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(54) Title: SARS-COV-2 INHIBITORS

(57) Abstract: Polypeptide inhibitors of SARS-CoV-2 are disclosed comprising an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 1-17, 19-21, 23-34 and 100-101, and their use for treating and limiting development of SARS-CoV-2 infection.

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SARS-COV-2 inhibitors**Cross reference**

This application claims priority to U.S. Provisional Patent Application Serial Nos. 63/051,474 filed July 14, 2020 and 63/067,593 filed August 19, 2020, each incorporated by reference herein in its entirety.

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Background

SARS -CoV-2 infection is thought to often start in the nose, with virus replicating there for several before spreading to the broader respiratory system. Delivery of a high concentration of a viral inhibitor into the nose and into the respiratory system generally could therefore potentially provide prophylactic protection, and therapeutic efficacy early in infection, and could be particularly useful for health care workers and others coming into frequent contact with infected individuals.

Summary

In a first aspect the disclosure provides polypeptides comprising an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS:1-17, 19-21, 23-34 and 100-101, wherein the polypeptide

binds to SARS-CoV-2 Spike glycoprotein receptor binding domain (RBD). In one embodiment, amino acid substitutions relative to the reference polypeptide amino acid sequence are selected from the exemplary amino acid substitutions provided in Table 1. In another embodiment, interface residues are identical to those in the reference polypeptide or are conservatively substituted relative to interface residues in the reference polypeptide. In a further embodiment the polypeptides comprise two or more copies of the amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 1-17, 19-21, 23-34 and 100-101. In one embodiment, the polypeptide comprises the formula Z1-Z2-Z3, wherein:

Z1 comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 1-17, 19-21, 23-34 and 100-164;

Z2 comprises an optional amino acid linker; and

Z3 comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 1-17, 19-21, 23-34 and 100-164;

wherein Z1 and Z3 may be identical or different.

In another embodiment, the polypeptides comprises the formula B1-B2-Z1-Z2-Z3-B3-B4, wherein:

Z1, Z2, and Z3 are as defined;

B2 and B3 comprise optional amino acid linkers; and

one or both of B1 and B4 independently comprise an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 1-17, 19-21, 23-34 and 100-164, wherein one of B1 and B4 may be absent.

In one embodiment, the polypeptides comprise an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 47-60, 193-355 and 454-588, and a genus selected from those recited in the right hand column of Table 8 wherein genus positions X1, X2, X3, and X4 may be present or absent, and when present may be any sequence of 1 or more amino acids.

In another embodiment, the polypeptide comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 356-453 and 595-692, and a genus selected from those recited in the middle column of Table 9 wherein genus positions X1, X2, X3, and X4 may be present or absent, and when present may be any sequence of 1 or more amino acids.

In a further embodiment, the polypeptide comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 65-96, wherein in embodiments where a secretion signal is present (MARAWIFFLLCLAGRALA; SEQ ID NO:63) it can be replaced with any other secretion signal.

In other aspects, the disclosure provides nucleic acids encoding the polypeptide of the disclosure, expression vectors comprising the nucleic acids operatively linked to a promoter, host cell comprising a polypeptide, nucleic acid, and/or expression vector of the disclosure, oligomers of the polypeptides of the disclosure, compositions comprising 2, 3, 4, or more copies of the polypeptide any embodiment of the disclosure attached to a support, including but not limited to a polypeptide particle support, and pharmaceutical compositions, comprising a polypeptide, nucleic acid, expression vector, host cell, oligomer, and/or composition of the disclosure, and a pharmaceutically acceptable carrier.

In another aspect, the disclosure provides methods for treating or limiting development of a severe acute respiratory syndrome (SARS) coronavirus infection (including SARS-Co-V and SARS-CoV-2), comprising administering to a subject in need thereof an amount of the polypeptide, the nucleic acid, the expression vector, the host cell, the oligomer, the composition, and/or the pharmaceutical composition of the disclosure, effective to treat or limit development of the infection.

Description of the Figures

Figure 1. Designed Minibinder Proteins For the SARS-CoV-2 Spike Receptor Binding Domain Designs for approach 1, and approach 2, were encoded in long oligonucleotides, and screened for binding to fluorescently tagged RBD on the yeast cell surface. Deep sequencing identified 3 Ace2 helix scaffolded designs (approach 1), and 150 de novo interface designs (approach 2) that were clearly enriched following FACS sorting for RBD binding. Designs were expressed in *E. coli* and purified, and many were found to have

soluble expression, to bind RBD in biolayer interferometry experiments, and could effectively compete with ACE-2 for binding to RBD (example shown in Figure 2). Based on BLI data (e.g. See Figure 2) the RBD binding affinities of minibinders are: LCB1 <1nM, LCB3 <1nM. The affinities of LCB2, LCB4, LCB5, LCB6, LCB7, LCB8 range from 1~20nM, with relative strength of different binders being LCB4 > LCB2 > LCB9 = LCB5 > LCB6 > LCB7.

Figure 2. High Affinity Binding of De novo Designed Minibinder to SARS-CoV-2 Spike RBD. Biotinylated Spike RBD protein was loaded to a streptavidin biolayer interferometry (BLI) tip (ForteBio Octet™) and after washing, the tip was dipped into purified Combo 1 anti-RBD minibinder at different concentrations. After loading the tips were placed into buffer alone. (Left and middle) Response curves indicate ~Kd of 300 pM affinity. (Right) If ACE-2 is loaded to RBD tips and then Combo 1 is added, the minibinder rapidly displaces ACE-2 off of the BLI tip.

Figure 3. De novo Designed Minibinder to SARS-CoV-2 Spike RBD is Heat Stable. Purified Combo 1 minibinder was measured for in a circular dichroism spectrometer at 25C, 95C and at 25C after heating to 95C. The CD spectra were all very similar in shape indicating that the protein remains folded in all conditions.

Figure 4. De novo Designed Minibinder to SARS-CoV-2 Spike RBD are Potent in Virus Neutralization Assays. SARS-CoV-2 strain 2019 n-CoV/USA_WA1/2020 was obtained from the Centers for Disease Control and Prevention (gift of Natalie Thornburg). Virus stocks were produced in Vero CCL81 cells (ATCC) and titrated by focus-forming assay on Vero E6 cells. Serial dilutions of mAbs or minibinder were incubated with 102 focus-forming units (FFU) of SARS-CoV-2 for 1 h at 37C. RBD minibinder (or mAb)-virus complexes were added to Vero E6 cell monolayers in 96-well plates and incubated at 37C for 1 h. Subsequently, cells were overlaid with 1% (w/v) methylcellulose in MEM supplemented with 2% FBS. Plates were harvested 30 h later by removing overlays and fixed with 4% PFA in PBS for 20 min at room temperature. Plates were washed and sequentially incubated with 1 µg/mL of CR3022 ([1]) anti-S antibody and HRP-conjugated goat anti-human IgG in PBS supplemented with 0.1% saponin and 0.1% BSA. SARS-CoV-2-infected cell foci were visualized using TrueBlue™ peroxidase substrate (KPL) and quantitated on an ImmunoSpot™ microanalyzer (Cellular Technologies). Data were processed using Prism software (GraphPad Prism™ 8.0).

Figure 5(A-J). LCB1-Fc prophylaxis protects against SARS-CoV-2 infection. (A) Molecular surface representation of three LCB1v1.3 miniproteins bound to individual

protomers of the SARS-CoV-2 spike protein trimer (left: side view; right: top view). (B) Binding curves of purified LCB1v1.3 and LCB1-Fc to SARS-CoV-2 RBD as monitored by biolayer interferometry (one experiment performed in technical duplicate). (C) Neutralization curves of LCB1v1.3, LCB1-Fc, or control binder against a SARS-CoV-2 WA1/2020 isolate (EC₅₀ values: 14.4 pM, 71.8 pM, and >10,000 nM respectively; average of two experiments, each performed in duplicate). (D-J) 7 to 8-week-old female and male K18-hACE2 transgenic mice received 250 µg of LCB1-Fc or control binder by i.p. injection one day prior to i.n. inoculation with 10³ PFU of SARS-CoV-2. Tissues were collected at 4 and 7 dpi. (D) Weight change following LCB1-Fc administration (mean ± SEM; n = 8, two experiments: two-way ANOVA with Sidak's post-test: *** $P < 0.001$, **** $P < 0.0001$). (E) Infectious virus measured by plaque assay at 4 or 7 dpi in the lung (n = 8, two experiments: Mann-Whitney test; *** $P < 0.001$). (F-J) Viral RNA levels at 4 or 7 dpi in the lung, heart, spleen, brain, or nasal wash (n = 8, two experiments: Mann-Whitney test: ns, not significant, * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$, **** $P < 0.0001$).

Figure 6(A-C). LCB1-Fc prophylaxis prevents SARS-CoV-2-mediated lung disease. (A) Respiratory mechanics parameters: inspiratory capacity, resistance, elastance tissue damping, quasi-static compliance, and pressure-volume loops measured at 7 dpi (n = 3-6, two experiments: two-way ANOVA with Tukey's post-test: ns, not significant, * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$ between indicated groups). (B) Hematoxylin and eosin staining of lung sections from mice treated at D-1 and collected at 7 dpi with SARS-CoV-2. Images show low (left) and high (right; boxed region from left) magnification. Scale bars for all images, 100 µm. Representative images from n = 3 mice per group. (C) Heat-map of cytokine mRNA levels from lung tissues of SARS-CoV-2 infected mice at 4 dpi. For each cytokine, the fold-change was calculated relative to age-matched naïve control animals after normalization to *Gapdh* and the Log₂(fold change) was plotted (n = 8 mice/group relative to n = 3 naïve controls).

Figure 7(A-J). Post-exposure delivery of anti-RBD binders reduces SARS-CoV-2 burden. (A-G) 7 to 8-week-old female and male K18-hACE2 transgenic mice received 250 µg of LCB1-Fc or control binder by i.p. injection one day after i.n. inoculation with 10³ PFU of SARS-CoV-2. Tissues were collected at 4 or 7 dpi. (A) Weight change following LCB1-Fc administration (mean ± SEM; n = 6, two experiments: two-way ANOVA with Sidak's post-test: ** $P < 0.01$, **** $P < 0.0001$). (B) Infectious virus in the lung measured by plaque assay at 4 or 7 dpi in the lung (n = 6, two experiments: ** $P < 0.01$). (C-G) Viral RNA levels

at 4 or 7 dpi in the lung, heart, spleen, brain, or nasal wash ($n = 6$, two experiments: Mann-Whitney test: ns, not significant, * $P < 0.05$, ** $P < 0.01$). (H) Hematoxylin and eosin staining of lung sections from mice treated at D+1 and collected at 7 dpi with SARS-CoV-2. Images show low (left) and high (right; boxed region from left) magnification. Scale bars for all images, 100 μm . Representative images from $n = 3$ mice per group. (I-J) 7 to 8-week-old male K18-hACE2 transgenic mice received a single 50 μg i.n. dose of LCB1v1.3 or control binder at one- or two-days post-inoculation with 10^3 PFU of SARS-CoV-2. Viral RNA levels at 7 dpi in the lung (I) or nasal wash (J) ($n = 6$, two experiments: one-way ANOVA: ns, not significant, * $P < 0.05$, **** $P < 0.0001$).

Figure 8(A-K). Intranasal administration of LCB1v1.3 reduces viral infection even when given 5 days prior to SARS-CoV-2 exposure. (A-D) 7 to 8-week-old female K18-hACE2 transgenic mice received a single i.n. 50 μg dose of LCB1v1.3 or control binder at the indicated time prior to i.n. inoculation with 10^3 PFU of SARS-CoV-2. Tissues were collected at 4 or 7 dpi and viral RNA levels were determined ($n = 5-6$ animals per group, two-experiments: two-way ANOVA with Sidak's post-test: ns, not significant, * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$, **** $P < 0.0001$). (E-J) 7 to 8-week-old female K18-hACE2 transgenic mice received the indicated i.n. dose of LCB1v1.3 or control binder at one day prior to i.n. inoculation with 10^3 PFU of SARS-CoV-2. (E) Weight change following LCB1v1.3 or control binder administration (mean $\pm$ SEM; $n = 6$, two experiments: two-way ANOVA with Sidak's post-test compared to the control binder treated group: ** $P < 0.01$, **** $P < 0.0001$). (F-J) Viral RNA levels at 7 dpi in the lung, heart, spleen, brain, or nasal wash ($n = 6$, two experiments: Kruskal-Wallis ANOVA with Dunn's post-test: * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$). (K) Hematoxylin and eosin staining of lung sections from mice treated with a single i.n. 50 μg dose of LCB1v1.3 or control binder at D-1 and collected at 7 dpi with SARS-CoV-2. Images show low (left) and high (right; boxed region from left) magnification. Scale bars for all images, 100 μm . Representative images from $n = 3$ mice per group.

Figure 9(A-H). Immunogenicity of LCB1v1.3 and protection from challenge. (A) Scheme of experimental details. K18-hACE2 transgenic mice ($n = 10$ to 12 per group) were treated every 3 days with 50 μg of LCB1v1.3 or control binder by i.n. administration. On day 18 post-treatment, animals were bled and anti-LCB1v1.3 antibodies were measured. The following day, animals were challenged with 10^3 PFU of SARS-CoV-2, and tissues were collected at 7 dpi. (B) Binding of serum antibodies to LCB1v1.3 as measured by ELISA

(three experiments). Dashed line indicated limit of detection of the assay. (C) Weight change following LCB1v1.3 or control binder administration (mean $\pm$ SEM; two experiments: two-way ANOVA with Sidak's post-test: **** $P < 0.0001$). (D-H) Viral RNA levels at 7 dpi in the lung, heart, spleen, brain, or nasal wash (two experiments: Mann-Whitney test: * $P < 0.05$, ** $P < 0.01$, **** $P < 0.0001$).

Figure 10(A-M). LCB1v1.3 protects mice against B.1.1.7 variant and WA1/2020 E484K/N501Y/D614G strains. (A) Neutralization of LCB1v1.3 against B.1.1.7 or WA1/2020 E484K/N501Y/D614G SARS-CoV-2 (EC_{50} values: 802 pM and 667 pM, respectively; mean of two experiments, each performed in duplicate). (B-G) 7 to 8-week-old female K18-hACE2 transgenic mice were treated with a single 50 μ g i.n. dose of LCB1v1.3 or control binder at 1 day prior to i.n. inoculation with 10^3 PFU of B.1.1.7. (B) Weight change following LCB1v1.3 or control binder administration (mean $\pm$ SEM; $n = 6$, two experiments: two-way ANOVA with Sidak's post-test: *** $P < 0.001$, **** $P < 0.0001$). (C-G) Viral RNA levels at 6 dpi in the lung, heart, spleen, nasal wash, or brain ($n = 6$, two experiments: Mann-Whitney test: * $P < 0.05$, ** $P < 0.01$). (H-M) 8-week-old male K18-hACE2 transgenic mice were treated with a single 50 μ g i.n. dose of LCB1v1.3 or control binder at 1 day prior to i.n. inoculation with 10^3 PFU of WA1/2020 E484K/N501Y/D614G. (H) Weight change following LCB1v1.3 or control binder administration (mean $\pm$ SEM; $n = 6$, two experiments: two-way ANOVA with Sidak's post-test: * $P < 0.05$, **** $P < 0.0001$). (I-M) Viral RNA levels at 6 dpi in the lung, heart, spleen, nasal wash, or brain ($n = 6$, two experiments: Mann-Whitney test: * $P < 0.05$, ** $P < 0.01$).

Figure 11. Cytokine and chemokine induction following SARS-CoV-2 infection. Individual plots for cytokine and chemokine RNA levels in the lungs of SARS-CoV-2 infected mice at 4 dpi following treatment with control or LCB1-Fc binders ($n = 8$ per group, two experiments: Mann-Whitney test: ns, not significant, * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$). Data were used to generate the heat-map in Figure 6C.

Figure 12(A-C). Intranasal delivery of LCB1v1.3 at 1 or 2 days post-SARS-CoV-2 infection reduces viral burden, Related to Fig 7. (A-C) 7 to 8-week-old male K18-hACE2 transgenic mice received a single 50 μ g i.n. dose of LCB1v1.3 or control binder at one- or two-days post-inoculation with 10^3 PFU of SARS-CoV-2. Viral RNA levels at 7 dpi in the heart (A), spleen (B), or brain (C) ($n = 6$, two experiments: one-way ANOVA: * $P < 0.05$, ** $P < 0.01$).

Figure 13. Intranasal prophylaxis of LCB1v1.3 reduces weight loss, Related to

Fig 8. 7 to 8-week-old female K18-hACE2 transgenic mice received a single 50 µg i.n. dose of LCB1v1.3 or control binder at the indicated time prior to i.n. inoculation with 10^3 PFU of SARS-CoV-2. Weight change was recorded daily (mean $\pm$ SEM; n = 6, two experiments:

two-way ANOVA with Sidak's post-test: * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$, **** $P < 0.0001$).

Figure 14(A-B). Multivalent minibinders simultaneously engage multiple epitopes on the pre-fusion SARS-CoV-2 spike protein resulting in extremely slow dissociation rates.

(A,B) Dissociation of the minibinder construct and the receptor binding domain (RBD) **(A)** or the hexapropyl spike protein (S6P) **(B)** complex was monitored via competition with 100-fold molar excess of untagged M1 using AlphaLISA™ (Mean $\pm$ SEM, n=3).

Figure 15(A-F). Cryo-EM structures of multivalent minibinders in complex with the SARS-CoV-2 S glycoprotein. **(A)** Ribbon diagram representations of all three minibinders bound to the RBD. **(B)** Cryo-EM map of F31-G10 in complex with two RBDs. **(C)** Cryo-EM map of F231-P24 in complex with three RBDs. **(D)** Design model of H2-1 bound to the S glycoprotein. **(E)** Cryo-EM map of H2-1 in complex with the S glycoprotein in two orthogonal orientations. **(F)** Cryo-EM map showing the interacting residues of the H2-1 and S glycoprotein interface.

Figure 16(A-F). Multivalency enhances both the breadth and potency of neutralization against SARS-CoV-2 variants by minibinders. **(A)** Dissociation of minibinder constructs from S6P variants after 24 hours was measured via competition with untagged H2-0 using AlphaLISA (mean, n=3). Cells containing an X indicate insufficient signal in the no competitor condition to quantify the fraction of protein bound. **(B)** Competition of minibinder constructs with ACE2 for S6P was measured via ELISA (mean, n=2). **(C)** Neutralization curves of minibinder constructs against SARS-CoV-2 pseudovirus variants (mean, n=2) **(D)** Table summarizing neutralization potencies of multivalent minibinder constructs against SARS-CoV-2 pseudovirus variants. N/A indicates an IC_{50} value above the tested concentration range and an IC_{50} greater than 50,000 pM. **(E)** Neutralization curves of minibinder constructs against authentic SARS-CoV-2 isolates (mean, n=2). **(F)** Table summarizing neutralization potencies of multivalent minibinder constructs against authentic SARS-CoV-2 isolates.

Figure 17(A-C). Top multivalent minibinder candidates are escape resistant and protect mice from SARS-CoV-2 infection via pre-exposure intranasal administration. **(A)**

Plaque assays were performed to isolate VSV-SARS-CoV-2 chimera virus escape mutants against a control neutralizing antibody (2B04) and the F231-P12 and H2-1 multivalent minibinders. Images are representative of 35 replicate wells per multivalent minibinder.

Large plaques, highlighted by black arrows, are indicative of escape. **(B, C)** K18-hACE2-

transgenic mice (n=6/timepoint) were dosed with 50ug H2-0 by intranasal administration (i.n., 2 x 25 µl doses per nostril, 100 µl total) 24h prior (T-24h) to infection with 10³ plaque forming units of SARS-CoV-2 Variants B.1.1.7, B.1.351, B.1.1.24 intranasally at Day 0. **(B)**

Daily weight change following infection (mean ± SEM; n = 6, two-way ANOVA with Sidak's post-test: * P < 0.05, *** P < 0.001, **** P < 0.0001). **(C)** After days post infection (6dpi) animals (n=6/timepoint) were sacrificed and analyzed for the presence of SARS-CoV-2 viral RNA by quantitative real time RT-PCR in the lung, heart, spleen, brain, or nasal wash (n = 6: Mann-Whitney test: ns, not significant, * P < 0.05, ** P < 0.01).

Detailed Description

All references cited are herein incorporated by reference in their entirety. Within this application, unless otherwise stated, the techniques utilized may be found in any of several well-known references such as: Molecular Cloning: A Laboratory Manual (Sambrook, et al., 1989, Cold Spring Harbor Laboratory Press), Gene Expression Technology (Methods in Enzymology, Vol. 185, edited by D. Goeddel, 1991. Academic Press, San Diego, CA), "Guide to Protein Purification" in Methods in Enzymology (M.P. Deutscher, ed., (1990) Academic Press, Inc.); PCR Protocols: A Guide to Methods and Applications (Innis, et al. 1990. Academic Press, San Diego, CA), Culture of Animal Cells: A Manual of Basic Technique, 2nd Ed. (R.I. Freshney. 1987. Liss, Inc. New York, NY), Gene Transfer and Expression Protocols, pp. 109-128, ed. E.J. Murray, The Humana Press Inc., Clifton, N.J.), and the Ambion 1998 Catalog (Ambion, Austin, TX).

As used herein, the singular forms "a", "an" and "the" include plural referents unless the context clearly dictates otherwise.

As used herein, the amino acid residues are abbreviated as follows: alanine (Ala; A), asparagine (Asn; N), aspartic acid (Asp; D), arginine (Arg; R), cysteine (Cys; C), glutamic acid (Glu; E), glutamine (Gln; Q), glycine (Gly; G), histidine (His; H), isoleucine (Ile; I), leucine (Leu; L), lysine (Lys; K), methionine (Met; M), phenylalanine (Phe; F), proline (Pro; P), serine (Ser; S), threonine (Thr; T), tryptophan (Trp; W), tyrosine (Tyr; Y), and valine (Val; V).

In all embodiments of polypeptides disclosed herein, an N-terminal methionine residue is optional (i.e.: may be present or absent).

All embodiments of any aspect of the disclosure can be used in combination, unless the context clearly dictates otherwise.

5 Unless the context clearly requires otherwise, throughout the description and the claims, the words ‘comprise’, ‘comprising’, and the like are to be construed in an inclusive sense as opposed to an exclusive or exhaustive sense; that is to say, in the sense of “including, but not limited to”. Words using the singular or plural number also include the plural and singular number, respectively. Additionally, the words “herein,” “above,” and
10 “below” and words of similar import, when used in this application, shall refer to this application as a whole and not to any particular portions of the application.

In a first aspect, the disclosure provides polypeptides comprising an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the
15 group consisting of SEQ ID NOS: 1-17, 19-21, 23-34 and 100-101, wherein the polypeptide binds to SARS-CoV-2 Spike glycoprotein receptor binding domain (RBD).

>LCB1-1

DKEWILQKIYEIMRLLDDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVE (SEQ ID NO:1)

20 >LCB1-2

DKEEILNKIYEIMRLLDDELGNAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVE (SEQ ID NO:2)

>LCB1-3

DKEWILQKIYEIMRLLDDELGHAEASMRVSDLIYEFMKQGDERLLEEAERLLEEVE (SEQ ID NO:3)

>LCB1-4

25 DKENILQKIYEIMKTLDQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVE (SEQ ID NO:4)

>LCB1-5

DKENILQKIYEIMKTLDQLGHAEASMNVSVDLIYEFMKQGDERLLEEAERLLEEVE (SEQ ID NO:5)

LCB1_v1.1_Cys

DKENILQKIYEIMKTLDQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVE (SEQ ID NO:6)

30 >LCB1_v1.2

DKENILQKIYEIMKTLDQLGHAEASMYVSDLIYEFMKQGDERLLEEAERLLEEVE (SEQ ID NO:7)

>LCB1_v1.3

DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVE (SEQ ID NO:8)

>LCB1_v1.4

DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDNLLLEEAEQLLQEVER (SEQ ID NO:9)

>LCB1_v1.5 (LCB1_v1.3 with N-link Glycosylation)

DKENILQKIYEIMKTLEQLGHAEASMNVSVDLIYEFMKQGDRLLEEAEERLLEEVEER (SEQ ID NO:10)

5 >LCB2-1

SDDSDSVRYLLYMAELRYEQGNPEKAKKILEMAEFTAKRNNNEELERLVREVKKRL (SEQ ID NO:11)

>LCB2-2

SDDSDAVRYLLYMAELLYKQGNPEEAKKLELAEFTAKRNNNEELERLVREVKKRL (SEQ ID NO:12)

>LCB3-1

10 NDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLERLLS (SEQ ID NO:13)

>LCB3-2

NDDELLMLVTDLVAEALLFAKDEEIKKRVFTLFELADKAYKNNDRTLSKVSELKELLERLQ (SEQ ID NO:14)

15 > LCB3_v1.2

NDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO:15)

>LCB3-4

20 NDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFENATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO:16)

>LCB3_v1.1

NDDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNNDRQKLEKVVEELKELLERLLS (SEQ ID NO:17)

>LCB3_v1.3

25 NDDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO:19)

>LCB3_v1.4

NDDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKARKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO:20)

30 >LCB3_v1.5

NDDELHMQMTDLVYEALHFAKDEEMQKRVFQLFEQADKAYKTKDRQKLEKVVEELKELLERLLS (SEQ ID NO:21)

- >LCB4-1
QREKRLKQLEMLLEYAIERNDPYLMFDVAVEMLRRLAEENNDERIIERAKRILEEYE (SEQ ID NO:23)
- >LCB4-2
DREERLKYLEMLLELAVERNDPYLIFDVAIELRLRLAEENNDERIYERAKRILEEVE (SEQ ID NO:24)
- 5 >LCB5-1
SLEELKEQVKELKKELSPEMRRLIEEALRFLEEGNPAMAMVLSDLVYQLGDPRVIDLYMLVTKT (SEQ ID NO:25)
- >LCB5-2
SLEEVKEILKELKKELSPEDRRLIEEALRLLEEGNPAMASVLSDLVFLLGDPRIELMLVTKT (SEQ ID NO:26)
- 10 >LCB6-1
DREQRLVRFLVRLASKFNLSPEQILQLFEVLEELLERGVSEEEIRKQLEEVAKELG (SEQ ID NO:27)
- >LCB6-2
DREQRLVRFLVRLASKFNLSMEQILILFDVLEELLERGVSEEEIRKILEEVAKEL (SEQ ID NO:28)
- 15 >LCB7-1
DDDIRYLIYMAKLRLEQGNPEEAKEKVLEMARFLAERLGMEELLKEVRELLRKIEELR (SEQ ID NO:29)
- >LCB7-2
DDDVRYLIYMAKLLLEQGNPEEAKEKVLESARFAAELLGNEELLKEVRELLRKIEELR (SEQ ID NO:30)
- >LCB8-1
20 PIIELLREAKEKNDEFASDALYLVNELLQRTGDPRLEEVLVLIWRALKEKDPRLLDRAIELFER (SEQ ID NO:31)
- >LCB8-2
PVTELLREAKEKNDPMAISDALFLVFELAQRTGDPRLEEVLFLIWRALKEKDPRLLDRAIELFER (SEQ ID NO:32)
- 25 >AHB1-1
DEDLEELERLYRKAAEEVAKEAKDASRRGDDERAKEQMERAMRLFDQVFELAQELQEKQTDGNRQKATHLDKAVKE
AADELYQVRV (SEQ ID NO:33)
- >AHB1-2
DEDLEELERLYRKAAEEVAKEAEEASRRGDKERAKELLERLALHLFDQVFELAQELQEKLTDEKRQKATHLDKAVHE
30 AADELYQVRV (SEQ ID NO:34)
- >AHB2-1
ELEERVMHLLDQVSELAHELLHKLGTGEELQRATHFDKWANEAILIKSDDEREIREIEEEARRILEHLEELARK
(SEQ ID NO:100)
- >AHB2-2_

ELEEQVMHVLDDQVSELAHELLHKLITGEELERAAYFNWWATEMMLLELIKSDDEREIREIEEEEARRILEHLEELARK
(SEQ ID NO:101)

As detailed in the examples that follows, the polypeptides bind with high affinity to the SARS-CoV-2 Spike glycoprotein receptor binding domain (RBD).

In all of embodiments herein, the percent identity requirement does not include any additional functional domain that may be incorporated in the polypeptide. In one embodiment, 1, 2, or 3 amino acids may be deleted from the N and/or C terminus.

The polypeptides have been subjected to extensive mutational analysis as described in the examples that follow, permitting determination of allowable substitutions at each residue within the polypeptide. Exemplary substitutions are as shown in **Table 1** (The number denotes the residue number, and the letters denote the single letter amino acids that can be present at that residue). Thus, in one embodiment, amino acid substitutions relative to the reference polypeptide amino acid sequence (i.e.: one of SEQ ID NOS: 1-17, 19-21, 23-34 and 100-101) are selected from the exemplary amino acid substitutions provided in Table 1.

Table 1: Exemplary substitutions:

LCB1 (SEQ ID NOS:1-10 and 102-136)

1	--	A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y	
20	2	--	A, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
	3	--	A, D, E, F, G, H, K, L, M, N, P, Q, R, S, T, V, W, Y
	4	--	A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
	5	--	A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
	6	--	A, C, I, L, M, Q, T, V
25	7	--	A, C, D, E, F, G, H, M, N, P, Q, R, S, V, W, Y
	8	--	A, C, D, E, F, G, H, I, K, L, M, N, Q, R, S, T, V, W, Y
	9	--	C, I, L, M, N, Q, T, V
	10	--	C, F, V, W, Y
	11	--	A, C, D, E, F, G, H, I, K, L, M, N, Q, R, S, T, V, W, Y
30	12	--	A, C, D, H, I, L, M, N, S, T, V, Y
	13	--	C, I, M, Q
	14	--	A, C, D, E, F, G, H, I, K, L, M, N, Q, R, S, T, V, W, Y
	15	--	A, C, D, E, F, G, H, I, K, L, M, N, Q, R, S, T, V, W, Y
	16	--	C, F, I, L, M, T, V
35	17	--	A, C, D, E, F, G, H, I, K, L, M, N, Q, R, S, T, V, W, Y
	18	--	A, C, D, E, F, G, H, I, K, L, M, N, Q, R, S, T, V, W, Y
	19	--	A, C, D, E, F, G, H, I, K, L, M, N, Q, R, S, T, V, W, Y
	20	--	A, C, D, E, F, G, H, K, L, M, N, Q, R, S, T, W

- 21 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y
 22 -- A,C,D,F,G,H,I,L,M,N,P,Q,S,T,V,W,Y
 23 -- C,E,M,N,P,Q,S,T,V
 24 -- A,C,D,E,F,G,H,K,L,M,N,P,Q,R,S,T,V,W,Y
 5 25 -- A,C,G,M,N,Q,S,T,V
 26 -- M,N,V
 27 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y
 28 -- A,C,G,I,L,S,T,V
 29 -- A,C,S,V,W
 10 30 -- D
 31 -- A,C,D,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y
 32 -- C,F,H,I,L,M,N,P,T,V
 33 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
 34 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
 15 35 -- A,C,D,F,H,M,Q,V,W,Y
 36 -- A,C,D,E,G,H,I,L,M,N,Q,R,S,T,V,W,Y
 37 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
 38 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y
 39 -- A,C,D,E,F,G,H,K,L,M,N,P,Q,R,S,T,V,W,Y
 20 40 -- D,E,G,H,N,P,Q
 41 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
 42 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
 43 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
 44 -- A,C,D,E,F,G,H,I,K,L,M,Q,R,S,V,W,Y
 25 45 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
 46 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
 47 -- A,C,G,P,S,T,V
 48 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y
 49 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y
 30 50 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y
 51 -- A,C,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y
 52 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
 53 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
 54 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
 35 55 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
 56 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

 LCB2 (SEQ ID NOS:11-12)
 1 -- A,C,D,E,G,N,P,S,T
 40 2 -- D,M,P,Q,Y
 3 -- A,D,E,N,Q

- 4 -- C,D,E,V
 5 -- D
 6 -- A,C,D,E,G,N,Q,S,T,V
 7 -- A,C,G,I,L,M,P,S,T,V
 5 8 -- A,C,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y
 9 -- D,N,Y
 10 -- I,L,T
 11 -- C,E,G,I,L,M,W
 12 -- F,H,Y
 10 13 -- E,M,Q,R,V
 14 -- A,C,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y
 15 -- A,C,D,E,G,H,I,K,L,M,N,Q,R,S,T,V
 16 -- C,H,L,T
 17 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
 15 18 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y
 19 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
 20 -- A,C,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,Y
 21 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
 22 -- A,C,D,E,G,I,K,L,N,P,Q,R,S,T,V
 20 23 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
 24 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
 25 -- A,C,E,G,H,I,K,N,P,Q,R,S,T,Y
 26 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
 27 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
 25 28 -- H,K,R,T,Y
 29 -- C,D,E,H,I,K,L,M,N,P,Q,R,S,T,V,Y
 30 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,S,T,V,W,Y
 31 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,Y
 32 -- F,H,I,K,L,M,P,Q,R,Y
 30 33 -- A,C,G,P,S,T
 34 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y
 35 -- F,H,Y
 36 -- A,C,E,H,I,L,M,S,V
 37 -- A,C,E,G,H,L,M,Q,R,S,T,V,W
 35 38 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
 39 -- A,C,D,E,G,H,I,K,L,M,N,P,Q,R,S,T,V
 40 -- A,C,D,E,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
 41 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
 42 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
 40 43 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
 44 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

45 -- A,C,E,F,I,L,M,P,S,T,V,W,Y
 46 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
 47 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
 48 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
 5 49 -- A,C,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
 50 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
 51 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
 52 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
 53 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
 10 54 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
 55 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
 56 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

 LCB3 (SEQ ID NOS:13-17, 19-21 and 137-163)
 15 1 -- C,E,F,I,M,N,T,W
 2 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
 3 -- D,G,L,M,N,S,Y
 4 -- A,C,E,F,H,K,Q,T
 5 -- A,C,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y
 20 6 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
 7 -- A,C,D,F,I,L,M,P,R,S,V,W
 8 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y
 9 -- A,C,E,F,G,H,I,L,M,N,Q,R,S,T,V,Y
 10 -- A,C,F,G,H,K,M,N,Q,R,S,T,Y
 25 11 -- D,F,H,L,M,N,Q
 12 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
 13 -- A,F,I,L,M,N,Q,S,T,V
 14 -- A,C,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
 15 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
 30 16 -- A,C,D,E,F,G,H,I,L,M,N,P,Q,R,S,T,V,W,Y
 17 -- A,C,D,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W
 18 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
 19 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
 20 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
 35 21 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
 22 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
 23 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
 24 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
 25 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
 40 26 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
 27 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

- 28 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
29 -- A, C, D, E, F, G, I, L, M, N, P, S, T, V, W, Y
30 -- C, E, F, H, L, N, S, W, Y
31 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
5 32 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
33 -- A, C, E, F, I, K, P, Q, S, V, W, Y
34 -- A, D, E, F, G, H, M, N, P, Q, R, S, V, W, Y
35 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
36 -- A, C, E, G, H, I, M, N, Q, S, T, V
10 37 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
38 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
39 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
40 -- A, C, D, E, F, G, H, K, L, M, N, P, Q, R, S, T, V, W, Y
41 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
15 42 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
43 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
44 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
45 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
46 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
20 47 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
48 -- A, C, E, F, G, I, K, L, M, N, P, Q, S, T, V, W
49 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
50 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
51 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
25 52 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
53 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
54 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
55 -- A, C, E, F, G, H, I, K, L, M, N, Q, S, T, V, W, Y
56 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
30 57 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
58 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
59 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
60 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
61 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
35 62 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
63 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
64 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y

LCB4 (SEQ ID NO:23-24)

- 40 1 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
2 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y

- 3 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
- 4 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
- 5 -- C, D, H, K, N, Q, R, Y
- 6 -- A, C, F, G, I, K, L, M, P, Q, R, S, T, V, Y
- 5 7 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
- 8 -- A, C, H, I, M, N, Q, R, S, T, V, Y
- 9 -- A, C, D, G, H, I, K, L, M, N, Q, R, S, T, V, Y
- 10 -- A, C, D, E, M, N, P, Q, S, T, V
- 11 -- C, D, G, H, I, K, L, M, N, P, R, S, T, V
- 10 12 -- F, G, I, L
- 13 -- F, I, L, M, S, V, Y
- 14 -- A, C, D, E, G, L, M, N, Q, R, S, T, V
- 15 -- C, E, F, G, H, I, L, M, S, V, W, Y
- 16 -- A, G, T, Y
- 15 17 -- A, C, D, E, F, G, H, I, K, L, M, N, Q, R, S, T, V, W, Y
- 18 -- A, C, D, E, F, G, H, I, K, L, M, N, Q, R, S, T, V, W, Y
- 19 -- A, C, D, E, F, G, H, I, K, L, M, N, Q, R, S, T, V, W, Y
- 20 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
- 21 -- C, D, Q, Y
- 20 22 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
- 23 -- E, F, H, Y
- 24 -- A, F, G, I, L, M, W
- 25 -- A, C, E, G, H, I, K, L, M, N, Q, R, S, T, V, Y
- 26 -- C, F, H, I, L, N, S, T, V, W
- 25 27 -- D, Q, W, Y
- 28 -- A, C, D, I, L, V, Y
- 29 -- A, C, E, G, K, L, N, Q, R, S, T
- 30 -- C, I, L, M, P, T, V
- 31 -- C, D, E
- 30 32 -- A, C, E, I, L, M, Q, S, T, V, Y
- 33 -- A, C, E, F, G, H, I, K, L, M, Q, R, S, T, V, Y
- 34 -- C, D, F, G, H, L, M, N, P, R, S, T, W, Y
- 35 -- A, C, E, F, G, H, I, K, L, N, P, R, T, V, W
- 36 -- A, C, G, S, T, V
- 35 37 -- A, C, D, E, G, H, I, K, L, M, N, P, Q, R, S, T, V, Y
- 38 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
- 39 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
- 40 -- A, C, D, E, F, G, H, I, K, L, M, N, Q, R, S, T, V, Y
- 41 -- A, C, D, E, G, H, K, N, Q, S, W
- 40 42 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
- 43 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, Y

- 44 -- A, E, F, G, H, I, K, L, M, N, Q, R, S, T, V
- 45 -- A, C, E, F, G, H, I, K, L, M, N, Q, R, S, T, V, W, Y
- 46 -- A, C, D, E, F, G, H, I, K, L, M, N, Q, R, S, T, V, W, Y
- 47 -- A, C, D, E, F, G, H, I, K, L, M, N, Q, R, S, T, V, W, Y
- 5 48 -- A, C, M, S, T, V
- 49 -- A, H, I, K, L, M, N, Q, R, S, T, V, W, Y
- 50 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
- 51 -- A, F, I, K, L, M, R, T, V, W, Y
- 52 -- F, I, K, L, M, V
- 10 53 -- A, C, D, E, F, G, H, I, K, L, M, N, Q, R, S, T, V, W, Y
- 54 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
- 55 -- A, C, F, G, H, I, K, L, M, N, Q, R, S, T, V, W, Y
- 56 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
- 15 LCB5 (SEQ ID NO:25-26)
- 1 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
- 2 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
- 3 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
- 4 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
- 20 5 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
- 6 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
- 7 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
- 8 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
- 9 -- A, C, E, F, G, H, I, L, M, N, Q, S, T, V, W, Y
- 25 10 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
- 11 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
- 12 -- A, C, D, E, F, G, H, I, L, M, N, P, Q, R, S, T, V, W, Y
- 13 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
- 14 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
- 30 15 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
- 16 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
- 17 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
- 18 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
- 19 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
- 35 20 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
- 21 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
- 22 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
- 23 -- A, C, D, E, F, G, H, I, L, M, N, P, Q, R, S, T, W, Y
- 24 -- A, C, D, E, F, G, H, I, L, M, N, P, Q, S, T, V, W, Y
- 40 25 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
- 26 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y

- 27 -- A,C,G,H,I,S,T,V
28 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y
29 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
30 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
5 31 -- A,C,E,F,H,I,K,L,M,N,Q,S,T,V,W,Y
32 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
33 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
34 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
35 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y
10 36 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
37 -- A,C,D,E,F,G,H,I,L,M,N,P,Q,R,S,T,V,W,Y
38 -- A,C,D,E,G,I,L,M,N,P,Q,S,T,V,W
39 -- A,C,F,G,L,M,N,S,T,V,W
40 -- A,C,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,Y
15 41 -- C,H,I,L,M,P,R
42 -- A,C,E,G,H,I,L,M,P,T,V,Y
43 -- C,I,L,M,Q,T,V
44 -- A,C,D,F,G,H,I,M,S,T
45 -- D,Y
20 46 -- A,C,D,F,I,L,R,V
47 -- C,E,G,I,V
48 -- F,I,V,W,Y
49 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y
50 -- A,C,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y
25 51 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
52 -- C,D,E,H,I,K,N,P,Q,R,S,T,Y
53 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
54 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
55 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
30 56 -- F,I,L,M,T,V,W
57 -- A,C,D,E,F,G,H,N,P,Q,R,S,T,W,Y
58 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
59 -- A,C,F,I,L,M,T,V,Y
60 -- C,F,M,N,V,Y
35 61 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y
62 -- A,C,F,G,I,L,M,S,T,V,W
63 -- A,C,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y
64 -- A,C,E,F,G,H,K,L,N,P,R,S,T,W,Y
65 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
40

LCB6 (SEQ ID NO:27-28)

- 1 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
 2 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
 3 -- E, W
 4 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
 5 5 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
 6 -- F, L, M, R, S
 7 -- H, T, V
 8 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
 9 -- F, M
 10 10 -- A, K, L, W
 11 -- D, E, G, V, Y
 12 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
 13 -- E, L
 14 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
 15 15 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
 16 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
 17 -- F, N, P, S
 18 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
 19 -- L, N, Q, V
 20 20 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
 21 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
 22 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
 23 -- C, D, P, Q, R, W
 24 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
 25 25 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
 26 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
 27 -- D, H, L, S, W
 28 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
 29 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
 30 30 -- L, Q, V, W
 31 -- I, K, L, S
 32 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
 33 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
 34 -- A, F, L, T, V
 35 35 -- C, D, G, H, K, L, N, T
 36 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
 37 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
 38 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
 39 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
 40 40 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
 41 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y

42 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
43 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
44 -- F,I
45 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
5 46 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
47 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
48 -- L,Q,R,T
49 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
50 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
10 51 -- C,V,Y
52 -- A,E,H,K
53 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
54 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
55 -- C,F,H,L,P,W,Y
15 56 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

LCB7 (SEQ ID NO:29-30)

1 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
2 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
20 3 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
4 -- I,T,V
5 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
6 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
7 -- L,P,Y
25 8 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
9 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
10 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
11 -- A
12 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
30 13 -- A,L,P
14 -- H,L,R,T,Y
15 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
16 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
17 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
35 18 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
19 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
20 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
21 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
22 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
40 23 -- A,S
24 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

- 25 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
 26 -- C, G, S, V, Y
 27 -- K, L, M, W
 28 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
 5 29 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
 30 -- A, Y
 31 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
 32 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
 33 -- A, C, F, I, K, L, V, W
 10 34 -- A, H, L
 35 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
 36 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
 37 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
 38 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
 15 39 -- A, C, K, L, M, N
 40 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
 41 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
 42 -- A, C, D, L, V
 43 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
 20 44 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
 45 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
 46 -- Q, S, V
 47 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
 48 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
 25 49 -- E, L
 50 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
 51 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
 52 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
 53 -- I
 30 54 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
 55 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
 56 -- L, M, N, R
 57 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
 35 LCB8 (SEQ ID NO:31-32)
 1 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
 2 -- C, F, I, L, M, S, V, W, Y
 3 -- A, C, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
 4 -- A, C, D, E, F, G, H, I, K, L, M, N, Q, R, S, T, V, W, Y
 40 5 -- A, C, F, G, I, K, L, M, Q, S, T, V, W, Y
 6 -- H, I, K, L, M

- 7 -- A, H, I, K, L, M, N, P, Q, R, W, Y
- 8 -- A, C, D, E, F, G, H, I, K, L, M, N, Q, R, S, T, V, W, Y
- 9 -- A, C, F, G, I, L, M, S, Y
- 10 -- A, F, H, K, L, M, Q, R, S
- 5 11 -- A, C, D, E, F, G, H, I, K, L, M, N, Q, R, S, T, V, W, Y
- 12 -- A, C, D, E, G, H, I, K, L, M, N, Q, R, S, T, V, W, Y
- 13 -- A, C, D, E, F, G, H, M, N, Q, S, W, Y
- 14 -- C, D, E, H, N, Q, S
- 15 -- A, D, E, F, H, I, L, M, N, P, Q, S, T, V, W, Y
- 10 16 -- C, F, M, N, R, Y
- 17 -- A, C, I, L, M, Q, R, V
- 18 -- A, C, F, H, I, L, M, T, V, Y
- 19 -- I, Q, S
- 20 -- D, N
- 15 21 -- A, C, G, S, V
- 22 -- A, C, I, L, M, V
- 23 -- C, F, R, T, W, Y
- 24 -- A, C, D, E, F, G, H, I, L, M, N, Q, R, S, T, V, W, Y
- 25 -- C, E, S, T, V, Y
- 20 26 -- A, C, D, E, F, G, H, N, Q, S, T
- 27 -- A, C, D, E, G, H, I, K, L, M, N, Q, R, S, T, V
- 28 -- C, E, F, G, H, I, K, L, M, Q, R, W, Y
- 29 -- A, C, F, G, H, I, K, L, M, N, Q, R, S, T, V, Y
- 30 -- A, C, E, G, H, K, M, N, P, Q, R, T
- 25 31 -- A, C, D, E, F, G, H, I, K, L, M, N, Q, R, S, T, V, Y
- 32 -- A, C, D, E, G, H, I, K, N, Q, R, S, T, W
- 33 -- A, C, E, G, H, K, M, N, P, Q, R, S, W, Y
- 34 -- C, D, E, F, H, M, N, W, Y
- 35 -- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, Y
- 30 36 -- A, C, D, E, F, G, H, K, L, M, N, Q, R, S, T, V, W, Y
- 37 -- F, G, H, I, L, M, S, T, Y
- 38 -- D, E, H, Q, W, Y
- 39 -- C, D, E, F, G, H, K, L, M, N, P, Q, R, S, T, V, W, Y
- 40 -- A, C, E, G, H, I, K, M, P, V, Y
- 35 41 -- C, F, H, I, K, L, M, R, S, T, V
- 42 -- E, F, I, T, W, Y
- 43 -- A, C, D, E, F, H, I, L, M, N, Q, R, S, T, V, W, Y
- 44 -- C, G, I, K, L, M, T, V, Y
- 45 -- G, S, W, Y
- 40 46 -- C, I, K, L, M, N, Q, R, S, T
- 47 -- A, C, E, N, Q, S, T, V

- 48 -- C,D,E,F,H,I,L,M,W
 49 -- C,D,F,H,K,L,M,N,Q,R,T
 50 -- A,C,D,E,N,Y
 51 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
 5 52 -- A,C,D,E,G,H,K,L,M,N,Q,R,S,T
 53 -- A,C,D,E,F,G,H,I,L,M,N,P,Q,S,T,V,W,Y
 54 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
 55 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,S,T,V,W,Y
 56 -- C,I,L,M
 10 57 -- A,C,D,E,G,I,N,Q,S,T
 58 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
 59 -- A,C,G,P,S
 60 -- A,C,E,F,G,I,L,M,N,Q,S,T,V
 61 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
 15 62 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y
 63 -- A,C,E,F,G,H,I,L,M,N,Q,S,T,V,W,Y
 64 -- A,C,D,E,G,H,I,K,L,M,N,P,Q,S,T,V
 65 -- A,C,D,E,G,H,I,K,L,M,N,P,Q,R,S,T,W,Y
 20 AHB1 (SEQ ID NOS:33-34)
 1 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
 2 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
 3 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
 4 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
 25 5 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
 6 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
 7 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
 8 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
 9 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
 30 10 -- A,C,F,H,I,K,L,M,N,Q,R,S,T,V,W,Y
 11 -- F,N,Y
 12 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
 13 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
 14 -- A,D,G
 35 15 -- A,C,D,E,G,H,I,K,L,M,N,Q,R,S,T,V
 16 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
 17 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y
 18 -- A,C,D,E,F,G,H,I,L,M,N,Q,S,T,V,W,Y
 19 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
 40 20 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
 21 -- A,C,E,G,S,V

	22	-- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
	23	-- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
	24	-- A, C, D, E, F, H, K, L, M, N, Q, R, S, T, V, Y
	25	-- A, C, D, F, G, H, L, M, N, Q, R, S, T, V, W, Y
5	26	-- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
	27	-- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
	28	-- A, C, D, E, F, G, H, K, L, M, N, P, Q, R, S, T, Y
	29	-- A, C, D, E, F, G, H, I, K, L, M, N, Q, R, S, T, V, W, Y
	30	-- A, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
10	31	-- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
	32	-- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
	33	-- A, G, S
	34	-- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
	35	-- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
15	36	-- A, C, D, E, F, G, H, K, L, M, N, P, Q, R, S, T, V, W, Y
	37	-- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
	38	-- A, C, E, G, H, M, P, Q
	39	-- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
	40	-- A, C, D, E, G, K, N, Q, R, S, T
20	41	-- A, C, D, E, F, G, H, I, L, M, N, P, Q, S, T, V, W, Y
	42	-- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
	43	-- A, C, D, E, F, G, H, I, K, L, M, N, Q, S, T, V, W, Y
	44	-- E, F, H, Q, S, W, Y
	45	-- D, N
25	46	-- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
	47	-- C, T, V
	48	-- F, S, W, Y
	49	-- A, C, D, E, F, G, H, I, K, L, M, N, Q, R, S, T, V, W, Y
	50	-- A, C, F, H, I, K, L, M, N, Q, R, S, T, V, W, Y
30	51	-- A, D, G, H, N, S
	52	-- H, K, Q, R
	53	-- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
	54	-- A, C, H, I, K, L, M, N, P, Q, R, S, T, V
	55	-- A, C, E, G, H, K, N, Q, R, S, T
35	56	-- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
	57	-- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
	58	-- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
	59	-- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
	60	-- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
40	61	-- A, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
	62	-- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y

	63	-- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
	64	-- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
	65	-- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
	66	-- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
5	67	-- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
	68	-- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
	69	-- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
	70	-- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
	71	-- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
10	72	-- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
	73	-- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
	74	-- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
	75	-- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
	76	-- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
15	77	-- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
	78	-- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
	79	-- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
	80	-- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
	81	-- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
20	82	-- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
	83	-- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
	84	-- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
	85	-- A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
25	AHB2 (SEQ ID NO:101-102 and 164)	
	1	-- C, G, A, V, F, Y, W, S, Q, D, E, R, K
	2	-- C, P, G, V, I, M, L, F, Y, W, S, N, Q, D, E, R, H
	3	-- C, G, A, V, I, F, S, T, D, E, K
	4	-- C, P, G, A, V, I, M, L, F, Y, W, S, T, N, Q, D, E, R, K, H
30	5	-- C, P, G, A, V, M, L, Y, W, S, N, Q, D, E, R, K, H
	6	-- G, A, V, I, F, S, T, D, H
	7	-- C, P, G, V, I, M, L, F, W, S, T, N, Q, E, R, K, H
	8	-- C, P, G, A, V, M, L, Y, W, S, T, N, Q, D, E, R, K, H
	9	-- C, P, G, A, V, I, M, L, F, W, S, T, N, Q, D, E, R, K, H
35	10	-- C, P, G, A, V, I, L, Y, W, S, T, N, E, R, K
	11	-- C, P, G, A, V, I, M, L, F, Y, W, S, T, N, Q, D, E, R, H
	12	-- C, P, G, A, V, I, L, F, Y, W, S, T, N, Q, D, E, R, K, H
	13	-- C, G, A, V, M, L, F, W, S, T, N, E, H
	14	-- C, P, G, A, V, I, Y, S, T, N, D, E, R, H
40	15	-- C, G, A, V, I, M, L, F, Y, W, S, T, N, Q, D, E, R, K
	16	-- C, P, G, A, V, I, M, L, F, Y, W, S, T, N, Q, D, E, R, K, H

17 -- C,P,G,A,V,L,Y,W,S,T,Q,D,E,R
18 -- C,P,A,V,I,M,F,Y,N,Q,R,K,H
19 -- C,P,G,A,V,I,M,L,F,Y,W,S,T,N,Q,D,E,R,K,H
20 -- C,P,G,A,V,M,L,Y,W,N,Q,E,R,K,H
5 21 -- C,P,G,A,V,I,M,L,F,Y,W,S,N,Q,E,R,K,H
22 -- C,P,G,A,V,M,L,F,Y,S,T,N,Q,D,E,R,K,H
23 -- C,P,G,A,V,I,M,L,F,Y,W,S,T,N,Q,E,R,K
24 -- C,P,G,A,V,I,M,L,F,Y,W,S,Q,E,R,H
25 -- C,P,G,A,V,I,M,L,F,Y,W,S,T,N,Q,D,R,H
10 26 -- C,G,A,V,L,Y,S,N,D,R,K,H
27 -- C,P,G,A,V,I,M,L,F,Y,W,S,T,N,Q,D,E,R,K,H
28 -- C,P,G,A,V,I,M,L,F,Y,W,S,T,N,Q,D,E,R,K,H
29 -- C,P,G,V,I,M,L,F,Y,W,S,T,N,Q,D,R,K,H
30 -- C,P,G,A,V,I,M,L,F,Y,W,S,T,N,Q,D,E,R,K,H
15 31 -- C,G,A,V,I,M,L,F,Y,W,S,T,Q,D,E,R,K,H
32 -- P,G,A,V,I,L,W,S,T,D,R,H
33 -- C,P,G,A,V,I,M,L,F,Y,W,S,T,N,Q,E,R,K,H
34 -- C,G,A,V,I,M,L,F,Y,W,S,T,N,Q,D,E,R,K,H
35 -- C,P,G,A,V,I,M,L,F,Y,W,S,T,N,Q,D,E,R,K,H
20 36 -- C,P,G,A,V,I,L,F,Y,S,T,N,Q,D,E,R,H
37 -- C,G,A,V,I,M,L,F,Y,W,S,T,N,Q,D,E,R,K,H
38 -- C,P,G,A,V,I,M,L,F,Y,W,S,T,Q,E,R,K
39 -- C,P,G,A,V,I,W,S,Q,E,R,H
40 -- C,P,G,A,V,I,L,Y,W,S,T,N,D,E,R,K,H
25 41 -- C,P,G,A,V,I,M,L,Y,W,S,T,N,Q,D,E,R,K,H
42 -- C,P,G,A,V,M,L,Y,W,S,T,N,Q,D,E,R,K,H
43 -- C,G,A,V,I,M,L,F,Y,W,S,T,N,Q,D,E,R,K,H
44 -- C,P,G,A,V,I,M,L,F,W,S,T,Q,D,E,R,H
45 -- C,G,A,V,I,M,L,F,Y,W,S,T,N,Q,D,E,R,K,H
30 46 -- C,P,G,A,V,I,M,L,F,S,T,Q,E,R,K
47 -- C,G,A,V,I,M,L,F,W,S,T,N,Q,D,E,R,H
48 -- C,P,G,A,V,I,M,L,F,Y,W,S,N,Q,E,R,K
49 -- C,P,G,A,V,M,L,F,Y,W,S,T,N,Q,D,E,R,K,H
50 -- C,P,G,A,V,I,M,L,F,Y,W,S,T,N,Q,D,E,R,K,H
35 51 -- C,G,A,V,I,M,L,F,Y,W,S,T,N,Q,D,E,R,K,H
52 -- C,P,G,A,V,I,M,L,F,Y,W,S,T,N,Q,D,E,R,K,H
53 -- C,P,G,A,V,I,M,L,F,Y,W,S,T,N,D,E,R,K,H
54 -- C,P,G,A,V,I,M,L,F,Y,W,S,T,N,Q,D,E,R,K,H
55 -- C,P,G,A,V,I,M,L,F,Y,S,T,N,Q,D,E,R,K,H
40 56 -- C,P,G,A,V,I,M,L,F,Y,W,S,T,N,Q,D,E,R,K,H
57 -- C,P,G,A,V,I,M,L,F,Y,W,S,T,N,Q,D,E,R,K,H

	58	-- C, G, A, V, I, M, L, F, Y, W, S, T, N, E, R, K, H
	59	-- C, P, G, A, V, I, M, L, F, Y, W, S, T, N, Q, D, E, R, K, H
	60	-- C, G, A, V, I, M, L, F, Y, W, S, T, Q, D, E, R, K
	61	-- C, P, G, A, V, I, M, L, F, Y, W, S, N, Q, D, E, R, K, H
5	62	-- C, G, A, V, L, S, T, N, D, E, K, H
	63	-- C, P, G, A, V, I, L, F, Y, W, S, T, N, Q, D, E, R, K, H
	64	-- C, P, G, A, V, I, M, L, F, Y, W, S, T, N, Q, D, E, R, H
	65	-- C, G, A, V, I, M, L, F, Y, S, T, N, R, K, H
	66	-- C, P, G, A, V, I, M, L, W, T, Q, E, R
10	67	-- C, P, G, A, V, I, M, L, F, Y, W, S, T, N, Q, D, E, R, K, H
	68	-- C, P, G, A, V, I, L, F, Y, W, S, T, N, Q, D, E, R, H
	69	-- P, G, V, I, M, L, Y, W, S, T, Q, R, K
	70	-- C, P, G, A, V, I, M, L, F, Y, W, S, T, N, Q, D, E, R, K, H
	71	-- C, G, A, V, L, F, W, S, Q, D, E, R, K
15	72	-- C, V, I, L, S
	73	-- P, G, A, V, S, T, E
	74	-- C, A, L, F, Y, S, T, R, H
	75	-- C, P, G, V, I, L, F, W, S, N, D, E, R, K

The residue numbers of the interface residues which are within 8Å to the RBD target are listed in **Table 2** for the various design types. In another embodiment, amino acid residues at the interface residues listed in Table 2 are either identical at that residue to the reference sequence, or may be substituted by a conservative amino acid substitution. Such conservative amino acid substitutions involve replacing a residue by a residue having similar physiochemical characteristics, e.g., substituting one aliphatic residue for another (such as Ile, Val, Leu, or Ala for one another), or substitution of one polar residue for another (such as between Lys and Arg; Glu and Asp; or Gln and Asn). Other such conservative substitutions, e.g., substitutions of entire regions having similar hydrophobicity characteristics, are known. Amino acids can be grouped according to similarities in the properties of their side chains (in A. L. Lehninger, in Biochemistry, second ed., pp. 73-75, Worth Publishers, New York (1975)): (1) non-polar: Ala (A), Val (V), Leu (L), Ile (I), Pro (P), Phe (F), Trp (W), Met (M); (2) uncharged polar: Gly (G), Ser (S), Thr (T), Cys (C), Tyr (Y), Asn (N), Gln (Q); (3) acidic: Asp (D), Glu (E); (4) basic: Lys (K), Arg (R), His (H). Alternatively, naturally occurring residues can be divided into groups based on common side-chain properties: (1) hydrophobic: Norleucine, Met, Ala, Val, Leu, Ile; (2) neutral hydrophilic: Cys, Ser, Thr, Asn, Gln; (3) acidic: Asp, Glu; (4) basic: His, Lys, Arg; (5) residues that influence chain orientation: Gly, Pro; (6) aromatic: Trp, Tyr, Phe. Non-conservative substitutions will entail exchanging a member of one of these classes for another class. Particular conservative substitutions

include, for example; Ala into Gly or into Ser; Arg into Lys; Asn into Gln or into His; Asp into Glu; Cys into Ser; Gln into Asn; Glu into Asp; Gly into Ala or into Pro; His into Asn or into Gln; Ile into Leu or into Val; Leu into Ile or into Val; Lys into Arg, into Gln or into Glu; Met into Leu, into Tyr or into Ile; Phe into Met, into Leu or into Tyr; Ser into Thr; Thr into Ser; Trp into Tyr; Tyr into Trp; and/or Phe into Val, into Ile or into Leu.

Table 2: Interface residues

'LCB1': [3, 6, 7, 10, 13, 17, 20, 22, 23, 25, 26, 29, 32, 33, 36],

'LCB2': [1, 2, 5, 6, 9, 12, 13, 16, 20, 32, 35, 39],

10 'LCB3': [1, 3, 4, 6, 7, 10, 11, 13, 14, 15, 18, 27, 30, 33, 34, 37],

'LCB4': [8, 11, 12, 15, 23, 24, 26, 27, 28, 30, 31, 34, 56],

'LCB5': [35, 37, 38, 40, 41, 44, 47, 48, 53, 56, 60, 63],

'LCB6': [3, 4, 7, 8, 11, 12, 14, 15, 21, 24, 25, 28, 31, 32, 35],

'LCB7': [2, 3, 6, 7, 9, 10, 13, 17, 29, 32, 33, 36],

15 'LCB8': [14, 15, 16, 19, 22, 23, 26, 29, 30, 38, 41, 42, 45],

'AHB1', [34, 38, 41, 45, 48, 49, 52, 63, 64, 67, 68, 70, 71, 74, 78, 81, 82, 85],

'AHB2', [4, 7, 11, 14, 15, 18, 21, 26, 29, 30, 33, 34, 36, 37, 40, 43, 44, 47, 48].

20 In one embodiment, amino acid residues at the interface residues listed in Table 2 are identical at that residue to the reference sequence.

In another embodiment, the polypeptide comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS:1-10, 13-17, 19-21, 33-34, and 100-101.

25 In one embodiment, the polypeptides comprise an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS:1-10 and 102-136 (see Table 3).

30 **Table 3: LCB1 exemplary variants**

Name	Binder Protein
LCB1_4N	DKENILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKGDERLLEEAERLLEEVEE (SEQ ID NO: 102)
LCB1_4K	DKEKILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKGDERLLEEAERLLEEVEE (SEQ ID NO: 103)
LCB1_14K	DKEWILQKIYEIMKLLDELGHAEASMRVSDLIYEFMKGDERLLEEAERLLEEVEE (SEQ ID NO: 104)

	ID NO: 104)
LCB1_15T	DKEWILQKIYEIMRTLDELGHAEASMRVSDLIYEFMKGDERLLEEAERLLEEVEVER (SEQ ID NO: 105)
LCB1_18Q	DKEWILQKIYEIMRLLDQLGHAEASMRVSDLIYEFMKGDERLLEEAERLLEEVEVER (SEQ ID NO: 106)
LCB1_18K	DKEWILQKIYEIMRLLDKLGHAEASMRVSDLIYEFMKGDERLLEEAERLLEEVEVER (SEQ ID NO: 107)
LCB1_27Q	DKEWILQKIYEIMRLLDDELGHAEASMQVSDLIYEFMKGDERLLEEAERLLEEVEVER (SEQ ID NO: 108)
LCB1_27Y	DKEWILQKIYEIMRLLDDELGHAEASMYVSDLIYEFMKGDERLLEEAERLLEEVEVER (SEQ ID NO: 109)
LCB1_17E	DKEWILQKIYEIMRLLEELGHAEASMRVSDLIYEFMKGDERLLEEAERLLEEVEVER (SEQ ID NO: 110)
LCB1_17R	DKEWILQKIYEIMRLRLRELGHAEASMRVSDLIYEFMKGDERLLEEAERLLEEVEVER (SEQ ID NO: 111)
LCB1_42N	DKEWILQKIYEIMRLLDDELGHAEASMRVSDLIYEFMKGDENLLEEAERLLEEVEVER (SEQ ID NO: 112)
LCB1_49Q	DKEWILQKIYEIMRLLDDELGHAEASMRVSDLIYEFMKGDERLLEEAQEQLLEEVEVER (SEQ ID NO: 113)
LCB1_52Q	DKEWILQKIYEIMRLLDDELGHAEASMRVSDLIYEFMKGDERLLEEAERLLQEVEVER (SEQ ID NO: 114)
LCB1_32L	DKEWILQKIYEIMRLLDDELGHAEASMRVSDLLYEFMKGDERLLEEAERLLEEVEVER (SEQ ID NO: 115)
LCB1_28A	DKEWILQKIYEIMRLLDDELGHAEASMRASDLIYEFMKGDERLLEEAERLLEEVEVER (SEQ ID NO: 116)
LCB1_v1.3_ACH1	DKENILQKIYEIMKTLEQLGHAEASMYVSDLIYEFMKGDERLLEEAERLLEEVEVER (SEQ ID NO: 117)
LCB1_v1.3_ACH2	DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKGDENLLEEAERLLEEVEVER (SEQ ID NO: 118)
LCB1_v1.3_ACH3	DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKGDERLLEEAQEQLLEEVEVER (SEQ ID NO: 119)
LCB1_v1.3_ACH4	DKENILQKIYEIMKTLEQLGHAEASMYVSDLIYEFMKGDENLLEEAQEQLLEEVEVER (SEQ ID NO: 120)
LCB1_v1.3_ACH5	DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKGDENLLEEAQEQLLEEVEVER (SEQ ID NO: 121)
LCB1_v1.3_1	DRENILQKIYEIMKELEKLGHAEASMQVSDLIYEFMQDKDERLLEEAERLLEEVEVKR (SEQ ID NO: 122)
LCB1_v1.3_2	DRENILQKIYEIMKELRQLGHAEASMQVSDLIYEFMKTDKRLLLEEAERLLEEVEVKR (SEQ ID NO: 123)
LCB1_v1.3_3	DRENILQKIYEIMKTLRRLGHAEASMQVSDLIYEFMQDKDKRLLLEEAERLLEEVEVQR (SEQ ID NO: 124)
LCB1_v1.3_4	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTDKDERLLEEAERLLEEVEVKR (SEQ ID NO: 125)
LCB1_v1.3_5	DRENILQKIYEIMKTLEKLGHAEASMQASDLIYEFMKTDKDERLLEEAERLLEEVEVQR (SEQ ID NO: 126)
LCB1_v1.3_6	DKENILQKIYEIMKTLRALGHAEASMQVSDLIYEFMQTKDERLLEEAERLLEEVEVKR (SEQ ID NO: 127)
LCB1_v1.3_7	DKENVLQKIYEIMKTLEKLGHAEASMQVSDLIYEFMQTKDKRLLLEEAERLLEEVEVQR (SEQ ID NO: 128)
LCB1_v1.3_15	DRENILQKIYEIMKELEKLGHAEASMQVSDLIYEFMQDKDENLLEEAERLLEEVEVKR (SEQ ID NO: 129)
LCB1_v1.3_16	DRENILQKIYEIMKELRQLGHAEASMQVSDLIYEFMKTDKDNLLLEEAERLLEEVEVKR (SEQ ID NO: 130)
LCB1_v1.3_17	DRENILQKIYEIMKTLRRLGHAEASMQVSDLIYEFMQDKDKNLLLEEAERLLEEVEVQR (SEQ ID NO: 131)
LCB1_v1.3_19	DRENILQKIYEIMKTLEKLGHAEASMQASDLIYEFMKTDKDENLLEEAERLLEEVEVQR (SEQ ID NO: 132)
LCB1_v1.3_20	DKENILQKIYEIMKTLRALGHAEASMQVSDLIYEFMQTKDENLLEEAERLLEEVEVKR (SEQ ID NO: 133)
LCB1_v1.3_21	DKENVLQKIYEIMKTLEKLGHAEASMQVSDLIYEFMQTKDKNLLLEEAERLLEEVEVQR (SEQ ID NO: 134)

LCB1_v2.2 DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVR (SEQ ID NO: 135)
 LCB1_v2.2_ompT DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVT (SEQ ID NO: 136)

The polypeptides may contain a substantial number of mutations while retaining binding activity, as detailed in the examples that follow. In one embodiment, the polypeptide comprises an amino acid substitution relative to the amino acid sequence of SEQ ID NO:1 at 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, or all 18 residues selected from the group consisting of 2, 4, 5, 14, 15, 17, 18, 27, 28, 32, 37, 38, 39, 41, 42, 49, 52, and 55. In another embodiment, the substitutions are selected from the substitutions listed in Table 4, either individually (i.e.: any single mutation listed in the Table) or in combinations in a given row.

