Gly Ile Ser Ser Leu Gln Thr Ser Asp His Gly Thr Val
625 630 635 640

Gln Pro Gly Glu Thr Ile Gln Ser Gln Ile Lys Cys Thr Pro Ile Lys
645 650 655

Thr Gly Pro Lys Lys Phe Ile Val Lys Leu Ser Ser Lys Gln Val Lys
660 665 670

Glu Ile Asn Ala Gln Lys Ile Val Leu Ile Thr Lys
675 680

<210> 661

<211> 1124

<212> PRT

<213> Artificial Sequence

<220>

<223> TIE2__Homo_sapiens__Q02763

<400> 661

ITI-08-PCT_Sequence_Listing_ST25.txt

```

Met Asp Ser Leu Ala Ser Leu Val Leu Cys Gly Val Ser Leu Leu Leu
1          5          10          15

Ser Gly Thr Val Glu Gly Ala Met Asp Leu Ile Leu Ile Asn Ser Leu
          20          25          30

Pro Leu Val Ser Asp Ala Glu Thr Ser Leu Thr Cys Ile Ala Ser Gly
          35          40          45

Trp Arg Pro His Glu Pro Ile Thr Ile Gly Arg Asp Phe Glu Ala Leu
          50          55          60

Met Asn Gln His Gln Asp Pro Leu Glu Val Thr Gln Asp Val Thr Arg
65          70          75          80

Glu Trp Ala Lys Lys Val Val Trp Lys Arg Glu Lys Ala Ser Lys Ile
          85          90          95

Asn Gly Ala Tyr Phe Cys Glu Gly Arg Val Arg Gly Glu Ala Ile Arg
          100          105          110

Ile Arg Thr Met Lys Met Arg Gln Gln Ala Ser Phe Leu Pro Ala Thr
          115          120          125

Leu Thr Met Thr Val Asp Lys Gly Asp Asn Val Asn Ile Ser Phe Lys
          130          135          140

Lys Val Leu Ile Lys Glu Glu Asp Ala Val Ile Tyr Lys Asn Gly Ser
145          150          155          160

Phe Ile His Ser Val Pro Arg His Glu Val Pro Asp Ile Leu Glu Val
          165          170          175

His Leu Pro His Ala Gln Pro Gln Asp Ala Gly Val Tyr Ser Ala Arg
          180          185          190

Tyr Ile Gly Gly Asn Leu Phe Thr Ser Ala Phe Thr Arg Leu Ile Val
          195          200          205

Arg Arg Cys Glu Ala Gln Lys Trp Gly Pro Glu Cys Asn His Leu Cys
          210          215          220

Thr Ala Cys Met Asn Asn Gly Val Cys His Glu Asp Thr Gly Glu Cys
225          230          235          240

Ile Cys Pro Pro Gly Phe Met Gly Arg Thr Cys Glu Lys Ala Cys Glu
          245          250          255

Leu His Thr Phe Gly Arg Thr Cys Lys Glu Arg Cys Ser Gly Gln Glu
          260          265          270

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Gly Cys Lys Ser Tyr Val Phe Cys Leu Pro Asp Pro Tyr Gly Cys Ser
275 280 285

Cys Ala Thr Gly Trp Lys Gly Leu Gln Cys Asn Glu Ala Cys His Pro
290 295 300

Gly Phe Tyr Gly Pro Asp Cys Lys Leu Arg Cys Ser Cys Asn Asn Gly
305 310 315 320

Glu Met Cys Asp Arg Phe Gln Gly Cys Leu Cys Ser Pro Gly Trp Gln
325 330 335

Gly Leu Gln Cys Glu Arg Glu Gly Ile Gln Arg Met Thr Pro Lys Ile
340 345 350

Val Asp Leu Pro Asp His Ile Glu Val Asn Ser Gly Lys Phe Asn Pro
355 360 365

Ile Cys Lys Ala Ser Gly Trp Pro Leu Pro Thr Asn Glu Glu Met Thr
370 375 380

Leu Val Lys Pro Asp Gly Thr Val Leu His Pro Lys Asp Phe Asn His
385 390 395 400

Thr Asp His Phe Ser Val Ala Ile Phe Thr Ile His Arg Ile Leu Pro
405 410 415

Pro Asp Ser Gly Val Trp Val Cys Ser Val Asn Thr Val Ala Gly Met
420 425 430

Val Glu Lys Pro Phe Asn Ile Ser Val Lys Val Leu Pro Lys Pro Leu
435 440 445

Asn Ala Pro Asn Val Ile Asp Thr Gly His Asn Phe Ala Val Ile Asn
450 455 460

Ile Ser Ser Glu Pro Tyr Phe Gly Asp Gly Pro Ile Lys Ser Lys Lys
465 470 475 480

Leu Leu Tyr Lys Pro Val Asn His Tyr Glu Ala Trp Gln His Ile Gln
485 490 495

Val Thr Asn Glu Ile Val Thr Leu Asn Tyr Leu Glu Pro Arg Thr Glu
500 505 510

Tyr Glu Leu Cys Val Gln Leu Val Arg Arg Gly Glu Gly Gly Glu Gly
515 520 525

His Pro Gly Pro Val Arg Arg Phe Thr Thr Ala Ser Ile Gly Leu Pro
530 535 540

Pro Pro Arg Gly Leu Asn Leu Leu Pro Lys Ser Gln Thr Thr Leu Asn

ITI-08-PCT_Sequence_Listing_ST25.txt

```

545          550          555          560
Leu Thr Trp Gln Pro Ile Phe Pro Ser Ser Glu Asp Asp Phe Tyr Val
          565          570          575
Glu Val Glu Arg Arg Ser Val Gln Lys Ser Asp Gln Gln Asn Ile Lys
          580          585          590
Val Pro Gly Asn Leu Thr Ser Val Leu Leu Asn Asn Leu His Pro Arg
          595          600          605
Glu Gln Tyr Val Val Arg Ala Arg Val Asn Thr Lys Ala Gln Gly Glu
          610          615          620
Trp Ser Glu Asp Leu Thr Ala Trp Thr Leu Ser Asp Ile Leu Pro Pro
          625          630          635          640
Gln Pro Glu Asn Ile Lys Ile Ser Asn Ile Thr His Ser Ser Ala Val
          645          650          655
Ile Ser Trp Thr Ile Leu Asp Gly Tyr Ser Ile Ser Ser Ile Thr Ile
          660          665          670
Arg Tyr Lys Val Gln Gly Lys Asn Glu Asp Gln His Val Asp Val Lys
          675          680          685
Ile Lys Asn Ala Thr Ile Thr Gln Tyr Gln Leu Lys Gly Leu Glu Pro
          690          695          700
Glu Thr Ala Tyr Gln Val Asp Ile Phe Ala Glu Asn Asn Ile Gly Ser
          705          710          715          720
Ser Asn Pro Ala Phe Ser His Glu Leu Val Thr Leu Pro Glu Ser Gln
          725          730          735
Ala Pro Ala Asp Leu Gly Gly Gly Lys Met Leu Leu Ile Ala Ile Leu
          740          745          750
Gly Ser Ala Gly Met Thr Cys Leu Thr Val Leu Leu Ala Phe Leu Ile
          755          760          765
Ile Leu Gln Leu Lys Arg Ala Asn Val Gln Arg Arg Met Ala Gln Ala
          770          775          780
Phe Gln Asn Val Arg Glu Glu Pro Ala Val Gln Phe Asn Ser Gly Thr
          785          790          795          800
Leu Ala Leu Asn Arg Lys Val Lys Asn Asn Pro Asp Pro Thr Ile Tyr
          805          810          815
Pro Val Leu Asp Trp Asn Asp Ile Lys Phe Gln Asp Val Ile Gly Glu
          820          825          830

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Gly Asn Phe Gly Gln Val Leu Lys Ala Arg Ile Lys Lys Asp Gly Leu
835 840 845

Arg Met Asp Ala Ala Ile Lys Arg Met Lys Glu Tyr Ala Ser Lys Asp
850 855 860

Asp His Arg Asp Phe Ala Gly Glu Leu Glu Val Leu Cys Lys Leu Gly
865 870 875 880

His His Pro Asn Ile Ile Asn Leu Leu Gly Ala Cys Glu His Arg Gly
885 890 895

Tyr Leu Tyr Leu Ala Ile Glu Tyr Ala Pro His Gly Asn Leu Leu Asp
900 905 910

Phe Leu Arg Lys Ser Arg Val Leu Glu Thr Asp Pro Ala Phe Ala Ile
915 920 925

Ala Asn Ser Thr Ala Ser Thr Leu Ser Ser Gln Gln Leu Leu His Phe
930 935 940

Ala Ala Asp Val Ala Arg Gly Met Asp Tyr Leu Ser Gln Lys Gln Phe
945 950 955 960

Ile His Arg Asp Leu Ala Ala Arg Asn Ile Leu Val Gly Glu Asn Tyr
965 970 975

Val Ala Lys Ile Ala Asp Phe Gly Leu Ser Arg Gly Gln Glu Val Tyr
980 985 990

Val Lys Lys Thr Met Gly Arg Leu Pro Val Arg Trp Met Ala Ile Glu
995 1000 1005

Ser Leu Asn Tyr Ser Val Tyr Thr Thr Asn Ser Asp Val Trp Ser
1010 1015 1020

Tyr Gly Val Leu Leu Trp Glu Ile Val Ser Leu Gly Gly Thr Pro
1025 1030 1035

Tyr Cys Gly Met Thr Cys Ala Glu Leu Tyr Glu Lys Leu Pro Gln
1040 1045 1050

Gly Tyr Arg Leu Glu Lys Pro Leu Asn Cys Asp Asp Glu Val Tyr
1055 1060 1065

Asp Leu Met Arg Gln Cys Trp Arg Glu Lys Pro Tyr Glu Arg Pro
1070 1075 1080

Ser Phe Ala Gln Ile Leu Val Ser Leu Asn Arg Met Leu Glu Glu
1085 1090 1095

ITI-08-PCT_Sequence_Listing_ST25.txt

Arg Lys Thr Tyr Val Asn Thr Thr Leu Tyr Glu Lys Phe Thr Tyr
1100 1105 1110

Ala Gly Ile Asp Cys Ser Ala Glu Glu Ala Ala
1115 1120

<210> 662

<211> 596

<212> PRT

<213> Artificial Sequence

<220>

<223> TKTL1__Homo_sapiens__P51854

<400> 662

Met Ala Asp Ala Glu Ala Arg Ala Glu Phe Pro Glu Glu Ala Arg Pro
1 5 10 15

Asp Arg Gly Thr Leu Gln Val Leu Gln Asp Met Ala Ser Arg Leu Arg
20 25 30

Ile His Ser Ile Arg Ala Thr Cys Ser Thr Ser Ser Gly His Pro Thr
35 40 45

Ser Cys Ser Ser Ser Ser Glu Ile Met Ser Val Leu Phe Phe Tyr Ile
50 55 60

Met Arg Tyr Lys Gln Ser Asp Pro Glu Asn Pro Asp Asn Asp Arg Phe
65 70 75 80

Val Leu Ala Lys Arg Leu Ser Phe Val Asp Val Ala Thr Gly Trp Leu
85 90 95

Gly Gln Gly Leu Gly Val Ala Cys Gly Met Ala Tyr Thr Gly Lys Tyr
100 105 110

Phe Asp Arg Ala Ser Tyr Arg Val Phe Cys Leu Met Ser Asp Gly Glu
115 120 125

Ser Ser Glu Gly Ser Val Trp Glu Ala Met Ala Phe Ala Ser Tyr Tyr
130 135 140

Ser Leu Asp Asn Leu Val Ala Ile Phe Asp Val Asn Arg Leu Gly His
145 150 155 160

Ser Gly Ala Leu Pro Ala Glu His Cys Ile Asn Ile Tyr Gln Arg Arg
165 170 175

Cys Glu Ala Phe Gly Trp Asn Thr Tyr Val Val Asp Gly Arg Asp Val
180 185 190

ITI-08-PCT_Sequence_Listing_ST25.txt

Glu Ala Leu Cys Gln Val Phe Trp Gln Ala Ser Gln Val Lys His Lys
 195 200 205
 Pro Thr Ala Val Val Ala Lys Thr Phe Lys Gly Arg Gly Thr Pro Ser
 210 215 220
 Ile Glu Asp Ala Glu Ser Trp His Ala Lys Pro Met Pro Arg Glu Arg
 225 230 235 240
 Ala Asp Ala Ile Ile Lys Leu Ile Glu Ser Gln Ile Gln Thr Ser Arg
 245 250 255
 Asn Leu Asp Pro Gln Pro Pro Ile Glu Asp Ser Pro Glu Val Asn Ile
 260 265 270
 Thr Asp Val Arg Met Thr Ser Pro Pro Asp Tyr Arg Val Gly Asp Lys
 275 280 285
 Ile Ala Thr Arg Lys Ala Cys Gly Leu Ala Leu Ala Lys Leu Gly Tyr
 290 295 300
 Ala Asn Asn Arg Val Val Val Leu Asp Gly Asp Thr Arg Tyr Ser Thr
 305 310 315 320
 Phe Ser Glu Ile Phe Asn Lys Glu Tyr Pro Glu Arg Phe Ile Glu Cys
 325 330 335
 Phe Met Ala Glu Gln Asn Met Val Ser Val Ala Leu Gly Cys Ala Ser
 340 345 350
 Arg Gly Arg Thr Ile Ala Phe Ala Ser Thr Phe Ala Ala Phe Leu Thr
 355 360 365
 Arg Ala Phe Asp His Ile Arg Ile Gly Gly Leu Ala Glu Ser Asn Ile
 370 375 380
 Asn Ile Ile Gly Ser His Cys Gly Val Ser Val Gly Asp Asp Gly Ala
 385 390 395 400
 Ser Gln Met Ala Leu Glu Asp Ile Ala Met Phe Arg Thr Ile Pro Lys
 405 410 415
 Cys Thr Ile Phe Tyr Pro Thr Asp Ala Val Ser Thr Glu His Ala Val
 420 425 430
 Ala Leu Ala Ala Asn Ala Lys Gly Met Cys Phe Ile Arg Thr Thr Arg
 435 440 445
 Pro Glu Thr Met Val Ile Tyr Thr Pro Gln Glu Arg Phe Glu Ile Gly
 450 455 460
 Gln Ala Lys Val Leu Arg His Cys Val Ser Asp Lys Val Thr Val Ile

ITI-08-PCT Sequence Listing ST25.txt

465 470 475 480

Gly Ala Gly Ile Thr Val Tyr Glu Ala Leu Ala Ala Ala Asp Glu Leu
485 490 495

Ser Lys Gln Asp Ile Phe Ile Arg Val Ile Asp Leu Phe Thr Ile Lys
500 505 510

Pro Leu Asp Val Ala Thr Ile Val Ser Ser Ala Lys Ala Thr Glu Gly
515 520 525

Arg Ile Ile Thr Val Glu Asp His Tyr Pro Gln Gly Gly Ile Gly Glu
530 535 540

Ala Val Cys Ala Ala Val Ser Met Asp Pro Asp Ile Gln Val His Ser
545 550 555 560

Leu Ala Val Ser Gly Val Pro Gln Ser Gly Lys Ser Glu Glu Leu Leu
565 570 575

Asp Met Tyr Gly Ile Ser Ala Arg His Ile Ile Val Ala Val Lys Cys
580 585 590

Met Leu Leu Asn
595

<210> 663

<211> 286

<212> PRT

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> TPI/m Homo sapiens P60174

<400> 663

Met Ala Glu Asp Gly Glu Glu Ala Glu Phe His Phe Ala Ala Leu Tyr
1 5 10 15

Ile Ser Gly Gln Trp Pro Arg Leu Arg Ala Asp Thr Asp Leu Gln Arg
20 25 30

Leu Gly Ser Ser Ala Met Ala Pro Ser Arg Lys Phe Phe Val Gly Gly
35 40 45

Asn Trp Lys Met Asn Gly Arg Lys Gln Ser Leu Gly Glu Leu Ile Gly
50 55 60

Thr Leu Asn Ala Ala Lys Val Pro Ala Asp Thr Glu Val Val Cys Ala
65 70 75 80

Pro Pro Thr Ala Tyr Ile Asp Phe Ala Arg Gln Lys Leu Asp Pro Lys

ITI-08-PCT_Sequence_Listing_ST25.txt

85 90 95

Ile Ala Val Ala Ala Gln Asn Cys Tyr Lys Val Thr Asn Gly Ala Phe
100 105 110

Thr Gly Glu Ile Ser Pro Gly Met Ile Lys Asp Cys Gly Ala Thr Trp
115 120 125

Val Val Leu Gly His Ser Glu Arg Arg His Val Phe Gly Glu Ser Asp
130 135 140

Glu Leu Ile Gly Gln Lys Val Ala His Ala Leu Ala Glu Gly Leu Gly
145 150 155 160

Val Ile Ala Cys Ile Gly Glu Lys Leu Asp Glu Arg Glu Ala Gly Ile
165 170 175

Thr Glu Lys Val Val Phe Glu Gln Thr Lys Val Ile Ala Asp Asn Val
180 185 190

Lys Asp Trp Ser Lys Val Val Leu Ala Tyr Glu Pro Val Trp Ala Ile
195 200 205

Gly Thr Gly Lys Thr Ala Thr Pro Gln Gln Ala Gln Glu Val His Glu
210 215 220

Lys Leu Arg Gly Trp Leu Lys Ser Asn Val Ser Asp Ala Val Ala Gln
225 230 235 240

Ser Thr Arg Ile Ile Tyr Gly Gly Ser Val Thr Gly Ala Thr Cys Lys
245 250 255

Glu Leu Ala Ser Gln Pro Asp Val Asp Gly Phe Leu Val Gly Gly Ala
260 265 270

Ser Leu Lys Pro Glu Phe Val Asp Ile Ile Asn Ala Lys Gln
275 280 285

<210> 664

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> TRGV11__Homo_sapiens__Q99601

<400> 664

Met Pro Leu Val Val Ala Val Ile Phe Phe Ser Leu Trp Val Phe Ala
1 5 10 15

Leu Gly Gln Leu Glu Gln Pro Glu Ile Ser Ile Ser Arg Pro Ala Asn

ITI-08-PCT_Sequence_Listing_ST25.txt

20

25

30

Lys Ser Ala His Ile Ser Trp Lys Ala Ser Ile Gln Gly Phe Ser Ser
35 40 45

Lys Ile Ile His Trp Tyr Trp Gln Lys Pro Asn Lys Gly Leu Glu Tyr
50 55 60

Leu Leu His Val Phe Leu Thr Ile Ser Ala Gln Asp Cys Ser Gly Gly
65 70 75 80

Lys Thr Lys Lys Leu Glu Val Ser Lys Asn Ala His Thr Ser Thr Ser
85 90 95

Thr Leu Lys Ile Lys Phe Leu Glu Lys Glu Asp Glu Val Val Tyr His
100 105 110

Cys Ala Cys Trp Ile Arg His
115

<210> 665

<211> 137

<212> PRT

<213> Artificial Sequence

<220>

<223> TRGV9__Homo_sapiens__A4D1X2

<400> 665

Met Leu Ser Leu Leu His Thr Ser Thr Leu Ala Val Leu Gly Ala Leu
1 5 10 15

Cys Val Tyr Gly Ala Gly His Leu Glu Gln Pro Gln Ile Ser Ser Thr
20 25 30

Lys Thr Leu Ser Lys Thr Ala Arg Leu Glu Cys Val Val Ser Gly Ile
35 40 45

Thr Ile Ser Ala Thr Ser Val Tyr Trp Tyr Arg Glu Arg Pro Gly Glu
50 55 60

Val Ile Gln Phe Leu Val Ser Ile Ser Tyr Asp Gly Thr Val Arg Lys
65 70 75 80

Glu Ser Gly Ile Pro Ser Gly Lys Phe Glu Val Asp Arg Ile Pro Glu
85 90 95

Thr Ser Thr Ser Thr Leu Thr Ile His Asn Val Glu Lys Gln Asp Ile
100 105 110

Ala Thr Tyr Tyr Cys Ala Leu Trp Glu Val His Ser Ser Arg Gln Phe

ITI-08-PCT_Sequence_Listing_ST25.txt

115 120 125

Glu Pro Ser His Ser Ile Asn Val Tyr
130 135

<210> 666
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> TRGV9__Homo_sapiens__Q99603