Table 4: Exemplary LCB1 substitutions

Name	Parent	Mutations from WT											
LCB1_1	LCB1	W4N	R14K	L15T	E18Q	R27Q	K38Q						
LCB1_2	LCB1	W4N	R14K	L15T	E18Q	R27Y	K38Q						
LCB1_3	LCB1	W4N	R14K	L15T	D17E	E18Q	R27Q	K38Q					
LCB1_4	LCB1	W4N	R14K	L15T	D17E	E18Q	R27Q	K38Q	R42N	R49Q	E52Q		
LCB1_4N	LCB1	W4N											
LCB1_4K	LCB1	W4K											
LCB1_14K	LCB1	R14K											
LCB1_15T	LCB1	L15T											
LCB1_18Q	LCB1	E18Q											
LCB1_18K	LCB1	E18K											
LCB1_27Q	LCB1	R27Q											
LCB1_27Y	LCB1	R27Y											
LCB1_38Q	LCB1	K38Q											
LCB1_17E	LCB1	D17E											
LCB1_17R	LCB1	D17R											
LCB1_42N	LCB1	R42N											
LCB1_49Q	LCB1	R49Q											
LCB1_52Q	LCB1	E52Q											
LCB1_32L	LCB1	I32L											
LCB1_28A	LCB1	V28A											
LCB1_v1.3	LCB1	W4N	R14K	L15T	D17E	E18Q	R27Q	K38Q					
LCB1_v1.3_ACH1	LCB1_v1.3	W4N	R14K	L15T	D17E	E18Q	R27Y	K38Q					
LCB1_v1.3_ACH2	LCB1_v1.3	W4N	R14K	L15T	D17E	E18Q	R27Q	K38Q	R42N				
LCB1_v1.3_ACH3	LCB1_v1.3	W4N	R14K	L15T	D17E	E18Q	R27Q	K38Q	R49Q				
LCB1_v1.3_ACH4	LCB1_v1.3	W4N	R14K	L15T	D17E	E18Q	R27Y	K38Q	R42N	R49Q			
LCB1_v1.3_ACH5	LCB1_v1.3	W4N	R14K	L15T	D17E	E18Q	R27Q	K38Q	R42N	R49Q			
LCB1_v1.3_1	LCB1_v1.3	K2R	W4N	R14K	L15E	D17E	E18K	R27Q	K37Q	K38D	G39K		
		E55K											

5	LCB1_v1.3_2	LCB1_v1.3 E55K	K2R	W4N	R14K	L15E	D17R	E18Q	R27Q	K38T	G39K	E41K
	LCB1_v1.3_3	LCB1_v1.3 E41K	K2R E55Q	W4N	R14K	L15T	D17R	E18R	R27Q	K37Q	K38D	G39K
	LCB1_v1.3_4	LCB1_v1.3	W4N	I5V	R14K	L15E	D17E	E18R	R27Q	K38T	G39K	E55K
	LCB1_v1.3_5	LCB1_v1.3 E55Q	K2R	W4N	R14K	L15T	D17E	E18K	R27Q	V28A	K38T	G39K
	LCB1_v1.3_6	LCB1_v1.3	W4N	R14K	L15T	D17R	E18A	R27Q	K37Q	K38T	G39K	E55K
10	LCB1_v1.3_7	LCB1_v1.3 E41K	W4N E55Q	I5V	R14K	L15T	D17E	E18K	R27Q	K37Q	K38T	G39K
	LCB1_v1.3_15	LCB1_v1.3 R42N	K2R E55K	W4N	R14K	L15E	D17E	E18K	R27Q	K37Q	K38D	G39K
	LCB1_v1.3_16	LCB1_v1.3 R42N	K2R E55K	W4N	R14K	L15E	D17R	E18Q	R27Q	K38T	G39K	E41K
15	LCB1_v1.3_17	LCB1_v1.3 E41K	K2R R42N	W4N E55Q	R14K	L15T	D17R	E18R	R27Q	K37Q	K38D	G39K
	LCB1_v1.3_19	LCB1_v1.3 R42N	K2R E55Q	W4N	R14K	L15T	D17E	E18K	R27Q	V28A	K38T	G39K
	LCB1_v1.3_20	LCB1_v1.3 E55K	W4N	R14K	L15T	D17R	E18A	R27Q	K37Q	K38T	G39K	R42N
20	LCB1_v1.3_21	LCB1_v1.3 E41K	W4N R42N	I5V E55Q	R14K	L15T	D17E	E18K	R27Q	K37Q	K38T	G39K
	LCB1_v2.2	LCB1_v1.3 E55K	W4N	I5V	R14K	L15E	D17E	E18R	R27Q	K38T	G39K	R42N
	LCB1_v2.2_ompT	LCB1_v1.3 E55T	W4N	I5V	R14K	L15E	D17E	E18R	R27Q	K38T	G39K	R42N

In another embodiment, the polypeptides comprise an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 13-17, 19-21 and 137-163 (see Table 5).

Table 5: LCB3 exemplary variants

Name	Binder Protein
LCB3_8Q	NDDELHMQMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLE RLLS (SEQ ID NO: 137)
LCB3_8T	NDDELHMTMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLE RLLS (SEQ ID NO: 138)
LCB3_19K	NDDELHMLMTDLVYEALHKAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLE RLLS (SEQ ID NO: 139)
LCB3_19I	NDDELHMLMTDLVYEALHIAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLE RLLS (SEQ ID NO: 140)
LCB3_25F	NDDELHMLMTDLVYEALHFAKDEEFKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLE RLLS (SEQ ID NO: 141)
LCB3_25M	NDDELHMLMTDLVYEALHFAKDEEMKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLE RLLS (SEQ ID NO: 142)
LCB3_26Q	NDDELHMLMTDLVYEALHFAKDEEIQKRVFQLFELADKAYKNNDRQKLEKVVEELKELLE RLLS (SEQ ID NO: 143)
LCB3_28H	NDDELHMLMTDLVYEALHFAKDEEIKKHVFQLFELADKAYKNNDRQKLEKVVEELKELLE RLLS (SEQ ID NO: 144)
LCB3_35K	NDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFEKADKAYKNNDRQKLEKVVEELKELLE RLLS (SEQ ID NO: 145)
LCB3_37T	NDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELATKAYKNNDRQKLEKVVEELKELLE

	RLLS (SEQ ID NO: 146)
LCB3_40R	NDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKARKNNDRQKLEKVVEELKELLE RLLS (SEQ ID NO: 147)
LCB3_43K	NDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNKDRQKLEKVVEELKELLE RLLS (SEQ ID NO: 148)
LCB3_34G	NDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFGLADKAYKNNDNRQKLEKVVEELKELLE RLLS (SEQ ID NO: 149)
LCB3_34Y	NDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFYLDKAYKNNDNRQKLEKVVEELKELLE RLLS (SEQ ID NO: 150)
LCB3_34T	NDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFTLADKAYKNNDNRQKLEKVVEELKELLE RLLS (SEQ ID NO: 151)
LCB3_49K	NDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDNRQKLKKVVEELKELLE RLLS (SEQ ID NO: 152)
LCB3_v1.2_AC H1	NDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFGKATKAYKNKDRQKLEKVVEELKELLE RLLS (SEQ ID NO: 153)
LCB3_v1.2_AC H2	NDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFYKATKAYKNKDRQKLEKVVEELKELLE RLLS (SEQ ID NO: 154)
LCB3_v2.2	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLE RLLS (SEQ ID NO: 155)
LCB3_v1.3_2	NDDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLE RLLS (SEQ ID NO: 156)
LCB3_v1.3_3	NDDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKARKAYKNKDRQKLEKVVEELKELLE RLLS (SEQ ID NO: 157)
LCB3_v1.3_4	NDDELHMQMTDLVWEALHFAKDEEFQKHVFQLFEKARKAYKNKDRQKLEKVVEELKELLE RLLS (SEQ ID NO: 158)
LCB3_v1.3_5	NDDELHMQMTDLVWEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLE RLLS (SEQ ID NO: 159)
LCB3_v1.3_6	NEDELHMQMTDLVWEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLE RLLS (SEQ ID NO: 160)
LCB3_v1.3_7	NDDELHMQMTDLVWEALHFAKTEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLE RLLS (SEQ ID NO: 161)
LCB3_v1.3_15	NLDELHMQMTDLVYEALHFAKTEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLE RLLS (SEQ ID NO: 162)
LCB3_v2.3	NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLE RILS (SEQ ID NO: 163)

The polypeptides may contain a substantial number of mutations while retaining binding activity, as detailed in the examples that follow. In one embodiment, the polypeptide comprises an amino acid substitution relative to the amino acid sequence of SEQ ID NO:13 at 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or all 20 residues selected from the group consisting 2, 6, 8, 9, 13, 14, 19, 22, 25, 26, 28, 29, 34, 35, 37, 40, 43, 45, 49, and 62. In another embodiment, the substitutions are selected from the substitutions listed in Table 6, either individually or in combinations in a given row.

Table 6: Exemplary LCB3 substitutions

Name	Parent	Mutations from WT						
LCB3_1	LCB3	L8Q	I25F	K26Q	R28H	L35K	D37T	
LCB3_2	LCB3	L8Q	K26Q	R28H	L35K	D37T	N43K	
LCB3_3	LCB3	L8Q	I25F	K26Q	R28H	L35K	D37T	N43K

LCB3_4	LCB3	L8Q	F19K	I25F	K26Q	R28H	L35K	D37T	Y40R, N43K
LCB3_8Q	LCB3	L8Q							
LCB3_8T	LCB3	L8T							
LCB3_19K	LCB3	F19K							
LCB3_19I	LCB3	F19I							
LCB3_25F	LCB3	I25F							
LCB3_25M	LCB3	I25M							
LCB3_26Q	LCB3	K26Q							
LCB3_28H	LCB3	R28H							
LCB3_35K	LCB3	L35K							
LCB3_37T	LCB3	D37T							
LCB3_40R	LCB3	Y40R							
LCB3_43K	LCB3	N43K							
LCB3_34G	LCB3	E34G							
LCB3_34Y	LCB3	E34Y							
LCB3_34T	LCB3	E34T							
LCB3_49K	LCB3	E49K							
LCB3_v1.2	LCB3	L8Q	K26Q	R28H	L35K	D37T	N43K		
LCB3_v1.2_ACH1	LCB3_v1.2	L8Q	K26Q	R28H	E34G	L35K	D37T	N43K	
LCB3_v1.2_ACH2	LCB3_v1.2	L8Q	K26Q	R28H	E34Y	L35K	D37T	N43K	
LCB3_v2.2	LCB3_v1.3	D2L	L8Q	I25F	K26Q	R28H	L35K	D37T	N43K
LCB3_v1.3_2	LCB3_v1.3	L8Q	D22T	I25F	K26Q	R28H	L35K	D37T	N43K
LCB3_v1.3_3	LCB3_v1.3	L8Q	I25F	K26Q	R28H	L35K	D37R	N43K	
LCB3_v1.3_4	LCB3_v1.3	L8Q	Y14W	I25F	K26Q	R28H	L35K	D37R	N43K
LCB3_v1.3_5	LCB3_v1.3	L8Q	Y14W	I25F	K26Q	R28H	L35K	D37T	N43K
LCB3_v1.3_6	LCB3_v1.3	D2E	L8Q	Y14W	I25F	K26Q	R28H	L35K	D37T, N43K
LCB3_v1.3_7	LCB3_v1.3	L8Q	Y14W	D22T	I25F	K26Q	R28H	L35K	D37T, N43K
LCB3_v1.3	LCB3_v1.2	L8Q	I25F	K26Q	R28H	L35K	D37T	N43K	
LCB3_v1.3_15	LCB3_v1.3	D2L	L8Q	D22T	I25F	K26Q	R28H	L35K	D37T, N43K, R28H, V29A, L35K, D37T, N43K, R45K, L62I
LCB3_v2.3	LCB1_v2.1	D2I	H6L	L8Q	M9V	V13I	I25F	K26Q	

In a further embodiment, the polypeptides comprise an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS:33-34 and 100-101 and 164 (see Table 7).

Table 7: AHB2 exemplary variant

AHB2	ELEEQVMHVLDOVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEAARILEH
v2	LEELART (SEQ ID NO: 164)

In one embodiment, the polypeptide comprises an amino acid substitution relative to the amino acid sequence of SEQ ID NO:101 at or both residues selected from the group consisting 63 and 75. In a further embodiment, the substitutions comprise R63A and/or K75T.

In all embodiments disclosed herein, the polypeptides may comprise one or more additional functional groups or residues as deemed appropriate for an intended use. In one embodiment, the polypeptides may further comprise one or more added cysteine residues at the N-terminus and/or C-terminus. In another embodiment, the polypeptides may further comprise an N-linked glycosylation site (i.e.: NX(S/T), where X is any amino acid).

In another embodiment, the polypeptides may comprise two or more (i.e.: 2, 3, 4, 5, or more) copies of the amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 1-17, 19-21, 23-34 and 100-101. In this embodiment, 2 or more of the binders are linked. In one embodiment, the two or more copies of the polypeptide are all identical; in another embodiment, the two or more copies of the polypeptide are not all identical. In any of these embodiments, the two or more copies of the polypeptide may be separated by amino acid linker sequences, though such linkers are not required. The amino acid linkers may be of any length and amino acid composition as suitable for an intended purpose. In one embodiment, the amino acid linkers are independently between 2-100 or 3-100 amino acids in length.

In another embodiment, the amino acid linker sequences comprise Gly-Ser rich (at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% Gly-Ser residues) amino acid linkers. In a further embodiment, the Gly-Ser rich linkers comprise an amino acid sequence selected from the group consisting of GG and SEQ ID NOS:35-46 and 165-171

GSGS (SEQ ID NO:35)

GGSGGS (SEQ ID NO:36)

SGGSGGSGGSG (SEQ ID NO:37)

GGSGGSGGSGGSG (SEQ ID NO:38)

GGSGSSGGSGSGSG (SEQ ID NO:39)

GGSGSGGSGSGSGGS (SEQ ID NO:40)

SGGSGSGSGSGSGGS (SEQ ID NO:41)

GGGSGGGSSGGSGGSSGGSGGGS (SEQ ID NO:42)

GGGSGGGGSGGGGSGGGGSGGGGSGGGGSG (SEQ ID NO:43)

GGGSGGGSGGS GGS GGGSGGGSGGS GGGSGGGS (SEQ ID NO:44)

[illegible][illegible]

GGSGGGGSGGGGSGGGGSGG (SEQ ID NO: 165)

GGSGGGGSGGGGSGG (SEQ ID NO: 166)

GGSGGGGSGG (SEQ ID NO: 167)

10 GGGGSGGGG (SEQ ID NO: 168)

GGGSGGG (SEQ ID NO: 169)

GGSGG (SEQ ID NO: 170)

GGSGSSG (SEQ ID NO: 171)

15 In another embodiment, the amino acid linker sequences may comprise Pro-rich (at least 15%, 20%, 25%, or greater Pro residues) amino acid linkers. Non-limiting and exemplary embodiments may comprise an amino acid sequence selected from the group consisting of SEQ ID NOs:97-98 and 172-176.

AGSGGGSGGSGGSPVPSTPPTPSPSTPPTPSPSPVPSTPPTPSPSTPPTPSPSPVPSTPPTPSPSTPPTPSPSPASG (SEQ ID NO: 97)

20 NO:97)
GSGGSGGSGGSPVPSTPPTPSPSTPPTPSPSGGSGNSSGSGGSPVPSTPPTPSPSTPPTPSPSAS (SEQ ID NO:98)

GGASPAAPAPASPAAPAPSAPAGG (SEQ ID NO: 172)

GGASPAAPAPASPAGG (SEQ ID NO: 173)

GGASPAAPAPGG (SEQ ID NO: 174)

25 GGASPAAPAGG (SEQ ID NO: 175)

GGSSGPSTPPTPSPSTPPTPSPSPGGSSG (SEQ ID NO: 176)

In further non-limiting embodiments, the amino acid linkers may comprise the amino acid sequence selected from the group consisting of SEQ ID NOS: 99 and 177-178.

GGSSAGSPTSTGTSSATPSGSGTGG(SEQ ID NO: 177)

GGSSGEAAAKEAAAKEAAAKGSSGG (SEQ ID NO: 178)

GGSSGQIFVKTLTGKTITLEVEPSDTIENVKAKIQDKEGIPPDQQRLLIFAGKQLEDGRTLSDYNIQKESTLHLVL
RLRGGGGSSG (SEQ ID NO: 99)

In one embodiment, the polypeptide comprises the formula Z1-Z2-Z3, wherein:

Z1 comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 1-17, 19-21, 23-34 and 100-164;

Z2 comprises an optional amino acid linker; and

Z3 comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 1-17, 19-21, 23-34 and 100-164;

5 wherein Z1 and Z3 may be identical or different. In one embodiment, Z1 and Z3 are identical; in another embodiment Z1 and Z3 are different. In embodiments where Z1 and Z3 differ, each may be a variant of a given starting monomer (ex: Z1 comprises the amino acid sequence of SEQ ID NO:1 (LCB1), and Z3 comprises the amino acid sequence of SEQ ID NO: 102-136. Any such combination of the monomers disclosed herein may be used. It will
10 further be understood that the polypeptides may comprise 2, 3, 4, 5, or more monomers of any embodiment disclosed herein. In embodiments where there are 3 or more monomers, all 3 monomers may be identical; 2 monomers may be identical and one may differ, or all 3 monomers may be different.

In one embodiment employing LCB1 and variants thereof, Z1 comprises an amino
15 acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 1-10 and 102-136; and

Z3 comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the
20 amino acid sequence selected from the group consisting of SEQ ID NOS: 1-10 and 102-136.

In another embodiment employing LCB3 and variants thereof,

Z1 comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 13-17, 19-21 and
25 137-163; and

Z3 comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 13-17, 19-21 and
137-163.

In another embodiment employing AHB and variants thereof,

Z1 comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 33-34, 100-101, and 164; and

Z3 comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 33-34, 100-101, and 164.

5 In one embodiment, one of Z1 and Z3 comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 1-10 and 102-136; and

the other of Z1 and Z3 comprises an amino acid sequence at least 50%, 55%, 60%,
10 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 13-17, 19-21 and 137-163.

In another embodiment, one of Z1 and Z3 comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%,
15 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 1-10 and 102-136; and

the other of Z1 and Z3 comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID
20 NOS: 33-34, 100-100, and 164.

In a further embodiment, one of Z1 and Z3 comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 13-17, 19-21 and 137-163; and

25 the other of Z1 and Z3 comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 33-34, 100-100, and 164.

In another embodiment of any of the other embodiments disclosed herein, the
30 polypeptide comprises at least 3 monomers (i.e.: 3, 4, 5, or more). In one such embodiment, the polypeptide comprises the formula B1-B2-Z1-Z2-Z3-B3-B4, wherein:

Z1, Z2, and Z3 are as defined above;

B2 and B3 comprise optional amino acid linkers; and

one or both of B1 and B4 independently comprise an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 1-17, 19-21, 23-34 and 100-164, wherein one of B1 and B4 may be absent. In one embodiment, one of B1 and B4 is absent. In another embodiment, both B1 and B4 are present. In one embodiment, B1 and B4 independently comprise an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 1-17, 19-21, 23-34 and 100-164. In this embodiment, B1 and B4 may be identical or may be different. In one embodiment, B1 when present and B4 when present, are identical to one or both of Z1 and Z3. In another embodiment, B1 when present and B4 when present, are not identical to either of Z1 and Z3.

In one embodiment, B1 when present, and B4 when present, independently comprise an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 1-10, 13-17, 19-21, 33-34, 100-101, and 102-164.

In another embodiment, B1 when present, and B4 when present, independently comprise an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 1-10 and 102-136.

In a further embodiment, B1 when present, and B4 when present, independently comprise an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 13-17, 19-21 and 137-163.

In a still further embodiment, B1 when present, and B4 when present, independently comprise an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 33-34, 100-101, and 164.

In various embodiments when both B1 and B4 are present,

- one of B1 and B4 comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 1-10 and 102-136, and the other comprises an amino acid sequence at least

50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 13-17, 19-21 and 137-163;

- one of B1 and B4 comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 1-10 and 102-136, and the other comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 33-34, 100-101, and 164, or
- one of B1 and B4 comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 13-17, 19-21 and 137-163, and the other comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 33-34, 100-101, and 164.

In various non-limiting embodiments, the polypeptides comprise an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 47-60, 193-355, and 454-588 and a genus selected from those recited in the right hand column of Table 8 wherein genus positions X1, X2, X3, and X4 may be present or absent, and when present may be any sequence of 1 or more amino acids. In all embodiments, any N-terminal methionine residues may be present or absent in the polypeptide. In one embodiment, any N-terminal methionine residues are absent in the polypeptide.

>LCB1-6GS-LCB1

DKEWILQKIYEIMRLDDELGHAEASMRVSDLIYEFMKGDERLLEEAERLLEEVERGSGGSDKEWILQKIYEIMRLDDELGHAEASMRVSDLIYEFMKGDERLLEEAERLLEEVE (SEQ ID NO: 47)

>LCB1-12GS-LCB1

DKEWILQKIYEIMRLDDELGHAEASMRVSDLIYEFMKGDERLLEEAERLLEEVERGSGGSGSGSGDKEWILQKIYEIMRLDDELGHAEASMRVSDLIYEFMKGDERLLEEAERLLEEVE (SEQ ID NO: 48)

>LCB1-24GS-LCB1

DKEWILQKIYEIMRLLDDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVEVRGGGSGGGSSGGSGGGSSGGGSDKE
WILQKIYEIMRLLDDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVEVR (SEQ ID NO:49)

>LCB1-36GS-LCB1

5 DKEWILQKIYEIMRLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVE
GGGGSGGGSDDKEWILQKIYEIMRLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVE (SEQ ID NO:50)

```
>LCB1 v1.1-GSLCB1 v1.1(1GS1)
```

[illegible]

```
>LCB1 v1.1-PRO-LCB1 v1.1(1PRO1)
```

15 DKENILQKIYEIMKTLDQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVERAGSGSGSGSGSPVPSTPPTPSPSTPP
TPSPSPVPSTPPTPSPSTPPTPSPSPVPSTPPTPSPSTPPTPSPSASGDKENILQKIYEIMKTLDQLGHAEASMQVSDLIYEF
MKQGDERLLEEAERLLEE (SEQ ID NO:52)

```
>LCB3 v1.2-GS3-LCB3 v1.2 (3GS3)
```

20 NDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGGGSGGGGSGGGGSGGGG
SGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGNDDELHMQMTDLVYEALHFAKDEEIQK
HVFQLF EKATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO:53)

```
>LCB3 v1.2-PRO-LCB3 v1.2(3PRO3)
```

25 NDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSAGSGGGSGGSGSPVPSTPP
TPSPSTPPTSPSPVPSTPPTSPSTPPTSPSPVPSTPPTSPSTPPTSPSPASGNDELHMQMTDLVYEALHFAKDEEIQK
HVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO:54)

```
>LCB1 v1.1-GS-LCB3 v1.2(1GS3)
```

30 DKENILQKIYEIMKTLDQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVE
GGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGG
GGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGG
NDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEK
 ATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO:55)

```
>LCB3 v1.2-GS-LCB1 v1.1 (3GS1)
```

35 NDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGGSGGGSGGGSGGGG
SGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSDKENILQKIYEIMKTLDLGHAEASMQ
 VSDLIYEFMKQGDRLLEEAERLLEEVER (SEQ ID NO:56)

```
>LCB3 v1.2-10GS-LCB1 v1.1(LCB3-GS10-LCB1)
```

40 NDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSGGSGGSGDKENILQKI
YEIMKTLDLGLHAEASMQVSDLIYEFMKQGDERLLEEAEERLLEEVEER (SEQ ID NO: 57)

```
>LCB1 v1.1-PRO-LCB3 v1.2(1PRO3)
```

45 DKENILQKIYEIMKTLDQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVERAGSGGSGGSGGSPVPSTPPTPSPSTPP
TPSPSPVPSTPPTPSPSTPPTPSPSPVSTPPTPSPSTPPTPSPSASGNDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEK
ATKAYKNKDROKLEKVVEELKELLERLLS (SEQ ID NO:58)

```
>LCB3 v1.2-PRO-LCB1 v1.1(3PRO1)
```

50 NDDELHMQMTDLVYEALHFAKDEEIQKHVQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSAGSGGGSGGSPVPSTPP
TPSPSTPPTSPSPVPSTPPTSPSTPPTSPSPVPSTPPTSPSTPPTSPSPSASGDKENILQKIYEIMKTLDLGHAEASMQ
VSDLIYEFMKQGDRLLEEAERLLEEVER (SEQ ID NO:59)

```
>36175(5 LCB1 linker14)
```

55 DKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKGKDERLLEEAERLLEEVE
RRLDELGHAEASMRVSDLIYEFMKGKDERLLEEAERLLEEVE
RVSDLIYEFMKGKDERLLEEAERLLEEVE
RGSGSGSGSGSGSGSGSGDKEWILQKIYEIMRLLDELGHAEASM
RVSDLIYEFMKGKDERLLEEAERLLEEVE
RGSGSGSGSGSGSGSGSGDKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKGK

DERLLEEAERLLEEVERGSGSGSSGGSGSGSGDKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLE
EVER (SEQ ID NO:60)

Table 8. Daisy Chain Designs

5

Name	Protein	Annotated: X1, X2, X3, and X4 may be present or absent, and when present may be any sequence of 1 or more amino acids
1GS1	MEKKIGSSAWSHPQFEKGGGSGGGSGGSAWSPQFE KGGSGSSGGGGDKENILQKIYEIMKTLTDQLGHAEAS MQVSDLIYEFMKQGDERLLEEAERLLEEVEERGGGGSG GGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSG GGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSDK ENILQKIYEIMKTLTDQLGHAEASMQVSDLIYEFMKQ GDERLLEEAERLLEEVEER (SEQ ID NO: 193)	X1- DKENILQKIYEIMKTLTDQLGHAEASMQVSDLIYEF MKQGDERLLEEAERLLEEVEER (SEQ ID NO:4) - X2- DKENILQKIYEIMKTLTDQLGHAEASMQVSDLIYEF MKQGDERLLEEAERLLEEVEER (SEQ ID NO:4)
1PRO1	MEKKIGSSAWSHPQFEKGGGSGGGSGGSAWSPQFE KGGSGSSGGGGDKENILQKIYEIMKTLTDQLGHAEAS MQVSDLIYEFMKQGDERLLEEAERLLEEVEERAGSGG SGGSGGSPVPSTPPTPSPSTPPTPSPSPVPSTPPTP SPSTPPTPSPSPVPSTPPTPSPSTPPTPSPSPASGDK ENILQKIYEIMKTLTDQLGHAEASMQVSDLIYEFMKQ GDERLLEEAERLLEEVEER (SEQ ID NO: 194)	X1- DKENILQKIYEIMKTLTDQLGHAEASMQVSDLIYEF MKQGDERLLEEAERLLEEVEER (SEQ ID NO:4) - X2- DKENILQKIYEIMKTLTDQLGHAEASMQVSDLIYEF MKQGDERLLEEAERLLEEVEER (SEQ ID NO:4)
3GS3	MEKKIGSSAWSHPQFEKGGGSGGGSGGSAWSPQFE KGGSGSSGGGGNDELHMQMTDLVYEALHFAKDEEI QKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLER LLSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGG SGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSG SGGGSGNDELHMQMTDLVYEALHFAKDEEIQKHVF QLFEKATKAYKNKDRQKLEKVVEELKELLERLLS (S EQ ID NO: 195)	X1- NDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO:15) -X2- NDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO:15)
3PRO3	MEKKIGSSAWSHPQFEKGGGSGGGSGGSAWSPQFE KGGSGSSGGGGNDELHMQMTDLVYEALHFAKDEEI QKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLER LLSAGSGGGSGGGSPVPSTPPTPSPSTPPTPSPSP VPSTPPTPSPSTPPTPSPSPVPSTPPTPSPSTPPTP SPSASGNDELHMQMTDLVYEALHFAKDEEIQKHVF QLFEKATKAYKNKDRQKLEKVVEELKELLERLLS (S EQ ID NO: 196)	X1- NDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO:15) -X2- NDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO:15)
1GS3	MEKKIGSSAWSHPQFEKGGGSGGGSGGSAWSPQFE KGGSGSSGGGGDKENILQKIYEIMKTLTDQLGHAEAS MQVSDLIYEFMKQGDERLLEEAERLLEEVEERGGGGSG GGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSG GGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSD DELHMQMTDLVYEALHFAKDEEIQKHVFQLFEKATK AYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 197)	X1- DKENILQKIYEIMKTLTDQLGHAEASMQVSDLIYEF MKQGDERLLEEAERLLEEVEER (SEQ ID NO:4) - X2- NDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO:15)
3GS1	MEKKIGSSAWSHPQFEKGGGSGGGSGGSAWSPQFE KGGSGSSGGGGNDELHMQMTDLVYEALHFAKDEEI QKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLER LLSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGG SGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSG SGGGSGDKENILQKIYEIMKTLTDQLGHAEASMQVSD LIYEFMKQGDERLLEEAERLLEEVEER (SEQ ID NO: 198)	X1- NDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO:15) -X2- DKENILQKIYEIMKTLTDQLGHAEASMQVSDLIYEF MKQGDERLLEEAERLLEEVEER (SEQ ID NO:4)
1PRO3	MEKKIGSSAWSHPQFEKGGGSGGGSGGSAWSPQFE KGGSGSSGGGGDKENILQKIYEIMKTLTDQLGHAEAS MQVSDLIYEFMKQGDERLLEEAERLLEEVEERAGSGG SGGSGGSPVPSTPPTPSPSTPPTPSPSPVPSTPPTP SPSTPPTPSPSPVPSTPPTPSPSTPPTPSPSPASGN DELHMQMTDLVYEALHFAKDEEIQKHVFQLFEKATK AYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 199)	X1- DKENILQKIYEIMKTLTDQLGHAEASMQVSDLIYEF MKQGDERLLEEAERLLEEVEER (SEQ ID NO:4) - X2- NDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO:15)

NO: 199)	MEKKIGSSAWSHPQFEKGGSGGGSGGSAWHPQFEKGGSGSSGGGNDDELHMQMTDLVYEALHFAKDEEI QKHVFQLF EKATKAYKNKDRQKLEKVVEELKELLER LLSAGSGSGSGSGSPVPSTPPTSPSTPPTSPSP VPSTPPTSPSTPPTSPSPVPSTPPTSPSTPPTSPSASGDKENILQKIYEIMKTL DQ LGHAEASMQVSD LIYEFMKQ GDERLLEEAERLLEEVEE (SEQ ID NO: 200)	ID NO:15)	X1- NDELHMQMTDLVYEALHFAKDEEI QKHVFQLF EKATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO:15) -X2- DKENILQKIYEIMKTL DQ LGHAEASMQVSD LIYEF MKQ GDERLLEEAERLLEEVEE (SEQ ID NO:4)
3PRO1	MEKKISAWSHPQFEKGGSGGGSGGSAWHPQFEKG GSGSSGDKEWILQKIYEIMRLDELGHAEASMRVSD LIYEFMKK GDERLLEEAERLLEEVEE GGGSGGGGS GGGSGDKEWILQKIYEIMRLDELGHAEASMRVSD LIYEFMKK GDERLLEEAERLLEEVEE (SEQ ID NO: 201)		X1- DKEWILQKIYEIMRLDELGHAEASMRVSD LIYEF MKK GDERLLEEAERLLEEVEE (SEQ ID NO: 1) -X2- DKEWILQKIYEIMRLDELGHAEASMRVSD LIYEF MKK GDERLLEEAERLLEEVEE (SEQ ID NO: 1)
CSL- LCB1- GS15- LCB1	MEKKISAWSHPQFEKGGSGGGSGGSAWHPQFEKG GSGSSGNDELHMLMTDLVYEALHFAKDEEIKKRVF QLFELADKAYKNDRQKLEKVVEELKELLERLLSGG GSGSGGGSGGGSGNDDELHMLMTDLVYEALHFAKDE EIKKRVFQLFELADKAYKNDRQKLEKVVEELKELL ERLLS (SEQ ID NO: 202)		X1- NDELHMLMTDLVYEALHFAKDEEIKKRVFQLFEL ADKAYKNDRQKLEKVVEELKELLERLLS (SEQ ID NO:13) -X2- NDELHMLMTDLVYEALHFAKDEEIKKRVFQLFEL ADKAYKNDRQKLEKVVEELKELLERLLS (SEQ ID NO:13)
CSL- LCB3- GS15- LCB3	MEKKISAWSHPQFEKGGSGGGSGGSAWHPQFEKG GSGSSGDKEWILQKIYEIMRLDELGHAEASMRVSD LIYEFMKK GDERLLEEAERLLEEVEE GGGSGGGGS GGGSGDKEWILQKIYEIMRLDELGHAEASMRVSD LIYEFMKK GDERLLEEAERLLEEVEE (SEQ ID NO: 203)		X1- DKEWILQKIYEIMRLDELGHAEASMRVSD LIYEF MKK GDERLLEEAERLLEEVEE (SEQ ID NO: 1) -X2- DKEWILQKIYEIMRLDELGHAEASMRVSD LIYEF MKK GDERLLEEAERLLEEVEE (SEQ ID NO: 1)
CSL- LCB1- GS20- LCB1	MEKKISAWSHPQFEKGGSGGGSGGSAWHPQFEKG GSGSSGNDELHMLMTDLVYEALHFAKDEEIKKRVF QLFELADKAYKNDRQKLEKVVEELKELLERLLSGG GSGSGGGSGGGSGGGSGNDDELHMLMTDLVYEALH FAKDEEIKKRVFQLFELADKAYKNDRQKLEKVVEE LKELLERLLS (SEQ ID NO: 204)		X1- NDELHMLMTDLVYEALHFAKDEEIKKRVFQLFEL ADKAYKNDRQKLEKVVEELKELLERLLS (SEQ ID NO:13) -X2- NDELHMLMTDLVYEALHFAKDEEIKKRVFQLFEL ADKAYKNDRQKLEKVVEELKELLERLLS (SEQ ID NO:13)
CSL- LCB3- GS20- LCB3	MEKKISAWSHPQFEKGGSGSSGDKEWILQKIYEIMR LDELGHAEASMRVSD LIYEFMKK GDERLLEEAERL LEEVEE GSSGSSGSSGSSGSSGSDKEWILQKIY EIMRLDELGHAEASMRVSD LIYEFMKK GDERLLEE AERLLEEVEE GSSSGSSGSSSGSSGSDKEWIL QKIYEIMRLDELGHAEASMRVSD LIYEFMKK GDER LLEEAERLLEEVEE (SEQ ID NO: 205)		X1- DKEWILQKIYEIMRLDELGHAEASMRVSD LIYEF MKK GDERLLEEAERLLEEVEE (SEQ ID NO: 1) -X2- DKEWILQKIYEIMRLDELGHAEASMRVSD LIYEF MKK GDERLLEEAERLLEEVEE (SEQ ID NO: 1) -X3- DKEWILQKIYEIMRLDELGHAEASMRVSD LIYEF MKK GDERLLEEAERLLEEVEE (SEQ ID NO: 1)
CSL- LCB1- GS20- LCB1- GS20- LCB1	MEKKISAWSHPQFEKGGSGSSGNDELHMLMTDLVY EALHFAKDEEIKKRVFQLFELADKAYKNDRQKLEK VVEELKELLERLLSGSSGSSGSSGSSGSDKEWILQKIY EIMRLDELGHAEASMRVSD LIYEFMKK GDERLLEE AERLLEEVEE GSSSGSSGSSSGSSGSDKEWILQKIY EIMRLDELGHAEASMRVSD LIYEFMKK GDER LLEEAERLLEEVEE (SEQ ID NO: 206)		X1- NDELHMLMTDLVYEALHFAKDEEIKKRVFQLFEL ADKAYKNDRQKLEKVVEELKELLERLLS (SEQ ID NO:13) -X2- DDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELA DKAYKNDRQKLEKVVEELKELLERLLS (SEQ ID NO:13) -X3- NDELHMLMTDLVYEALHFAKDEEIKKRVFQLFEL ADKAYKNDRQKLEKVVEELKELLERLLS (SEQ ID NO:13)
CSL- LCB3- GS20- LCB3- GS20- LCB3	MEKKISAWSHPQFEKGGSGGGSGGSAWHPQFEKG GSGSSGDKEWILQKIYEIMRLDELGHAEASMRVSD LIYEFMKK GDERLLEEAERLLEEVEE GSGAGSPAGS PTSTGTSTSGDKEWILQKIYEIMRLDELGHAEASMRVSD LIYEFMKK GDERLLEEAERLLEEVEE (SEQ ID NO: 207)		X1- DKEWILQKIYEIMRLDELGHAEASMRVSD LIYEF MKK GDERLLEEAERLLEEVEE (SEQ ID NO: 1) -X2- DKEWILQKIYEIMRLDELGHAEASMRVSD LIYEF MKK GDERLLEEAERLLEEVEE (SEQ ID NO: 1)
CSL- LCB1- XTENx 2	MEKKISAWSHPQFEKGGSGGGSGGSAWHPQFEKG GSGSSGDKEWILQKIYEIMRLDELGHAEASMRVSD LIYEFMKK GDERLLEEAERLLEEVEE GSGAGSPAGS PTSTGTSTSGDKEWILQKIYEIMRLDELGHAEASMRVSD LIYEFMKK GDERLLEEAERLLEEVEE (SEQ ID NO: 207)		x1- DKEWILQKIYEIMRLDELGHAEASMRVSD LIYEF MKK GDERLLEEAERLLEEVEE (SEQ ID NO: 1)
CSL- LCB1- XTENx	MEKKISAWSHPQFEKGGSGGGSGGSAWHPQFEKG GSGSSGDKEWILQKIYEIMRLDELGHAEASMRVSD LIYEFMKK GDERLLEEAERLLEEVEE GSGAGSPAGS PTSTGTSTSGDKEWILQKIYEIMRLDELGHAEASMRVSD LIYEFMKK GDERLLEEAERLLEEVEE (SEQ ID NO: 207)		x1- DKEWILQKIYEIMRLDELGHAEASMRVSD LIYEF MKK GDERLLEEAERLLEEVEE (SEQ ID NO: 1)

[illegible]

GS_2X	GGSSGGSSGGSSGGSDKENILQKIYEIMKTLEQLGHA AEASMQVSDLIYEFMKQGDRLLEEAERLLEEVEE (SEQ ID NO: 215)	NO: 8) -X2- DKENILQKIYEIMKTLEQLGHAESMQVSDLIYEF MKQGDRLLEEAERLLEEVEE (SEQ ID NO: 8)
LCB1_	MEKKISAWSHPPQFEKGGGSGGGSGGSAWSHPPQFEK GGSSGDKENILQKIYEIMKTLEQLGHAESMQVSD LIYEFMKQGDRLLEEAERLLEEVEE GGGSSAGSPTS	X1- DKENILQKIYEIMKTLEQLGHAESMQVSDLIYEF MKQGDRLLEEAERLLEEVEE (SEQ ID NO: 8) -
v1.3_	TGTSSATPSGSGTGGDKENILQKIYEIMKTLEQLGHA AEASMQVSDLIYEFMKQGDRLLEEAERLLEEVEE (SEQ ID NO: 216)	X2- DKENILQKIYEIMKTLEQLGHAESMQVSDLIYEF MKQGDRLLEEAERLLEEVEE (SEQ ID NO: 8)
XTEN_		
2X		
LCB1_	MEKKISAWSHPPQFEKGGGSGGGSGGSAWSHPPQFEK GGSSGDKENILQKIYEIMKTLEQLGHAESMQVSD LIYEFMKQGDRLLEEAERLLEEVEE GGGSSGAAAK EAAAKEAAKGGSSGDKENILQKIYEIMKTLEQLGHA AEASMQVSDLIYEFMKQGDRLLEEAERLLEEVEE (SEQ ID NO: 217)	X1- DKENILQKIYEIMKTLEQLGHAESMQVSDLIYEF MKQGDRLLEEAERLLEEVEE (SEQ ID NO: 8) -
v1.3_		X2- DKENILQKIYEIMKTLEQLGHAESMQVSDLIYEF MKQGDRLLEEAERLLEEVEE (SEQ ID NO: 8)
EAAAK_		
2X		
LCB1_	MEKKISAWSHPPQFEKGGGSGGGSGGSAWSHPPQFEK GGSSGDKENILQKIYEIMKTLEQLGHAESMQVSD LIYEFMKQGDRLLEEAERLLEEVEE GGGSSGPSTPP TPSPSTPPTPSPSPGGSSGDKENILQKIYEIMKTLE QLGHAESMQVSDLIYEFMKQGDRLLEEAERLLEEVEE (SEQ ID NO: 218)	X1- DKENILQKIYEIMKTLEQLGHAESMQVSDLIYEF MKQGDRLLEEAERLLEEVEE (SEQ ID NO: 8) -
v1.3_		X2- DKENILQKIYEIMKTLEQLGHAESMQVSDLIYEF MKQGDRLLEEAERLLEEVEE (SEQ ID NO: 8)
Pro_2		
X		
LCB1_	MEKKISAWSHPPQFEKGGGSGGGSGGSAWSHPPQFEK GGSSGDKENILQKIYEIMKTLEQLGHAESMQVSD LIYEFMKQGDRLLEEAERLLEEVEE GGGSSGQIFVK TLTGKTITLEVEPSDTIENVKAKIQDKEGIPPDQQR LIFAGKQLEDGRTLSDYNIQKESTLHLVLRRLGGGG SSGDKENILQKIYEIMKTLEQLGHAESMQVSDLIY EFMKQGDRLLEEAERLLEEVEE (SEQ ID NO: 219)	X1- DKENILQKIYEIMKTLEQLGHAESMQVSDLIYEF MKQGDRLLEEAERLLEEVEE (SEQ ID NO: 8) -
v1.3_		X2- DKENILQKIYEIMKTLEQLGHAESMQVSDLIYEF MKQGDRLLEEAERLLEEVEE (SEQ ID NO: 8)
Ub_2X		
LCB1_	MEKKISAWSHPPQFEKGGGSGGGSGGSAWSHPPQFEK GGSSGDKENILQKIYEIMKTLEQLGHAESMQVSD LIYEFMKQGDRLLEEAERLLEEVEE GGGSSAGSPTS TGTSSATPSGSGTGGDKENILQKIYEIMKTLEQLGHA AEASMQVSDLIYEFMKQGDRLLEEAERLLEEVEE GGGSSAGSPTSTGTSSATPSGSGTGGDKENILQKIYEI MKTLEQLGHAESMQVSDLIYEFMKQGDRLLEEAERLLEEVEE (SEQ ID NO: 220)	X1- DKENILQKIYEIMKTLEQLGHAESMQVSDLIYEF MKQGDRLLEEAERLLEEVEE (SEQ ID NO: 8) -
v1.3_		X2- DKENILQKIYEIMKTLEQLGHAESMQVSDLIYEF MKQGDRLLEEAERLLEEVEE (SEQ ID NO: 8) -
XTEN_		X3- DKENILQKIYEIMKTLEQLGHAESMQVSDLIYEF MKQGDRLLEEAERLLEEVEE (SEQ ID NO: 8)
3X		
LCB1_	MEKKISAWSHPPQFEKGGGSGGGSGGSAWSHPPQFEK GGSSGDKENILQKIYEIMKTLEQLGHAESMQVSD LIYEFMKQGDRLLEEAERLLEEVEE GGGSSGAAAK EAAAKEAAKGGSSGDKENILQKIYEIMKTLEQLGHA AEASMQVSDLIYEFMKQGDRLLEEAERLLEEVEE GGGSSGAAAKEAAKGGSSGDKENILQKIYEI MKTLEQLGHAESMQVSDLIYEFMKQGDRLLEEAERLLEEVEE (SEQ ID NO: 221)	X1- DKENILQKIYEIMKTLEQLGHAESMQVSDLIYEF MKQGDRLLEEAERLLEEVEE (SEQ ID NO: 8) -
v1.3_		X2- DKENILQKIYEIMKTLEQLGHAESMQVSDLIYEF MKQGDRLLEEAERLLEEVEE (SEQ ID NO: 8) -
EAAAK_		X3- DKENILQKIYEIMKTLEQLGHAESMQVSDLIYEF MKQGDRLLEEAERLLEEVEE (SEQ ID NO: 8)
3X		
LCB1_	MEKKISAWSHPPQFEKGGGSGGGSGGSAWSHPPQFEK GGSSGDKENILQKIYEIMKTLEQLGHAESMQVSD LIYEFMKQGDRLLEEAERLLEEVEE GGGSSGPSTPP TPSPSTPPTPSPSPGGSSGDKENILQKIYEIMKTLE QLGHAESMQVSDLIYEFMKQGDRLLEEAERLLEEVEE GGGSSGPSTPPTPSPSGGSDKEN ILQKIYEIMKTLEQLGHAESMQVSDLIYEFMKQGD ERLLEEAERLLEEVEE (SEQ ID NO: 222)	X1- DKENILQKIYEIMKTLEQLGHAESMQVSDLIYEF MKQGDRLLEEAERLLEEVEE (SEQ ID NO: 8) -
v1.3_		X2- DKENILQKIYEIMKTLEQLGHAESMQVSDLIYEF MKQGDRLLEEAERLLEEVEE (SEQ ID NO: 8) -
Pro_3		X3- DKENILQKIYEIMKTLEQLGHAESMQVSDLIYEF MKQGDRLLEEAERLLEEVEE (SEQ ID NO: 8)
X		
LCB1_	MEKKISAWSHPPQFEKGGGSGGGSGGSAWSHPPQFEK GGSSGDKENILQKIYEIMKTLEQLGHAESMQVSD LIYEFMKQGDRLLEEAERLLEEVEE GGGSSGQIFVK TLTGKTITLEVEPSDTIENVKAKIQDKEGIPPDQQR LIFAGKQLEDGRTLSDYNIQKESTLHLVLRRLGGGG SSGDKENILQKIYEIMKTLEQLGHAESMQVSDLIY EFMKQGDRLLEEAERLLEEVEE GGGSSGQIFVKTLT	X1DKENILQKIYEIMKTLEQLGHAESMQVSDLIY EFMKQGDRLLEEAERLLEEVEE (SEQ ID NO: 8) -X2- DKENILQKIYEIMKTLEQLGHAESMQVSDLIYEF MKQGDRLLEEAERLLEEVEE (SEQ ID NO: 8) -
v1.3_		X3- DKENILQKIYEIMKTLEQLGHAESMQVSDLIYEF
Ub_3X		

	GKTTITLEVEPSDTIENVKAKIQDKEGIPPDQORLIF AGKQLEDGRTLSDYNIQKESTLHLVLRRLGGSSSG DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFM KQGDERLLEEAERLLEEVEVER (SEQ ID NO: 223)	MKQGDERLLEEAERLLEEVEVER (SEQ ID NO: 8)
1GS1 _NTS	MEKKISAWSHQPFEKGGSSGGSSGSSAWSHQPFEK GGSSSGDKENVLQKIYEIMKELERLGHAEASMQVSD LIYEFMKTNDENLLEEAERLLEEVRKGGSSGGSSG GGSSGGSSGGSSSGDKENVLQKIYEIMKELERLGH AEASMQVSDLIYEFMKTNDENLLEEAERLLEEVRK (SEQ ID NO: 224)	X1- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTNDENLLEEAERLLEEVRK (SEQ ID NO: 135) -X2- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTNDENLLEEAERLLEEVRK (SEQ ID NO: 135)
1Pro1 _NTS	MEKKISAWSHQPFEKGGSSGGSSGSSAWSHQPFEK GGSSSGDKENVLQKIYEIMKELERLGHAEASMQVSD LIYEFMKTNDENLLEEAERLLEEVRKGGSSGPSTPP TPSPSTPPTPSPSPGGSSSGDKENVLQKIYEIMKE RLGHAEASMQVSDLIYEFMKTNDENLLEEAERLLEE VKR (SEQ ID NO: 225)	X1- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTNDENLLEEAERLLEEVRK (SEQ ID NO: 135) -X2- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTNDENLLEEAERLLEEVRK (SEQ ID NO: 135)
3GS3 _NTS	MEKKISAWSHQPFEKGGSSGGSSGSSAWSHQPFEK GGSSSGNDELHMQMTDLVYEALHFAKDEEFQKHVF QLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGG SSGGSSGGSSGGSSGGSSGNDELHMQMTDLV YEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLE KVVEELKELLERLLS (SEQ ID NO: 226)	X1- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155) -X2- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155)
3Pro3 _NTS	MEKKISAWSHQPFEKGGSSGGSSGSSAWSHQPFEK GGSSSGNDELHMQMTDLVYEALHFAKDEEFQKHVF QLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGG SSGPSTPPTPSPSTPPTPSPSPGGSSGNDELHMQMT DLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDR QKLEKVVEELKELLERLLS (SEQ ID NO: 227)	X1- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155) -X2- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155)
1GS1 _CTS	MEKKIDKENVLQKIYEIMKELERLGHAEASMQVSD LIYEFMKTNDENLLEEAERLLEEVRKGGSSGGSSG SSGGSSGGSSGGSSSGDKENVLQKIYEIMKELERLGH AEASMQVSDLIYEFMKTNDENLLEEAERLLEEVRKGG SSGSSGSAWSHQPFEKGGSSGGSSGSSAWSHQPFEK (SEQ ID NO: 228)	X1- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTNDENLLEEAERLLEEVRK (SEQ ID NO: 135) -X2- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTNDENLLEEAERLLEEVRK (SEQ ID NO: 135) -X3
1Pro1 _CTS	MEKKIDKENVLQKIYEIMKELERLGHAEASMQVSD LIYEFMKTNDENLLEEAERLLEEVRKGGSSGPSTPPT PSPSTPPTPSPSPGGSSSGDKENVLQKIYEIMKELER LGHAEASMQVSDLIYEFMKTNDENLLEEAERLLEEVR KGGSSGSSGSAWSHQPFEKGGSSGGSSGSSAWSHQP FEK (SEQ ID NO: 229)	X1- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTNDENLLEEAERLLEEVRK (SEQ ID NO: 135) -X2- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTNDENLLEEAERLLEEVRK (SEQ ID NO: 135) -X3
3GS3 _CTS	MEKKINDELHMQMTDLVYEALHFAKDEEFQKHVFQ LFEKATKAYKNKDRQKLEKVVEELKELLERLLSGG SSGGSSGGSSGGSSGGSSGNDELHMQMTDLVY EALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEK VVEELKELLERLLSGGSSGSSGSAWSHQPFEKGGSSG GGSSGSAWSHQPFEK (SEQ ID NO: 230)	X1- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155) -X2- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155) -X3
3Pro3 _CTS	MEKKINDELHMQMTDLVYEALHFAKDEEFQKHVFQ LFEKATKAYKNKDRQKLEKVVEELKELLERLLSGG SGPSTPPTPSPSTPPTPSPSPGGSSGNDELHMQMT DLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQ KLEKVVEELKELLERLLSGGSSGSSGSAWSHQPFEK GGSSGGSSGSSGSAWSHQPFEK (SEQ ID NO: 231)	X1- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155) -X2- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155) -X3
1GS1G S1_NT	MEKKISAWSHQPFEKGGSSSGDKENVLQKIYEIMK ELERLGHAEASMQVSDLIYEFMKTNDENLLEEAERL LEEVRKGGSSGGSSGGSSGGSSGGSSSGDKENV	X1- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTNDENLLEEAERLLEEVRK (SEQ ID NO: 135)

S	LQKIYEIMKELERLGHAEASMQVSDLIYEFMKTDE NLLEEAERLLEEVRKGGSSGGSSGGSSGGSSGG SSGDKENVLQKIYEIMKELERLGHAEASMQVSDLI YEFMKTDENLLEEAERLLEEVR (SEQ ID NO: 232)	135)-X2- DENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTDENLLEEAERLLEEVR (SEQ ID NO: 135)-X3- DENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTDENLLEEAERLLEEVR (SEQ ID NO: 135)
1Pro1 Pro1_ NTS	MEKKISAWSHQPFEKGGSSGDKENVLQKIYEIMK ELERLGHAEASMQVSDLIYEFMKTDENLLEEAERL LEEVRKGGSSGPSTPPTPSPSTPPTPSPGGSSGD KENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKT TKDENLLEEAERLLEEVRKGGSSGPSTPPTPSPSTP PTPSPSGSSGDKENVLQKIYEIMKELERLGHAEAS MQVSDLIYEFMKTDENLLEEAERLLEEVR (SEQ ID NO: 233)	X1- DENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTDENLLEEAERLLEEVR (SEQ ID NO: 135)-X2- DENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTDENLLEEAERLLEEVR (SEQ ID NO: 135)-X3- DENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTDENLLEEAERLLEEVR (SEQ ID NO: 135)
3GS3G S3_NT S	MEKKISAWSHQPFEKGGSSGNLDELHMOMTDLVY EALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEK VVEELKELLERLLSGSSGGSSGGSSGGSSGGSSGG SSGNLDELHMOMTDLVYEALHFAKDEEFQKHVFQLF EKATKAYKNKDRQKLEKVVEELKELLERLLSGSSG GGSSGGSSGGSSGGSSGNLDELHMOMTDLVYEA LHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKV EELKELLERLLS (SEQ ID NO: 234)	N1- DELHMOMTDLVYEALHFAKDEEFQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155)-X2- DELHMOMTDLVYEALHFAKDEEFQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155)-X3- DELHMOMTDLVYEALHFAKDEEFQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155)
3Pro3 Pro3_ NTS	MEKKISAWSHQPFEKGGSSGNLDELHMOMTDLVY EALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEK VVEELKELLERLLSGSSGPSTPPTPSPSTPPTPSP SPGGSSGNLDELHMOMTDLVYEALHFAKDEEFQKH VQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSG SSSGSPSTPPTPSPSTPPTPSPSGSSGNLDELHMOM TDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDR QKLEKVVEELKELLERLLS (SEQ ID NO: 235)	N1- DELHMOMTDLVYEALHFAKDEEFQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155)-X2- DELHMOMTDLVYEALHFAKDEEFQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155)-X3- DELHMOMTDLVYEALHFAKDEEFQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155)
1GS1G S1_CT S	MEKKIDKENVLQKIYEIMKELERLGHAEASMQVSDLI YEFMKTDENLLEEAERLLEEVRKGGSSGGSSGG SSGGSSGGSSGDKENVLQKIYEIMKELERLGHAEAS MQVSDLIYEFMKTDENLLEEAERLLEEVRKGGSSGG SSGGSSGGSSGGSSGDKENVLQKIYEIMKELERLGHAEAS MQVSDLIYEFMKTDENLLEEAERLLEEVRKGGSSGSAW SHQPFEK (SEQ ID NO: 236)	X1- DENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTDENLLEEAERLLEEVR (SEQ ID NO: 135)-X2- DENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTDENLLEEAERLLEEVR (SEQ ID NO: 135)-X3- DENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTDENLLEEAERLLEEVR (SEQ ID NO: 135)-X4
1Pro1 Pro1_ CTS	MEKKIDKENVLQKIYEIMKELERLGHAEASMQVSDLI YEFMKTDENLLEEAERLLEEVRKGGSSGPSTPPT PSPSTPPTPSPSGSSGDKENVLQKIYEIMKELERL GHAEASMQVSDLIYEFMKTDENLLEEAERLLEEVR KGGSSGPSTPPTPSPSTPPTPSPSGSSGDKENVL QKIYEIMKELERLGHAEASMQVSDLIYEFMKTDE NLLEEAERLLEEVRKGGSSGSAWSHQPFEK (SEQ ID NO: 237)	N1- DENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTDENLLEEAERLLEEVR (SEQ ID NO: 135)-X2- DENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTDENLLEEAERLLEEVR (SEQ ID NO: 135)-X3- DENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTDENLLEEAERLLEEVR (SEQ ID NO: 135)-X4
3GS3G S3_CT S	MEKKINLDELHMOMTDLVYEALHFAKDEEFQKHVFQ LFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGS SGSSGGSSGGSSGGSSGNLDELHMOMTDLVY EALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEK	N1- DELHMOMTDLVYEALHFAKDEEFQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155)-X2-

	VVEELKELLERLLSSGGSSGGSSGGSSGGSSGGSSGGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLF EKGATKAYKNKDRQKLEKVVEELKELLERLLSSGGSSGSAWSHPQFEK (SEQ ID NO: 238)	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLF ATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155)-X3- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLF ATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155)-X4
3Pro3 Pro3 CTS	MEKKINLDELHMQMTDLVYEALHFAKDEEFQKHVFQ LFKATKAYKNKDRQKLEKVVEELKELLERLLSSGSGPSTPPTPSPSTPPTPSPSPGGSSGNLDELHMQMT DLVYEALHFAKDEEFQKHVFQLFKATKAYKNKDRQ KLEKVVEELKELLERLLSSGSGPSTPPTPSPSTPPTPSPSPGGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLF KATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 239)	X1- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLF ATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155)-X2- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLF ATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155)-X3- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLF ATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155)-X4
1GS3 NTS	MEKKISAWSHPQFEKGGSSGGSSGGSSAWSHPQFEK GSGSSGDKENVLQKIYEIMKELERLGHAEASMQVSD LIYEFMKTNDENLLEEAERLLEEVRGSGSSGGSSG GGSSGGSSGGSSGNLDELHMQMTDLVYEALHFAK DEEFQKHVFQLFKATKAYKNKDRQKLEKVVEELKE LLERLLS (SEQ ID NO: 240)	X1- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTNDENLLEEAERLLEEVR (SEQ ID NO: 135)-X2- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLF ATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155)
1Pro3 NTS	MEKKISAWSHPQFEKGGSSGGSSGGSSAWSHPQFEK GSGSSGDKENVLQKIYEIMKELERLGHAEASMQVSD LIYEFMKTNDENLLEEAERLLEEVRGSGSSGPSTP TPSPSTPPTPSPSPGGSSGNLDELHMQMTDLVYEAL HFAKDEEFQKHVFQLFKATKAYKNKDRQKLEKVVE ELKELLERLLS (SEQ ID NO: 241)	X1- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTNDENLLEEAERLLEEVR (SEQ ID NO: 135)-X2- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLF ATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155)
3GS1 NTS	MEKKISAWSHPQFEKGGSSGGSSGGSSAWSHPQFEK GSGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVF QLFEKATKAYKNKDRQKLEKVVEELKELLERLLSSG SSGGSSGGSSGGSSGGSSGDKENVLQKIYEIM KELERLGHAEASMQVSDLIYEFMKTNDENLLEEAER LLEEVR (SEQ ID NO: 242)	X1- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLF ATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155)-X2- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTNDENLLEEAERLLEEVR (SEQ ID NO: 135)
3Pro1 NTS	MEKKISAWSHPQFEKGGSSGGSSGGSSAWSHPQFEK GSGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVF QLFEKATKAYKNKDRQKLEKVVEELKELLERLLSSG SSGPSTPPTPSPSTPPTPSPSPGGSSGDKENVLQKI YEIMKELERLGHAEASMQVSDLIYEFMKTNDENLLE EAERLLEEVR (SEQ ID NO: 243)	X1- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLF ATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155)-X2- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTNDENLLEEAERLLEEVR (SEQ ID NO: 135)
1GS3 CTS	MEKKIDKENVLQKIYEIMKELERLGHAEASMQVSD LIYEFMKTNDENLLEEAERLLEEVRGSGSSGGSSG SSGGSSGGSSGGSSGNLDELHMQMTDLVYEALHFAK DEEFQKHVFQLFKATKAYKNKDRQKLEKVVEELKE LLERLLSSGSSGSSAWSHPQFEKGGSSGGSSGSSA WSHPQFEK (SEQ ID NO: 244)	X1- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLF ATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155)-X3
1Pro3 CTS	MEKKIDKENVLQKIYEIMKELERLGHAEASMQVSD LIYEFMKTNDENLLEEAERLLEEVRGSGSSGPSTPPT PSPSTPPTPSPSPGGSSGNLDELHMQMTDLVYEALH FAKDEEFQKHVFQLFKATKAYKNKDRQKLEKVVEE LKELLERLLSSGSSGSSAWSHPQFEKGGSSGGSSG SAWSHPQFEK (SEQ ID NO: 245)	X1- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTNDENLLEEAERLLEEVR (SEQ ID NO: 135)-X2- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLF ATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155)-X3
3GS1 CTS	MEKKINLDELHMQMTDLVYEALHFAKDEEFQKHVFQ LFKATKAYKNKDRQKLEKVVEELKELLERLLSSG SSGGSSGGSSGGSSGGSSGDKENVLQKIYEIMK ELERLGHAEASMQVSDLIYEFMKTNDENLLEEAERL	X1- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLF ATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155)-X2-

	LEEVRKGGSSGSSGSAWSHPQFEKGGGSGGGSSGSSGSAWSHPQFEK (SEQ ID NO: 246)	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVR (SEQ ID NO: 135) -X3
3Pro1 _CTS	MEKKINLDELHMQMTDLVYEALHFAKDEEFQKHVFQ LFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSGPSTPPTPSPSTPPTPSPSPGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTCDENLLEE AERLLEEVRKGGSSGSSGSAWSHPQFEKGGGSGGGSSGSAWSHPQFEK (SEQ ID NO: 247)	X1- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQ LFEKATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155) -X2- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVR (SEQ ID NO: 135) -X3
3- GS10- 1- L_NTS	MEKKISAWSHPOFEKGGGSGGGSSGSSGSAWSHPQFEKGSGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQ LFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSGGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTCDENLLEE AERLLEEVR (SEQ ID NO: 248)	X1- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQ LFEKATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155) -X2- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVR (SEQ ID NO: 135)
3- GS10- 1_NTS	MEKKISAWSHPOFEKGGGSGGGSSGSSGSAWSHPQFEKGSGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQ LFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSSGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTCDENLLEE AERLLEEVR (SEQ ID NO: 249)	X1- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQ LFEKATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155) -X2- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVR (SEQ ID NO: 135)
3- GS15- 1_NTS	MEKKISAWSHPOFEKGGGSGGGSSGSSGSAWSHPQFEKGSGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQ LFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSSGGSSGSGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTCDENLLEE AERLLEEVR (SEQ ID NO: 250)	X1- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQ LFEKATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155) -X2- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVR (SEQ ID NO: 135)
3- GS20- 1_NTS	MEKKISAWSHPOFEKGGGSGGGSSGSSGSAWSHPQFEKGSGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQ LFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSSGGSSGSGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTCDENLLEE AERLLEEVR (SEQ ID NO: 251)	X1- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQ LFEKATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155) -X2- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVR (SEQ ID NO: 135)
1- GS10- 1_NTS	MEKKISAWSHPOFEKGGGSGGGSSGSSGSAWSHPQFEKGSGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTCDENLLEE AERLLEEVRKGGSSGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTCDENLLEE AERLLEEVR (SEQ ID NO: 252)	X1- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVR (SEQ ID NO: 135) -X2- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVR (SEQ ID NO: 135)
1- GS15- 1_NTS	MEKKISAWSHPOFEKGGGSGGGSSGSSGSAWSHPQFEKGSGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTCDENLLEE AERLLEEVRKGGSSGGSSGSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTCDENLLEE AERLLEEVR (SEQ ID NO: 253)	X1- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVR (SEQ ID NO: 135) -X2- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVR (SEQ ID NO: 135)
1- GS20- 1_NTS	MEKKISAWSHPOFEKGGGSGGGSSGSSGSAWSHPQFEKGSGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTCDENLLEE AERLLEEVRKGGSSGGSSGQVSDLIYEFMKTCDENLLEE AERLLEEVR (SEQ ID NO: 254)	X1- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVR (SEQ ID NO: 135) -X2- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVR (SEQ ID NO: 135)
2- 1_GS1 0	MSKIKSAWSHPQFEKGGGSGGGSSGSSGSAWSHPQFEKGSGSSGELEEQVMHVLDQVSELAHELLHKLGTGEELE RAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSSGGSSGDKENVLQKIYEIMKE	X1- ELEEQVMHVLDQVSELAHELLHKLGTGEELE RAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK (SEQ ID NO: 101) -X2-

	RLGHAEASMQVSDLIYEFMKTCDERLLEEAERLLEE VKR (SEQ ID NO: 255)	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTCDERLLEEAERLLEEVKR (SEQ ID NO: 125)
2- 1_GS1 5	MSKIKSAWSHPQFEKGGGSGGGSGGSAWSHPQFEKG GSGSSGELEEQVMHVLDQVSELAHELLHKLGTGEELE RAAYFNWWATEMMLELIKSDDEREIREIEEEEARRIL EHLEELARKGGSSGGGSSGGSSGDKENVLQKIYEI MKELERLGHAEASMQVSDLIYEFMKTCDERLLEEA RLLEEVKR (SEQ ID NO: 256)	X1- ELEEQVMHVLDQVSELAHELLHKLGTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE ELARK (SEQ ID NO: 101)-X2- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTCDERLLEEAERLLEEVKR (SEQ ID NO: 125)
2- 1_GS2 0	MSKIKSAWSHPQFEKGGGSGGGSGGSAWSHPQFEKG GSGSSGELEEQVMHVLDQVSELAHELLHKLGTGEELE RAAYFNWWATEMMLELIKSDDEREIREIEEEEARRIL EHLEELARKGGSSGGGSSGGSSGDKENVLQ KIYEIMKELERLGHAEASMQVSDLIYEFMKTCDERL LEEAERLLEEVKR (SEQ ID NO: 257)	X1- ELEEQVMHVLDQVSELAHELLHKLGTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE ELARK (SEQ ID NO: 101)-X2- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTCDERLLEEAERLLEEVKR (SEQ ID NO: 125)
2-2- 1_GS1 0	MSKIKSAWSHPQFEKGGGSGGGSGGSAWSHPQFEKG GSGSSGELEEQVMHVLDQVSELAHELLHKLGTGEELE RAAYFNWWATEMMLELIKSDDEREIREIEEEEARRIL EHLEELARKGGSSGGGSSGELEEQVMHVLDQVSELA HELLHKLGTGEELERAAYFNWWATEMMLELIKSDDER EIREIEEEEARRILEHLEELARKGGSSGGGSSGDKEN VLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTCD ERLLEEAERLLEEVKR (SEQ ID NO: 258)	X1- ELEEQVMHVLDQVSELAHELLHKLGTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE ELARK (SEQ ID NO: 101)-X2- ELEEQVMHVLDQVSELAHELLHKLGTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE ELARK (SEQ ID NO: 101)-X3
2-2- 1_GS1 5	MSKIKSAWSHPQFEKGGGSGGGSGGSAWSHPQFEKG GSGSSGELEEQVMHVLDQVSELAHELLHKLGTGEELE RAAYFNWWATEMMLELIKSDDEREIREIEEEEARRIL EHLEELARKGGSSGGGSSGGSSGELEEQVMHVLDQ VSELAHELLHKLGTGEELERAAYFNWWATEMMLELIK SDDEREIREIEEEEARRILEHLEELARKGGSSGGGSS GGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSD LIYEFMKTCDERLLEEAERLLEEVKR (SEQ ID NO: 259)	X1- ELEEQVMHVLDQVSELAHELLHKLGTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE ELARK (SEQ ID NO: 101)-X2- ELEEQVMHVLDQVSELAHELLHKLGTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE ELARK (SEQ ID NO: 101)-X3
2-2- 1_GS2 0	MSKIKSAWSHPQFEKGGGSGGGSGGSAWSHPQFEKG GSGSSGELEEQVMHVLDQVSELAHELLHKLGTGEELE RAAYFNWWATEMMLELIKSDDEREIREIEEEEARRIL EHLEELARKGGSSGGGSSGGGSSGELEEQVMHVLDQ VSELAHELLHKLGTGEELERAAYFNWWATEMM LELIKSDDEREIREIEEEEARRILEHLEELARKGGSS GGGSSGGGSSGGSSGDKENVLQKIYEIMKELERLGH AEASMQVSDLIYEFMKTCDERLLEEAERLLEEVKR (SEQ ID NO: 260)	X1- ELEEQVMHVLDQVSELAHELLHKLGTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE ELARK (SEQ ID NO: 101)-X2- ELEEQVMHVLDQVSELAHELLHKLGTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE ELARK (SEQ ID NO: 101)-X3
2- 2_GS1 0	MSKIKSAWSHPQFEKGGGSGGGSGGSAWSHPQFEKG GSGSSGELEEQVMHVLDQVSELAHELLHKLGTGEELE RAAYFNWWATEMMLELIKSDDEREIREIEEEEARRIL EHLEELARKGGSSGGGSSGELEEQVMHVLDQVSELA HELLHKLGTGEELERAAYFNWWATEMMLELIKSDDER EIREIEEEEARRILEHLEELARK (SEQ ID NO: 261)	X1- ELEEQVMHVLDQVSELAHELLHKLGTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE ELARK (SEQ ID NO: 101)-X2- ELEEQVMHVLDQVSELAHELLHKLGTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE ELARK (SEQ ID NO: 101)
2- 2_GS1 5	MSKIKSAWSHPQFEKGGGSGGGSGGSAWSHPQFEKG GSGSSGELEEQVMHVLDQVSELAHELLHKLGTGEELE RAAYFNWWATEMMLELIKSDDEREIREIEEEEARRIL EHLEELARKGGSSGGGSSGGGSSGELEEQVMHVLDQ VSELAHELLHKLGTGEELERAAYFNWWATEMMLELIK SDDEREIREIEEEEARRILEHLEELARK (SEQ ID NO: 262)	X1- ELEEQVMHVLDQVSELAHELLHKLGTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE ELARK (SEQ ID NO: 101)-X2- ELEEQVMHVLDQVSELAHELLHKLGTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE ELARK (SEQ ID NO: 101)
2- 2_GS2 0	MSKIKSAWSHPQFEKGGGSGGGSGGSAWSHPQFEKG GSGSSGELEEQVMHVLDQVSELAHELLHKLGTGEELE RAAYFNWWATEMMLELIKSDDEREIREIEEEEARRIL EHLEELARKGGSSGGGSSGGGSSGGGSSGELEEQVM HVLDQVSELAHELLHKLGTGEELERAAYFNWWATEMM LELIKSDDEREIREIEEEEARRILEHLEELARK (SEQ	X1- ELEEQVMHVLDQVSELAHELLHKLGTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE ELARK (SEQ ID NO: 101)-X2- ELEEQVMHVLDQVSELAHELLHKLGTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE

	ID NO: 263) MSKIKSAWSHPQFEKGGGSGGGSGGSAWSHPQFEKG GSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELE RAAYFNWWATEMMLELIKSDDEREIREIEEEEARRIL EHLEELARKGGSSGGGSSGELEEQVMHVLDQVSELA HELLHKLTGEELERAAYFNWWATEMMLELIKSDDER EIREIEEEEARRILEHLEELARKGGSSGGGSSGELEE QVMHVLDQVSELAHELLHKLTGEELERAAYFNWWAT EMMLELIKSDDEREIREIEEEEARRILEHLEELARK (SEQ ID NO: 264) MSKIKSAWSHPQFEKGGGSGGGSGGSAWSHPQFEKG GSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELE RAAYFNWWATEMMLELIKSDDEREIREIEEEEARRIL EHLEELARKGGSSGGGSSGGGSSGELEEQVMHVLDQ VSELAHELLHKLTGEELERAAYFNWWATEMMLELIK SDDEREIREIEEEEARRILEHLEELARKGGSSGGGSS GGGSSGELEEQVMHVLDQVSELAHELLHKLTGEELE RAAYFNWWATEMMLELIKSDDEREIREIEEEEARRIL EHLEELARK (SEQ ID NO: 265) MSKIKSAWSHPQFEKGGGSGGGSGGSAWSHPQFEKG GSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELE RAAYFNWWATEMMLELIKSDDEREIREIEEEEARRIL EHLEELARKGGSSGGGSSGGGSSGGGSSGELEEQVM HVLDQVSELAHELLHKLTGEELERAAYFNWWATEMM LELIKSDDEREIREIEEEEARRILEHLEELARKGGSS GGGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEEARRILEHLEELARK (SEQ ID NO: 266) MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKG GSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELE RAAYFNWWATEMMLELIKSDDEREIREIEEEEARRIL EHLEELARKGGASPAAPAPASPAAPAPSAPAGGELE EQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWA TEMLELIKSDDEREIREIEEEEARRILEHLEELARK (SEQ ID NO: 267) MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKG GSGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVF QLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGG ASPAAPAPASPAAPAPSAPAGGDKENVLQKIYEIMK ELERLGHAEASMQVSDLIYEFMKTDERLLEEAERL LEEVKR (SEQ ID NO: 268) MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKG GSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELE RAAYFNWWATEMMLELIKSDDEREIREIEEEEARRIL EHLEELARKGGASPAAPAPASPAAPAPSAPAGGDKE NVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKT DERLLEEAERLLEEVKR (SEQ ID NO: 269) MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKG GSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELE RAAYFNWWATEMMLELIKSDDEREIREIEEEEARRIL EHLEELARKGGASPAAPAPASPAAPAPSAPAGGELE EQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWA TEMLELIKSDDEREIREIEEEEARRILEHLEELARK GGASPAAPAPASPAAPAPSAPAGGELEEQVMHVLDQ VSELAHELLHKLTGEELERAAYFNWWATEMMLELIK SDDEREIREIEEEEARRILEHLEELARK (SEQ ID NO: 270) MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKG GSGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVF	ELARK (SEQ ID NO: 101) X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE ELARK (SEQ ID NO: 101)-X2- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE ELARK (SEQ ID NO: 101)-X3- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE ELARK (SEQ ID NO: 101) X1ELEEQVMHVLDQVSELAHELLHKLTGEELERAA YFNWWATEMMLELIKSDDEREIREIEEEEARRILEH LEELARK (SEQ ID NO: 101)-X2- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE ELARK (SEQ ID NO: 101)-X3- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE ELARK (SEQ ID NO: 101) X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE ELARK (SEQ ID NO: 101)-X2- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE ELARK (SEQ ID NO: 101)-X3- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE ELARK (SEQ ID NO: 101) X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE ELARK (SEQ ID NO: 101)-X2- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE ELARK (SEQ ID NO: 101) X1- NLDLHMQMTDLVYEALHFAKDEEFQKHVFQLF EATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155)-X2- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTDERLLEEAERLLEEVKR (SEQ ID NO: 125) X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE ELARK (SEQ ID NO: 101)-X2- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTDERLLEEAERLLEEVKR (SEQ ID NO: 125) X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE ELARK (SEQ ID NO: 101)-X2- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE ELARK (SEQ ID NO: 101)-X3- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE ELARK (SEQ ID NO: 101) X1NLDLHMQMTDLVYEALHFAKDEEFQKHVFQLF EATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ
2-2- 2_GS1 0		
2-2- 2_GS1 5		
2-2- 2_GS2 0		
AHB2- AHB2- PAS		
LCB3- LCB1- PAS		
AHB2- LCB1- PAS		
AHB2- 3x_PA S		
3-2- 1_PAS		

	QLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGG ASPAAPAPASPAAPAPASAPAGGELEEQVMHVLDQVS ELAHELLHKLTGEELERAAYFNWWATEMMLELIKSD DEREIREIEEEEARRILEHLEELARKGGASPAAPAPA SPAAPAPASAPAGGDKENVLQKIYEIMKELERLGHA ASMQVSDLIYEFMKTCKDERLLEEAERLLEEVKR (SE Q ID NO: 271)	ID NO: 155)-X2- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE ELARK (SEQ ID NO: 101)-X3
2-3- 1_PAS	MEKKISAWSHQPFEKGGSGGGSGGSAWSHQPFEK GSGSGGELEEQVMHVLDQVSELAHELLHKLTGEELE RAAYFNWWATEMMLELIKSDDEREIREIEEEEARRIL EHLEELARKGGASPAAPAPASPAAPAPASAPAGGNLD ELHMQMTDLVYEALHFAKDEEFQKHVFQLFKATKA YKNKDRQKLEKVVEELKELLERLLSGGASPAAPAPA SPAAPAPASAPAGGDKENVLQKIYEIMKELERLGHA ASMQVSDLIYEFMKTCKDERLLEEAERLLEEVKR (SE Q ID NO: 272)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE ELARK (SEQ ID NO: 101)-X2- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFK ATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155)-X3
1-1- 1_PAS 24	MEKKISAWSHQPFEKGGSGGGSGGSAWSHQPFEK GSGSGGDKENVLQKIYEIMKELERLGHAASMQVSD LIYEFMKTCKDENLLEEAERLLEEVKRGASPAAPAP ASPAAPAPASAPAGGDKENVLQKIYEIMKELERLGHA EASMQVSDLIYEFMKTCKDENLLEEAERLLEEVKRG ASPAAPAPASPAAPAPASAPAGGDKENVLQKIYEIM ELERLGHAASMQVSDLIYEFMKTCKDENLLEEAERL LEEVKR (SEQ ID NO: 273)	X1- DKENVLQKIYEIMKELERLGHAASMQVSDLIYEF MKTCKDENLLEEAERLLEEVKR (SEQ ID NO: 135)-X2- DKENVLQKIYEIMKELERLGHAASMQVSDLIYEF MKTCKDENLLEEAERLLEEVKR (SEQ ID NO: 135)-X3- DKENVLQKIYEIMKELERLGHAASMQVSDLIYEF MKTCKDENLLEEAERLLEEVKR (SEQ ID NO: 135)
2-2- 2_PAS 24	MEKKISAWSHQPFEKGGSGGGSGGSAWSHQPFEK GSGSGGELEEQVMHVLDQVSELAHELLHKLTGEELE RAAYFNWWATEMMLELIKSDDEREIREIEEEEARRIL EHLEELARKGGASPAAPAPASPAAPAPASAPAGGELE EQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWA TEMMLELIKSDDEREIREIEEEEARRILEHLEELARK GGASPAAPAPASPAAPAPASAPAGGELEEQVMHVLDQ VSELAHELLHKLTGEELERAAYFNWWATEMMLELIK SDDEREIREIEEEEARRILEHLEELARK (SEQ ID NO: 274)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE ELARK (SEQ ID NO: 101)-X2- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE ELARK (SEQ ID NO: 101)-X3- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE ELARK (SEQ ID NO: 101)
3-3- 3_PAS 24	MEKKISAWSHQPFEKGGSGGGSGGSAWSHQPFEK GSGSGGNLDELHMQMTDLVYEALHFAKDEEFQKHVF QLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGG ASPAAPAPASPAAPAPASAPAGGNLDELHMQMTDLVY EALHFAKDEEFQKHVFQLFKATKAYKNKDRQKLEK VVEELKELLERLLSGGASPAAPAPASPAAPAPASAPA GGLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFK KATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 275)	X1- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFK ATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155)-X2- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFK ATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155)-X3- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFK ATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155)
2-2- 1_PAS 24	MEKKISAWSHQPFEKGGSGGGSGGSAWSHQPFEK GSGSGGELEEQVMHVLDQVSELAHELLHKLTGEELE RAAYFNWWATEMMLELIKSDDEREIREIEEEEARRIL EHLEELARKGGASPAAPAPASPAAPAPASAPAGGELE EQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWA TEMMLELIKSDDEREIREIEEEEARRILEHLEELARK GGASPAAPAPASPAAPAPASAPAGGDKENVLQKIYEI MKELERLGHAASMQVSDLIYEFMKTCKDENLLEAE RLLEEVKR (SEQ ID NO: 276)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE ELARK (SEQ ID NO: 101)-X2- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDE- REIREIEEEEARRILEHLEELARK (SEQ ID NO: 101) X3- DKENVLQKIYEIMKELERLGHAASMQVSDLIYEF MKTCKDENLLEEAERLLEEVKR (SEQ ID NO: 135)
2- 2_PAS 16	MEKKISAWSHQPFEKGGSGGGSGGSAWSHQPFEK GSGSGGELEEQVMHVLDQVSELAHELLHKLTGEELE RAAYFNWWATEMMLELIKSDDEREIREIEEEEARRIL EHLEELARKGGASPAAPAPASAPAGGELEEQVMHVLD QVSELAHELLHKLTGEELERAAYFNWWATEMMLELI KSDDEREIREIEEEEARRILEHLEELARK (SEQ ID NO: 277)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE ELARK (SEQ ID NO: 101)-X2- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE ELARK (SEQ ID NO: 101)

2- 2_PAS 11	MEKKISAWSHQPFEKGGGSGGGSGGSAWSHQPFEKG GSGSSGELEEQVMHVLDQVSELAHELLHKLGTGEELE RAAYFNWWATEMMLELIKSDDEREIREIEEEEARRIL EHLEELARKGGASPAAPAGGELEEQVMHVLDQVSEL AHELLHKLGTGEELERAAYFNWWATEMMLELIKSDDE REIREIEEEEARRILEHLEELARK (SEQ ID NO: 278)	X1- ELEEQVMHVLDQVSELAHELLHKLGTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE ELARK (SEQ ID NO:101)-X2- ELEEQVMHVLDQVSELAHELLHKLGTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE ELARK (SEQ ID NO:101)
3- 1_PAS 16	MEKKISAWSHQPFEKGGGSGGGSGGSAWSHQPFEKG GSGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVF QLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGG ASPAAPAPASPAGEKENVLQKIYEIMKELERLGHAE EASMQVSDLIYEFMKTCDERLLEEAERLLEEVR (S EQ ID NO: 279)	X1- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO:155)-X2- KENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTCDERLLEEAERLLEEVR (SEQ ID NO:125)
3- 1_PAS 11	MEKKISAWSHQPFEKGGGSGGGSGGSAWSHQPFEKG GSGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVF QLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGG ASPAAPAGGDKENVLQKIYEIMKELERLGHAEASMQ VSDLIYEFMKTCDERLLEEAERLLEEVR (SEQ ID NO: 280)	X1- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO:155)-X2- KENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTCDERLLEEAERLLEEVR (SEQ ID NO:125)
2- 1_PAS 16	MEKKISAWSHQPFEKGGGSGGGSGGSAWSHQPFEKG GSGSSGELEEQVMHVLDQVSELAHELLHKLGTGEELE RAAYFNWWATEMMLELIKSDDEREIREIEEEEARRIL EHLEELARKGGASPAAPAPASPAGEKENVLQKIYE IMKELERLGHAEASMQVSDLIYEFMKTCDERLLEEA ERLLEEVR (SEQ ID NO: 281)	X1- ELEEQVMHVLDQVSELAHELLHKLGTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE ELARK (SEQ ID NO:101)-X2- KENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTCDERLLEEAERLLEEVR (SEQ ID NO:125)
2- 1_PAS 11	MEKKISAWSHQPFEKGGGSGGGSGGSAWSHQPFEKG GSGSSGELEEQVMHVLDQVSELAHELLHKLGTGEELE RAAYFNWWATEMMLELIKSDDEREIREIEEEEARRIL EHLEELARKGGASPAAPAGGDKENVLQKIYEIMKEL ERLGHAEASMQVSDLIYEFMKTCDERLLEEAERLLE EVKR (SEQ ID NO: 282)	X1- ELEEQVMHVLDQVSELAHELLHKLGTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE ELARK (SEQ ID NO:101)-X2- KENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTCDERLLEEAERLLEEVR (SEQ ID NO:125)
3v2.3 -2- 1_PAS 24	MEKKISAWSHQPFEKGGGSGGGSGGSAWSHQPFEKG GSGSSGNIDELLMQVTDLIYEALHFAKDEEFQKHAF QLFEKATKAYKNKDKQKLEKVVEELKELLERILSGG ASPAAPAPASPAAPASAPAGGELEEQVMHVLDQVS ELAHLLHKLGTGEELERAAYFNWWATEMMLELIKSD DEREIREIEEEEARRILEHLEELARKGGASPAAPAPA SPAAPASAPAGGDKENVLQKIYEIMKELERLGHAE ASMQVSDLIYEFMKTCDERLLEEAERLLEEVR (SE Q ID NO: 283)	X1- NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEK ATKAYKNKDKQKLEKVVEELKELLERILS (SEQ ID NO: 163)-X2- ELEEQVMHVLDQVSELAHELLHKLGTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE ELARK (SEQ ID NO:101)-X3
2- 3v2.3 - 1_PAS 24	MEKKISAWSHQPFEKGGGSGGGSGGSAWSHQPFEKG GSGSSGELEEQVMHVLDQVSELAHELLHKLGTGEELE RAAYFNWWATEMMLELIKSDDEREIREIEEEEARRIL EHLEELARKGGASPAAPAPASPAAPASAPAGGNID ELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKA YKNKDKQKLEKVVEELKELLERILSGGASPAAPAPA SPAAPASAPAGGDKENVLQKIYEIMKELERLGHAE ASMQVSDLIYEFMKTCDERLLEEAERLLEEVR (SE Q ID NO: 284)	X1- ELEEQVMHVLDQVSELAHELLHKLGTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE ELARK (SEQ ID NO:101)-X2- NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEK ATKAYKNKDKQKLEKVVEELKELLERILS (SEQ ID NO: 163)-X3
2-2- 2_PAS 24 om pT	MEKKISAWSHQPFEKGGGSGGGSGGSAWSHQPFEKG GSGSSGELEEQVMHVLDQVSELAHELLHKLGTGEELE RAAYFNWWATEMMLELIKSDDEREIREIEEEEARRIL EHLEELARTGGASPAAPAPASPAAPASAPAGGELE EQVMHVLDQVSELAHELLHKLGTGEELERAAYFNWWA TEMMLELIKSDDEREIREIEEEEARRILEHLEELART GGASPAAPAPASPAAPASAPAGGELEEQVMHVLDQ VSELAHELLHKLGTGEELERAAYFNWWATEMMLELIK SDDEREIREIEEEEARRILEHLEELART (SEQ ID NO: 285)	X1- ELEEQVMHVLDQVSELAHELLHKLGTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE ELART (SEQ ID NO: 164)-X2- ELEEQVMHVLDQVSELAHELLHKLGTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE ELART (SEQ ID NO: 164)-X3- ELEEQVMHVLDQVSELAHELLHKLGTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE ELART (SEQ ID NO: 164)

1-1-	MEKKISAWSHPPQFEKGGGSGGGSGGSAWSHPPQFEKG	X1-	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF
1_PAS	GS GSSGD KENVLQKIYEIMKELERLGHAEASMQVSD	MKT KDERLLEEAERLLEEVR (SEQ ID	NO: 125) -X2-
24_om	LIYEFMKT K DENLLEEAERLLEEVT RGGASPAAPAP	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF	MKT KDERLLEEAERLLEEVR (SEQ ID
pT	ASPAAPAPASAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKT K DENLLEEAERLLEEVT RGG	NO: 125) -X3-	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF
	ASPAAPAPASPAAPAPASAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKT K DENLLEEAERLLEEVT R (SEQ ID NO: 286)	MKT KDERLLEEAERLLEEVR (SEQ ID	NO: 125)
	MEKKISAWSHPPQFEKGGGSGGGSGGSAWSHPPQFEKG		
3v2.3	GS GSSGNIDELLMQVTDLIYEALHFAKDEEFQKHAF	X1-	NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLF EK
-2-	QLFEKATKAYKNKDKQKLEKVVEELKELLERILSGG	ATKAYKNKDKQKLEKVVEELKELLERILS (SEQ	ID NO: 163) -X2-
1_PAS	ASPAAPAPASPAAPAPASAPAGGELEE QVMHVLDQVS	ELEE QVMHVLDQVSELAHELLHKLTGEELERAAYF	NWWATEMMLELIKSDDEREIREIEEEAARILEHLE
24_om	ELAHELLHKLTGEELERAAYFNWWATEMMLELIKSD	ELART (SEQ ID NO: 164) -X3	
pT	DEREIREIEEEAARILEHLEELARTGGASPAAPAPA		
	SPAAPAPASAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKT K DERLLEEAERLLEEVR (SEQ ID NO: 287)		
	MEKKISAWSHPPQFEKGGGSGGGSGGSAWSHPPQFEKG		
2-	GS GSSGELEE QVMHVLDQVSELAHELLHKLTGEELE	X1-	ELEE QVMHVLDQVSELAHELLHKLTGEELERAAYF
3v2.3	RAAYFNWWATEMMLELIKSDDEREIREIEEEAARIL	NWWATEMMLELIKSDDEREIREIEEEAARILEHLE	ELART (SEQ ID NO: 164) -X2-
-	EHLEELARTGGASPAAPAPASPAAPAPASAPAGGNID	NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLF EK	ATKAYKNKDKQKLEKVVEELKELLERILS (SEQ
1_PAS	ELLMQVTDLIYEALHFAKDEEFQKHAFQLF EKATKA	ID NO: 163) -X3	
24_om	YKNKDKQKLEKVVEELKELLERILSGGASPAAPAPA		
pT	SPAAPAPASAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKT K DERLLEEAERLLEEVR (SEQ ID NO: 288)		
	MEKKISAWSHPPQFEKGGGSGGGSGGSAWSHPPQFEKG		
3v2.3	GS GSSGNIDELLMQVTDLIYEALHFAKDEEFQKHAF	X1-	NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLF EK
-2-	QLFEKATKAYKNKDKQKLEKVVEELKELLERILSGG	ATKAYKNKDKQKLEKVVEELKELLERILS (SEQ	ID NO: 163) -X2-
1_PAS	ASPAAPAPASPAAPAPASAPAGGELEE QVMHVLDQVS	ELEE QVMHVLDQVSELAHELLHKLTGEELERAAYF	NWWATEMMLELIKSDDEREIREIEEEAARILEHLE
24	ELAHELLHKLTGEELERAAYFNWWATEMMLELIKSD	ELARK (SEQ ID NO: 101) -X3-	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF
	DEREIREIEEEAARILEHLEELARKGGASPAAPAPA	MKT K DENLLEEAERLLEEVR (SEQ ID NO:	135)
	SPAAPAPASAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKT K DENLLEEAERLLEEVR (SEQ ID NO: 289)		
	MEKKISAWSHPPQFEKGGGSGGGSGGSAWSHPPQFEKG		
2-	GS GSSGELEE QVMHVLDQVSELAHELLHKLTGEELE	X1-	ELEE QVMHVLDQVSELAHELLHKLTGEELERAAYF
3v2.3	RAAYFNWWATEMMLELIKSDDEREIREIEEEAARIL	NWWATEMMLELIKSDDEREIREIEEEAARILEHLE	ELARK (SEQ ID NO: 101) -X2-
-	EHLEELARKGGASPAAPAPASPAAPAPASAPAGGNID	NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLF EK	ATKAYKNKDKQKLEKVVEELKELLERILS (SEQ
1_PAS	ELLMQVTDLIYEALHFAKDEEFQKHAFQLF EKATKA	ID NO: 163) -X3-	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF
24	YKNKDKQKLEKVVEELKELLERILSGGASPAAPAPA	MKT K DENLLEEAERLLEEVR (SEQ ID NO:	135)
	SPAAPAPASAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKT K DENLLEEAERLLEEVR (SEQ ID NO: 290)		
	MEKKISAWSHPPQFEKGGGSGGGSGGSAWSHPPQFEKG		
3v2.3	GS GSSGNIDELLMQVTDLIYEALHFAKDEEFQKHAF	X1-	NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLF EK
-2-	QLFEKATKAYKNKDKQKLEKVVEELKELLERILSGG	ATKAYKNKDKQKLEKVVEELKELLERILS (SEQ	ID NO: 163) -X2-
1_PAS	ASPAAPAPASPAAPAPASAPAGGELEE QVMHVLDQVS	ELEE QVMHVLDQVSELAHELLHKLTGEELERAAYF	NWWATEMMLELIKSDDEREIREIEEEAARILEHLE
24_om	ELAHELLHKLTGEELERAAYFNWWATEMMLELIKSD	ELART (SEQ ID NO: 164) -X3-	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF
pT	DEREIREIEEEAARILEHLEELARTGGASPAAPAPA	MKT K DENLLEEAERLLEEVR (SEQ ID NO:	135)
	SPAAPAPASAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKT K DENLLEEAERLLEEVR (SEQ ID NO: 291)		
	MEKKISAWSHPPQFEKGGGSGGGSGGSAWSHPPQFEKG		
2-	GS GSSGELEE QVMHVLDQVSELAHELLHKLTGEELE	X1-	ELEE QVMHVLDQVSELAHELLHKLTGEELERAAYF
3v2.3	RAAYFNWWATEMMLELIKSDDEREIREIEEEAARIL	NWWATEMMLELIKSDDEREIREIEEEAARILEHLE	ELART (SEQ ID NO: 164) -X2-
-	EHLEELARTGGASPAAPAPASPAAPAPASAPAGGNID	NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLF EK	ATKAYKNKDKQKLEKVVEELKELLERILS (SEQ
1_PAS	ELLMQVTDLIYEALHFAKDEEFQKHAFQLF EKATKA		
24_om	YKNKDKQKLEKVVEELKELLERILSGGASPAAPAPA		
pT			

	SPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAE ASMQVSDLIYEFMKTNDENLLEEAERLLEEVKR (SEQ ID NO: 292)	ID NO: 163)-X3- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTNDENLLEEAERLLEEVKR (SEQ ID NO: 135)
2- 3v2.3 - 1_PAS 24_N- His- TEV	MEKKIHSHHHHSGENLYFQSGSGSSGELEEQVMHV LDQVSELAHELLHKLTGEELERAAYFNWWATEMMLE LIKSDDEREIREIEEEEARRILEHLEELARKGGASPA APAPASPAAPAPSAPAGGNIDELLMQVTDLIYEALH FAKDEEFQKHAFQLFKATKAYKNKDKQKLEKVVEE LKELLERILSGGASPAAPAPASPAAPAPSAPAGGDK ENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKT NDENLLEEAERLLEEVKR (SEQ ID NO: 293)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE ELARK (SEQ ID NO: 101)-X2- NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFK ATKAYKNKDKQKLEKVVEELKELLERILS (SEQ ID NO: 163)-X3- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTNDENLLEEAERLLEEVKR (SEQ ID NO: 135)
2- 3v2.3 - 1_PAS 24_om pT_N- His- TEV	MEKKIHSHHHHSGENLYFQSGSGSSGELEEQVMHV LDQVSELAHELLHKLTGEELERAAYFNWWATEMMLE LIKSDDEREIREIEEEEARRILEHLEELARTGGASPA APAPASPAAPAPSAPAGGNIDELLMQVTDLIYEALH FAKDEEFQKHAFQLFKATKAYKNKDKQKLEKVVEE LKELLERILSGGASPAAPAPASPAAPAPSAPAGGDK ENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKT NDENLLEEAERLLEEVKR (SEQ ID NO: 294)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE ELART (SEQ ID NO: 164)-X2- NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFK ATKAYKNKDKQKLEKVVEELKELLERILS (SEQ ID NO: 163)-X3- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTNDENLLEEAERLLEEVKR (SEQ ID NO: 135)
2-3- 1_PAS 24_NT SF	MEKKIDYKDDDDKSGSSAWSHPQFEKGGSGGGSG GSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSEL ELLHKLTGEELERAAYFNWWATEMMLELIKSDDERE IREIEEEEARRILEHLEELARKGGASPAAPAPASPA PAPSAPAGGNIDELLMQVTDLIYEALHFAKDEEFQK HAFQLFKATKAYKNKDKQKLEKVVEELKELLERIL SGGASPAAPAPASPAAPAPSAPAGGDKENVLQKIYE IMKELERLGHAEASMQVSDLIYEFMKTNDENLLEEA ERLLEEVKR (SEQ ID NO: 295)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE ELARK (SEQ ID NO: 101)-X2- NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFK ATKAYKNKDKQKLEKVVEELKELLERILS (SEQ ID NO: 163)-X3- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTNDENLLEEAERLLEEVKR (SEQ ID NO: 135)
2-3- 1_PAS 24_NT S3F	MEKKIDYKDHDGDYKDHDIDYKDDDDKSGSSAWSH PQFEKGGSGGGSGSSAWSHPQFEKGGSGSSGELEE QVMHVLDQVSELAHELLHKLTGEELERAAYFNWWAT EMMLELIKSDDEREIREIEEEEARRILEHLEELARKG GASPAAPAPASPAAPAPSAPAGGNIDELLMQVTDLI YEALHFAKDEEFQKHAFQLFKATKAYKNKDKQKLE KVVEELKELLERILSGGASPAAPAPASPAAPAPSAP AGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIY EFMKTNDENLLEEAERLLEEVKR (SEQ ID NO: 296)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE ELARK (SEQ ID NO: 101)-X2- NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFK ATKAYKNKDKQKLEKVVEELKELLERILS (SEQ ID NO: 163)-X3- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTNDENLLEEAERLLEEVKR (SEQ ID NO: 135)
2-3- 1_PAS 24_NT SM	MEKKIEQKLISEEDLGSGSSAWSHPQFEKGGSGGG SGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSEL AHELLHKLTGEELERAAYFNWWATEMMLELIKSDDE REIREIEEEEARRILEHLEELARKGGASPAAPAPASP AAPAPSAPAGGNIDELLMQVTDLIYEALHFAKDEEF QKHAFQLFKATKAYKNKDKQKLEKVVEELKELLER ILSGGASPAAPAPASPAAPAPSAPAGGDKENVLQKI YEIMKELERLGHAEASMQVSDLIYEFMKTNDENLLE EAERLLEEVKR (SEQ ID NO: 297)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE ELARK (SEQ ID NO: 101)-X2- NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFK ATKAYKNKDKQKLEKVVEELKELLERILS (SEQ ID NO: 163)-X3- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTNDENLLEEAERLLEEVKR (SEQ ID NO: 135)
2- PAS24 -3- PAS16 - 1_NTS 3F	MEKKIDYKDHDGDYKDHDIDYKDDDDKSGSSAWSH PQFEKGGSGGGSGSSAWSHPQFEKGGSGSSGELEE QVMHVLDQVSELAHELLHKLTGEELERAAYFNWWAT EMMLELIKSDDEREIREIEEEEARRILEHLEELARKG GASPAAPAPASPAAPAPSAPAGGNIDELLMQVTDLI YEALHFAKDEEFQKHAFQLFKATKAYKNKDKQKLE KVVEELKELLERILSGGASPAAPAPASPAAGGDKENV LQKIYEIMKELERLGHAEASMQVSDLIYEFMKTND NLEEAERLLEEVKR (SEQ ID NO: 298)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE ELARK (SEQ ID NO: 101)-X2- NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFK ATKAYKNKDKQKLEKVVEELKELLERILS (SEQ ID NO: 163)-X3- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTNDENLLEEAERLLEEVKR (SEQ ID NO: 135)

	MEKKIDYKDHDG DYKDHDIDYKDDDDK GSGSSAWSH PQFEKGGGSGGGSGGSAWSHPQFEKGGGSSS GELEE	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE
2-	QVMHVLDQVSELAHELLHKLTGEELERAAYFNWWAT	ELARK (SEQ ID NO:101)-X2-
PAS16	EMMLELIKSDDEREIREIEEEEARRILEHLEELARKG	NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEK
-3-	GASPAAPAPASPAGGNIDELLMQVTDLIYEALHFAK	ATKAYKNKDKQKLEKVVEELKELLERILS (SEQ
PAS16	DEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKE	ID NO: 163)-X3-
-	LLERILSGGASPAAPAPASPAGGDKENVLQKIYEIM	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF
1_NTS	KELERLGHAEASMQVSDLIYEFMKT KDENLLEEAER	MKT KDENLLEEAERLLEEVR (SEQ ID NO:
3F	LLEEVR (SEQ ID NO: 299)	135)
	MEKKIDYKDHDG DYKDHDIDYKDDDDK GSGSSAWSH PQFEKGGGSGGGSGGSAWSHPQFEKGGGSSS GELEE	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE
2-	QVMHVLDQVSELAHELLHKLTGEELERAAYFNWWAT	ELARK (SEQ ID NO:101)-X2-
PAS11	EMMLELIKSDDEREIREIEEEEARRILEHLEELARKG	NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEK
-3-	GASPAAPAGGNIDELLMQVTDLIYEALHFAKDEEFQ	ATKAYKNKDKQKLEKVVEELKELLERILS (SEQ
PAS16	KHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERI	ID NO: 163)-X3-
-	LSGGASPAAPAPASPAGGDKENVLQKIYEIMKELER	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF
1_NTS	LGHAESMQVSDLIYEFMKT KDENLLEEAERLLEEVR	MKT KDENLLEEAERLLEEVR (SEQ ID NO:
3F	KR (SEQ ID NO: 300)	135)
	MEKKIDYKDHDG DYKDHDIDYKDDDDK GSGSSAWSH PQFEKGGGSGGGSGGSAWSHPQFEKGGGSSS GELEE	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE
2-	QVMHVLDQVSELAHELLHKLTGEELERAAYFNWWAT	ELARK (SEQ ID NO:101)-X2-
PAS24	EMMLELIKSDDEREIREIEEEEARRILEHLEELARKG	NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEK
-3-	GASPAAPAPASPAPAPASPAGGNIDELLMQVTDLI	ATKAYKNKDKQKLEKVVEELKELLERILS (SEQ
PAS11	YEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLE	ID NO: 163)-X3-
-	KVVEELKELLERILSGGASPAAPAGGDKENVLQKIY	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF
1_NTS	EIMKELERLGHAEASMQVSDLIYEFMKT KDENLLEE	MKT KDENLLEEAERLLEEVR (SEQ ID NO:
3F	AERLLEEVR (SEQ ID NO: 301)	135)
	MEKKIDYKDHDG DYKDHDIDYKDDDDK GSGSSAWSH PQFEKGGGSGGGSGGSAWSHPQFEKGGGSSS GELEE	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE
2-	QVMHVLDQVSELAHELLHKLTGEELERAAYFNWWAT	ELARK (SEQ ID NO:101)-X2-
PAS16	EMMLELIKSDDEREIREIEEEEARRILEHLEELARKG	NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEK
-3-	GASPAAPAPASPAGGNIDELLMQVTDLIYEALHFAK	ATKAYKNKDKQKLEKVVEELKELLERILS (SEQ
PAS11	DEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKE	ID NO: 163)-X3-
-	LLERILSGGASPAAPAGGDKENVLQKIYEIMKELER	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF
1_NTS	LGHAESMQVSDLIYEFMKT KDENLLEEAERLLEEVR	MKT KDENLLEEAERLLEEVR (SEQ ID NO:
3F	KR (SEQ ID NO: 302)	135)
	MEKKIDYKDHDG DYKDHDIDYKDDDDK GSGSSAWSH PQFEKGGGSGGGSGGSAWSHPQFEKGGGSSS GELEE	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE
2-	QVMHVLDQVSELAHELLHKLTGEELERAAYFNWWAT	ELARK (SEQ ID NO:101)-X2-
PAS11	EMMLELIKSDDEREIREIEEEEARRILEHLEELARKG	NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEK
-3-	GASPAAPAGGNIDELLMQVTDLIYEALHFAKDEEFQ	ATKAYKNKDKQKLEKVVEELKELLERILS (SEQ
PAS11	KHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERI	ID NO: 163)-X3-
-	LSGGASPAAPAGGDKENVLQKIYEIMKELERLGHAE	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF
1_NTS	ASMQVSDLIYEFMKT KDENLLEEAERLLEEVR (SE	MKT KDENLLEEAERLLEEVR (SEQ ID NO:
3F	Q ID NO: 303)	135)
	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKG	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE
2-	GSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELE	ELARK (SEQ ID NO:101)-X2-
PAS11	RAAYFNWWATEMMLELIKSDDEREIREIEEEEARRIL	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF
-3-	EHLEELARKGGGGELEEQVMHVLDQVSELAHELLHK	NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE
PAS11	LTGEELERAAYFNWWATEMMLELIKSDDEREIREIE	ELARK (SEQ ID NO:101)
-	EEARRILEHLEELARK (SEQ ID NO: 304)	
2_G4		
	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKG	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE
2-	GSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELE	ELARK (SEQ ID NO:101)-X2-
PAS11	RAAYFNWWATEMMLELIKSDDEREIREIEEEEARRIL	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF
-3-	EHLEELARKGGGGELEEQVMHVLDQVSELAHELLHKLT	NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE
PAS11	GEELERAAYFNWWATEMMLELIKSDDEREIREIEEEE	ELARK (SEQ ID NO:101)
-	ARRILEHLEELARK (SEQ ID NO: 305)	
2_G2		

2- 3_PAS 24	MEKKISAWSHQPFEKGGGSGGGSGGSAWSHQPFEKG GSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELE RAAYFNWWATEMMLELIKSDDEREIREIEEEEARRIL EHLEELARKGGASPAAPAPASPAAPAPSAPAGGNID ELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKA YKNKDKQKLEKVVEELKELLERILS (SEQ ID NO: 306)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE ELARK (SEQ ID NO:101)-X2- NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEK ATKAYKNKDKQKLEKVVEELKELLERILS (SEQ ID NO: 163)
2- 3_PAS 16	MEKKISAWSHQPFEKGGGSGGGSGGSAWSHQPFEKG GSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELE RAAYFNWWATEMMLELIKSDDEREIREIEEEEARRIL EHLEELARKGGASPAAPAPASPAAGNIDELLMQVTD LIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQK LEKVVEELKELLERILS (SEQ ID NO: 307)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE ELARK (SEQ ID NO:101)-X2- NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEK ATKAYKNKDKQKLEKVVEELKELLERILS (SEQ ID NO: 163)
2- 3_PAS 11	MEKKISAWSHQPFEKGGGSGGGSGGSAWSHQPFEKG GSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELE RAAYFNWWATEMMLELIKSDDEREIREIEEEEARRIL EHLEELARKGGASPAAPAGGNIDELLMQVTDLIYEA LHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKV EELKELLERILS (SEQ ID NO: 308)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE ELARK (SEQ ID NO:101)-X2- NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEK ATKAYKNKDKQKLEKVVEELKELLERILS (SEQ ID NO: 163)
1-2- 1_PAS 24	MEKKISAWSHQPFEKGGGSGGGSGGSAWSHQPFEKG GSGSSGDKENVLQKIYEIMKELERLGHAEASMQVSD LIYEFMKTNDENLLEEAERLLEEVKRGASPAAPAP ASPAAPAPSAPAGGELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKSDDEREIREI EEEARLILEHLEELARKGGASPAAPAPASPAAPAPS APAGGDKENVLQKIYEIMKELERLGHAEASMQVSD LIYEFMKTNDENLLEEAERLLEEVKR (SEQ ID NO: 309)	X1- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTNDENLLEEAERLLEEVKR (SEQ ID NO: 135)-X2- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE ELARK (SEQ ID NO:101)-X3- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTNDENLLEEAERLLEEVKR (SEQ ID NO: 135)
2- PAS24 -3- PAS24 - 1_NTS	MEKKISAWSHQPFEKGGGSGGGSGGSAWSHQPFEKG GSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELE RAAYFNWWATEMMLELIKSDDEREIREIEEEEARRIL EHLEELARKGGASPAAPAPASPAAPAPSAPAGGNLD ELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKA YKNKDRQKLEKVVEELKELLERLLSGGASPAAPAPA SPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAE ASMQVSDLIYEFMKTNDENLLEEAERLLEEVKR (SE Q ID NO: 310)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE ELARK (SEQ ID NO:101)-X2- NIDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155)-X3- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTNDENLLEEAERLLEEVKR (SEQ ID NO: 135)
2- PAS24 -3- PAS16 - 1_NTS	MEKKISAWSHQPFEKGGGSGGGSGGSAWSHQPFEKG GSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELE RAAYFNWWATEMMLELIKSDDEREIREIEEEEARRIL EHLEELARKGGASPAAPAPASPAAPAPSAPAGGNLD ELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKA YKNKDRQKLEKVVEELKELLERLLSGGASPAAPAPA SPAGGDKENVLQKIYEIMKELERLGHAEASMQVSD LIYEFMKTNDENLLEEAERLLEEVKR (SEQ ID NO: 311)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE ELARK (SEQ ID NO:101)-X2- NIDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155)-X3- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTNDENLLEEAERLLEEVKR (SEQ ID NO: 135)
2- PAS16 -3- PAS24 - 1_NTS	MEKKISAWSHQPFEKGGGSGGGSGGSAWSHQPFEKG GSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELE RAAYFNWWATEMMLELIKSDDEREIREIEEEEARRIL EHLEELARKGGASPAAPAPASPAAPAPSAPAGG (SEQ ID NO: 155) GGASPAAPAPASPAAPAPSAPAGGDKENVLQK IYEIMKELERLGHAEASMQVSDLIYEFMKTNDENLL EEAERLLEEVKR (SEQ ID NO: 312)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE ELARK (SEQ ID NO:101)-X2- NIDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155)-X3- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTNDENLLEEAERLLEEVKR (SEQ ID NO: 135)
2- PAS16 -3-	MEKKISAWSHQPFEKGGGSGGGSGGSAWSHQPFEKG GSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELE RAAYFNWWATEMMLELIKSDDEREIREIEEEEARRIL	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE

PAS16	EHLEELARKGGASPAAPAPASPAGGNLDELHMQMTD	ELARK (SEQ ID NO: 101) -X2-
-	LVYEALHFAKDEEFQKHVFQLF EKATKAYKNKDRQK	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLF EK
1_NTS	LEKVVEELKELLERLLSGGASPAAPAPASPAGGDKE	ATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ
	NVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKT	ID NO: 155) -X3-
	DENLLEEAERLLEEVKR (SEQ ID NO: 313)	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF
		MKTKDENLLEEAERLLEEVKR (SEQ ID NO:
		135)
		X1-
	MEKKISAWSHQPFEKGGSGGGSGGSAWSHQPFEK	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF
	GGSGSSELEEQVMHVLDQVSELAHELLHKLTGEELE	NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE
2-	RAAYFNWWATEMMLELIKSDDEREIREIEEEEARRIL	ELARK (SEQ ID NO: 101) -X2-
PAS11	EHLEELARKGGASPAAPAGGNLDELHMQMTDLVYEA	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLF EK
-3-	LHFAKDEEFQKHVFQLF EKATKAYKNKDRQKLEKV	ATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ
PAS16	EELKELLERLLSGGASPAAPAPASPAGGDKENVLQK	ID NO: 155) -X3-
-	IYEIMKELERLGHAEASMQVSDLIYEFMKT	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF
1_NTS	KDENLLEEAERLLEEVKR (SEQ ID NO: 314)	MKTKDENLLEEAERLLEEVKR (SEQ ID NO:
		135)
		X1-
	MEKKISAWSHQPFEKGGSGGGSGGSAWSHQPFEK	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF
	GGSGSSELEEQVMHVLDQVSELAHELLHKLTGEELE	NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE
2-	RAAYFNWWATEMMLELIKSDDEREIREIEEEEARRIL	ELARK (SEQ ID NO: 101) -X2-
PAS24	EHLEELARKGGASPAAPAPASPAPAPAGGNLD	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLF EK
-3-	ELHMQMTDLVYEALHFAKDEEFQKHVFQLF EKATK	ATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ
PAS11	YKNKDRQKLEKVVEELKELLERLLSGGASPAAPAGG	ID NO: 155) -X3-
-	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFM	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF
1_NTS	KTKDENLLEEAERLLEEVKR (SEQ ID NO: 315)	MKTKDENLLEEAERLLEEVKR (SEQ ID NO:
		135)
		X1-
	MEKKISAWSHQPFEKGGSGGGSGGSAWSHQPFEK	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF
	GGSGSSELEEQVMHVLDQVSELAHELLHKLTGEELE	NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE
2-	RAAYFNWWATEMMLELIKSDDEREIREIEEEEARRIL	ELARK (SEQ ID NO: 101) -X2-
PAS16	EHLEELARKGGASPAAPAPASPAGGNLDELHMQMTD	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLF EK
-3-	LVYEALHFAKDEEFQKHVFQLF EKATKAYKNKDRQK	ATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ
PAS11	LEKVVEELKELLERLLSGGASPAAPAGGDKENVLQK	ID NO: 155) -X3-
-	IYEIMKELERLGHAEASMQVSDLIYEFMKT	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF
1_NTS	KDENLLEEAERLLEEVKR (SEQ ID NO: 316)	MKTKDENLLEEAERLLEEVKR (SEQ ID NO:
		135)
		X1-
	MEKKISAWSHQPFEKGGSGGGSGGSAWSHQPFEK	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF
	GGSGSSELEEQVMHVLDQVSELAHELLHKLTGEELE	NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE
2-	RAAYFNWWATEMMLELIKSDDEREIREIEEEEARRIL	ELARK (SEQ ID NO: 101) -X2-
PAS11	EHLEELARKGGASPAAPAGGNLDELHMQMTDLVYEA	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLF EK
-3-	LHFAKDEEFQKHVFQLF EKATKAYKNKDRQKLEKV	ATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ
PAS11	EELKELLERLLSGGASPAAPAGGDKENVLQKIYEIM	ID NO: 155) -X3-
-	KELERLGHAEASMQVSDLIYEFMKT	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF
1_NTS	KDENLLEEAERLLEEVKR (SEQ ID NO: 317)	MKTKDENLLEEAERLLEEVKR (SEQ ID NO:
		135)
		X1-
	MEKKISAWSHQPFEKGGSGGGSGGSAWSHQPFEK	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF
	GGSGSSELEEQVMHVLDQVSELAHELLHKLTGEELE	NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE
2-	RAAYFNWWATEMMLELIKSDDEREIREIEEEEARRIL	ELARK (SEQ ID NO: 101) -X2-
PAS11	EHLEELARKGGASPAAPAGGNLDELHMQMTDLVYEA	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLF EK
-3-	LHFAKDEEFQKHVFQLF EKATKAYKNKDRQKLEKV	ATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ
PAS11	EELKELLERLLSGGASPAAPAGGDKENVLQKIYEIM	ID NO: 155) -X3-
-	KELERLGHAEASMQVSDLIYEFMKT	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF
1_NTS	KDENLLEEAERLLEEVKR (SEQ ID NO: 318)	MKTKDENLLEEAERLLEEVKR (SEQ ID NO:
		135)
		X1-
	MEKKISAWSHQPFEKGGSGGGSGGSAWSHQPFEK	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF
	GGSGSSELEEQVMHVLDQVSELAHELLHKLTGEELE	NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE
2-3-	RAAYFNWWATEMMLELIKSDDEREIREIEEEEARRIL	ELARK (SEQ ID NO: 101) -X2-
1_PAS	EHLEELARKGGASAGGNLDELHMQMTDLVYEALHFA	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLF EK
7	KDEEFQKHVFQLF EKATKAYKNKDRQKLEKVVEELK	ATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ
	ELLERLLSGGASAGGDKENVLQKIYEIMKELERLGH	ID NO: 155) -X3-
	AEASMQVSDLIYEFMKT	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF
	KDENLLEEAERLLEEVKR (SEQ ID NO: 318)	MKTKDENLLEEAERLLEEVKR (SEQ ID NO:
		135)
		X1-
	MEKKISAWSHQPFEKGGSGGGSGGSAWSHQPFEK	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF
	GGSGSSELEEQVMHVLDQVSELAHELLHKLTGEELE	NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE
2-3-	RAAYFNWWATEMMLELIKSDDEREIREIEEEEARRIL	ELARK (SEQ ID NO: 101) -X2-
1_GS7	EHLEELARKGGSGGGGNLDELHMQMTDLVYEALHF	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLF EK
	AKDEEFQKHVFQLF EKATKAYKNKDRQKLEKVVEEL	ATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ
	KELLERLLSGGSGGGGDKENVLQKIYEIMKELERL	ID NO: 155) -X3-
	GHAEASMQVSDLIYEFMKT	
	KDENLLEEAERLLEEVK	

	R (SEQ ID NO: 319)	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTCDENLLEEAERLLEEVKR (SEQ ID NO: 135)
2-3- 1_GS5	MEKKISAWSHQPFEKGGSGGGSGGSAWSHQPFEKG GSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELE RAAYFNWWATEMMLELIKSDDEREIREIEEEEARRIL EHLEELARKGGSGGNLDELHMQMTDLVYEALHFAKD EEFQKHVFQLFKATKAYKNKDRQKLEKVVEELKEL LERLLSGGSGGDKENVLQKIYEIMKELERLGHAEAS MQVSDLIYEFMKTCDENLLEEAERLLEEVKR (SEQ ID NO: 320)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE ELARK (SEQ ID NO:101)-X2- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFK ATKAYKNKDRQKLEKVVEELKELERLLS (SEQ ID NO: 155)-X3- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTCDENLLEEAERLLEEVKR (SEQ ID NO: 135)
2-3- 1_GS1 1	MEKKISAWSHQPFEKGGSGGGSGGSAWSHQPFEKG GSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELE RAAYFNWWATEMMLELIKSDDEREIREIEEEEARRIL EHLEELARKGGSGGGSGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFKATKAYKNKDRQKLEKVV EELKELLERLLSGGSGGGSGGDKENVLQKIYEIM KELERLGHAEASMQVSDLIYEFMKTCDENLLEEAER LLEEVKR (SEQ ID NO: 321)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE ELARK (SEQ ID NO:101)-X2- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFK ATKAYKNKDRQKLEKVVEELKELERLLS (SEQ ID NO: 155)-X3- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTCDENLLEEAERLLEEVKR (SEQ ID NO: 135)
2-2- 2_PAS 11	MEKKISAWSHQPFEKGGSGGGSGGSAWSHQPFEKG GSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELE RAAYFNWWATEMMLELIKSDDEREIREIEEEEARRIL EHLEELARKGGSPAPAGGELEEQVMHVLDQVSEL AHELLHKLTGEELERAAYFNWWATEMMLELIKSDDE REIREIEEEEARRILEHLEELARKGGSPAPAGGEL EEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWW ATEMMLELIKSDDEREIREIEEEEARRILEHLEELAR K (SEQ ID NO: 322)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE ELARK (SEQ ID NO:101)-X2- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE ELARK (SEQ ID NO:101)-X3- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE ELARK (SEQ ID NO:101)
2-2- 2_GS1 1	MEKKISAWSHQPFEKGGSGGGSGGSAWSHQPFEKG GSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELE RAAYFNWWATEMMLELIKSDDEREIREIEEEEARRIL EHLEELARKGGSGGGSGGELEEQVMHVLDQVSEL AHELLHKLTGEELERAAYFNWWATEMMLELIKSDDE REIREIEEEEARRILEHLEELARKGGSGGGSGGGEL EEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWW ATEMMLELIKSDDEREIREIEEEEARRILEHLEELAR K (SEQ ID NO: 323)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE ELARK (SEQ ID NO:101)-X2- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE ELARK (SEQ ID NO:101)-X3- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE ELARK (SEQ ID NO:101)
2-2- 2_GS8	MEKKISAWSHQPFEKGGSGGGSGGSAWSHQPFEKG GSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELE RAAYFNWWATEMMLELIKSDDEREIREIEEEEARRIL EHLEELARKGGSGGGSGGELEEQVMHVLDQVSELAHE LLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEIEEEEARRILEHLEELARKGGSGGGSGGELEEQVMH VLDQVSELAHELLHKLTGEELERAAYFNWWATEMML ELIKSDDEREIREIEEEEARRILEHLEELARK (SEQ ID NO: 324)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE ELARK (SEQ ID NO:101)-X2- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE ELARK (SEQ ID NO:101)-X3- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE ELARK (SEQ ID NO:101)
2-2- 2_GS5	MEKKISAWSHQPFEKGGSGGGSGGSAWSHQPFEKG GSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELE RAAYFNWWATEMMLELIKSDDEREIREIEEEEARRIL EHLEELARKGGSGGELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKSDDEREIREIE EEEARRILEHLEELARKGGSGGELEEQVMHVLDQVS ELAHELLHKLTGEELERAAYFNWWATEMMLELIKSD DEREIREIEEEEARRILEHLEELARK (SEQ ID NO: 325)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE ELARK (SEQ ID NO:101)-X2- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE ELARK (SEQ ID NO:101)-X3- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE ELARK (SEQ ID NO:101)

	MEKKISAWSHPOFEKGGGSGGGSSGSWSHPQFEKG GSGSSGELEEQVMHVLDQVSELAHELLHKLGTGEELE RAAYFNWWATEMMLELIKSDDEREIREIEEEEARRIL EHLEELARKGGSGGGSGGGSGGNLDELHMOMTDL VYEALHFADDEEFQKHVFQLFEKATKAYKNKDRQKL EKVVVEELKELLERLLSGGSGGGSGGGSGGDKENV LQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKE NLLEEAERLLEEVR(SEQ ID NO: 326)	NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE ELARK(SEQ ID NO:101)-X2- NLDELHMOMTDLVYEALHFADDEEFQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155)-X3- DKNENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVR(SEQ ID NO: 135)
2-3- 1_GGG GS15		X1-E- LEEQVMHVLDQVSELAHELLHKLGTGEELERAAYFN WWATEMMLELIKSDDEREIREIEEEEARRILEHLE LARK (SEQ ID No: 101)-X2- NLDELHMOMTDLVYEALHFADDEEFQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155)-X3- DKNENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVR(SEQ ID NO: 135)
	MEKKISAWSHPOFEKGGGSGGGSSGSWSHPQFEKG GSGSSGELEEQVMHVLDQVSELAHELLHKLGTGEELE RAAYFNWWATEMMLELIKSDDEREIREIEEEEARRIL EHLEELARKGGSGGGSGGGSNLDELHMOMTDLVYE ALHFADDEEFQKHVFQLFEKATKAYKNKDRQKLEKV VEELKELLERLLSGGSGGGSGGGSGGDKENVLQKIYE IMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEA ERLLEEVR(SEQ ID NO: 327)	X1- ELEEQVMHVLDQVSELAHELLHKLGTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE ELARK(SEQ ID NO:101)-X2- NLDELHMOMTDLVYEALHFADDEEFQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155)-X3- DKNENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVR(SEQ ID NO: 135)
2-3- 1_GGG GS12		X1- ELEEQVMHVLDQVSELAHELLHKLGTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE ELARK(SEQ ID NO:101)-X2- NLDELHMOMTDLVYEALHFADDEEFQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155)-X3- DKNENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVR(SEQ ID NO: 135)
	MEKKISAWSHPOFEKGGGSGGGSSGSWSHPQFEKG GSGSSGELEEQVMHVLDQVSELAHELLHKLGTGEELE RAAYFNWWATEMMLELIKSDDEREIREIEEEEARRIL EHLEELARKGGSGGGSGGGSNLDELHMOMTDLVYEALH FAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEE LKELLERLLSGGSGGGSGGGDKENVLQKIYEIMKELE RLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEE VKR(SEQ ID NO: 328)	X1- ELEEQVMHVLDQVSELAHELLHKLGTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE ELARK(SEQ ID NO:101)-X2- NLDELHMOMTDLVYEALHFADDEEFQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155)-X3- DKNENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVR(SEQ ID NO: 135)
2-3- 1_GGG GS9		X1- ELEEQVMHVLDQVSELAHELLHKLGTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLE ELARK(SEQ ID NO:101)-X2- NLDELHMOMTDLVYEALHFADDEEFQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155)-X3- DKNENVLQKIYEIMKELERLG(SEQ ID NO: 135) HAEASMQVSDLIYEFMKTKDENLLEEAERLL EEVR
	MEKKISAWSHPOFEKGGGSGGGSSGSWSHPQFEKG GSGSSGELEEQVMHVLDQVSELAHELLHKLGTGEELE RAAYFNWWATEMMLELIKSDDEREIREIEEEEARRIL EHLEELARKGGSGGGSGGGSNLDELHMOMTDLVYEALHFA KDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELK ELLERLLSGGSGGGDKENVLQKIYEIMKELERLGH AEASMQVSDLIYEFMKTKDENLLEEAERLLEEVR(SEQ ID NO: 329)	X1- DKNENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVR(SEQ ID NO: 135)-X2- DKNENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVR(SEQ ID NO: 135)-X3
2-3- 1_GGG GS7		X1- DKNENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVR(SEQ ID NO: 135)-X2- DKNENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVR(SEQ ID NO: 135)-X3
	MEKKIGGGDKENVLQKIYEIMKELERLGHAEASMQV SDLIYEFMKTKDENLLEEAERLLEEVRGGSGGGGS GGGSGGGSGGGSGGGDKENVLQKIYEIMKELERL GHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVR RGSGSGGSAWSHPQFEKGGGSGGGSSGSWSHPQF EK(SEQ ID NO: 330)	X1- DKNENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVR(SEQ ID NO: 135)-X2- DKNENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVR(SEQ ID NO: 135)-X3
1- 1_GGG GS25		X1- DKNENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVR(SEQ ID NO: 135)-X2- DKNENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVR(SEQ ID NO: 135)-X3
	MEKKIGGGDKENVLQKIYEIMKELERLGHAEASMQV SDLIYEFMKTKDENLLEEAERLLEEVRGGSGGGGS GGGSGGGSGGGSGGGDKENVLQKIYEIMKELERLGHAEA SMQVSDLIYEFMKTKDENLLEEAERLLEEVRGGGS GGGSAWSHPQFEKGGGSGGGSSGSWSHPQFEK (SE Q ID NO: 331)	X1- DKNENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVR(SEQ ID NO: 135)-X2- DKNENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVR(SEQ ID NO: 135)-X3
1- 1_GGG GS20		X1- DKNENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVR(SEQ ID NO: 135)-X2- DKNENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVR(SEQ ID NO: 135)-X3
	MEKKIGGGDKENVLQKIYEIMKELERLGHAEASMQV SDLIYEFMKTKDENLLEEAERLLEEVRGGSGGGGS GGGSGGGDKENVLQKIYEIMKELERLGHAEASMQVS DLIYEFMKTKDENLLEEAERLLEEVRGGSGGGSSA WSHPQFEKGGGSGGGSSGSWSHPQFEK (SEQ ID NO: 332)	X1- DKNENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVR(SEQ ID NO: 135)-X2- DKNENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVR(SEQ ID NO: 135)-X3
1- 1_GGG GS15		X1- DKNENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVR(SEQ ID NO: 135)-X2- DKNENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVR(SEQ ID NO: 135)-X3
1- 1_GGG	MEKKIGGGDKENVLQKIYEIMKELERLGHAEASMQV SDLIYEFMKTKDENLLEEAERLLEEVRGGSGGGGS GGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYE	X1- DKNENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVR(SEQ ID NO:

GS10	FMKTKDENLLEEAERLLEEVRKGGGSGGSAWSHPQFEKGGGSGGSAWSHPQFEK (SEQ ID NO: 333)	135)-X2- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTCDENLLEEAERLLEEVRK (SEQ ID NO: 135)-X3
2- 1_GGG GS10	MEKKIGGGELEEQVMHVLDQVSELAHELLHKLTGEE LERAAYFNWWATEMMLELIKSDDEREIREIEEEARR ILEHLEELARKGGSGGGSGGDKENVLQKIYEIMKE LERLGHAEASMQVSDLIYEFMKTCDENLLEEAERLL EEVRKGGGSGGSAWSHPQFEKGGGSGGSAWS HPQFEK (SEQ ID NO: 334)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEARRILEHLE ELARK (SEQ ID NO: 101)-X2- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTCDENLLEEAERLLEEVRK (SEQ ID NO: 135)-X3
3- 1_GGG GS10	MEKKIGGGNDELHMQMTDLVYEALHFAKDEEFQKH VFQFEKATKAYKNKDRQKLEKVVEELKELLERLLS GGSGGGSGGDKENVLQKIYEIMKELERLGHAEASM QVSDLIYEFMKTCDENLLEEAERLLEEVRKGGGSGG GSAWSHPQFEKGGGSGGSAWSHPQFEK (SEQ ID NO: 335)	X1- NDELHMQMTDLVYEALHFAKDEEFQKHVFQFEK ATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155)-X2- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTCDENLLEEAERLLEEVRK (SEQ ID NO: 135)-X3
2- 3_GGG GS10	MEKKIGGGELEEQVMHVLDQVSELAHELLHKLTGEE LERAAYFNWWATEMMLELIKSDDEREIREIEEEARR ILEHLEELARKGGSGGGSGGNDELHMQMTDLVYE ALHFAKDEEFQKHVFQFEKATKAYKNKDRQKLEKV VEELKELLERLLSGGSGGSAWSHPQFEKGGGSGG SGGSAWSHPQFEK (SEQ ID NO: 336)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEARRILEHLE ELARK (SEQ ID NO: 101)-X2- NDELHMQMTDLVYEALHFAKDEEFQKHVFQFEK ATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155)-X3
3- 2_GGG GS10	MEKKIGGGNDELHMQMTDLVYEALHFAKDEEFQKH VFQFEKATKAYKNKDRQKLEKVVEELKELLERLLS GGSGGGSGGELEEQVMHVLDQVSELAHELLHKLTG EELERAAYFNWWATEMMLELIKSDDEREIREIEEEA RRILEHLEELARKGGSGGSAWSHPQFEKGGGSGG SGGSAWSHPQFEK (SEQ ID NO: 337)	X1- NDELHMQMTDLVYEALHFAKDEEFQKHVFQFEK ATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155)-X2- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEARRILEHLE ELARK (SEQ ID NO: 101)-X3
2-3- 1_GGG GS10	MEKKIGGGELEEQVMHVLDQVSELAHELLHKLTGEE LERAAYFNWWATEMMLELIKSDDEREIREIEEEARR ILEHLEELARKGGSGGGSGGNDELHMQMTDLVYE ALHFAKDEEFQKHVFQFEKATKAYKNKDRQKLEKV VEELKELLERLLSGGSGGGSGGDKENVLQKIYEIM KELERLGHAEASMQVSDLIYEFMKTCDENLLEEAER LLEEVRKGGGSGGSAWSHPQFEKGGGSGGSGGSA WSHPQFEK (SEQ ID NO: 338)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEARRILEHLE ELARK (SEQ ID NO: 101)-X2- NDELHMQMTDLVYEALHFAKDEEFQKHVFQFEK ATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155)-X3- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTCDENLLEEAERLLEEVRK (SEQ ID NO: 135)-X4
3-2- 1_GGG GS10	MEKKIGGGNDELHMQMTDLVYEALHFAKDEEFQKH VFQFEKATKAYKNKDRQKLEKVVEELKELLERLLS GGSGGGSGGELEEQVMHVLDQVSELAHELLHKLTG EELERAAYFNWWATEMMLELIKSDDEREIREIEEEA RRILEHLEELARKGGSGGGSGGDKENVLQKIYEIM KELERLGHAEASMQVSDLIYEFMKTCDENLLEEAER LLEEVRKGGGSGGSAWSHPQFEKGGGSGGSGGSA WSHPQFEK (SEQ ID NO: 339)	X1- NDELHMQMTDLVYEALHFAKDEEFQKHVFQFEK ATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155)-X2- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEARRILEHLE ELARK (SEQ ID NO: 101)-X3- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTCDENLLEEAERLLEEVRK (SEQ ID NO: 135)-X4
2-3- 1_GGG GS15	MEKKIGGGELEEQVMHVLDQVSELAHELLHKLTGEE LERAAYFNWWATEMMLELIKSDDEREIREIEEEARR ILEHLEELARKGGSGGGSGGGSGGNDELHMQMT DLVYEALHFAKDEEFQKHVFQFEKATKAYKNKDRQ KLEKVVEELKELLERLLSGGSGGGSGGGSGGDK ENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKT CDENLLEEAERLLEEVRKGGGSGGSAWSHPQFEKGG SGGSGGSAWSHPQFEK (SEQ ID NO: 340)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEARRILEHLE ELARK (SEQ ID NO: 101)-X2- NDELHMQMTDLVYEALHFAKDEEFQKHVFQFEK ATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155)-X3- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTCDENLLEEAERLLEEVRK (SEQ ID NO: 135)-X4
3-2-	MEKKIGGGNDELHMQMTDLVYEALHFAKDEEFQKH	X1-

1_GGG GS15	VFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS GGSGGGSGGGSGGEEQVMHVLDQVSELAHELL HKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGSGGGSGGGSGGDK NVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKT DENLLEEAERLLEEVKRGSGSGGSAWSHPQFEKGG GSGGGSGGSAWSHPQFEK (SEQ ID NO: 341)	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155)-X2- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEARRILEHLE ELARK (SEQ ID NO: 101)-X3- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTCDENLLEEAERLLEEVKR (SEQ ID NO: 135)-X4
LCB3- LCB1- PAS12	MEKKINLDELHMQMTDLVYEALHFAKDEEFQKHVFQ LFEKATKAYKNKDRQKLEKVVEELKELLERLLS SPAAPAPGGDKENVLQKIYEIMKELERLGHAEASMQ VSDLIYEFMKTCDENLLEEAERLLEEVKRGSGSGS SAWSHPQFEKGGSGSGGSAWSHPQFEK (SEQ ID NO: 342)	X1NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLF EKATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155)-X2- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTCDENLLEEAERLLEEVKR (SEQ ID NO: 135)-X3
AHB2- LCB1- PAS12	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELER AAYFNWWATEMMLELIKSDDEREIREIEEEARRILE HLEELARKGGASPAAPAPGGDKENVLQKIYEIMKEL ERLGHAEASMQVSDLIYEFMKTCDENLLEEAERLLE EVKRGSGSGGSAWSHPQFEKGGSGSGGSAWSH PQFEK (SEQ ID NO: 343)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEARRILEHLE ELARK (SEQ ID NO: 101)-X2- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTCDENLLEEAERLLEEVKR (SEQ ID NO: 135)-X3
AHB2- LCB3- PAS12	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELER AAYFNWWATEMMLELIKSDDEREIREIEEEARRILE HLEELARKGGASPAAPAPGGNDELHMQMTDLVYEAL HFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVV LFEKELLERLLSGSGSGGSAWSHPQFEKGGSGGG SGGSAWSHPQFEK (SEQ ID NO: 344)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEARRILEHLE ELARK (SEQ ID NO: 101)-X2- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155)-X3
LCB3- AHB2- PAS12	MEKKINLDELHMQMTDLVYEALHFAKDEEFQKHVFQ LFEKATKAYKNKDRQKLEKVVEELKELLERLLS SPAAPAPGGEELEEQVMHVLDQVSELAHELLHKLTGE ELERAAYFNWWATEMMLELIKSDDEREIREIEEEAR RI LEHLEELARKGGSGSGGSAWSHPQFEKGGSGGG SGGSAWSHPQFEK (SEQ ID NO: 345)	X1- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155)-X2- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEARRILEHLE ELARK (SEQ ID NO: 101)-X3
AHB2- LCB3- LCB1- PAS12	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELER AAYFNWWATEMMLELIKSDDEREIREIEEEARRILE HLEELARKGGASPAAPAPGGNDELHMQMTDLVYEAL HFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVV EELKELLERLLSGGASPAAPAPGGDKENVLQKIYEI MKELERLGHAEASMQVSDLIYEFMKTCDENLLEEA RLLEEVKRGSGSGGSAWSHPQFEKGGSGGGSGGS AWSHPQFEK (SEQ ID NO: 346)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEARRILEHLE ELARK (SEQ ID NO: 101)-X2- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155)-X3- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTCDENLLEEAERLLEEVKR (SEQ ID NO: 135)-X4
LCB3- AHB2- LCB1- PAS12	MEKKINLDELHMQMTDLVYEALHFAKDEEFQKHVFQ LFEKATKAYKNKDRQKLEKVVEELKELLERLLS SPAAPAPGGEELEEQVMHVLDQVSELAHELLHKLTGE ELERAAYFNWWATEMMLELIKSDDEREIREIEEEAR RI LEHLEELARKGGASPAAPAPGGDKENVLQKIYEI MKELERLGHAEASMQVSDLIYEFMKTCDENLLEEA RLLEEVKRGSGSGGSAWSHPQFEKGGSGGGSGGS AWSHPQFEK (SEQ ID NO: 347)	X1- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155)-X2- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEARRILEHLE ELARK (SEQ ID NO: 101)-X3- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTCDENLLEEAERLLEEVKR (SEQ ID NO: 135)-X4
LCB3- AHB2- LCB1- PAS24	MEKKINLDELHMQMTDLVYEALHFAKDEEFQKHVFQ LFEKATKAYKNKDRQKLEKVVEELKELLERLLS SPAAPAPASPAAPAPSAPAGGELEEQVMHVLDQVSE LAHELLHKLTGEELERAAYFNWWATEMMLELIKSD EREIREIEEEARRILEHLEELARKGGASPAAPAPAS PAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAE ASMQVSDLIYEFMKTCDENLLEEAERLLEEVKRGSG SGGSAWSHPQFEKGGSGGGSGGSAWSHPQFEK (SE	X1- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155)-X2- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEARRILEHLE ELARK (SEQ ID NO: 101)-X3- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF

	Q ID NO: 348)	MKTKDENLLEEAERLLEEVRK (SEQ ID NO: 135) -X4
AHB2v 2- LCB1_ PAS12	MEKKIELEEQVMHVLDQVSELAHELLHKLGTGEELER AAYFNWWATEMMLELIKSDDEREIREIEEEAARILE HLEELARTGGASPAAPAPGGDKENVLQKIYEIMKEL ERLGHAEASMQVSDLIYEFMKT KDENLLEEAERLLE EVKRGSGSGSSGSAWSHPQFEKGGGSGGSGGSAWSH PQFEK (SEQ ID NO: 349)	X1- ELEEQVMHVLDQVSELAHELLHKLGTGEELERAAAYF NWWATEMMLELIKSDDEREIREIEEEAARILEHLE ELART (SEQ ID NO: 164) -X2- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKT KDENLLEEAERLLEEVRK (SEQ ID NO: 135) -X3
AHB2v 2- LCB3_ PAS12	MEKKIELEEQVMHVLDQVSELAHELLHKLGTGEELER AAYFNWWATEMMLELIKSDDEREIREIEEEAARILE HLEELARTGGASPAAPAPGGNLDLHMOMTDLVYEA LHFAKDEEFQKHVFQLFEEKATKAYKNKDRQKLEKVV EELKELLERLRLSGGSGSSGSAWSHPQFEKGGGSGGG SGGSAWSHPQFEK (SEQ ID NO: 350)	X1- ELEEQVMHVLDQVSELAHELLHKLGTGEELERAAAYF NWWATEMMLELIKSDDEREIREIEEEAARILEHLE ELART (SEQ ID NO: 164) -X2- NLDELHMOMTDLVYEALHFAKDEEFQKHVFQLFEEK ATKAYKNKDRQKLEKVVVEELKELLERLLS (SEQ ID NO: 155) -X3
LCB3- AHB2v 2_PAS 12	MEKKINLDELHMOMTDLVYEALHFAKDEEFQKHVFQ LFEEKATKAYKNKDRQKLEKVVVEELKELLERLLSGGA SPAAPAPGGEELEEQVMHVLDQVSELAHELLHKLGTGE ELERAAAYFNWWATEMMLELIKSDDEREIREIEEEAAR RILEHLEELARTGGSGSSGSAWSHPQFEKGGGSGGG SGGSAWSHPQFEK (SEQ ID NO: 351)	X1- NLDELHMOMTDLVYEALHFAKDEEFQKHVFQLFEEK ATKAYKNKDRQKLEKVVVEELKELLERLLS (SEQ ID NO: 155) -X2- ELEEQVMHVLDQVSELAHELLHKLGTGEELERAAAYF NWWATEMMLELIKSDDEREIREIEEEAARILEHLE ELART (SEQ ID NO: 164) -X3
AHB2v 2- LCB3- LCB1_ PAS12	MEKKIELEEQVMHVLDQVSELAHELLHKLGTGEELER AAYFNWWATEMMLELIKSDDEREIREIEEEAARILE HLEELARTGGASPAAPAPGGNLDLHMOMTDLVYEA LHFAKDEEFQKHVFQLFEEKATKAYKNKDRQKLEKVV EELKELLERLRLSGGASPAAPAPGGDKENVLQKIYEI MKELERLGHAEASMQVSDLIYEFMKT KDENLLEEA RLLEEVRKGGSGSSGSAWSHPQFEKGGGSGGGSGGS AWSHPQFEK (SEQ ID NO: 352)	X1- ELEEQVMHVLDQVSELAHELLHKLGTGEELERAAAYF NWWATEMMLELIKSDDEREIREIEEEAARILEHLE ELART (SEQ ID NO: 164) -X2- NLDELHMOMTDLVYEALHFAKDEEFQKHVFQLFEEK ATKAYKNKDRQKLEKVVVEELKELLERLLS (SEQ ID NO: 155) -X3- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKT KDENLLEEAERLLEEVRK (SEQ ID NO: 135) -X4
LCB3- AHB2v 2- LCB1_ PAS12	MEKKINLDELHMOMTDLVYEALHFAKDEEFQKHVFQ LFEEKATKAYKNKDRQKLEKVVVEELKELLERLLSGGA SPAAPAPGGEELEEQVMHVLDQVSELAHELLHKLGTGE ELERAAAYFNWWATEMMLELIKSDDEREIREIEEEAAR RILEHLEELARTGGASPAAPAPGGDKENVLQKIYEI MKELERLGHAEASMQVSDLIYEFMKT KDENLLEEA RLLEEVRKGGSGSSGSAWSHPQFEKGGGSGGGSGGS AWSHPQFEK (SEQ ID NO: 353)	X1- NLDELHMOMTDLVYEALHFAKDEEFQKHVFQLFEEK ATKAYKNKDRQKLEKVVVEELKELLERLLS (SEQ ID NO: 155) -X2- ELEEQVMHVLDQVSELAHELLHKLGTGEELERAAAYF NWWATEMMLELIKSDDEREIREIEEEAARILEHLE ELART (SEQ ID NO: 164) -X3- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKT KDENLLEEAERLLEEVRK (SEQ ID NO: 135) -X4
AHB2v 2- LCB3- LCB1_ PAS24	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEK GGSGSGEELEEQVMHVLDQVSELAHELLHKLGTGEE RAAYFNWWATEMMLELIKSDDEREIREIEEEAARIL EHLEELARTGGASPAAPAPASPAAPAPSAPAGGNLD ELHMOMTDLVYEALHFAKDEEFQKHVFQLFEEKATKA YKNKDRQKLEKVVVEELKELLERLLSGGASPAAPAPA SPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAE ASMQVSDLIYEFMKT KDENLLEEAERLLEEVRK (SE Q ID NO: 354)	X1- ELEEQVMHVLDQVSELAHELLHKLGTGEELERAAAYF NWWATEMMLELIKSDDEREIREIEEEAARILEHLE ELART (SEQ ID NO: 164) -X2- NLDELHMOMTDLVYEALHFAKDEEFQKHVFQLFEEK ATKAYKNKDRQKLEKVVVEELKELLERLLS (SEQ ID NO: 155) -X3- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKT KDENLLEEAERLLEEVRK (SEQ ID NO: 135)
LCB3- AHB2v 2- LCB1_ PAS24	MEKKINLDELHMOMTDLVYEALHFAKDEEFQKHVFQ LFEEKATKAYKNKDRQKLEKVVVEELKELLERLLSGGA SPAAPAPASPAAPAPSAPAGGELEEQVMHVLDQVSE LAHELLHKLGTGEELERAAAYFNWWATEMMLELIKSD EREIREIEEEAARILEHLEELARTGGASPAAPAPAS PAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAE SMQVSDLIYEFMKT KDENLLEEAERLLEEVRKGGSG SSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK (SE Q ID NO: 355)	X1- NLDELHMOMTDLVYEALHFAKDEEFQKHVFQLFEEK ATKAYKNKDRQKLEKVVVEELKELLERLLS (SEQ ID NO: 155) -X2- ELEEQVMHVLDQVSELAHELLHKLGTGEELERAAAYF NWWATEMMLELIKSDDEREIREIEEEAARILEHLE ELART (SEQ ID NO: 164) -X3- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKT KDENLLEEAERLLEEVRK (SEQ ID NO: 135)