<400> 666

Met Leu Ser Leu Leu His Thr Ser Thr Leu Ala Val Leu Gly Ala Leu
1 5 10 15

Cys Val Tyr Gly Ala Gly His Leu Glu Gln Pro Gln Ile Ser Ser Thr
20 25 30

Lys Thr Leu Ser Lys Thr Ala Arg Leu Glu Cys Val Val Ser Gly Ile
35 40 45

Thr Ile Ser Ala Thr Ser Val Tyr Trp Tyr Arg Glu Arg Pro Gly Glu
50 55 60

Val Ile Gln Phe Leu Val Ser Ile Ser Tyr Asp Gly Thr Val Arg Lys
65 70 75 80

Glu Ser Gly Ile Pro Ser Gly Lys Phe Glu Val Asp Arg Ile Pro Glu
85 90 95

Thr Ser Thr Ser Thr Leu Thr Ile His Asn Val Glu Lys Gln Asp Ile
100 105 110

Ala Thr Tyr Tyr Cys Ala Leu Trp Glu Val
115 120

<210> 667
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> TRGV9__Homo_sapiens__Q99604

<400> 667

Met Leu Ser Leu Leu His Thr Ser Thr Leu Ala Val Leu Gly Ala Leu
1 5 10 15

ITI-08-PCT_Sequence_Listing_ST25.txt

Cys Val Tyr Gly Ala Gly His Leu Glu Gln Pro Gln Ile Ser Ser Thr
20 25 30

Lys Thr Leu Ser Lys Thr Ala Arg Leu Glu Cys Val Val Ser Gly Ile
35 40 45

Lys Ile Ser Ala Thr Ser Val Tyr Trp Tyr Arg Glu Arg Pro Gly Glu
50 55 60

Val Ile Gln Phe Leu Val Ser Ile Ser Tyr Asp Gly Thr Val Arg Lys
65 70 75 80

Glu Ser Gly Ile Pro Ser Gly Lys Phe Glu Val Asp Arg Ile Pro Glu
85 90 95

Thr Ser Thr Ser Thr Leu Thr Ile His Asn Val Glu Lys Gln Asp Ile
100 105 110

Ala Thr Tyr Tyr Cys Ala Leu Trp Glu Val
115 120

<210> 668

<211> 793

<212> PRT

<213> Artificial Sequence

<220>

<223> TRPC1__Homo_sapiens__P48995

<400> 668

Met Met Ala Ala Leu Tyr Pro Ser Thr Asp Leu Ser Gly Ala Ser Ser
1 5 10 15

Ser Ser Leu Pro Ser Ser Pro Ser Ser Ser Pro Asn Glu Val Met
20 25 30

Ala Leu Lys Asp Val Arg Glu Val Lys Glu Glu Asn Thr Leu Asn Glu
35 40 45

Lys Leu Phe Leu Leu Ala Cys Asp Lys Gly Asp Tyr Tyr Met Val Lys
50 55 60

Lys Ile Leu Glu Glu Asn Ser Ser Gly Asp Leu Asn Ile Asn Cys Val
65 70 75 80

Asp Val Leu Gly Arg Asn Ala Val Thr Ile Thr Ile Glu Asn Glu Asn
85 90 95

Leu Asp Ile Leu Gln Leu Leu Leu Asp Tyr Gly Cys Gln Ser Ala Asp
100 105 110

ITI-08-PCT_Sequence_Listing_ST25.txt

Ala	Leu	Leu	Val	Ala	Ile	Asp	Ser	Glu	Val	Val	Gly	Ala	Val	Asp	Ile	115	120	125	
Leu	Leu	Asn	His	Arg	Pro	Lys	Arg	Ser	Ser	Arg	Pro	Thr	Ile	Val	Lys	130	135	140	
Leu	Met	Glu	Arg	Ile	Gln	Asn	Pro	Glu	Tyr	Ser	Thr	Thr	Met	Asp	Val	145	150	155	160
Ala	Pro	Val	Ile	Leu	Ala	Ala	His	Arg	Asn	Asn	Tyr	Glu	Ile	Leu	Thr	165	170	175	
Met	Leu	Leu	Lys	Gln	Asp	Val	Ser	Leu	Pro	Lys	Pro	His	Ala	Val	Gly	180	185	190	
Cys	Glu	Cys	Thr	Leu	Cys	Ser	Ala	Lys	Asn	Lys	Lys	Asp	Ser	Leu	Arg	195	200	205	
His	Ser	Arg	Phe	Arg	Leu	Asp	Ile	Tyr	Arg	Cys	Leu	Ala	Ser	Pro	Ala	210	215	220	
Leu	Ile	Met	Leu	Thr	Glu	Glu	Asp	Pro	Ile	Leu	Arg	Ala	Phe	Glu	Leu	225	230	235	240
Ser	Ala	Asp	Leu	Lys	Glu	Leu	Ser	Leu	Val	Glu	Val	Glu	Phe	Arg	Asn	245	250	255	
Asp	Tyr	Glu	Glu	Leu	Ala	Arg	Gln	Cys	Lys	Met	Phe	Ala	Lys	Asp	Leu	260	265	270	
Leu	Ala	Gln	Ala	Arg	Asn	Ser	Arg	Glu	Leu	Glu	Val	Ile	Leu	Asn	His	275	280	285	
Thr	Ser	Ser	Asp	Glu	Pro	Leu	Asp	Lys	Arg	Gly	Leu	Leu	Glu	Glu	Arg	290	295	300	
Met	Asn	Leu	Ser	Arg	Leu	Lys	Leu	Ala	Ile	Lys	Tyr	Asn	Gln	Lys	Glu	305	310	315	320
Phe	Val	Ser	Gln	Ser	Asn	Cys	Gln	Gln	Phe	Leu	Asn	Thr	Val	Trp	Phe	325	330	335	
Gly	Gln	Met	Ser	Gly	Tyr	Arg	Arg	Lys	Pro	Thr	Cys	Lys	Lys	Ile	Met	340	345	350	
Thr	Val	Leu	Thr	Val	Gly	Ile	Phe	Trp	Pro	Val	Leu	Ser	Leu	Cys	Tyr	355	360	365	
Leu	Ile	Ala	Pro	Lys	Ser	Gln	Phe	Gly	Arg	Ile	Ile	His	Thr	Pro	Phe	370	375	380	
Met	Lys	Phe	Ile	Ile	His	Gly	Ala	Ser	Tyr	Phe	Thr	Phe	Leu	Leu	Leu				

ITI-08-PCT_Sequence_Listing_ST25.txt

```

385          390          395          400
Leu Asn Leu Tyr Ser Leu Val Tyr Asn Glu Asp Lys Lys Asn Thr Met
      405          410          415
Gly Pro Ala Leu Glu Arg Ile Asp Tyr Leu Leu Ile Leu Trp Ile Ile
      420          425          430
Gly Met Ile Trp Ser Asp Ile Lys Arg Leu Trp Tyr Glu Gly Leu Glu
      435          440          445
Asp Phe Leu Glu Glu Ser Arg Asn Gln Leu Ser Phe Val Met Asn Ser
      450          455          460
Leu Tyr Leu Ala Thr Phe Ala Leu Lys Val Val Ala His Asn Lys Phe
465          470          475          480
His Asp Phe Ala Asp Arg Lys Asp Trp Asp Ala Phe His Pro Thr Leu
      485          490          495
Val Ala Glu Gly Leu Phe Ala Phe Ala Asn Val Leu Ser Tyr Leu Arg
      500          505          510
Leu Phe Phe Met Tyr Thr Thr Ser Ser Ile Leu Gly Pro Leu Gln Ile
      515          520          525
Ser Met Gly Gln Met Leu Gln Asp Phe Gly Lys Phe Leu Gly Met Phe
      530          535          540
Leu Leu Val Leu Phe Ser Phe Thr Ile Gly Leu Thr Gln Leu Tyr Asp
545          550          555          560
Lys Gly Tyr Thr Ser Lys Glu Gln Lys Asp Cys Val Gly Ile Phe Cys
      565          570          575
Glu Gln Gln Ser Asn Asp Thr Phe His Ser Phe Ile Gly Thr Cys Phe
      580          585          590
Ala Leu Phe Trp Tyr Ile Phe Ser Leu Ala His Val Ala Ile Phe Val
      595          600          605
Thr Arg Phe Ser Tyr Gly Glu Glu Leu Gln Ser Phe Val Gly Ala Val
      610          615          620
Ile Val Gly Thr Tyr Asn Val Val Val Val Ile Val Leu Thr Lys Leu
625          630          635          640
Leu Val Ala Met Leu His Lys Ser Phe Gln Leu Ile Ala Asn His Glu
      645          650          655
Asp Lys Glu Trp Lys Phe Ala Arg Ala Lys Leu Trp Leu Ser Tyr Phe
      660          665          670

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Asp Asp Lys Cys Thr Leu Pro Pro Pro Phe Asn Ile Ile Pro Ser Pro
675 680 685

Lys Thr Ile Cys Tyr Met Ile Ser Ser Leu Ser Lys Trp Ile Cys Ser
690 695 700

His Thr Ser Lys Gly Lys Val Lys Arg Gln Asn Ser Leu Lys Glu Trp
705 710 715 720

Arg Asn Leu Lys Gln Lys Arg Asp Glu Asn Tyr Gln Lys Val Met Cys
725 730 735

Cys Leu Val His Arg Tyr Leu Thr Ser Met Arg Gln Lys Met Gln Ser
740 745 750

Thr Asp Gln Ala Thr Val Glu Asn Leu Asn Glu Leu Arg Gln Asp Leu
755 760 765

Ser Lys Phe Arg Asn Glu Ile Arg Asp Leu Leu Gly Phe Arg Thr Ser
770 775 780

Lys Tyr Ala Met Phe Tyr Pro Arg Asn
785 790

<210> 669

<211> 1104

<212> PRT

<213> Artificial Sequence

<220>

<223> TRP-p8__Homo_sapiens__Q7Z2W7

<400> 669

Met Ser Phe Arg Ala Ala Arg Leu Ser Met Arg Asn Arg Arg Asn Asp
1 5 10 15

Thr Leu Asp Ser Thr Arg Thr Leu Tyr Ser Ser Ala Ser Arg Ser Thr
20 25 30

Asp Leu Ser Tyr Ser Glu Ser Asp Leu Val Asn Phe Ile Gln Ala Asn
35 40 45

Phe Lys Lys Arg Glu Cys Val Phe Phe Thr Lys Asp Ser Lys Ala Thr
50 55 60

Glu Asn Val Cys Lys Cys Gly Tyr Ala Gln Ser Gln His Met Glu Gly
65 70 75 80

Thr Gln Ile Asn Gln Ser Glu Lys Trp Asn Tyr Lys Lys His Thr Lys
85 90 95

ITI-08-PCT_Sequence_Listing_ST25.txt

Glu	Phe	Pro	Thr	Asp	Ala	Phe	Gly	Asp	Ile	Gln	Phe	Glu	Thr	Leu	Gly	100	105	110
Lys	Lys	Gly	Lys	Tyr	Ile	Arg	Leu	Ser	Cys	Asp	Thr	Asp	Ala	Glu	Ile	115	120	125
Leu	Tyr	Glu	Leu	Leu	Thr	Gln	His	Trp	His	Leu	Lys	Thr	Pro	Asn	Leu	130	135	140
Val	Ile	Ser	Val	Thr	Gly	Gly	Ala	Lys	Asn	Phe	Ala	Leu	Lys	Pro	Arg	145	150	155
Met	Arg	Lys	Ile	Phe	Ser	Arg	Leu	Ile	Tyr	Ile	Ala	Gln	Ser	Lys	Gly	165	170	175
Ala	Trp	Ile	Leu	Thr	Gly	Gly	Thr	His	Tyr	Gly	Leu	Met	Lys	Tyr	Ile	180	185	190
Gly	Glu	Val	Val	Arg	Asp	Asn	Thr	Ile	Ser	Arg	Ser	Ser	Glu	Glu	Asn	195	200	205
Ile	Val	Ala	Ile	Gly	Ile	Ala	Ala	Trp	Gly	Met	Val	Ser	Asn	Arg	Asp	210	215	220
Thr	Leu	Ile	Arg	Asn	Cys	Asp	Ala	Glu	Gly	Tyr	Phe	Leu	Ala	Gln	Tyr	225	230	235
Leu	Met	Asp	Asp	Phe	Thr	Arg	Asp	Pro	Leu	Tyr	Ile	Leu	Asp	Asn	Asn	245	250	255
His	Thr	His	Leu	Leu	Leu	Val	Asp	Asn	Gly	Cys	His	Gly	His	Pro	Thr	260	265	270
Val	Glu	Ala	Lys	Leu	Arg	Asn	Gln	Leu	Glu	Lys	Tyr	Ile	Ser	Glu	Arg	275	280	285
Thr	Ile	Gln	Asp	Ser	Asn	Tyr	Gly	Gly	Lys	Ile	Pro	Ile	Val	Cys	Phe	290	295	300
Ala	Gln	Gly	Gly	Gly	Lys	Glu	Thr	Leu	Lys	Ala	Ile	Asn	Thr	Ser	Ile	305	310	315
Lys	Asn	Lys	Ile	Pro	Cys	Val	Val	Val	Glu	Gly	Ser	Gly	Gln	Ile	Ala	325	330	335
Asp	Val	Ile	Ala	Ser	Leu	Val	Glu	Val	Glu	Asp	Ala	Leu	Thr	Ser	Ser	340	345	350
Ala	Val	Lys	Glu	Lys	Leu	Val	Arg	Phe	Leu	Pro	Arg	Thr	Val	Ser	Arg	355	360	365

ITI-08-PCT_Sequence_Listing_ST25.txt

Leu Pro Glu Glu Glu Thr Glu Ser Trp Ile Lys Trp Leu Lys Glu Ile
 370 375 380
 Leu Glu Cys Ser His Leu Leu Thr Val Ile Lys Met Glu Glu Ala Gly
 385 390 395 400
 Asp Glu Ile Val Ser Asn Ala Ile Ser Tyr Ala Leu Tyr Lys Ala Phe
 405 410 415
 Ser Thr Ser Glu Gln Asp Lys Asp Asn Trp Asn Gly Gln Leu Lys Leu
 420 425 430
 Leu Leu Glu Trp Asn Gln Leu Asp Leu Ala Asn Asp Glu Ile Phe Thr
 435 440 445
 Asn Asp Arg Arg Trp Glu Ser Ala Asp Leu Gln Glu Val Met Phe Thr
 450 455 460
 Ala Leu Ile Lys Asp Arg Pro Lys Phe Val Arg Leu Phe Leu Glu Asn
 465 470 475 480
 Gly Leu Asn Leu Arg Lys Phe Leu Thr His Asp Val Leu Thr Glu Leu
 485 490 495
 Phe Ser Asn His Phe Ser Thr Leu Val Tyr Arg Asn Leu Gln Ile Ala
 500 505 510
 Lys Asn Ser Tyr Asn Asp Ala Leu Leu Thr Phe Val Trp Lys Leu Val
 515 520 525
 Ala Asn Phe Arg Arg Gly Phe Arg Lys Glu Asp Arg Asn Gly Arg Asp
 530 535 540
 Glu Met Asp Ile Glu Leu His Asp Val Ser Pro Ile Thr Arg His Pro
 545 550 555 560
 Leu Gln Ala Leu Phe Ile Trp Ala Ile Leu Gln Asn Lys Lys Glu Leu
 565 570 575
 Ser Lys Val Ile Trp Glu Gln Thr Arg Gly Cys Thr Leu Ala Ala Leu
 580 585 590
 Gly Ala Ser Lys Leu Leu Lys Thr Leu Ala Lys Val Lys Asn Asp Ile
 595 600 605
 Asn Ala Ala Gly Glu Ser Glu Glu Leu Ala Asn Glu Tyr Glu Thr Arg
 610 615 620
 Ala Val Glu Leu Phe Thr Glu Cys Tyr Ser Ser Asp Glu Asp Leu Ala
 625 630 635 640
 Glu Gln Leu Leu Val Tyr Ser Cys Glu Ala Trp Gly Gly Ser Asn Cys

ITI-08-PCT_Sequence_Listing_ST25.txt

645 650 655

Leu Glu Leu Ala Val Glu Ala Thr Asp Gln His Phe Ile Ala Gln Pro
660 665 670

Gly Val Gln Asn Phe Leu Ser Lys Gln Trp Tyr Gly Glu Ile Ser Arg
675 680 685

Asp Thr Lys Asn Trp Lys Ile Ile Leu Cys Leu Phe Ile Ile Pro Leu
690 695 700

Val Gly Cys Gly Phe Val Ser Phe Arg Lys Lys Pro Val Asp Lys His
705 710 715 720

Lys Lys Leu Leu Trp Tyr Tyr Val Ala Phe Phe Thr Ser Pro Phe Val
725 730 735

Val Phe Ser Trp Asn Val Val Phe Tyr Ile Ala Phe Leu Leu Leu Phe
740 745 750

Ala Tyr Val Leu Leu Met Asp Phe His Ser Val Pro His Pro Pro Glu
755 760 765

Leu Val Leu Tyr Ser Leu Val Phe Val Leu Phe Cys Asp Glu Val Arg
770 775 780

Gln Trp Tyr Val Asn Gly Val Asn Tyr Phe Thr Asp Leu Trp Asn Val
785 790 795 800

Met Asp Thr Leu Gly Leu Phe Tyr Phe Ile Ala Gly Ile Val Phe Arg
805 810 815

Leu His Ser Ser Asn Lys Ser Ser Leu Tyr Ser Gly Arg Val Ile Phe
820 825 830

Cys Leu Asp Tyr Ile Ile Phe Thr Leu Arg Leu Ile His Ile Phe Thr
835 840 845

Val Ser Arg Asn Leu Gly Pro Lys Ile Ile Met Leu Gln Arg Met Leu
850 855 860

Ile Asp Val Phe Phe Phe Leu Phe Leu Phe Ala Val Trp Met Val Ala
865 870 875 880

Phe Gly Val Ala Arg Gln Gly Ile Leu Arg Gln Asn Glu Gln Arg Trp
885 890 895

Arg Trp Ile Phe Arg Ser Val Ile Tyr Glu Pro Tyr Leu Ala Met Phe
900 905 910

Gly Gln Val Pro Ser Asp Val Asp Gly Thr Thr Tyr Asp Phe Ala His
915 920 925

ITI-08-PCT_Sequence_Listing_ST25.txt

Cys Thr Phe Thr Gly Asn Glu Ser Lys Pro Leu Cys Val Glu Leu Asp
 930 935 940
 Glu His Asn Leu Pro Arg Phe Pro Glu Trp Ile Thr Ile Pro Leu Val
 945 950 955 960
 Cys Ile Tyr Met Leu Ser Thr Asn Ile Leu Leu Val Asn Leu Leu Val
 965 970 975
 Ala Met Phe Gly Tyr Thr Val Gly Thr Val Gln Glu Asn Asn Asp Gln
 980 985 990
 Val Trp Lys Phe Gln Arg Tyr Phe Leu Val Gln Glu Tyr Cys Ser Arg
 995 1000 1005
 Leu Asn Ile Pro Phe Pro Phe Ile Val Phe Ala Tyr Phe Tyr Met
 1010 1015 1020
 Val Val Lys Lys Cys Phe Lys Cys Cys Cys Lys Glu Lys Asn Met
 1025 1030 1035
 Glu Ser Ser Val Cys Cys Phe Lys Asn Glu Asp Asn Glu Thr Leu
 1040 1045 1050
 Ala Trp Glu Gly Val Met Lys Glu Asn Tyr Leu Val Lys Ile Asn
 1055 1060 1065
 Thr Lys Ala Asn Asp Thr Ser Glu Glu Met Arg His Arg Phe Arg
 1070 1075 1080
 Gln Leu Asp Thr Lys Leu Asn Asp Leu Lys Gly Leu Leu Lys Glu
 1085 1090 1095
 Ile Ala Asn Lys Ile Lys
 1100
 <210> 670
 <211> 698
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> TSG10__Homo_sapiens__Q9BZW7
 <400> 670
 Met Met Arg Ser Arg Ser Lys Ser Pro Arg Arg Pro Ser Pro Thr Ala
 1 5 10 15
 Arg Gly Ala Asn Cys Asp Val Glu Leu Leu Lys Thr Thr Thr Arg Asp
 20 25 30

ITI-08-PCT_Sequence_Listing_ST25.txt

Arg	Glu	Glu	Leu	Lys	Cys	Met	Leu	Glu	Lys	Tyr	Glu	Arg	His	Leu	Ala	35	40	45	
Glu	Ile	Gln	Gly	Asn	Val	Lys	Val	Leu	Lys	Ser	Glu	Arg	Asp	Lys	Ile	50	55	60	
Phe	Leu	Leu	Tyr	Glu	Gln	Ala	Gln	Glu	Glu	Ile	Thr	Arg	Leu	Arg	Arg	65	70	75	80
Glu	Met	Met	Lys	Ser	Cys	Lys	Ser	Pro	Lys	Ser	Thr	Thr	Ala	His	Ala	85	90	95	
Ile	Leu	Arg	Arg	Val	Glu	Thr	Glu	Arg	Asp	Val	Ala	Phe	Thr	Asp	Leu	100	105	110	
Arg	Arg	Met	Thr	Thr	Glu	Arg	Asp	Ser	Leu	Arg	Glu	Arg	Leu	Lys	Ile	115	120	125	
Ala	Gln	Glu	Thr	Ala	Phe	Asn	Glu	Lys	Ala	His	Leu	Glu	Gln	Arg	Ile	130	135	140	
Glu	Glu	Leu	Glu	Cys	Thr	Val	His	Asn	Leu	Asp	Asp	Glu	Arg	Met	Glu	145	150	155	160
Gln	Met	Ser	Asn	Met	Thr	Leu	Met	Lys	Glu	Thr	Ile	Ser	Thr	Val	Glu	165	170	175	
Lys	Glu	Met	Lys	Ser	Leu	Ala	Arg	Lys	Ala	Met	Asp	Thr	Glu	Ser	Glu	180	185	190	
Leu	Gly	Arg	Gln	Lys	Ala	Glu	Asn	Asn	Ser	Leu	Arg	Leu	Leu	Tyr	Glu	195	200	205	
Asn	Thr	Glu	Lys	Asp	Leu	Ser	Asp	Thr	Gln	Arg	His	Leu	Ala	Lys	Lys	210	215	220	
Lys	Tyr	Glu	Leu	Gln	Leu	Thr	Gln	Glu	Lys	Ile	Met	Cys	Leu	Asp	Glu	225	230	235	240
Lys	Ile	Asp	Asn	Phe	Thr	Arg	Gln	Asn	Ile	Ala	Gln	Arg	Glu	Glu	Ile	245	250	255	
Ser	Ile	Leu	Gly	Gly	Thr	Leu	Asn	Asp	Leu	Ala	Lys	Glu	Lys	Glu	Cys	260	265	270	
Leu	Gln	Ala	Cys	Leu	Asp	Lys	Lys	Ser	Glu	Asn	Ile	Ala	Ser	Leu	Gly	275	280	285	
Glu	Ser	Leu	Ala	Met	Lys	Glu	Lys	Thr	Ile	Ser	Gly	Met	Lys	Asn	Ile	290	295	300	

ITI-08-PCT_Sequence_Listing_ST25.txt

Ile Ala Glu Met Glu Gln Ala Ser Arg Gln Cys Thr Glu Ala Leu Ile
305 310 315 320

Val Cys Glu Gln Asp Val Ser Arg Met Arg Arg Gln Leu Asp Glu Thr
325 330 335

Asn Asp Glu Leu Ala Gln Ile Ala Arg Glu Arg Asp Ile Leu Ala His
340 345 350

Asp Asn Asp Asn Leu Gln Glu Gln Phe Ala Lys Ala Lys Gln Glu Asn
355 360 365

Gln Ala Leu Ser Lys Lys Leu Asn Asp Thr His Asn Glu Leu Asn Asp
370 375 380

Ile Lys Gln Lys Val Gln Asp Thr Asn Leu Glu Val Asn Lys Leu Lys
385 390 395 400

Asn Ile Leu Lys Ser Glu Glu Ser Glu Asn Arg Gln Met Met Glu Gln
405 410 415

Leu Arg Lys Ala Asn Glu Asp Ala Glu Asn Trp Glu Asn Lys Ala Arg
420 425 430

Gln Ser Glu Ala Asp Asn Asn Thr Leu Lys Leu Glu Leu Ile Thr Ala
435 440 445

Glu Ala Glu Gly Asn Arg Leu Lys Glu Lys Val Asp Ser Leu Asn Arg
450 455 460

Glu Val Glu Gln His Leu Asn Ala Glu Arg Ser Tyr Lys Ser Gln Ile
465 470 475 480

Ser Thr Leu His Lys Ser Val Val Lys Met Glu Glu Glu Leu Gln Lys
485 490 495

Val Gln Phe Glu Lys Val Ser Ala Leu Ala Asp Leu Ser Ser Thr Arg
500 505 510

Glu Leu Cys Ile Lys Leu Asp Ser Ser Lys Glu Leu Leu Asn Arg Gln
515 520 525

Leu Val Ala Lys Asp Gln Glu Ile Glu Met Arg Glu Asn Glu Leu Asp
530 535 540

Ser Ala His Ser Glu Ile Glu Leu Leu Arg Ser Gln Met Ala Asn Glu
545 550 555 560

Arg Ile Ser Met Gln Asn Leu Glu Ala Leu Leu Val Ala Asn Arg Asp
565 570 575

Lys Glu Tyr Gln Ser Gln Ile Ala Leu Gln Glu Lys Glu Ser Glu Ile

ITI-08-PCT_Sequence_Listing_ST25.txt

580

585

590

Gln Leu Leu Lys Glu His Leu Cys Leu Ala Glu Asn Lys Met Ala Ile
595 600 605

Gln Ser Arg Asp Val Ala Gln Phe Arg Asn Val Val Thr Gln Leu Glu
610 615 620

Ala Asp Leu Asp Ile Thr Lys Arg Gln Leu Gly Thr Glu Arg Phe Glu
625 630 635 640

Arg Glu Arg Ala Val Gln Glu Leu Arg Arg Gln Asn Tyr Ser Ser Asn
645 650 655

Ala Tyr His Met Ser Ser Thr Met Lys Pro Asn Thr Lys Cys His Ser
660 665 670

Pro Glu Arg Ala His His Arg Ser Pro Asp Arg Gly Leu Asp Arg Ser
675 680 685

Leu Glu Glu Asn Leu Cys Tyr Arg Asp Phe
690 695

<210> 671

<211> 308

<212> PRT

<213> Artificial Sequence

<220>

<223> TSPY1__Homo_sapiens__Q01534

<400> 671

Met Arg Pro Glu Gly Ser Leu Thr Tyr Arg Val Pro Glu Arg Leu Arg
1 5 10 15

Gln Gly Phe Cys Gly Val Gly Arg Ala Ala Gln Ala Leu Val Cys Ala
20 25 30

Ser Ala Lys Glu Gly Thr Ala Phe Arg Met Glu Ala Val Gln Glu Gly
35 40 45

Ala Ala Gly Val Glu Ser Glu Gln Ala Ala Leu Gly Glu Glu Ala Val
50 55 60

Leu Leu Leu Asp Asp Ile Met Ala Glu Val Glu Val Val Ala Glu Glu
65 70 75 80

Glu Gly Leu Val Glu Arg Arg Glu Glu Ala Gln Arg Ala Gln Gln Ala
85 90 95

Val Pro Gly Pro Gly Pro Met Thr Pro Glu Ser Ala Pro Glu Glu Leu

ITI-08-PCT_Sequence_Listing_ST25.txt

100

105

110

Leu Ala Val Gln Val Glu Leu Glu Pro Val Asn Ala Gln Ala Arg Lys
115 120 125

Ala Phe Ser Arg Gln Arg Glu Lys Met Glu Arg Arg Arg Lys Pro His
130 135 140

Leu Asp Arg Arg Gly Ala Val Ile Gln Ser Val Pro Gly Phe Trp Ala
145 150 155 160

Asn Val Ile Ala Asn His Pro Gln Met Ser Ala Leu Ile Thr Asp Glu
165 170 175

Asp Glu Asp Met Leu Ser Tyr Met Val Ser Leu Glu Val Gly Glu Glu
180 185 190

Lys His Pro Val His Leu Cys Lys Ile Met Leu Phe Phe Arg Ser Asn
195 200 205

Pro Tyr Phe Gln Asn Lys Val Ile Thr Lys Glu Tyr Leu Val Asn Ile
210 215 220

Thr Glu Tyr Arg Ala Ser His Ser Thr Pro Ile Glu Trp Tyr Pro Asp
225 230 235 240

Tyr Glu Val Glu Ala Tyr Arg Arg Arg His His Asn Ser Ser Leu Asn
245 250 255

Phe Phe Asn Trp Phe Ser Asp His Asn Phe Ala Gly Ser Asn Lys Ile
260 265 270

Ala Glu Ile Leu Cys Lys Asp Leu Trp Arg Asn Pro Leu Gln Tyr Tyr
275 280 285

Lys Arg Met Lys Pro Pro Glu Glu Gly Thr Glu Thr Ser Gly Asp Ser
290 295 300

Gln Leu Leu Ser
305

<210> 672

<211> 122

<212> PRT

<213> Artificial Sequence

<220>

<223> TVC_(TRGV3)___Homo_sapiens__M13231.1

<400> 672

Met Arg Trp Ala Leu Leu Val Leu Leu Ala Phe Leu Ser Pro Ala Ser

ITI-08-PCT_Sequence_Listing_ST25.txt

```

1             5             10             15
Gln Lys Ser Ser Asn Leu Glu Gly Arg Thr Lys Ser Val Thr Arg Gln
      20             25             30
Thr Gly Ser Ser Ala Glu Ile Thr Cys Asp Leu Thr Val Thr Asn Thr
      35             40             45
Phe Tyr Ile His Trp Tyr Leu His Gln Glu Gly Lys Ala Pro Gln Arg
      50             55             60
Leu Leu Tyr Tyr Asp Val Ser Thr Ala Arg Asp Val Leu Glu Ser Gly
65             70             75             80
Leu Ser Pro Gly Lys Tyr Tyr Thr His Thr Pro Arg Arg Trp Ser Trp
      85             90             95
Ile Leu Arg Leu Gln Asn Leu Ile Glu Asn Asp Ser Gly Val Tyr Tyr
      100            105            110
Cys Ala Thr Trp Asp Arg Gln Lys Leu Leu
      115            120

```

<210> 673

<211> 267

<212> PRT

<213> Artificial Sequence

<220>

<223> TX101__Homo_sapiens__Q9BY14-2

<400> 673

```

Met Gly Ala Arg Gln Ile Gln Thr Ser Ser Ser Gln Thr Ser Pro Glu
1             5             10             15
Glu Ala Met Gly Thr Pro Arg Ile Gln His Leu Leu Ile Leu Leu Val
      20             25             30
Leu Gly Ala Ser Leu Leu Thr Ser Gly Leu Glu Leu Tyr Cys Gln Lys
      35             40             45
Gly Leu Ser Met Thr Val Glu Ala Asp Pro Ala Asn Met Phe Asn Trp
      50             55             60
Thr Thr Glu Glu Val Glu Thr Cys Asp Lys Gly Ala Leu Cys Gln Glu
65             70             75             80
Thr Ile Leu Ile Ile Lys Ala Gly Thr Glu Thr Ala Ile Leu Ala Thr
      85             90             95
Lys Gly Cys Ile Pro Glu Gly Glu Glu Ala Ile Thr Ile Val Gln His

```


ITI-08-PCT_Sequence_Listing_ST25.txt

100

105

110

Ser Ser Pro Pro Gly Leu Ile Val Thr Ser Tyr Ser Asn Tyr Cys Glu
115 120 125

Asp Ser Phe Cys Asn Asp Lys Asp Ser Leu Ser Gln Phe Trp Glu Phe
130 135 140

Ser Glu Thr Thr Ala Ser Thr Val Ser Thr Thr Leu His Cys Pro Thr
145 150 155 160

Cys Val Ala Leu Gly Thr Cys Phe Ser Ala Pro Ser Leu Pro Cys Pro
165 170 175

Asn Gly Thr Thr Arg Cys Tyr Gln Gly Lys Leu Glu Ile Thr Gly Gly
180 185 190

Gly Ile Glu Ser Ser Val Glu Val Lys Gly Cys Thr Ala Met Ile Gly
195 200 205

Cys Arg Leu Met Ser Gly Ile Leu Ala Val Gly Pro Met Phe Val Arg
210 215 220

Glu Ala Cys Pro His Gln Leu Leu Thr Gln Pro Arg Lys Thr Glu Asn
225 230 235 240

Gly Ala Thr Cys Leu Pro Ile Pro Val Trp Gly Leu Gln Leu Leu Leu
245 250 255

Pro Leu Leu Leu Pro Ser Phe Ile His Phe Ser
260 265

<210> 674

<211> 529

<212> PRT

<213> Artificial Sequence

<220>

<223> tyrosinase__Homo_sapiens__A0A024DBG7

<400> 674

Met Leu Leu Ala Val Leu Tyr Cys Leu Leu Trp Ser Phe Gln Thr Ser
1 5 10 15

Ala Gly His Phe Pro Arg Ala Cys Val Ser Ser Lys Asn Leu Met Glu
20 25 30

Lys Glu Cys Cys Pro Pro Trp Ser Gly Asp Arg Ser Pro Cys Gly Gln
35 40 45

Leu Ser Gly Arg Gly Ser Cys Gln Asn Ile Leu Leu Ser Asn Ala Pro

ITI-08-PCT_Sequence_Listing_ST25.txt

50						55						60					
Leu	Gly	Pro	Gln	Phe	Pro	Phe	Thr	Gly	Val	Asp	Asp	Arg	Glu	Ser	Trp		
65					70					75					80		
Pro	Ser	Val	Phe	Tyr	Asn	Arg	Thr	Cys	Gln	Cys	Ser	Gly	Asn	Phe	Met		
				85					90					95			
Gly	Phe	Asn	Cys	Gly	Asn	Cys	Lys	Phe	Gly	Phe	Trp	Gly	Pro	Asn	Cys		
			100					105					110				
Thr	Glu	Arg	Arg	Leu	Leu	Val	Arg	Arg	Asn	Ile	Phe	Asp	Leu	Ser	Ala		
		115					120					125					
Pro	Glu	Lys	Asp	Lys	Phe	Phe	Ala	Tyr	Leu	Thr	Leu	Ala	Lys	His	Thr		
	130					135					140						
Ile	Ser	Ser	Asp	Tyr	Val	Ile	Pro	Ile	Gly	Thr	Tyr	Gly	Gln	Met	Lys		
145					150					155					160		
Asn	Gly	Ser	Thr	Pro	Met	Phe	Asn	Asp	Ile	Asn	Ile	Tyr	Asp	Leu	Phe		
				165					170					175			
Val	Trp	Met	His	Tyr	Tyr	Val	Ser	Met	Asp	Ala	Leu	Leu	Gly	Gly	Ser		
			180					185					190				
Glu	Ile	Trp	Arg	Asp	Ile	Asp	Phe	Ala	His	Glu	Ala	Pro	Ala	Phe	Leu		
		195					200					205					
Pro	Trp	His	Arg	Leu	Phe	Leu	Leu	Arg	Trp	Glu	Gln	Glu	Ile	Gln	Lys		
	210					215					220						
Leu	Thr	Gly	Asp	Glu	Asn	Phe	Thr	Ile	Pro	Tyr	Trp	Asp	Trp	Arg	Asp		
225					230					235					240		
Ala	Glu	Lys	Cys	Asp	Ile	Cys	Thr	Asp	Glu	Tyr	Met	Gly	Gly	Gln	His		
				245					250					255			
Pro	Thr	Asn	Pro	Asn	Leu	Leu	Ser	Pro	Ala	Ser	Phe	Phe	Ser	Ser	Trp		
			260					265					270				
Gln	Ile	Val	Cys	Ser	Arg	Leu	Glu	Glu	Tyr	Asn	Ser	His	Gln	Ser	Leu		
		275					280					285					
Cys	Asn	Gly	Thr	Pro	Glu	Gly	Pro	Leu	Arg	Arg	Asn	Pro	Gly	Asn	His		
	290					295					300						
Asp	Lys	Ser	Arg	Thr	Pro	Arg	Leu	Pro	Ser	Ser	Ala	Asp	Val	Glu	Phe		
305					310					315					320		
Cys	Leu	Ser	Leu	Thr	Gln	Tyr	Glu	Ser	Gly	Ser	Met	Asp	Lys	Ala	Ala		
				325					330					335			

ITI-08-PCT_Sequence_Listing_ST25.txt

```

Asn Phe Ser Phe Arg Asn Thr Leu Glu Gly Phe Ala Ser Pro Leu Thr
      340                      345                      350