135) -X4

Table 8A

SEQ ID	Name	Sequence
51	1GS1	DKENILQKIYEIMKTLTDLQGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVE RG GGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGG GSGGGSGGGSGGGSGGGSDKENILQKIYEIMKTLTDLQGHAEASMQVSDLIYEFMKQGD ERLLEEAERLLEEVE
52	1PRO1	DKENILQKIYEIMKTLTDLQGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVE RA GSGGSGGGSGGSPVPSTPPTPSPSTPPTPSPSPVPSTPPTPSPSTPPTPSPSPVPSTP PTPSPSTPPTPSPSPASGDKENILQKIYEIMKTLTDLQGHAEASMQVSDLIYEFMKQGD ERLLEEAERLLEEVE
53	3GS3	NDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE LLERLLSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGG GGGGSGGGSGGGSGGGSGGGSGGGSDNDELHMQMTDLVYEALHFAKDEEIQKHVFQL FEKATKAYKNKDRQKLEKVVEELKELLERLLS
54	3PRO3	NDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE LLERLLSAGSGGGSGGSGGSPVPSTPPTPSPSTPPTPSPSPVPSTPPTPSPSTPPTPS PSPVPSTPPTPSPSTPPTPSPSPASGNDDELHMQMTDLVYEALHFAKDEEIQKHVFQL FEKATKAYKNKDRQKLEKVVEELKELLERLLS
55	1GS3	DKENILQKIYEIMKTLTDLQGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVE RG GGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGG GSGGGSGGGSGGGSGGGSDNDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEKATKAY KNKDRQKLEKVVEELKELLERLLS
56	3GS1	NDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE LLERLLSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGG GGGGSGGGSGGGSGGGSGGGSGGGSDKENILQKIYEIMKTLTDLQGHAEASMQVSDLI YEFMKQGDERLLEEAERLLEEVE
58	1PRO3	DKENILQKIYEIMKTLTDLQGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVE RA GSGGSGGGSGGSPVPSTPPTPSPSTPPTPSPSPVPSTPPTPSPSTPPTPSPSPVPSTP PTPSPSTPPTPSPSPASGNDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEKATKAY KNKDRQKLEKVVEELKELLERLLS
59	3PRO1	NDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE LLERLLSAGSGGGSGGSGGSPVPSTPPTPSPSTPPTPSPSPVPSTPPTPSPSTPPTPS PSPVPSTPPTPSPSTPPTPSPSPASGDKENILQKIYEIMKTLTDLQGHAEASMQVSDLI YEFMKQGDERLLEEAERLLEEVE
454	CSL- LCB1- GS15- LCB1	DKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVE RG GGGSGGGSGGGSGGGSGGGSDKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERL LEEAERLLEEVE
455	CSL- LCB3- GS15- LCB3	NDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKE LLERLLSGGGSGGGSGGGSGGGSDNDELHMLMTDLVYEALHFAKDEEIKKRVFQLFEL ADKAYKNNDRQKLEKVVEELKELLERLLS
456	CSL- LCB1- GS20- LCB1	DKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVE RG GGGSGGGSGGGSGGGSGGGSDKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKK GDERLLEEAERLLEEVE
457	CSL- LCB3- GS20- LCB3	NDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKE LLERLLSGGGSGGGSGGGSGGGSDNDELHMLMTDLVYEALHFAKDEEIKKRVFQLFEL ADKAYKNNDRQKLEKVVEELKELLERLLS
458	CSL- LCB1- GS20- LCB1	DKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVE RG SSGSGSSGSGSSGSGSGSDKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKK GDERLLEEAERLLEEVE RGSSSGSSSGSSSGSGSDKEWILQKIYEIMRLLDEL GHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVE

	GS20- LCB1	
	CSL- LCB3-	NDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKE
	GS20- LCB3-	LLERLLSGSSSGSSGSSGSSGSSGSSGSSGNDELHMLMTDLVYEALHFAKDEEIKKRVF
	GS20- LCB3	QLFELADKAYKNNDRQKLEKVVEELKELLERLLSGSSSGSSSGSSSGSSSGSSGNDD
459	CSL- LCB1- XTENx2	ELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLE RLLS
	CSL- LCB1- XTENx2	DKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKGDERLLEEAERLLEEVEERG SAGGSPAGSPTSTGTSTSGDKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKG GDERLLEEAERLLEEVEERG
	CSL- LCB1- XTENx3	DKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKGDERLLEEAERLLEEVEERG SAGGSPAGSPTSTGTSTSGDKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKG GDERLLEEAERLLEEVEERGSAGGSPAGSPTSTGTSTSGDKEWILQKIYEIMRLLDEL GHAEASMRVSDLIYEFMKGDERLLEEAERLLEEVEERG
461	CSL- LCB3- XTENx2	NDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKE LLERLLSGSAGGSPAGSPTSTGTSTSGGNDELHMLMTDLVYEALHFAKDEEIKKRVF QLFELADKAYKNNDRQKLEKVVEELKELLERLLS
462	CSL- LCB3- XTENx3	NDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKE LLERLLSGSAGGSPAGSPTSTGTSTSGGNDELHMLMTDLVYEALHFAKDEEIKKRVF QLFELADKAYKNNDRQKLEKVVEELKELLERLLSGSAGGSPAGSPTSTGTSTSGGNDD ELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLE RLLS
463	C- LCB1- GS20- LCB1- GS20- LCB1- LS	DKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKGDERLLEEAERLLEEVEERG SSGSGSSSGSSGSSGSSGSSGSDKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKG GDERLLEEAERLLEEVEERGSSSGSSSGSSSGSSSGSSGSDKEWILQKIYEIMRLLDEL GHAEASMRVSDLIYEFMKGDERLLEEAERLLEEVEERG
458	C- LCB3- GS20- LCB3- GS20- LCB3- LS	NDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKE LLERLLSGSSSGSSGSSGSSGSSGSSGSSGNDELHMLMTDLVYEALHFAKDEEIKKRVF QLFELADKAYKNNDRQKLEKVVEELKELLERLLSGSSSGSSSGSSSGSSSGSSGNDD ELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLE RLLS
459	CSL- LCB1- XTEN25 x3	DKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKGDERLLEEAERLLEEVEERG GSSAGSPTSTGTSSATPSGSGTGGDKEWILQKIYEIMRLLDELGHAEASMRVSDLIY EFMKGDERLLEEAERLLEEVEERGSSAGSPTSTGTSSATPSGSGTGGDKEWILQKI YEIMRLLDELGHAEASMRVSDLIYEFMKGDERLLEEAERLLEEVEERG
464	CSL- LCB3- XTEN25 x3	NDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKE LLERLLSGGSAGSPTSTGTSSATPSGSGTGGNDELHMLMTDLVYEALHFAKDEEIKKRVF QLFELADKAYKNNDRQKLEKVVEELKELLERLLSGGSAGSPTSTGTSSATP SGSGTGGNDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEK VVEELKELLERLLS
465	LCB1_v 1.3_GS _2X	DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKGQDERLLEEAERLLEEVEERG GSSGGGSSGGGSSGGGSSGGSSGSDKENILQKIYEIMKTLEQLGHAEASMQVSDLIY EFMKGQDERLLEEAERLLEEVEERG
466	LCB1_v 1.3_XT EN_2X	DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKGQDERLLEEAERLLEEVEERG GSSAGSPTSTGTSSATPSGSGTGGDKENILQKIYEIMKTLEQLGHAEASMQVSDLIY EFMKGQDERLLEEAERLLEEVEERG
467	LCB1_v 1.3_EA AAK_2X	DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKGQDERLLEEAERLLEEVEERG GSSGEAAAKEAAAKEAAAKSSGGDKENILQKIYEIMKTLEQLGHAEASMQVSDLIY EFMKGQDERLLEEAERLLEEVEERG
468	LCB1_v 1.3_Pr o_2X	DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKGQDERLLEEAERLLEEVEERG GSSGPSTPPTSPSTPPTSPSPSGSSGDKENILQKIYEIMKTLEQLGHAEASMQVS DLIYEFMKGQDERLLEEAERLLEEVEERG
469	LCB1_v 1.3_Ub	DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKGQDERLLEEAERLLEEVEERG GSSGQIFVKTLTGTKTITLEVEPSDTIENVKAKIQDKEGIPPDQORLIFAGQLEDGFG
470		

	_2X	TLSDYNIQKESTLHLVLRRLRGGGGSSGDKENILQKIYEIMKTLEQLGHAEASMQVSD LIYEFMKQGDERLLEEAERLLEEVEER
	LCB1_v	DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVEER
	1.3_XT	GSSAGSPTSTGTSSATPSGSGTGGDKENILQKIYEIMKTLEQLGHAEASMQVSDLIY
471	EN_3X	EFMKQGDERLLEEAERLLEEVEERGGSSAGSPTSTGTSSATPSGSGTGGDKENILQKI YEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVEER
	LCB1_v	DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVEER
	1.3_EA	GSSGEAAAKEAAAKEAAAKGSSGGDKENILQKIYEIMKTLEQLGHAEASMQVSDLIY
472	AAK_3X	EFMKQGDERLLEEAERLLEEVEERGGSSGEAAAKEAAAKEAAAKGSSGGDKENILQKI YEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVEER
	LCB1_v	DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVEER
	1.3_Pr	GSSGPSTPPTPSPSTPPTPSPSPGGSSGDKENILQKIYEIMKTLEQLGHAEASMQVS
473	o_3X	DLIYEFMKQGDERLLEEAERLLEEVEERGGSSGPSTPPTPSPSTPPTPSPSPGGSSGD KENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVEER
		DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVEER
		GSSGQIFVKTLTGKTTITLEVEPSDTIENVKAKIQDKEGIPPDQQRILFAGKQLEDGR
		TLSDYNIQKESTLHLVLRRLRGGGGSSGDKENILQKIYEIMKTLEQLGHAEASMQVSD
	LCB1_v	LIYEFMKQGDERLLEEAERLLEEVEERGGSSGQIFVKTLTGKTTITLEVEPSDTIENVK
474	1.3_Ub	AKIQDKEGIPPDQQRILFAGKQLEDGRTLSDYNIQKESTLHLVLRRLRGGGGSSGDKE NILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVEER
	1GS1_N	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTNDENLLEEAERLLEEVEKRG
475	TS	GSSGGSSGGSSGGSSGGSSGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIY EFMKTNDENLLEEAERLLEEVEKRG
	1Pro1_	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTNDENLLEEAERLLEEVEKRG
476	NTS	GSSGPSTPPTPSPSTPPTPSPSPGGSSGDKENVLQKIYEIMKELERLGHAEASMQVS DLIYEFMKTNDENLLEEAERLLEEVEKRG
	3GS3_N	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE
477	TS	LLERLLSGSSGGSSGGSSGGSSGGSSGGSSGNLDELHMQMTDLVYEALHFAKDEEF QKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS
	3Pro3_	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE
478	NTS	LLERLLSGSSGPSTPPTPSPSTPPTPSPSPGGSSGNLDELHMQMTDLVYEALHFAK DEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS
	1GS1_C	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTNDENLLEEAERLLEEVEKRG
475	TS	GSSGGSSGGSSGGSSGGSSGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIY EFMKTNDENLLEEAERLLEEVEKRG
	1Pro1_	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTNDENLLEEAERLLEEVEKRG
476	CTS	GSSGPSTPPTPSPSTPPTPSPSPGGSSGDKENVLQKIYEIMKELERLGHAEASMQVS DLIYEFMKTNDENLLEEAERLLEEVEKRG
	3GS3_C	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE
477	TS	LLERLLSGSSGGSSGGSSGGSSGGSSGGSSGNLDELHMQMTDLVYEALHFAKDEEF QKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS
	3Pro3_	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE
478	CTS	LLERLLSGSSGPSTPPTPSPSTPPTPSPSPGGSSGNLDELHMQMTDLVYEALHFAK DEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS
		DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTNDENLLEEAERLLEEVEKRG
		GSSGGSSGGSSGGSSGGSSGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIY
	1GS1GS	DLIYEFMKTNDENLLEEAERLLEEVEKRGSSGGSSGGSSGGSSGGSSGDKENVLQKI
479	1_NTS	YEIMKELERLGHAEASMQVSDLIYEFMKTNDENLLEEAERLLEEVEKRG
		DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTNDENLLEEAERLLEEVEKRG
		GSSGPSTPPTPSPSTPPTPSPSPGGSSGDKENVLQKIYEIMKELERLGHAEASMQVS
	1Pro1P	DLIYEFMKTNDENLLEEAERLLEEVEKRGSSGPSTPPTPSPSTPPTPSPSPGGSSGD
480	ro1_NT	KENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTNDENLLEEAERLLEEVEKRG
	S	
		NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE
		LLERLLSGSSGGSSGGSSGGSSGGSSGGSSGNLDELHMQMTDLVYEALHFAKDEEF
		QKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGSSGGSSGGSSGGSSGGSS
	3GS3GS	SGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEK
481	3_NTS	VVEELKELLERLLS
	3Pro3P	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE
482	ro3_NT	LLERLLSGSSGPSTPPTPSPSTPPTPSPSPGGSSGNLDELHMQMTDLVYEALHFAK

S DEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSSGPSTPPTPSP
STPPTPSPSPGGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKN
KDRQKLEKVVEELKELLERLLS

1GS1GS
479 1_CTS DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTCDENLLEEAERLLEEVRK
GSSGGSSGGSSGGSSGGSSGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIY
EFMKTCDENLLEEAERLLEEVRKGGSSGGSSGGSSGGSSGGSSGDKENVLQKI
YEIMKELERLGHAEASMQVSDLIYEFMKTCDENLLEEAERLLEEVRK

1Pro1P
480 rol_CT S DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTCDENLLEEAERLLEEVRK
GSSGPSTPPTPSPSTPPTPSPSPGGSSGDKENVLQKIYEIMKELERLGHAEASMQVS
DLIYEFMKTCDENLLEEAERLLEEVRKGGSSGPSTPPTPSPSTPPTPSPSPGGSSGD
KENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTCDENLLEEAERLLEEVRK

3GS3GS
481 3_CTS NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE
LLERLLSGSSGGSSGGSSGGSSGGSSGGSSGNLDELHMQMTDLVYEALHFAKDEEF
QKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGSSGGSSGGSSGGSSGGSS
SGGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEK
VVEELKELLERLLS

3Pro3P
482 ro3_CT S NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE
LLERLLSGSSGPSTPPTPSPSTPPTPSPSPGGSSGNLDELHMQMTDLVYEALHFAK
DEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGSSGPSTPPTPSP
STPPTPSPSPGGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKN
KDRQKLEKVVEELKELLERLLS

1GS3_N
483 TS DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTCDENLLEEAERLLEEVRK
GSSGGSSGGSSGGSSGGSSGGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLF
EKATKAYKNKDRQKLEKVVEELKELLERLLS

1Pro3_N
484 NTS DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTCDENLLEEAERLLEEVRK
GSSGPSTPPTPSPSTPPTPSPSPGGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHV
FQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS

3GS1_N
485 TS NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE
LLERLLSGSSGGSSGGSSGGSSGGSSGGSSGDKENVLQKIYEIMKELERLGHAEAS
MQVSDLIYEFMKTCDENLLEEAERLLEEVRK

3Pro1_N
486 NTS NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE
LLERLLSGSSGPSTPPTPSPSTPPTPSPSPGGSSGDKENVLQKIYEIMKELERLGH
AEASMQVSDLIYEFMKTCDENLLEEAERLLEEVRK

1GS3_C
483 TS DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTCDENLLEEAERLLEEVRK
GSSGGSSGGSSGGSSGGSSGGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLF
EKATKAYKNKDRQKLEKVVEELKELLERLLS

1Pro3_C
484 TS DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTCDENLLEEAERLLEEVRK
GSSGPSTPPTPSPSTPPTPSPSPGGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHV
FQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS

3GS1_C
485 TS NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE
LLERLLSGSSGGSSGGSSGGSSGGSSGGSSGDKENVLQKIYEIMKELERLGHAEAS
MQVSDLIYEFMKTCDENLLEEAERLLEEVRK

3Pro1_C
486 TS NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE
LLERLLSGSSGPSTPPTPSPSTPPTPSPSPGGSSGDKENVLQKIYEIMKELERLGH
AEASMQVSDLIYEFMKTCDENLLEEAERLLEEVRK

3-
487 GS10-
1-
L_NTS NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE
LLERLLSGSSGGSSGGSSGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTCD
ENLLEEAERLLEEVRK

3-
488 GS10-
1_NTS NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE
LLERLLSGSSGGSSGGSSGGSSGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTCD
ENLLEEAERLLEEVRK

3-
489 GS15-
1_NTS NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE
LLERLLSGSSGGSSGGSSGGSSGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF
MKTCDENLLEEAERLLEEVRK

3-
490 GS20-
1_NTS NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE
LLERLLSGSSGGSSGGSSGGSSGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSD
LIYEFMKTCDENLLEEAERLLEEVRK

491	1-	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKT	DENLLEEAERLLEEVRG
	GS10-	GSSGGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKT	DENLLEEAERLLEEVRG
	1_NTS		
492	1-	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKT	DENLLEEAERLLEEVRG
	GS15-	GSSGGGSSGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKT	DENLLEEAERLLEEVRG
	1_NTS		
493	1-	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKT	DENLLEEAERLLEEVRG
	GS20-	GSSGGGSSGGSSGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKT	DENLLEEAERLLEEVRG
	1_NTS		
494	2-	ELEEQVMHVLQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE	IEEEARRILEHLEELARKGGSSGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKT
	1_GS10		
495	2-	ELEEQVMHVLQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE	IEEEARRILEHLEELARKGGSSGGSSGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKT
	1_GS15		
496	2-	ELEEQVMHVLQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE	IEEEARRILEHLEELARKGGSSGGSSGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKT
	1_GS20		
497	2-2-	ELEEQVMHVLQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE	IEEEARRILEHLEELARKGGSSGEELEEQVMHVLQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	1_GS10		
498	2-2-	ELEEQVMHVLQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE	IEEEARRILEHLEELARKGGSSGGSSGEELEEQVMHVLQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	1_GS15		
499	2-2-	ELEEQVMHVLQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE	IEEEARRILEHLEELARKGGSSGGSSGGSSGEELEEQVMHVLQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	1_GS20		
500	2-	ELEEQVMHVLQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE	IEEEARRILEHLEELARKGGSSGGSSGEELEEQVMHVLQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	2_GS10		
501	2-	ELEEQVMHVLQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE	IEEEARRILEHLEELARKGGSSGGSSGEELEEQVMHVLQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	2_GS15		
502	2-	ELEEQVMHVLQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE	IEEEARRILEHLEELARKGGSSGGSSGGSSGEELEEQVMHVLQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	2_GS20		
503	2-2-	ELEEQVMHVLQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE	IEEEARRILEHLEELARKGGSSGEELEEQVMHVLQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	2_GS10		
504	2-2-	ELEEQVMHVLQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE	IEEEARRILEHLEELARKGGSSGGSSGGSSGEELEEQVMHVLQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	2_GS15		
505	2-2-	ELEEQVMHVLQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE	IEEEARRILEHLEELARKGGSSGGSSGGSSGEELEEQVMHVLQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	2_GS20		
506	AHB2-	ELEEQVMHVLQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE	IEEEARRILEHLEELARKGGASPAAPAPASPAAPAPASAPAGGELEEQVMHVLQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	AHB2_P		
	AS		

		ARK
507	LCB3- LCB1_P AS	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE LLERLLSGGASPAAPAPASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASM QVSDLIYEFMKTCDERLLEEAERLLEEVR
508	AHB2- LCB1_P AS	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGASPAAPAPASPAAPAPSAPAGGDKENVLQKIYEIMKE LERLGHAEASMQVSDLIYEFMKTCDERLLEEAERLLEEVR
509	AHB2_3 x_PAS	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGASPAAPAPASPAAPAPSAPAGGELEEQVMHVLDQVSE LAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEEL ARKGGASPAAPAPASPAAPAPSAPAGGELEEQVMHVLDQVSELAHELLHKLTGEELE RAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK
510	3-2- 1_PAS	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE LLERLLSGGASPAAPAPASPAAPAPSAPAGGELEEQVMHVLDQVSELAHELLHKLTG EELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAP APASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTCDER LLEEAERLLEEVR
511	2-3- 1_PAS	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGASPAAPAPASPAAPAPSAPAGGNLDELHMQMTDLVYE ALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAP APASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTCDER LLEEAERLLEEVR
512	1-1- 1_PAS2 4	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTCDENLLEEAERLLEEVRG GASPAAPAPASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYE FMKTCDENLLEEAERLLEEVRGKGGASPAAPAPASPAAPAPSAPAGGDKENVLQKIYE IMKELERLGHAEASMQVSDLIYEFMKTCDENLLEEAERLLEEVR
509	2-2- 2_PAS2 4	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGASPAAPAPASPAAPAPSAPAGGELEEQVMHVLDQVSE LAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEEL ARKGGASPAAPAPASPAAPAPSAPAGGELEEQVMHVLDQVSELAHELLHKLTGEELE RAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK
513	3-3- 3_PAS2 4	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE LLERLLSGGASPAAPAPASPAAPAPSAPAGGNLDELHMQMTDLVYEALHFAKDEEFQ KHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAPAPASPAAPAPS APAGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKV EELKELLERLLS
514	2-2- 1_PAS2 4	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGASPAAPAPASPAAPAPSAPAGGELEEQVMHVLDQVSE LAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEEL ARKGGASPAAPAPASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSD LIYEFMKTCDENLLEEAERLLEEVR
515	2- 2_PAS1 6	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGASPAAPAPASPAAGGELEEQVMHVLDQVSELAHELLHK LTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK
516	2- 2_PAS1 1	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGASPAAPAGGELEEQVMHVLDQVSELAHELLHKLTGEE LERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK
517	3- 1_PAS1 6	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE LLERLLSGGASPAAPAPASPAAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYE FMKTCDERLLEEAERLLEEVR
518	3- 1_PAS1 1	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE LLERLLSGGASPAAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKT CDERLLEEAERLLEEVR
519	2- 1_PAS1 6	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGASPAAPAPASPAAGGDKENVLQKIYEIMKELERLGHAE ASMQVSDLIYEFMKTCDERLLEEAERLLEEVR
520	2- 1_PAS1 1	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGASPAAPAGGDKENVLQKIYEIMKELERLGHAEASMQV SDLIYEFMKTCDERLLEEAERLLEEVR

			NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKE
	3v2.3-		LLERILSGGASPAAPAPASPAAPAPSAPAGGELEEQVMHVLDDQVSELAHELLHKLGT
	2-		EELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAP
521	1_PAS2		APASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKE
	4		RLLEEAERLLEEVKR
			ELEEQVMHVLDDQVSELAHELLHKLGTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	2-		IEEEARRILEHLEELARKGGASPAAPAPASPAAPAPSAPAGGNIDELLMQVTDLIYE
	3v2.3-		ALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAP
522	1_PAS2		APASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKE
	4		RLLEEAERLLEEVKR
			ELEEQVMHVLDDQVSELAHELLHKLGTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	2-2-		IEEEAARILEHLEELARTGGASPAAPAPASPAAPAPSAPAGGELEEQVMHVLDDQVSE
	2_PAS2		LAHELLHKLGTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEAARILEHLEEL
523	4_ompT		ARTGGASPAAPAPASPAAPAPSAPAGGELEEQVMHVLDDQVSELAHELLHKLGTGEELE
			RAAYFNWWATEMMLELIKSDDEREIREIEEEAARILEHLEELART
			DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKE
	1-1-		LLLEEAERLLEEVTRG
	1_PAS2		GASPAAPAPASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYE
524	4_ompT		FMKTKE
			NLLEEAERLLEEVTRGASPAAPAPASPAAPAPSAPAGGDKENVLQKIYE
			IMKELERLGHAEASMQVSDLIYEFMKTKE
			NLLEEAERLLEEVTR
			NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKE
	3v2.3-		LLERILSGGASPAAPAPASPAAPAPSAPAGGELEEQVMHVLDDQVSELAHELLHKLGT
	2-		EELERAAYFNWWATEMMLELIKSDDEREIREIEEEAARILEHLEELARTGGASPAAP
525	1_PAS2		APASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKE
	4_ompT		RLLEEAERLLEEVKR
			ELEEQVMHVLDDQVSELAHELLHKLGTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	2-		IEEEAARILEHLEELARTGGASPAAPAPASPAAPAPSAPAGGNIDELLMQVTDLIYE
	3v2.3-		ALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAP
526	1_PAS2		APASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKE
	4_ompT		RLLEEAERLLEEVKR
			NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKE
	3v2.3-		LLERILSGGASPAAPAPASPAAPAPSAPAGGELEEQVMHVLDDQVSELAHELLHKLGT
	2-		EELERAAYFNWWATEMMLELIKSDDEREIREIEEEAARILEHLEELARTGGASPAAP
527	1_PAS2		APASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKE
	4		NLLEEAERLLEEVKR
			ELEEQVMHVLDDQVSELAHELLHKLGTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	2-		IEEEARRILEHLEELARKGGASPAAPAPASPAAPAPSAPAGGNIDELLMQVTDLIYE
	3v2.3-		ALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAP
528	1_PAS2		APASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKE
	4		NLLEEAERLLEEVKR
			NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKE
	3v2.3-		LLERILSGGASPAAPAPASPAAPAPSAPAGGELEEQVMHVLDDQVSELAHELLHKLGT
	2-		EELERAAYFNWWATEMMLELIKSDDEREIREIEEEAARILEHLEELARTGGASPAAP
529	1_PAS2		APASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKE
	4_ompT		NLLEEAERLLEEVKR
			ELEEQVMHVLDDQVSELAHELLHKLGTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	2-		IEEEAARILEHLEELARTGGASPAAPAPASPAAPAPSAPAGGNIDELLMQVTDLIYE
	3v2.3-		ALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAP
530	1_PAS2		APASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKE
	4_ompT		NLLEEAERLLEEVKR
			ELEEQVMHVLDDQVSELAHELLHKLGTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	2-		IEEEARRILEHLEELARKGGASPAAPAPASPAAPAPSAPAGGNIDELLMQVTDLIYE
	3v2.3-		ALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAP
	1_PAS2		APASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKE
538	4_N-His-TEV		NLLEEAERLLEEVKR
			ELEEQVMHVLDDQVSELAHELLHKLGTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	2-		IEEEAARILEHLEELARTGGASPAAPAPASPAAPAPSAPAGGNIDELLMQVTDLIYE
	3v2.3-		ALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAP
	1_PAS2		APASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKE
530	4_ompT_N-His-		NLLEEAERLLEEVKR

		TEV
		ELEEQVMHVLDDQVSELAHELLHKLGTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGASPAAPAPASPAAPAPSAPAGGNIDELLMQVTDLIYE
	2-3-	ALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAP
	1_PAS2	APASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKT KDE
531	4_NTSF	NLLEEAERLLEEVR
		ELEEQVMHVLDDQVSELAHELLHKLGTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGASPAAPAPASPAAPAPSAPAGGNIDELLMQVTDLIYE
	2-3-	ALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAP
	1_PAS2	APASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKT KDE
531	4_NTS3	NLLEEAERLLEEVR
	F	
		ELEEQVMHVLDDQVSELAHELLHKLGTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGASPAAPAPASPAAPAPSAPAGGNIDELLMQVTDLIYE
	2-3-	ALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAP
	1_PAS2	APASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKT KDE
531	4_NTSM	NLLEEAERLLEEVR
	2-	
	PAS24-	ELEEQVMHVLDDQVSELAHELLHKLGTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	3-	IEEEARRILEHLEELARKGGASPAAPAPASPAAPAPSAPAGGNIDELLMQVTDLIYE
	PAS16-	ALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAP
	1_NTS3	APASPAAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKT K DENLLEEAER
532	F	LLEEVR
	2-	
	PAS16-	ELEEQVMHVLDDQVSELAHELLHKLGTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	3-	IEEEARRILEHLEELARKGGASPAAPAPASPAAGGNIDELLMQVTDLIYEALHFAKDE
	PAS16-	EFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAPAPASPAAGG
533	1_NTS3	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKT K DENLLEEAERLLEEVR
	F	
	2-	
	PAS11-	ELEEQVMHVLDDQVSELAHELLHKLGTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	3-	IEEEARRILEHLEELARKGGASPAAPAGGNIDELLMQVTDLIYEALHFAKDEEFQKH
	PAS16-	AFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAPAPASPAAGGDKENV
534	1_NTS3	LQKIYEIMKELERLGHAEASMQVSDLIYEFMKT K DENLLEEAERLLEEVR
	F	
	2-	
	PAS24-	ELEEQVMHVLDDQVSELAHELLHKLGTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	3-	IEEEARRILEHLEELARKGGASPAAPAPASPAAPAPSAPAGGNIDELLMQVTDLIYE
	PAS11-	ALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAP
	1_NTS3	AGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKT K DENLLEEAERLLEEVR
535	F	KR
	2-	
	PAS16-	ELEEQVMHVLDDQVSELAHELLHKLGTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	3-	IEEEARRILEHLEELARKGGASPAAPAPASPAAGGNIDELLMQVTDLIYEALHFAKDE
	PAS11-	EFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAPAGGDKENV
536	1_NTS3	LQKIYEIMKELERLGHAEASMQVSDLIYEFMKT K DENLLEEAERLLEEVR
	F	
	2-	
	PAS11-	ELEEQVMHVLDDQVSELAHELLHKLGTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	3-	IEEEARRILEHLEELARKGGASPAAPAGGNIDELLMQVTDLIYEALHFAKDEEFQKH
	PAS11-	AFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAPAGGDKENVLQKIY
537	1_NTS3	EIMKELERLGHAEASMQVSDLIYEFMKT K DENLLEEAERLLEEVR
	F	
	2-	
	PAS11-	ELEEQVMHVLDDQVSELAHELLHKLGTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	3-	IEEEARRILEHLEELARKGGASPAAPAGGNIDELLMQVTDLIYEALHFAKDEEFQKH
	PAS11-	AFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAPAGGDKENVLQKIY
537	1_NTS3	EIMKELERLGHAEASMQVSDLIYEFMKT K DENLLEEAERLLEEVR
	F	
	2-	
	PAS11-	ELEEQVMHVLDDQVSELAHELLHKLGTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	3-	IEEEARRILEHLEELARKGGASPAAPAGGNIDELLMQVTDLIYEALHFAKDEEFQKH
	PAS11-	AFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAPAGGDKENVLQKIY
537	1_NTS3	EIMKELERLGHAEASMQVSDLIYEFMKT K DENLLEEAERLLEEVR
	F	
	2-	
	PAS11-	ELEEQVMHVLDDQVSELAHELLHKLGTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	3-	IEEEARRILEHLEELARKGGASPAAPAGGNIDELLMQVTDLIYEALHFAKDEEFQKH
	PAS11-	AFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAPAGGDKENVLQKIY
537	1_NTS3	EIMKELERLGHAEASMQVSDLIYEFMKT K DENLLEEAERLLEEVR
	F	
	2-	
	PAS11-	ELEEQVMHVLDDQVSELAHELLHKLGTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	3-	IEEEARRILEHLEELARKGGASPAAPAGGNIDELLMQVTDLIYEALHFAKDEEFQKH
	PAS11-	AFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAPAGGDKENVLQKIY
537	1_NTS3	EIMKELERLGHAEASMQVSDLIYEFMKT K DENLLEEAERLLEEVR
	F	
	2-	
	PAS11-	ELEEQVMHVLDDQVSELAHELLHKLGTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	3-	IEEEARRILEHLEELARKGGASPAAPAGGNIDELLMQVTDLIYEALHFAKDEEFQKH
	PAS11-	AFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAPAGGDKENVLQKIY
537	1_NTS3	EIMKELERLGHAEASMQVSDLIYEFMKT K DENLLEEAERLLEEVR
	F	
	2-	
	PAS11-	ELEEQVMHVLDDQVSELAHELLHKLGTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	3-	IEEEARRILEHLEELARKGGASPAAPAGGNIDELLMQVTDLIYEALHFAKDEEFQKH
	PAS11-	AFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAPAGGDKENVLQKIY
537	1_NTS3	EIMKELERLGHAEASMQVSDLIYEFMKT K DENLLEEAERLLEEVR
	F	

	4	ALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILS
	2-	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	3_PAS1	IEEEARRILEHLEELARKGGASPAAPAPASPAGGNIDELLMQVTDLIYEALHFAKDE
541	6	EFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILS
	2-	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	3_PAS1	IEEEARRILEHLEELARKGGASPAAPAGGNIDELLMQVTDLIYEALHFAKDEEFQKH
542	1	AFQLFEKATKAYKNKDKQKLEKVVEELKELLERILS
		DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTCDENLLEEAERLLEEVKRG
		GASPAAPAPASPAAPASAPAGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAY
	1-2-	FNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAPASPAAP
	1_PAS2	APSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTCDENLLEEAER
543	4	LLEEVKR
	2-	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	PAS24-	IEEEARRILEHLEELARKGGASPAAPAPASPAAPASAPAGGNLDELHMQMTDLVYE
	3-	ALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAP
	PAS24-	APASPAAPASAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTCD
544	1_NTS	NLLEEAERLLEEVKR
	2-	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	PAS24-	IEEEARRILEHLEELARKGGASPAAPAPASPAAPASAPAGGNLDELHMQMTDLVYE
	3-	ALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAP
	PAS16-	APASAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTCDENLLEEAER
545	1_NTS	LLEEVKR
	2-	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	PAS16-	IEEEARRILEHLEELARKGGASPAAPAPASPAGGNLDELHMQMTDLVYEALHFAKDE
	3-	EFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAPASPAAP
	PAS24-	APSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTCDENLLEEAER
546	1_NTS	LLEEVKR
	2-	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	PAS16-	IEEEARRILEHLEELARKGGASPAAPAPASPAGGNLDELHMQMTDLVYEALHFAKDE
	3-	EFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAPAPASPAGG
	PAS16-	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTCDENLLEEAERLLEEVKR
547	1_NTS	
	2-	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	PAS11-	IEEEARRILEHLEELARKGGASPAAPAGGNLDELHMQMTDLVYEALHFAKDEEFQKH
	3-	VFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAPAPASPAGGDKENV
	PAS16-	LQKIYEIMKELERLGHAEASMQVSDLIYEFMKTCDENLLEEAERLLEEVKR
548	1_NTS	
	2-	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	PAS24-	IEEEARRILEHLEELARKGGASPAAPAPASPAAPASAPAGGNLDELHMQMTDLVYE
	3-	ALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAP
	PAS11-	AGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTCDENLLEEAERLLEEV
549	1_NTS	KR
	2-	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	PAS16-	IEEEARRILEHLEELARKGGASPAAPAPASPAGGNLDELHMQMTDLVYEALHFAKDE
	3-	EFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAPAGGDKENV
	PAS11-	LQKIYEIMKELERLGHAEASMQVSDLIYEFMKTCDENLLEEAERLLEEVKR
550	1_NTS	
	2-	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	PAS11-	IEEEARRILEHLEELARKGGASPAAPAGGNLDELHMQMTDLVYEALHFAKDEEFQKH
	3-	VFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAPAGGDKENVLQKIY
	PAS11-	EIMKELERLGHAEASMQVSDLIYEFMKTCDENLLEEAERLLEEVKR
551	1_NTS	
		ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
		IEEEARRILEHLEELARKGGASAGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQL
	2-3-	FEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASAGGDKENVLQKIYEIMKELER
552	1_PAS7	LGHAEASMQVSDLIYEFMKTCDENLLEEAERLLEEVKR
		ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
		IEEEARRILEHLEELARKGGSGSGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQ
	2-3-	LFEKATKAYKNKDRQKLEKVVEELKELLERLLSGSGSGGDKENVLQKIYEIMKEL
553	1_GS7	ERLGHAEASMQVSDLIYEFMKTCDENLLEEAERLLEEVKR

[illegible]

569	3-	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE
	1_GGGG S10	LLERLLSGSGGGSGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKD ENLLEEAERLLEEVR
570	2-	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	3_GGGG S10	IEEEARRILEHLEELARKGGSGGGSGGNLDELHMQMTDLVYEALHFAKDEEFQKHV FQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS
571	3-	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE
	2_GGGG S10	LLERLLSGSGGGSGGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWAT EMMLELIKSDDEREIREIEEEARRILEHLEELARK
572	2-3-	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	1_GGGG S10	IEEEARRILEHLEELARKGGSGGGSGGNLDELHMQMTDLVYEALHFAKDEEFQKHV FQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGSGGGSGGDKENVLQKIYEI MKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVR
573	3-2-	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE
	1_GGGG S10	LLERLLSGSGGGSGGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWAT EMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSGGGSGGDKENVLQKIYEI MKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVR
560	2-3-	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	1_GGGG S15	IEEEARRILEHLEELARKGGSGGGSGGGSGGNLDELHMQMTDLVYEALHFAKDEE FQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGSGGGSGGGSGGDK ENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVR
574	3-2-	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE
	1_GGGG S15	LLERLLSGSGGGSGGGSGGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSGGGSGGGSGGDK ENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVR
575	LCB3-	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE
	LCB1_P AS12	LLERLLSGGASPAAPAPGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKT KDENLLEEAERLLEEVR
576	AHB2-	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	LCB1_P AS12	IEEEARRILEHLEELARKGGASPAAPAPGGDKENVLQKIYEIMKELERLGHAEASMQ VSDLIYEFMKTKDENLLEEAERLLEEVR
577	AHB2-	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	LCB3_P AS12	IEEEARRILEHLEELARKGGASPAAPAPGGNDELHMQMTDLVYEALHFAKDEEFQK HVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS
578	LCB3-	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE
	AHB2_P AS12	LLERLLSGGASPAAPAPGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWW ATEMMLELIKSDDEREIREIEEEARRILEHLEELARK
579	AHB2-	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	LCB3- LCB1_P AS12	IEEEARRILEHLEELARKGGASPAAPAPGGNDELHMQMTDLVYEALHFAKDEEFQK HVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAPAPGGDKENVLQK IYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVR
580	LCB3-	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE
	AHB2- LCB1_P AS12	LLERLLSGGASPAAPAPGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWW ATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAPGGDKENVLQK IYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVR
581	LCB3-	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE
	AHB2- LCB1_P AS24	LLERLLSGGASPAAPAPASPAAPASAPAGGELEEQVMHVLDQVSELAHELLHKLTG EELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAP APASPAAPASAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTDE NLLEEAERLLEEVR
582	AHB2v2 -	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	LCB1_P AS12	IEEEAARILEHLEELARTGGASPAAPAPGGDKENVLQKIYEIMKELERLGHAEASMQ VSDLIYEFMKTKDENLLEEAERLLEEVR
583	AHB2v2 -	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	LCB3_P AS12	IEEEAARILEHLEELARTGGASPAAPAPGGNDELHMQMTDLVYEALHFAKDEEFQK HVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS

584	LCB3-	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE
	AHB2v2	LLERLLSGGASPAAPAPGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWW
	_PAS12	ATEMMLELIKSDDEREIREIEEEAARILEHLEELART
585	AHB2v2	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	-LCB3-	IEEEAARILEHLEELARTGGASPAAPAPGGNDELHMQMTDLVYEALHFAKDEEFQK
	LCB1_P	HVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAPAPGGDKENVLQK
586	AS12	IYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVR
	LCB3-	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE
	AHB2v2	LLERLLSGGASPAAPAPGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWW
587	-	ATEMMLELIKSDDEREIREIEEEAARILEHLEELARTGGASPAAPAPGGDKENVLQK
	LCB1_P	IYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVR
	AS12	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
588	AHB2v2	IEEEAARILEHLEELARTGGASPAAPAPASPAAPASAPAGGNDELHMQMTDLVYE
	-LCB3-	ALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAP
	LCB1_P	APASPAAPASAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDE
589	AS24	NLEEAERLLEEVR
	LCB3-	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE
	AHB2v2	LLERLLSGGASPAAPAPASPAAPASAPAGGELEEQVMHVLDQVSELAHELLHKLTG
590	-	EELERAAYFNWWATEMMLELIKSDDEREIREIEEEAARILEHLEELARTGGASPAAP
	LCB1_P	APASPAAPASAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDE
	AS24	NLEEAERLLEEVR

In some embodiments, the polypeptides comprise an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of a genus selected from those recited in the middle column of Table 8. In these embodiments, X1, X2, X3 (when recited in the genus), and X4 (when recited in the genus) may be present or absent, and when present may be any sequence of 1 or more amino acids. By way of example, the genus in the middle column, first row of sequences in Table 8 is X1-(SEQ ID NO:4)-X2-(SEQ ID NO:4). In this embodiment, X2 may be present or absent and, when present, may (for example) comprise an amino acid linker of any suitable length and amino acid composition as deemed appropriate. X1 may be present or absent, and when present may comprise any amino acid residue or residues as deemed appropriate, including but not limited to a leader sequence, a detectable tag, a purification tag, etc.

In another example, the genus in the middle column, last row of sequences in Table 8 is X1-(SEQ ID NO: 155)-X2-(SEQ ID NO: 164)-X3-(SEQ ID NO: 135)-X4. In this embodiment, X2 and X3 may be present or absent and, when present, may (for example) comprise an amino acid linker of any suitable length and amino acid composition as deemed appropriate. X1 and X4 may be present or absent, and when present may comprise any amino acid residue or residues as deemed appropriate, including but not limited to a leader sequence, a detectable tag, a purification tag, secretion signal etc.

In some embodiments, the optional domain that is present between monomer domains is present and may comprise an amino acid linker. Under this embodiment, (a) in the first example above X2 would be present and comprise an amino acid linker of any appropriate length and amino acid composition, and X1 may be present or absent; and (b) in the second example above one or both of X2 and X3 would be present and comprise an amino acid linker of any appropriate length and amino acid composition, and X1 and X4 may independently be present or absent.

In any embodiment or combination of embodiments of the polypeptides disclosed herein, the polypeptide may further comprise one or more additional functional peptide domain. Any such additional functional peptide domain may be used as appropriate for an intended purpose. In various non-limiting embodiments, the additional functional peptide domain may comprise, for example, a targeting domain, a detectable domain, a scaffold domain, a secretion signal, an Fc domain, or a further therapeutic peptide domain. In one embodiment, the additional functional domain comprises an Fc domain, including but not limited to an Fc domain comprising an amino acid sequence comprising the amino acid sequence of SEQ ID NO:64.

Fc domain:

EPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS
TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEW
ESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSQSVMEALHNHYTQKSLSLSPGK (SEQ ID NO:64)

In another embodiment, the added functional domain may comprise an oligomerization domain. Any oligomerization domain may be used as suitable to generate an oligomer as suitable for an intended purpose. In one non-limiting embodiment, the oligomerization domain may comprise a homotrimerization domain. Exemplary oligomerization domains may comprises an amino acid sequence selected from the group consisting of SEQ ID NOS:179-189 and 589-594.

1rfo GYIPEAPRDGQAYVRKDGWVLLSTFL (SEQ ID NO: 179)

1na0

_int EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYY

2-R3 QKALELDPNNAEAKQNLGNAKQKQG (SEQ ID NO: 180)

1na0 EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALEL

_int DPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNLGNAKQKQG (SEQ ID NO:
2 181)

6msr

GSEYEIRKALEELKASTAELKRATASLRASTEELKKNPSEDALVENNRLIVEHNA

IIVENNRIIAAVLELIVRAIK (SEQ ID NO: 182)

1gcm RMKQIEDKIEEILSKIYHIENEIARIKKLIGER (SEQ ID NO: 183)

pRO-
2-
noHi GSEYEIRKALEELKASTAELKRSTASLRASTEELKKNPSEDALVENNRLIVENNA
s IIVENNRIIAAVLELIVRAIK (SEQ ID NO: 184)

1na0 NLAEKMYKAGNAMYRKQYTTIAITLALLKDPNNAEAWYNLGNAAAYKKGEYDEAIEAYQKALELDP
_3 NNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNLGNKQKQ (SEQ ID NO: 185)

4pn9 GEIAKSLKEIAKSLKEIAWSLKEIAKSLKG (SEQ ID NO: 186)

SB17 SEALEELEKALRELKKSTDELERSTEELEKNPSEDALVENNRLIVENNKIIVE
5 VLRRIIAKVLK (SEQ ID NO: 187)

SB17 SPELEKALRELKKSTDELERSTEELEKNGSPEALVENNRLIVENNKIIVEVLR
5.1 IIAK (SEQ ID NO: 188)

SB17 SEKALRELKKSTDELERSTEELEKNGSPEALVENNRLIVENNKIIVEVLR (SEQ ID NO: 189)
5.2

5L6H SEELRAVADLQRLNIELARKLLEAVARLQELNIDLVRKTSELTDEKTIREE
C3_1 IRKVKEESKRIVEEAEIRRAKEESRKIADSR (SEQ ID NO: 589)

3672 EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQG
9.2 DYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDP
NNAEAWYNLGNAYYKQGDYDEAIEYYQKALEL (SEQ ID NO: 590)

1na0
_int
2-R3 EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQG
v2 DYDEAIEYYQKALELDPNNAEAKQNLGNKQKQ (SEQ ID NO: 591)

1na0
_int
2-R3 EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQG
v3 DYDEAIEYYQKALELDPNNAEAKQNLGNKQKQ (SEQ ID NO: 592)

1na0 EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQG
_int DYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPN
2 v2 NAEAKQNLGNKQKQ (SEQ ID NO: 593)

6msr EYEIRKALEELKASTAELKRATASLRASTEELKKNPSEDALVENNRLIVEH
v2 NAIIVENNRIIAAVLELIVRAIK (SEQ ID NO: 594)

In one embodiment, the polypeptide comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of

5 SEQ ID NOS 356-453 and 595-692 and a genus selected from those recited in the right hand column of Table 9 wherein genus positions X1, X2, X3, and X4 may be present or absent, and when present may be any sequence of 1 or more amino acids. In all embodiments, any N-terminal methionine residues may be present or absent in the polypeptide. In one embodiment, any N-terminal methionine residues are absent in the polypeptide.

Name	Protein	Annotated: X1, X2, X3, and X4 may be present or absent, and when present may be any sequence of 1 or more amino acids
AHB2- 6GS-1rfo	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEEARRILEHLEELARKG SGSGSGYIPEAPRDGQAYVRKDGWVLL LSTFLGGSGSSGSAWSHPQFEKGGGSGG GGSGGSAWSHPQFEK (SEQ ID NO: 356)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEEARRILEHLEELAR K (SEQ ID NO:101)-X2- GYIPEAPRDGQAYVRKDGWVLLSTFL (SEQ ID NO: 179)-X3
AHB2- 28GS- AHB2- 6GS-1rfo	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEEARRILEHLEELARKG SGSGSGSGSGSGSGSGSGSGSGSGSGS ELEEQVMHVLDQVSELAHELLHKLTGE ELERAAAYFNWWATEMMLELIKSDDERE IREIEEEEARRILEHLEELARKGSGSGS GYIPEAPRDGQAYVRKDGWVLLSTFL GGSGSGSAWSHPQFEKGGGSGGSGG SAWSHPQFEK (SEQ ID NO: 357)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEEARRILEHLEELAR K (SEQ ID NO:101)-X2- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEEARRILEHLEELAR K (SEQ ID NO:101)-X3- GYIPEAPRDGQAYVRKDGWVLLSTFL (SEQ ID NO: 179)-X4
AHB2- 5GS-1rfo	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEEARRILEHLEELARKG SGSGGYIPEAPRDGQAYVRKDGWVLL STFLGGSGSSGSAWSHPQFEKGGGSGG GGSGSAWSHPQFEK (SEQ ID NO: 358)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEEARRILEHLEELAR K (SEQ ID NO:101)-X2- GYIPEAPRDGQAYVRKDGWVLLSTFL (SEQ ID NO: 179)-X3
AHB2- 4GS-1rfo	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEEARRILEHLEELARKG SGSGYIPEAPRDGQAYVRKDGWVLLS TFLGGSGSSGSAWSHPQFEKGGGSGGG GGSAWSHPQFEK (SEQ ID NO: 359)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEEARRILEHLEELAR K (SEQ ID NO:101)-X2- GYIPEAPRDGQAYVRKDGWVLLSTFL (SEQ ID NO: 179)-X3
AHB2- 3GS-1rfo	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEEARRILEHLEELARKG SGGYIPEAPRDGQAYVRKDGWVLLST FLGGSGSSGSAWSHPQFEKGGGSGGGG GGSAWSHPQFEK (SEQ ID NO: 360)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEEARRILEHLEELAR K (SEQ ID NO:101)-X2- GYIPEAPRDGQAYVRKDGWVLLSTFL (SEQ ID NO: 179)-X3
AHB2- 28GS- AHB2- 3GS-1rfo	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEEARRILEHLEELARKG SGSGSGSGSGSGSGSGSGSGSGSGSGS ELEEQVMHVLDQVSELAHELLHKLTGE ELERAAAYFNWWATEMMLELIKSDDERE IREIEEEEARRILEHLEELARKGSGGYI PEAPRDGQAYVRKDGWVLLSTFLGGG SSGSAWSHPQFEKGGGSGGGSGGSAW SHPQFEK (SEQ ID NO: 361)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEEARRILEHLEELAR K (SEQ ID NO:101)-X2- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEEARRILEHLEELAR K (SEQ ID NO:101)-X3- GYIPEAPRDGQAYVRKDGWVLLSTFL (SEQ ID NO: 179)-X4
AHB2- 4GS- 5L6HC3_1	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEEARRILEHLEELARKG SGSSEELRAVADLQRLNIELARKLLEA VARLQELNIDLVRKTSELTDEKTIREE IRKVKEESKRIVEEAEIEIRRAKEESR KIADESRRGGSGSSGSAWSHPQFEKGGG SGGGSGGSAWSHPQFEK (SEQ ID NO: 362)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEEARRILEHLEELAR K (SEQ ID NO:101)-X2- SEELRAVADLQRLNIELARKLLEAVARLQELNIDLVR KTSELTDEKTIREEIRKVKEESKRIVEEAEIEIRRAK EESRKIADES (SEQ ID NO: 589)

80

4GS-	GS	SGSGSGSGSGSGSGSNLDELHMQMTD	NO: 155)-X2-
5L6HC3_1		LVYEALHFAKDEEFQKHVFQLFKATK AYKNKDRQKLEKVVEELKELLERLLSG SGSSEELRAVADLQRLNIELARKLLEA VARLQELNIDLVRKTSELTDEKTIREE IRKVKEESKRIVEEAEIIRAKEESR KIADESRRGGSGSSSAWSHPQFEKGGG SGGGSGGSAWSHPQFEK (SEQ ID NO: 370)	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFKAT KAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155)-X3
		MEKKINLDELHMQMTDLVYEALHFAKD EEFQKHVFQLFKATKAYKNKDRQKLE KVVEELKELLERLLSGSGSGSGSGSGS SGSGSGSGSGSGSGSNLDELHMQMTD LVYEALHFAKDEEFQKHVFQLFKATK AYKNKDRQKLEKVVEELKELLERLLSG SGSGSEELRAVADLQRLNIELARKLLE AVARLQELNIDLVRKTSELTDEKTIRE EIRKVKEESKRIVEEAEIIRAKEES RKIADESRRGGSGSSSAWSHPQFEKGG SGGGSGGSAWSHPQFEK (SEQ ID NO: 371)	X1- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFKAT KAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155)-X2- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFKAT KAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155)-X3
LCB3- 28GS- LCB3- 5GS- 5L6HC3_1		MEKKIEEAELAYLLGELAYKLGEYRIA IRAYRIALKRDPNNAEAWYNLGNAYYK QGDYDEAIEYYQKALELDPNNAEAWYN LGNAYYKQGDYDEAIEYYQKALELDPN NAEAWYNLGNAYYKQGDYDEAIEYYQK ALELGS GSDKENVLQKIYEIMKELE RLGHAEASMQVSDLIYEFMKTNDENLL EEAERLLEEVRKGGSGSSGSAWSHPQF EKGGSGGGSGGSAWSHPQFEK (SEQ ID NO: 372)	X1- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMK TKDENLLEEAEERLLEEVRK (SEQ ID NO: 135)-X2- EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNA EAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAW YNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNL GNAYYKQGDYDEAIEYYQKALEL (SEQ ID NO: 590)
36729.2_ LCB1v2.2_ _6GS		MEKKIEEAELAYLLGELAYKLGEYRIA IRAYRIALKRDPNNAEAWYNLGNAYYK QGDYDEAIEYYQKALELDPNNAEAWYN LGNAYYKQGDYDEAIEYYQKALELDPN NAEAWYNLGNAYYKQGDYDEAIEYYQK ALELGS GSDKENVLQKIYEIMKELERL GHAEASMQVSDLIYEFMKTNDENLLEE AERLLEEVRKGGSGSSGSAWSHPQFEK GGSGGGSGGSAWSHPQFEK (SEQ ID NO: 373)	X1- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMK TKDENLLEEAEERLLEEVRK (SEQ ID NO: 135)-X2- EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNA EAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAW YNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNL GNAYYKQGDYDEAIEYYQKALEL (SEQ ID NO: 590)
36729.2_ LCB1v2.2_ _2GS		MEKKIEEAELAYLLGELAYKLGEYRIA IRAYRIALKRDPNNAEAWYNLGNAYYK QGDYDEAIEYYQKALELDPNNAEAWYN LGNAYYKQGDYDEAIEYYQKALELDPN NAEAWYNLGNAYYKQGDYDEAIEYYQK ALELGS DKENVLQKIYEIMKELERLGH AEASMQVSDLIYEFMKTNDENLLEEAE RLLEEVRKGGSGSSGSAWSHPQFEKGG SGGGSGGSAWSHPQFEK (SEQ ID NO: 374)	X1- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMK TKDENLLEEAEERLLEEVRK (SEQ ID NO: 135)-X2- EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNA EAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAW YNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNL GNAYYKQGDYDEAIEYYQKALEL (SEQ ID NO: 590)
LCB3- PAS24- LCB3- 4GS- 5L6HC3_1		MEKKINLDELHMQMTDLVYEALHFAKD EEFQKHVFQLFKATKAYKNKDRQKLE KVVEELKELLERLLSGGASPAAPAPAS PAAPAPASAGGNLDELHMQMTDLVYE ALHFAKDEEFQKHVFQLFKATKAYKN KDRQKLEKVVEELKELLERLLSGSGSS EELRAVADLQRLNIELARKLLEAVARL QELNIDLVRKTSELTDEKTIREEIRKV KEESKRIVEEAEIIRAKEESRKIAD ESRRGGSGSSGSAWSHPQFEKGGSGGG SGGSAWSHPQFEK (SEQ ID NO: 375)	- X1NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFKAT ATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155)-X2- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFKAT KAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155)-X3
LCB3-		MEKKINLDELHMQMTDLVYEALHFAKD	X1-

PAS24- LCB3- 5GS- 5L6HC3_1	EEFQKHVFQLFEEKATKAYKNKDRQKLE KVVEELKELLERLLSGGASPAAPAPAS PAAPAPSAPAGGNLDELHMQMTDLVYE ALHFAKDEEFQKHVFQLFEEKATKAYKN KDRQKLEKVVEELKELLERLLSGSGSG SEELRAVADLQRLNIELARKLLEAVAR LQELNIDLVRKTSELTDEKTIREEIRK VKEESKRIVEEAEETRRAKEESRKIA DESRGGSGSGSAWSHPQFEKGGGSGG SGSGSAWSHPQFEK (SEQ ID NO: 376)	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEEKAT KAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155) -X2- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEEKAT KAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155) -X3
LCB1- 10GS- AHB2- 4GS-1rfo	MEKKIDKENVLQKIYEIMKELERLGHAE EASMQVSDLIYEFMKTCDENLLEEAER LLEEVKRGSGSGSGSGSGSGSGSGSG DQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEARR ILEHLEELARKSGSGGYIPEAPRDGQA YVRKDGEWVLLSTFLGGSGSGSAWSH PQFEKGGSGSGSGSGSAWSHPQFEK (S EQ ID NO: 377)	X1- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMK TKDENLLEEAERLLEEVKR (SEQ ID NO: 135) -X2- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEARRILEHLEELAR K (SEQ ID NO: 101) -X3- GYIPEAPRDGQAYVRKDGEWVLLSTFL (SEQ ID NO: 179) -X4
LCB1- 28GS- AHB2- 4GS-1rfo	MEKKIDKENVLQKIYEIMKELERLGHAE EASMQVSDLIYEFMKTCDENLLEEAER LLEEVKRGSGSGSGSGSGSGSGSGSG SGSGSGSGSELEEQVMHVLDQVSELAHE LLHKLTGEELERAAYFNWWATEMMLEL IKSDDEREIREIEEEARRILEHLEELAR RKSGSGGYIPEAPRDGQAYVRKDGEWV LLSTFLGGSGSGSGSAWSHPQFEKGGGS GGSGSGSAWSHPQFEK (SEQ ID NO: 378)	X1- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMK TKDENLLEEAERLLEEVKR (SEQ ID NO: 135) -X2- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEARRILEHLEELAR K (SEQ ID NO: 101) -X3- GYIPEAPRDGQAYVRKDGEWVLLSTFL (SEQ ID NO: 179) -X4
LCB3- 10GS- AHB2- 4GS-1rfo	MEKKINLDELHMQMTDLVYEALHFAKD EEFQKHVFQLFEEKATKAYKNKDRQKLE KVVEELKELLERLLSGSGSGSGSGSGSG EEQVMHVLDQVSELAHELLHKLTGEEL ERAAAYFNWWATEMMLELIKSDDEREIR EIEEEARRILEHLEELARKSGSGGYIP EAPRDGQAYVRKDGEWVLLSTFLGGSG SSGSAWSHPQFEKGGSGSGSGSGSAWS HPQFEK (SEQ ID NO: 379)	X1- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEEKAT KAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155) -X2- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEARRILEHLEELAR K (SEQ ID NO: 101) -X3- GYIPEAPRDGQAYVRKDGEWVLLSTFL (SEQ ID NO: 179) -X4
LCB3- 16GS- AHB2- 4GS-1rfo	MEKKINLDELHMQMTDLVYEALHFAKD EEFQKHVFQLFEEKATKAYKNKDRQKLE KVVEELKELLERLLSGSGSGSGSGSGSG SGSGSELEEQVMHVLDQVSELAHELLHK LTGEELERAAYFNWWATEMMLELIKSD DEREIREIEEEARRILEHLEELARKGS SGGYIPEAPRDGQAYVRKDGEWVLLST FLGGSGSGSGSAWSHPQFEKGGSGSGGS GSAWSHPQFEK (SEQ ID NO: 380)	X1- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEEKAT KAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155) -X2- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEARRILEHLEELAR K (SEQ ID NO: 101) -X3- GYIPEAPRDGQAYVRKDGEWVLLSTFL (SEQ ID NO: 179) -X4
36729.2_ 6GS_LCB1 v2.2- 28GS- LCB3	MEKKISAWSHPOFEKGGSGSGSGSGSA WSHPQFEKGGSGSGSGMEEAELAYLLGE LAYKLGEYRIAIRAYRIALKRDPNNAE AWYNLGNAYYKQGDYDEAIEYYQKALE LDPNNAEAWYNLGNAYYKQGDYDEAIE YYQKALELDPNNAEAWYNLGNAYYKQG DYDEAIEYYQKALELGGSGSGSDKENVL QKIYEIMKELERLGHAEASMQVSDLIY EFMKTCDENLLEEAERLLEEVKRGSGS SGSGSGSGSGSGSGSGSGSGSGSNLD ELHMQMTDLVYEALHFAKDEEFQKHVF QLFEKATKAYKNKDRQKLEKVVEELKE LLERLLS (SEQ ID NO: 381)	X1- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMK TKDENLLEEAERLLEEVKR (SEQ ID NO: 135) -X2- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEEKAT KAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155)
36729.2_ 6GS_LCB1	MEKKISAWSHPOFEKGGSGSGSGSGSA WSHPQFEKGGSGSGSGMEEAELAYLLGE	X1- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMK

v2.2- 9GS-LCB3	LAYKLG EYRIAIRAYRIALKRDPNNAE AWYNLGNAYYKQGDYDEAIEYYQKALE LDPNNAEAWYNLGNAYYKQGDYDEAIE YYQKALELDPNNAEAWYNLGNAYYKQG DYDEAIEYYQKALELGS GSGSDKENVL QKIYEIMKELERLGHAEASMQVSDLIY EFMKT K DENLLEEAERLLEEVKRGSGS GSGSGNLDELHMQMTDLVYEALHFAKD EEFQKHVFQLF EKATKAYKNKDRQKLE KVVEELKELLERLLS (SEQ ID NO: 382)	TKDENLLEEAERLLEEVKR (SEQ ID NO: 135) -X2- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLF EKAT KAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155)
36729.2_ 6GS_LCB1 v2.2- 28GS- AHB2	MEKKISAWSH PQFEKGGSGGGSGGSA WSHPQFEKGGSGSGMEEAELAYLLGE LAYKLG EYRIAIRAYRIALKRDPNNAE AWYNLGNAYYKQGDYDEAIEYYQKALE LDPNNAEAWYNLGNAYYKQGDYDEAIE YYQKALELDPNNAEAWYNLGNAYYKQG DYDEAIEYYQKALELGS GSGSDKENVL QKIYEIMKELERLGHAEASMQVSDLIY EFMKT K DENLLEEAERLLEEVKRGSGS GSGSGSGSGSGSGSGSGSGSGSELE EQVMHVL DQVSELAHELLHKLTGEELE RAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARK (SEQ ID NO: 383)	X1- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMK TKDENLLEEAERLLEEVKR (SEQ ID NO: 135) -X2- ELEEQVMHVL DQVSELAHELLHKLTGEELE RAAYFNW WATEMMLELIKSDDEREIREIEEEARRILEHLEELAR K (SEQ ID NO:101)
36729.2_ 6GS_LCB1 v2.2- 9GS-AHB2	MEKKISAWSH PQFEKGGSGGGSGGSA WSHPQFEKGGSGSGMEEAELAYLLGE LAYKLG EYRIAIRAYRIALKRDPNNAE AWYNLGNAYYKQGDYDEAIEYYQKALE LDPNNAEAWYNLGNAYYKQGDYDEAIE YYQKALELDPNNAEAWYNLGNAYYKQG DYDEAIEYYQKALELGS GSGSDKENVL QKIYEIMKELERLGHAEASMQVSDLIY EFMKT K DENLLEEAERLLEEVKRGSGS GSGSGELEE QVMHVL DQVSELAHELLH KLTGEELE RAAYFNWWATEMMLELIK SDDEREIREIEEEARRILEHLEELARK (SEQ ID NO: 384)	X1- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMK TKDENLLEEAERLLEEVKR (SEQ ID NO: 135) -X2- ELEEQVMHVL DQVSELAHELLHKLTGEELE RAAYFNW WATEMMLELIKSDDEREIREIEEEARRILEHLEELAR K (SEQ ID NO:101)
LCB1- 10GS- LCB3- 4GS-1rfo	MEKKIDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKT K DENLLEEAERLLEEVKRGSGSGSGSGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLF EKATKAYKNKDRQKLEKVVEELKELLERLLS GSGSGYIPEAPRDGQAYVRKDG EWVLLSTFLGSGSGSAWSHPQFEK (SEQ ID NO: 385)	X1- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMK TKDENLLEEAERLLEEVKR (SEQ ID NO: 135) -X2- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLF EKAT KAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155) -X3- GYIPEAPRDGQAYVRKDG EWVLLSTFL (SEQ ID NO: 179) -X4
LCB1- 28GS- LCB3- 4GS-1rfo	MEKKIDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKT K DENLLEEAERLLEEVKRGSGSGSGSGSGSGSGSGSGSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLF EKATKAYKNKDRQKLEKVVEELKELLERLLSGSGSGYIPEAPRDGQAYVRKDG EWVLLSTFLGSGSGSAWSHPQFEK (SEQ ID NO: 386)	X1- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMK TKDENLLEEAERLLEEVKR (SEQ ID NO: 135) -X2- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLF EKAT KAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155) -X3- GYIPEAPRDGQAYVRKDG EWVLLSTFL (SEQ ID NO: 179) -X4
AHB2- 10GS- LCB3- 4GS-1rfo	MEKKIELEE QVMHVL DQVSELAHELLHKLTGEELE RAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSGSGSGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLF EKATKAYKNKDRQKLEKVVEELKELLERLLSGSGSGYIPEAPRDGQAYVRKDG EWVLLSTFLGSGSGSAWSHPQFEKGGSGSGSGSAWS	X1- ELEEQVMHVL DQVSELAHELLHKLTGEELE RAAYFNW WATEMMLELIKSDDEREIREIEEEARRILEHLEELAR K (SEQ ID NO:101) -X2- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLF EKAT KAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155) -X3- GYIPEAPRDGQAYVRKDG EWVLLSTFL (SEQ ID

	HPQFEK (SEQ ID NO: 387)	NO: 179) -X4
AHB2- 16GS- LCB3- 4GS-1rfo	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEARRILEHLEELARKG SGSGSGSGSGSGSGSNLDELHMQMTDL VYEALHFAKDEEFQKHVFQLFEEKATKA YKNKDRQKLEKVVEELKELLERLLSGS GSGYIPEAPRDGQAYVRKDGWVLLST FLGGSGSGSAWSHPQFEKGGGSGGGS GGSAWSHPQFEK (SEQ ID NO: 388)	X1- ELEEQVMHVLDQVSELAHELLHKL TGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEARRILEHLEELAR K (SEQ ID NO: 101) -X2- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEEKAT KAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155) -X3- GYIPEAPRDGQAYVRKDGWVLLSTFL (SEQ ID NO: 179) -X4
LCB1- 9GS- LCB3- 5GS- 5L6HC3_1	MEKKIDKENVLQKIYEIMKELERLGH EASMQVSDLIYEFMKTNDENLLEEAE RLLVEVKRSGSGSGSGSNLDELHMQMTD LVYEALHFAKDEEFQKHVFQLFEEKATK AYKNKDRQKLEKVVEELKELLERLLSG SGSGSEELRAVADLQRLNIELARKLLE AVARLQELNIDLVRKTSELTDEKTIRE EIRKVKEESKRIVEEAEERIRAKEES RKIADESRRGSGSGSSSAWSHPQFEKGG GSGGSGSGSAWSHPQFEK (SEQ ID NO: 389)	X1- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKT NDENLLEEAEERLLEEVR (SEQ ID NO: 135) -X2- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEEKAT KAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155) -X3
AHB2- 9GS- LCB3- 5GS- 5L6HC3_1	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEARRILEHLEELARKG SGSGSGSGSNLDELHMQMTDLVYEALHF AKDEEFQKHVFQLFEEKATKAYKNKDRQ KLEKVVEELKELLERLLSGSGSEEL RAVADLQRLNIELARKLLEAVARLQEL NIDLVRKTSELTDEKTIREEIRKVKEE SKRIVEEAEERIRAKEESRKIADES GGSGSGSGSAWSHPQFEKGGGSGGSGG SAWSHPQFEK (SEQ ID NO: 390)	X1- ELEEQVMHVLDQVSELAHELLHKL TGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEARRILEHLEELAR K (SEQ ID NO: 101) -X2- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEEKAT KAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155) -X3
AHB2- 4GS- 1na0_int 2-R3	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEARRILEHLEELARKG SGSEEAELAYLLGELAYKLGEYRIAIR AYRIALKRDPNNAEAWYNLGNAYYKQG DYDEAIYYQKALEDPNNAEAKQNLGN AKQKQGGGSGSSSAWSHPQFEKGGGS GGGSGGSAWSHPQFEK (SEQ ID NO: 391)	X1- ELEEQVMHVLDQVSELAHELLHKL TGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEARRILEHLEELAR K (SEQ ID NO: 101) -X2- EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNA EAWYNLGNAYYKQGDYDEAIYYQKALEDPNNAEAKQ NLGNAKQKQ (SEQ ID NO: 591)
AHB2- 6GS- 1na0_int 2-R3	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEARRILEHLEELARKG SGSGSEEAELAYLLGELAYKLGEYRIAIR IRAYRIALKRDPNNAEAWYNLGNAYYK QGDYDEIYYQKALEDPNNAEAKQNL GNAKQKQGGGSGSSSAWSHPQFEKGG GSGGSGGSAWSHPQFEK (SEQ ID NO: 392)	X1- ELEEQVMHVLDQVSELAHELLHKL TGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEARRILEHLEELAR K (SEQ ID NO: 101) -X2- EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNA EAWYNLGNAYYKQGDYDEIYYQKALEDPNNAEAKQ NLGNAKQKQ (SEQ ID NO: 592)
AHB2- 4GS- 1na0_int 2	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEARRILEHLEELARKG SGSEEAELAYLLGELAYKLGEYRIAIR AYRIALKRDPNNAEAWYNLGNAYYKQG DYDEAIYYQKALEDPNNAEAWYNLGN AYYKQGDYDEAIYYQKALEDPNNAE AKQNLGNKQKQGGGSGSSSAWSHPQF EKGGGSGGSGGSAWSHPQFEK (SEQ ID NO: 393)	X1- ELEEQVMHVLDQVSELAHELLHKL TGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEARRILEHLEELAR K (SEQ ID NO: 101) -X2- EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNA EAWYNLGNAYYKQGDYDEAIYYQKALEDPNNAEAWY NLGNAYYKQGDYDEAIYYQKALEDPNNAEAKQNLG NKQKQ (SEQ ID NO: 593)
AHB2- 6GS-	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS	X1- ELEEQVMHVLDQVSELAHELLHKL TGEELERAAYFNW