Gly Ile Ala Asp Ala Ser Gln Ser Ser Met His Asn Ala Leu His Ile
      355                      360                      365

Tyr Met Asn Gly Thr Met Ser Gln Val Gln Gly Ser Ala Asn Asp Pro
      370                      375                      380

Ile Phe Leu Leu His His Ala Phe Val Asp Ser Ile Phe Glu Gln Trp
385                      390                      395                      400

Leu Arg Arg His Arg Pro Leu Gln Glu Val Tyr Pro Glu Ala Asn Ala
      405                      410                      415

Pro Ile Arg His Asn Arg Glu Ser Tyr Met Val Pro Phe Ile Pro Leu
      420                      425                      430

Tyr Arg Asn Gly Asp Phe Phe Ile Ser Ser Lys Asp Leu Gly Tyr Asp
      435                      440                      445

Tyr Ser Tyr Leu Gln Asp Ser Asp Pro Asp Ser Phe Gln Asp Tyr Ile
      450                      455                      460

Lys Ser Tyr Leu Glu Gln Ala Ser Arg Ile Trp Ser Trp Leu Leu Gly
465                      470                      475                      480

Ala Ala Met Val Gly Ala Val Leu Thr Ala Leu Leu Ala Gly Leu Val
      485                      490                      495

Ser Leu Leu Cys Arg His Lys Arg Lys Gln Leu Pro Glu Glu Lys Gln
      500                      505                      510

Pro Leu Leu Met Glu Lys Glu Asp Tyr His Ser Leu Tyr Gln Ser His
      515                      520                      525

```

Leu

```

<210> 675
<211> 529
<212> PRT
<213> Artificial Sequence

<220>
<223> tyrosinase__Homo_sapiens__L8B082

<400> 675

```

```

Met Leu Leu Ala Val Leu Tyr Cys Leu Leu Trp Ser Phe Gln Thr Ser
1                      5                      10                      15

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Ala Gly His Phe Pro Arg Ala Cys Val Ser Ser Lys Asn Leu Met Glu
20 25 30

Lys Glu Cys Cys Pro Pro Trp Ser Gly Asp Arg Ser Pro Cys Gly Gln
35 40 45

Leu Ser Gly Arg Gly Ser Cys Gln Asn Ile Leu Leu Ser Asn Ala Pro
50 55 60

Leu Gly Pro Gln Phe Pro Phe Thr Gly Val Asp Asp Arg Glu Ser Trp
65 70 75 80

Pro Ser Val Phe Tyr Asn Arg Thr Cys Gln Cys Ser Gly Asn Phe Met
85 90 95

Gly Phe Asn Cys Gly Asn Cys Lys Phe Gly Phe Trp Gly Pro Asn Cys
100 105 110

Thr Glu Arg Arg Leu Leu Val Arg Arg Asn Ile Phe Asp Leu Ser Ala
115 120 125

Pro Glu Lys Asp Lys Phe Phe Ala Tyr Leu Thr Leu Ala Lys His Thr
130 135 140

Ile Ser Ser Asp Tyr Val Ile Pro Ile Gly Thr Tyr Gly Gln Met Lys
145 150 155 160

Asn Gly Ser Thr Pro Met Phe Asn Asp Ile Asn Ile Tyr Asp Leu Phe
165 170 175

Val Trp Met His Tyr Tyr Val Ser Met Asp Ala Leu Leu Gly Gly Ser
180 185 190

Glu Ile Trp Arg Asp Ile Asp Phe Ala His Glu Ala Pro Ala Phe Leu
195 200 205

Pro Trp His Arg Leu Phe Leu Leu Arg Trp Glu Gln Glu Ile Gln Lys
210 215 220

Leu Thr Gly Asp Glu Asn Phe Thr Ile Pro Tyr Trp Asp Trp Arg Asp
225 230 235 240

Ala Glu Lys Cys Asp Ile Cys Thr Asp Glu Tyr Met Gly Gly Gln His
245 250 255

Pro Thr Asn Pro Asn Leu Leu Ser Pro Ala Ser Phe Phe Ser Ser Trp
260 265 270

Gln Ile Val Cys Ser Arg Leu Glu Glu Tyr Asn Ser His Gln Ser Leu
275 280 285

Cys Asn Gly Thr Pro Glu Gly Pro Leu Arg Arg Asn Pro Gly Asn His

ITI-08-PCT_Sequence_Listing_ST25.txt

290

295

300

Asp Lys Ser Arg Thr Pro Arg Leu Pro Ser Ser Ala Asp Val Glu Phe
305 310 315 320

Cys Leu Ser Leu Thr Gln Tyr Glu Ser Gly Ser Met Asp Lys Ala Ala
325 330 335

Asn Phe Ser Phe Arg Asn Thr Leu Glu Gly Phe Ala Ser Pro Leu Thr
340 345 350

Gly Ile Ala Asp Ala Ser Gln Ser Ser Met His Asn Ala Leu His Ile
355 360 365

Tyr Met Asn Gly Thr Met Ser Gln Val Gln Gly Ser Ala Asn Asp Pro
370 375 380

Ile Phe Leu Leu His His Ala Phe Val Asp Ser Ile Phe Glu Gln Trp
385 390 395 400

Leu Arg Arg His Arg Pro Leu Gln Glu Val Tyr Pro Glu Ala Asn Ala
405 410 415

Pro Ile Gly His Asn Arg Glu Ser Tyr Met Val Pro Phe Ile Pro Leu
420 425 430

Tyr Arg Asn Gly Asp Phe Phe Ile Ser Ser Lys Asp Leu Gly Tyr Asp
435 440 445

Tyr Ser Tyr Leu Gln Asp Ser Asp Pro Asp Ser Phe Gln Asp Tyr Ile
450 455 460

Lys Ser Tyr Leu Glu Gln Ala Ser Arg Ile Trp Ser Trp Leu Leu Gly
465 470 475 480

Ala Ala Met Val Gly Ala Val Leu Thr Ala Leu Leu Ala Gly Leu Val
485 490 495

Ser Leu Leu Cys Arg His Lys Arg Lys Gln Leu Pro Glu Glu Lys Gln
500 505 510

Pro Leu Leu Met Glu Lys Glu Asp Tyr His Ser Leu Tyr Gln Ser His
515 520 525

Leu

<210> 676

<211> 529

<212> PRT

<213> Artificial Sequence

<220>

ITI-08-PCT_Sequence_Listing_ST25.txt

<223> tyrosinase__Homo_sapiens__L8B086

<400> 676

```

Met Leu Leu Ala Val Leu Tyr Cys Leu Leu Trp Ser Phe Gln Thr Ser
1          5          10          15

Ala Gly His Phe Pro Arg Ala Cys Val Ser Ser Lys Asn Leu Met Glu
20          25          30

Lys Glu Cys Cys Pro Pro Trp Ser Gly Asp Arg Ser Pro Cys Gly Gln
35          40          45

Leu Ser Gly Arg Gly Ser Cys Gln Asn Ile Leu Leu Ser Asn Ala Pro
50          55          60

Leu Gly Pro Gln Phe Pro Phe Thr Gly Val Asp Asp Arg Glu Ser Trp
65          70          75          80

Pro Ser Val Phe Tyr Asn Arg Thr Cys Gln Cys Ser Gly Asn Phe Met
85          90          95

Gly Phe Asn Cys Gly Asn Cys Lys Phe Gly Phe Trp Gly Pro Asn Cys
100         105         110

Thr Glu Arg Arg Leu Leu Val Arg Arg Asn Ile Phe Asp Leu Ser Ala
115         120         125

Pro Glu Lys Asp Lys Phe Phe Ala Tyr Leu Thr Leu Ala Lys His Thr
130         135         140

Ile Ser Ser Asp Tyr Val Ile Pro Ile Gly Thr Tyr Gly Gln Met Lys
145         150         155         160

Asn Gly Ser Thr Pro Met Phe Asn Asp Ile Asn Ile Tyr Asp Leu Phe
165         170         175

Val Trp Met His Tyr Tyr Val Ser Met Asp Ala Leu Leu Gly Gly Ser
180         185         190

Glu Ile Trp Arg Asp Ile Asp Phe Ala His Glu Ala Pro Ala Phe Leu
195         200         205

Pro Trp His Arg Leu Phe Leu Leu Arg Trp Glu Gln Glu Ile Gln Lys
210         215         220

Leu Thr Gly Asp Glu Asn Phe Thr Ile Pro Tyr Trp Asp Trp Arg Asp
225         230         235         240

Ala Glu Lys Cys Asp Ile Cys Thr Asp Glu Tyr Met Gly Gly Gln His
245         250         255

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Pro	Thr	Asn	Pro	Asn	Leu	Leu	Ser	Pro	Ala	Ser	Phe	Phe	Ser	Ser	Trp
			260					265					270		
Gln	Ile	Val	Cys	Ser	Arg	Leu	Glu	Glu	Tyr	Asn	Ser	His	Gln	Ser	Leu
		275					280					285			
Cys	Asn	Gly	Thr	Pro	Glu	Gly	Pro	Leu	Arg	Arg	Asn	Pro	Gly	Asn	His
	290					295					300				
Asp	Lys	Ser	Arg	Thr	Pro	Arg	Leu	Pro	Ser	Ser	Ala	Asp	Val	Glu	Phe
305					310					315					320
Cys	Leu	Ser	Leu	Thr	Gln	Tyr	Glu	Ser	Gly	Ser	Met	Asp	Lys	Ala	Ala
				325					330					335	
Asn	Phe	Ser	Phe	Arg	Asn	Thr	Leu	Glu	Gly	Phe	Ala	Ser	Pro	Leu	Thr
			340					345					350		
Gly	Ile	Ala	Asp	Ala	Ser	Gln	Ser	Ser	Met	His	Asn	Ala	Leu	His	Ile
		355					360					365			
Tyr	Met	Asn	Gly	Thr	Met	Ser	Gln	Val	Gln	Gly	Ser	Ala	Asn	Asp	Pro
	370					375					380				
Ile	Phe	Leu	Leu	His	His	Ala	Phe	Val	Asp	Ser	Ile	Phe	Glu	Gln	Trp
385					390					395					400
Leu	Gln	Arg	His	Arg	Pro	Leu	Gln	Glu	Val	Tyr	Pro	Glu	Ala	Asn	Ala
				405					410					415	
Pro	Ile	Gly	His	Asn	Arg	Glu	Ser	Tyr	Met	Val	Pro	Phe	Ile	Pro	Leu
			420					425					430		
Tyr	Arg	Asn	Gly	Asp	Phe	Phe	Ile	Ser	Ser	Lys	Asp	Leu	Gly	Tyr	Asp
		435					440					445			
Tyr	Ser	Tyr	Leu	Gln	Asp	Ser	Asp	Pro	Asp	Ser	Phe	Gln	Asp	Tyr	Ile
	450					455					460				
Lys	Ser	Tyr	Leu	Glu	Gln	Ala	Ser	Arg	Ile	Trp	Ser	Trp	Leu	Leu	Gly
465					470					475					480
Ala	Ala	Met	Val	Gly	Ala	Val	Leu	Thr	Ala	Leu	Leu	Ala	Gly	Leu	Val
				485					490					495	
Ser	Leu	Leu	Cys	Arg	His	Lys	Arg	Lys	Gln	Leu	Pro	Glu	Glu	Lys	Gln
			500					505					510		
Pro	Leu	Leu	Met	Glu	Lys	Glu	Asp	Tyr	His	Ser	Leu	Tyr	Gln	Ser	His
			515				520					525			
Leu															

ITI-08-PCT_Sequence_Listing_ST25.txt

<210> 677
 <211> 529
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> tyrosinase__Homo_sapiens__L8B0B9

<400> 677

```

Met Leu Leu Ala Val Leu Tyr Cys Leu Leu Trp Ser Phe Gln Thr Ser
1           5           10           15

Ala Gly His Phe Pro Arg Ala Cys Val Ser Ser Lys Asn Leu Met Glu
          20           25           30

Lys Glu Cys Cys Pro Pro Trp Ser Gly Asp Arg Ser Pro Cys Gly Gln
          35           40           45

Leu Ser Gly Arg Gly Ser Cys Gln Asn Ile Leu Leu Ser Asn Ala Pro
          50           55           60

Leu Gly Pro Gln Phe Pro Phe Thr Gly Val Asp Asp Arg Glu Ser Trp
65           70           75           80

Pro Ser Val Phe Tyr Asn Arg Thr Cys Gln Cys Ser Gly Asn Phe Met
          85           90           95

Gly Phe Asn Cys Gly Asn Cys Lys Phe Gly Phe Trp Gly Pro Asn Cys
          100          105          110

Thr Glu Arg Arg Leu Leu Val Arg Arg Asn Ile Phe Asp Leu Ser Ala
          115          120          125

Pro Glu Lys Asp Lys Phe Phe Ala Tyr Leu Thr Leu Ala Lys His Thr
          130          135          140

Ile Ser Ser Asp Tyr Val Ile Pro Ile Gly Thr Tyr Gly Gln Met Lys
145          150          155          160

Asn Gly Ser Thr Pro Met Phe Asn Asp Ile Asn Ile Tyr Asp Leu Phe
          165          170          175

Val Trp Met His Tyr Tyr Val Ser Met Asp Ala Leu Leu Gly Gly Tyr
          180          185          190

Glu Ile Trp Arg Asp Ile Asp Phe Ala His Glu Ala Pro Ala Phe Leu
          195          200          205

Pro Trp His Arg Leu Phe Leu Leu Arg Trp Glu Gln Glu Ile Gln Lys
210          215          220
    
```


ITI-08-PCT_Sequence_Listing_ST25.txt

```

Leu Thr Gly Asp Glu Asn Phe Thr Ile Pro Tyr Trp Asp Trp Arg Asp
225                230                235                240

Ala Glu Lys Cys Asp Ile Cys Thr Asp Glu Tyr Met Gly Gly Gln His
                245                250                255

Pro Thr Asn Pro Asn Leu Leu Ser Pro Ala Ser Phe Phe Ser Ser Trp
                260                265                270

Gln Ile Val Cys Ser Arg Leu Glu Glu Tyr Asn Ser His Gln Ser Leu
                275                280                285

Cys Asn Gly Thr Pro Glu Gly Pro Leu Arg Arg Asn Pro Gly Asn His
                290                295                300

Asp Lys Ser Arg Thr Pro Arg Leu Pro Ser Ser Ala Asp Val Glu Phe
305                310                315                320

Cys Leu Ser Leu Thr Gln Tyr Glu Ser Gly Ser Met Asp Lys Ala Ala
                325                330                335

Asn Phe Ser Phe Arg Asn Thr Leu Glu Gly Phe Ala Ser Pro Leu Thr
                340                345                350

Gly Ile Ala Asp Ala Ser Gln Ser Ser Met His Asn Ala Leu His Ile
                355                360                365

Tyr Met Asn Gly Thr Met Ser Gln Val Gln Gly Ser Ala Asn Asp Pro
370                375                380

Ile Phe Leu Leu His His Ala Phe Val Asp Ser Ile Phe Glu Gln Trp
385                390                395                400

Leu Arg Arg His Arg Pro Leu Gln Glu Val Tyr Pro Glu Ala Asn Ala
                405                410                415

Pro Ile Gly His Asn Arg Glu Ser Tyr Met Val Pro Phe Ile Pro Leu
                420                425                430

Tyr Arg Asn Gly Asp Phe Phe Ile Ser Ser Lys Asp Leu Gly Tyr Asp
435                440                445

Tyr Ser Tyr Leu Gln Asp Ser Asp Pro Asp Ser Phe Gln Asp Tyr Ile
450                455                460

Lys Ser Tyr Leu Glu Gln Ala Ser Arg Ile Trp Ser Trp Leu Leu Gly
465                470                475                480

Ala Ala Met Val Gly Ala Val Leu Thr Ala Leu Leu Ala Gly Leu Val
                485                490                495

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Ser Leu Leu Cys Arg His Lys Arg Lys Gln Leu Pro Glu Glu Lys Gln
500 505 510