1na0_int 2	DDEREIREIEEEEARRILEHLEELARKG SGSGSEEAELAYLLGELAYKLGEYRIA IRAYRIALKRDPNNAEAWYNLGNAYYK QGDYDEAIYYQKALELDPNNAEAWYNL GNAYYKQGDYDEAIEYYQKALELDPNN AEAKQNLGNKQKQGGGSGSGSAWSHP QFEKGGGSGGGSGGSAWSHPQFEK (SEQ ID NO: 394)	WATEMMLELIKSDDEREIREIEEEEARRILEHLEELAR K (SEQ ID NO: 101) -X2- EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNA EAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWY NLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNLG NKQKQ (SEQ ID NO: 593)
AHB2- 4GS-6ms r	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIK DDEREIREIEEEEARRILEHLEELARKG SGSGSEYEIRKALEELKASTAELKRAT ASLRASTEELKKNPSEDALVENNRLIV EHNNAIIVENRIIAAVLELIVRAIKGGS GSSGSAWSHPQFEKGGGSGGGSGGSAW SHPQFEK (SEQ ID NO: 395)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEEARRILEHLEELAR K (SEQ ID NO: 101) -X2- EYEIRKALEELKASTAELKRATASLRASTEELKKNPS EDALVENNRLIVEHNNAIIVENRIIAAVLELIVRAIK (SEQ ID NO: 594)
AHB2- 6GS-6ms r	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIK DDEREIREIEEEEARRILEHLEELARKG SGSGSGSEYEIRKALEELKASTAELKR ATASLRASTEELKKNPSEDALVENNRL IVEHNNAIIVENRIIAAVLELIVRAIKG GSGSGSAWSHPQFEKGGGSGGGSGGSAW SHPQFEK (SEQ ID NO: 396)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEEARRILEHLEELAR K (SEQ ID NO: 101) -X2- EYEIRKALEELKASTAELKRATASLRASTEELKKNPS EDALVENNRLIVEHNNAIIVENRIIAAVLELIVRAIK (SEQ ID NO: 594)
36729.2 LCB1v2.2 _6GS	MEKKISAWSHPPQFEKGGGSGGGSGGSA WSHPQFEKGGGSGSGSEEAELAYLLGEL AYKLGEYRIAIRAYRIALKRDPNNAEA WYNLGNAYYKQGDYDEAIEYYQKALEL DPNNAEAWYNLGNAYYKQGDYDEAIEY YQKALELDPNNAEAWYNLGNAYYKQGD YDEAIEYYQKALELGS GSDKENVLQ KIYEIMKELERLGHAEASMQVSDLIYE FMKTKDENLLEEAERLLEEVR (SEQ ID NO: 397)	X1- EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNA EAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAW YNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNL GNAYYKQGDYDEAIEYYQKALEL (SEQ ID NO: 590) -X2- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMK TKDENLLEEAERLLEEVR (SEQ ID NO: 135)
36729.2 LCB1v2.2 _4GS	MEKKISAWSHPPQFEKGGGSGGGSGGSA WSHPQFEKGGGSGSGSEEAELAYLLGEL AYKLGEYRIAIRAYRIALKRDPNNAEA WYNLGNAYYKQGDYDEAIEYYQKALEL DPNNAEAWYNLGNAYYKQGDYDEAIEY YQKALELDPNNAEAWYNLGNAYYKQGD YDEAIEYYQKALELGS GSDKENVLQKI YEIMKELERLGHAEASMQVSDLIYEFM KTKDENLLEEAERLLEEVR (SEQ ID NO: 398)	X1- EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNA EAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAW YNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNL GNAYYKQGDYDEAIEYYQKALEL (SEQ ID NO: 590) -X2- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMK TKDENLLEEAERLLEEVR (SEQ ID NO: 135)
36729.2 LCB1v2.2 _2GS	MEKKISAWSHPPQFEKGGGSGGGSGGSA WSHPQFEKGGGSGSGSEEAELAYLLGEL AYKLGEYRIAIRAYRIALKRDPNNAEA WYNLGNAYYKQGDYDEAIEYYQKALEL DPNNAEAWYNLGNAYYKQGDYDEAIEY YQKALELDPNNAEAWYNLGNAYYKQGD YDEAIEYYQKALELGS GSDKENVLQKIYE IMKELERLGHAEASMQVSDLIYEFMKT KDNENLLEEAERLLEEVR (SEQ ID NO: 399)	X1- EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNA EAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAW YNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNL GNAYYKQGDYDEAIEYYQKALEL (SEQ ID NO: 590) -X2- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMK TKDENLLEEAERLLEEVR (SEQ ID NO: 135)
AHB2- 8GS- 1na0_int 2-R3	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIK DDEREIREIEEEEARRILEHLEELARKG SGSGSGSEEAELAYLLGELAYKLGEYR IAIRAYRIALKRDPNNAEAWYNLGNAY YKQGDYDEAIEYYQKALELDPNNAEAK QNLGNAKQKQGGGSGSGSAWSHPQFE KGGGSGGGSGGSAWSHPQFEK (SEQ ID NO: 400)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEEARRILEHLEELAR K (SEQ ID NO: 101) -X2- EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNA EAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAK QNLGNAKQKQ (SEQ ID NO: 180) -X3

AHB2- 8GS- 1na0_int 2	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEEARRILEHLEELARKG SGSGSGSSEAEALAYLLGELAYKLGEYR IAIRAYRIALKRDPNNAEAWYNLGNAY YKQGDYDEAIEYYQKALELDPNNAEAW YNLGNAYYKQGDYDEAIEYYQKALELD PNNAEAKQNLGNAKQKQGGSGSSGSA WSHPQFEKGGSGGGSGGSAWSHPQFE K(SEQ ID NO: 401)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEEARRILEHLEELAR K(SEQ ID NO:101)-X2- EEAEALAYLLGELAYKLGEYRIAIRAYRIALKRDPNNA EAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAW YNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNL GNAKQKQG(SEQ ID NO: 181)-X3
AHB2- 8GS-6msr	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEEARRILEHLEELARKG SGSGSGSGSSEYEIRKALEELKASTAEL KRATASLRASTEELKKNPSEDALVENN RLIVEHNAIIVENNRIIAAVLELIVRA IKGGSGSSGSAWSHPQFEKGGSGGGG GSAWSHPQFEK(SEQ ID NO: 402)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEEARRILEHLEELAR K(SEQ ID NO:101)-X2- GSEYEIRKALEELKASTAELKRATASLRASTEELKKN PSEDALVENNRLIVEHNAIIVENNRIIAAVLELIVRA IK(SEQ ID NO: 182)-X3
AHB2- 10GS- 6msr	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEEARRILEHLEELARKG SGSGSGSGSGSSEYEIRKALEELKASTA ELKRATASLRASTEELKKNPSEDALVE NNRLIVEHNAIIVENNRIIAAVLELIV RAIKGGSGSSGSAWSHPQFEKGGSGGG GSGGSAWSHPQFEK(SEQ ID NO: 403)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEEARRILEHLEELAR K(SEQ ID NO:101)-X2- GSEYEIRKALEELKASTAELKRATASLRASTEELKKN PSEDALVENNRLIVEHNAIIVENNRIIAAVLELIVRA IK(SEQ ID NO: 182)-X3
AHB2- 10GS- 1na0_int 2-R3	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEEARRILEHLEELARKG SGSGSGSGSSEAEALAYLLGELAYKLGE YRIAIRAYRIALKRDPNNAEAWYNLGN AYYKQGDYDEAIEYYQKALELDPNNAE AKQNLGNAKQKQGGSGSGSWSHPQ FEKGGSGGGSGGSAWSHPQFEK(SEQ ID NO: 404)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEEARRILEHLEELAR K(SEQ ID NO:101)-X2- EEAEALAYLLGELAYKLGEYRIAIRAYRIALKRDPNNA EAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAK QNLGNAKQKQG(SEQ ID NO: 180)-X3
AHB2- 10GS- 1na0_int 2	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEEARRILEHLEELARKG SGSGSGSGSSEAEALAYLLGELAYKLGE YRIAIRAYRIALKRDPNNAEAWYNLGN AWYNLGNAYYKQGDYDEAIEYYQKALE LDPNNAEAKQNLGNAKQKQGGSGSGSSG SAWSHPQFEKGGSGGGSGGSAWSHPQ FEK(SEQ ID NO: 405)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEEARRILEHLEELAR K(SEQ ID NO:101)-X2- EEAEALAYLLGELAYKLGEYRIAIRAYRIALKRDPNNA EAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAW YNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNL GNAKQKQG(SEQ ID NO: 181)-X3
AHB2- 4GS-1gcm	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEEARRILEHLEELARKG SGSRMKQIEDKIEEILSKIYHIENEIA RIKKLIGERGGSGSSGSAWSHPQFEK GGSGGGSGGSAWSHPQFEK(SEQ ID NO: 406)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEEARRILEHLEELAR K(SEQ ID NO:101)-X2- RMKQIEDKIEEILSKIYHIENEIARIKKLIGER (SEQ ID NO: 183)-X3
AHB2- 8GS-1gcm	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEEARRILEHLEELARKG SGSGSGSRMKQIEDKIEEILSKIYHIE NEIARIKKLIGERGGSGSSGSAWSHPQ FEKGGSGGGSGGSAWSHPQFEK(SEQ ID NO: 407)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEEARRILEHLEELAR K(SEQ ID NO:101)-X2- RMKQIEDKIEEILSKIYHIENEIARIKKLIGER(SEQ ID NO: 183)-X3
AHB2- 4GS-pRO-	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEEARRILEHLEELARKG	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEEARRILEHLEELAR

2-noHis	SGSGSEYEIRKALEELKASTAELKRST ASLRASTEELKKNPSEDALVENNRLIV ENNAIIVENNRIIAAVLELIVRAIKGG SGSSGSAWSHPQFEKGGGSGGSGSSA WSHPQFEK (SEQ ID NO: 408)	K (SEQ ID NO: 101) -X2- GSEYEIRKALEELKASTAELKRSTASLRASTEELKKN PSEDALVENNRLIVENNAIIVENNRIIAAVLELIVRA IK (SEQ ID NO: 184) -X3
AHB2- 8GS-PRO- 2-noHis	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEEARRILEHLEELARKG SGSGSGSGSEYEIRKALEELKASTAEL KRSTASLRASTEELKKNPSEDALVENN RLIVENNAIIVENNRIIAAVLELIVRA IKGGSGSSGSAWSHPQFEKGGGSGGGS GSAWSHPQFEK (SEQ ID NO: 409)	X1ELEEQVMHVLDQVSELAHELLHKLKTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEEARRILEHLEEL ARK (SEQ ID NO: 101) -X2- GSEYEIRKALEELKASTAELKRSTASLRASTEELKKN PSEDALVENNRLIVENNAIIVENNRIIAAVLELIVRA IK (SEQ ID NO: 184) -X3
AHB2- 6GS- 1na0_3	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEEARRILEHLEELARKG SGSGSNLAEKMYKAGNAMYRKQYTI IIAYTLALLKDPNNAEAWYNLGNAAAYK KGEYDEAIEAYQKALELDPNNAEAWYN LGNAYYKQGDYDEAIEYYQKALELDPN NAEAKQNLGNKQKQGGGSGSSGSAWS HPQFEKGGGSGGSGGSAWSHPQFEK (SEQ ID NO: 410)	X1- ELEEQVMHVLDQVSELAHELLHKLKTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEEARRILEHLEELAR K (SEQ ID NO: 101) -X2- NLAEKMYKAGNAMYRKQYTI IIAYTLALLKDPNNAEAWYNLGNAAAYKKGEYDEAIEAYQKALELDPNNAEAW YNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNL GNKQKQ (SEQ ID NO: 185) -X3
AHB2- 10GS- 1na0_3	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEEARRILEHLEELARKG SGSGSGSGSNLAEKMYKAGNAMYRKQ YTI IIAYTLALLKDPNNAEAWYNLGN AAYKKGEYDEAIEAYQKALELDPNNAE AWYNLGNAYYKQGDYDEAIEYYQKALE LDPNNAEAKQNLGNKQKQGGGSGSSG SAWSHPQFEKGGGSGGSGGSAWSHPQ FEK (SEQ ID NO: 411)	X1- ELEEQVMHVLDQVSELAHELLHKLKTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEEARRILEHLEELAR K (SEQ ID NO: 101) -X2- NLAEKMYKAGNAMYRKQYTI IIAYTLALLKDPNNAEAWYNLGNAAAYKKGEYDEAIEAYQKALELDPNNAEAW YNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNL GNKQKQ (SEQ ID NO: 185) -X3
AHB2- 6GS-4pn9	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEEARRILEHLEELARKG SGSGSGEIAKSLKEIAKSLKEIAWSLK EIAKSLKGGGSGSSGSAWSHPQFEKGG GSGGSGGSAWSHPQFEK (SEQ ID NO: 412)	X1- ELEEQVMHVLDQVSELAHELLHKLKTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEEARRILEHLEELAR K (SEQ ID NO: 101) -X2- GEIAKSLKEIAKSLKEIAWSLKKEIAKSLK (SEQ ID NO: 186) -X3
AHB2- 10GS- 4pn9	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEEARRILEHLEELARKG SGSGSGSGSGEIAKSLKEIAKSLKEIA WSLKKEIAKSLKGGGSGSSGSAWSHPQF EKGGGSGGSGGSAWSHPQFEK (SEQ ID NO: 413)	X1- ELEEQVMHVLDQVSELAHELLHKLKTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEEARRILEHLEELAR K (SEQ ID NO: 101) -X2- GEIAKSLKEIAKSLKEIAWSLKKEIAKSLK (SEQ ID NO: 186) -X3
AHB2- GGGGS5- 1na0_int 2-R3	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEEARRILEHLEELARKG GSGGEEAELAYLLGELAYKLGEYRI AIRAYRIALKRDPNNAEAWYNLGNAYYKQ GDYDEAIEYYQKALELDPNNAEAKQNL GNKQKQGGGSGSSGSAWSHPQFEKGG GSGGSGGSAWSHPQFEK (SEQ ID NO: 414)	X1- ELEEQVMHVLDQVSELAHELLHKLKTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEEARRILEHLEELAR K (SEQ ID NO: 101) -X2- EEAELAYLLGELAYKLGEYRI AIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAK QNLGNKQKQ (SEQ ID NO: 180) -X3
AHB2- GGGGS7- 1na0_int 2-R3	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEEARRILEHLEELARKG GSGGGEAAELAYLLGELAYKLGEYRI AIRAYRIALKRDPNNAEAWYNLGNAYY KQGDYDEAIEYYQKALELDPNNAEAKQ NLGNKQKQGGGSGSSGSAWSHPQFEK	X1- ELEEQVMHVLDQVSELAHELLHKLKTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEEARRILEHLEELAR K (SEQ ID NO: 101) -X2- EEAELAYLLGELAYKLGEYRI AIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAK

	GGGSGGGSGGSAWSHPQFEK (SEQ ID NO: 415)	QNLGNKQKQG (SEQ ID NO: 180) -X3
AHB2- GGGS9- lna0_int 2-R3	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEARRILEHLEELARKG GGSGGGGEEAELAYLLGELAYKLGEY RIAIRAYRIALKRDPNNAEAWYNLGN YYKQGDYDEAIEYYQKALELDPNNAE KQNLGNKQKQGGSGSSGSAWSHPQF EKGGSGGGSGGSAWSHPQFEK (SEQ ID NO: 416)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEARRILEHLEELAR K (SEQ ID NO: 101) -X2- EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNA EAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAK QNLGNKQKQG (SEQ ID NO: 180) -X3
AHB2- GGGS5- lna0_int 2	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEARRILEHLEELARKG GSGGEEAELAYLLGELAYKLGEYRIAI RAYRIALKRDPNNAEAWYNLGNAYYKQ GDYDEAIEYYQKALELDPNNAEAWYNL GNAYYKQGDYDEAIEYYQKALELDPNN AEAKQNLGNKQKQGGSGSSGSAWSH PQFEKGGSGGGSGGSAWSHPQFEK (S EQ ID NO: 417)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEARRILEHLEELAR K (SEQ ID NO: 101) -X2- EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNA EAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAW YNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNL GNKQKQG (SEQ ID NO: 181) -X3
AHB2- GGGS7- lna0_int 2	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEARRILEHLEELARKG GGSGGGGEEAELAYLLGELAYKLGEYRI AIRAYRIALKRDPNNAEAWYNLGNAYY KQGDYDEAIEYYQKALELDPNNAEAWY NLGNAYYKQGDYDEAIEYYQKALELDP NNAEAKQNLGNKQKQGGSGSSGSAW SHPQFEKGGSGGGSGGSAWSHPQFEK (SEQ ID NO: 418)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEARRILEHLEELAR K (SEQ ID NO: 101) -X2- EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNA EAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAW YNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNL GNKQKQG (SEQ ID NO: 181) -X3
AHB2- GGGS9- lna0_int 2	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEARRILEHLEELARKG GGSGGGGEEAELAYLLGELAYKLGEY RIAIRAYRIALKRDPNNAEAWYNLGN YYKQGDYDEAIEYYQKALELDPNNAE WYNLGNAYYKQGDYDEAIEYYQKALEL DPNNAEAKQNLGNKQKQGGSGSSG SAWSHPQFEKGGSGGGSGGSAWSHPQF EK (SEQ ID NO: 419)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEARRILEHLEELAR K (SEQ ID NO: 101) -X2- EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNA EAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAW YNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNL GNKQKQG (SEQ ID NO: 181) -X3
AHB2- GGGS5- 6msr	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEARRILEHLEELARKG GSGGGSEYEIRKALEELKASTAELKRA TASLRASTEELKKNPSEDALVENNRLI VEHNAIIVENNRIIAAVLELIVRAIKG GSGSSGSAWSHPQFEKGGSGGGSGG SAWSHPQFEK (SEQ ID NO: 420)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEARRILEHLEELAR K (SEQ ID NO: 101) -X2- GSEYEIRKALEELKASTAELKATASLRASTEELKKN PSEDALVENNRLIVEHNAIIVENNRIIAAVLELIVRA IK (SEQ ID NO: 182) -X3
AHB2- GGGS7- 6msr	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEARRILEHLEELARKG GGSGGGGSEYEIRKALEELKASTAELK RATASLRASTEELKKNPSEDALVENNR LIVEHNAIIVENNRIIAAVLELIVRAI KGGSGSSGSAWSHPQFEKGGSGGGSG GSAWSHPQFEK (SEQ ID NO: 421)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEARRILEHLEELAR K (SEQ ID NO: 101) -X2- GSEYEIRKALEELKASTAELKATASLRASTEELKKN PSEDALVENNRLIVEHNAIIVENNRIIAAVLELIVRA IK (SEQ ID NO: 182) -X3
AHB2- GGGS9- 6msr	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEARRILEHLEELARKG GGSGGGGSEYEIRKALEELKASTAEL LKRATASLRASTEELKKNPSEDALVEN NRLIVEHNAIIVENNRIIAAVLELIVR AIKGGSGSSGSAWSHPQFEKGGSGGGG	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEARRILEHLEELAR K (SEQ ID NO: 101) -X2- GSEYEIRKALEELKASTAELKATASLRASTEELKKN PSEDALVENNRLIVEHNAIIVENNRIIAAVLELIVRA

	SGGSAWSHPQFEK (SEQ ID NO: 422)	IK (SEQ ID NO: 182) -X3
AHB2- GGGS5- lgcm	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEARRILEHLEELARKG GSGGRMKQIEDKIEEILSKIYHIENEI ARIKKLIGERGGSGSSGSAWSHPQFEK (SEQ ID NO: 423)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEARRILEHLEELAR K (SEQ ID NO: 101) -X2- RMKQIEDKIEEILSKIYHIENEIARIKKLIGER (SEQ ID NO: 183) -X3
AHB2- GGGS7- lgcm	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEARRILEHLEELARKG GSGGGGRMKQIEDKIEEILSKIYHIEN EIARIKKLIGERGGSGSSGSAWSHPQF EKGGSGSGSGSAWSHPQFEK (SEQ ID NO: 424)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEARRILEHLEELAR K (SEQ ID NO: 101) -X2- RMKQIEDKIEEILSKIYHIENEIARIKKLIGER (SEQ ID NO: 183) -X3
AHB2- GGGS9- lgcm	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEARRILEHLEELARKG GGSGGGGRMKQIEDKIEEILSKIYHI ENEIARIKKLIGERGGSGSSGSAWSHP QFEKGGSGSGSGSAWSHPQFEK (SE Q ID NO: 425)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEARRILEHLEELAR K (SEQ ID NO: 101) -X2- RMKQIEDKIEEILSKIYHIENEIARIKKLIGER (SEQ ID NO: 183) -X3
AHB2- GGGS5- pRO-2- noHis	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEARRILEHLEELARKG GSGGGSEYEIRKALEELKASTAELKRS TASLRASTEELKKNPSEDALVENNRLI VENNAIIVENNRIIAAVLELIVRAIKG GSGSSGSAWSHPQFEKGGSGSGSGSGS AWSHPQFEK (SEQ ID NO: 426)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEARRILEHLEELAR K (SEQ ID NO: 101) -X2- GSEYEIRKALEELKASTAELKRSTASLRASTEELKKN PSEDALVENNRLIVENNAIIVENNRIIAAVLELIVRA IK (SEQ ID NO: 184) -X3
AHB2- GGGS7- pRO-2- noHis	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEARRILEHLEELARKG GGSGGGGSEYEIRKALEELKASTAELK RSTASLRASTEELKKNPSEDALVENNR LIVENNAIIVENNRIIAAVLELIVRAI KGGSGSSGSAWSHPQFEKGGSGSGSGS GSAWSHPQFEK (SEQ ID NO: 427)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEARRILEHLEELAR K (SEQ ID NO: 101) -X2- GSEYEIRKALEELKASTAELKRSTASLRASTEELKKN PSEDALVENNRLIVENNAIIVENNRIIAAVLELIVRA IK (SEQ ID NO: 184) -X3
AHB2- GGGS9- pRO-2- noHis	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEARRILEHLEELARKG GGSGGGGGGSEYEIRKALEELKASTAE LKRSTASLRASTEELKKNPSEDALVEN NRLIVENNAIIVENNRIIAAVLELIVR AIKGGSGSSGSAWSHPQFEKGGSGSGG SGGSAWSHPQFEK (SEQ ID NO: 428)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEARRILEHLEELAR K (SEQ ID NO: 101) -X2- GSEYEIRKALEELKASTAELKRSTASLRASTEELKKN PSEDALVENNRLIVENNAIIVENNRIIAAVLELIVRA IK (SEQ ID NO: 184) -X3
AHB2- GGGS5- lna0_3	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEARRILEHLEELARKG GSGGNLAEKMYKAGNAMYRKQYTI IAYTLALLKDPNNAEAWYNLGNAA YKKGEYDEAIEAYQKALELDPNNAEAW YNLGNAYYKQGDYDEAIEYYQKALELDP NNAEAKQNLGNKQKQGGSGSSGSAWSH PQFEKGGSGSGSGSGSAWSHPQFEK (S EQ ID NO: 429)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEARRILEHLEELAR K (SEQ ID NO: 101) -X2- NLAEKMYKAGNAMYRKQYTI IAYTLALLKDPNNAEAWYNLGNAA YKKGEYDEAIEAYQKALELDPNNAEAW YNLGNAYYKQGDYDEAIEYYQKALELDP NNAEAKQNLGNKQKQ (SEQ ID NO: 185) -X3
AHB2- GGGS7- lna0_3	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEARRILEHLEELARKG GSGGGNLAEKMYKAGNAMYRKQYTI AIAYTLALLKDPNNAEAWYNLGNAA Y	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEARRILEHLEELAR K (SEQ ID NO: 101) -X2- NLAEKMYKAGNAMYRKQYTI AIAYTLALLKDPNNA

	KKGEYDEAIEAYQKALELDPNNAEAWY NLGNAYYKQGDYDEAIEYYQKALELDP NNAEAKQNLGNAKQKQGGGSGSSGSAW SHPQFEKGGGSGGSGGSAWSHPQFEK (SEQ ID NO: 430)	EAWYNLGNAAAYKKGEYDEAIEAYQKALELDPNNAEAW YNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNL GNAKQKQG (SEQ ID NO: 185) -X3
AHB2- GGGGS5- lna0_3	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEEARRILEHLEELARKG GGGSGGGGNLAEKMYKAGNAMYRKQY TIAI IAYTLALLKDPNNAEAWYNLGN AYKKGEYDEAIEAYQKALELDPNNAE WYNLGNAYYKQGDYDEAIEYYQKALEL DPNNAEAKQNLGNAKQKQGGGSGSSG AWSHPQFEKGGGSGGSGGSAWSHPQF EK (SEQ ID NO: 431)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEEARRILEHLEELAR K (SEQ ID NO: 101) -X2- NLAEKMYKAGNAMYRKQYTIAI IAYTLALLKDPNNA EAWYNLGNAAAYKKGEYDEAIEAYQKALELDPNNAEAW YNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNL GNAKQKQG (SEQ ID NO: 185) -X3
AHB2- GGGGS5- 4pn9	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEEARRILEHLEELARKG GSGGGEIAKSLKEIAKSLKEIAWSLKE IAKSLKGGGSGSSGSAWSHPQFEKGGG SGGSGGSAWSHPQFEK (SEQ ID NO: 432)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEEARRILEHLEELAR K (SEQ ID NO: 101) -X2- GEIAKSLKEIAKSLKEIAWSLKEIAKSLKG (SEQ ID NO: 186) -X3
AHB2- GGGGS7- 4pn9	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEEARRILEHLEELARKG GGSGGGGEIAKSLKEIAKSLKEIAWSL KEIAKSLKGGGSGSSGSAWSHPQFEK GGSGGSGGSAWSHPQFEK (SEQ ID NO: 433)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEEARRILEHLEELAR K (SEQ ID NO: 101) -X2- GEIAKSLKEIAKSLKEIAWSLKEIAKSLKG (SEQ ID NO: 186) -X3
AHB2- GGGGS9- 4pn9	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEEARRILEHLEELARKG GGGSGGGGGEIAKSLKEIAKSLKEIAW SLKEIAKSLKGGGSGSSGSAWSHPQFE KGGGSGGSGGSAWSHPQFEK (SEQ ID NO: 434)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEEARRILEHLEELAR K (SEQ ID NO: 101) -X2- GEIAKSLKEIAKSLKEIAWSLKEIAKSLKG (SEQ ID NO: 186) -X3
AHB2- 2GS- SB175	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEEARRILEHLEELARKG GSEALEELEKALRELKKSTDELERSTE ELEKNPSEDALVENNRLIVENNKIIVE VLRIIAKVLKGGSGSSGSAWSHPQFEK GGGSGGGSGGSAWSHPQFEK (SEQ ID NO: 435)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEEARRILEHLEELAR K (SEQ ID NO: 101) -X2- SEALEELEKALRELKKSTDELERSTEELEKNPSEDAL VENNRLIVENNKIIVEVLRIIAKVLK (SEQ ID NO: 187) -X3
AHB2- 4GS- SB175	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEEARRILEHLEELARKG GGSSALEELEKALRELKKSTDELE RSTEELEKNPSEDALVENNRLIVENNKI IVEVLRIIAKVLKGGSGSSGSAWSHPQF EKGSGSGGSGGSAWSHPQFEK (SEQ ID NO: 436)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEEARRILEHLEELAR K (SEQ ID NO: 101) -X2- SEALEELEKALRELKKSTDELERSTEELEKNPSEDAL VENNRLIVENNKIIVEVLRIIAKVLK (SEQ ID NO: 187) -X3
AHB2- 6GS- SB175	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEEARRILEHLEELARKG GGSGSEALEELEKALRELKKSTDELE RSTEELEKNPSEDALVENNRLIVENNK IIVEVLRIIAKVLKGGSGSSGSAWSHP QFEKGGGSGGSGGSAWSHPQFEK (SE Q ID NO: 437)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEEARRILEHLEELAR K (SEQ ID NO: 101) -X2- SEALEELEKALRELKKSTDELERSTEELEKNPSEDAL VENNRLIVENNKIIVEVLRIIAKVLK (SEQ ID NO: 187) -X3
AHB2- 2GS-	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW

SB175.1	DDEREIREIEEEEARRILEHLEELARKG GSPELEKALRELKKSTDELERSTEELE KNGSPEALVENNRLIVENNKIIVEVL IIAKGGSSGSSSAWSHPQFEKGGGSGG GSGGSAWSHPQFEK (SEQ ID NO: 438)	WATEMMLELIKSDDEREIREIEEEEARRILEHLEELAR K (SEQ ID NO:101)-X2- SPELEKALRELKKSTDELERSTEELEKNGSPEALVEN NRLIVENNKIIVEVLRIIAK (SEQ ID NO: 188) - X3
AHB2- 4GS- SB175.1	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIK DDEREIREIEEEEARRILEHLEELARKG GGSSPELEKALRELKKSTDELERSTEE LEKNGSPEALVENNRLIVENNKIIVEV LRIIAKGGSSGSSSAWSHPQFEKGGGS GGGSGGSAWSHPQFEK (SEQ ID NO: 439)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEEARRILEHLEELAR K (SEQ ID NO:101)-X2- SPELEKALRELKKSTDELERSTEELEKNGSPEALVEN NRLIVENNKIIVEVLRIIAK (SEQ ID NO: 188) - X3
AHB2- 6GS- SB175.1	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIK DDEREIREIEEEEARRILEHLEELARKG GGGSSPELEKALRELKKSTDELERST EELEKNGSPEALVENNRLIVENNKIIV EVLRIIAKGGSSGSSSAWSHPQFEKGG GSGGSGGSAWSHPQFEK (SEQ ID NO: 440)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEEARRILEHLEELAR K (SEQ ID NO:101)-X2- SPELEKALRELKKSTDELERSTEELEKNGSPEALVEN NRLIVENNKIIVEVLRIIAK (SEQ ID NO: 188) - X3
AHB2- 2GS- SB175.2	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIK DDEREIREIEEEEARRILEHLEELARKG GSEKALRELKKSTDELERSTEELEKNG SPEALVENNRLIVENNKIIVEVLRGGS GSSGSAWSHPQFEKGGGSGGSGGSAW SHPQFEK (SEQ ID NO: 441)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEEARRILEHLEELAR K (SEQ ID NO:101)-X2- SEKALRELKKSTDELERSTEELEKNGSPEALVENNRL IVENNKIIVEVL (SEQ ID NO: 189) -X3
AHB2- 4GS- SB175.2	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIK DDEREIREIEEEEARRILEHLEELARKG GGSSSEKALRELKKSTDELERSTEELEK NGSPEALVENNRLIVENNKIIVEVLRG GSSGSGSAWSHPQFEKGGGSGGSGGSAW SHPQFEK (SEQ ID NO: 442)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEEARRILEHLEELAR K (SEQ ID NO:101)-X2- SEKALRELKKSTDELERSTEELEKNGSPEALVENNRL IVENNKIIVEVL (SEQ ID NO: 189) -X3
AHB2- 6GS- SB175.2	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIK DDEREIREIEEEEARRILEHLEELARKG GGGSGSEKALRELKKSTDELERSTEEL EKNGSPEALVENNRLIVENNKIIVEVL RGGGSSGSAWSHPQFEKGGGSGGSGGSAW SHPQFEK (SEQ ID NO: 443)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEEARRILEHLEELAR K-X2- SEKALRELKKSTDELERSTEELEKNGSPEALVENNRL IVENNKIIVEVL (SEQ ID NO: 189) -X3
SB175- 6GS- LCB1v2.2	MEKKISAWSHPQFEKGGGSGGSGGSA WSHPQFEKGGGSGGSGSEALEELEKALR ELKKSTDELERSTEELEKNPSEDALVE NNRLIVENNKIIVEVLRIIAKVLKGGG GSGDKENVLQKIYEIMKELERLGHAEA SMQVSDLIYEFMKTCDENLLEEAERLL EEVKR (SEQ ID NO: 444)	X1- SEALEELEKALRELKKSTDELERSTEELEKNPSEDAL VENNRLIVENNKIIVEVLRIIAKVLK (SEQ ID NO:187) -X2- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMK TKDENLLEEAERLLEEVKR (SEQ ID NO: 135)
SB175- 10GS- LCB1v2.2	MEKKISAWSHPQFEKGGGSGGSGGSA WSHPQFEKGGGSGGSGSEALEELEKALR ELKKSTDELERSTEELEKNPSEDALVE NNRLIVENNKIIVEVLRIIAKVLKGGG GSGGSGDKENVLQKIYEIMKELERLG HAEASMQVSDLIYEFMKTCDENLLEEA ERLLEEVKR (SEQ ID NO: 445)	X1- SEALEELEKALRELKKSTDELERSTEELEKNPSEDAL VENNRLIVENNKIIVEVLRIIAKVLK (SEQ ID NO:187) -X2- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMK TKDENLLEEAERLLEEVKR (SEQ ID NO: 135)
SB175.1- 6GS- LCB1v2.2	MEKKISAWSHPQFEKGGGSGGSGGSA WSHPQFEKGGGSGGSGSPELEKALRELK KSTDELERSTEELEKNGSPEALVENNR LIVENNKIIVEVLRIIAKGGGSGGSGDKE	X1- SPELEKALRELKKSTDELERSTEELEKNGSPEALVEN NRLIVENNKIIVEVLRIIAK (SEQ ID NO: 188) - X2-

	NVLQKIYEIMKELERLGHAEASMQVSD LIYEFMKTNDENLLEEAERLLEEVRK (SEQ ID NO: 446)	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMK TKDENLLEEAERLLEEVRK (SEQ ID NO: 135)
SB175.1- 10GS- LCB1v2.2	MEKKISAWSHPPQFEKGGGSGGGSGGSA WSHPPQFEKGGSGSSGSPELEKALRELK KSTDELERSTEELEKNGSPEALVENNR LIVENNKIIVEVLRIIAKGGGSGGGG SDKENVLQKIYEIMKELERLGHAEASM QVSDLIYEFMKTNDENLLEEAERLLEE VKR (SEQ ID NO: 447)	X1- SPELEKALRELKKSTDELERSTEELEKNGSPEALVEN NRLIVENNKIIVEVLRIIAK (SEQ ID NO: 188) - X2 DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMK TKDENLLEEAERLLEEVRK (SEQ ID NO: 135)
LCB3- 8GS- SB175	MEKKINLDELHMQMTDLVYEALHFAKD EEFQKHVFQLFKATKAYKNKDRQKLE KVVEELKELLERLLSGGGSGGGSEAL EELEKALRELKKSTDELERSTEELEKN PSEDALVENNRLIVENNKIIVEVLRII AKVLKGGASPAAPAGGSAWSHPPQFEK GGSGGGSGGSAWSHPPQFEK (SEQ ID NO: 448)	X1- NLDELHMQMTDLVYEALHFAKD EEFQKHVFQLFKAT KAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155) -X2- SEALEELEKALRELKKSTDELERSTEELEKNPSEDAL VENNRLIVENNKIIVEVLRIIAKVLK (SEQ ID NO: 187) -X3
LCB3- 6GS- SB175	MEKKINLDELHMQMTDLVYEALHFAKD EEFQKHVFQLFKATKAYKNKDRQKLE KVVEELKELLERLLSGGGSGGSEALEE LEKALRELKKSTDELERSTEELEKNPS EDALVENNRLIVENNKIIVEVLRIIAK VLKGGASPAAPAGGSAWSHPPQFEKGGG SGGGSGGSAWSHPPQFEK (SEQ ID NO: 449)	X1- NLDELHMQMTDLVYEALHFAKD EEFQKHVFQLFKAT KAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155) -X2- SEALEELEKALRELKKSTDELERSTEELEKNPSEDAL VENNRLIVENNKIIVEVLRIIAKVLK (SEQ ID NO: 187) -X3
LCB3- 4GS- SB175	MEKKINLDELHMQMTDLVYEALHFAKD EEFQKHVFQLFKATKAYKNKDRQKLE KVVEELKELLERLLSGGGSGSEALEE KALRELKKSTDELERSTEELEKNPSED ALVENNRLIVENNKIIVEVLRIIAKVL KGGASPAAPAGGSAWSHPPQFEKGGGSG GGSGGSAWSHPPQFEK (SEQ ID NO: 450)	X1- NLDELHMQMTDLVYEALHFAKD EEFQKHVFQLFKAT KAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155) -X2- SEALEELEKALRELKKSTDELERSTEELEKNPSEDAL VENNRLIVENNKIIVEVLRIIAKVLK (SEQ ID NO: 187) -X3
LCB3- 2GS- SB175	MEKKINLDELHMQMTDLVYEALHFAKD EEFQKHVFQLFKATKAYKNKDRQKLE KVVEELKELLERLLSGGSEALEELEKA LRELKKSTDELERSTEELEKNPSEDAL VENNRLIVENNKIIVEVLRIIAKVLK GASPAAPAGGSAWSHPPQFEKGGGSGGG GGGSAWSHPPQFEK (SEQ ID NO: 451)	X1- NLDELHMQMTDLVYEALHFAKD EEFQKHVFQLFKAT KAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155) -X2- SEALEELEKALRELKKSTDELERSTEELEKNPSEDAL VENNRLIVENNKIIVEVLRIIAKVLK (SEQ ID NO: 187) -X3
AHB2v1- 2GS- SB175	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEAARI LEHLEELARKG GSEALEELEKALRELKKSTDELERSTE ELEKNPSEDALVENNRLIVENNKIIVE VLRIIAKVLKGGSGSGGSAWSHPPQFEK GGGSGGGSGGSAWSHPPQFEK (SEQ ID NO: 452)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEAARI LEHLEELAR K (SEQ ID NO: 101) -X2- SEALEELEKALRELKKSTDELERSTEELEKNPSEDAL VENNRLIVENNKIIVEVLRIIAKVLK (SEQ ID NO: 187) -X3
AHB2v2- 2GS- SB175	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEAARI LEHLEELARTG GSEALEELEKALRELKKSTDELERSTE ELEKNPSEDALVENNRLIVENNKIIVE VLRIIAKVLKGGSGSGGSAWSHPPQFEK GGGSGGGSGGSAWSHPPQFEK (SEQ ID NO: 453)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEAARI LEHLEELAR T (SEQ ID NO: 164) -X2- SEALEELEKALRELKKSTDELERSTEELEKNPSEDAL VENNRLIVENNKIIVEVLRIIAKVLK (SEQ ID NO: 187) -X3

Table 9A

SEQ	Name	Sequence

ID		
595	AHB2-6GS- 1rfo	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGSGSGSGYIPEAPRDGQAYVRKDG EWVLLSTFL
596	AHB2-28GS- AHB2-6GS- 1rfo	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSELEEQVMHVLD QVSELAHELLHKLTGEELERAAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEH LEELARKGSGSGSGYIPEAPRDGQAYVRKDG EWVLLSTFL
597	AHB2-5GS- 1rfo	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGSGSGGYIPEAPRDGQAYVRKDG EWVLLSTFL
598	AHB2-4GS- 1rfo	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGSGSGYIPEAPRDGQAYVRKDG EWVLLSTFL
599	AHB2-3GS- 1rfo	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGSGGYIPEAPRDGQAYVRKDG EWVLLSTFL
600	AHB2-28GS- AHB2-3GS- 1rfo	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSELEEQVMHVLD QVSELAHELLHKLTGEELERAAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEH LEELARKGSGGYIPEAPRDGQAYVRKDG EWVLLSTFL
601	AHB2-4GS- 5L6HC3_1	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGSGSSEELRAVADLQRLNIELARKLLEAVARLQELNIDL VRKTSSELTDEKTIREEIRKVKEESKRIVEEAEIEIRRAKEESRKIADESR
602	AHB2-5GS- 5L6HC3_1	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGSGSGSEELRAVADLQRLNIELARKLLEAVARLQELNIDL LVRKTSSELTDEKTIREEIRKVKEESKRIVEEAEIEIRRAKEESRKIADESR
603	AHB2-28GS- AHB2-4GS- 5L6HC3_1	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSELEEQVMHVLD QVSELAHELLHKLTGEELERAAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEH LEELARKGSGSSEELRAVADLQRLNIELARKLLEAVARLQELNIDLVRKTSSELTDEK TIREEIRKVKEESKRIVEEAEIEIRRAKEESRKIADESR
604	AHB2-28GS- AHB2-5GS- 5L6HC3_1	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSELEEQVMHVLD QVSELAHELLHKLTGEELERAAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEH LEELARKGSGSGSEELRAVADLQRLNIELARKLLEAVARLQELNIDLVRKTSSELTDE KTIREEIRKVKEESKRIVEEAEIEIRRAKEESRKIADESR
605	LCB3-6GS- 1rfo	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLF EKATKAYKNKDRQKLEKVVEELKE LLERLLSGSGSGGYIPEAPRDGQAYVRKDG EWVLLSTFL
606	LCB3-5GS- 1rfo	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLF EKATKAYKNKDRQKLEKVVEELKE LLERLLSGSGSGGYIPEAPRDGQAYVRKDG EWVLLSTFL
607	LCB3-4GS- 1rfo	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLF EKATKAYKNKDRQKLEKVVEELKE LLERLLSGSGSGGYIPEAPRDGQAYVRKDG EWVLLSTFL
608	LCB3-5GS- 5L6HC3_1	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLF EKATKAYKNKDRQKLEKVVEELKE LLERLLSGSGSGSEELRAVADLQRLNIELARKLLEAVARLQELNIDLVRKTSSELTDE KTIREEIRKVKEESKRIVEEAEIEIRRAKEESRKIADESR
609	LCB3-28GS- LCB3-4GS- 5L6HC3_1	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLF EKATKAYKNKDRQKLEKVVEELKE LLERLLSGSGSGSGSGSGSGSGSGSGSGSGSGSGSNLDELHMQMTDLVYEALHFAK EEFQKHVFQLF EKATKAYKNKDRQKLEKVVEELKELLERLLSGSGSGSEELRAVADLQ RLNIELARKLLEAVARLQELNIDLVRKTSSELTDEKTIREEIRKVKEESKRIVEEAE EIRRAKEESRKIADESR
610	LCB3-28GS- LCB3-5GS- 5L6HC3_1	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLF EKATKAYKNKDRQKLEKVVEELKE LLERLLSGSGSGSGSGSGSGSGSGSGSGSGSGSGSNLDELHMQMTDLVYEALHFAK EEFQKHVFQLF EKATKAYKNKDRQKLEKVVEELKELLERLLSGSGSGSEELRAVADLQ RLNIELARKLLEAVARLQELNIDLVRKTSSELTDEKTIREEIRKVKEESKRIVEEAE EIRRAKEESRKIADESR
611	36729.2_LCB 1v2.2_6GS	EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAI EYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGN YYKQGDYDEAIEYYQKALELGS GSGSDKENVLQKIYEIMKELERLGHAEASMQVSDL IYEFMKT KDENLLEEAERLLEEVR
612	36729.2_LCB	EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAI

	1v2.2_4GS	EYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELGS GSDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKT KDENLLEEERLLEEVR
		EAEELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELGS GSDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKT KDENLLEEERLLEEVR
613	36729.2_LCB1v2.2_2GS	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAPAPASPAAPASAPAGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGSGSSEELRAVADLQRLNI ELARKLLEAVARLQELNIDLVRKTS ELTDEKTIREEIRKVKEESKRIVEEAEIEIRAKEESRKIADES R
614	LCB3-PAS24-LCB3-4GS-5L6HC3_1	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAPAPASPAAPASAPAGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGSGSSEELRAVADLQRLNI ELARKLLEAVARLQELNIDLVRKTS ELTDEKTIREEIRKVKEESKRIVEEAEIEIRAKEESRKIADES R
615	LCB3-PAS24-LCB3-5GS-5L6HC3_1	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAPAPASPAAPASAPAGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGSGSSEELRAVADLQRLNI ELARKLLEAVARLQELNIDLVRKTS ELTDEKTIREEIRKVKEESKRIVEEAEIEIRAKEESRKIADES R
616	LCB1-10GS-AHB2-4GS-1rfo	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKT KDENLLEEERLLEEVRKGSGSGSGSGGELEEQVMHVL DQVSELAHELLHKL TGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGSGYIPEAPRDGQAYVRKDGEWVLLSTFL
617	LCB1-28GS-AHB2-4GS-1rfo	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKT KDENLLEEERLLEEVRKGSGSGSGSGSGSGSGSGSGSGSELEEQVMHVL DQVSELAHELLHKL TGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGSGYIPEAPRDGQAYVRKDGEWVLLSTFL
618	LCB3-10GS-AHB2-4GS-1rfo	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGGSGGGSGGGELEEQVMHVL DQVSELAHELLHKL TGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGSGYIPEAPRDGQAYVRKDGEWVLLSTFL
619	LCB3-16GS-AHB2-4GS-1rfo	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGSGSGSGSGSGSGSGSGSGSELEEQVMHVL DQVSELAHELLHKL TGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGSGYIPEAPRDGQAYVRKDGEWVLLSTFL
620	36729.2_6GS_LCB1v2.2-28GS-LCB3	EAEELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELGS GSDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKT KDENLLEEERLLEEVRKGSGSGSGSGSGSGSGSGSGSGSGSNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS
621	36729.2_6GS_LCB1v2.2-9GS-LCB3	EAEELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELGS GSDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKT KDENLLEEERLLEEVRKGSGSGSGSGSNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS
622	36729.2_6GS_LCB1v2.2-28GS-AHB2	EAEELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELGS GSDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKT KDENLLEEERLLEEVRKGSGSGSGSGSGSGSGSGSGSGSGSELEEQVMHVL DQVSELAHELLHKL TGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK
623	36729.2_6GS_LCB1v2.2-9GS-AHB2	EAEELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELGS GSDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKT KDENLLEEERLLEEVRKGSGSGSGSGSGSGSGSGSGSGSGSELEEQVMHVL DQVSELAHELLHKL TGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK
624	LCB1-10GS-LCB3-4GS-1rfo	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKT KDENLLEEERLLEEVRKGSGSGSGSGSNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGSGSGYIPEAPRDGQAYVRKDGEWVLLSTFL
625	LCB1-28GS-LCB3-4GS-	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKT KDENLLEEERLLEEVRKGSGSGSGSGSGSGSGSGSGSGSGSNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGSGSGSGSGSGSGSGSGSGSGSELEEQVMHVL DQVSELAHELLHKL TGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK

	1rfo	QLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGSGSGYIPEAPRDGQAYVRKDGE WVLLSTFL
	AHB2-10GS- LCB3-4GS- 1rfo	ELEEQVMHVLDQVSELAHELLHKLTEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGSGSGSGGNLDELHMQMTDLVYEALHFAKDEEFQKHV FQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGSGSGYIPEAPRDGQAYVRKDG EWVLLSTFL
626		
	AHB2-16GS- LCB3-4GS- 1rfo	ELEEQVMHVLDQVSELAHELLHKLTEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGSGSGSGSGSGSNLDELHMQMTDLVYEALHFAKDE EFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGSGSGYIPEAPRDGQA YVRKDGEWVLLSTFL
627		
	LCB1-9GS- LCB3-5GS- 5L6HC3_1	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTCDENLLEEERLLEEVKRG SGSGSGSNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLE KVVEELKELLERLLSGSGSGSEELRAVADLQRLNIELARKLLEAVARLQELNIDLVR KTSELTDEKTIREEIRKVKEESKRIVEEAEERIRAKEESRRIADESR
	AHB2-9GS- LCB3-5GS- 5L6HC3_1	ELEEQVMHVLDQVSELAHELLHKLTEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGSGSGSGSNLDELHMQMTDLVYEALHFAKDEEFQKHVF QLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGSGSGSEELRAVADLQRLNIELA RKLLEAVARLQELNIDLVRKTSELTDEKTIREEIRKVKEESKRIVEEAEERIRAKE ESRRIADESR
629		
	AHB2-4GS- 1na0_int2- R3	ELEEQVMHVLDQVSELAHELLHKLTEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGSGSEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPN NAEAWYNLGNAYYKQGDYDEAIYYQKALELDPNNAEAKQNLGNKQKQ
630		
	AHB2-6GS- 1na0_int2- R3	ELEEQVMHVLDQVSELAHELLHKLTEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGSGSEEAELAYLLGELAYKLGEYRIAIRAYRIALKRD PNNAEAWYNLGNAYYKQGDYDEAIYYQKALELDPNNAEAKQNLGNKQKQ
631		
	AHB2-4GS- 1na0_int2	ELEEQVMHVLDQVSELAHELLHKLTEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGSGSEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPN NAEAWYNLGNAYYKQGDYDEAIYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAI YYQKALELDPNNAEAKQNLGNKQKQ
632		
	AHB2-6GS- 1na0_int2	ELEEQVMHVLDQVSELAHELLHKLTEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGSGSEEAELAYLLGELAYKLGEYRIAIRAYRIALKRD PNNAEAWYNLGNAYYKQGDYDEAIYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAI EYYQKALELDPNNAEAKQNLGNKQKQ
633		
	AHB2-4GS- 6ms r	ELEEQVMHVLDQVSELAHELLHKLTEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGSGSEYEIRKALEELKASTAELKRATASLRASTEELK KNPSEDALVENNRLIVEHNAIIVENRIIAAVLELIVRAIK
634		
	AHB2-6GS- 6ms r	ELEEQVMHVLDQVSELAHELLHKLTEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGSGSEYEIRKALEELKASTAELKRATASLRASTEEL LKKNPSEDALVENNRLIVEHNAIIVENRIIAAVLELIVRAIK
635		
	36729.2_LCB 1v2.2_6GS	EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAI EYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIYYQKALELDPNNAEAWYNLGN AYYKQGDYDEAIYYQKALELGSFGSDKENVLQKIYEIMKELERLGHAEASMQVSDL IYEFMKTCDENLLEEERLLEEVKR
636		
	36729.2_LCB 1v2.2_4GS	EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAI EYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIYYQKALELDPNNAEAWYNLGN AYYKQGDYDEAIYYQKALELGSFGSDKENVLQKIYEIMKELERLGHAEASMQVSDLIY EFMKTCDENLLEEERLLEEVKR
637		
	36729.2_LCB 1v2.2_2GS	EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAI EYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIYYQKALELDPNNAEAWYNLGN AYYKQGDYDEAIYYQKALELGSFGSDKENVLQKIYEIMKELERLGHAEASMQVSDLIY EFMKTCDENLLEEERLLEEVKR
638		
	AHB2-8GS- 1na0_int2- R3	ELEEQVMHVLDQVSELAHELLHKLTEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGSGSGSEEAELAYLLGELAYKLGEYRIAIRAYRIALK RDPNNAEAWYNLGNAYYKQGDYDEAIYYQKALELDPNNAEAKQNLGNKQKQ
639		
	AHB2-8GS- 1na0_int2	ELEEQVMHVLDQVSELAHELLHKLTEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGSGSGSEEAELAYLLGELAYKLGEYRIAIRAYRIALK RDPNNAEAWYNLGNAYYKQGDYDEAIYYQKALELDPNNAEAWYNLGNAYYKQGDYD EAIYYQKALELDPNNAEAKQNLGNKQKQ
640		

ELEEQVMHVLDQVSELAHELLHKLKTGEELERAAYFNWWATEMMLELIKSDDEREIRE
IEEEEARRILEHLEELARKGSGSGSGSGSGSEYEIRKALEELKASTAELKRATASLRST
EELKKNPSEDALVENNRLIVEHNAIIVENNRIIAAVLELIVRAIK

ELEEQVMHVLDQVSELAHELLHKLKTGEELERAAYFNWWATEMMLELIKSDDEREIRE
IEEEEARRILEHLEELARKGSGSGSGSGSGSGSEYEIRKALEELKASTAELKRATASLR
STEELKKNPSEDALVENNRLIVEHNAIIVENNRIIAAVLELIVRAIK

ELEEQVMHVLDQVSELAHELLHKLKTGEELERAAYFNWWATEMMLELIKSDDEREIRE
IEEEEARRILEHLEELARKGSGSGSGSGSGSGSEAEALAYLLGELAYKLGEYRIAIRAYRIA
LKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNLGNAKQKQG

ELEEQVMHVLDQVSELAHELLHKLKTGEELERAAYFNWWATEMMLELIKSDDEREIRE
IEEEEARRILEHLEELARKGSGSGSGSGSGSGSEAEALAYLLGELAYKLGEYRIAIRAYRIA
LKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGD
YDEAIEYYQKALELDPNNAEAKQNLGNAKQKQG

ELEEQVMHVLDQVSELAHELLHKLKTGEELERAAYFNWWATEMMLELIKSDDEREIRE
IEEEEARRILEHLEELARKGSGSRMKQIEDKIEEILSKIYHIENEIARIKKLIGER

ELEEQVMHVLDQVSELAHELLHKLKTGEELERAAYFNWWATEMMLELIKSDDEREIRE
IEEEEARRILEHLEELARKGSGSGSGSGSRMKQIEDKIEEILSKIYHIENEIARIKKLIG
ER

ELEEQVMHVLDQVSELAHELLHKLKTGEELERAAYFNWWATEMMLELIKSDDEREIRE
IEEEEARRILEHLEELARKGSGSGSGSEYEIRKALEELKASTAELKRSTASLRSTEEELK
KNPSEDALVENNRLIVENNAIIVENNRIIAAVLELIVRAIK

ELEEQVMHVLDQVSELAHELLHKLKTGEELERAAYFNWWATEMMLELIKSDDEREIRE
IEEEEARRILEHLEELARKGSGSGSGSGSGSEYEIRKALEELKASTAELKRSTASLRST
EELKKNPSEDALVENNRLIVENNAIIVENNRIIAAVLELIVRAIK

ELEEQVMHVLDQVSELAHELLHKLKTGEELERAAYFNWWATEMMLELIKSDDEREIRE
IEEEEARRILEHLEELARKGSGSGSNLAEKMYKAGNAMYRKQYTTIAI IAYTLALLKD
PNNAEAWYNLGNAAAYKKGEYDEAIEAYQKALELDPNNAEAWYNLGNAYYKQGDYDEA
IEYYQKALELDPNNAEAKQNLGNAKQKQG

ELEEQVMHVLDQVSELAHELLHKLKTGEELERAAYFNWWATEMMLELIKSDDEREIRE
IEEEEARRILEHLEELARKGSGSGSGSGSGSNLAEKMYKAGNAMYRKQYTTIAI IAYTLA
LLKDPNNAEAWYNLGNAAAYKKGEYDEAIEAYQKALELDPNNAEAWYNLGNAYYKQGD
YDEAIEYYQKALELDPNNAEAKQNLGNAKQKQG

ELEEQVMHVLDQVSELAHELLHKLKTGEELERAAYFNWWATEMMLELIKSDDEREIRE
IEEEEARRILEHLEELARKGSGSGSGSGSGEIAKSLKEIAKSLKEIAWSLKEIAKSLKG

ELEEQVMHVLDQVSELAHELLHKLKTGEELERAAYFNWWATEMMLELIKSDDEREIRE
IEEEEARRILEHLEELARKGSGSGSGSGSGSGEIAKSLKEIAKSLKEIAWSLKEIAKSLK
G

ELEEQVMHVLDQVSELAHELLHKLKTGEELERAAYFNWWATEMMLELIKSDDEREIRE
IEEEEARRILEHLEELARKGGSGGEEAEALAYLLGELAYKLGEYRIAIRAYRIALKRDP
NNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNLGNAKQKQG

ELEEQVMHVLDQVSELAHELLHKLKTGEELERAAYFNWWATEMMLELIKSDDEREIRE
IEEEEARRILEHLEELARKGGGSGGGGEEAEALAYLLGELAYKLGEYRIAIRAYRIALKR
DPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNLGNAKQKQG

ELEEQVMHVLDQVSELAHELLHKLKTGEELERAAYFNWWATEMMLELIKSDDEREIRE
IEEEEARRILEHLEELARKGGGSGGGGEEAEALAYLLGELAYKLGEYRIAIRAYRIALKR
DPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEA
IEYYQKALELDPNNAEAKQNLGNAKQKQG

ELEEQVMHVLDQVSELAHELLHKLKTGEELERAAYFNWWATEMMLELIKSDDEREIRE
IEEEEARRILEHLEELARKGGGSGGGGEEAEALAYLLGELAYKLGEYRIAIRAYRIALKR
DPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEA
AIEYYQKALELDPNNAEAKQNLGNAKQKQG

ELEEQVMHVLDQVSELAHELLHKLKTGEELERAAYFNWWATEMMLELIKSDDEREIRE
IEEEEARRILEHLEELARKGGGSGGGGEEAEALAYLLGELAYKLGEYRIAIRAYRIALKR
DPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEA
AIEYYQKALELDPNNAEAKQNLGNAKQKQG

	AHB2- GGGS9- 1na0_int2	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGGSGGGGEEAELAYLLGELAYKLGEYRIAIRAYRIAL KRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDY DEAIEYYQKALELDPNNAEAKQNLGNAKQKQG
658		
	AHB2- GGGS5-6msr	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGSGGGSEYEIRKALEELKASTAELKRATASLRASTEEL KKNPSEDALVENNRLIVEHNAIIVENNRIIAAVLELIVRAIK
659		
	AHB2- GGGS7-6msr	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGSGGGGSEYEIRKALEELKASTAELKRATASLRASTE ELKKNPSEDALVENNRLIVEHNAIIVENNRIIAAVLELIVRAIK
660		
	AHB2- GGGS9-6msr	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGGSGGGGSEYEIRKALEELKASTAELKRATASLRAS TEELKKNPSEDALVENNRLIVEHNAIIVENNRIIAAVLELIVRAIK
661		
	AHB2- GGGS5-1gcm	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGSGGRMKQIEDKIEEILSKIYHIENEIARIKKLIGER
662		
	AHB2- GGGS7-1gcm	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGSGGRMKQIEDKIEEILSKIYHIENEIARIKKLIGE R
663		
	AHB2- GGGS9-1gcm	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGSGGGGRMKQIEDKIEEILSKIYHIENEIARIKKLI GER
664		
	AHB2- GGGS5-pRO- 2-noHis	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGSGGGSEYEIRKALEELKASTAELKRSTASLRASTEEL KKNPSEDALVENNRLIVENNAIIVENNRIIAAVLELIVRAIK
665		
	AHB2- GGGS7-pRO- 2-noHis	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGSGGGGSEYEIRKALEELKASTAELKRSTASLRASTE ELKKNPSEDALVENNRLIVENNAIIVENNRIIAAVLELIVRAIK
666		
	AHB2- GGGS9-pRO- 2-noHis	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGSGGGGSEYEIRKALEELKASTAELKRSTASLRAS TEELKKNPSEDALVENNRLIVENNAIIVENNRIIAAVLELIVRAIK
667		
	AHB2- GGGS5- 1na0_3	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGSGGNLAEKMYKAGNAMYRKQYTIATIIAYTLALLKDP NNAEAWYNLGNAAAYKKGEYDEAIEAYQKALELDPNNAEAWYNLGNAYYKQGDYDEAI EYYQKALELDPNNAEAKQNLGNAKQKQG
668		
	AHB2- GGGS7- 1na0_3	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGSGGGNLAEKMYKAGNAMYRKQYTIATIIAYTLALLK DPNNAEAWYNLGNAAAYKKGEYDEAIEAYQKALELDPNNAEAWYNLGNAYYKQGDYDE AIEYYQKALELDPNNAEAKQNLGNAKQKQG
669		
	AHB2- GGGS9- 1na0_3	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGSGGGNLAEKMYKAGNAMYRKQYTIATIIAYTLALL LKDPNNAEAWYNLGNAAAYKKGEYDEAIEAYQKALELDPNNAEAWYNLGNAYYKQGDY DEAIEYYQKALELDPNNAEAKQNLGNAKQKQG
670		
	AHB2- GGGS5-4pn9	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGSGGGEIAKSLKEIAKSLKEIAWSLKEIAKSLKG
671		
	AHB2- GGGS7-4pn9	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGSGGGEIAKSLKEIAKSLKEIAWSLKEIAKSLKG
672		
	AHB2- GGGS9-4pn9	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGSGGGGGEIAKSLKEIAKSLKEIAWSLKEIAKSLKG
673		
	AHB2-2GS- SB175	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGSEALEELEKALRELKKSTDELERSTEELEKNPSEDAL VENNRLIVENNKIIVEVLRIIAKVLK
674		
	AHB2-4GS- SB175	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGSGSEALEELEKALRELKKSTDELERSTEELEKNPSED ALVENNRLIVENNKIIVEVLRIIAKVLK
675		
	AHB2-6GS- SB175	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGSGSEALEELEKALRELKKSTDELERSTEELEKNPS EDALVENNRLIVENNKIIVEVLRIIAKVLK
676		

677	AHB2-2GS-SB175.1	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGSPLEKALRELKKSTDELERSTEELEKNGSPEALVEN NRLIVENNKIIVEVLRIIAK
678	AHB2-4GS-SB175.1	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGSSPELEKALRELKKSTDELERSTEELEKNGSPEALV ENNRLIVENNKIIVEVLRIIAK
679	AHB2-6GS-SB175.1	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGSGSPELEKALRELKKSTDELERSTEELEKNGSPEA LVENNRLIVENNKIIVEVLRIIAK
680	AHB2-2GS-41 SB175.2	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGSEKALRELKKSTDELERSTEELEKNGSPEALVENNRL IVENNKIIVEVLR
681	AHB2-4GS-SB175.2	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGSSSEKALRELKKSTDELERSTEELEKNGSPEALVENN RLIVENNKIIVEVLR
682	AHB2-6GS-SB175.2	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGSGSEKALRELKKSTDELERSTEELEKNGSPEALVE NNRLIVENNKIIVEVLR
683	SB175-6GS-LCB1v2.2	SEALEELEKALRELKKSTDELERSTEELEKNPSEDALVENNRLIVENNKIIVEVLRI IAKVLKGGGGSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTNDENLLE EAERLLEEVR
684	SB175-10GS-LCB1v2.2	SEALEELEKALRELKKSTDELERSTEELEKNPSEDALVENNRLIVENNKIIVEVLRI IAKVLKGGGGSGGGGSDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTND NLEEAERLLEEVR
685	SB175.1-6GS-LCB1v2.2	SPELEKALRELKKSTDELERSTEELEKNGSPEALVENNRLIVENNKIIVEVLRIIAK GGGGSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTNDENLLEEAERLL EEVVR
686	SB175.1-10GS-LCB1v2.2	SPELEKALRELKKSTDELERSTEELEKNGSPEALVENNRLIVENNKIIVEVLRIIAK GGGGSGGGGSDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTNDENLLEEA ERLLEEVR
687	LCB3-8GS-SB175	NLDELHMQMTDLVYEALHFADDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE LLERLLSGGGSGGGSEALEELEKALRELKKSTDELERSTEELEKNPSEDALVENNR LIVENNKIIVEVLRIIAKVLK
688	LCB3-6GS-SB175	NLDELHMQMTDLVYEALHFADDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE LLERLLSGGGSGSEALEELEKALRELKKSTDELERSTEELEKNPSEDALVENNRLI VENNKIIVEVLRIIAKVLK
689	LCB3-4GS-SB175	NLDELHMQMTDLVYEALHFADDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE LLERLLSGGGSEALEELEKALRELKKSTDELERSTEELEKNPSEDALVENNRLIVE NNKIIVEVLRIIAKVLK
690	LCB3-2GS-SB175	NLDELHMQMTDLVYEALHFADDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE LLERLLSGGSEALEELEKALRELKKSTDELERSTEELEKNPSEDALVENNRLIVEN NKIIVEVLRIIAKVLK
691	AHB2v1-2GS-SB175	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGSEALEELEKALRELKKSTDELERSTEELEKNPSEDAL VENNRLIVENNKIIVEVLRIIAKVLK
692	AHB2v2-2GS-SB175	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAAYFNWWATEMMLELIKSDDEREIRE IEEEAARILEHLEELARTGGSEALEELEKALRELKKSTDELERSTEELEKNPSEDAL VENNRLIVENNKIIVEVLRIIAKVLK

In some embodiments, the polypeptides comprise an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of a genus selected from those

5 recited in the middle column of Table 9. In these embodiments, X1, X2, X3 (when recited in

the genus), and X4 (when recited in the genus) may be present or absent, and when present may be any sequence of 1 or more amino acids, as described above for embodiments listed in Table 8. In some embodiments, the optional domain that is present between monomer domains is present and may comprise an amino acid linker, as described above for

embodiments listed in Table 8.

In another embodiment, the polypeptides comprise an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to an amino acid sequence comprising the amino acid sequence selected from the group consisting of SEQ ID NOS:693 to 701, wherein any N-terminal methionine residue may be absent or present, and wherein residues in parentheses may be present or absent (preferably absent) and are not considered in determining percent identity.

In one embodiment, the N-terminal methionine residue is absent and the optional residues are absent.

Table 9B

Name	Sequence
C389_AHB2v1_2GS-SB175	MELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEEARR ILEHLEELARKGGSEALEELEKALRELKKSTDELERSTEELEKNPSEDALVENNRLIVENNKIIV EVLRIIAKVLK (SEQ ID NO: 693)
AHB2v2_12PAS_LCB3v2.2_12PAS_LCB1v2.2	MELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEEARR ILEHLEELARTGGASPAAPAPGGNLDLHMOMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKN KDRQKLEKVVEELKELLERLLSGGASPAAPAPGGDKENVLQKIYEIMKELERLGHAEASMQVSDLI IYEFMKTCDENLLEEAERLLEEVR (SEQ ID NO: 694)
AHB2v2_24PAS_LCB3v2.2_24PAS_LCB1v2.2	MELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEEARR ILEHLEELARTGGASPAAPAPASPAAPAPSAPAGGNLDLHMOMTDLVYEALHFAKDEEFQKHVF QLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAPAPASPAAPAPSAPAGGDKENVLQ KIYEIMKELERLGHAEASMQVSDLIYEFMKTCDENLLEEAERLLEEVR (SEQ ID NO: 695)
C398_SB175_6GS_LCB1v2.2	MELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEEARR ILEHLEELARKGGGSEALEELEKALRELKKSTDELERSTEELEKNPSEDALVENNRLIVENNKI IVEVLRIIAKVLK (SEQ ID NO: 696)
AHB2v1_10GS_LCB3v2.2_10GS_LCB1v2.2	MELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEEARR ILEHLEELARKGGGSGGGSGGNLDLHMOMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKD RQKLEKVVEELKELLERLLSGGGSGGGSGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTCDENLLEEAERLLEEVR (SEQ ID NO: 697)
C390-AHB2v1-4GS-SB175	MELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEEARR ILEHLEELARKGGGSEALEELEKALRELKKSTDELERSTEELEKNPSEDALVENNRLIVENNKI IVEVLRIIAKVLK (SEQ ID NO: 696)
C326-AHB2v1-4GS-1rfo	MELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEEARR ILEHLEELARKGGSGGYIPEAPRDGQAYVRKDGWVLLSTFL (SEQ ID NO: 698)
AHB2v1-10GS-LCB3_v2.3-10GS-LCB1_v2.2 with His Tev tag	(MSHHHHHHHSENLYFQSGG) ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMM LELIKSDDEREIREIEEEEARRILEHLEELARKGGGSGGGSGGNIDELLMQVTDLIYEALHFAKDE EFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGGSGGGSGGDKENVLQKIYEIMK ELERLGHAEASMQVSDLIYEFMKTCDENLLEEAERLLEEVR (SEQ ID NO: 699)

LCBlv3 with (MSHHHHHHHHSENLYFQSGGG) DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDER
His Tev tag LLEEAERLLEEVEE (SEQ ID NO: 700)

[illegible]

The polypeptide of any embodiment or combination of embodiments described here may further be linked to a stabilization domain to promote increased residency time upon administration to a subject. Any suitable stabilization domain may be used for an intended purpose. Exemplary stabilization domains include, but are not limited to, polyethylene glycol (PEG), albumin, hydroxyethyl starch (HES), conformationally disordered polypeptide sequence composed of the amino acids Pro, Ala, and/or Ser ('PASylation'), and/or a mucin diffusivity polypeptide composed of amino acids Lys and Ala, with or without Glu.

Non-limiting embodiments of such mucin diffusivity polypeptides include, but are not limited to:

Mucin domain: AKAKAKAKAKAKAKAKAKGG (SEQ ID NO:61); GGAKAKAKAKAKAKAKAKAK (SEQ ID NO:62)

Exemplary polypeptides of these embodiments may, for example, comprise an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 65-96, wherein in embodiments where a secretion signal is present (MARAWIFFLLCLAGRALA; SEQ ID NO:63) it can be replaced with any other secretion signal.

>Mucin_LCB1_v1.1_Cys_
AKAKAKAKAKAKAKAKAGGDKENILQKIYEIMKTLDQLGHAEASMQVSDLIYEFMKQGDRLLEEAERLLEEVC
(SEQ ID NO:65)

>Mucin_LCB1_v1.3
AKAKAKAKAKAKAKAKAKGDKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVEE (SEQ
ID NO:66)

>LCB1_v1.3_Mucin
DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAEERLLEEVEERGKAKAKAKAKAKAKAKAKAKAK SEQ
ID NO:67)

FC Fusions (**Bold = Secretion Signal**, underline = LCB, Yellow is the GS Linker, Green is Fc)

>LCB1-Fc1 (BM40-LCB1-GS4-Fc-Opt-WT) (The LCB1 sequences = **LCB1-1** of first provisional)

MARAWIFFLLCLAGRALADKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKGDERLLEEAERLLEEVERGSGSEPKSS
DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR
SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ
PENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:68)

> LCB1-Fc2 (BM40-LCB1-GS15-Fc-Opt-WT) (The LCB1 sequence = **LCB1-1** of first provisional)

MARAWIFFLLCLAGRALADKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKGDERLLEEAERLLEEVERGSGSGSGSG
SGSGSGSEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR
EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPS
DIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK (SEQ ID
NO:69)

>LCB1-Fc3 (BM40-Fc-Opt- GS15-2-LCB1-WT) (The LCB1 sequence = **LCB1-1** of first provisional)

MARAWIFFLLCLAGRALAEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD
GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQV
SLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPG
KSGSGSGSGSGSGSGS DKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKGDERLLEEAERLLEEVE (SEQ ID
NO: 70)

>LCB1-Fc4 (BM40-LCB1-GS15-Fc-Opt-GS15-2-LCB1-WT) (The LCB1 sequences = **LCB1-1** of first provisional)

MARAWIFFLLCLAGRALADKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKGDERLLEEAERLLEEVERGSGSGSGSG
SGSGSGSEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR
EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPS
DIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGKSGSGSGSGSGSG
SGSDKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKGDERLLEEAERLLEEVE (SEQ ID NO:71)

>LCB1-Fc5 (BM40-LCB1-GS4-Fc-Opt-Q38) (The LCB1 sequence = **LCB1-3** of first provisional)

MARAWIFFLLCLAGRALADKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKGDERLLEEAERLLEEVERGSGSEPKSS
DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVV
SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ
PENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:72)

>LCB1-Fc6 (BM40-LCB1-GS15-Fc-Opt-Q38) (The LCB1 sequence = **LCB1-3** of first provisional)

MARAWIFFLLCLAGRALADKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKGDERLLEEAERLLEEVERGSGSGSGSG
SGSGSGSEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR
EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPS
DIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK (SEQ ID
NO:73)

>LCB1-Fc7 (BM40-Fc-Opt-GS15-2-LCB1-Q38) (The LCB1 sequence = **LCB1-3** of first provisional)

MARAWIFFLLCLAGRALAEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD
GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQV
SLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPG
KSGSGSGSGSGSGSGSDKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKGDERLLEEAERLLEEVE (SEQ ID
NO:74)

>LCB1-Fc8 (BM40-LCB1-Q38-GS15-Fc-Opt-GS15-2-LCB1-Q38) (The LCB1 sequences = **LCB1-3** of first provisional)

MARAWIFFLLCLAGRALADKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKGDERLLEEAERLLEEVERGSGSGSGSG
SGSGSGSEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR

EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPS
 DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKSGSGSGSGSGS
 GSGSDKEWILQKIYEIMRLDELGHAEASMRVSDLIYEFMKQGDRLLEEAERLLEEVEVER (SEQ ID NO:75)

5 > LCB1-6M-Fc9 (BM40-LCB1-6M -4N,14K,15T,18Q,27Q,38Q -GS15-Fc-Opt)
 (The LCB1 sequence = **LCB1_v1.1 of this provisional**)
MARAWIFFLLCLAGRALADKENILQKIYEIMKTL DQLGHAEASMQVSDLIYEFMKQGDRLLEEAERLLEEVEVERGGSGSGSGSG
 SGSGSGSEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR
 10 EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPS
 DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK (SEQ ID
 NO:76)

15 > LCB1-6M-Ngly-Fc10 (BM40-LCB1-6M-Ngly -4N,14K,15T,18Q,27N,38Q -GS15-Fc-Opt) (The
 LCB1 sequence = **LCB1-5 of the original provisional** = LCB1_v1.1 = LCB1-4 with N-link
 Glycosylation)
MARAWIFFLLCLAGRALADKENILQKIYEIMKTL DQLGHAEASMNVS DLIYEFMKQGDRLLEEAERLLEEVEVERGGSGSGSGSG
 SGSGSGSEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR
 20 EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPS
 DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK (SEQ ID
 NO:77)

25 > LCB3-6M-Fc11 (BM40-LCB3-6M -8Q,26Q,28H,35K,37T,43K -GS15-Fc-Opt)
 (LCB sequence is the same as **LCB3-3** of First Provisional)
MARAWIFFLLCLAGRALANDDELHMQMTDLVYEALHFAKDEEIQKHVFQLF EKATKAYKNKDRQKLEKVVEELKELLERLLSG
 GSGSGSGSGSGSGSEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV
 HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTC
 30 LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK
 (SEQ ID NO:78)

35 > LCB3-6M-Ngly-Fc12 (BM40-LCB3-6M-Ngly -8Q,26Q,28H,35N,37T,43K -GS15-Fc-Opt) (LCB
 sequence is the same as **LCB3-4** of First Provisional which is LCB3-3 with N-link
 Glycosylation)
MARAWIFFLLCLAGRALANDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFENATKAYKNKDRQKLEKVVEELKELLERLLSG
 GSGSGSGSGSGSGSEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV
 HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTC
 40 LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK
 (SEQ ID NO:79)

45 > LCB1-6M-GPGcP-Fc13 (BM40-LCB1-6M -4N,14K,15T,18Q,27Q,38Q -GPGcP-Fc-Opt) (LCB
 sequence is the same as **LCB3-3** of First Provisional)
MARAWIFFLLCLAGRALADKENILQKIYEIMKTL DQLGHAEASMQVSDLIYEFMKQGDRLLEEAERLLEEVEVERAGSGSGSGS
 GSGSPVSTPPTSPSTPPTSPSPSGSGSGSGSPVSTPPTSPSTPPTSPSPASEPKSSDKTHTCPPCPAPELLGGPSVF
 LFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVS
 50 NKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY
 SKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:80)

55 > LCB3-6M-GPGcP-Fc14 (BM40-LCB3-6M -8Q,26Q,28H,35K,37T,43K -GPGcP-Fc-Opt) (LCB
 sequence is the same as **LCB3-3** of First Provisional)
MARAWIFFLLCLAGRALANDDELHMQMTDLVYEALHFAKDEEIQKHVFQLF EKATKAYKNKDRQKLEKVVEELKELLERLLSA
 GSGSGSGSGSGSPVSTPPTSPSTPPTSPSPSGSGSGSGSPVSTPPTSPSTPPTSPSPASEPKSSDKTHTCPPCPAPE
 LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNG
 KEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD
 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:81)

- 5 > LCB1-6M-GS30-Fc15 (BM40-LCB1-6M -4N,14K,15T,18Q,27Q,38Q -GS30-Fc-Opt) LCB1-4
MARAWIFFLLCLAGRALADKENILQKIYEIMKTLDQLGHAEASMQVSDLIYEFMKQGDRLLEEAERLLEEVEVERGGSGGGSG
 GGGSGGGSGGGSGGGSGGGSGGEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK
 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSL
 SPGK (SEQ ID NO:82)
- 10 > LCB3-6M-GS30-Fc16 (BM40-LCB3-6M -8Q,26Q,28H,35K,37T,43K -GS30-Fc-Opt) (LCB
 sequence is the same as **LCB3-3** of First Provisional)
MARAWIFFLLCLAGRALADNDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSG
 GSGSGGGSGGGSGGGSGGGSGGGSGGEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED
 DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP
 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNH
 YTQKSLSLSPGK (SEQ ID NO:83)
- 20 > LCB1-v1.3-Fc17 (BM40-LCB1-v1.3 -4N,14K,15T,17E,18Q,27Q,38Q -GS15-Fc-Opt)
MARAWIFFLLCLAGRALADKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDRLLEEAERLLEEVEVERGGSGGGSG
 SGSGGSEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR
 EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPS
 DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK (SEQ ID
 NO:84)
- 25 > LCB1-v1.3-Ngly-Fc18 (BM40-LCB1-v1.3 Ngly -4N,14K,15T,17E,18Q,27N,38Q -GS15-Fc-
 Opt) (>LCB1_v1.5 (= LCB1_v1.3 with N-link Glycosylation)
MARAWIFFLLCLAGRALADKENILQKIYEIMKTLEQLGHAEASMNVSVDLIYEFMKQGDRLLEEAERLLEEVEVERGGSGGGSG
 SGSGGSEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR
 EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPS
 DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK (SEQ ID
 NO:85)
- 30 > LCB1-v1.3-GPGcP-Fc19 (BM40-LCB1-v1.3-Fc19 -4N,14K,15T,17E,18Q,27Q,38Q-GPGcP-Fc-
 Opt)
MARAWIFFLLCLAGRALADKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDRLLEEAERLLEEVEVERAGSGGGSGGS
 GGSPVPSTPPTSPSTPPTSPSGSGNSGSGGSPVPSTPPTSPSTPPTSPSPASEPKSSDKTHTCPPCPAPELLGGPSVF
 LFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVS
 NKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY
 SKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:86)
- 40 > LCB1-v1.3-GS30-Fc20 (BM40-LCB1-v1.3 -4N,14K,15T,17E,18Q,27Q,38Q -GS30-Fc-Opt)
MARAWIFFLLCLAGRALADKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDRLLEEAERLLEEVEVERGGSGGGSG
 GGGSGGGSGGGSGGGSGGGSGGEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK
 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSL
 SPGK (SEQ ID NO:87)

Fc21-
 LCB1v2.2-
 FcIgG1_WT

MARAWIFFLLCLAGRALADKENVLQKIYEIMKELERLGHAESMQVSDLIYEFMKTCDENL
 LEEAERLLEEVRGGSGGGSGGGSGGGSEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPK
 DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVL
 HQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVK
 GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEA
 LHNHYTQKSLSLSPGK (SEQ ID NO: 88)

Fc22-
 LCB1v2.2-
 FcIgG3_WT

MARAWIFFLLCLAGRALADKENVLQKIYEIMKELERLGHAESMQVSDLIYEFMKTCDENL
 LEEAERLLEEVRGGSGGGSGGGSGGGSEPKSSDKTHTCPRCPAPELLGGPSVFLFPPKPK
 DTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTKPREEQFNSTFRVSVLTVL
 HQDWLNGKEYKCKVSNKALPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVK
 GFYPSDIAVEWESSGQPENNYNTTPPMLSDGSFFLYSKLTVDKSRWQQGNIFSCVMHEA

LHNRFQTQKSLSLSPGK (SEQ ID NO: 89)

Fc23_LCB3_v
2.3-10GS-
LCB1_v2.2_F
cIgG1_WT

MARAWIFFLLCLAGRALANIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNK
DKQKLEKVVEELKELLERILSGGGSGGGSGGDKENVLQKIYEIMKELERLGHAEASMQVSD
LIYEFMKTNDENLLEEAERLLEEVKRGSGSGSGSGSGGSEPKSSDKTHTCPPCPAPELL
GGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY
NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE
LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ
QGNVFSCSVMEALHNHYTQKSLSLSPGK (SEQ ID NO: 90)

Fc24_AHB2-
10GS-
LCB3_v2.3-
10GS-
LCB1_v2.2_F
cIgG1_WT

MARAWIFFLLCLAGRALAELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMM
LELIKSDDEREIREIEEEEARRILEHLEELARKGGGSGGGSGGNIDELLMQVTDLIYEALHF
AKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGGSGGGSGGDKENVL
QKIYEIMKELERLGHAEASMQVSDLIYEFMKTNDENLLEEAERLLEEVKRGSGSGSGSG
SGGSEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE
KTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK (SEQ ID
NO: 91)

Fc25_LCB3_v
2.3-10GS-
AHB2-10GS-
LCB1_v2.2_F
cIgG1_WT

MARAWIFFLLCLAGRALANIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNK
DKQKLEKVVEELKELLERILSGGGSGGGSGGDELEEQVMHVLDQVSELAHELLHKLTGEEL
RAAYFNWWATEMMLELIKSDDEREIREIEEEEARRILEHLEELARKGGGSGGGSGGDKENVL
QKIYEIMKELERLGHAEASMQVSDLIYEFMKTNDENLLEEAERLLEEVKRGSGSGSGSG
SGGSEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE
KTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK (SEQ ID
NO: 92)

Fc26_LCB3_v
2.3-10GS-
LCB1_v2.2_F
cIgG1_GA

MARAWIFFLLCLAGRALANIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNK
DKQKLEKVVEELKELLERILSGGGSGGGSGGDKENVLQKIYEIMKELERLGHAEASMQVSD
LIYEFMKTNDENLLEEAERLLEEVKRGSGSGSGSGSGGSEPKSSDKTHTCPPCPAPELL
AGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY
NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE
LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ
QGNVFSCSVMEALHNHYTQKSLSLSPGK (SEQ ID NO: 93)

Fc27_LCB3_v
2.3-10GS-
LCB1_v2.2_F
cIgG1_GRLR

MARAWIFFLLCLAGRALANIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNK
DKQKLEKVVEELKELLERILSGGGSGGGSGGDKENVLQKIYEIMKELERLGHAEASMQVSD
LIYEFMKTNDENLLEEAERLLEEVKRGSGSGSGSGSGGSEPKSSDKTHTCPPCPAPELL
RGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY
NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE
LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ
QGNVFSCSVMEALHNHYTQKSLSLSPGK (SEQ ID NO: 94)

Fc28_LCB3_v
2.3-10GS-
LCB1_v2.2_F
cIgG1_GAALI
E

MARAWIFFLLCLAGRALANIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNK
DKQKLEKVVEELKELLERILSGGGSGGGSGGDKENVLQKIYEIMKELERLGHAEASMQVSD
LIYEFMKTNDENLLEEAERLLEEVKRGSGSGSGSGSGGSEPKSSDKTHTCPPCPAPELL
AGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY
NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPLPEEKTISKAKGQPREPQVYTLPPSRDE
LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ
QGNVFSCSVMEALHNHYTQKSLSLSPGK (SEQ ID NO: 95)

Fc29_LCB3_v
2.3-10GS-
LCB1_v2.2_F
cIgG1_GAALI
ELS

MARAWIFFLLCLAGRALANIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNK
DKQKLEKVVEELKELLERILSGGGSGGGSGGDKENVLQKIYEIMKELERLGHAEASMQVSD
LIYEFMKTNDENLLEEAERLLEEVKRGSGSGSGSGSGGSEPKSSDKTHTCPPCPAPELL
AGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY
NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPLPEEKTISKAKGQPREPQVYTLPPSRDE
LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ
QGNVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO: 96)

The disclosure further provides oligomers of the polypeptide of any embodiment or combination of embodiments herein. In one embodiment, the oligomers are oligomers of polypeptides disclosed herein that comprise oligomerization domains. In one embodiment, the oligomer comprises a trimer, including but not limited to a homotrimer.

5 In another embodiment, the disclosure provides compositions, comprising 2, 3, 4, or more copies of the polypeptide of any embodiment or combination of embodiments herein attached to a support, including but not limited to a polypeptide particle support, such as a nanoparticle or virus like particle.

As disclosed herein, the polypeptides bind to the SARS-CoV-2 Spike glycoprotein, and thus are useful (for example), as therapeutics to treat SARS-CoV-2 infection. In one
10 embodiment, the polypeptides bind to the SARS-CoV-2 Spike glycoprotein with an affinity of at least 10 nM, measured as described in the attached examples.

In another aspect, the disclosure provides nucleic acids encoding a polypeptide of the disclosure. The nucleic acid sequence may comprise RNA (such as mRNA) or DNA. Such
15 nucleic acid sequences may comprise additional sequences useful for promoting expression and/or purification of the encoded protein, including but not limited to polyA sequences, modified Kozak sequences, and sequences encoding epitope tags, export signals, and secretory signals, nuclear localization signals, and plasma membrane localization signals. It will be apparent to those of skill in the art, based on the teachings herein, what nucleic acid
20 sequences will encode the proteins of the invention.

In another aspect, the disclosure provides expression vectors comprising the nucleic acid of any embodiment or combination of embodiments of the disclosure operatively linked to a suitable control sequence. "Expression vector" includes vectors that operatively link a nucleic acid coding region or gene to any control sequences capable of effecting expression
25 of the gene product. "Control sequences" operably linked to the nucleic acid sequences of the disclosure are nucleic acid sequences capable of effecting the expression of the nucleic acid molecules. The control sequences need not be contiguous with the nucleic acid sequences, so long as they function to direct the expression thereof. Thus, for example, intervening untranslated yet transcribed sequences can be present between a promoter sequence and the
30 nucleic acid sequences and the promoter sequence can still be considered "operably linked" to the coding sequence. Other such control sequences include, but are not limited to, polyadenylation signals, termination signals, and ribosome binding sites. Such expression vectors can be of any type known in the art, including but not limited to plasmid and viral-based expression vectors. The control sequence used to drive expression of the disclosed

nucleic acid sequences in a mammalian system may be constitutive (driven by any of a variety of promoters, including but not limited to, CMV, SV40, RSV, actin, EF) or inducible (driven by any of a number of inducible promoters including, but not limited to, tetracycline, ecdysone, steroid-responsive).

5 In one aspect, the present disclosure provides cells comprising the polypeptide, the composition, the nucleic acid, and/or the expression vector of any embodiment or combination of embodiments of the disclosure, wherein the cells can be either prokaryotic or eukaryotic, such as mammalian cells. In one embodiment the cells may be transiently or stably transfected with the nucleic acids or expression vectors of the disclosure. Such
10 transfection of expression vectors into prokaryotic and eukaryotic cells can be accomplished via any technique known in the art. A method of producing a polypeptide according to the invention is an additional part of the invention. The method comprises the steps of (a) culturing a host according to this aspect of the invention under conditions conducive to the expression of the polypeptide, and (b) optionally, recovering the expressed polypeptide. In
15 other embodiments, the polypeptides may be produced via any other suitable technique, including but not limited to using cell-free protein synthesis (or in vitro transcription and translation).

In another aspect, the disclosure provides pharmaceutical compositions/vaccines comprising

- 20 (a) the polypeptide, the nucleic acid, the expression vector, and/or the host cell of any embodiment or combination of embodiments herein; and
(b) a pharmaceutically acceptable carrier.

The compositions may further comprise (a) a lyoprotectant; (b) a surfactant; (c) a bulking agent; (d) a tonicity adjusting agent; (e) a stabilizer; (f) a preservative and/or (g) a
25 buffer. In some embodiments, the buffer in the pharmaceutical composition is a Tris buffer, a histidine buffer, a phosphate buffer, a citrate buffer or an acetate buffer. The composition may also include a lyoprotectant, e.g. sucrose, sorbitol or trehalose. In certain embodiments, the composition includes a preservative e.g. benzalkonium chloride, benzethonium, chlorohexidine, phenol, m-cresol, benzyl alcohol, methylparaben, propylparaben,
30 chlorobutanol, o-cresol, p-cresol, chlorocresol, phenylmercuric nitrate, thimerosal, benzoic acid, and various mixtures thereof. In other embodiments, the composition includes a bulking agent, like glycine. In yet other embodiments, the composition includes a surfactant e.g., polysorbate-20, polysorbate-40, polysorbate- 60, polysorbate-65, polysorbate-80 polysorbate-85, poloxamer-188, sorbitan monolaurate, sorbitan monopalmitate, sorbitan monostearate,

sorbitan monooleate, sorbitan trilaurate, sorbitan tristearate, sorbitan trioleate, or a combination thereof. The composition may also include a tonicity adjusting agent, e.g., a compound that renders the formulation substantially isotonic or isoosmotic with human blood. Exemplary tonicity adjusting agents include sucrose, sorbitol, glycine, methionine, mannitol, dextrose, inositol, sodium chloride, arginine and arginine hydrochloride. In other embodiments, the composition additionally includes a stabilizer, e.g., a molecule which substantially prevents or reduces chemical and/or physical instability of the nanostructure, in lyophilized or liquid form. Exemplary stabilizers include sucrose, sorbitol, glycine, inositol, sodium chloride, methionine, arginine, and arginine hydrochloride.

The polypeptide, the nucleic acid, the expression vector, and/or the host cell may be the sole active agent in the composition, or the composition may further comprise one or more other agents suitable for an intended use.

In a further aspect, the disclosure provides methods for treating a severe acute respiratory syndrome (SARS) coronavirus infection (including SARS-Co-V and SARS-CoV-2), comprising administering to a subject in need thereof an amount of the polypeptide, the nucleic acid, the expression vector, the host cell, the oligomer, the composition, and/or the pharmaceutical composition of any of the preceding claims, effective to treat the infection. In one embodiment, the SARS coronavirus comprises SARS-CoV-2.

In another aspect, the disclosure provides methods for limiting development of a severe acute respiratory syndrome (SARS) coronavirus infection (including SARS-Co-V and SARS-CoV-2), comprising administering to a subject in need thereof an amount of the polypeptide, the nucleic acid, the expression vector, the host cell, the oligomer, the composition, and/or the pharmaceutical composition of any of the preceding claims, effective to treat the infection. In one embodiment, the SARS coronavirus comprises SARS-CoV-2.

The polypeptide, the nucleic acid, the expression vector, the host cell, and/or the pharmaceutical composition may be administered via any suitable administrative route as deemed appropriate by attending medical personnel. In one embodiment, the polypeptide, the nucleic acid, the expression vector, the host cell, the oligomer, the composition, and/or the pharmaceutical composition is administered intra-nasally. In another embodiment, the polypeptide, the nucleic acid, the expression vector, the host cell, the oligomer, the composition, and/or the pharmaceutical composition is administered systemically.

When the method comprises treating a SARS coronavirus infection, the one or more polypeptides, nucleic acids, expression vectors, host cells, and/or pharmaceutical compositions are administered to a subject that has already been diagnosed as having a SARS

coronavirus infection. As used herein, "treat" or "treating" means accomplishing one or more of the following: (a) reducing severity of symptoms of the infection in the subject; (b) limiting increase in symptoms in the subject; (c) increasing survival; (d) decreasing the duration of symptoms; (e) limiting or preventing development of symptoms; and (f) decreasing the need for hospitalization and/or the length of hospitalization for treating the infection.

When the method comprises limiting development of SARS coronavirus infection, the one or more polypeptides, nucleic acids, expression vectors, host cells, and/or pharmaceutical compositions are administered prophylactically to a subject that is not known to have a SARS coronavirus infection, but may be at risk of such an infection. As used herein, "limiting" means to limit development of a SARS coronavirus infection in subjects at risk of such infection, which may be any subject.

The subject may be any subject, such as a human subject

Exemplary symptoms of SARS-CoV-2 infection include, but are not limited to, fever, fatigue, cough, shortness of breath, chest pressure and/or pain, loss or diminution of the sense of smell, loss or diminution of the sense of taste, and respiratory issues including but not limited to pneumonia, bronchitis, severe acute respiratory syndrome (SARS), and upper and lower respiratory tract infections.

As used herein, an "effective amount" refers to an amount of the composition that is effective for treating and/or limiting SARS-CoV-2 infection. The polypeptide, composition, nucleic acid, or composition of any embodiment herein are typically formulated as a pharmaceutical composition, such as those disclosed above, and can be administered via any suitable route, including orally, parentally, by inhalation spray, rectally, or topically in dosage unit formulations containing conventional pharmaceutically acceptable carriers, adjuvants, and vehicles. The term parenteral as used herein includes, subcutaneous, intravenous, intra-arterial, intramuscular, intrasternal, intratendinous, intraspinal, intracranial, intrathoracic, infusion techniques or intraperitoneally. Polypeptide compositions may also be administered via microspheres, liposomes, immune-stimulating complexes (ISCOMs), or other microparticulate delivery systems or sustained release formulations introduced into suitable tissues (such as blood). Dosage regimens can be adjusted to provide the optimum desired response (e.g., a therapeutic or prophylactic response). A suitable dosage range may, for instance, be 0.1 µg/kg-100 mg/kg body weight of the polypeptide or nanoparticle thereof. The composition can be delivered in a single bolus, or may be administered more than once (e.g., 2, 3, 4, 5, or more times) as determined by attending medical personnel.

The disclosure also provides methods for designing polypeptides that bind to the receptor binding site (RBD) of SARS-Cov-2, wherein the methods comprise steps as described in the examples that follow. Such methods may comprise the steps of polypeptide design (as described in any embodiment or combination of embodiments in the examples),
5 cell-free synthesis, and evaluation for SARS-Cov-2 RBD binding using any suitable technique.

Examples

Summary

10 Effective therapeutics for SARS-CoV-2 are needed. We sought to use computational protein design to generate high affinity binders to the receptor binding site (RBD) of SARS-Cov-2 that block the interaction with the Ace2 receptor required for cell entry. We generated small protein scaffolds with shape complementary to the Ace2 binding site on the RBD using two strategies: first, scaffolds were built around the helix in Ace2 that makes the majority of
15 the interactions with the RBD, and second, diverse de novo designed scaffolds less than 65 residues in length were docked against this region. In both cases, the scaffold residues at the RBD interface were then optimized for high affinity binding and those in the remainder of the protein, for folding to the target structure and stability. The 50,000 designs predicted to bind most strongly to the virus were encoded in large oligonucleotide arrays, and screened using
20 yeast surface display for binding to the RBD with fluorescence activated cell sorting; deep sequencing of the population before and after sorting identified hundreds of designs that bind the target. The binding modes of the highest affinity (most enriched by sorting) binders were confirmed by high resolution sequence mapping, and the affinities were further increased by combining 1-4 beneficial substitutions. Eight of the optimized designs with different binding
25 sites surrounding the Ace2 interface on the RBD, and completely different sequences, were found to express at high levels in E coli, and to bind the RBD with K_d 's ranging from 100pM to 10nM. The designs blocked infection of vero-6 cells by live virus with IC_{50} 's ranging from 10nM to 20pM. The polypeptides are thus useful, for example, in both intra-nasal and systemic SARS-CoV-2 therapeutics, and, more generally, our results demonstrate the power
30 of computational protein design for rapidly generating potential therapeutic candidates against pandemic threats.

SARS -CoV-2 infection is thought to often start in the nose, with virus replicating there for several before spreading to the broader respiratory system. Delivery of a high concentration of a viral inhibitor into the nose and into the respiratory system generally could

therefore potentially provide prophylactic protection, and therapeutic efficacy early in infection, and could be particularly useful for health care workers and others coming into frequent contact with infected individuals. A number of monoclonal antibodies are in development as systemic SARS-CoV-2 therapeutics, but these compounds are not ideal for intranasal delivery as antibodies are large and often not extremely stable molecules, and the density of binding sites is low (two per 150Kd antibody); the Fc domain provides little added benefit. More desirable would be protein inhibitory with the very high affinity for the virus of the monoclonals, but with higher stability and very much smaller size to maximize the density of inhibitory domains and enable direct delivery into the respiratory system through nebulization.

We set out to *de novo* design high affinity binders to the RBD that compete with Ace2 binding. We explored two strategies: first we attempted to scaffold the alpha helix in Ace2 that makes the majority of the interactions with the RBD in a small designed protein that makes additional interactions with the RBD to attain higher affinity, and second, we sought to design binders completely from scratch that do not incorporate any known binding interaction with the RBD. An advantage of the second approach is that the range of possibilities for design is much larger, and so potentially higher affinity binding modes can be identified. For the first approach, we used the RosettaTM blue print builder to generate small proteins which incorporate the Ace2 helix and for the second approach, RIF docking and design using large miniprotein libraries. The designs interact with distinct regions of the RBD surface surrounding the Ace2 binding sites (**Figure 1**). Designs for approach 1, and approach 2, were encoded in long oligonucleotides, and screened for binding to fluorescently tagged RBD on the yeast cell surface. Deep sequencing identified 3 Ace2 helix scaffolded designs (approach 1), and 150 de novo interface designs (approach 2) that were clearly enriched following FACS sorting for RBD binding. Designs were expressed in *E. coli* and purified, and many were found to have soluble expression and to bind RBD in biolayer interferometry experiments and could effectively compete with ACE-2 for binding to RBD (example shown in Figure 2). Based on BLI data (e.g. See **Figure 2**) the RBD binding affinities of minibinders are: LCB1 <1nM, LCB3 <1nM. The affinities of LCB2, LCB4, LCB5, LCB6, LCB7, LCB8 range from 1~20nM, with relative strength of different binders being LCB4 > LCB2 > LCB9 = LCB5 > LCB6 > LCB7.

To determine whether the designs binding the RBD through the designed interfaces, site saturation libraries in which every residue in each design was substituted with each of the 20 amino acids one at a time were constructed, and subjected to FACS sorting for RBD

binding. Deep sequencing showed that the binding interface residues and protein core residues were conserved in many of the designs for which such site saturation libraries (SSM's) were constructed (SSMs were used to define allowable positions for amino acid changes in **Table 1**). For most of the designs, a small number of substitutions were enriched in the FACS sorting, suggesting they increase binding affinity for RBD. For the highest affinity of the approach 1 designs, and 8 of the approach 2 designs, combinatorial libraries incorporating these substitutions were constructed and again screened for binding with FACS; because of the very high binding affinity the concentrations used in the sorting were as low as 20pM. Each library converged on a small number of closely related sequences, and for each design, one of the optimized variants was expressed in *E. coli* and purified.

The binding of the 8 optimized designs with different binding modes to RBD (Figure1) was investigated by biolayer interferometry. For a number of the designs, the K_d 's ranged from 1-20nM, and for the remainder, the K_d 's were below 1nM, too strong to measure reliably with this technique (See Figure 2). Circular dichroism spectra of the designs were consistent with the design models, and the designs retained full binding activity after a number of days at room temperature (**Figure 3**).

We investigated the ability of the designs to block infection of human cells by live virus. 100 FFU of SARS-CoV-2 was added to $2.5-3 \times 10^4$ vero cells in the presence of varying amounts of the designed binders. Details are provided in the legend to **Figure 4**. We observed potent inhibition of infection for all of the designs with IC_{50} 's ranging from 1 nM to 0.02 nM.

Details on specific designs are provided in Table 10.

Table 10

Construct Name	Seq ID	Expression Host	Vector	Expression Method	Estimated Level of Soluble Production (mg / L)	Estimated K_d for Spike (nM)	Estimated K_d for RBD (nM)	SARS-CoV-2 Neutralization IC_{50} (nM)
LCB1-1	(SEQ ID NO:1)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
LCB1-2	(SEQ ID NO:2)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
LCB1-3	(SEQ ID NO:3)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
LCB1-4	(SEQ ID NO:4)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
LCB1-5	(SEQ ID NO:5)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01

LCB1_v1.1_Cy s	(SEQ ID NO:6)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
LCB1_v1.2	(SEQ ID NO:7)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
LCB1_v1.3	(SEQ ID NO:8)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
LCB1_v1.4	(SEQ ID NO:9)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
LCB1_v1.5 (LCB1_v1.3 with N-link Glycosylation)	(SEQ ID NO:10)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
LCB2-1	(SEQ ID NO:11)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
LCB2-2	(SEQ ID NO:12)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
LCB3-1	(SEQ ID NO:13)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
LCB3-2	(SEQ ID NO:14)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
LCB3-3	(SEQ ID NO:15)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
LCB3-4	(SEQ ID NO:16)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
LCB3_v1.1	(SEQ ID NO:17)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
LCB3_v1.2	(SEQ ID NO:15)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
LCB3_v1.3	(SEQ ID NO:19)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
LCB3_v1.4	(SEQ ID NO:20)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
LCB3_v1.5	(SEQ ID NO:21)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
LCB3-4	(SEQ ID NO:16)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
LCB4-1	(SEQ ID NO:23)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
LCB4-2	(SEQ ID NO:24)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
LCB5-1	(SEQ ID NO:25)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
LCB5-2	(SEQ ID NO:26)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
LCB6-1	(SEQ ID NO:27)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
LCB6-2	(SEQ ID NO:28)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
LCB7-1	(SEQ ID NO:29)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
LCB7-2	(SEQ ID NO:30)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
LCB8-1	(SEQ ID NO:31)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
LCB8-2	(SEQ ID NO:32)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
AHB1-1	(SEQ ID NO:33)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
AHB1-2	(SEQ ID NO:34)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
AHB2-1	(SEQ ID NO:100)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
AHB2-2	(SEQ ID	E. coli	pET	Autoinduction	10	0.2	0.1	0.01

	NO:101)			37 C				
LCB1-6GS-	(SEQ ID			Autoinduction				
LCB1	NO:47)	E. coli	pET	37 C	10	0.2	0.1	0.01
LCB1-12GS-	(SEQ ID			Autoinduction				
LCB1	NO:48)	E. coli	pET	37 C	10	0.2	0.1	0.01
LCB1-24GS-	(SEQ ID			Autoinduction				
LCB1	NO:49)	E. coli	pET	37 C	10	0.2	0.1	0.01
LCB1-36GS-	(SEQ ID			Autoinduction				
LCB1	NO:50)	E. coli	pET	37 C	10	0.2	0.1	0.01
LCB1_v1.1-	(SEQ ID			Autoinduction				
GSLCB1_v1.1(1GS1)	NO:51)	E. coli	pET	37 C	10	0.2	0.1	0.01
LCB1_v1.1-	(SEQ ID			Autoinduction				
PRO-	NO:52)			37 C				
LCB1_v1.1(1P RO1)		E. coli	pET	37 C	10	0.2	0.1	0.01
LCB3_v1.2-	(SEQ ID			Autoinduction				
GS3-	NO:53)			37 C				
LCB3_v1.2(3G S3)		E. coli	pET	37 C	10	0.2	0.1	0.01
LCB3_v1.2-	(SEQ ID			Autoinduction				
PRO-	NO:54)			37 C				
LCB3_v1.2(3P RO3)		E. coli	pET	37 C	10	0.2	0.1	0.01
LCB1_v1.1-	(SEQ ID			Autoinduction				
GS-	NO:55)			37 C				
LCB3_v1.2(1G S3)		E. coli	pET	37 C	10	0.2	0.1	0.01
LCB3_v1.2-	(SEQ ID			Autoinduction				
GS-	NO:56)			37 C				
LCB1_v1.1(3G S1)		E. coli	pET	37 C	10	0.2	0.1	0.01
LCB3_v1.2-	(SEQ ID			Autoinduction				
10GS-	NO:57)			37 C				
LCB1_v1.1(LC B3-GS10-								
LCB1)		E. coli	pET	37 C	10	0.2	0.1	0.01
LCB1_v1.1-	(SEQ ID			Autoinduction				
PRO-	NO:58)			37 C				
LCB3_v1.2(1P RO3)		E. coli	pET	37 C	10	0.2	0.1	0.01
LCB3_v1.2-	(SEQ ID			Autoinduction				
PRO-	NO:59)			37 C				
LCB1_v1.1(3P RO1)		E. coli	pET	37 C	10	0.2	0.1	0.01
(5_LCB1_link er14)	(SEQ ID			Autoinduction				
	NO:60)	E. coli	pET	37 C	20.38	0.2	0.1	0.01141
Mucin_LCB1_v	(SEQ ID			Autoinduction				
1.1_Cys	NO:65)	E. coli	pET	37 C	10	0.2	0.1	0.01
Mucin_LCB1_v	(SEQ ID			Autoinduction				
1.3	NO:66)	E. coli	pET	37 C	10	0.2	0.1	0.01
LCB1_v1.3_Mu cin	(SEQ ID			Autoinduction				
	NO:67)	E. coli	pET	37 C	10	0.2	0.1	0.01
LCB1-Fc1 (BM40-LCB1-GS4-Fc-Opt-WT) (The LCB1 sequences = LCB1-1 of first provisional)	(SEQ ID			Autoinduction				
	NO:68)	Human		Transient Transfection				
		293	pCMVR	37 C	12	0.2	0.1	0.01
LCB1-Fc2 (BM40-LCB1-	(SEQ ID			Transient Transfection				
	NO:69)	Human	pCMVR	37 C	12	0.2	0.1	0.01

GS15-Fc-Opt-WT) (The LCB1 sequence = LCB1-1 of first provisional)		cells		37 C				
LCB1-Fc3 (BM40-Fc-Opt- GS15-2- LCB1-WT) (The LCB1 sequence = LCB1-1 of first provisional)	(SEQ ID NO: 70)	Human 293 cells	pCMVR	Transient Transfection 37 C	12	0.2	0.1	0.01
LCB1-Fc4 (BM40-LCB1-GS15-Fc-Opt-GS15-2-LCB1-WT) (The LCB1 sequences = LCB1-1 of first provisional)	(SEQ ID NO:71)	Human 293 cells	pCMVR	Transient Transfection 37 C	2	0.2	0.1	0.01
LCB1-Fc5 (BM40-LCB1-GS4-Fc-Opt-Q38) (The LCB1 sequence = LCB1-3 of first provisional)	(SEQ ID NO:72)	Human 293 cells	pCMVR	Transient Transfection 37 C	6	0.2	0.1	0.01
LCB1-Fc6 (BM40-LCB1-GS15-Fc-Opt-Q38) (The LCB1 sequence = LCB1-3 of first provisional)	(SEQ ID NO:73)	Human 293 cells	pCMVR	Transient Transfection 37 C	5	0.2	0.1	0.01
LCB1-Fc7 (BM40-Fc-Opt-GS15-2-LCB1-Q38) (The LCB1 sequence = LCB1-3 of first provisional)	(SEQ ID NO:74)	Human 293 cells	pCMVR	Transient Transfection 37 C	10	0.2	0.1	0.01
LCB1-Fc8 (BM40-LCB1-Q38-GS15-Fc-Opt-GS15-2-LCB1-Q38) (The LCB1 sequences = LCB1-3 of first provisional)	(SEQ ID NO:75)	Human 293 cells	pCMVR	Transient Transfection 37 C	1	0.2	0.1	0.01
LCB1-6M-Fc9 (BM40-LCB1-6M -	(SEQ ID NO:76)	Human 293 cells	pCMVR	Transient Transfection 37 C	20	0.2	0.1	0.01

4N,14K,15T,1 8Q,27Q,38Q - GS15-Fc-Opt)								
LCB1-6M- Ngly-Fc10 (BM40-LCB1- 6M-Ngly - 4N,14K,15T,1 8Q,27N,38Q - GS15-Fc-Opt) (The LCB1 sequence = LCB1-5 of the original provisional = LCB1_v1.1 = LCB1-4 with N-link Glycosylation)	(SEQ ID NO:77)	Human 293 cells	pCMVR	Transient Transfection 37 C	20	0.2	0.1	0.01
LCB3-6M-Fc11 (BM40-LCB3- 6M - 8Q,26Q,28H,3 5K,37T,43K - GS15-Fc-Opt) (LCB sequence is the same as LCB3-3 of First Provisional)	(SEQ ID NO:78)	Human 293 cells	pCMVR	Transient Transfection 37 C	5	0.2	0.1	0.01
LCB3-6M- NGly-Fc12 (BM40-LCB3- 6M-Ngly - 8Q,26Q,28H,3 5N,37T,43K - GS15-Fc-Opt) (LCB sequence is the same as LCB3-4 of First Provisional which is LCB3-3 with N-link Glycosylation)	(SEQ ID NO:79)	Human 293 cells	pCMVR	Transient Transfection 37 C	5	0.2	0.1	0.01
LCB1-6M- GPGcP-Fc13 (BM40-LCB1- 6M - 4N,14K,15T,1 8Q,27Q,38Q - GPGcP-Fc- Opt) (LCB sequence is the same as LCB3-3 of First Provisional)	(SEQ ID NO:80)	Human 293 cells	pCMVR	Transient Transfection 37 C	2	0.2	0.1	0.01
LCB3-6M- GPGcP-Fc14 (BM40-LCB3-	(SEQ ID NO:81)	Human 293 cells	pCMVR	Transient Transfection 37 C	2	0.2	0.1	0.01

6M - 8Q,26Q,28H,3 5K,37T,43K - GPGcP-Fc- Opt) (LCB sequence is the same as LCB3-3 of First Provisional)								
LCB1-6M- GS30-Fc15 (BM40-LCB1- 6M - 4N,14K,15T,1 8Q,27Q,38Q - GS30-Fc- Opt) LCB1-4	(SEQ ID NO:82)	Human 293 cells	pCMVR	Transient Transfection 37 C	1	0.2	0.1	0.01
LCB3-6M- GS30-Fc16 (BM40-LCB3- 6M - 8Q,26Q,28H,3 5K,37T,43K - GS30-Fc-Opt) (LCB sequence is the same as LCB3-3 of First Provisional)	(SEQ ID NO:83)	Human 293 cells	pCMVR	Transient Transfection 37 C	1	0.2	0.1	0.01
LCB1-v1.3- Fc17 (BM40- LCB1-v1.3 - 4N,14K,15T,1 7E,18Q,27Q,3 8Q -GS15-Fc- Opt)	(SEQ ID NO:84)	Human 293 cells	pCMVR	Transient Transfection 37 C	5	0.2	0.1	0.01
LCB1-v1.3- Ngly-Fc18 (BM40-LCB1- v1.3 Ngly - 4N,14K,15T,1 7E,18Q,27N,3 8Q -GS15-Fc- Opt) (>LCB1_v1.5 (= LCB1_v1.3 with N-link Glycosylation)	(SEQ ID NO:85)	Human 293 cells	pCMVR	Transient Transfection 37 C	5	0.2	0.1	0.01
LCB1-v1.3- GPGcP-Fc19 (BM40-LCB1- v1.3-Fc19 - 4N,14K,15T,1 7E,18Q,27Q,3 8Q-GPGcP-Fc- Opt)	(SEQ ID NO:86)	Human 293 cells	pCMVR	Transient Transfection 37 C	5	0.2	0.1	0.01
LCB1-v1.3- GS30-Fc20 (BM40-LCB1- v1.3 - 4N,14K,15T,1 7E,18Q,27Q,3 8Q -GS30-Fc-	(SEQ ID NO:87)	Human 293 cells	pCMVR	Transient Transfection 37 C	5	0.2	0.1	0.01

Opt)									

The designed binders have several advantages over antibodies as potential therapeutics. Together, they span a range of binding modes, and in combination viral escape would be quite unlikely. The retention of activity after extended time at elevated temperatures suggests they would not require a cold chain. The designs are 20 fold smaller than a full antibody molecule, and hence in an equal mass have 20 fold more potential neutralizing sites, increasing the potential efficacy of a locally administered drug. The cost of goods and the ability to scale to very high production should be lower for the much simpler miniproteins, which unlike antibodies, do not require expression in mammalian cells for proper folding. The small size and high stability should make them amenable to direct delivery into the respiratory system by nebulization. Immunogenicity is a potential problem with any foreign molecule, but for previously characterized small de novo designed proteins little or no immune response has been observed, perhaps because the high solubility and stability together with the small size makes presentation on dendritic cells less likely.

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Ultrapotent miniproteins targeting the receptor-binding domain protect against SARS-CoV-2 infection and disease

Despite the introduction of public health measures and spike protein-based vaccines to mitigate the COVID-19 pandemic, SARS-CoV-2 infections and deaths continue to rise.. Here, we investigated the capacity of modified versions of one lead binder, LCB1, to protect against SARS-CoV-2-mediated lung disease in human ACE2-expressing transgenic mice. Systemic administration of LCB1-Fc reduced viral burden, diminished immune cell infiltration and inflammation, and completely prevented lung disease and pathology. A single

intranasal dose of LCB1v1.3 reduced SARS-CoV-2 infection in the lung even when given as many as five days before or two days after virus inoculation. Importantly, LCB1v1.3 protected *in vivo* against a historical strain (WA1/2020), an emerging B.1.1.7 strain, and a strain encoding key E484K and N501Y spike protein substitutions. These data support the use of LCB1v1.3 for prevention or treatment of SARS-CoV-2 infection.

Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2), the cause of the Coronavirus Disease 2019 (COVID-19) pandemic, has resulted in global disease, suffering, and economic hardship. Despite implementation of public health measures, SARS-CoV-2 transmission persists principally through human-to-human spread (Day, 2020; Li et al., 2020; Standl et al., 2020). SARS-CoV-2-induced clinical manifestations range from asymptomatic infection to severe pneumonia, multi-organ failure, and death. Although the underlying mechanisms that dictate disease severity are poorly understood, the immunocompromised, the elderly, and those with specific comorbidities (*e.g.*, history of cardiovascular disease, diabetes, or obesity) are at increased risk for poor outcome (Zhou et al., 2020).

Here, using a stringent model of SARS-CoV-2 disease pathogenesis in human ACE2 (hACE2)-expressing transgenic mice (Golden et al., 2020; Winkler et al., 2020a), we evaluated the efficacy *in vivo* of exemplary miniprotein binder, LCB1. For our *in vivo* experiments, we evaluated two versions of LCB1: (a) an Fc-modified bivalent form, LCB1-hIgG-Fc9 (LCB1-Fc) that should extend half-life *in vivo* and engage effector arms of the immune system; and (b) a further optimized, monomeric form of LCB1 lacking an Fc domain, LCB1v1.3. Intraperitoneal administration of LCB1-Fc at one day pre- or post SARS-CoV-2 exposure conferred substantial protection including an absence of weight loss, reductions in viral burden approaching the limit of detection, and inhibition of lung inflammation and pathology. Intranasal delivery of LCB1v1.3 conferred protection as many as five days before or two days after SARS-CoV-2 inoculation. Dosing experiments revealed that LCB1v1.3 retained efficacy at pharmacologically attainable concentrations and was weakly immunogenic. Most importantly, LCB1v1.3 protected animals against the currently emerging B.1.1.7 United Kingdom variant and a SARS-CoV-2 strain encoding key spike substitutions E484K and N501Y present in both the South Africa (B.1.351) and Brazil (B.1.1.248) variants of concern. Overall, these studies establish LCB1-Fc and LCB1v1.3 as possible treatments to prevent or mitigate SARS-CoV-2 disease.

RESULTS

LCB1v1.3 prophylaxis limits viral burden and clinical disease. We modified LCB1 to generate two versions for *in vivo* testing: (a) we introduced polar mutations into

LCB1 to increase expression yield and solubility without altering RBD binding (LCB1v1.3) and (b) we modified LCB1 by fusing it to a human IgG1 Fc domain (LCB1-Fc) to enhance bioavailability. LCB1v1.3 and LCB1-Fc bound avidly to a single RBD within the S trimer (**Fig 5A**) with dissociation constants (K_D) of less than 625 and 156 pM, respectively (**Fig 5B**). LCB1v1.3 and LCB1-Fc also potently neutralized an authentic SARS-CoV-2 isolate (2019n-CoV/USA_WA1/2020 [WA1/2020]) (EC_{50} of 14.4 and 71.8 pM, respectively; **Fig 5C**).

To determine the protective potential of these miniproteins against SARS-CoV-2, we utilized K18 human hACE2-expressing transgenic mice, which develop severe lung infection and disease after intranasal inoculation of SARS-CoV-2 (Golden et al., 2020; Winkler et al., 2020a). In prophylaxis studies, a single 250 μ g (10 mg/kg) dose of LCB1-Fc administered by intraperitoneal injection (i.p.) one day prior to intranasal (i.n.) inoculation with 10^3 PFU of SARS-CoV-2 WA1/2020 prevented weight loss compared to animals given a control protein (influenza A virus hemagglutinin minibinder) designed using similar computational methods (**Fig 5D**). After LCB1-Fc prophylaxis, infectious virus was not detected in the lungs at 4- or 7-days post-infection (dpi), whereas high levels were observed in animals administered control protein (**Fig 5E, top and bottom**). Similarly, viral RNA levels in the lung, heart, spleen, and brain of LCB1-Fc treated animals were at or near the limit of detection of the assay at 4 or 7 dpi (**Fig 5F-I**). LCB1-Fc treatment had no effect on viral RNA levels in nasal wash samples obtained at 4 dpi (**Fig 5J**), results that are similar to a recent study of a neutralizing human antibody in hamsters (Zhou et al., 2021). However, viral RNA levels were reduced at 7 dpi, suggesting that LCB1-Fc treatment accelerated viral clearance or prevented spread in the upper respiratory tract.

Diffuse alveolar damage, inflammation, and pneumonia are manifestations of COVID-19 lung disease, culminating in respiratory failure and a requirement for mechanical ventilation (Johnson et al., 2020; Kordzadeh-Kermani et al., 2020). We evaluated the capacity of LCB1-Fc to prevent the compromised lung function seen after SARS-CoV-2 infection of K18-hACE2 mice (Winkler et al., 2020a). At 7 dpi, mechanical ventilation tests of lung biomechanics in animals treated with LCB1-Fc showed no difference from naïve animals (**Fig 6A**), whereas mice receiving the control binder protein showed decreased inspiratory capacity and lung compliance as well as increased pulmonary resistance, elastance, and tissue damping, all consistent with compromised lung function. These biophysical properties resulted in disparate pressure-volume loops between control binder

and LCB1-Fc treated or naïve animals. We also assessed the effect of LCB1-Fc treatment on SARS-CoV-2-induced lung pathology. Lung sections of animals collected at 7 dpi with SARS-CoV-2 showed widespread inflammation characterized by a cellular infiltrate and airspace consolidation in control protein-treated but not LCB1-Fc treated or naïve mice (**Fig 6B**). At 4 dpi, inflammatory cytokine and chemokine RNA signatures in the lung were absent in LCB1-Fc treated but not control binder treated animals, suggesting that LCB1-Fc treatment prevents virus infection and inflammation in the lung (**Fig 6C and 11**).

Post-exposure therapy with anti-RBD binders reduces viral burden. To evaluate its efficacy in a post-exposure setting, we administered LCB1-Fc by i.p. injection at 1 dpi. Therapy with LCB1-Fc prevented weight loss (**Fig 7A**) and reduced viral burden in all tested tissues at 4 and 7 dpi (**Fig 7B-G**). Infectious virus was not recovered from the lungs of LCB1-Fc treated animals collected at either timepoint. Lung sections confirmed that therapy with LCB1-Fc improved pathological outcome (**Fig 7H**). At 7 dpi, immune cell infiltrates were absent in the lung sections of LCB1-Fc treated but not control binder-treated animals.

We next tested the efficacy of LCB1v1.3 as an i.n.-delivered post-exposure therapy. I.n. delivery, might enable self-administration of an anti-SARS-CoV-2 biological drug. Indeed, miniprotein inhibitors against influenza virus have shown efficacy as a nasal mist (Chevalier et al., 2017). For these studies, we used LCB1v1.3 because it can bind an increased number of RBD molecules for a given mass dose, resulting in increased neutralization activity (**Fig 5C**). Whereas high levels of SARS-CoV-2 RNA were detected in the lungs and other peripheral tissues of control binder-treated animals at 7 dpi, infection was reduced in animals receiving LCB1v1.3 by i.n. administration at D+1 or D+2 after inoculation with SARS-CoV-2 (**Fig 7I and 12**). Levels of viral RNA were reduced in the nasal washes of animals receiving LCB1v1.3 after treatment at D+1 but not D+2 compared to control binder-treated animals (**Fig 7J**).

Intranasal delivery of LCB1v1.3 confers protection against SARS-CoV-2 when administered up to 5 days before infection. We next evaluated the durability of LCB1v1.3 administered via i.n. prophylaxis. At 5 days, 3 days, 1 day, or 6 hours prior to inoculation with 10^3 PFU of SARS-CoV-2, K18-hACE2 transgenic mice received a single 50 μ g i.n. dose of LCB1v1.3 or the control binder. At 4 or 7 dpi, viral burden in tissues was determined by RT-qPCR. As expected, protection by LCB1v1.3 was better when administered closer to the time of SARS-CoV-2 exposure, as reflected by greater reductions in viral load and weight loss (**Fig 8A-D and S3**). However, even mice receiving LCB1v1.3 five days prior to

inoculation and collected at 7 dpi showed reduced viral RNA levels in the lung compared to control binder treated animals. Regardless of the collection timepoint, lung viral RNA levels were reduced in animals receiving LCB1v1.3 three days prior to inoculation with SARS-CoV-2.

We tested a range of i.n. doses LCB1v1.3 for efficacy (**Fig 8E-J**). Treatment with as little as 2 µg (0.1 mg/kg) of LCB1v1.3 prevented SARS-CoV-2-induced weight loss. Doses between 2 and 10 µg (0.1 to 0.5 mg/kg) of LCB1v1.3 reduced viral RNA levels in the lung, heart, and spleen at 7 dpi relative to control binder-treated animals. Moreover, animals receiving a 50 µg dose of LCB1v1.3 showed minimal, if any, lung inflammation (**Fig 8K**).

Collectively, these results indicate that even low doses of LCB1v1.3, when administered via an i.n. route prior to exposure, can limit SARS-CoV-2 infection and disease in the stringent K18-hACE transgenic mouse model of pathogenesis.

LCB1v1.3 is weakly immunogenic and retains protective activity after repeated dosing. We treated K18-hACE2 transgenic mice with 50 µg of control binder or LCB1v1.3 every three days for a total of 18 days (**Fig 9A**). At this time, we collected sera and assessed the presence of anti-LCB1v1.3 antibodies. Only 1 of 10 mice developed IgG antibodies against LCB1v1.3 (**Fig 9B**). To determine if repeated dosing affected LCB1v1.3-mediated protection, we challenged the cohort with 10^3 PFU of SARS-CoV-2. Again, substantial protection against weight loss (**Fig 9C**) and viral infection in the lung and other organs was observed in all animals receiving LCB1v1.3 (**Fig 9D-H**).

LCB1v1.3 protects against emerging SARS-CoV-2 variants. We evaluated the activity of LCB1v1.3 against a B.1.1.7 isolate containing deletions at 69-70 and 144-145, and substitutions at N501Y, A570D, D614G, and P681H, and against a recombinant WA1/2020 strain containing key substitutions present in the B.1.351 and B.1.248 variant strains at residues E484K, N501Y, and D614G (Xie et al., 2021a). Although the neutralizing activity of LCB1v1.3 against the B.1.1.7 and E484K/N501Y/D614G strains was approximately 45 to 50-fold lower than for the WA1/2020 strain, the EC_{50} values still were ~800 pM and 667 pM, respectively (**Fig 10A**). To determine whether LCB1v1.3 could protect *in vivo* against SARS-CoV-2 strains with concerning spike protein substitutions, we treated K18-hACE2 transgenic mice with a single i.n. 50 µg dose of LCB1v1.3 or control binder one day prior to inoculation with 10^3 PFU of B.1.1.7 or E484K/N501/D614G SARS-CoV-2. Notably, LCB1v1.3 treatment before challenge with either variant strain protected against weight loss (**Fig 10B**

and 10H) and viral infection in all tissues collected at 6 dpi (**Fig 10C-G and 10I-M**). Thus, LCB1v1.3 is effective against both circulating and emerging strains of SARS-CoV-2.

DISCUSSION

Here, using the stringent K18-hACE2 mouse model of SARS-CoV-2 pathogenesis, we show that LCB1-Fc prevented SARS-CoV-2 infection and disease when administered one day before or after virus inoculation. Lung biomechanics of mice treated with LCB1-Fc mirrored those of naïve animals in all parameters tested.

We also evaluated the efficacy of LCB1v1.3, an optimized, monomeric form of LCB1 without an Fc domain. A single i.n. dose of LCB1v1.3 reduced viral burden when administered as many as five days before or two days after SARS-CoV-2 infection. Our i.n. delivery approach is unique. I.n. therapy of SARS-CoV-2 has been reported only with type I interferon in a hamster model of disease (Hoagland et al., 2021) and efficacy was limited. The K18-hACE2 mouse model recapitulates several aspects of severe COVID-19, including lung inflammation and reduced pulmonary function (Golden et al., 2020; Winkler et al., 2020a). Since K18-hACE2 mice are highly vulnerable to infection, the therapeutic window of treatment is limited (Winkler et al., 2020b) and for our miniproteins, might only curb viral infection. Importantly, our data demonstrate that LCB1v1.3 binder treatment before or after infection limited immune cell infiltration and lung inflammation, which prevented tissue damage and compromise of respiratory function. As part of our proof-of-principle studies for a nasal prophylaxis, we observed little immunogenicity of LCB1v1.3, suggesting that repeated dosing may be possible.

Although several antibody-based therapies demonstrate promise against SARS-CoV-2, and a few have been granted EUA status, viral evolution could jeopardize these interventions as evidenced by the emerging variants in the United Kingdom (B.1.1.7), South Africa (B.1.351), Brazil (B.1.248), and elsewhere. Indeed, we and others have observed that many monoclonal and polyclonal antibodies showed reduced neutralization activity against several of these variant strains (Chen et al., 2021; Wang et al., 2021a; Wang et al., 2021b; Wibmer et al., 2021; Xie et al., 2021b). In comparison, LCB1v1.3 showed efficacy against historical (WA1/2020) and emerging (B.1.1.7 and E484K/N501Y/D614G) SARS-CoV-2 strains. Based on the cryo-EM structure of the parent LCB1 binder in complex with SARS-CoV-2 RBD (Cao et al., 2020), only the N501Y mutation is expected to affect binding. While we observed a decrease in the neutralizing activity of LCB1v1.3 against the emerging variants, EC₅₀ values were still less than 800 pM, suggesting substantial potency was retained.

Compared to other potential SARS-CoV-2 antibody-based treatments, miniproteins have several benefits: (a) due to their smaller size, they can bind each protomer of a single trimeric spike, resulting in greater potency for a given dose; (b) they can be manufactured cost-effectively; and (c) they can be mixed using linker proteins to generate multimerized constructs that limit resistance.

EXPERIMENTAL MODEL AND SUBJECT DETAILS

Cells and viruses. Vero E6 (CRL-1586, American Type Culture Collection (ATCC), Vero CCL81 (ATCC), Vero-furin (Mukherjee et al., 2016), and Vero-hACE2-TMPRSS2 (a gift of A. Creanga and B. Graham, NIH) were cultured at 37°C in Dulbecco's Modified Eagle medium (DMEM) supplemented with 10% fetal bovine serum (FBS), 10 mM HEPES pH 7.3, 1 mM sodium pyruvate, 1× non-essential amino acids, and 100 U/ml of penicillin–streptomycin. Additionally, Vero-hACE2-TMPRSS2 cells were cultured in the presence of 5 µg/mL puromycin. The WA1/202 (2019n-CoV/USA_WA1/2020) isolate of SARS-CoV-2 was obtained from the US Centers for Disease Control (CDC). The B.1.1.7 and WA1/2020 E484K/N501Y/D614G viruses have been described previously (Chen et al., 2021; Xie et al., 2021a). Infectious stocks were propagated by inoculating Vero CCL81 or Vero-hACE2-TMPRSS2 cells. Supernatant was collected, aliquoted, and stored at -80°C. All work with infectious SARS-CoV-2 was performed in Institutional Biosafety Committee-approved BSL3 and A-BSL3 facilities at Washington University School of Medicine using positive pressure air respirators and protective equipment.

Mouse experiments. Animal studies were carried out in accordance with the recommendations in the Guide for the Care and Use of Laboratory Animals of the National Institutes of Health. The protocols were approved by the Institutional Animal Care and Use Committee at the Washington University School of Medicine (assurance number A3381–01). Virus inoculations were performed under anesthesia that was induced and maintained with ketamine hydrochloride and xylazine, and all efforts were made to minimize animal suffering.

Heterozygous K18-hACE c57BL/6J mice (strain: 2B6.Cg-Tg(K18-ACE2)2Prlmn/J) were obtained from The Jackson Laboratory. Animals were housed in groups and fed standard chow diets. Mice of different ages and both sexes were administered 10³ PFU of SARS-CoV-2 via intranasal administration.

METHOD DETAILS

Miniprotein production. LCB1-Fc was synthesized and cloned by GenScript into pCMVR plasmid, with kanamycin resistance. Plasmids were transformed into the NEB 5-alpha strain of *E. coli* (New England Biolabs) to recover DNA for transient transfection into Expi293F mammalian cells. Expi293F cells were grown in suspension using Expi293F expression medium (Life Technologies) at 33°C, 70% humidity, and 8% CO₂ rotating at 150 rpm. The cultures were transfected using PEI-MAX (Polyscience) with cells grown to a density of 3×10^6 cells per mL and cultivated for 3 days. Supernatants were clarified by centrifugation (5 min at 4000 x g, addition of PDADMAC solution to a final concentration of 0.0375% (Sigma Aldrich, #409014), and a second spin (5 min at 4000 x g). Clarified supernatants were purified using a MabSelect PrismaTM 2.6×5 cm column (Cytiva) on an AKTA Avant150 FPLC (Cytiva). Bound protein was washed with five column volumes of 20 mM NaPO₄ and 150 mM NaCl pH 7.2, then five column volumes of 20 mM NaPO₄ and 1 M NaCl pH 7.4, and eluted with three column volumes of 100 mM glycine at pH 3.0. The eluate was neutralized with 2 M Tris base to a final concentration of 50 mM. SDS-PAGE was used to assess protein purity. The protein was passed through a 0.22 µm filter and stored at 4°C until use.

LCB1v1.3 with polar mutations (4N, 14K, 15T, 17E, 18Q, 27Q, 38Q) relative to the original LCB1 was cloned into a pet29b vector. LCB1v1.3 was expressed in Lemo21(DE3) (NEB) in terrific broth media and grown in 2 L baffled shake flasks. Bacteria were propagated at 37°C to an O.D.600 of ~0.8, and then induced with 1 mM IPTG. Expression temperature was reduced to 18°C, and the cells were shaken for ~16 h. The cells were harvested and lysed using heat treatment and incubated at 80°C for 10 min with stirring. Lysates were clarified by centrifugation at 24,000 × g for 30 min and applied to a 2.6×10 cm Ni SepharoseTM 6 FF column (Cytiva) for purification by IMAC on an AKTA Avant150 FPLC system (Cytiva). Proteins were eluted over a linear gradient of 30 mM to 500 mM imidazole in a buffer of 50 mM Tris pH 8.0 and 500 mM NaCl. Peak fractions were pooled, concentrated in 10 kDa MWCO centrifugal filters (Millipore), sterile filtered (0.22 µm) and applied to either a SuperdexTM 200 Increase 10/300, or HiLoad S200 pg GL SEC column (Cytiva) using 50 mM phosphate pH 7.4, 150 mM NaCl buffer. After size exclusion chromatography, bacterial-derived components were tested to confirm low levels of endotoxin.

Biolayer interferometry. Biolayer interferometry data were collected using an OctetTM RED96 (ForteBio) and processed using the instrument's integrated software. Briefly, biotinylated RBD (Acro Biosystems) was loaded onto streptavidin-coated biosensors (SA

ForteBio) at 20 nM in binding buffer (10 mM HEPES (pH 7.4), 150 mM NaCl, 3 mM EDTA, 0.05% surfactant P20, and 0.5% non-fat dry milk) for 360 s. Analyte proteins (LCB1v1.3 or LCB1-Fc) were diluted from concentrated stocks into binding buffer. After baseline measurement in the binding buffer alone, the binding kinetics were monitored by dipping the biosensors in wells containing the target protein at the indicated concentration (association step) for 3,600 s and then dipping the sensors back into baseline/buffer (dissociation) for 7,200 s.

Plaque assay. Vero-furin cells (Mukherjee et al., 2016) were seeded at a density of 2.5×10^5 cells per well in flat-bottom 12-well tissue culture plates. The following day, medium was removed and replaced with 200 μ L of 10-fold serial dilutions of the material to be titrated, diluted in DMEM+2% FBS, and plates incubated at 37°C with rocking at regular intervals. One hour later, 1 mL of methylcellulose overlay was added. Plates were incubated at 37°C for 72 h, then fixed with 4% paraformaldehyde (final concentration) in PBS for 20 min. Fixed cell monolayers were stained with 0.05% (w/v) crystal violet in 20% methanol and washed twice with distilled, deionized water.

Measurement of viral burden. Tissues were weighed and homogenized with zirconia beads in a MagNA LyserTM instrument (Roche Life Science) in 1,000 μ L of DMEM media supplemented with 2% heat-inactivated FBS. Tissue homogenates were clarified by centrifugation at 10,000 rpm for 5 min and stored at -80°C. RNA was extracted using the MagMax mirVanaTM Total RNA isolation kit (Thermo Scientific) on a Kingfisher Flex extraction robot (Thermo Scientific). RNA was reverse transcribed and amplified using the TaqManTM RNA-to-CT 1-Step Kit (ThermoFisher). Reverse transcription was carried out at 48°C for 15 min followed by 2 min at 95°C. Amplification was accomplished over 50 cycles as follows: 95°C for 15 s and 60°C for 1 min. Copies of SARS-CoV-2 N gene RNA in samples were determined using a previously published assay (Case et al., 2020; Hassan et al., 2020). Briefly, a TaqManTM assay was designed to target a highly conserved region of the N gene (Forward primer: ATGCTGCAATCGTGCTACAA (SEQ ID NO: 190); Reverse primer: GACTGCCGCCTCTGCTC (SEQ ID NO: 191); Probe: /56-FAM/TCAAGGAAC/ZEN/AACATTGCCAA/3IABkFQ/) (SEQ ID NO: 192). This region was included in an RNA standard to allow for copy number determination down to 10 copies per reaction. The reaction mixture contained final concentrations of primers and probe of 500 and 100 nM, respectively.

Cytokine and chemokine mRNA measurements. RNA was isolated from lung homogenates as described above. cDNA was synthesized from DNase-treated RNA using

the High-Capacity cDNA Reverse Transcription kit (Thermo Scientific) with the addition of RNase inhibitor following the manufacturer's protocol. Cytokine and chemokine expression was determined using TaqManTM Fast Universal PCR master mix (Thermo Scientific) with commercial primers/probe sets specific for *IFN-g* (IDT: Mm.PT.58.41769240), *IL-6* (Mm.PT.58.10005566), *IL-1b* (Mm.PT.58.41616450), *Tnfa* (Mm.PT.58.12575861), *CXCL10* (Mm.PT.58.43575827), *CCL2* (Mm.PT.58.42151692), *CCL5* (Mm.PT.58.43548565), *CXCL11* (Mm.PT.58.10773148.g), *Ifnb* (Mm.PT.58.30132453.g), *CXCL1* (Mm.PT.58.42076891) and results were normalized to *GAPDH* (Mm.PT.39a.1) levels. Fold change was determined using the $2^{-\Delta\Delta C_t}$ method comparing treated mice to naïve controls.

Lung Pathology. Animals were euthanized before harvest and fixation of tissues. The left lung was first tied off at the left main bronchus and collected for viral RNA analysis. The right lung was inflated with approximately 1.2 mL of 10% neutral buffered formalin using a 3-mL syringe and catheter inserted into the trachea. Tissues were embedded in paraffin, and sections were stained with hematoxylin and eosin. Slides were scanned using a Hamamatsu NanoZoomerTM slide scanning system, and images were viewed using NDP view software (ver.1.2.46).

Respiratory mechanics. Mice were anesthetized with ketamine/xylazine (100 mg/kg and 10 mg/kg, i.p., respectively). The trachea was isolated via dissection of the neck area and cannulated using an 18-gauge blunt metal cannula (typical resistance of 0.18 cmH₂O.s/mL), which was secured in place with a nylon suture. The mouse then was connected to the flexiVentTM computer-controlled piston ventilator (SCIREQ Inc.) via the cannula, which was attached to the FX adaptor Y-tubing. Mechanical ventilation was initiated, and mice were given an additional 100 mg/kg of ketamine and 0.1 mg/mouse of the paralytic pancuronium bromide via intraperitoneal route to prevent breathing against the ventilator and during measurements. Mice were ventilated using default settings for mice, which consisted in a positive end expiratory pressure at 3 cm H₂O, a 10 mL/kg tidal volume (V_t), a respiratory rate at 150 breaths per minute (bpm), and a fraction of inspired oxygen (FiO₂) of 0.21 (*i.e.*, room air). Respiratory mechanics were assessed using the forced oscillation technique, as previously described (McGovern et al., 2013), using the latest version of the flexiVentTM operating software (flexiWare v8.1.3). Pressure-volume loops and measurements of inspiratory capacity also were performed.

Neutralization assay. Serial dilutions of binder proteins were incubated with 10² focus-forming units (FFU) of SARS-CoV-2 for 1 h at 37°C. Binder-virus complexes were

added to Vero E6 (WA1/2020) or Vero-hACE2-TMPRSS2 (B.1.1.7 and WA1/2020 E484K/N501Y/D614G) cell monolayers in 96-well plates and incubated at 37°C for 1 h. Subsequently, cells were overlaid with 1% (w/v) methylcellulose in MEM supplemented with 2% FBS. Plates were harvested 24-30 h later by removing overlays and fixed with 4% PFA in PBS for 20 min at room temperature. Plates were washed and sequentially incubated with an oligoclonal pool of SARS2-2, SARS2-11, SARS2-16, SARS2-31, SARS2-38, SARS2-57, and SARS2-71 anti-spike protein antibodies (Zhou et al., 2021) and HRP-conjugated goat anti-mouse IgG in PBS supplemented with 0.1% saponin and 0.1% bovine serum albumin. SARS-CoV-2-infected cell foci were visualized using TrueBlue™ peroxidase substrate (KPL) and quantitated on an ImmunoSpot™ microanalyzer (Cellular Technologies). Data were processed using Prism™ software (GraphPad Prism™ 8.0).