Pro Leu Leu Met Glu Lys Glu Asp Tyr His Ser Leu Tyr Gln Ser His
515 520 525

Leu

<210> 678

<211> 237

<212> PRT

<213> Artificial Sequence

<220>

<223> tyrosinase__Homo_sapiens__075767

<400> 678

Met Ser Pro Leu Trp Trp Gly Phe Leu Leu Ser Cys Leu Gly Cys Lys
1 5 10 15

Ile Leu Pro Gly Ala Gln Gly Gln Phe Pro Arg Val Cys Met Thr Val
20 25 30

Asp Ser Leu Val Asn Lys Glu Cys Cys Pro Arg Leu Gly Ala Glu Ser
35 40 45

Ala Asn Val Cys Gly Ser Gln Gln Gly Arg Gly Gln Cys Thr Glu Val
50 55 60

Arg Ala Asp Thr Arg Pro Trp Ser Gly Pro Tyr Ile Leu Arg Asn Gln
65 70 75 80

Asp Asp Arg Glu Leu Trp Pro Arg Lys Phe Phe His Arg Thr Cys Lys
85 90 95

Cys Thr Gly Asn Phe Ala Gly Tyr Asn Cys Gly Asp Cys Lys Phe Gly
100 105 110

Trp Thr Gly Pro Asn Cys Glu Arg Lys Lys Pro Pro Val Ile Arg Gln
115 120 125

Asn Ile His Ser Leu Ser Pro Gln Glu Arg Glu Gln Phe Leu Gly Ala
130 135 140

Leu Asp Leu Ala Lys Lys Arg Val His Pro Asp Tyr Val Ile Thr Thr
145 150 155 160

Gln His Trp Val Gly Leu Leu Gly Pro Asn Gly Thr Gln Pro Gln Phe
165 170 175

Ala Asn Cys Ser Val Tyr Asp Phe Phe Val Trp Leu His Tyr Tyr Ser

ITI-08-PCT_Sequence_Listing_ST25.txt

180

185

190

Val Arg Asp Thr Leu Leu Gly Gly Phe Phe Pro Trp Leu Lys Val Tyr
195 200 205

Tyr Tyr Arg Phe Val Ile Gly Leu Arg Val Trp Gln Trp Glu Val Ile
210 215 220

Ser Cys Lys Leu Ile Lys Arg Ala Thr Thr Arg Gln Pro
225 230 235

<210> 679

<211> 529

<212> PRT

<213> Artificial Sequence

<220>

<223> tyrosinase__Homo_sapiens__P14679

<400> 679

Met Leu Leu Ala Val Leu Tyr Cys Leu Leu Trp Ser Phe Gln Thr Ser
1 5 10 15

Ala Gly His Phe Pro Arg Ala Cys Val Ser Ser Lys Asn Leu Met Glu
20 25 30

Lys Glu Cys Cys Pro Pro Trp Ser Gly Asp Arg Ser Pro Cys Gly Gln
35 40 45

Leu Ser Gly Arg Gly Ser Cys Gln Asn Ile Leu Leu Ser Asn Ala Pro
50 55 60

Leu Gly Pro Gln Phe Pro Phe Thr Gly Val Asp Asp Arg Glu Ser Trp
65 70 75 80

Pro Ser Val Phe Tyr Asn Arg Thr Cys Gln Cys Ser Gly Asn Phe Met
85 90 95

Gly Phe Asn Cys Gly Asn Cys Lys Phe Gly Phe Trp Gly Pro Asn Cys
100 105 110

Thr Glu Arg Arg Leu Leu Val Arg Arg Asn Ile Phe Asp Leu Ser Ala
115 120 125

Pro Glu Lys Asp Lys Phe Phe Ala Tyr Leu Thr Leu Ala Lys His Thr
130 135 140

Ile Ser Ser Asp Tyr Val Ile Pro Ile Gly Thr Tyr Gly Gln Met Lys
145 150 155 160

Asn Gly Ser Thr Pro Met Phe Asn Asp Ile Asn Ile Tyr Asp Leu Phe

ITI-08-PCT_Sequence_Listing_ST25.txt

165

170

175

Val Trp Met His Tyr Tyr Val Ser Met Asp Ala Leu Leu Gly Gly Ser
 180 185 190

Glu Ile Trp Arg Asp Ile Asp Phe Ala His Glu Ala Pro Ala Phe Leu
 195 200 205

Pro Trp His Arg Leu Phe Leu Leu Arg Trp Glu Gln Glu Ile Gln Lys
 210 215 220

Leu Thr Gly Asp Glu Asn Phe Thr Ile Pro Tyr Trp Asp Trp Arg Asp
 225 230 235 240

Ala Glu Lys Cys Asp Ile Cys Thr Asp Glu Tyr Met Gly Gly Gln His
 245 250 255

Pro Thr Asn Pro Asn Leu Leu Ser Pro Ala Ser Phe Phe Ser Ser Trp
 260 265 270

Gln Ile Val Cys Ser Arg Leu Glu Glu Tyr Asn Ser His Gln Ser Leu
 275 280 285

Cys Asn Gly Thr Pro Glu Gly Pro Leu Arg Arg Asn Pro Gly Asn His
 290 295 300

Asp Lys Ser Arg Thr Pro Arg Leu Pro Ser Ser Ala Asp Val Glu Phe
 305 310 315 320

Cys Leu Ser Leu Thr Gln Tyr Glu Ser Gly Ser Met Asp Lys Ala Ala
 325 330 335

Asn Phe Ser Phe Arg Asn Thr Leu Glu Gly Phe Ala Ser Pro Leu Thr
 340 345 350

Gly Ile Ala Asp Ala Ser Gln Ser Ser Met His Asn Ala Leu His Ile
 355 360 365

Tyr Met Asn Gly Thr Met Ser Gln Val Gln Gly Ser Ala Asn Asp Pro
 370 375 380

Ile Phe Leu Leu His His Ala Phe Val Asp Ser Ile Phe Glu Gln Trp
 385 390 395 400

Leu Arg Arg His Arg Pro Leu Gln Glu Val Tyr Pro Glu Ala Asn Ala
 405 410 415

Pro Ile Gly His Asn Arg Glu Ser Tyr Met Val Pro Phe Ile Pro Leu
 420 425 430

Tyr Arg Asn Gly Asp Phe Phe Ile Ser Ser Lys Asp Leu Gly Tyr Asp
 435 440 445

ITI-08-PCT_Sequence_Listing_ST25.txt

Tyr Ser Tyr Leu Gln Asp Ser Asp Pro Asp Ser Phe Gln Asp Tyr Ile
450 455 460

Lys Ser Tyr Leu Glu Gln Ala Ser Arg Ile Trp Ser Trp Leu Leu Gly
465 470 475 480

Ala Ala Met Val Gly Ala Val Leu Thr Ala Leu Leu Ala Gly Leu Val
485 490 495

Ser Leu Leu Cys Arg His Lys Arg Lys Gln Leu Pro Glu Glu Lys Gln
500 505 510

Pro Leu Leu Met Glu Lys Glu Asp Tyr His Ser Leu Tyr Gln Ser His
515 520 525

Leu

<210> 680

<211> 529

<212> PRT

<213> Artificial Sequence

<220>

<223> tyrosinase__Homo_sapiens__U3M8N0

<400> 680

Met Leu Leu Ala Val Leu Tyr Cys Leu Leu Trp Ser Phe Gln Thr Ser
1 5 10 15

Ala Gly His Phe Pro Arg Ala Cys Val Ser Ser Lys Asn Leu Met Glu
20 25 30

Lys Glu Cys Cys Pro Pro Trp Ser Gly Asp Arg Ser Pro Cys Gly Gln
35 40 45

Leu Ser Gly Arg Gly Ser Cys Gln Asn Ile Leu Leu Ser Asn Ala Pro
50 55 60

Leu Gly Pro Gln Phe Pro Phe Thr Gly Val Asp Asp Arg Glu Ser Trp
65 70 75 80

Pro Ser Val Phe Tyr Asn Arg Thr Cys Gln Cys Ser Gly Asn Phe Met
85 90 95

Gly Phe Asn Cys Gly Asn Cys Lys Phe Gly Phe Trp Gly Pro Asn Cys
100 105 110

Thr Glu Arg Arg Leu Leu Val Arg Arg Asn Ile Phe Asp Leu Ser Ala
115 120 125

ITI-08-PCT_Sequence_Listing_ST25.txt

Pro Glu Lys Asp Lys Phe Phe Ala Tyr Leu Thr Leu Ala Lys His Thr
130 135 140

Ile Ser Ser Asp Tyr Val Ile Pro Ile Gly Thr Tyr Gly Gln Met Lys
145 150 155 160

Asn Gly Ser Thr Pro Met Phe Asn Asp Ile Asn Ile Tyr Asp Leu Phe
165 170 175

Val Trp Met His Tyr Tyr Val Ser Met Asp Ala Leu Leu Gly Gly Ser
180 185 190

Glu Ile Trp Arg Asp Ile Asp Phe Ala His Glu Ala Pro Ala Phe Leu
195 200 205

Pro Trp His Arg Leu Phe Leu Leu Arg Trp Glu Gln Glu Ile Gln Lys
210 215 220

Leu Thr Gly Asp Glu Asn Phe Thr Ile Pro Tyr Trp Asp Trp Arg Asp
225 230 235 240

Ala Glu Lys Cys Asp Ile Cys Thr Asp Glu Tyr Val Gly Gly Gln His
245 250 255

Pro Thr Asn Pro Asn Leu Leu Ser Pro Ala Ser Phe Phe Ser Ser Trp
260 265 270

Gln Ile Val Cys Ser Arg Leu Glu Glu Tyr Asn Ser His Gln Ser Leu
275 280 285

Cys Asn Gly Thr Pro Glu Gly Pro Leu Arg Arg Asn Pro Gly Asn His
290 295 300

Asp Lys Ser Arg Thr Pro Arg Leu Pro Ser Ser Ala Asp Val Glu Phe
305 310 315 320

Cys Leu Ser Leu Thr Gln Tyr Glu Ser Gly Ser Met Asp Lys Ala Ala
325 330 335

Asn Phe Ser Phe Arg Asn Thr Leu Glu Gly Phe Ala Ser Pro Leu Thr
340 345 350

Gly Ile Ala Asp Ala Ser Gln Ser Ser Met His Asn Ala Leu His Ile
355 360 365

Tyr Met Asn Gly Thr Met Ser Gln Val Gln Gly Ser Ala Asn Asp Pro
370 375 380

Ile Phe Leu Leu His His Ala Phe Val Asp Ser Ile Phe Glu Gln Trp
385 390 395 400

Leu Arg Arg His Arg Pro Leu Gln Glu Val Tyr Pro Glu Ala Asn Ala

ITI-08-PCT_Sequence_Listing_ST25.txt

405 410 415

Pro Ile Gly His Asn Arg Glu Ser Tyr Met Val Pro Phe Ile Pro Leu
420 425 430

Tyr Arg Asn Gly Asp Phe Phe Ile Ser Ser Lys Asp Leu Gly Tyr Asp
435 440 445

Tyr Ser Tyr Leu Gln Asp Ser Asp Pro Asp Ser Phe Gln Asp Tyr Ile
450 455 460

Lys Ser Tyr Leu Glu Gln Ala Ser Arg Ile Trp Ser Trp Leu Leu Gly
465 470 475 480

Ala Ala Met Val Gly Ala Val Leu Thr Ala Leu Leu Ala Gly Leu Val
485 490 495

Ser Leu Leu Cys Arg His Lys Arg Lys Gln Leu Pro Glu Glu Lys Gln
500 505 510

Pro Leu Leu Met Glu Lys Glu Asp Tyr His Ser Leu Tyr Gln Ser His
515 520 525

Leu

<210> 681

<211> 529

<212> PRT

<213> Artificial Sequence

<220>

<223> tyrosinase__Homo_sapiens__U3M9D5

<400> 681

Met Leu Leu Ala Val Leu Tyr Cys Leu Leu Trp Ser Phe Gln Thr Ser
1 5 10 15

Ala Gly His Phe Pro Arg Ala Cys Val Ser Ser Lys Asn Leu Met Glu
20 25 30

Lys Glu Cys Cys Pro Pro Trp Ser Gly Asp Arg Ser Pro Cys Gly Gln
35 40 45

Leu Ser Gly Arg Gly Ser Cys Gln Asn Ile Leu Leu Ser Asn Ala Pro
50 55 60

Leu Gly Pro Gln Phe Pro Phe Thr Gly Val Asp Asp Arg Glu Ser Trp
65 70 75 80

Pro Ser Val Phe Tyr Asn Arg Thr Cys Gln Cys Ser Gly Asn Phe Met
85 90 95

ITI-08-PCT_Sequence_Listing_ST25.txt

Gly	Phe	Asn	Cys	Gly	Asn	Cys	Lys	Phe	Gly	Phe	Trp	Gly	Pro	Asn	Cys	
			100					105					110			
Thr	Glu	Arg	Arg	Leu	Leu	Val	Arg	Arg	Asn	Ile	Phe	Asp	Leu	Ser	Ala	
		115					120					125				
Pro	Glu	Lys	Asp	Lys	Phe	Phe	Ala	Tyr	Leu	Thr	Leu	Ala	Lys	His	Thr	
	130					135					140					
Ile	Ser	Ser	Asp	Tyr	Val	Ile	Pro	Ile	Gly	Thr	Tyr	Gly	Gln	Met	Lys	
145					150					155					160	
Asn	Gly	Ser	Thr	Pro	Met	Phe	Asn	Asp	Ile	Asn	Ile	Tyr	Asp	Leu	Phe	
				165					170					175		
Val	Trp	Met	His	Tyr	Tyr	Val	Ser	Met	Asp	Ala	Leu	Leu	Gly	Gly	Ser	
			180					185					190			
Glu	Ile	Trp	Arg	Asp	Ile	Asp	Phe	Ala	His	Glu	Ala	Pro	Ala	Phe	Leu	
		195					200					205				
Pro	Trp	His	Arg	Leu	Phe	Leu	Leu	Arg	Trp	Glu	Gln	Glu	Ile	Gln	Lys	
	210					215					220					
Leu	Thr	Gly	Asp	Glu	Asn	Phe	Thr	Ile	Pro	Tyr	Trp	Asp	Trp	Arg	Asp	
225					230				235						240	
Ala	Glu	Lys	Cys	Asp	Ile	Cys	Thr	Asp	Glu	Tyr	Met	Gly	Gly	Gln	His	
			245						250					255		
Pro	Thr	Asn	Pro	Asn	Leu	Leu	Ser	Pro	Ala	Ser	Phe	Phe	Ser	Ser	Trp	
			260					265					270			
Gln	Ile	Val	Cys	Ser	Arg	Leu	Glu	Glu	Tyr	Asn	Ser	His	Gln	Ser	Leu	
		275					280					285				
Cys	Asn	Gly	Thr	Pro	Glu	Gly	Pro	Leu	Arg	Arg	Asn	Pro	Gly	Asn	His	
	290					295					300					
Asp	Lys	Ser	Arg	Thr	Pro	Arg	Leu	Pro	Ser	Ser	Ala	Asp	Val	Glu	Phe	
305					310					315					320	
Cys	Leu	Ser	Leu	Thr	Gln	Tyr	Glu	Ser	Gly	Ser	Met	Asp	Lys	Ala	Ala	
				325					330					335		
Asn	Phe	Ser	Phe	Arg	Asn	Thr	Leu	Glu	Gly	Phe	Ala	Ser	Pro	Leu	Thr	
			340					345					350			
Gly	Ile	Ala	Asp	Ala	Ser	Gln	Ser	Ser	Met	His	Asn	Ala	Leu	His	Ile	
		355					360					365				

ITI-08-PCT_Sequence_Listing_ST25.txt

Tyr Met Asn Gly Thr Met Ser Gln Val Gln Gly Ser Ala Asn Asp Pro
370 375 380

Ile Phe Leu Leu His His Ala Phe Val Asp Ser Ile Phe Glu Gln Trp
385 390 395 400

Leu Arg Arg His Arg Leu Leu Gln Glu Val Tyr Pro Glu Ala Asn Ala
405 410 415

Pro Ile Gly His Asn Arg Glu Ser Tyr Met Val Pro Phe Ile Pro Leu
420 425 430

Tyr Arg Asn Gly Asp Phe Phe Ile Ser Ser Lys Asp Leu Gly Tyr Asp
435 440 445

Tyr Ser Tyr Leu Gln Asp Ser Asp Pro Asp Ser Phe Gln Asp Tyr Ile
450 455 460

Lys Ser Tyr Leu Glu Gln Ala Ser Arg Ile Trp Ser Trp Leu Leu Gly
465 470 475 480

Ala Ala Met Val Gly Ala Val Leu Thr Ala Leu Leu Ala Gly Leu Val
485 490 495

Ser Leu Leu Cys Arg His Lys Arg Lys Gln Leu Pro Glu Glu Lys Gln
500 505 510

Pro Leu Leu Met Glu Lys Glu Asp Tyr His Ser Leu Tyr Gln Ser His
515 520 525

Leu

<210> 682

<211> 529

<212> PRT

<213> Artificial Sequence

<220>

<223> tyrosinase__Homo_sapiens__U3M9J2

<400> 682

Met Leu Leu Ala Val Leu Tyr Cys Leu Leu Trp Ser Phe Gln Thr Ser
1 5 10 15

Ala Gly His Phe Pro Arg Ala Cys Val Ser Ser Lys Asn Leu Met Glu
20 25 30

Lys Glu Cys Cys Pro Pro Trp Ser Gly Asp Arg Ser Pro Cys Gly Gln
35 40 45

Leu Ser Gly Arg Gly Ser Cys Gln Asn Ile Leu Leu Ser Asn Ala Pro

ITI-08-PCT_Sequence_Listing_ST25.txt

50	55	60														
Leu	Gly	Pro	Gln	Phe	Pro	Phe	Thr	Gly	Val	Asp	Asp	Arg	Glu	Ser	Trp	
65					70					75					80	
Pro	Ser	Val	Phe	Tyr	Asn	Arg	Thr	Cys	Gln	Cys	Ser	Gly	Asn	Phe	Met	
				85					90					95		
Gly	Phe	Asn	Cys	Gly	Asn	Cys	Lys	Phe	Gly	Phe	Trp	Gly	Pro	Asn	Cys	
			100					105					110			
Thr	Glu	Arg	Arg	Leu	Leu	Val	Arg	Arg	Asn	Ile	Phe	Asp	Leu	Ser	Ala	
		115					120					125				
Pro	Glu	Lys	Asp	Lys	Phe	Phe	Ala	Tyr	Leu	Thr	Leu	Ala	Lys	His	Thr	
	130					135					140					
Ile	Ser	Ser	Asp	Tyr	Val	Ile	Pro	Ile	Gly	Thr	Tyr	Gly	Gln	Met	Lys	
145					150					155					160	
Asn	Gly	Ser	Thr	Pro	Met	Phe	Asn	Asp	Ile	Asn	Ile	Tyr	Asp	Leu	Phe	
				165					170					175		
Val	Trp	Met	His	Tyr	Tyr	Val	Ser	Met	Asp	Ala	Leu	Leu	Gly	Gly	Ser	
			180					185					190			
Glu	Ile	Trp	Arg	Asp	Ile	Asp	Phe	Ala	His	Glu	Ala	Pro	Ala	Phe	Leu	
		195					200					205				
Pro	Trp	His	Arg	Leu	Phe	Leu	Leu	Arg	Trp	Glu	Gln	Glu	Ile	Gln	Lys	
	210					215					220					
Leu	Thr	Gly	Asp	Glu	Asn	Phe	Thr	Ile	Pro	Tyr	Trp	Asp	Trp	Arg	Asp	
225					230					235					240	
Ala	Glu	Lys	Cys	Asp	Ile	Cys	Thr	Asp	Glu	Tyr	Met	Gly	Gly	Gln	His	
				245					250					255		
Pro	Thr	Asn	Pro	Asn	Leu	Leu	Ser	Pro	Ala	Ser	Phe	Phe	Ser	Ser	Trp	
			260					265					270			
Gln	Ile	Val	Cys	Ser	Arg	Leu	Glu	Glu	Tyr	Asn	Ser	His	Gln	Ser	Leu	
		275					280					285				
Cys	Asn	Gly	Thr	Pro	Glu	Gly	Pro	Leu	Arg	Arg	Asn	Pro	Gly	Asn	His	
	290					295					300					
Asp	Lys	Ser	Arg	Thr	Pro	Arg	Leu	Pro	Ser	Ser	Ala	Asp	Val	Glu	Phe	
305					310					315					320	
Cys	Leu	Ser	Leu	Thr	Gln	Tyr	Glu	Ser	Gly	Ser	Met	Asp	Lys	Ala	Ala	
				325					330					335		

ITI-08-PCT_Sequence_Listing_ST25.txt

```

Asn Phe Ser Phe Arg Asn Thr Leu Glu Gly Phe Ala Ser Pro Leu Thr
      340                      345                      350

Gly Ile Ala Asp Ala Ser Gln Ser Ser Met His Asn Ala Leu His Ile
      355                      360                      365

Tyr Met Asn Gly Thr Met Ser Gln Val Gln Gly Ser Ala Asn Asp Pro
      370                      375                      380

Ile Phe Leu Leu His His Ala Phe Val Asp Ser Met Phe Glu Gln Trp
385                      390                      395                      400

Leu Arg Arg His Arg Pro Leu Gln Glu Val Tyr Pro Glu Ala Asn Ala
      405                      410                      415

Pro Ile Gly His Asn Arg Glu Ser Tyr Met Val Pro Phe Ile Pro Leu
      420                      425                      430

Tyr Arg Asn Gly Asp Phe Phe Ile Ser Ser Lys Asp Leu Gly Tyr Asp
      435                      440                      445

Tyr Ser Tyr Leu Gln Asp Ser Asp Pro Asp Ser Phe Gln Asp Tyr Ile
      450                      455                      460

Lys Ser Tyr Leu Glu Gln Ala Ser Arg Ile Trp Ser Trp Leu Leu Gly
465                      470                      475                      480

Ala Ala Met Val Gly Ala Val Leu Thr Ala Leu Leu Ala Gly Leu Val
      485                      490                      495

Ser Leu Leu Cys Arg His Lys Arg Lys Gln Leu Pro Glu Glu Lys Gln
      500                      505                      510

Pro Leu Leu Met Glu Lys Glu Asp Tyr His Ser Leu Tyr Gln Ser His
      515                      520                      525