ELISA. C-terminal biotinylated LCB1.1v3 was immobilized on streptavidin-coated plates (RayBiotech #7C-SCP-1) at 2.5 µg/mL in 100 µL total volume per well and incubated at 4°C overnight. Plates were washed with wash buffer (TBS + 0.1% (w/v) BSA + 0.05% (v/v) Tween20) and blocked with 200 µL/well blocking buffer (TBS + 2% (w/v) BSA + 0.05% (v/v) Tween20) for 1 h at room temperature. Plates were rinsed with wash buffer using 200 µL/well, and 100 µL of 1:100 diluted sera samples in blocking buffer were added to respective wells. For a positive control, Fc-RBD was serially diluted 1:5 starting at 240 ng/mL in 100 µL of blocking buffer. All samples were incubated for 1 h at room temperature. Plates were washed using 200 µL/well of wash buffer. For the serum samples, HRP-conjugated horse anti-mouse IgG antibody (Vector Laboratories #PI-2000-1) was diluted 1:200 in blocking buffer, and 100 µL was incubated in each well at room temperature for 30 min. For the positive control, HRP-conjugated mouse anti-human IgG antibody (Invitrogen #05-4220) was diluted 1:500 in blocking buffer, and 100 µL was incubated in each well at room temperature for 30 min. Plates were rinsed with wash buffer, and 100 µL of TMB (SeraCare) was added to each well for 2 min. The reaction was quenched by adding 100 µL of 1N HCl. Optical densities were determined at 450nm on a Synergy Neo2™ plate reader (BioTek Instruments).

QUANTIFICATION AND STATISTICAL ANALYSIS

Statistical significance was assigned when P values were < 0.05 using Prism™ Version 8 (GraphPad). Tests, number of animals, median values, and statistical comparison groups are indicated in each of the Figure legends. Analysis of weight change was determined by two-way ANOVA. Changes in functional parameters or immune parameters

were compared to control binder-treated animals and analyzed by one-way ANOVA with multiple comparisons tests. Statistical analyses of viral burden between two groups were determined by Mann-Whitney test.

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Multivalent Designs

15 Escape variants of SARS-CoV-2 are threatening to considerably prolong the COVID-19 pandemic. Here we develop multivalent minibinders as potential prophylactic and therapeutic agents to address this problem. We designed multivalent minibinders containing three copies of a minibinder (self-assembled homotrimer), or three linked distinct minibinders (multi-domain fusion) targeting different sites, geometrically matched to the spike trimer and

20 optimized their composition using a rapid cell-free expression and evaluation workflow. The optimized designs have greatly slowed dissociation rates from the SARS-CoV-2-S-glycoprotein with complex half-lives of more than two weeks. Cryo-EM of the structures reveal that both homotrimer and fusion minibinder constructs can engage all three RBDs on a single spike protein. The top trimeric and fusion candidates neutralize the wild-type SARS-

25 CoV-2 virus in addition to the B.1.1.7, B.1.351, B.1.1.28 variants of concern with IC₅₀s in the low pM range. Additionally, the top homotrimer candidate provided prophylactic protection in a human ACE2-expressing transgenic mice against the same variant strains. Our approach highlights the utility of computational protein design coupled to rapid experimental prototyping to design potent multivalent inhibitors that can broadly neutralize widely

30 circulating variants of concern.

We sought to develop multivalent versions of our computationally designed miniproteins that block the SARS-CoV-2 receptor binding domain (RBD) interaction with its host receptor ACE2. In principle, the small size of the designed minibinders enables simultaneous engagement of multiple RBDs within a single spike protein trimer. We

hypothesized that this multivalent binding would lead to ultra-high affinity inhibitors that are more resistant to escape mutations than their monomeric counterparts. The resulting avidity from these multivalent interactions could ameliorate the effects of mutations that would escape individual domains. Additionally, single proteins containing domains targeting multiple distinct epitopes or containing different sets of contacts with the target epitope could further increase the robustness of the designs to mutational escape. Starting with the LCB1, AHB2, and LCB3 minibinders (hereafter referred to as M1, M2, and M3 respectively; Table 11) and their known binding modes we pursued two parallel strategies for designing multivalent inhibitors, self-assembled homotrimers and multi-domain fusions.

ID	Protein
M1	LCB1_v2.2
M2	AHB2
M3	LCB3_v2.2
F23-P12	AHB2_v2-PAS12-LCB3_v2.2
F31-P12	LCB3_v2.2-PAS12-LCB1_v2.2
F231-P12	AHB2_v2-PAS12-LCB3_v2.2-PAS12-LCB1_v2.2
F231-P24	AHB2_v2-PAS24-LCB3_v2.2-PAS24-LCB1_v2.2
F23-G10	AHB2_v2-GS10-LCB3_v2.2
F31-F10	LCB3_v2.2-GS10-LCB1_v2.2
F231-G10	AHB2_v2-GS10-LCB3_v2.2-GS10-LCB1_v2.2
H1-1	SB175-6GS-LCB1_v2.2
H2-0	AHB2-4GS-1rfo
H2-1	AHB2-2GS-SB175
H3-1	LCB3_v2.2-6GS-SB175

Table 11. List of abbreviations used to describe multivalent minibinders

To enable rapid prototyping of the designed proteins, we developed a cell-free DNA assembly and protein expression workflow enabling a greatly shortened design-build-test cycle better matched to the urgency of a pandemic. The workflow combines a cell-free DNA assembly step utilizing Gibson assembly followed by PCR to generate linear expression templates that are used to drive cell-free protein synthesis (CFPS). The developed workflow allows us to translate synthetic DNA to purified protein in as little as 6 hours, is easily scaled

to high-throughput formats (e.g., 96- or 384-well plates), and is amenable to automated liquid handling. Furthermore, we coupled this cell-free workflow to an AlphaLISATM protein-protein interaction (PPI) competition assay to enable comparison of dissociation rates of the designed proteins against either the monomeric RBD or the trimeric hexaprotein SARS-CoV-2-S-glycoprotein (S6P). Because multivalency largely only impacts the dissociation rate constant of the interaction, we reasoned that an in-solution off-rate screen would enable us to distinguish mono- from multi-valent binding. The resulting workflow can evaluate hundreds of candidate multivalent proteins per week.

10 Design and validation of multivalent binders

In the first strategy, we designed self-assembling trimeric versions of the M1, M2, and M3 miniproteins geometrically matched to the three RBDs in the spike trimer (hereafter referred to as H[binding domain #]-[homotrimer#]; for example, H1-1 represents a homotrimer of M1 with homotrimerization domain 1, Table 11). We designed, expressed, and evaluated more than one hundred different proteins containing various homotrimerization domains and linker lengths using our cell-free expression and multivalency screen workflow. We identified versions of each homotrimer that showed slow dissociation rates potentially indicating multivalent binding (Fig. 14).

In the second strategy, we generated two- and three-domain fusions of the M1, M2 and M3 binding domains separated by flexible linkers (hereafter referred to as F[binding domain #s]-[linker]; for example, F231-P12 represents a fusion of M2 to M3 to M1 all separated by a PAS12 linker, Table 11). We evaluated a range of linker lengths chosen to span the distances between the termini of the domains when bound to the “open” and “closed” states of the RBD. We again expressed and evaluated more than one hundred different designs varying binding domain connectivity and linker length to optimize multivalency. Several identified two- and three-domain fusions show slow dissociation rates comparable to the homo-trimeric constructs described above (Fig. 14).

The best candidates from each strategy showed little to no dissociation after 14 days of with competitor, with further measurements being limited by the stability of S6P. From these data we estimate the complex has a dissociation rate constant of slower than $1 \times 10^{-7} \text{ s}^{-1}$. To our knowledge, these are the slowest measured dissociation rate constant for a synthetic protein-protein interactions ever reported.

We next used single particle cryo-electron microscopy (cryo-EM) to characterize the complex between S6P and the top candidate minibinders constructs (Fig. 15). The Cryo-EM

structures of the H2-1, F31-G10, and the F231-P24 constructs were determined at resolutions of 2.6, 4.5, and 3.9 Å respectively. H2-1 was found to simultaneously engage all three RBDs, causing all three RBDs to adopt the open state. The design model accurately closely matches the observed structure. F31-G10 bound to two RBDs, both appearing to adopt the open conformation upon binding. The structure indicates this linker length enabled simultaneous binding of two RBDs in their native state. The third free RBD adopted either the open or closed conformation in the structure. F231-P24 bound to three RBDs, with M1 binding a closed conformation RBD and M2 and M3 binding to open conformation RBDs. This suggests the linker length is sufficiently long enough to enable all three binding domains to simultaneously engage all three RBDs without significant distortion of the native state. In both F31-G10 and F231-P24 the maps are highly suggestive of multivalent binding, though the flexible linkers yield no density in the EM map to confirm linkage of the domains.

Multivalent minibinders neutralize widely circulating SARS-CoV-2 variants

We next sought to determine ability of the multivalent constructs to neutralize SARS-CoV-2 variants. We screened the off rate of the best multivalent minibinders against a panel of mutant spike proteins (Fig. 16). The homotrimers showed the most mutational resistance, with the H2 homotrimers showing little dissociation after 24 hours against any of the mutant spikes. The two-domain fusions showed little increased resilience to the tested point mutants. The three-domain fusions showed considerably more consistent binding to the tested point mutants, though some still impacted binding.

We additionally evaluated the potency of these proteins via neutralization assays against both a SARS-CoV-2 HIV pseudovirus in addition to authentic SARS-CoV-2 isolates (Fig. 16). The H2-0 and H2-1 homotrimers consistently performed the best across all constructs tested, with IC₅₀s in the low pM range. The three-domain fusions also performed well, with IC₅₀s in the sub nM range for all tested variants. The greater neutralization breadth of the H2 homotrimers likely reflects the closer mimicking of the ACE2 binding site by the M2 monomer, a unique advantage enabled by protein design.

Multivalent minibinders resist viral escape

In addition to evaluating the top candidate's ability to neutralize currently circulating SARS-CoV-2 mutants, we also tested the ability of the inhibitors to resist escape viral escape (Fig. 17). To do this, plaque assays were performed with a VSV-SARS-CoV-2 chimera virus were replicated on Vero E6 cells. To select mutants that were resistant to the inhibitor, the

inhibitor was included in the overlay to halt replication of non-resistant viruses. In positive control neutralizing antibody (2B04), multiple escape mutants were selected per plate. For both F231-P12 and H2-1 no escape mutants were isolated in 35 replicate wells of each inhibitor.

5

H2-0 provides prophylactic protection in human ACE2-expressing transgenic mice

To determine the ability of our multivalent minibinders to protect in an in vivo model, we evaluated them as a pre-exposure prophylactic treatment in human ACE2-expressing transgenic mice (Fig. 17). A single 50 µg dose of H2-0 was administered intranasally (i.n.) one day prior to inoculation with 10³ focus forming units of SARS-CoV-2 Variants B.1.1.7, B1.351, B.1.1.24. In all cases, i.n. administration of H2-0 protected the mice against SARS-CoV-2-induced weight loss. At 6 days post infection viral burden was determined via RT-qPCR in a variety in tissues. Notably, viral loads in the lungs were reduced in all cases. These results indicate that H2-0 given via i.n. administration can provide prophylactic protection against SARS-CoV-2 infection in a relevant mouse model.

10
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Conclusions

We anticipate that the cell-free protein expression and evaluation workflow will find utility in many different applications where the evaluation of individual protein variants is the limiting process step. In addition, our developed multivalency screen will accelerate the ability of researchers to develop multivalent protein therapeutics.

20

The designed protein constructs could have a number of advantages over monoclonal antibodies for preventing and treating COVID-19 infection. 1) direct administration into respiratory system, 2) low cost of goods and amenability to very large-scale production, 3) high stability and lack of need for cold chain, and 4) very broad resistance to escape mutants in single compounds. More generally, designed high affinity multivalent minibinders could provide a powerful platform for combating viral pandemics.

25

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We claim

1. A polypeptide comprising an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 1-17, 19-21, 23-34 and 100-101, wherein the polypeptide binds to SARS-CoV-2 Spike glycoprotein receptor binding domain (RBD).
5
2. The polypeptide of claim 1, wherein amino acid substitutions relative to the reference polypeptide amino acid sequence are selected from the exemplary amino acid substitutions provided in Table 1.
10
3. The polypeptide of claim 1 or 2, wherein interface residues are identical to those in the reference polypeptide or are conservatively substituted relative to interface residues in the reference polypeptide.
15
4. The polypeptide of any one of claims 1-3, comprising an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS:1-10, 13-17, 19-21, 33-34, and 100-101.
20
5. The polypeptide of any one of claims 1-4, comprising an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS:1-10 and 102-136.
25
6. The polypeptide of claim 5, wherein the polypeptide comprises an amino acid substitution relative to the amino acid sequence of SEQ ID NO:1 at 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, or all 18 residues selected from the group consisting of 2, 4, 5, 14, 15, 17, 18, 27, 28, 32, 37, 38, 39, 41, 42, 49, 52, and 55.
30
7. The polypeptide of claim 6, wherein the substitutions are selected from the substitutions listed in Table 4, either individually or in combinations in a given row.

8. The polypeptide of any one of claims 1-4, comprising an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 13-17, 19-21 and 137-163.

5

9. The polypeptide of claim 8, wherein the polypeptide comprises an amino acid substitution relative to the amino acid sequence of SEQ ID NO:13 at 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or all 20 residues selected from the group consisting 2, 6, 8, 9, 13, 14, 19, 22, 25, 26, 28, 29, 34, 35, 37, 40, 43, 45, 49, and 62.

10

10. The polypeptide of claim 6, wherein the substitutions are selected from the substitutions listed in Table 6, either individually or in combinations in a given row.

11. The polypeptide of any one of claims 1-4, comprising an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS:33-34 and 100-101 and 164.

12. The polypeptide of claim 11, wherein the polypeptide comprises an amino acid substitution relative to the amino acid sequence of SEQ ID NO:101 at or both residues selected from the group consisting 63 and 75.

13. The polypeptide of claim 12, wherein the substitutions comprise R63A and/or K75T.

14. The polypeptide of any one of claims 1-13, further comprising one or more added cysteine residues at the N-terminus and/or C-terminus.

15. The polypeptide of any one of claims 1-14, comprising an N-linked glycosylation site (i.e.: NX(S/T), where X is any amino acid).

30

16. The polypeptide of any one of claims 1-15, comprising two or more copies of the amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 1-17, 19-21, 23-34 and 100-101.

17. The polypeptide of claim 16, wherein the two or more copies of the polypeptide are all identical.

5 18. The polypeptide of claim 16, wherein the two or more copies of the polypeptide are not all identical.

19. The polypeptide of any one of claims 16-18, wherein the two or more copies of the polypeptide are separated by amino acid linker sequences.

10

20. The polypeptide of claim 9, wherein amino acid linker sequences comprise Gly-Ser rich (at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% Gly-Ser residues) amino acid linkers.

15 21. The polypeptide of claim 20, wherein the Gly-Ser rich linkers comprise an amino acid sequence selected from the group consisting of GG and SEQ ID NOs:35-46 and 165-171

22. The polypeptide of claim 19, wherein amino acid linker sequences comprise Pro-rich (at least 15%, 20%, 25%, or greater Pro residues) amino acid linkers.

20

23. The polypeptide of claim 22, wherein the Pro-rich amino acid linkers comprise an amino acid sequence selected from the group consisting of SEQ ID NOs:97-98 and 172-176.

24. The polypeptide of claim 19, wherein the amino acid linker comprises the amino acid
25 sequence selected from the group consisting of SEQ ID NOS:99 and 177-178.

25. The polypeptide of any one of claims 19-24, wherein the amino acid linkers are independently between 2-100 amino acids in length.

30 26. The polypeptide of any one of claims 16-25, wherein the polypeptide comprises the formula Z1-Z2-Z3, wherein:

Z1 comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the

amino acid sequence selected from the group consisting of SEQ ID NOS: 1-17, 19-21, 23-34 and 100-164;

Z2 comprises an optional amino acid linker; and

5 Z3 comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 1-17, 19-21, 23-34 and 100-164;

Wherein Z1 and Z3 may be identical or different.

10 27. The polypeptide of claim 26, wherein Z1 and Z3 are identical.

28. The polypeptide of claim 26 wherein Z1 and Z3 are different.

29. The polypeptide of any one of claims 26-28, wherein:

15 Z1 comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 1-10 and 102-136; and

20 Z3 comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 1-10 and 102-136.

30. The polypeptide of any one of claims 26-28, wherein:

25 Z1 comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 13-17, 19-21 and 137-163; and

30 Z3 comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 13-17, 19-21 and 137-163.

31. The polypeptide of any one of claims 26-28, wherein:

Z1 comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 33-34, 100-100, and 164; and

5 Z3 comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 33-34, 100-100, and 164.

10 32. The polypeptide of any one of claims 26-28, wherein:

 one of Z1 and Z3 comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 1-10 and 102-136; and

15 the other of Z1 and Z3 comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 13-17, 19-21 and 137-163.

20 33. The polypeptide of any one of claims 26-28, wherein:

 one of Z1 and Z3 comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 1-10 and 102-136; and

25 the other of Z1 and Z3 comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 33-34, 100-100, and 164.

30 34. The polypeptide of any one of claims 26-28, wherein:

 one of Z1 and Z3 comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 13-17, 19-21 and 137-163; and

the other of Z1 and Z3 comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 33-34, 100-100, and 164.

5

35. The polypeptide of any one of claims 26-34, wherein the polypeptide comprises the formula B1-B2-Z1-Z2-Z3-B3-B4, wherein:

Z1, Z2, and Z3 are as defined in any one of claims 26-34;

B2 and B3 comprise optional amino acid linkers; and

10

one or both of B1 and B4 independently comprise an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 1-17, 19-21, 23-34 and 100-164, wherein one of B1 and B4 may be absent.

15

36. The polypeptide of claim 35, wherein one of B1 and B4 is absent.

37. The polypeptide of claim 35, wherein B1 and B4 independently comprise an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 1-17, 19-21, 23-34 and 100-164.

20

38. The polypeptide of claim 37, wherein B1 and B4 are identical.

39. The polypeptide of claim 37, wherein B1 and B4 are not identical.

25

40. The polypeptide of any one of claims 35-39, wherein B1 when present and B4 when present, are identical to one or both of Z1 and Z3, or wherein B1 when present and B4 when present, are not identical to either of Z1 and Z3.

30

41. The polypeptide of any one of claims 35-40, wherein B1 when present, and B4 when present, independently comprise an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 1-10, 13-17, 19-21, 33-34, and 100-164.

42. The polypeptide of any one of claims 35-40, wherein B1 when present, and B4 when present, independently comprise an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 1-10 and 102-136.

43. The polypeptide of any one of claims 35-40, wherein B1 when present, and B4 when present, independently comprise an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 13-17, 19-21 and 137-163.

44. The polypeptide of any one of claims 35-40, wherein B1 when present, and B4 when present, independently comprise an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 33-34, 100-101, and 164.

45. The polypeptide of any one of claims 35-40, wherein both B1 and B4 are present, and wherein

- one of B1 and B4 comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 1-10 and 102-136, and the other comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 13-17, 19-21 and 137-163;
- one of B1 and B4 comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 1-10 and 102-136, and the other comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%,

96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 33-34, 100-101, and 164, or

- one of B1 and B4 comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 13-17, 19-21 and 137-163, and the other comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 33-34, 100-101, and 164.

46. The polypeptide of any one of claims 1-45, comprising an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 47-60, 193-355, and 454-588 and a genus selected from those recited in the right hand column of Table 8 wherein genus positions X1, X2, X3, and X4 may be present or absent, and when present may be any sequence of 1 or more amino acids and wherein any N-terminal methionine residues may be present or absent in the polypeptide, preferably wherein the polypeptide comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 454-588 and most preferably wherein the polypeptide comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 693-701 wherein any N-terminal methionine residue may be absent or present, and wherein residues in parentheses may be present or absent (preferably absent) and are not considered in determining percent identity.

47. The polypeptide of any one of claims 1-46, further comprising an additional functional peptide domain.

48. The polypeptide of claim 47, wherein the additional functional peptide domain comprises a targeting domain, a detectable domain, a scaffold domain, a secretion signal, an Fc domain, or a further therapeutic peptide domain.

49. The polypeptide of claim 48, wherein the additional functional domain comprises an Fc domain, including but not limited to an Fc domain comprising an amino acid sequence comprising the amino acid sequence of SEQ ID NO:64.

5 50. The polypeptide of any one of claims 47-49, wherein the added functional domain comprises an oligomerization domain.

51. The polypeptide of claim 50, wherein the oligomerization domain comprises a homotrimerization domain.

10

52. The polypeptide of claim 50 or 51, wherein the oligomerization domain comprises an amino acid sequence selected from the group consisting of SEQ ID NOS:179-189 and 589-594.

15 53. The polypeptide of any one of claims 50-52, comprising an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 356-453 and 595-692, and a genus selected from those recited in the right hand column of Table 9 wherein genus positions X1, X2, X3, and X4 may be
20 present or absent, and when present may be any sequence of 1 or more amino acids and wherein any N-terminal methionine residues may be present or absent in the polypeptide,, preferably wherein the polypeptide comprises and amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID
25 NOS: 595-692.

54. The polypeptide of any one of claims 1-53, wherein the polypeptide is linked to a stabilization domain, including but not limited to polyethylene glycol (PEG), albumin, hydroxyethyl starch (HES), conformationally disordered polypeptide sequence composed of
30 the amino acids Pro, Ala, and/or Ser ('PASylation'), and/or a mucin diffusivity polypeptide composed of amino acids Lys and Ala, with or without Glu.

55 The polypeptide of any one of claims 1-54, comprising an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%,

97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 65-96, wherein in embodiments where a secretion signal is present (MARAWIFFLLCLAGRALA; SEQ ID NO:63) it can be replaced with any other secretion signal.

5

56. The polypeptide of any one of claims 1-55, wherein the polypeptide binds to the SARS-CoV-2 Spike glycoprotein with an affinity of at least 10 nM, measured as described in the attached examples.

10

57. A nucleic acid encoding the polypeptide of any one of claims 1-56.

58. An expression vector comprising the nucleic acid of claim 57 operatively linked to a promoter.

15

59. A host cell comprising the polypeptide, the nucleic acid, and/or the expression vector of any preceding claim.

60. An oligomer of the polypeptide of any one of claims 1-56.

20

61. The oligomer of claim 60, wherein the oligomer comprises a trimer, including but not limited to a homotrimer.

62. A composition, comprising 2, 3, 4, or more copies of the polypeptide of any one of claims 1-56 attached to a support, including but not limited to a polypeptide particle support.

25

63. A pharmaceutical composition, comprising the polypeptide, the nucleic acid, the expression vector, the host cell, the oligomer, and/or the composition of any of the preceding claims, and a pharmaceutically acceptable carrier.

30

64. A method for treating a severe acute respiratory syndrome (SARS) coronavirus infection (including SARS-Co-V and SARS-CoV-2), comprising administering to a subject in need thereof an amount of the polypeptide, the nucleic acid, the expression vector, the host

cell, the oligomer, the composition, and/or the pharmaceutical composition of any of the preceding claims, effective to treat the infection.

65. The method of claim 64, wherein the SARS coronavirus comprises SARS-CoV-2.

5

66. A method for limiting development of a severe acute respiratory syndrome (SARS) coronavirus infection (including SARS-Co-V and SARS-CoV-2), comprising administering to a subject in need thereof an amount of the polypeptide, the nucleic acid, the expression vector, the host cell, the oligomer, the composition, and/or the pharmaceutical composition of any of the preceding claims, effective to treat the infection.

10

67. The method of claim 66, wherein the SARS coronavirus comprises SARS-CoV-2.

68. The method of any one of claims 64-67, wherein the polypeptide, the nucleic acid, the expression vector, the host cell, the oligomer, the composition, and/or the pharmaceutical composition is administered intra-nasally.

15

69. The method of any one of claims 64-67, wherein the polypeptide, the nucleic acid, the expression vector, the host cell, the oligomer, the composition, and/or the pharmaceutical composition is administered systemically.

20

70. A method for designing polypeptides that bind to the receptor binding site (RBD) of SARS-Cov-2, wherein the methods comprise steps as described in any embodiment or combination of embodiments disclosed herein.

25

71. The method of claim 70, further comprising cell-free synthesis of the designed polypeptides, and evaluation of the synthesized polypeptides for SARS-Cov-2 RBD binding using any suitable technique.

72. A cell-free system comprising the polypeptide, the nucleic acid, and/or the expression vector of any preceding claim.

30

Designed minibinders target SARS-CoV-2 Spike

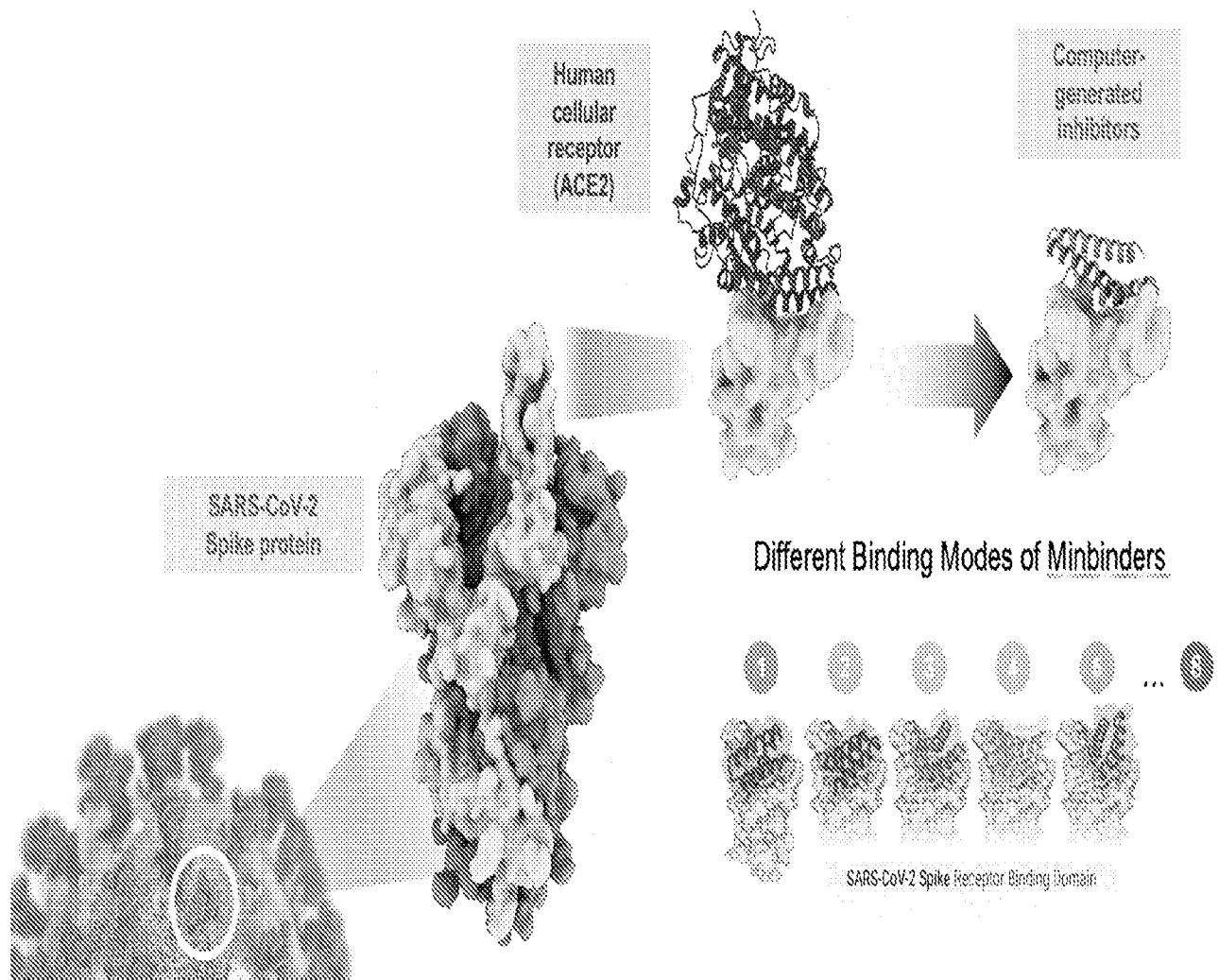
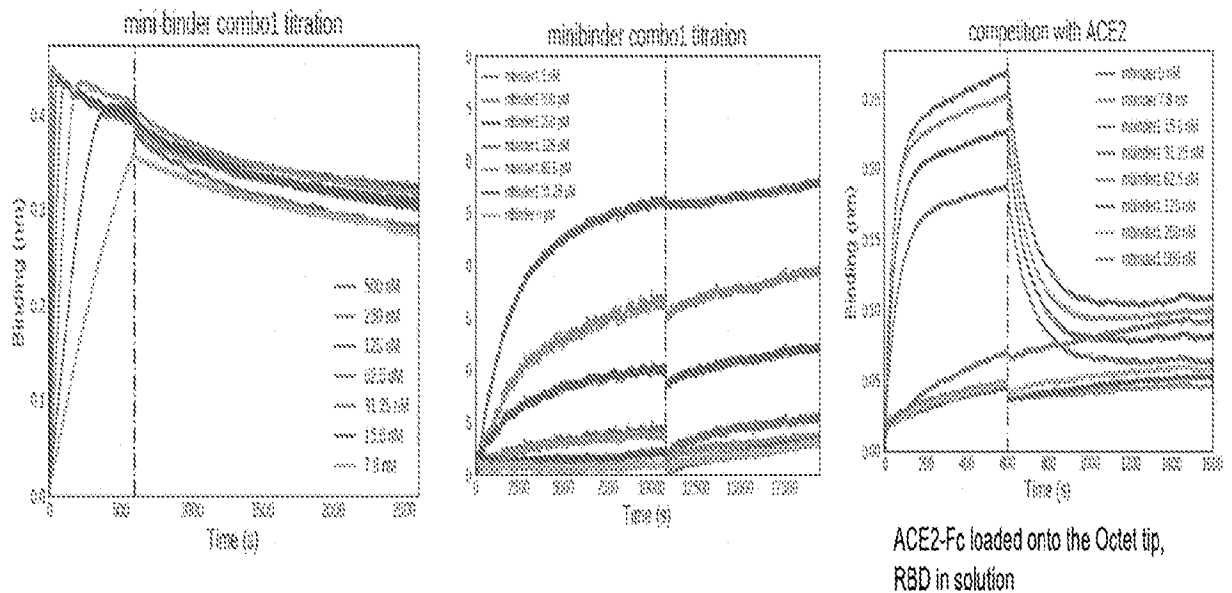


Figure 1

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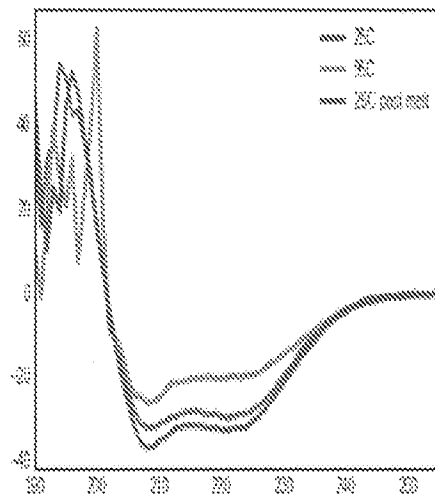
55 residue design binds RBD with ~300pM affinity and competes for binding with ACE2



Biolayer interferometry (BLI) data for combo 1 minibinder demonstrates ~300 pM affinity for Spike RBD and competes for binding to RBD by ACE-2.

Figure 2

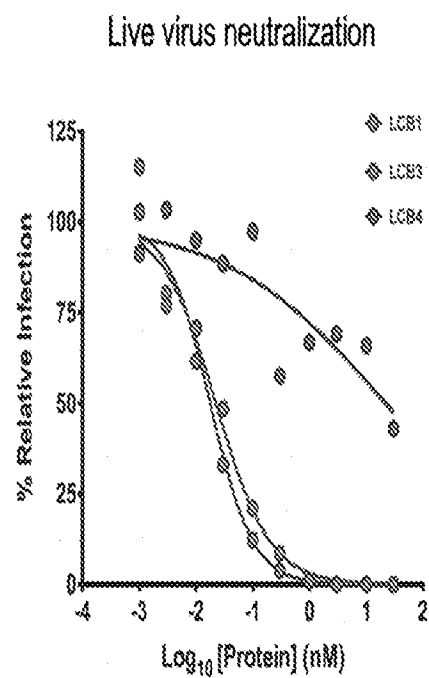
55 residue Spike RBD minibinder has high thermal stability



Circular Dichroism (CD) spectrum
for combo 1 minibinder
demonstrates extreme
heat stability up to 95°C

Figure 3

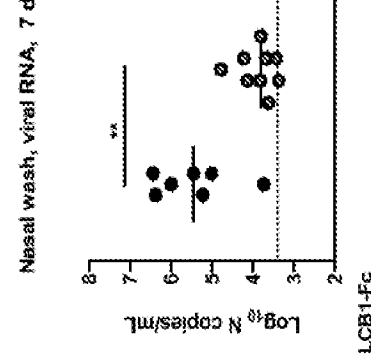
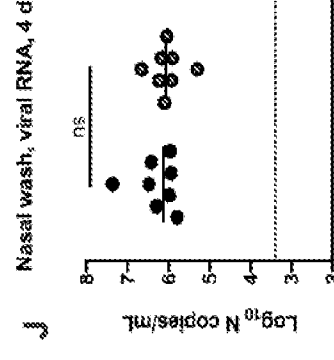
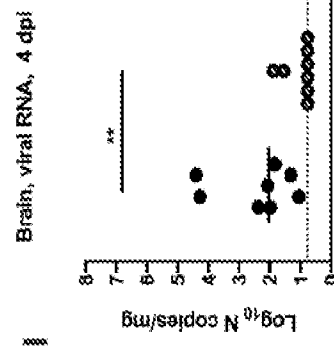
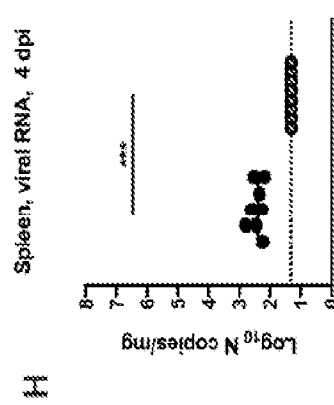
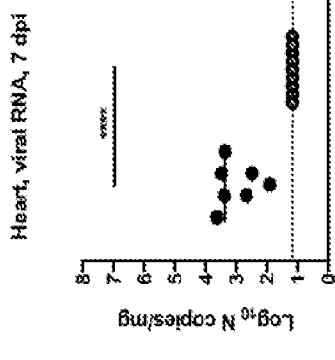
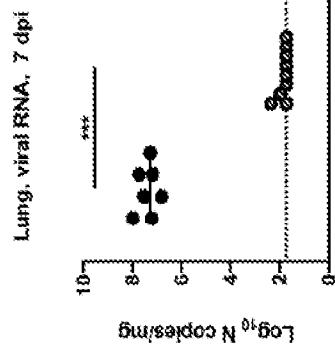
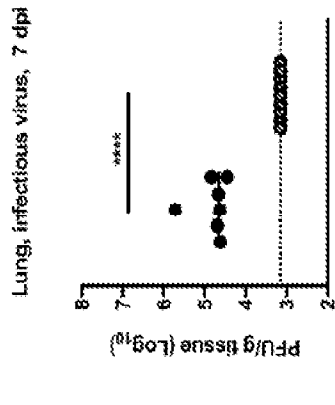
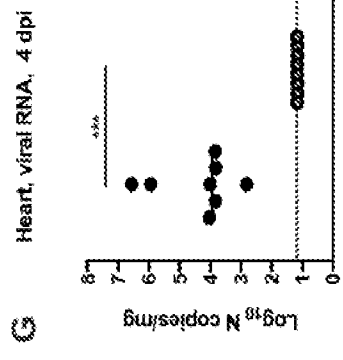
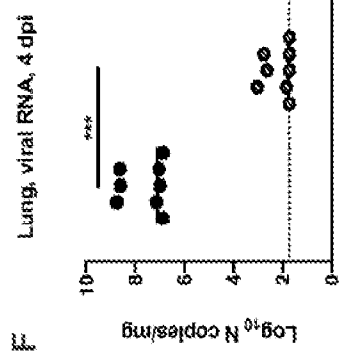
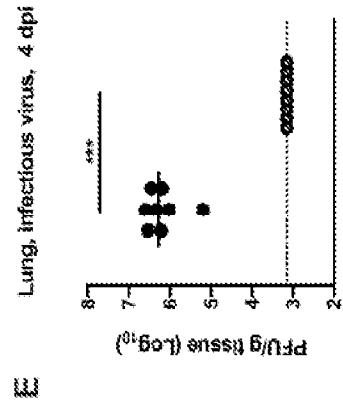
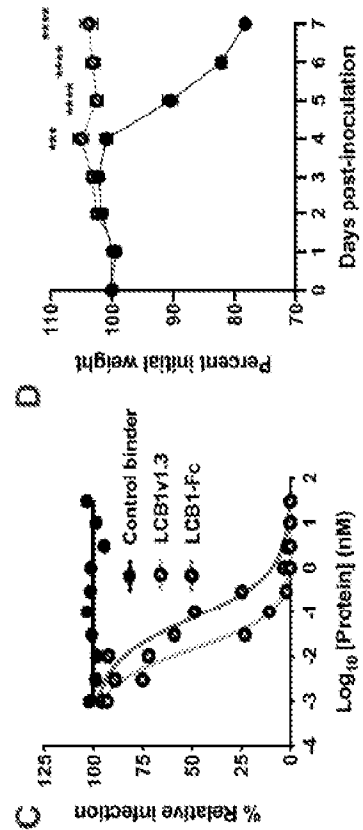
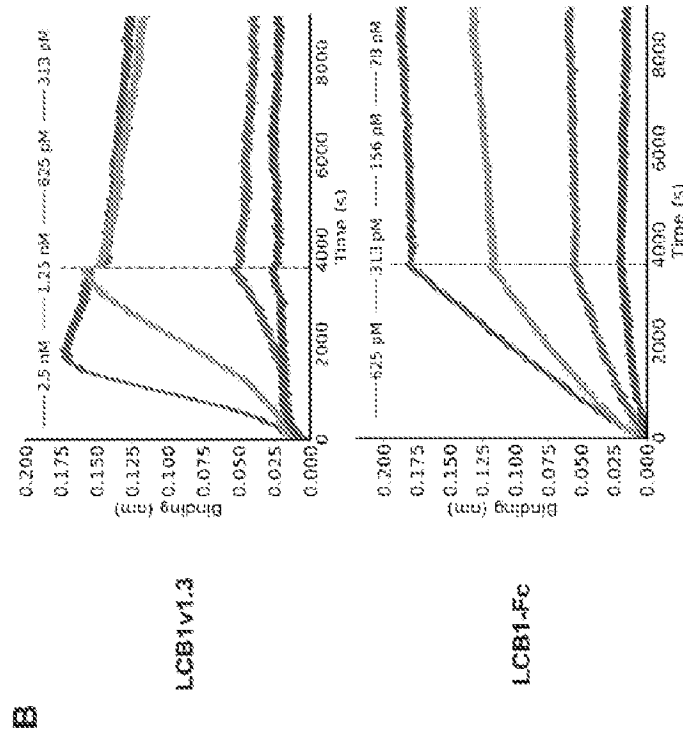
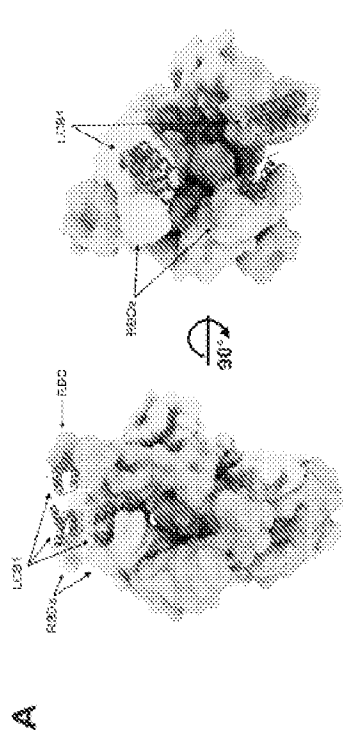
Minibinders potently neutralize live coronavirus

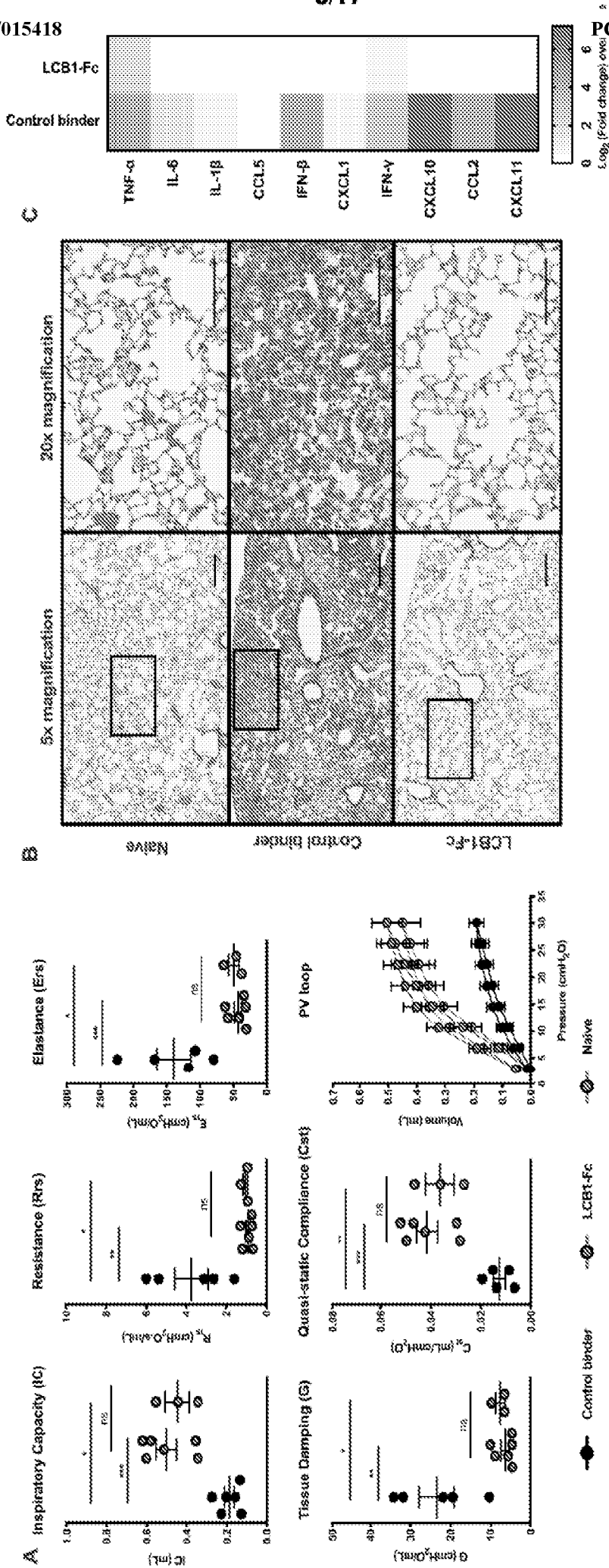


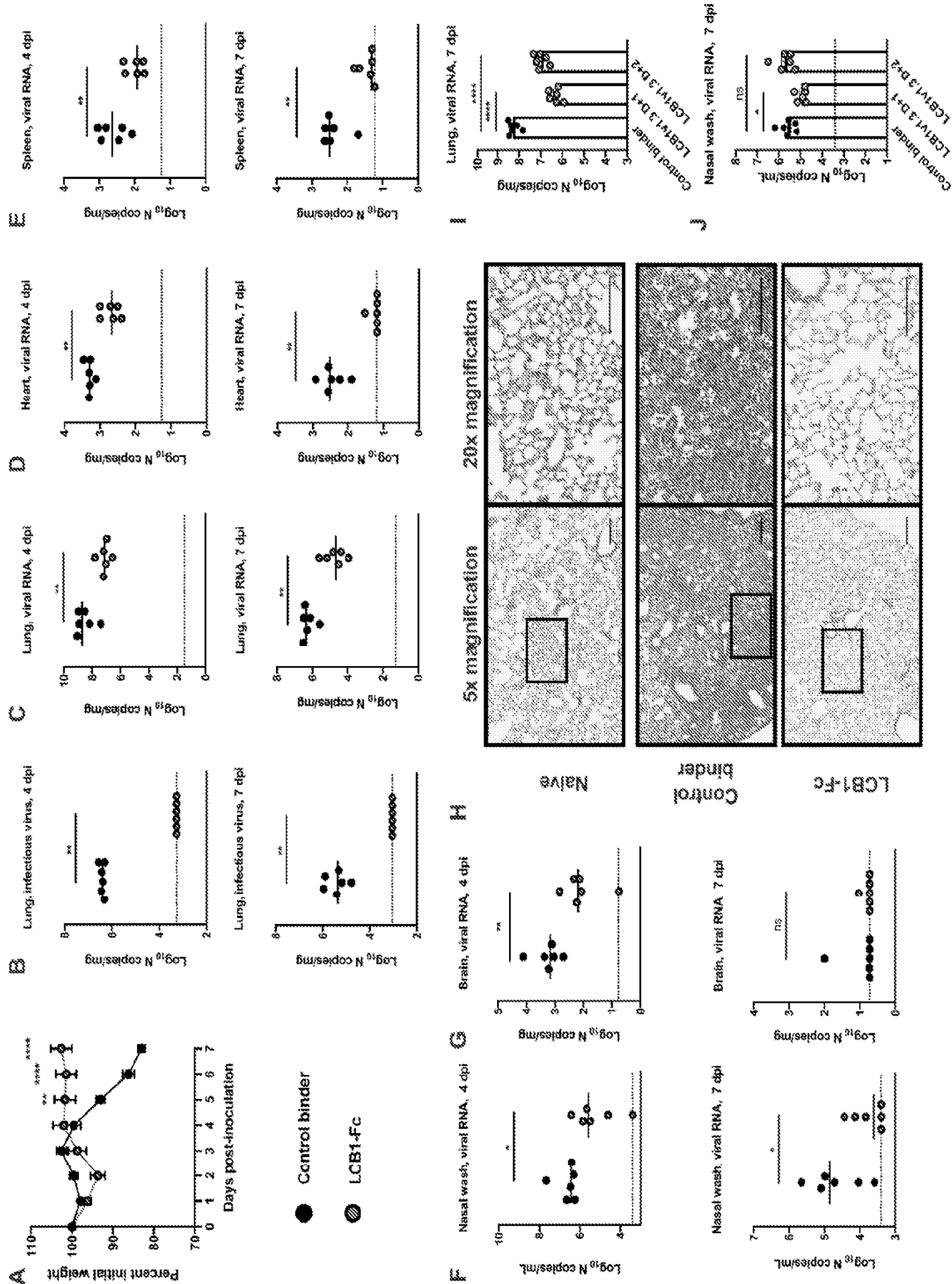
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Best mAb EC50:	1.5 ng/ml

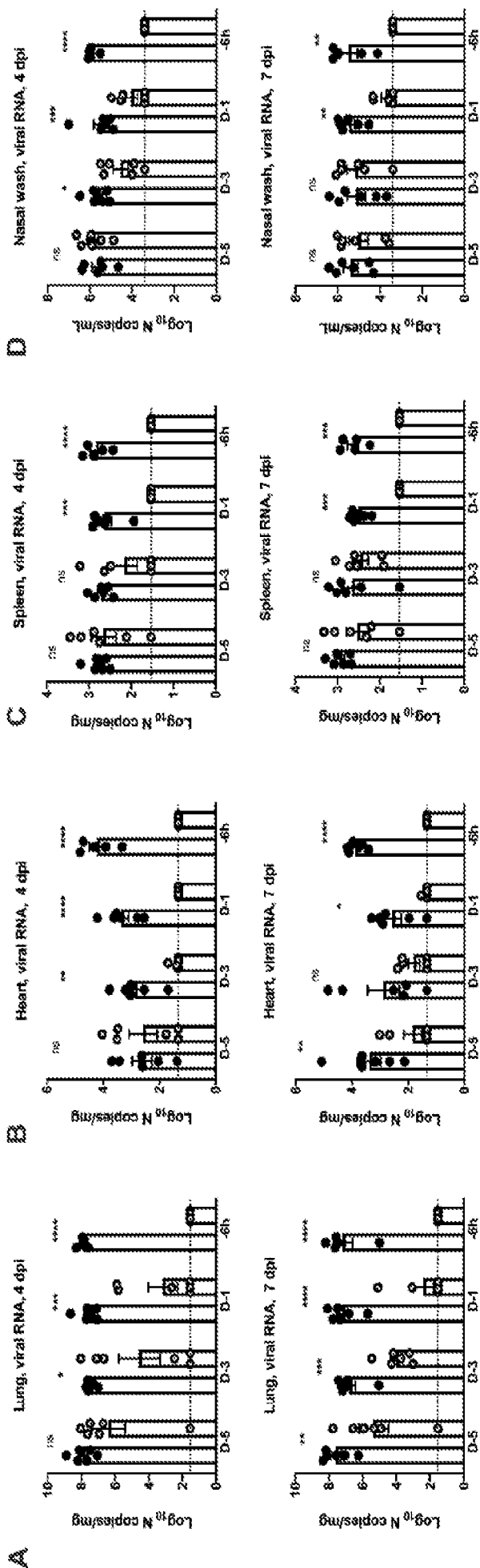
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Figure 4









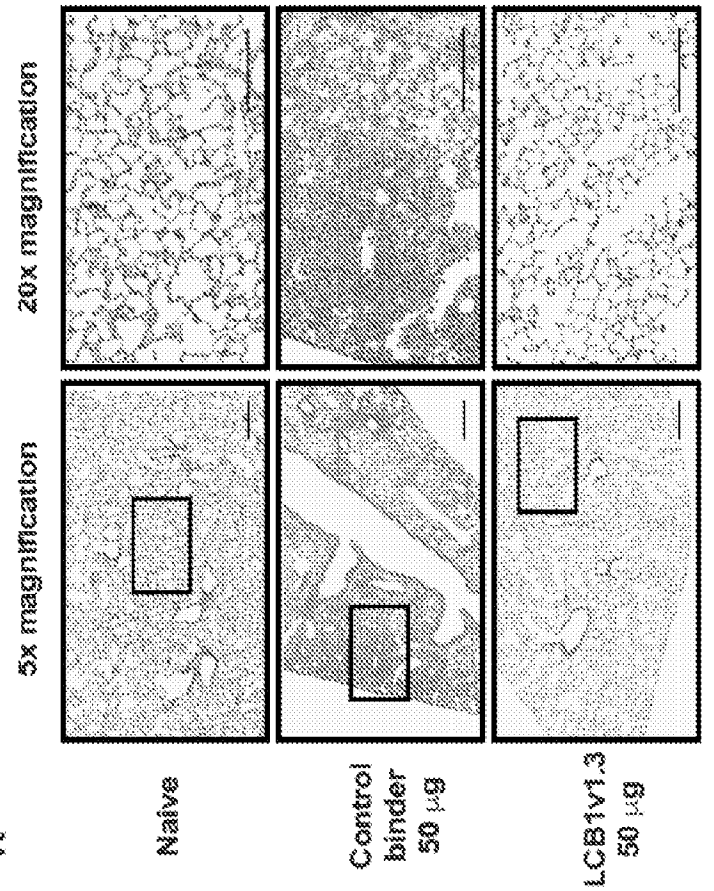
E

H

K

● Control binder

● LCB1v1.3



● Control binder ● 50 µg ● 10 µg ● 2 µg ● 0.4 µg

LCB1v1.3

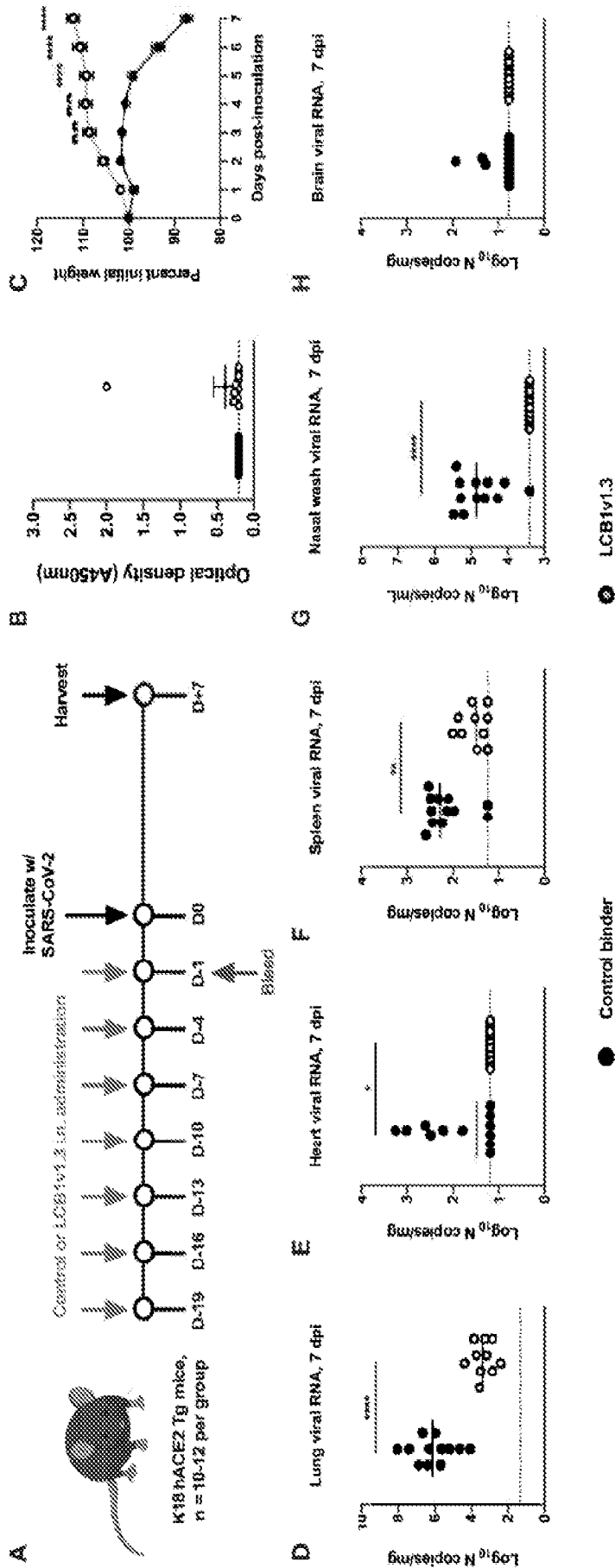
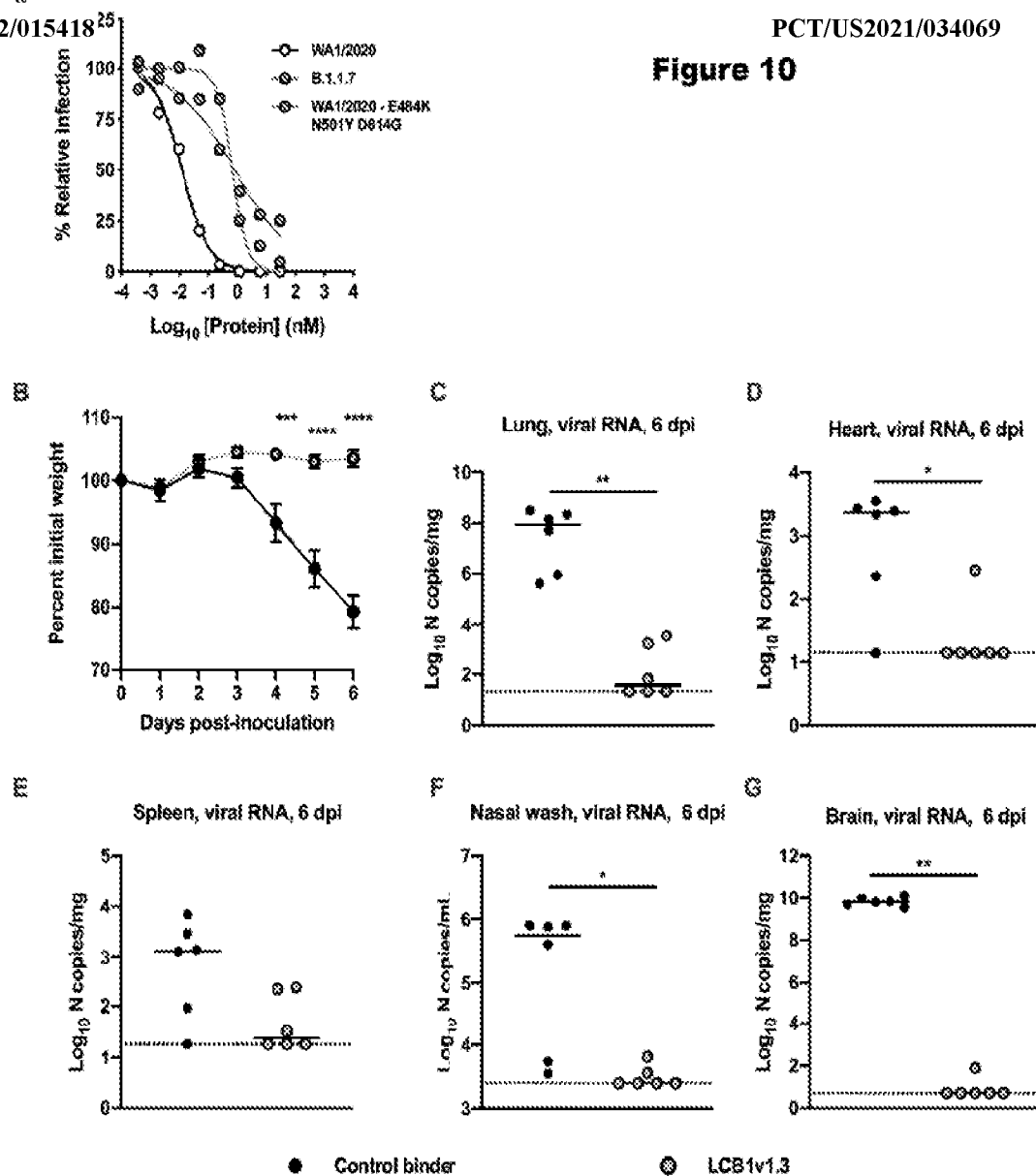
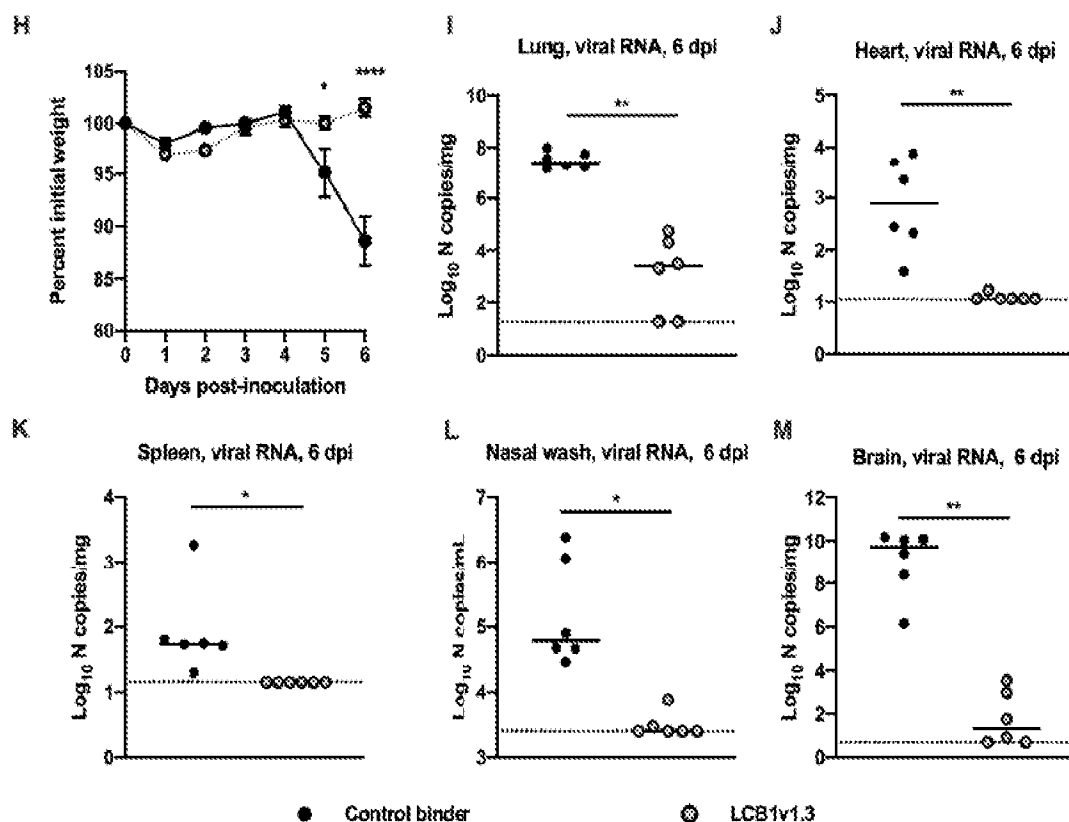


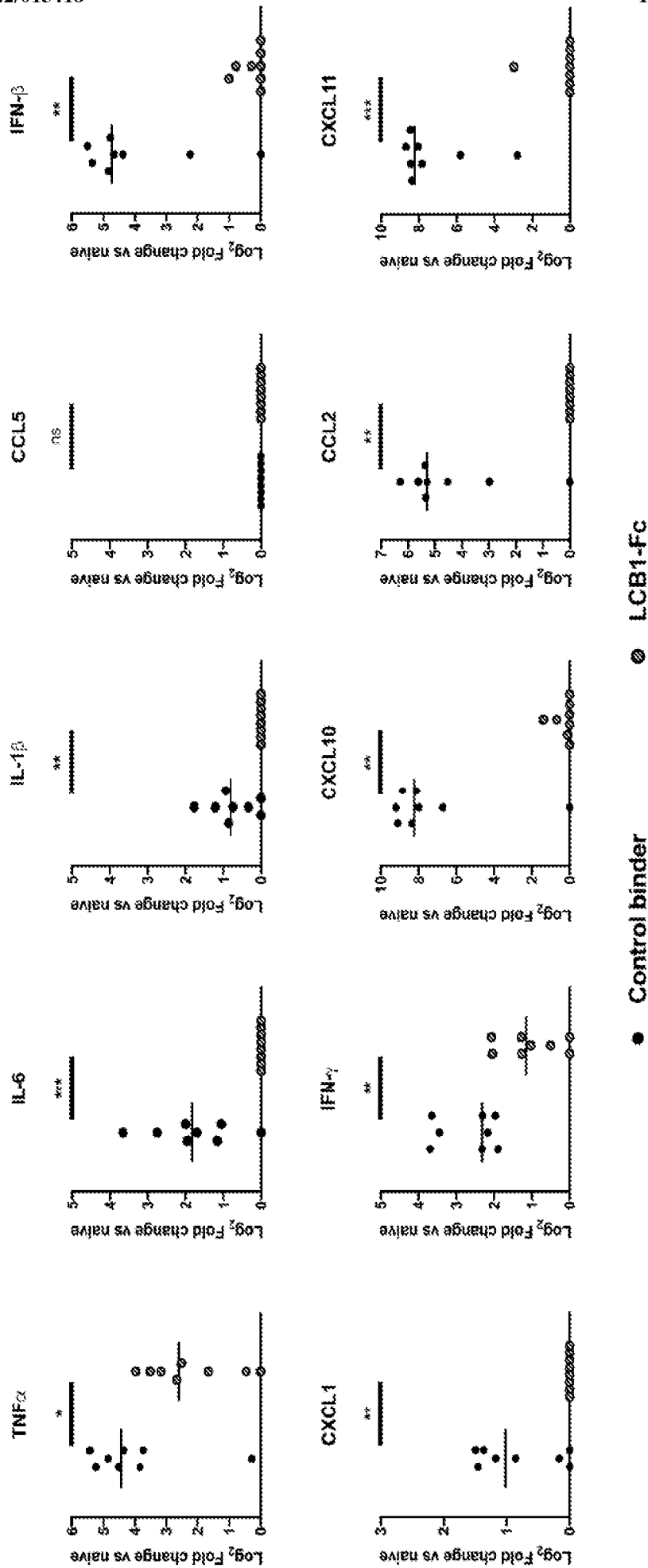
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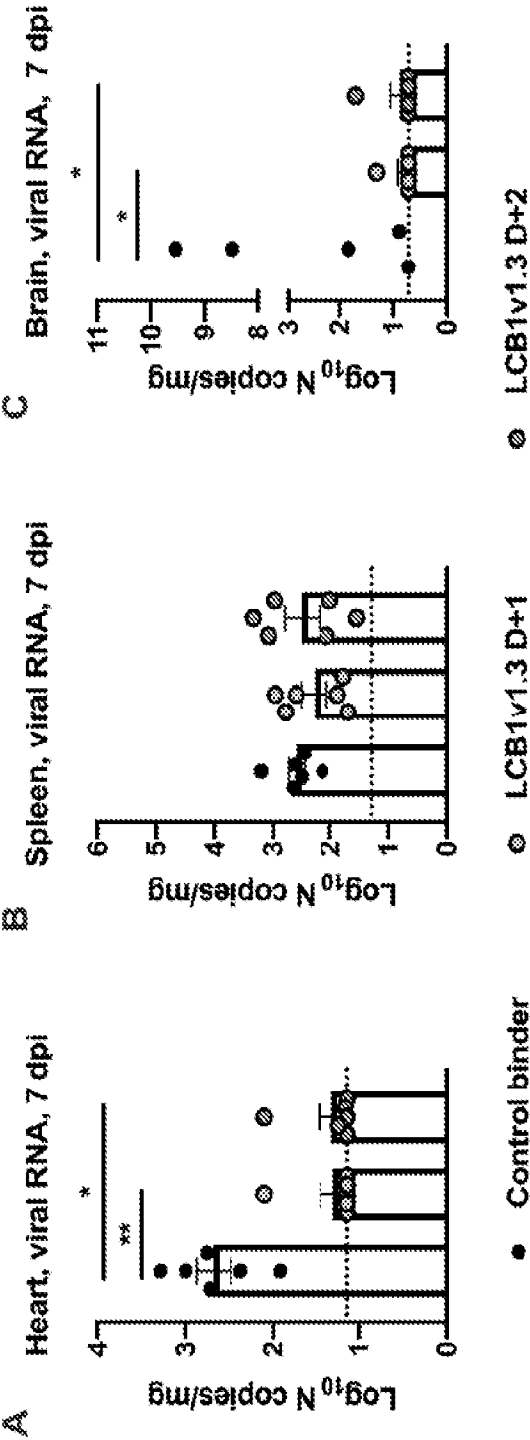
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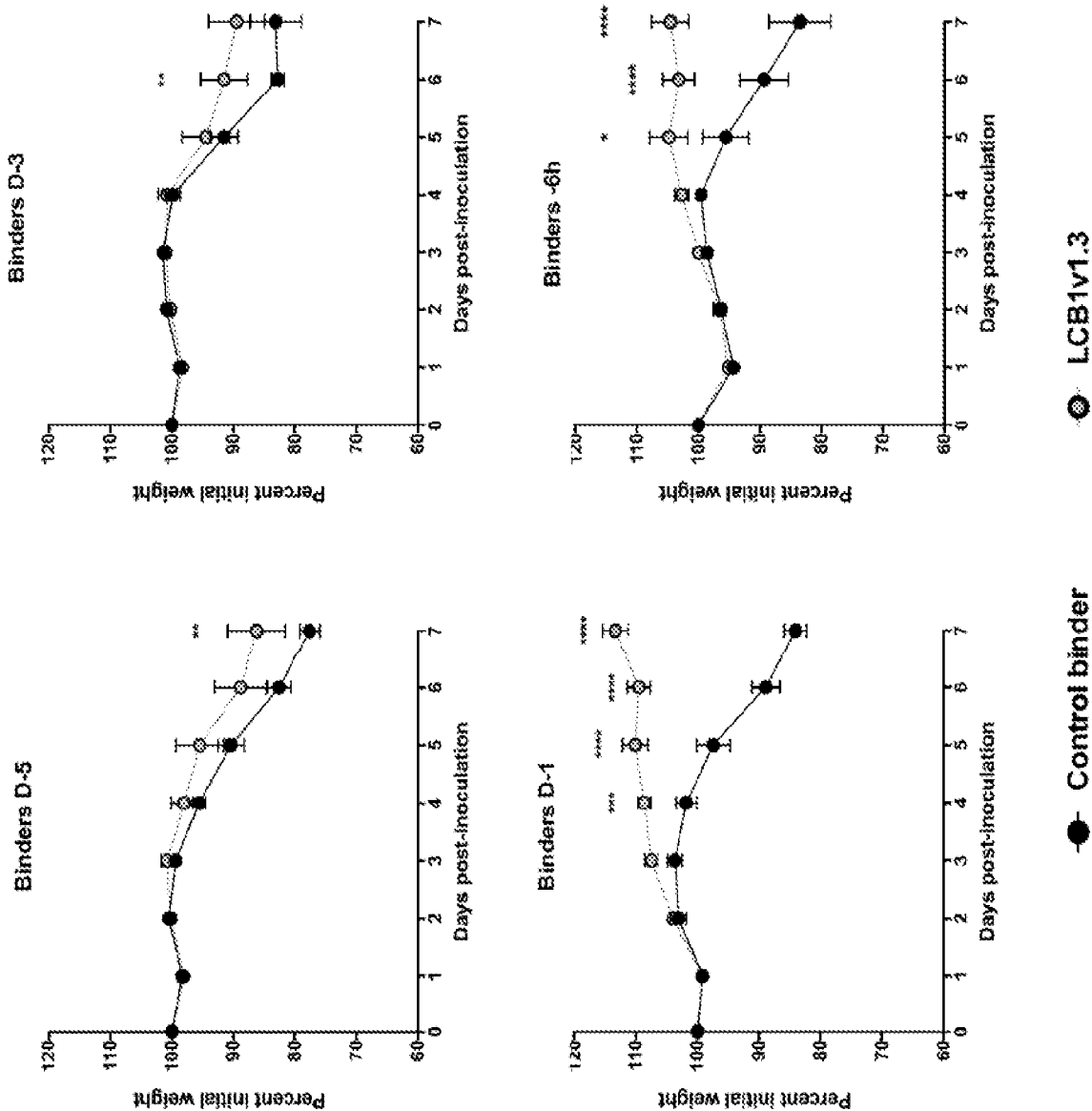