```

Leu

```

<210> 683
<211> 537
<212> PRT
<213> Artificial Sequence

<220>
<223> TYRP1__Homo_sapiens__P17643

<400> 683

```

```

Met Ser Ala Pro Lys Leu Leu Ser Leu Gly Cys Ile Phe Phe Pro Leu
1          5          10         15

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Leu Leu Phe Gln Gln Ala Arg Ala Gln Phe Pro Arg Gln Cys Ala Thr
 20 25 30
 Val Glu Ala Leu Arg Ser Gly Met Cys Cys Pro Asp Leu Ser Pro Val
 35 40 45
 Ser Gly Pro Gly Thr Asp Arg Cys Gly Ser Ser Ser Gly Arg Gly Arg
 50 55 60
 Cys Glu Ala Val Thr Ala Asp Ser Arg Pro His Ser Pro Gln Tyr Pro
 65 70 75 80
 His Asp Gly Arg Asp Asp Arg Glu Val Trp Pro Leu Arg Phe Phe Asn
 85 90 95
 Arg Thr Cys His Cys Asn Gly Asn Phe Ser Gly His Asn Cys Gly Thr
 100 105 110
 Cys Arg Pro Gly Trp Arg Gly Ala Ala Cys Asp Gln Arg Val Leu Ile
 115 120 125
 Val Arg Arg Asn Leu Leu Asp Leu Ser Lys Glu Glu Lys Asn His Phe
 130 135 140
 Val Arg Ala Leu Asp Met Ala Lys Arg Thr Thr His Pro Leu Phe Val
 145 150 155 160
 Ile Ala Thr Arg Arg Ser Glu Glu Ile Leu Gly Pro Asp Gly Asn Thr
 165 170 175
 Pro Gln Phe Glu Asn Ile Ser Ile Tyr Asn Tyr Phe Val Trp Thr His
 180 185 190
 Tyr Tyr Ser Val Lys Lys Thr Phe Leu Gly Val Gly Gln Glu Ser Phe
 195 200 205
 Gly Glu Val Asp Phe Ser His Glu Gly Pro Ala Phe Leu Thr Trp His
 210 215 220
 Arg Tyr His Leu Leu Arg Leu Glu Lys Asp Met Gln Glu Met Leu Gln
 225 230 235 240
 Glu Pro Ser Phe Ser Leu Pro Tyr Trp Asn Phe Ala Thr Gly Lys Asn
 245 250 255
 Val Cys Asp Ile Cys Thr Asp Asp Leu Met Gly Ser Arg Ser Asn Phe
 260 265 270
 Asp Ser Thr Leu Ile Ser Pro Asn Ser Val Phe Ser Gln Trp Arg Val
 275 280 285
 Val Cys Asp Ser Leu Glu Asp Tyr Asp Thr Leu Gly Thr Leu Cys Asn

ITI-08-PCT_Sequence_Listing_ST25.txt

290

295

300

Ser Thr Glu Asp Gly Pro Ile Arg Arg Asn Pro Ala Gly Asn Val Ala
305 310 315 320

Arg Pro Met Val Gln Arg Leu Pro Glu Pro Gln Asp Val Ala Gln Cys
325 330 335

Leu Glu Val Gly Leu Phe Asp Thr Pro Pro Phe Tyr Ser Asn Ser Thr
340 345 350

Asn Ser Phe Arg Asn Thr Val Glu Gly Tyr Ser Asp Pro Thr Gly Lys
355 360 365

Tyr Asp Pro Ala Val Arg Ser Leu His Asn Leu Ala His Leu Phe Leu
370 375 380

Asn Gly Thr Gly Gly Gln Thr His Leu Ser Pro Asn Asp Pro Ile Phe
385 390 395 400

Val Leu Leu His Thr Phe Thr Asp Ala Val Phe Asp Glu Trp Leu Arg
405 410 415

Arg Tyr Asn Ala Asp Ile Ser Thr Phe Pro Leu Glu Asn Ala Pro Ile
420 425 430

Gly His Asn Arg Gln Tyr Asn Met Val Pro Phe Trp Pro Pro Val Thr
435 440 445

Asn Thr Glu Met Phe Val Thr Ala Pro Asp Asn Leu Gly Tyr Thr Tyr
450 455 460

Glu Ile Gln Trp Pro Ser Arg Glu Phe Ser Val Pro Glu Ile Ile Ala
465 470 475 480

Ile Ala Val Val Gly Ala Leu Leu Leu Val Ala Leu Ile Phe Gly Thr
485 490 495

Ala Ser Tyr Leu Ile Arg Ala Arg Arg Ser Met Asp Glu Ala Asn Gln
500 505 510

Pro Leu Leu Thr Asp Gln Tyr Gln Cys Tyr Ala Glu Glu Tyr Glu Lys
515 520 525

Leu Gln Asn Pro Asn Gln Ser Val Val
530 535

<210> 684

<211> 519

<212> PRT

<213> Artificial Sequence

ITI-08-PCT_Sequence_Listing_ST25.txt

<220>

<223> TYRP2__Homo_sapiens__P40126

<400> 684

Met	Ser	Pro	Leu	Trp	Trp	Gly	Phe	Leu	Leu	Ser	Cys	Leu	Gly	Cys	Lys	1	5	10	15
Ile	Leu	Pro	Gly	Ala	Gln	Gly	Gln	Phe	Pro	Arg	Val	Cys	Met	Thr	Val	20	25	30	
Asp	Ser	Leu	Val	Asn	Lys	Glu	Cys	Cys	Pro	Arg	Leu	Gly	Ala	Glu	Ser	35	40	45	
Ala	Asn	Val	Cys	Gly	Ser	Gln	Gln	Gly	Arg	Gly	Gln	Cys	Thr	Glu	Val	50	55	60	
Arg	Ala	Asp	Thr	Arg	Pro	Trp	Ser	Gly	Pro	Tyr	Ile	Leu	Arg	Asn	Gln	65	70	75	80
Asp	Asp	Arg	Glu	Leu	Trp	Pro	Arg	Lys	Phe	Phe	His	Arg	Thr	Cys	Lys	85	90	95	
Cys	Thr	Gly	Asn	Phe	Ala	Gly	Tyr	Asn	Cys	Gly	Asp	Cys	Lys	Phe	Gly	100	105	110	
Trp	Thr	Gly	Pro	Asn	Cys	Glu	Arg	Lys	Lys	Pro	Pro	Val	Ile	Arg	Gln	115	120	125	
Asn	Ile	His	Ser	Leu	Ser	Pro	Gln	Glu	Arg	Glu	Gln	Phe	Leu	Gly	Ala	130	135	140	
Leu	Asp	Leu	Ala	Lys	Lys	Arg	Val	His	Pro	Asp	Tyr	Val	Ile	Thr	Thr	145	150	155	160
Gln	His	Trp	Leu	Gly	Leu	Leu	Gly	Pro	Asn	Gly	Thr	Gln	Pro	Gln	Phe	165	170	175	
Ala	Asn	Cys	Ser	Val	Tyr	Asp	Phe	Phe	Val	Trp	Leu	His	Tyr	Tyr	Ser	180	185	190	
Val	Arg	Asp	Thr	Leu	Leu	Gly	Pro	Gly	Arg	Pro	Tyr	Arg	Ala	Ile	Asp	195	200	205	
Phe	Ser	His	Gln	Gly	Pro	Ala	Phe	Val	Thr	Trp	His	Arg	Tyr	His	Leu	210	215	220	
Leu	Cys	Leu	Glu	Arg	Asp	Leu	Gln	Arg	Leu	Ile	Gly	Asn	Glu	Ser	Phe	225	230	235	240
Ala	Leu	Pro	Tyr	Trp	Asn	Phe	Ala	Thr	Gly	Arg	Asn	Glu	Cys	Asp	Val	245	250	255	

ITI-08-PCT_Sequence_Listing_ST25.txt

Cys	Thr	Asp	Gln	Leu	Phe	Gly	Ala	Ala	Arg	Pro	Asp	Asp	Pro	Thr	Leu	260	265	270
Ile	Ser	Arg	Asn	Ser	Arg	Phe	Ser	Ser	Trp	Glu	Thr	Val	Cys	Asp	Ser	275	280	285
Leu	Asp	Asp	Tyr	Asn	His	Leu	Val	Thr	Leu	Cys	Asn	Gly	Thr	Tyr	Glu	290	295	300
Gly	Leu	Leu	Arg	Arg	Asn	Gln	Met	Gly	Arg	Asn	Ser	Met	Lys	Leu	Pro	305	310	315
Thr	Leu	Lys	Asp	Ile	Arg	Asp	Cys	Leu	Ser	Leu	Gln	Lys	Phe	Asp	Asn	325	330	335
Pro	Pro	Phe	Phe	Gln	Asn	Ser	Thr	Phe	Ser	Phe	Arg	Asn	Ala	Leu	Glu	340	345	350
Gly	Phe	Asp	Lys	Ala	Asp	Gly	Thr	Leu	Asp	Ser	Gln	Val	Met	Ser	Leu	355	360	365
His	Asn	Leu	Val	His	Ser	Phe	Leu	Asn	Gly	Thr	Asn	Ala	Leu	Pro	His	370	375	380
Ser	Ala	Ala	Asn	Asp	Pro	Ile	Phe	Val	Val	Leu	His	Ser	Phe	Thr	Asp	385	390	395
Ala	Ile	Phe	Asp	Glu	Trp	Met	Lys	Arg	Phe	Asn	Pro	Pro	Ala	Asp	Ala	405	410	415
Trp	Pro	Gln	Glu	Leu	Ala	Pro	Ile	Gly	His	Asn	Arg	Met	Tyr	Asn	Met	420	425	430
Val	Pro	Phe	Phe	Pro	Pro	Val	Thr	Asn	Glu	Glu	Leu	Phe	Leu	Thr	Ser	435	440	445
Asp	Gln	Leu	Gly	Tyr	Ser	Tyr	Ala	Ile	Asp	Leu	Pro	Val	Ser	Val	Glu	450	455	460
Glu	Thr	Pro	Gly	Trp	Pro	Thr	Thr	Leu	Leu	Val	Val	Met	Gly	Thr	Leu	465	470	475
Val	Ala	Leu	Val	Gly	Leu	Phe	Val	Leu	Leu	Ala	Phe	Leu	Gln	Tyr	Arg	485	490	495
Arg	Leu	Arg	Lys	Gly	Tyr	Thr	Pro	Leu	Met	Glu	Thr	His	Leu	Ser	Ser	500	505	510
Lys	Arg	Tyr	Thr	Glu	Glu	Ala										515		

ITI-08-PCT_Sequence_Listing_ST25.txt

<210> 685
 <211> 151
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> UPA__Homo_sapiens__Q96NZ9

<400> 685

Met Arg Arg Leu Leu Leu Val Thr Ser Leu Val Val Val Leu Leu Trp
 1 5 10 15

Glu Ala Gly Ala Val Pro Ala Pro Lys Val Pro Ile Lys Met Gln Val
 20 25 30

Lys His Trp Pro Ser Glu Gln Asp Pro Glu Lys Ala Trp Gly Ala Arg
 35 40 45

Val Val Glu Pro Pro Glu Lys Asp Asp Gln Leu Val Val Leu Phe Pro
 50 55 60

Val Gln Lys Pro Lys Leu Leu Thr Thr Glu Glu Lys Pro Arg Gly Gln
 65 70 75 80

Gly Arg Gly Pro Ile Leu Pro Gly Thr Lys Ala Trp Met Glu Thr Glu
 85 90 95

Asp Thr Leu Gly His Val Leu Ser Pro Glu Pro Asp His Asp Ser Leu
 100 105 110

Tyr His Pro Pro Pro Glu Glu Asp Gln Gly Glu Glu Arg Pro Arg Leu
 115 120 125

Trp Val Met Pro Asn His Gln Val Leu Leu Gly Pro Glu Glu Asp Gln
 130 135 140

Asp His Ile Tyr His Pro Gln
 145 150

<210> 686
 <211> 174
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> VEGFR1__Homo_sapiens__B5A924

<400> 686

Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu Leu Ser
 1 5 10 15

ITI-08-PCT_Sequence_Listing_ST25.txt

Cys Leu Leu Leu Thr Gly Ser Ser Ser Gly Ser Lys Leu Lys Asp Pro
20 25 30

Glu Leu Ser Leu Lys Gly Thr Gln His Ile Met Gln Ala Gly Gln Thr
35 40 45

Leu His Leu Gln Cys Arg Gly Glu Ala Ala His Lys Trp Ser Leu Pro
50 55 60

Glu Met Val Ser Lys Glu Ser Glu Arg Leu Ser Ile Thr Lys Ser Ala
65 70 75 80

Cys Gly Arg Asn Gly Lys Gln Phe Cys Ser Thr Leu Thr Leu Asn Thr
85 90 95

Ala Gln Ala Asn His Thr Gly Phe Tyr Ser Cys Lys Tyr Leu Ala Val
100 105 110

Pro Thr Ser Lys Lys Lys Glu Thr Glu Ser Ala Ile Tyr Ile Phe Ile
115 120 125

Ser Asp Thr Gly Arg Pro Phe Val Glu Met Tyr Ser Glu Ile Pro Glu
130 135 140

Ile Ile His Met Thr Glu Gly Arg Glu Leu Val Ile Pro Cys Arg Val
145 150 155 160

Thr Ser Pro Asn Ile Thr Val Thr Leu Lys Lys Lys Lys Ala
165 170

<210> 687

<211> 249

<212> PRT

<213> Artificial Sequence

<220>

<223> WT1__Homo_sapiens__A0A0H5AUY0

<400> 687

Met Gly Ser Asp Val Arg Asp Leu Asn Ala Leu Leu Pro Ala Val Pro
1 5 10 15

Ser Leu Gly Gly Gly Gly Gly Cys Ala Leu Pro Val Ser Gly Ala Ala
20 25 30

Gln Trp Ala Pro Val Leu Asp Phe Ala Pro Pro Gly Ala Ser Ala Tyr
35 40 45

Gly Ser Leu Gly Gly Pro Ala Pro Pro Pro Ala Pro Pro Pro Pro Pro
50 55 60

ITI-08-PCT_Sequence_Listing_ST25.txt

Pro Pro Pro Pro His Ser Phe Ile Lys Gln Glu Pro Ser Trp Gly Gly
65 70 75 80

Ala Glu Pro His Glu Glu Gln Cys Leu Ser Ala Phe Thr Val His Phe
85 90 95

Ser Gly Gln Phe Thr Gly Thr Ala Gly Ala Cys Arg Tyr Gly Pro Phe
100 105 110

Gly Pro Pro Pro Pro Ser Gln Ala Ser Ser Gly Gln Ala Arg Met Phe
115 120 125

Pro Asn Ala Pro Tyr Leu Pro Ser Cys Leu Glu Ser Gln Pro Ala Ile
130 135 140

Arg Asn Gln Gly Tyr Ser Thr Val Thr Phe Asp Gly Thr Pro Ser Tyr
145 150 155 160

Gly His Thr Pro Ser His His Ala Ala Gln Phe Pro Asn His Ser Phe
165 170 175

Lys His Glu Asp Pro Met Gly Gln Gln Gly Ser Leu Gly Glu Gln Gln
180 185 190

Tyr Ser Val Pro Pro Pro Val Tyr Gly Cys His Thr Pro Thr Asp Ser
195 200 205

Cys Thr Gly Ser Gln Ala Leu Leu Leu Arg Thr Pro Tyr Ser Ser Asp
210 215 220

Asn Leu Tyr Gln Met Thr Ser Gln Leu Glu Cys Met Thr Trp Asn Gln
225 230 235 240

Met Asn Leu Gly Ala Thr Leu Lys Gly
245

<210> 688

<211> 449

<212> PRT

<213> Artificial Sequence

<220>

<223> WT1__Homo_sapiens__P19544

<400> 688

Met Gly Ser Asp Val Arg Asp Leu Asn Ala Leu Leu Pro Ala Val Pro
1 5 10 15

Ser Leu Gly Gly Gly Gly Gly Cys Ala Leu Pro Val Ser Gly Ala Ala
20 25 30

ITI-08-PCT_Sequence_Listing_ST25.txt

Gln Trp Ala Pro Val Leu Asp Phe Ala Pro Pro Gly Ala Ser Ala Tyr
35 40 45

Gly Ser Leu Gly Gly Pro Ala Pro Pro Pro Ala Pro Pro Pro Pro
50 55 60

Pro Pro Pro Pro His Ser Phe Ile Lys Gln Glu Pro Ser Trp Gly Gly
65 70 75 80

Ala Glu Pro His Glu Glu Gln Cys Leu Ser Ala Phe Thr Val His Phe
85 90 95

Ser Gly Gln Phe Thr Gly Thr Ala Gly Ala Cys Arg Tyr Gly Pro Phe
100 105 110

Gly Pro Pro Pro Pro Ser Gln Ala Ser Ser Gly Gln Ala Arg Met Phe
115 120 125

Pro Asn Ala Pro Tyr Leu Pro Ser Cys Leu Glu Ser Gln Pro Ala Ile
130 135 140

Arg Asn Gln Gly Tyr Ser Thr Val Thr Phe Asp Gly Thr Pro Ser Tyr
145 150 155 160

Gly His Thr Pro Ser His His Ala Ala Gln Phe Pro Asn His Ser Phe
165 170 175

Lys His Glu Asp Pro Met Gly Gln Gln Gly Ser Leu Gly Glu Gln Gln
180 185 190

Tyr Ser Val Pro Pro Pro Val Tyr Gly Cys His Thr Pro Thr Asp Ser
195 200 205

Cys Thr Gly Ser Gln Ala Leu Leu Leu Arg Thr Pro Tyr Ser Ser Asp
210 215 220

Asn Leu Tyr Gln Met Thr Ser Gln Leu Glu Cys Met Thr Trp Asn Gln
225 230 235 240

Met Asn Leu Gly Ala Thr Leu Lys Gly Val Ala Ala Gly Ser Ser Ser
245 250 255

Ser Val Lys Trp Thr Glu Gly Gln Ser Asn His Ser Thr Gly Tyr Glu
260 265 270

Ser Asp Asn His Thr Thr Pro Ile Leu Cys Gly Ala Gln Tyr Arg Ile
275 280 285

His Thr His Gly Val Phe Arg Gly Ile Gln Asp Val Arg Arg Val Pro
290 295 300

ITI-08-PCT_Sequence_Listing_ST25.txt

Gly Val Ala Pro Thr Leu Val Arg Ser Ala Ser Glu Thr Ser Glu Lys
305 310 315 320

Arg Pro Phe Met Cys Ala Tyr Pro Gly Cys Asn Lys Arg Tyr Phe Lys
325 330 335

Leu Ser His Leu Gln Met His Ser Arg Lys His Thr Gly Glu Lys Pro
340 345 350

Tyr Gln Cys Asp Phe Lys Asp Cys Glu Arg Arg Phe Ser Arg Ser Asp
355 360 365

Gln Leu Lys Arg His Gln Arg Arg His Thr Gly Val Lys Pro Phe Gln
370 375 380

Cys Lys Thr Cys Gln Arg Lys Phe Ser Arg Ser Asp His Leu Lys Thr
385 390 395 400

His Thr Arg Thr His Thr Gly Lys Thr Ser Glu Lys Pro Phe Ser Cys
405 410 415

Arg Trp Pro Ser Cys Gln Lys Lys Phe Ala Arg Ser Asp Glu Leu Val
420 425 430

Arg His His Asn Met His Gln Arg Asn Met Thr Lys Leu Gln Leu Ala
435 440 445

Leu

<210> 689

<211> 92

<212> PRT

<213> Artificial Sequence

<220>

<223> WT1__Homo_sapiens__Q06250

<400> 689

Met Gln Arg Arg Gly Gln Pro Leu Glu Asn His Val Ala Leu Ile His
1 5 10 15

Trp Gln Ser Ala Gly Ile Pro Ala Ser Lys Val His Asn Tyr Cys Asn
20 25 30

Met Lys Lys Ser Arg Leu Gly Arg Ser Arg Ala Val Arg Ile Ser Gln
35 40 45

Pro Leu Leu Ser Pro Arg Arg Cys Pro Leu His Leu Thr Glu Arg Gly
50 55 60

Ala Gly Leu Leu Gln Pro Gln Pro Gln Gly Pro Val Arg Thr Pro Gly

ITI-08-PCT_Sequence_Listing_ST25.txt

65 70 75 80

Pro Pro Ser Gly Ser His Pro Ala Ala Ala Asp Asn
85 90

<210> 690
<211> 81
<212> PRT
<213> Artificial Sequence

<220>
<223> XAGE1__Homo_sapiens__Q9HD64

<400> 690

Met Glu Ser Pro Lys Lys Lys Asn Gln Gln Leu Lys Val Gly Ile Leu
1 5 10 15

His Leu Gly Ser Arg Gln Lys Lys Ile Arg Ile Gln Leu Arg Ser Gln
20 25 30

Cys Ala Thr Trp Lys Val Ile Cys Lys Ser Cys Ile Ser Gln Thr Pro
35 40 45

Gly Ile Asn Leu Asp Leu Gly Ser Gly Val Lys Val Lys Ile Ile Pro
50 55 60

Lys Glu Glu His Cys Lys Met Pro Glu Ala Gly Glu Glu Gln Pro Gln
65 70 75 80

Val

<210> 691
<211> 178
<212> PRT
<213> Artificial Sequence

<220>
<223> IL-10__Homo_sapiens__P22301

<400> 691

Met His Ser Ser Ala Leu Leu Cys Cys Leu Val Leu Leu Thr Gly Val
1 5 10 15

Arg Ala Ser Pro Gly Gln Gly Thr Gln Ser Glu Asn Ser Cys Thr His
20 25 30

Phe Pro Gly Asn Leu Pro Asn Met Leu Arg Asp Leu Arg Asp Ala Phe
35 40 45

Ser Arg Val Lys Thr Phe Phe Gln Met Lys Asp Gln Leu Asp Asn Leu

ITI-08-PCT_Sequence_Listing_ST25.txt

50

55

60

Leu Leu Lys Glu Ser Leu Leu Glu Asp Phe Lys Gly Tyr Leu Gly Cys
65 70 75 80

Gln Ala Leu Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu Val Met Pro
85 90 95

Gln Ala Glu Asn Gln Asp Pro Asp Ile Lys Ala His Val Asn Ser Leu
100 105 110

Gly Glu Asn Leu Lys Thr Leu Arg Leu Arg Leu Arg Arg Cys His Arg
115 120 125

Phe Leu Pro Cys Glu Asn Lys Ser Lys Ala Val Glu Gln Val Lys Asn
130 135 140

Ala Phe Asn Lys Leu Gln Glu Lys Gly Ile Tyr Lys Ala Met Ser Glu
145 150 155 160

Phe Asp Ile Phe Ile Asn Tyr Ile Glu Ala Tyr Met Thr Met Lys Ile
165 170 175

Arg Asn

<210> 692

<211> 134

<212> PRT

<213> Artificial Sequence

<220>

<223> IL-5__Homo_sapiens__P05113

<400> 692

Met Arg Met Leu Leu His Leu Ser Leu Leu Ala Leu Gly Ala Ala Tyr
1 5 10 15

Val Tyr Ala Ile Pro Thr Glu Ile Pro Thr Ser Ala Leu Val Lys Glu
20 25 30

Thr Leu Ala Leu Leu Ser Thr His Arg Thr Leu Leu Ile Ala Asn Glu
35 40 45

Thr Leu Arg Ile Pro Val Pro Val His Lys Asn His Gln Leu Cys Thr
50 55 60

Glu Glu Ile Phe Gln Gly Ile Gly Thr Leu Glu Ser Gln Thr Val Gln
65 70 75 80

Gly Gly Thr Val Glu Arg Leu Phe Lys Asn Leu Ser Leu Ile Lys Lys
85 90 95

ITI-08-PCT_Sequence_Listing_ST25.txt

Tyr Ile Asp Gly Gln Lys Lys Lys Cys Gly Glu Glu Arg Arg Arg Val
100 105 110

Asn Gln Phe Leu Asp Tyr Leu Gln Glu Phe Leu Gly Val Met Asn Thr
115 120 125

Glu Trp Ile Ile Glu Ser
130

<210> 693

<211> 554

<212> PRT

<213> Artificial Sequence

<220>

<223> M-CSF__Homo_sapiens__P09603

<400> 693

Met Thr Ala Pro Gly Ala Ala Gly Arg Cys Pro Pro Thr Thr Trp Leu
1 5 10 15

Gly Ser Leu Leu Leu Val Cys Leu Leu Ala Ser Arg Ser Ile Thr
20 25 30

Glu Glu Val Ser Glu Tyr Cys Ser His Met Ile Gly Ser Gly His Leu
35 40 45

Gln Ser Leu Gln Arg Leu Ile Asp Ser Gln Met Glu Thr Ser Cys Gln
50 55 60

Ile Thr Phe Glu Phe Val Asp Gln Glu Gln Leu Lys Asp Pro Val Cys
65 70 75 80

Tyr Leu Lys Lys Ala Phe Leu Leu Val Gln Asp Ile Met Glu Asp Thr
85 90 95

Met Arg Phe Arg Asp Asn Thr Pro Asn Ala Ile Ala Ile Val Gln Leu
100 105 110

Gln Glu Leu Ser Leu Arg Leu Lys Ser Cys Phe Thr Lys Asp Tyr Glu
115 120 125

Glu His Asp Lys Ala Cys Val Arg Thr Phe Tyr Glu Thr Pro Leu Gln
130 135 140

Leu Leu Glu Lys Val Lys Asn Val Phe Asn Glu Thr Lys Asn Leu Leu
145 150 155 160

Asp Lys Asp Trp Asn Ile Phe Ser Lys Asn Cys Asn Asn Ser Phe Ala
165 170 175

ITI-08-PCT_Sequence_Listing_ST25.txt

Glu	Cys	Ser	Ser	Gln	Asp	Val	Val	Thr	Lys	Pro	Asp	Cys	Asn	Cys	Leu	180	185	190
Tyr	Pro	Lys	Ala	Ile	Pro	Ser	Ser	Asp	Pro	Ala	Ser	Val	Ser	Pro	His	195	200	205
Gln	Pro	Leu	Ala	Pro	Ser	Met	Ala	Pro	Val	Ala	Gly	Leu	Thr	Trp	Glu	210	215	220
Asp	Ser	Glu	Gly	Thr	Glu	Gly	Ser	Ser	Leu	Leu	Pro	Gly	Glu	Gln	Pro	225	230	235
Leu	His	Thr	Val	Asp	Pro	Gly	Ser	Ala	Lys	Gln	Arg	Pro	Pro	Arg	Ser	245	250	255
Thr	Cys	Gln	Ser	Phe	Glu	Pro	Pro	Glu	Thr	Pro	Val	Val	Lys	Asp	Ser	260	265	270
Thr	Ile	Gly	Gly	Ser	Pro	Gln	Pro	Arg	Pro	Ser	Val	Gly	Ala	Phe	Asn	275	280	285
Pro	Gly	Met	Glu	Asp	Ile	Leu	Asp	Ser	Ala	Met	Gly	Thr	Asn	Trp	Val	290	295	300
Pro	Glu	Glu	Ala	Ser	Gly	Glu	Ala	Ser	Glu	Ile	Pro	Val	Pro	Gln	Gly	305	310	315
Thr	Glu	Leu	Ser	Pro	Ser	Arg	Pro	Gly	Gly	Gly	Ser	Met	Gln	Thr	Glu	325	330	335
Pro	Ala	Arg	Pro	Ser	Asn	Phe	Leu	Ser	Ala	Ser	Ser	Pro	Leu	Pro	Ala	340	345	350
Ser	Ala	Lys	Gly	Gln	Gln	Pro	Ala	Asp	Val	Thr	Gly	Thr	Ala	Leu	Pro	355	360	365
Arg	Val	Gly	Pro	Val	Arg	Pro	Thr	Gly	Gln	Asp	Trp	Asn	His	Thr	Pro	370	375	380
Gln	Lys	Thr	Asp	His	Pro	Ser	Ala	Leu	Leu	Arg	Asp	Pro	Pro	Glu	Pro	385	390	395
Gly	Ser	Pro	Arg	Ile	Ser	Ser	Leu	Arg	Pro	Gln	Gly	Leu	Ser	Asn	Pro	405	410	415
Ser	Thr	Leu	Ser	Ala	Gln	Pro	Gln	Leu	Ser	Arg	Ser	His	Ser	Ser	Gly	420	425	430
Ser	Val	Leu	Pro	Leu	Gly	Glu	Leu	Glu	Gly	Arg	Arg	Ser	Thr	Arg	Asp	435	440	445

ITI-08-PCT_Sequence_Listing_ST25.txt

Arg Arg Ser Pro Ala Glu Pro Glu Gly Gly Pro Ala Ser Glu Gly Ala
450 455 460

Ala Arg Pro Leu Pro Arg Phe Asn Ser Val Pro Leu Thr Asp Thr Gly
465 470 475 480

His Glu Arg Gln Ser Glu Gly Ser Phe Ser Pro Gln Leu Gln Glu Ser
485 490 495

Val Phe His Leu Leu Val Pro Ser Val Ile Leu Val Leu Leu Ala Val
500 505 510

Gly Gly Leu Leu Phe Tyr Arg Trp Arg Arg Arg Ser His Gln Glu Pro
515 520 525

Gln Arg Ala Asp Ser Pro Leu Glu Gln Pro Glu Gly Ser Pro Leu Thr
530 535 540

Gln Asp Asp Arg Gln Val Glu Leu Pro Val
545 550

<210> 694
<211> 390
<212> PRT
<213> Artificial Sequence

<220>
<223> TGFbeta1__Homo_sapiens__P01137

<400> 694

Met Pro Pro Ser Gly Leu Arg Leu Leu Leu Leu Leu Leu Pro Leu Leu
1 5 10 15

Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu Ser Thr
20 25 30

Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala
35 40 45

Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser
50 55 60

Gln Gly Glu Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu
65 70 75 80

Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Ala Glu Pro Glu
85 90 95

Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu
100 105 110

ITI-08-PCT_Sequence_Listing_ST25.txt

Met	Val	Glu	Thr	His	Asn	Glu	Ile	Tyr	Asp	Lys	Phe	Lys	Gln	Ser	Thr	115	120	125	
His	Ser	Ile	Tyr	Met	Phe	Phe	Asn	Thr	Ser	Glu	Leu	Arg	Glu	Ala	Val	130	135	140	
Pro	Glu	Pro	Val	Leu	Leu	Ser	Arg	Ala	Glu	Leu	Arg	Leu	Leu	Arg	Leu	145	150	155	160
Lys	Leu	Lys	Val	Glu	Gln	His	Val	Glu	Leu	Tyr	Gln	Lys	Tyr	Ser	Asn	165	170	175	
Asn	Ser	Trp	Arg	Tyr	Leu	Ser	Asn	Arg	Leu	Leu	Ala	Pro	Ser	Asp	Ser	180	185	190	
Pro	Glu	Trp	Leu	Ser	Phe	Asp	Val	Thr	Gly	Val	Val	Arg	Gln	Trp	Leu	195	200	205	
Ser	Arg	Gly	Gly	Glu	Ile	Glu	Gly	Phe	Arg	Leu	Ser	Ala	His	Cys	Ser	210	215	220	
Cys	Asp	Ser	Arg	Asp	Asn	Thr	Leu	Gln	Val	Asp	Ile	Asn	Gly	Phe	Thr	225	230	235	240
Thr	Gly	Arg	Arg	Gly	Asp	Leu	Ala	Thr	Ile	His	Gly	Met	Asn	Arg	Pro	245	250	255	
Phe	Leu	Leu	Leu	Met	Ala	Thr	Pro	Leu	Glu	Arg	Ala	Gln	His	Leu	Gln	260	265	270	
Ser	Ser	Arg	His	Arg	Arg	Ala	Leu	Asp	Thr	Asn	Tyr	Cys	Phe	Ser	Ser	275	280	285	
Thr	Glu	Lys	Asn	Cys	Cys	Val	Arg	Gln	Leu	Tyr	Ile	Asp	Phe	Arg	Lys	290	295	300	
Asp	Leu	Gly	Trp	Lys	Trp	Ile	His	Glu	Pro	Lys	Gly	Tyr	His	Ala	Asn	305	310	315	320
Phe	Cys	Leu	Gly	Pro	Cys	Pro	Tyr	Ile	Trp	Ser	Leu	Asp	Thr	Gln	Tyr	325	330	335	
Ser	Lys	Val	Leu	Ala	Leu	Tyr	Asn	Gln	His	Asn	Pro	Gly	Ala	Ser	Ala	340	345	350	
Ala	Pro	Cys	Cys	Val	Pro	Gln	Ala	Leu	Glu	Pro	Leu	Pro	Ile	Val	Tyr	355	360	365	
Tyr	Val	Gly	Arg	Lys	Pro	Lys	Val	Glu	Gln	Leu	Ser	Asn	Met	Ile	Val	370	375	380	
Arg	Ser	Cys	Lys	Cys	Ser														

ITI-08-PCT_Sequence_Listing_ST25.txt

385

390

<210> 695

<211> 479

<212> PRT

<213> Artificial Sequence

<220>

<223> Caspase_8__Homo_sapiens__Q14790

<400> 695

Met Asp Phe Ser Arg Asn Leu Tyr Asp Ile Gly Glu Gln Leu Asp Ser
1 5 10 15

Glu Asp Leu Ala Ser Leu Lys Phe Leu Ser Leu Asp Tyr Ile Pro Gln
20 25 30

Arg Lys Gln Glu Pro Ile Lys Asp Ala Leu Met Leu Phe Gln Arg Leu
35 40 45

Gln Glu Lys Arg Met Leu Glu Glu Ser Asn Leu Ser Phe Leu Lys Glu
50 55 60

Leu Leu Phe Arg Ile Asn Arg Leu Asp Leu Leu Ile Thr Tyr Leu Asn
65 70 75 80

Thr Arg Lys Glu Glu Met Glu Arg Glu Leu Gln Thr Pro Gly Arg Ala
85 90 95

Gln Ile Ser Ala Tyr Arg Val Met Leu Tyr Gln Ile Ser Glu Glu Val
100 105 110

Ser Arg Ser Glu Leu Arg Ser Phe Lys Phe Leu Leu Gln Glu Glu Ile
115 120 125

Ser Lys Cys Lys Leu Asp Asp Asp Met Asn Leu Leu Asp Ile Phe Ile
130 135 140

Glu Met Glu Lys Arg Val Ile Leu Gly Glu Gly Lys Leu Asp Ile Leu
145 150 155 160

Lys Arg Val Cys Ala Gln Ile Asn Lys Ser Leu Leu Lys Ile Ile Asn
165 170 175

Asp Tyr Glu Glu Phe Ser Lys Glu Arg Ser Ser Ser Leu Glu Gly Ser
180 185 190

Pro Asp Glu Phe Ser Asn Gly Glu Glu Leu Cys Gly Val Met Thr Ile
195 200 205

Ser Asp Ser Pro Arg Glu Gln Asp Ser Glu Ser Gln Thr Leu Asp Lys

ITI-08-PCT_Sequence_Listing_ST25.txt

```

210                215                220
Val Tyr Gln Met Lys Ser Lys Pro Arg Gly Tyr Cys Leu Ile Ile Asn
225                230                235                240
Asn His Asn Phe Ala Lys Ala Arg Glu Lys Val Pro Lys Leu His Ser
                245                250                255
Ile Arg Asp Arg Asn Gly Thr His Leu Asp Ala Gly Ala Leu Thr Thr
                260                265                270
Thr Phe Glu Glu Leu His Phe Glu Ile Lys Pro His Asp Asp Cys Thr
                275                280                285
Val Glu Gln Ile Tyr Glu Ile Leu Lys Ile Tyr Gln Leu Met Asp His
                290                295                300
Ser Asn Met Asp Cys Phe Ile Cys Cys Ile Leu Ser His Gly Asp Lys
305                310                315                320
Gly Ile Ile Tyr Gly Thr Asp Gly Gln Glu Ala Pro Ile Tyr Glu Leu
                325                330                335
Thr Ser Gln Phe Thr Gly Leu Lys Cys Pro Ser Leu Ala Gly Lys Pro
                340                345                350
Lys Val Phe Phe Ile Gln Ala Cys Gln Gly Asp Asn Tyr Gln Lys Gly
                355                360                365
Ile Pro Val Glu Thr Asp Ser Glu Glu Gln Pro Tyr Leu Glu Met Asp
370                375                380
Leu Ser Ser Pro Gln Thr Arg Tyr Ile Pro Asp Glu Ala Asp Phe Leu
385                390                395                400
Leu Gly Met Ala Thr Val Asn Asn Cys Val Ser Tyr Arg Asn Pro Ala
                405                410                415
Glu Gly Thr Trp Tyr Ile Gln Ser Leu Cys Gln Ser Leu Arg Glu Arg
                420                425                430
Cys Pro Arg Gly Asp Asp Ile Leu Thr Ile Leu Thr Glu Val Asn Tyr
                435                440                445
Glu Val Ser Asn Lys Asp Asp Lys Lys Asn Met Gly Lys Gln Met Pro
450                455                460
Gln Pro Thr Phe Thr Leu Arg Lys Lys Leu Val Phe Pro Ser Asp
465                470                475

```

<210> 696

<211> 375

ITI-08-PCT_Sequence_Listing_ST25.txt

<212> PRT

<213> Artificial Sequence

<220>

<223> SERPINB5__Homo_sapiens__P36952

<400> 696

Met Asp Ala Leu Gln Leu Ala Asn Ser Ala Phe Ala Val Asp Leu Phe
1 5 10 15

Lys Gln Leu Cys Glu Lys Glu Pro Leu Gly Asn Val Leu Phe Ser Pro
20 25 30

Ile Cys Leu Ser Thr Ser Leu Ser Leu Ala Gln Val Gly Ala Lys Gly
35 40 45

Asp Thr Ala Asn Glu Ile Gly Gln Val Leu His Phe Glu Asn Val Lys
50 55 60

Asp Val Pro Phe Gly Phe Gln Thr Val Thr Ser Asp Val Asn Lys Leu
65 70 75 80

Ser Ser Phe Tyr Ser Leu Lys Leu Ile Lys Arg Leu Tyr Val Asp Lys
85 90 95

Ser Leu Asn Leu Ser Thr Glu Phe Ile Ser Ser Thr Lys Arg Pro Tyr
100 105 110

Ala Lys Glu Leu Glu Thr Val Asp Phe Lys Asp Lys Leu Glu Glu Thr
115 120 125

Lys Gly Gln Ile Asn Asn Ser Ile Lys Asp Leu Thr Asp Gly His Phe
130 135 140

Glu Asn Ile Leu Ala Asp Asn Ser Val Asn Asp Gln Thr Lys Ile Leu
145 150 155 160

Val Val Asn Ala Ala Tyr Phe Val Gly Lys Trp Met Lys Lys Phe Ser
165 170 175

Glu Ser Glu Thr Lys Glu Cys Pro Phe Arg Val Asn Lys Thr Asp Thr
180 185 190

Lys Pro Val Gln Met Met Asn Met Glu Ala Thr Phe Cys Met Gly Asn
195 200 205

Ile Asp Ser Ile Asn Cys Lys Ile Ile Glu Leu Pro Phe Gln Asn Lys
210 215 220

His Leu Ser Met Phe Ile Leu Leu Pro Lys Asp Val Glu Asp Glu Ser
225 230 235 240

ITI-08-PCT_Sequence_Listing_ST25.txt

Thr Gly Leu Glu Lys Ile Glu Lys Gln Leu Asn Ser Glu Ser Leu Ser
245 250 255

Gln Trp Thr Asn Pro Ser Thr Met Ala Asn Ala Lys Val Lys Leu Ser
260 265 270

Ile Pro Lys Phe Lys Val Glu Lys Met Ile Asp Pro Lys Ala Cys Leu
275 280 285

Glu Asn Leu Gly Leu Lys His Ile Phe Ser Glu Asp Thr Ser Asp Phe
290 295 300

Ser Gly Met Ser Glu Thr Lys Gly Val Ala Leu Ser Asn Val Ile His
305 310 315 320

Lys Val Cys Leu Glu Ile Thr Glu Asp Gly Gly Asp Ser Ile Glu Val
325 330 335

Pro Gly Ala Arg Ile Leu Gln His Lys Asp Glu Leu Asn Ala Asp His
340 345 350

Pro Phe Ile Tyr Ile Ile Arg His Asn Lys Thr Arg Asn Ile Ile Phe
355 360 365

Phe Gly Lys Phe Cys Ser Pro
370 375

<210> 697
<211> 212
<212> PRT
<213> Artificial Sequence

<220>
<223> calreticulin__Homo_sapiens__B4DHR1

<400> 697

Met Leu Leu Ser Val Tyr Phe Lys Glu Gln Phe Leu Asp Gly Asp Gly
1 5 10 15

Trp Thr Ser Arg Trp Ile Glu Ser Lys His Lys Ser Asp Phe Gly Lys
20 25 30

Phe Val Leu Ser Ser Gly Lys Phe Tyr Gly Asp Glu Glu Lys Asp Lys
35 40 45

Gly Leu Gln Thr Ser Gln Asp Ala Arg Phe Tyr Ala Leu Ser Ala Ser
50 55 60

Phe Glu Pro Phe Ser Asn Lys Gly Gln Thr Leu Val Val Gln Phe Thr
65 70 75 80

ITI-08-PCT_Sequence_Listing_ST25.txt

Val Lys His Glu Gln Asn Ile Asp Cys Gly Gly Gly Tyr Val Lys Leu
85 90 95

Phe Pro Asn Ser Leu Asp Gln Thr Asp Met His Gly Asp Ser Glu Tyr
100 105 110

Asn Ile Met Phe Gly Pro Asp Ile Cys Gly Pro Gly Thr Lys Lys Val
115 120 125

His Val Ile Phe Asn Tyr Lys Gly Lys Asn Val Leu Ile Asn Lys Asp
130 135 140

Ile Arg Cys Lys Asp Asp Glu Phe Thr His Leu Tyr Thr Leu Ile Val
145 150 155 160

Arg Pro Asp Asn Thr Tyr Glu Val Lys Ile Asp Asn Ser Gln Val Glu
165 170 175

Ser Gly Ser Leu Glu Asp Asp Trp Asp Phe Leu Pro Pro Lys Lys Ile
180 185 190

Lys Asp Pro Asp Ala Ser Lys Pro Glu Asp Trp Asp Glu Arg Ala Lys
195 200 205

Ile Asp Asp Pro
210

<210> 698
<211> 296
<212> PRT
<213> Artificial Sequence

<220>
<223> calreticulin__Homo_sapiens__B4E2Y9

<400> 698

Met His Gly Asp Ser Glu Tyr Asn Ile Met Phe Gly Pro Asp Ile Cys
1 5 10 15

Gly Pro Gly Thr Lys Lys Val His Val Ile Phe Asn Tyr Lys Gly Lys
20 25 30

Asn Val Leu Ile Asn Lys Asp Ile Arg Cys Lys Asp Asp Glu Phe Thr
35 40 45

His Leu Tyr Thr Leu Ile Val Arg Pro Asp Asn Thr Tyr Glu Val Lys
50 55 60

Ile Asp Asn Ser Gln Val Glu Ser Gly Ser Leu Glu Asp Asp Trp Asp
65 70 75 80

ITI-08-PCT_Sequence_Listing_ST25.txt

```

Phe Leu Pro Pro Lys Lys Ile Lys Asp Pro Asp Ala Ser Lys Pro Glu
      85                      90                      95

Asp Trp Asp Glu Arg Ala Lys Ile Asp Asp Pro Thr Asp Ser Lys Pro
      100                      105                      110

Glu Asp Trp Asp Lys Pro Glu His Ile Pro Asp Pro Asp Ala Lys Lys
      115                      120                      125

Pro Glu Asp Trp Asp Glu Glu Met Asp Gly Glu Trp Glu Pro Pro Val
      130                      135                      140

Ile Gln Asn Pro Glu Tyr Lys Gly Glu Trp Lys Pro Arg Gln Ile Asp
145                      150                      155                      160

Asn Pro Asp Tyr Lys Gly Thr Trp Ile His Pro Glu Ile Asp Asn Pro
      165                      170                      175

Glu Tyr Ser Pro Asp Pro Ser Ile Tyr Ala Tyr Asp Asn Phe Gly Val
      180                      185                      190

Leu Gly Leu Asp Leu Trp Gln Val Lys Ser Gly Thr Ile Phe Asp Asn
      195                      200                      205

Phe Leu Ile Thr Asn Asp Glu Ala Tyr Ala Glu Glu Phe Gly Asn Glu
      210                      215                      220

Thr Trp Gly Val Thr Lys Ala Ala Glu Lys Gln Met Lys Asp Lys Gln
225                      230                      235                      240

Asp Glu Glu Gln Arg Leu Lys Glu Glu Glu Glu Asp Lys Lys Arg Lys
      245                      250                      255

Glu Glu Glu Glu Ala Glu Asp Lys Glu Asp Asp Glu Asp Lys Asp Glu
      260                      265                      270

Asp Glu Glu Asp Glu Glu Asp Lys Glu Glu Asp Glu Glu Glu Asp Val
      275                      280                      285

Pro Gly Gln Ala Lys Asp Glu Leu
      290                      295

```

```

<210> 699
<211> 417
<212> PRT
<213> Artificial Sequence

<220>
<223> calreticulin__Homo_sapiens__P27797

<400> 699

```


ITI-08-PCT_Sequence_Listing_ST25.txt

```

Met Leu Leu Ser Val Pro Leu Leu Leu Gly Leu Leu Gly Leu Ala Val
1      5      10      15

Ala Glu Pro Ala Val Tyr Phe Lys Glu Gln Phe Leu Asp Gly Asp Gly
      20      25      30

Trp Thr Ser Arg Trp Ile Glu Ser Lys His Lys Ser Asp Phe Gly Lys
      35      40      45

Phe Val Leu Ser Ser Gly Lys Phe Tyr Gly Asp Glu Glu Lys Asp Lys
      50      55      60

Gly Leu Gln Thr Ser Gln Asp Ala Arg Phe Tyr Ala Leu Ser Ala Ser
65      70      75      80

Phe Glu Pro Phe Ser Asn Lys Gly Gln Thr Leu Val Val Gln Phe Thr
      85      90      95

Val Lys His Glu Gln Asn Ile Asp Cys Gly Gly Gly Tyr Val Lys Leu
      100      105      110

Phe Pro Asn Ser Leu Asp Gln Thr Asp Met His Gly Asp Ser Glu Tyr
      115      120      125

Asn Ile Met Phe Gly Pro Asp Ile Cys Gly Pro Gly Thr Lys Lys Val
      130      135      140

His Val Ile Phe Asn Tyr Lys Gly Lys Asn Val Leu Ile Asn Lys Asp
145      150      155      160

Ile Arg Cys Lys Asp Asp Glu Phe Thr His Leu Tyr Thr Leu Ile Val
      165      170      175

Arg Pro Asp Asn Thr Tyr Glu Val Lys Ile Asp Asn Ser Gln Val Glu
      180      185      190

Ser Gly Ser Leu Glu Asp Asp Trp Asp Phe Leu Pro Pro Lys Lys Ile
      195      200      205

Lys Asp Pro Asp Ala Ser Lys Pro Glu Asp Trp Asp Glu Arg Ala Lys
      210      215      220

Ile Asp Asp Pro Thr Asp Ser Lys Pro Glu Asp Trp Asp Lys Pro Glu
225      230      235      240

His Ile Pro Asp Pro Asp Ala Lys Lys Pro Glu Asp Trp Asp Glu Glu
      245      250      255

Met Asp Gly Glu Trp Glu Pro Pro Val Ile Gln Asn Pro Glu Tyr Lys
      260      265      270

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Gly Glu Trp Lys Pro Arg Gln Ile Asp Asn Pro Asp Tyr Lys Gly Thr
275 280 285

Trp Ile His Pro Glu Ile Asp Asn Pro Glu Tyr Ser Pro Asp Pro Ser
290 295 300

Ile Tyr Ala Tyr Asp Asn Phe Gly Val Leu Gly Leu Asp Leu Trp Gln
305 310 315 320

Val Lys Ser Gly Thr Ile Phe Asp Asn Phe Leu Ile Thr Asn Asp Glu
325 330 335

Ala Tyr Ala Glu Glu Phe Gly Asn Glu Thr Trp Gly Val Thr Lys Ala
340 345 350

Ala Glu Lys Gln Met Lys Asp Lys Gln Asp Glu Glu Gln Arg Leu Lys
355 360 365

Glu Glu Glu Glu Asp Lys Lys Arg Lys Glu Glu Glu Glu Ala Glu Asp
370 375 380

Lys Glu Asp Asp Glu Asp Lys Asp Glu Asp Glu Glu Asp Glu Glu Asp
385 390 395 400

Lys Glu Glu Asp Glu Glu Glu Asp Val Pro Gly Gln Ala Lys Asp Glu
405 410 415

Leu

<210> 700

<211> 384

<212> PRT

<213> Artificial Sequence

<220>

<223> calreticulin__Homo_sapiens__Q96L12

<400> 700

Met Ala Arg Ala Leu Val Gln Leu Trp Ala Ile Cys Met Leu Arg Val
1 5 10 15

Ala Leu Ala Thr Val Tyr Phe Gln Glu Glu Phe Leu Asp Gly Glu His
20 25 30

Trp Arg Asn Arg Trp Leu Gln Ser Thr Asn Asp Ser Arg Phe Gly His
35 40 45

Phe Arg Leu Ser Ser Gly Lys Phe Tyr Gly His Lys Glu Lys Asp Lys
50 55 60

Gly Leu Gln Thr Thr Gln Asn Gly Arg Phe Tyr Ala Ile Ser Ala Arg

ITI-08-PCT_Sequence_Listing_ST25.txt

```

65          70          75          80
Phe Lys Pro Phe Ser Asn Lys Gly Lys Thr Leu Val Ile Gln Tyr Thr
      85          90          95
Val Lys His Glu Gln Lys Met Asp Cys Gly Gly Gly Tyr Ile Lys Val
      100          105          110
Phe Pro Ala Asp Ile Asp Gln Lys Asn Leu Asn Gly Lys Ser Gln Tyr
      115          120          125
Tyr Ile Met Phe Gly Pro Asp Ile Cys Gly Phe Asp Ile Lys Lys Val
      130          135          140
His Val Ile Leu His Phe Lys Asn Lys Tyr His Glu Asn Lys Lys Leu
      145          150          155          160
Ile Arg Cys Lys Val Asp Gly Phe Thr His Leu Tyr Thr Leu Ile Leu
      165          170          175
Arg Pro Asp Leu Ser Tyr Asp Val Lys Ile Asp Gly Gln Ser Ile Glu
      180          185          190
Ser Gly Ser Ile Glu Tyr Asp Trp Asn Leu Thr Ser Leu Lys Lys Glu
      195          200          205
Thr Ser Pro Ala Glu Ser Lys Asp Trp Glu Gln Thr Lys Asp Asn Lys
      210          215          220
Ala Gln Asp Trp Glu Lys His Phe Leu Asp Ala Ser Thr Ser Lys Gln
      225          230          235          240
Ser Asp Trp Asn Gly Asp Leu Asp Gly Asp Trp Pro Ala Pro Met Leu
      245          250          255
Gln Lys Pro Pro Tyr Gln Asp Gly Leu Lys Pro Glu Gly Ile His Lys
      260          265          270
Asp Val Trp Leu His Arg Lys Met Lys Asn Thr Asp Tyr Leu Thr Gln
      275          280          285
Tyr Asp Leu Ser Glu Phe Glu Asn Ile Gly Ala Ile Gly Leu Glu Leu
      290          295          300
Trp Gln Val Arg Ser Gly Thr Ile Phe Asp Asn Phe Leu Ile Thr Asp
      305          310          315          320
Asp Glu Glu Tyr Ala Asp Asn Phe Gly Lys Ala Thr Trp Gly Glu Thr
      325          330          335
Lys Gly Pro Glu Arg Glu Met Asp Ala Ile Gln Ala Lys Glu Glu Met
      340          345          350

```

ITI-08-PCT_Sequence_Listing_ST25.txt

Lys Lys Ala Arg Glu Glu Glu Glu Glu Glu Leu Leu Ser Gly Lys Ile
355 360 365

Asn Arg His Glu His Tyr Phe Asn Gln Phe His Arg Arg Asn Glu Leu
370 375 380

<210> 701

<211> 464

<212> PRT

<213> Artificial Sequence

<220>

<223> N-myc__Homo_sapiens__P04198

<400> 701

Met Pro Ser Cys Ser Thr Ser Thr Met Pro Gly Met Ile Cys Lys Asn
1 5 10 15

Pro Asp Leu Glu Phe Asp Ser Leu Gln Pro Cys Phe Tyr Pro Asp Glu
20 25 30

Asp Asp Phe Tyr Phe Gly Gly Pro Asp Ser Thr Pro Pro Gly Glu Asp
35 40 45

Ile Trp Lys Lys Phe Glu Leu Leu Pro Thr Pro Pro Leu Ser Pro Ser
50 55 60

Arg Gly Phe Ala Glu His Ser Ser Glu Pro Pro Ser Trp Val Thr Glu
65 70 75 80

Met Leu Leu Glu Asn Glu Leu Trp Gly Ser Pro Ala Glu Glu Asp Ala
85 90 95

Phe Gly Leu Gly Gly Leu Gly Gly Leu Thr Pro Asn Pro Val Ile Leu
100 105 110

Gln Asp Cys Met Trp Ser Gly Phe Ser Ala Arg Glu Lys Leu Glu Arg
115 120 125

Ala Val Ser Glu Lys Leu Gln His Gly Arg Gly Pro Pro Thr Ala Gly
130 135 140

Ser Thr Ala Gln Ser Pro Gly Ala Gly Ala Ala Ser Pro Ala Gly Arg
145 150 155 160

Gly His Gly Gly Ala Ala Gly Ala Gly Arg Ala Gly Ala Ala Leu Pro
165 170 175

Ala Glu Leu Ala His Pro Ala Ala Glu Cys Val Asp Pro Ala Val Val
180 185 190

ITI-08-PCT_Sequence_Listing_ST25.txt

Phe	Pro	Phe	Pro	Val	Asn	Lys	Arg	Glu	Pro	Ala	Pro	Val	Pro	Ala	Ala	195	200	205
Pro	Ala	Ser	Ala	Pro	Ala	Ala	Gly	Pro	Ala	Val	Ala	Ser	Gly	Ala	Gly	210	215	220
Ile	Ala	Ala	Pro	Ala	Gly	Ala	Pro	Gly	Val	Ala	Pro	Pro	Arg	Pro	Gly	225	230	235
Gly	Arg	Gln	Thr	Ser	Gly	Gly	Asp	His	Lys	Ala	Leu	Ser	Thr	Ser	Gly	245	250	255
Glu	Asp	Thr	Leu	Ser	Asp	Ser	Asp	Asp	Glu	Asp	Asp	Glu	Glu	Glu	Asp	260	265	270
Glu	Glu	Glu	Glu	Ile	Asp	Val	Val	Thr	Val	Glu	Lys	Arg	Arg	Ser	Ser	275	280	285
Ser	Asn	Thr	Lys	Ala	Val	Thr	Thr	Phe	Thr	Ile	Thr	Val	Arg	Pro	Lys	290	295	300
Asn	Ala	Ala	Leu	Gly	Pro	Gly	Arg	Ala	Gln	Ser	Ser	Glu	Leu	Ile	Leu	305	310	315
Lys	Arg	Cys	Leu	Pro	Ile	His	Gln	Gln	His	Asn	Tyr	Ala	Ala	Pro	Ser	325	330	335
Pro	Tyr	Val	Glu	Ser	Glu	Asp	Ala	Pro	Pro	Gln	Lys	Lys	Ile	Lys	Ser	340	345	350
Glu	Ala	Ser	Pro	Arg	Pro	Leu	Lys	Ser	Val	Ile	Pro	Pro	Lys	Ala	Lys	355	360	365
Ser	Leu	Ser	Pro	Arg	Asn	Ser	Asp	Ser	Glu	Asp	Ser	Glu	Arg	Arg	Arg	370	375	380
Asn	His	Asn	Ile	Leu	Glu	Arg	Gln	Arg	Arg	Asn	Asp	Leu	Arg	Ser	Ser	385	390	395
Phe	Leu	Thr	Leu	Arg	Asp	His	Val	Pro	Glu	Leu	Val	Lys	Asn	Glu	Lys	405	410	415
Ala	Ala	Lys	Val	Val	Ile	Leu	Lys	Lys	Ala	Thr	Glu	Tyr	Val	His	Ser	420	425	430
Leu	Gln	Ala	Glu	Glu	His	Gln	Leu	Leu	Leu	Glu	Lys	Glu	Lys	Leu	Gln	435	440	445
Ala	Arg	Gln	Gln	Gln	Leu	Leu	Lys	Lys	Ile	Glu	His	Ala	Arg	Thr	Cys	450	455	460