WA1/2020 - E484K/N501Y/D614G









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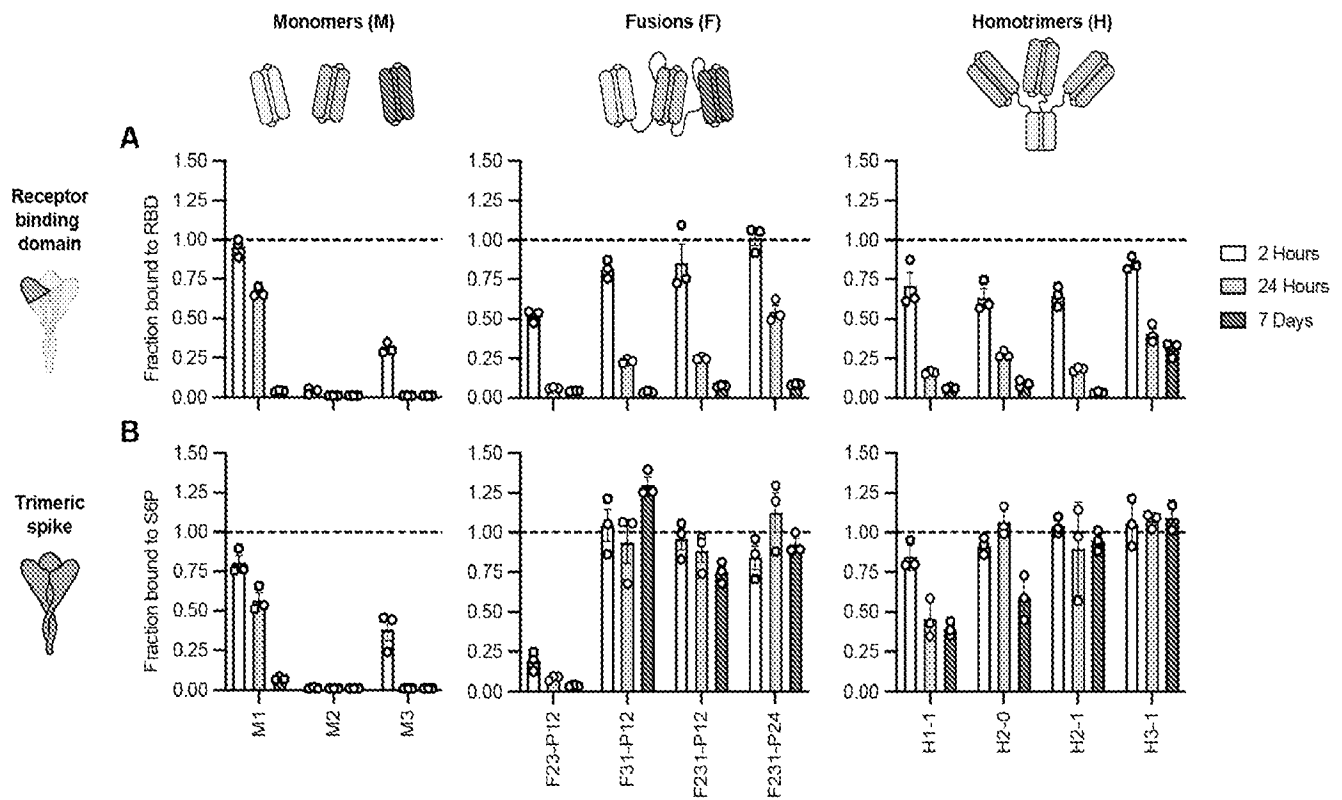


Figure 14

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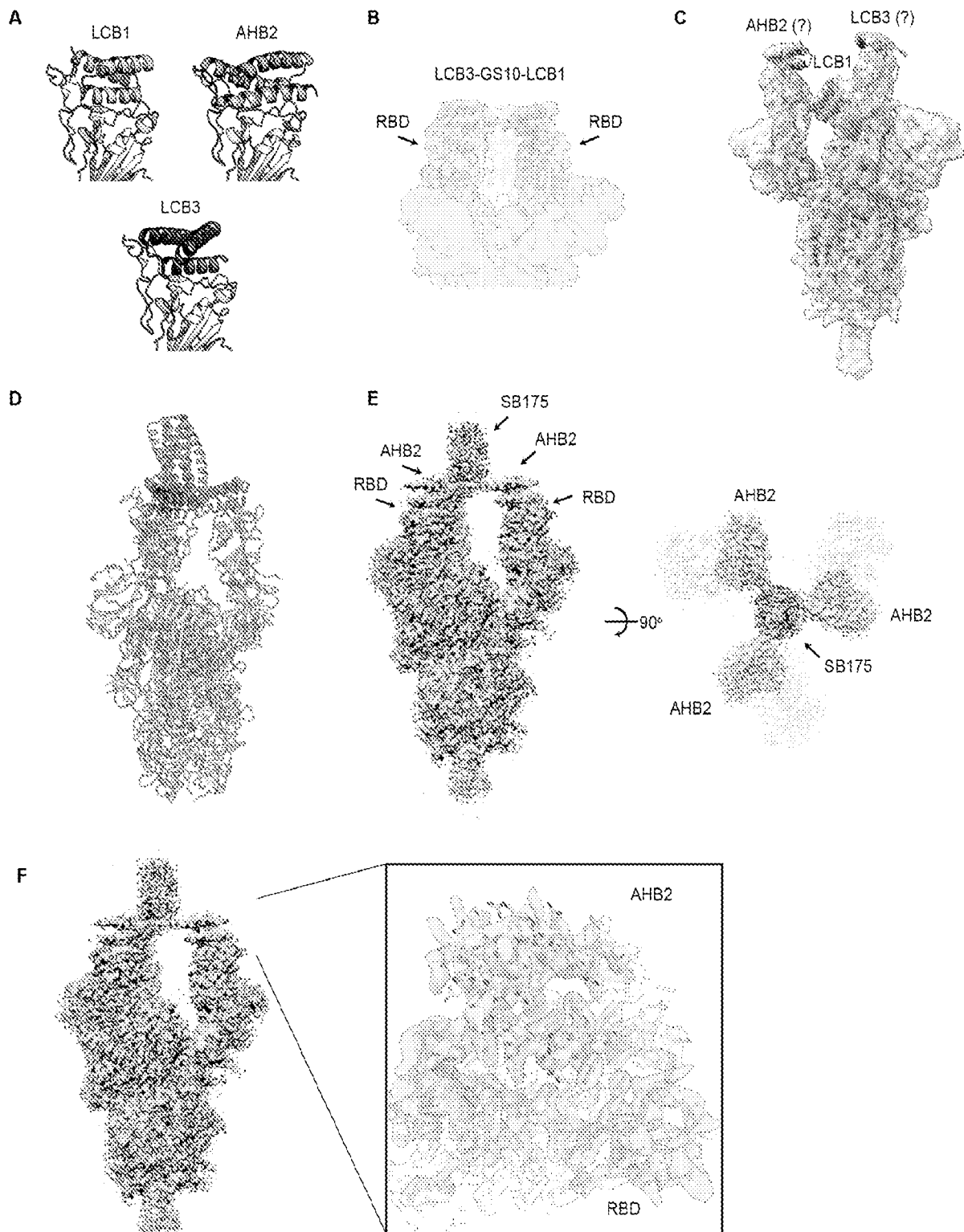


Figure 15

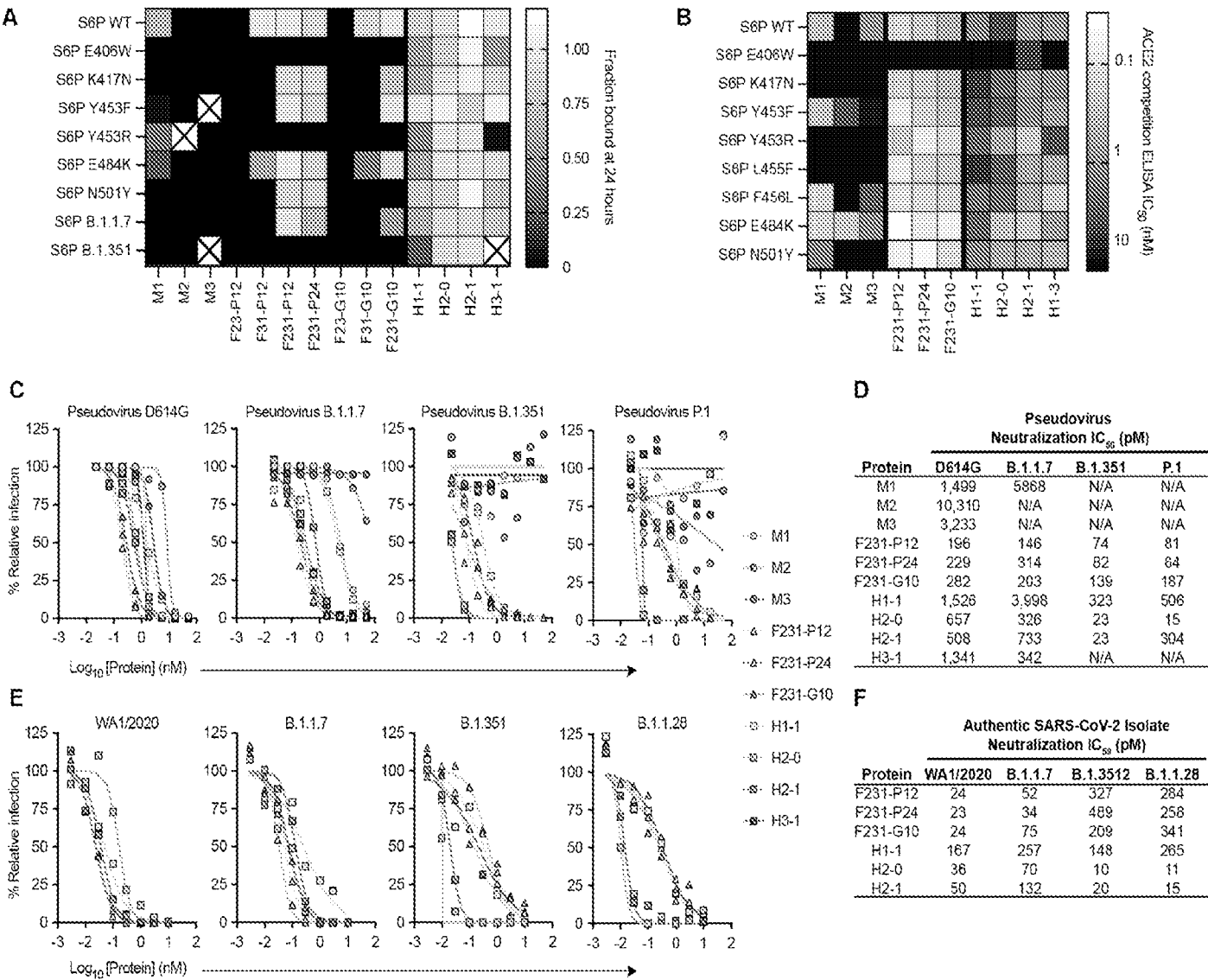


Figure 16

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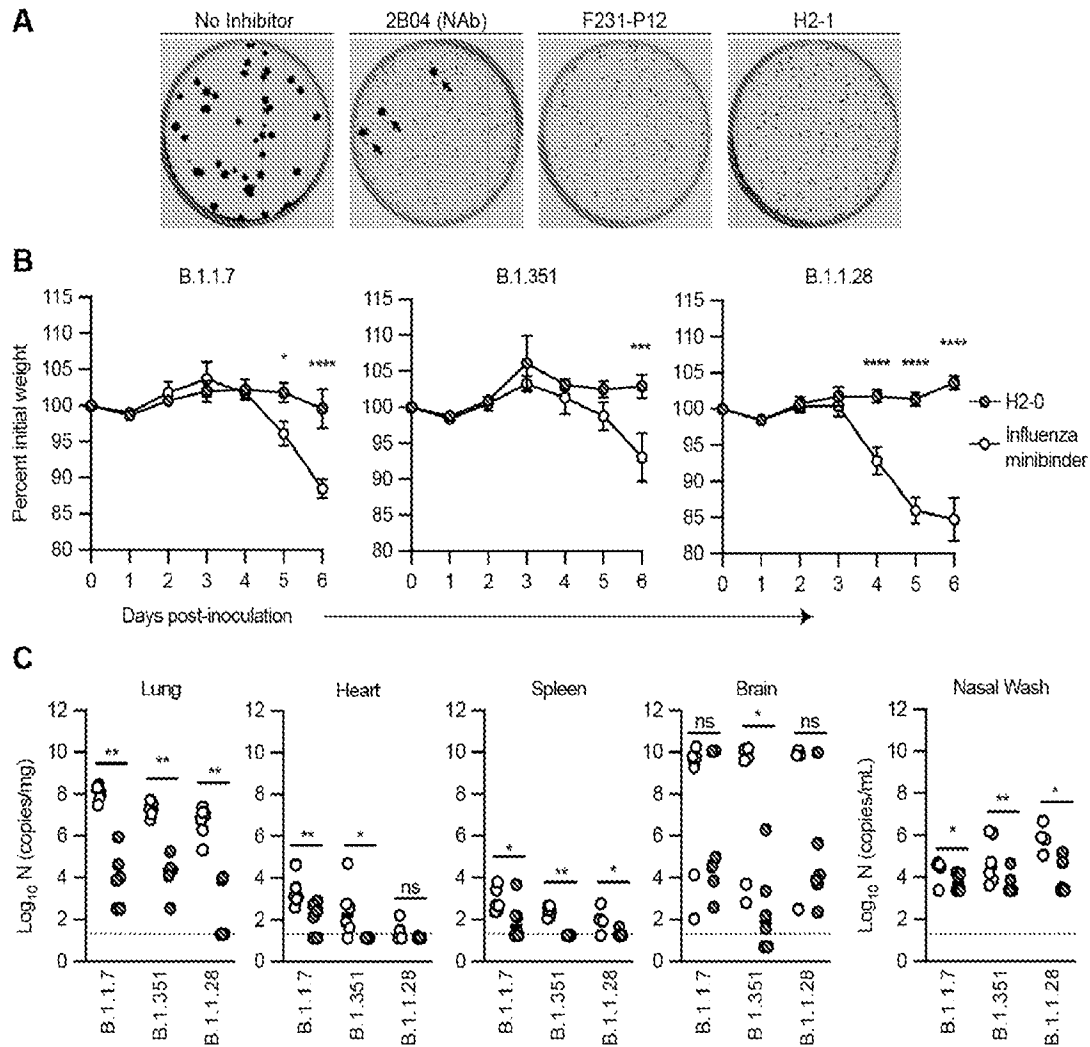


Figure 17

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<170> PatentIn version 3.5

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

Tyr Glu Phe Met Lys Gln Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu
35 40 45

Arg Leu Leu Glu Glu Val Glu Arg
50 55

<210> 8
<211> 56
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 8

Asp Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu
1 5 10 15

Glu Gln Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile

20

25

30

Tyr Glu Phe Met Lys Gln Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu
 35 40 45

Arg Leu Leu Glu Glu Val Glu Arg
 50 55

<210> 9

<211> 56

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 9

Asp Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu
 1 5 10 15

Glu Gln Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile
 20 25 30

Tyr Glu Phe Met Lys Gln Gly Asp Glu Asn Leu Leu Glu Glu Ala Glu
 35 40 45

Gln Leu Leu Gln Glu Val Glu Arg
 50 55

<210> 10

<211> 56

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 10

Asp Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu
 1 5 10 15

Glu Gln Leu Gly His Ala Glu Ala Ser Met Asn Val Ser Asp Leu Ile
 20 25 30

Tyr Glu Phe Met Lys Gln Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu
35 40 45

Arg Leu Leu Glu Glu Val Glu Arg
50 55

<210> 11
<211> 56
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 11

Ser Asp Asp Glu Asp Ser Val Arg Tyr Leu Leu Tyr Met Ala Glu Leu
1 5 10 15

Arg Tyr Glu Gln Gly Asn Pro Glu Lys Ala Lys Lys Ile Leu Glu Met
20 25 30

Ala Glu Phe Ile Ala Lys Arg Asn Asn Asn Glu Glu Leu Glu Arg Leu
35 40 45

Val Arg Glu Val Lys Lys Arg Leu
50 55

<210> 12
<211> 56
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 12

Ser Asp Asp Glu Asp Ala Val Arg Tyr Leu Leu Tyr Met Ala Glu Leu
1 5 10 15

Leu Tyr Lys Gln Gly Asn Pro Glu Glu Ala Lys Lys Leu Leu Glu Leu
20 25 30

Ala Glu Phe Ile Ala Lys Arg Asn Asn Asn Glu Glu Leu Glu Arg Leu

35

40

45

Val Arg Glu Val Lys Lys Arg Leu
 50 55

<210> 13
 <211> 64
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 13

Asn Asp Asp Glu Leu His Met Leu Met Thr Asp Leu Val Tyr Glu Ala
 1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Ile Lys Lys Arg Val Phe Gln Leu
 20 25 30

Phe Glu Leu Ala Asp Lys Ala Tyr Lys Asn Asn Asp Arg Gln Lys Leu
 35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
 50 55 60

<210> 14
 <211> 63
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 14

Asn Asp Asp Glu Leu Leu Met Leu Val Thr Asp Leu Val Ala Glu Ala
 1 5 10 15

Leu Leu Phe Ala Lys Asp Glu Glu Ile Lys Lys Arg Val Phe Thr Leu
 20 25 30

Phe Glu Leu Ala Asp Lys Ala Tyr Lys Asn Asn Asp Arg Asp Thr Leu
 35 40 45

Ser Lys Val Val Ser Glu Leu Lys Glu Leu Leu Glu Arg Leu Gln
50 55 60

<210> 15
<211> 64
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 15

Asn Asp Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Ile Gln Lys His Val Phe Gln Leu
20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

<210> 16
<211> 64
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 16

Asn Asp Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Ile Gln Lys His Val Phe Gln Leu
20 25 30

Phe Glu Asn Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser

50

55

60

<210> 17
 <211> 64
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 17

Asn Asp Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
 1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu
 20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Asn Asp Arg Gln Lys Leu
 35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
 50 55 60

<210> 18

<400> 18
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<210> 19
 <211> 64
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 19

Asn Asp Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
 1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu
 20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
 35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

<210> 20
<211> 64
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 20

Asn Asp Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Lys Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu
20 25 30

Phe Glu Lys Ala Thr Lys Ala Arg Lys Asn Lys Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

<210> 21
<211> 64
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 21

Asn Asp Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Lys Ala Lys Asp Glu Glu Met Gln Lys Arg Val Phe Gln Leu
20 25 30

Phe Glu Gln Ala Asp Lys Ala Tyr Lys Thr Lys Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

<210> 22

<400> 22
000

<210> 23

<211> 56

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 23

Gln Arg Glu Lys Arg Leu Lys Gln Leu Glu Met Leu Leu Glu Tyr Ala
1 5 10 15

Ile Glu Arg Asn Asp Pro Tyr Leu Met Phe Asp Val Ala Val Glu Met
20 25 30

Leu Arg Leu Ala Glu Glu Asn Asn Asp Glu Arg Ile Ile Glu Arg Ala
35 40 45

Lys Arg Ile Leu Glu Glu Tyr Glu
50 55

<210> 24

<211> 56

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 24

Asp Arg Glu Glu Arg Leu Lys Tyr Leu Glu Met Leu Leu Glu Leu Ala
1 5 10 15

Val Glu Arg Asn Asp Pro Tyr Leu Ile Phe Asp Val Ala Ile Glu Leu
20 25 30

Leu Arg Leu Ala Glu Glu Asn Asn Asp Glu Arg Ile Tyr Glu Arg Ala

35

40

45

Lys Arg Ile Leu Glu Glu Val Glu
 50 55

<210> 25

<211> 65

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 25

Ser Leu Glu Glu Leu Lys Glu Gln Val Lys Glu Leu Lys Lys Glu Leu
 1 5 10 15

Ser Pro Glu Met Arg Arg Leu Ile Glu Glu Ala Leu Arg Phe Leu Glu
 20 25 30

Glu Gly Asn Pro Ala Met Ala Met Met Val Leu Ser Asp Leu Val Tyr
 35 40 45

Gln Leu Gly Asp Pro Arg Val Ile Asp Leu Tyr Met Leu Val Thr Lys
 50 55 60

Thr
 65

<210> 26

<211> 65

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 26

Ser Leu Glu Glu Val Lys Glu Ile Leu Lys Glu Leu Lys Lys Glu Leu
 1 5 10 15

Ser Pro Glu Asp Arg Arg Leu Ile Glu Glu Ala Leu Arg Leu Leu Glu
 20 25 30

Glu Gly Asn Pro Ala Met Ala Ser Met Val Leu Ser Asp Leu Val Phe
35 40 45

Leu Leu Gly Asp Pro Arg Val Ile Glu Leu Leu Met Leu Val Thr Lys
50 55 60

Thr
65

<210> 27
<211> 56
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 27

Asp Arg Glu Gln Arg Leu Val Arg Phe Leu Val Arg Leu Ala Ser Lys
1 5 10 15

Phe Asn Leu Ser Pro Glu Gln Ile Leu Gln Leu Phe Glu Val Leu Glu
20 25 30

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

Glu Glu Val Ala Lys Glu Leu Gly
50 55

<210> 28
<211> 55
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 28

Asp Arg Glu Gln Arg Leu Val Arg Phe Leu Val Arg Leu Ala Ser Lys
1 5 10 15

Phe Asn Leu Ser Met Glu Gln Ile Leu Ile Leu Phe Asp Val Leu Glu

20

25

30

Glu Leu Leu Glu Arg Gly Val Ser Glu Glu Glu Ile Arg Lys Ile Leu
 35 40 45

Glu Glu Val Ala Lys Glu Leu
 50 55

<210> 29

<211> 57

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 29

Asp Asp Asp Ile Arg Tyr Leu Ile Tyr Met Ala Lys Leu Arg Leu Glu
 1 5 10 15

Gln Gly Asn Pro Glu Glu Ala Glu Lys Val Leu Glu Met Ala Arg Phe
 20 25 30

Leu Ala Glu Arg Leu Gly Met Glu Glu Leu Leu Lys Glu Val Arg Glu
 35 40 45

Leu Leu Arg Lys Ile Glu Glu Leu Arg
 50 55

<210> 30

<211> 57

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 30

Asp Asp Asp Val Arg Tyr Leu Ile Tyr Met Ala Lys Leu Leu Leu Glu
 1 5 10 15

Gln Gly Asn Pro Glu Glu Ala Glu Lys Val Leu Glu Ser Ala Arg Phe
 20 25 30

Ala Ala Glu Leu Leu Gly Asn Glu Glu Leu Leu Lys Glu Val Arg Glu
35 40 45

Leu Leu Arg Lys Ile Glu Glu Leu Arg
50 55

<210> 31
<211> 65
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 31

Pro Ile Ile Glu Leu Leu Arg Glu Ala Lys Glu Lys Asn Asp Glu Phe
1 5 10 15

Ala Ile Ser Asp Ala Leu Tyr Leu Val Asn Glu Leu Leu Gln Arg Thr
20 25 30

Gly Asp Pro Arg Leu Glu Glu Val Leu Tyr Leu Ile Trp Arg Ala Leu
35 40 45

Lys Glu Lys Asp Pro Arg Leu Leu Asp Arg Ala Ile Glu Leu Phe Glu
50 55 60

Arg
65

<210> 32
<211> 65
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 32

Pro Val Thr Glu Leu Leu Arg Glu Ala Lys Glu Lys Asn Asp Pro Met
1 5 10 15

Ala Ile Ser Asp Ala Leu Phe Leu Val Phe Glu Leu Ala Gln Arg Thr

20

25

30

Gly Asp Pro Arg Leu Glu Glu Val Leu Phe Leu Ile Trp Arg Ala Leu
 35 40 45

Lys Glu Lys Asp Pro Arg Leu Leu Asp Arg Ala Ile Glu Leu Phe Glu
 50 55 60

Arg
 65

<210> 33
 <211> 85
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 33

Asp Glu Asp Leu Glu Glu Leu Glu Arg Leu Tyr Arg Lys Ala Glu Glu
 1 5 10 15

Val Ala Lys Glu Ala Lys Asp Ala Ser Arg Arg Gly Asp Asp Glu Arg
 20 25 30

Ala Lys Glu Gln Met Glu Arg Ala Met Arg Leu Phe Asp Gln Val Phe
 35 40 45

Glu Leu Ala Gln Glu Leu Gln Glu Lys Gln Thr Asp Gly Asn Arg Gln
 50 55 60

Lys Ala Thr His Leu Asp Lys Ala Val Lys Glu Ala Ala Asp Glu Leu
 65 70 75 80

Tyr Gln Arg Val Arg
 85

<210> 34
 <211> 85
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Synthetic

<400> 34

Asp Glu Asp Leu Glu Glu Leu Glu Arg Leu Tyr Arg Lys Ala Glu Glu
1 5 10 15

Val Ala Lys Glu Ala Glu Glu Ala Ser Arg Arg Gly Asp Lys Glu Arg
20 25 30

Ala Lys Glu Leu Leu Glu Arg Ala Leu His Leu Phe Asp Gln Val Phe
35 40 45

Glu Leu Ala Gln Glu Leu Gln Glu Lys Leu Thr Asp Glu Lys Arg Gln
50 55 60

Lys Ala Thr His Leu Asp Lys Ala Val His Glu Ala Ala Asp Glu Leu
65 70 75 80

Tyr Gln Arg Val Arg
85

<210> 35

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 35

Gly Ser Gly Ser
1

<210> 36

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 36

Gly Gly Ser Gly Gly Ser

1

5

<210> 37
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 37

Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly
1 5 10

<210> 38
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 38

Gly Gly Ser Gly Gly Ser Gly Ser Gly Gly Ser Gly
1 5 10

<210> 39
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 39

Gly Gly Ser Gly Ser Ser Gly Gly Ser Gly Ser Gly Ser Gly
1 5 10

<210> 40
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 40

Gly Gly Ser Gly Ser Gly Gly Ser Gly Ser Gly Ser Gly Gly Ser
1 5 10 15

<210> 41
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 41

Ser Gly Gly Ser Gly Ser Gly Ser Gly Gly Ser Gly Ser Gly Ser
1 5 10 15

<210> 42
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 42

Gly Gly Gly Ser Gly Gly Gly Ser Ser Gly Gly Ser Gly Gly Ser Ser
1 5 10 15

Gly Gly Gly Ser Gly Gly Gly Ser
20

<210> 43
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 43

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
20 25 30

<210> 44
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 44

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly
1 5 10 15

Gly Ser Gly Gly Gly Ser Gly Ser Gly Gly Ser Gly Gly Gly Gly Ser
20 25 30

Gly Gly Gly Ser
35

<210> 45
<211> 75
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 45

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
20 25 30

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
35 40 45

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
50 55 60

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
65 70 75

<210> 46

<211> 76
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 46

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
20 25 30

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
35 40 45

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
50 55 60

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
65 70 75

<210> 47
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 47

Asp Lys Glu Trp Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg Leu Leu
1 5 10 15

Asp Glu Leu Gly His Ala Glu Ala Ser Met Arg Val Ser Asp Leu Ile
20 25 30

Tyr Glu Phe Met Lys Lys Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu
35 40 45

Arg Leu Leu Glu Glu Val Glu Arg Gly Gly Ser Gly Gly Ser Asp Lys
50 55 60

Glu Trp Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg Leu Leu Asp Glu
65 70 75 80

Leu Gly His Ala Glu Ala Ser Met Arg Val Ser Asp Leu Ile Tyr Glu
85 90 95

Phe Met Lys Lys Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu
100 105 110

Leu Glu Glu Val Glu Arg
115

<210> 48
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 48

Asp Lys Glu Trp Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg Leu Leu
1 5 10 15

Asp Glu Leu Gly His Ala Glu Ala Ser Met Arg Val Ser Asp Leu Ile
20 25 30

Tyr Glu Phe Met Lys Lys Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu
35 40 45

Arg Leu Leu Glu Glu Val Glu Arg Gly Gly Ser Gly Gly Ser Gly Ser
50 55 60

Gly Gly Ser Gly Asp Lys Glu Trp Ile Leu Gln Lys Ile Tyr Glu Ile
65 70 75 80

Met Arg Leu Leu Asp Glu Leu Gly His Ala Glu Ala Ser Met Arg Val
85 90 95

Ser Asp Leu Ile Tyr Glu Phe Met Lys Lys Gly Asp Glu Arg Leu Leu
100 105 110

Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Glu Arg
115 120

<210> 49
<211> 136
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 49

Asp Lys Glu Trp Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg Leu Leu
1 5 10 15

Asp Glu Leu Gly His Ala Glu Ala Ser Met Arg Val Ser Asp Leu Ile
20 25 30

Tyr Glu Phe Met Lys Lys Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu
35 40 45

Arg Leu Leu Glu Glu Val Glu Arg Gly Gly Gly Ser Gly Gly Gly Ser
50 55 60

Ser Gly Gly Ser Gly Gly Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser
65 70 75 80

Asp Lys Glu Trp Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg Leu Leu
85 90 95

Asp Glu Leu Gly His Ala Glu Ala Ser Met Arg Val Ser Asp Leu Ile
100 105 110

Tyr Glu Phe Met Lys Lys Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu
115 120 125

Arg Leu Leu Glu Glu Val Glu Arg
130 135

<210> 50
<211> 148
<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 50

Asp Lys Glu Trp Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg Leu Leu
1 5 10 15

Asp Glu Leu Gly His Ala Glu Ala Ser Met Arg Val Ser Asp Leu Ile
20 25 30

Tyr Glu Phe Met Lys Lys Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu
35 40 45

Arg Leu Leu Glu Glu Val Glu Arg Gly Gly Gly Ser Gly Gly Gly Ser
50 55 60

Gly Gly Ser Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Ser
65 70 75 80

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Asp Lys Glu Trp
85 90 95

Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg Leu Leu Asp Glu Leu Gly
100 105 110

His Ala Glu Ala Ser Met Arg Val Ser Asp Leu Ile Tyr Glu Phe Met
115 120 125

Lys Lys Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu
130 135 140

Glu Val Glu Arg
145

<210> 51

<211> 187

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 51

Asp Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu
1 5 10 15

Asp Gln Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile
20 25 30

Tyr Glu Phe Met Lys Gln Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu
35 40 45

Arg Leu Leu Glu Glu Val Glu Arg Gly Gly Gly Gly Ser Gly Gly Gly
50 55 60

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
65 70 75 80

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
85 90 95

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
100 105 110

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125

Gly Gly Ser Asp Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met
130 135 140

Lys Thr Leu Asp Gln Leu Gly His Ala Glu Ala Ser Met Gln Val Ser
145 150 155 160

Asp Leu Ile Tyr Glu Phe Met Lys Gln Gly Asp Glu Arg Leu Leu Glu
165 170 175

Glu Ala Glu Arg Leu Leu Glu Glu Val Glu Arg
180 185

<210> 52

<211> 187

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 52

Asp Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu
1 5 10 15

Asp Gln Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile
20 25 30

Tyr Glu Phe Met Lys Gln Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu
35 40 45

Arg Leu Leu Glu Glu Val Glu Arg Ala Gly Ser Gly Gly Ser Gly Gly
50 55 60

Ser Gly Gly Ser Pro Val Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser
65 70 75 80

Thr Pro Pro Thr Pro Ser Pro Ser Pro Val Pro Ser Thr Pro Pro Thr
85 90 95

Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Pro Val Pro Ser
100 105 110

Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser
115 120 125

Ala Ser Gly Asp Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met
130 135 140

Lys Thr Leu Asp Gln Leu Gly His Ala Glu Ala Ser Met Gln Val Ser
145 150 155 160

Asp Leu Ile Tyr Glu Phe Met Lys Gln Gly Asp Glu Arg Leu Leu Glu
165 170 175

Glu Ala Glu Arg Leu Leu Glu Glu Val Glu Arg
180 185

<210> 53
<211> 203
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 53

Asn Asp Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Ile Gln Lys His Val Phe Gln Leu
20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
65 70 75 80

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
85 90 95

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
100 105 110

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asn Asp Asp Glu Leu
130 135 140

His Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys
145 150 155 160

Asp Glu Glu Ile Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr
165 170 175

Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu
180 185 190

Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
195 200

<210> 54
<211> 203
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 54

Asn Asp Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Ile Gln Lys His Val Phe Gln Leu
20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

Ala Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Pro Val Pro Ser
65 70 75 80

Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser
85 90 95

Pro Val Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr
100 105 110

Pro Ser Pro Ser Pro Val Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser
115 120 125

Thr Pro Pro Thr Pro Ser Pro Ser Ala Ser Gly Asn Asp Asp Glu Leu
130 135 140

His Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys
145 150 155 160

Asp Glu Glu Ile Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr
165 170 175

Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu
180 185 190

Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
195 200

<210> 55
<211> 195
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 55

Asp Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu
1 5 10 15

Asp Gln Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile
20 25 30

Tyr Glu Phe Met Lys Gln Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu
35 40 45

Arg Leu Leu Glu Glu Val Glu Arg Gly Gly Gly Gly Ser Gly Gly Gly
50 55 60

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
65 70 75 80

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
85 90 95

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
100 105 110

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125

Gly Gly Ser Asn Asp Asp Glu Leu His Met Gln Met Thr Asp Leu Val
130 135 140

Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Ile Gln Lys His Val
145 150 155 160

Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg
165 170 175

Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg
180 185 190

Leu Leu Ser
195

<210> 56
<211> 195
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 56

Asn Asp Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Ile Gln Lys His Val Phe Gln Leu
20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
65 70 75 80

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
85 90 95

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
100 105 110

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Lys Glu Asn Ile
130 135 140

Leu Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu Asp Gln Leu Gly His
145 150 155 160

Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys
165 170 175

Gln Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu
180 185 190

Val Glu Arg
195

<210> 57
<211> 130
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 57

Asn Asp Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Ile Gln Lys His Val Phe Gln Leu
20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Asp Lys Glu Asn Ile Leu
65 70 75 80

Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu Asp Gln Leu Gly His Ala
85 90 95

Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Gln
100 105 110

Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val
115 120 125

Glu Arg
130

<210> 58
<211> 195
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 58

Asp Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu
1 5 10 15

Asp Gln Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile
20 25 30

Tyr Glu Phe Met Lys Gln Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu
35 40 45

Arg Leu Leu Glu Glu Val Glu Arg Ala Gly Ser Gly Gly Ser Gly Gly
50 55 60

Ser Gly Gly Ser Pro Val Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser
65 70 75 80

Thr Pro Pro Thr Pro Ser Pro Ser Pro Val Pro Ser Thr Pro Pro Thr
85 90 95

Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Pro Val Pro Ser
100 105 110

Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser
115 120 125

Ala Ser Gly Asn Asp Asp Glu Leu His Met Gln Met Thr Asp Leu Val
130 135 140

Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Ile Gln Lys His Val
145 150 155 160

Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg
165 170 175

Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg
180 185 190

Leu Leu Ser
195

<210> 59
<211> 195
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 59

Asn Asp Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Ile Gln Lys His Val Phe Gln Leu
20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

Ala Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Pro Val Pro Ser
65 70 75 80

Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser
85 90 95

Pro Val Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr
100 105 110

Pro Ser Pro Ser Pro Val Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser
115 120 125

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

Leu Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu Asp Gln Leu Gly His
145 150 155 160

Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys
165 170 175

Gln Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu
180 185 190

Val Glu Arg
195

<210> 60
<211> 336
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 60

Asp Lys Glu Trp Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg Leu Leu
1 5 10 15

Asp Glu Leu Gly His Ala Glu Ala Ser Met Arg Val Ser Asp Leu Ile
20 25 30

Tyr Glu Phe Met Lys Lys Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu
35 40 45

Arg Leu Leu Glu Glu Val Glu Arg Gly Gly Ser Gly Ser Ser Gly Gly
50 55 60

Ser Gly Ser Gly Ser Gly Asp Lys Glu Trp Ile Leu Gln Lys Ile Tyr
65 70 75 80

Glu Ile Met Arg Leu Leu Asp Glu Leu Gly His Ala Glu Ala Ser Met
85 90 95

Arg Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Lys Gly Asp Glu Arg
100 105 110

Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Glu Arg Gly Gly
115 120 125

Ser Gly Ser Ser Gly Gly Ser Gly Ser Gly Ser Gly Asp Lys Glu Trp
130 135 140

Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg Leu Leu Asp Glu Leu Gly
145 150 155 160

His Ala Glu Ala Ser Met Arg Val Ser Asp Leu Ile Tyr Glu Phe Met
165 170 175

Lys Lys Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu
180 185 190

Glu Val Glu Arg Gly Gly Ser Gly Ser Ser Gly Gly Ser Gly Ser Gly
195 200 205

Ser Gly Asp Lys Glu Trp Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg
210 215 220

Leu Leu Asp Glu Leu Gly His Ala Glu Ala Ser Met Arg Val Ser Asp

Gly Gly Ala Lys Ala Lys Ala Lys Ala Lys Ala Lys Ala Lys
1 5 10 15

Ala Lys Ala Lys Ala Lys
20

<210> 63
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 63

Met Ala Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala
1 5 10 15

Leu Ala

<210> 64
<211> 232
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 64

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln

65		70		75		80									
Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln
			85					90					95		
Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala
		100						105					110		
Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro
		115					120					125			
Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr
	130					135					140				
Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser
145					150					155					160
Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr
			165						170					175	
Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr
			180					185					190		
Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe
		195					200					205			
Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys
	210					215					220				
Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys								
225					230										

<210> 65
 <211> 79
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 65

Ala Lys Ala Lys Ala Lys Ala Lys Ala Lys Ala Lys Ala Lys Ala Lys

1	5	10	15
Ala Lys Ala Lys Gly Gly Asp Lys Glu Asn Ile Leu Gln Lys Ile Tyr	20	25	30
Glu Ile Met Lys Thr Leu Asp Gln Leu Gly His Ala Glu Ala Ser Met	35	40	45
Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Gln Gly Asp Glu Arg	50	55	60
Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Glu Arg Cys	65	70	75

<210> 66
 <211> 79
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 66

Ala Lys Ala Lys Ala Lys Ala Lys Ala Lys Ala Lys Ala Lys Ala Lys	1	5	10	15
Ala Lys Ala Lys Gly Gly Asp Lys Glu Asn Ile Leu Gln Lys Ile Tyr	20	25	30	
Glu Ile Met Lys Thr Leu Asp Gln Leu Gly His Ala Glu Ala Ser Met	35	40	45	
Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Gln Gly Asp Glu Arg	50	55	60	
Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Glu Arg Cys	65	70	75	

<210> 67
 <211> 78
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Synthetic

<400> 67

Asp Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu
1 5 10 15

Glu Gln Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile
20 25 30

Tyr Glu Phe Met Lys Gln Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu
35 40 45

Arg Leu Leu Glu Glu Val Glu Arg Gly Gly Ala Lys Ala Lys Ala Lys
50 55 60

Ala Lys Ala Lys Ala Lys Ala Lys Ala Lys Ala Lys Ala Lys
65 70 75

<210> 68

<211> 310

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 68

Met Ala Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala
1 5 10 15

Leu Ala Asp Lys Glu Trp Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg
20 25 30

Leu Leu Asp Glu Leu Gly His Ala Glu Ala Ser Met Arg Val Ser Asp
35 40 45

Leu Ile Tyr Glu Phe Met Lys Lys Gly Asp Glu Arg Leu Leu Glu Glu
50 55 60

Ala Glu Arg Leu Leu Glu Glu Val Glu Arg Gly Ser Gly Ser Glu Pro
65 70 75 80

Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
85 90 95

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
100 105 110

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
115 120 125

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
130 135 140

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
145 150 155 160

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
165 170 175

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
180 185 190

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
195 200 205

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
210 215 220

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
225 230 235 240

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
245 250 255

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
260 265 270

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
275 280 285

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu

290

295

300

Ser Leu Ser Pro Gly Lys
305 310

<210> 69

<211> 321

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 69

Met Ala Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala
1 5 10 15

Leu Ala Asp Lys Glu Trp Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg
20 25 30

Leu Leu Asp Glu Leu Gly His Ala Glu Ala Ser Met Arg Val Ser Asp
35 40 45

Leu Ile Tyr Glu Phe Met Lys Lys Gly Asp Glu Arg Leu Leu Glu Glu
50 55 60

Ala Glu Arg Leu Leu Glu Glu Val Glu Arg Gly Gly Ser Gly Ser Gly
65 70 75 80

Gly Ser Gly Ser Gly Ser Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys
85 90 95

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
100 105 110

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
115 120 125

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
130 135 140

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn

<400> 70

Met Ala Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala
1 5 10 15

Leu Ala Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys
20 25 30

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
35 40 45

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
50 55 60

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
65 70 75 80

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
85 90 95

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
100 105 110

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
115 120 125

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
130 135 140

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
145 150 155 160

Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
165 170 175

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
180 185 190

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
195 200 205

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
210 215 220

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
225 230 235 240

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Ser Gly Gly Ser Gly Ser
245 250 255

Gly Ser Gly Gly Ser Gly Ser Gly Ser Asp Lys Glu Trp Ile Leu Gln
260 265 270

Lys Ile Tyr Glu Ile Met Arg Leu Leu Asp Glu Leu Gly His Ala Glu
275 280 285

Ala Ser Met Arg Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Lys Gly
290 295 300

Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Glu
305 310 315 320

Arg

<210> 71
<211> 392
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 71

Met Ala Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala
1 5 10 15

Leu Ala Asp Lys Glu Trp Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg
20 25 30

Leu Leu Asp Glu Leu Gly His Ala Glu Ala Ser Met Arg Val Ser Asp
35 40 45

Leu Ile Tyr Glu Phe Met Lys Lys Gly Asp Glu Arg Leu Leu Glu Glu
50 55 60

Ala Glu Arg Leu Leu Glu Glu Val Glu Arg Gly Gly Ser Gly Ser Gly
65 70 75 80

Gly Ser Gly Ser Gly Ser Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys
85 90 95

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
100 105 110

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
115 120 125

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
130 135 140

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
145 150 155 160

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
165 170 175

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
180 185 190

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
195 200 205

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
210 215 220

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
225 230 235 240

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
245 250 255

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu

260

265

270

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
 275 280 285

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
 290 295 300

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
 305 310 315 320

Lys Ser Gly Gly Ser Gly Ser Gly Ser Gly Gly Ser Gly Ser Gly Ser
 325 330 335

Asp Lys Glu Trp Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg Leu Leu
 340 345 350

Asp Glu Leu Gly His Ala Glu Ala Ser Met Arg Val Ser Asp Leu Ile
 355 360 365

Tyr Glu Phe Met Lys Lys Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu
 370 375 380

Arg Leu Leu Glu Glu Val Glu Arg
 385 390

<210> 72

<211> 310

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 72

Met Ala Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala
 1 5 10 15

Leu Ala Asp Lys Glu Trp Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg
 20 25 30

Leu Leu Asp Glu Leu Gly His Ala Glu Ala Ser Met Arg Val Ser Asp

35

40

45

Leu Ile Tyr Glu Phe Met Lys Gln Gly Asp Glu Arg Leu Leu Glu Glu
 50 55 60

Ala Glu Arg Leu Leu Glu Glu Val Glu Arg Gly Ser Gly Ser Glu Pro
 65 70 75 80

Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
 85 90 95

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
 100 105 110

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
 115 120 125

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
 130 135 140

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
 145 150 155 160

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
 165 170 175

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
 180 185 190

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
 195 200 205

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
 210 215 220

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
 225 230 235 240

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
 245 250 255

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
260 265 270

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
275 280 285

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
290 295 300

Ser Leu Ser Pro Gly Lys
305 310

<210> 73
<211> 321
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 73

Met Ala Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala
1 5 10 15

Leu Ala Asp Lys Glu Trp Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg
20 25 30

Leu Leu Asp Glu Leu Gly His Ala Glu Ala Ser Met Arg Val Ser Asp
35 40 45

Leu Ile Tyr Glu Phe Met Lys Gln Gly Asp Glu Arg Leu Leu Glu Glu
50 55 60

Ala Glu Arg Leu Leu Glu Glu Val Glu Arg Gly Gly Ser Gly Ser Gly
65 70 75 80

Gly Ser Gly Ser Gly Ser Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys
85 90 95

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
100 105 110

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
115 120 125

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
130 135 140

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
145 150 155 160

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
165 170 175

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
180 185 190

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
195 200 205

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
210 215 220

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
225 230 235 240

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
245 250 255

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
260 265 270

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
275 280 285

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
290 295 300

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
305 310 315 320

Lys

<210> 74
<211> 321
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 74

Met Ala Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala
1 5 10 15

Leu Ala Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys
20 25 30

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
35 40 45

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
50 55 60

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
65 70 75 80

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
85 90 95

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
100 105 110

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
115 120 125

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
130 135 140

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
145 150 155 160

Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

165

170

175

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
 180 185 190

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
 195 200 205

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
 210 215 220

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
 225 230 235 240

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Ser Gly Gly Ser Gly Ser
 245 250 255

Gly Ser Gly Gly Ser Gly Ser Gly Ser Asp Lys Glu Trp Ile Leu Gln
 260 265 270

Lys Ile Tyr Glu Ile Met Arg Leu Leu Asp Glu Leu Gly His Ala Glu
 275 280 285

Ala Ser Met Arg Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Gln Gly
 290 295 300

Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Glu
 305 310 315 320

Arg

<210> 75

<211> 392

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 75

Met Ala Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala

1	5	10	15
Leu	Ala	Asp	Lys
	20		
Glu	Trp	Ile	Leu
			25
Gln	Lys	Ile	Tyr
Glu	Ile	Met	Arg
	30		
Leu	Leu	Asp	Glu
	35		
Leu	Gly	His	Ala
			40
Glu	Ala	Ser	Met
Arg	Val	Ser	Asp
			45
Leu	Ile	Tyr	Glu
	50		
Phe	Met	Lys	Gln
			55
Gly	Asp	Glu	Arg
			60
Leu	Leu	Glu	Glu
Ala	Glu	Arg	Leu
Leu	Glu	Glu	Val
			70
Glu	Arg	Gly	Gly
			75
Ser	Gly	Ser	Gly
Ala	Glu	Arg	Leu
			80
Gly	Ser	Gly	Ser
Gly	Ser	Gly	Gly
Ser	Glu	Pro	Lys
Ser	Ser	Asp	Lys
			95
Gly	Ser	Gly	Gly
Thr	His	Thr	Cys
			100
Pro	Pro	Cys	Pro
Ala	Pro	Glu	Leu
Leu	Leu	Gly	Gly
			110
Pro	Glu	Leu	Leu
Ser	Val	Phe	Leu
Phe	Pro	Pro	Lys
			120
Pro	Lys	Asp	Thr
Leu	Met	Ile	Ser
			125
Arg	Thr	Pro	Glu
Val	Thr	Cys	Val
			135
Val	Val	Val	Asp
Val	Ser	His	Glu
			140
Pro	Glu	Val	Thr
Val	Lys	Phe	Asn
			150
Trp	Tyr	Val	Asp
Gly	Val	Glu	Val
			155
His	Asn		
			160
Ala	Lys	Thr	Lys
Pro	Arg	Glu	Glu
Gln	Tyr	Asn	Ser
Thr	Tyr	Arg	Val
			175
Val	Ser	Val	Leu
Leu	Thr	Val	Leu
His	Gln	Asp	Trp
Leu	Asn	Gly	Lys
			190
Tyr	Lys	Cys	Lys
Val	Ser	Asn	Lys
Ala	Leu	Pro	Ala
Pro	Ile	Glu	Lys
Tyr	Thr		
Thr	Ile	Ser	Lys
Ala	Lys	Gly	Gln
Pro	Arg	Glu	Pro
Gln	Val	Tyr	Thr
Thr			
Thr	Ile	Ser	Lys
Ala	Lys	Gly	Gln
Pro	Arg	Glu	Pro
Gln	Val	Tyr	Thr
Thr			
Thr	Ile	Ser	Lys
Ala	Lys	Gly	Gln
Pro	Arg	Glu	Pro
Gln	Val	Tyr	Thr
Thr			
Thr	Ile	Ser	Lys
Ala	Lys	Gly	Gln
Pro	Arg	Glu	Pro
Gln	Val	Tyr	Thr
Thr			
Thr	Ile	Ser	Lys
Ala	Lys	Gly	Gln
Pro	Arg	Glu	Pro
Gln	Val	Tyr	Thr
Thr			
Thr	Ile	Ser	Lys
Ala	Lys	Gly	Gln
Pro	Arg	Glu	Pro
Gln	Val	Tyr	Thr
Thr			
Thr	Ile	Ser	Lys
Ala	Lys	Gly	Gln
Pro	Arg	Glu	Pro
Gln	Val	Tyr	Thr
Thr			
Thr	Ile	Ser	Lys
Ala	Lys	Gly	Gln
Pro	Arg	Glu	Pro
Gln	Val	Tyr	Thr
Thr			
Thr	Ile	Ser	Lys
Ala	Lys	Gly	Gln
Pro	Arg	Glu	Pro
Gln	Val	Tyr	Thr
Thr			
Thr	Ile	Ser	Lys
Ala	Lys	Gly	Gln
Pro	Arg	Glu	Pro
Gln	Val	Tyr	Thr
Thr			
Thr	Ile	Ser	Lys
Ala	Lys	Gly	Gln
Pro	Arg	Glu	Pro
Gln	Val	Tyr	Thr
Thr			
Thr	Ile	Ser	Lys
Ala	Lys	Gly	Gln
Pro	Arg	Glu	Pro
Gln	Val	Tyr	Thr
Thr			
Thr	Ile	Ser	Lys
Ala	Lys	Gly	Gln
Pro	Arg	Glu	Pro
Gln	Val	Tyr	Thr
Thr			
Thr	Ile	Ser	Lys
Ala	Lys	Gly	Gln
Pro	Arg	Glu	Pro
Gln	Val	Tyr	Thr
Thr			
Thr	Ile	Ser	Lys
Ala	Lys	Gly	Gln
Pro	Arg	Glu	Pro
Gln	Val	Tyr	Thr
Thr			
Thr	Ile	Ser	Lys
Ala	Lys	Gly	Gln
Pro	Arg	Glu	Pro
Gln	Val	Tyr	Thr
Thr			
Thr	Ile	Ser	Lys
Ala	Lys	Gly	Gln
Pro	Arg	Glu	Pro
Gln	Val	Tyr	Thr
Thr			
Thr	Ile	Ser	Lys
Ala	Lys	Gly	Gln
Pro	Arg	Glu	Pro
Gln	Val	Tyr	Thr
Thr			
Thr	Ile	Ser	Lys
Ala	Lys	Gly	Gln
Pro	Arg	Glu	Pro
Gln	Val	Tyr	Thr
Thr			
Thr	Ile	Ser	Lys
Ala	Lys	Gly	Gln
Pro	Arg	Glu	Pro
Gln	Val	Tyr	Thr
Thr			
Thr	Ile	Ser	Lys
Ala	Lys	Gly	Gln
Pro	Arg	Glu	Pro
Gln	Val	Tyr	Thr
Thr			
Thr	Ile	Ser	Lys
Ala	Lys	Gly	Gln
Pro	Arg	Glu	Pro
Gln	Val	Tyr	Thr
Thr			
Thr	Ile	Ser	Lys
Ala	Lys	Gly	Gln
Pro	Arg	Glu	Pro
Gln	Val	Tyr	Thr
Thr			
Thr	Ile	Ser	Lys
Ala	Lys	Gly	Gln
Pro	Arg	Glu	Pro
Gln	Val	Tyr	Thr
Thr			
Thr	Ile	Ser	Lys
Ala	Lys	Gly	Gln
Pro	Arg	Glu	Pro
Gln	Val	Tyr	Thr
Thr			
Thr	Ile	Ser	Lys
Ala	Lys	Gly	Gln
Pro	Arg	Glu	Pro
Gln	Val	Tyr	Thr
Thr			
Thr	Ile	Ser	Lys
Ala	Lys	Gly	Gln
Pro	Arg	Glu	Pro
Gln	Val	Tyr	Thr
Thr			
Thr	Ile	Ser	Lys
Ala	Lys	Gly	Gln
Pro	Arg	Glu	Pro
Gln	Val	Tyr	Thr
Thr			
Thr	Ile	Ser	Lys
Ala	Lys	Gly	Gln
Pro	Arg	Glu	Pro
Gln	Val	Tyr	Thr
Thr			
Thr	Ile	Ser	Lys

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
225 230 235 240

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
245 250 255

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
260 265 270

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
275 280 285

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
290 295 300

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
305 310 315 320

Lys Ser Gly Gly Ser Gly Ser Gly Ser Gly Gly Ser Gly Ser Gly Ser
325 330 335

Asp Lys Glu Trp Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg Leu Leu
340 345 350

Asp Glu Leu Gly His Ala Glu Ala Ser Met Arg Val Ser Asp Leu Ile
355 360 365

Tyr Glu Phe Met Lys Gln Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu
370 375 380

Arg Leu Leu Glu Glu Val Glu Arg
385 390

<210> 76
<211> 321
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 76

Met Ala Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala
1 5 10 15

Leu Ala Asp Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys
20 25 30

Thr Leu Asp Gln Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp
35 40 45

Leu Ile Tyr Glu Phe Met Lys Gln Gly Asp Glu Arg Leu Leu Glu Glu
50 55 60

Ala Glu Arg Leu Leu Glu Glu Val Glu Arg Gly Gly Ser Gly Ser Gly
65 70 75 80

Gly Ser Gly Ser Gly Ser Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys
85 90 95

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
100 105 110

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
115 120 125

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
130 135 140

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
145 150 155 160

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
165 170 175

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
180 185 190

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
195 200 205

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr

210

215

220

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
 225 230 235 240

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
 245 250 255

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
 260 265 270

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
 275 280 285

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
 290 295 300

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
 305 310 315 320

Lys

<210> 77

<211> 321

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 77

Met Ala Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala
 1 5 10 15

Leu Ala Asp Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys
 20 25 30

Thr Leu Asp Gln Leu Gly His Ala Glu Ala Ser Met Asn Val Ser Asp
 35 40 45

Leu Ile Tyr Glu Phe Met Lys Gln Gly Asp Glu Arg Leu Leu Glu Glu

50

55

60

Ala Glu Arg Leu Leu Glu Glu Val Glu Arg Gly Gly Ser Gly Ser Gly
65 70 75 80

Gly Ser Gly Ser Gly Ser Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys
85 90 95

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
100 105 110

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
115 120 125

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
130 135 140

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
145 150 155 160

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
165 170 175

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
180 185 190

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
195 200 205

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
210 215 220

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
225 230 235 240

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
245 250 255

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
260 265 270

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
275 280 285

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
290 295 300

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
305 310 315 320

Lys

<210> 78
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 78

Met Ala Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala
1 5 10 15

Leu Ala Asn Asp Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr
20 25 30

Glu Ala Leu His Phe Ala Lys Asp Glu Glu Ile Gln Lys His Val Phe
35 40 45

Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln
50 55 60

Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu
65 70 75 80

Leu Ser Gly Gly Ser Gly Ser Gly Gly Ser Gly Ser Gly Ser Gly Gly
85 90 95

Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
100 105 110

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
115 120 125

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
130 135 140

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
145 150 155 160

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
165 170 175

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
180 185 190

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
195 200 205

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
210 215 220

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
225 230 235 240

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
245 250 255

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
260 265 270

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
275 280 285

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
290 295 300

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
305 310 315 320

Lys Ser Leu Ser Leu Ser Pro Gly Lys

<210> 79
 <211> 329
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 79

Met Ala Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala
 1 5 10 15

Leu Ala Asn Asp Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr
 20 25 30

Glu Ala Leu His Phe Ala Lys Asp Glu Glu Ile Gln Lys His Val Phe
 35 40 45

Gln Leu Phe Glu Asn Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln
 50 55 60

Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu
 65 70 75 80

Leu Ser Gly Gly Ser Gly Ser Gly Gly Ser Gly Ser Gly Ser Gly Gly
 85 90 95

Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 100 105 110

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 115 120 125

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 130 135 140

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
 145 150 155 160

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu

165

170

175

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 180 185 190

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 195 200 205

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
 210 215 220

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
 225 230 235 240

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 245 250 255

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 260 265 270

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 275 280 285

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 290 295 300

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
 305 310 315 320

Lys Ser Leu Ser Leu Ser Pro Gly Lys
 325

<210> 80

<211> 372

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 80

Met Ala Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala

1	5	10	15
Leu Ala Asp Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys	20	25	30
Thr Leu Asp Gln Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp	35	40	45
Leu Ile Tyr Glu Phe Met Lys Gln Gly Asp Glu Arg Leu Leu Glu Glu	50	55	60
Ala Glu Arg Leu Leu Glu Glu Val Glu Arg Ala Gly Ser Gly Gly Ser	65	70	75
Gly Gly Ser Gly Gly Ser Pro Val Pro Ser Thr Pro Pro Thr Pro Ser	85	90	95
Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Gly Gly Ser Gly Asn Ser	100	105	110
Ser Gly Ser Gly Gly Ser Pro Val Pro Ser Thr Pro Pro Thr Pro Ser	115	120	125
Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Ala Ser Glu Pro Lys Ser	130	135	140
Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu	145	150	155
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu	165	170	175
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser	180	185	190
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu	195	200	205
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr	210	215	220

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
225 230 235 240

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
245 250 255

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
260 265 270

Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
275 280 285

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
290 295 300

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
305 310 315 320

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
325 330 335

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
340 345 350

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
355 360 365

Ser Pro Gly Lys
370

<210> 81
<211> 380
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 81

Met Ala Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala
1 5 10 15

Leu Ala Asn Asp Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr
20 25 30

Glu Ala Leu His Phe Ala Lys Asp Glu Glu Ile Gln Lys His Val Phe
35 40 45

Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln
50 55 60

Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu
65 70 75 80

Leu Ser Ala Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Pro Val
85 90 95

Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser
100 105 110

Pro Ser Gly Gly Ser Gly Asn Ser Ser Gly Ser Gly Gly Ser Pro Val
115 120 125

Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser
130 135 140

Pro Ser Ala Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro
145 150 155 160

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
165 170 175

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
180 185 190

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
195 200 205

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
210 215 220

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr

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

<210> 82
 <211> 336
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 82

Met	Ala	Arg	Ala	Trp	Ile	Phe	Phe	Leu	Leu	Cys	Leu	Ala	Gly	Arg	Ala
1				5				10					15		

Leu Ala Asp Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys

20

25

30

Thr Leu Asp Gln Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp
 35 40 45

Leu Ile Tyr Glu Phe Met Lys Gln Gly Asp Glu Arg Leu Leu Glu Glu
 50 55 60

Ala Glu Arg Leu Leu Glu Glu Val Glu Arg Gly Gly Gly Ser Gly Gly
 65 70 75 80

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
 85 90 95

Gly Ser Gly Gly Gly Gly Ser Gly Glu Pro Lys Ser Ser Asp Lys Thr
 100 105 110

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
 115 120 125

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
 130 135 140

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
 145 150 155 160

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
 165 170 175

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
 180 185 190

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
 195 200 205

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
 210 215 220

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
 225 230 235 240

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
245 250 255

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
260 265 270

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
275 280 285

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
290 295 300

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
305 310 315 320

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330 335

<210> 83
<211> 344
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 83

Met Ala Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala
1 5 10 15

Leu Ala Asn Asp Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr
20 25 30

Glu Ala Leu His Phe Ala Lys Asp Glu Glu Ile Gln Lys His Val Phe
35 40 45

Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln
50 55 60

Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu
65 70 75 80

Leu Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
85 90 95

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
100 105 110

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
115 120 125

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
130 135 140

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
145 150 155 160

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
165 170 175

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
180 185 190

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
195 200 205

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
210 215 220

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
225 230 235 240

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
245 250 255

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
260 265 270

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
275 280 285

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

290

295

300

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
 305 310 315 320

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

Ser Leu Ser Leu Ser Pro Gly Lys
 340

<210> 84

<211> 321

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 84

Met Ala Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala
 1 5 10 15

Leu Ala Asp Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys
 20 25 30

Thr Leu Glu Gln Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp
 35 40 45

Leu Ile Tyr Glu Phe Met Lys Gln Gly Asp Glu Arg Leu Leu Glu Glu
 50 55 60

Ala Glu Arg Leu Leu Glu Glu Val Glu Arg Gly Gly Ser Gly Ser Gly
 65 70 75 80

Gly Ser Gly Ser Gly Ser Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys
 85 90 95

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
 100 105 110

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser

115

120

125

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
 130 135 140

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
 145 150 155 160

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
 165 170 175

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
 180 185 190

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
 195 200 205

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
 210 215 220

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
 225 230 235 240

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
 245 250 255

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
 260 265 270

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
 275 280 285

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
 290 295 300

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
 305 310 315 320

Lys

<210> 85
<211> 321
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 85

Met Ala Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala
1 5 10 15

Leu Ala Asp Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys
20 25 30

Thr Leu Glu Gln Leu Gly His Ala Glu Ala Ser Met Asn Val Ser Asp
35 40 45

Leu Ile Tyr Glu Phe Met Lys Gln Gly Asp Glu Arg Leu Leu Glu Glu
50 55 60

Ala Glu Arg Leu Leu Glu Glu Val Glu Arg Gly Gly Ser Gly Ser Gly
65 70 75 80

Gly Ser Gly Ser Gly Ser Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys
85 90 95

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
100 105 110

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
115 120 125

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
130 135 140

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
145 150 155 160

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
165 170 175

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
180 185 190

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
195 200 205

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
210 215 220

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
225 230 235 240

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
245 250 255

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
260 265 270

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
275 280 285

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
290 295 300

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
305 310 315 320

Lys

<210> 86

<211> 372

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 86

Met Ala Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala
1 5 10 15

Leu Ala Asp Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys
20 25 30

Thr Leu Glu Gln Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp
35 40 45

Leu Ile Tyr Glu Phe Met Lys Gln Gly Asp Glu Arg Leu Leu Glu Glu
50 55 60

Ala Glu Arg Leu Leu Glu Glu Val Glu Arg Ala Gly Ser Gly Gly Ser
65 70 75 80

Gly Gly Ser Gly Gly Ser Pro Val Pro Ser Thr Pro Pro Thr Pro Ser
85 90 95

Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Gly Gly Ser Gly Asn Ser
100 105 110

Ser Gly Ser Gly Gly Ser Pro Val Pro Ser Thr Pro Pro Thr Pro Ser
115 120 125

Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Ala Ser Glu Pro Lys Ser
130 135 140

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
145 150 155 160

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
165 170 175

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
180 185 190

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
195 200 205

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
210 215 220

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn

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

<210> 87
 <211> 336
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 87

Met Ala Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala
 1 5 10 15

Leu Ala Asp Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys

20

25

30

Thr Leu Glu Gln Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp
 35 40 45

Leu Ile Tyr Glu Phe Met Lys Gln Gly Asp Glu Arg Leu Leu Glu Glu
 50 55 60

Ala Glu Arg Leu Leu Glu Glu Val Glu Arg Gly Gly Gly Ser Gly Gly
 65 70 75 80

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
 85 90 95

Gly Ser Gly Gly Gly Gly Ser Gly Glu Pro Lys Ser Ser Asp Lys Thr
 100 105 110

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
 115 120 125

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
 130 135 140

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
 145 150 155 160

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
 165 170 175

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
 180 185 190

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
 195 200 205

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
 210 215 220

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
 225 230 235 240

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
245 250 255

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
260 265 270

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
275 280 285

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
290 295 300

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
305 310 315 320

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330 335

<210> 88

<211> 321

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 88

Met Ala Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala
1 5 10 15

Leu Ala Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys
20 25 30

Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp
35 40 45

Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu
50 55 60

Ala Glu Arg Leu Leu Glu Glu Val Lys Arg Gly Gly Ser Gly Ser Gly
65 70 75 80

Gly Ser Gly Ser Gly Ser Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys
85 90 95

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
100 105 110

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
115 120 125

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
130 135 140

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
145 150 155 160

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
165 170 175

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
180 185 190

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
195 200 205

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
210 215 220

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
225 230 235 240

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
245 250 255

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
260 265 270

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
275 280 285

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu

290

295

300

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
 305 310 315 320

Lys

<210> 89

<211> 321

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 89

Met Ala Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala
 1 5 10 15

Leu Ala Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys
 20 25 30

Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp
 35 40 45

Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu
 50 55 60

Ala Glu Arg Leu Leu Glu Glu Val Lys Arg Gly Gly Ser Gly Ser Gly
 65 70 75 80

Gly Ser Gly Ser Gly Ser Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys
 85 90 95

Thr His Thr Cys Pro Arg Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
 100 105 110

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
 115 120 125

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp

130

135

140

Pro Glu Val Gln Phe Lys Trp Tyr Val Asp Gly Val Glu Val His Asn
 145 150 155 160

Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val
 165 170 175

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
 180 185 190

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
 195 200 205

Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
 210 215 220

Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
 225 230 235 240

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
 245 250 255

Ser Ser Gly Gln Pro Glu Asn Asn Tyr Asn Thr Thr Pro Pro Met Leu
 260 265 270

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
 275 280 285

Ser Arg Trp Gln Gln Gly Asn Ile Phe Ser Cys Ser Val Met His Glu
 290 295 300

Ala Leu His Asn Arg Phe Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
 305 310 315 320

Lys

<210> 90

<211> 395

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 90

Met Ala Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala
1 5 10 15

Leu Ala Asn Ile Asp Glu Leu Leu Met Gln Val Thr Asp Leu Ile Tyr
20 25 30

Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Ala Phe
35 40 45

Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Lys Gln
50 55 60

Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Ile
65 70 75 80

Leu Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Asp Lys Glu Asn
85 90 95

Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly
100 105 110

His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met
115 120 125

Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu
130 135 140

Glu Val Lys Arg Gly Gly Ser Gly Ser Gly Gly Ser Gly Ser Gly Ser
145 150 155 160

Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
165 170 175

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
180 185 190

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
195 200 205

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
210 215 220

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
225 230 235 240

Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
245 250 255

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
260 265 270

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
275 280 285

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
290 295 300

Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
305 310 315 320

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
325 330 335

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
340 345 350

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
355 360 365

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
370 375 380

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
385 390 395

<211> 480
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 91

Met Ala Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala
1 5 10 15

Leu Ala Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser
20 25 30

Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu
35 40 45

Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu
50 55 60

Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala
65 70 75 80

Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Gly
85 90 95

Ser Gly Gly Gly Ser Gly Gly Asn Ile Asp Glu Leu Leu Met Gln Val
100 105 110

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

Gln Lys His Ala Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys
130 135 140

Asn Lys Asp Lys Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu
145 150 155 160

Leu Leu Glu Arg Ile Leu Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
165 170 175

Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu

180

185

190

Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu
 195 200 205

Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala
 210 215 220

Glu Arg Leu Leu Glu Glu Val Lys Arg Gly Gly Ser Gly Ser Gly Gly
 225 230 235 240

Ser Gly Ser Gly Ser Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys Thr
 245 250 255

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
 260 265 270

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
 275 280 285

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
 290 295 300

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
 305 310 315 320

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
 325 330 335

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
 340 345 350

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
 355 360 365

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
 370 375 380

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
 385 390 395 400

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
405 410 415

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
420 425 430

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
435 440 445

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
450 455 460

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465 470 475 480

<210> 92
<211> 480
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 92

Met Ala Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala
1 5 10 15

Leu Ala Asn Ile Asp Glu Leu Leu Met Gln Val Thr Asp Leu Ile Tyr
20 25 30

Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Ala Phe
35 40 45

Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Lys Gln
50 55 60

Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Ile
65 70 75 80

Leu Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Glu Leu Glu Glu
85 90 95

Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu
100 105 110

Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn
115 120 125

Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu
130 135 140

Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His
145 150 155 160

Leu Glu Glu Leu Ala Arg Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly
165 170 175

Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu
180 185 190

Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu
195 200 205

Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala
210 215 220

Glu Arg Leu Leu Glu Glu Val Lys Arg Gly Gly Ser Gly Ser Gly Gly
225 230 235 240

Ser Gly Ser Gly Ser Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys Thr
245 250 255

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
260 265 270

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
275 280 285

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
290 295 300

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala

305		310		315		320
Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val	325	330	335			
Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr	340	345	350			
Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr	355	360	365			
Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu	370	375	380			
Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys	385	390	395	400		
Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser	405	410	415			
Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp	420	425	430			
Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser	435	440	445			
Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala	450	455	460			
Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys	465	470	475	480		

<210> 93
 <211> 395
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 93

Met Ala Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala

1	5	10	15
Leu	Ala	Asn	Ile
	20	25	30
Leu	Ala	Leu	His
	35	40	45
Gln	Leu	Phe	Glu
	50	55	60
Lys	Leu	Glu	Lys
	65	70	75
Leu	Ser	Gly	Gly
		85	90
Val	Leu	Gln	Lys
		100	105
His	Ala	Glu	Ala
		115	120
Lys	Thr	Lys	Asp
		130	135
Glu	Val	Lys	Arg
		145	150
Gly	Gly	Ser	Gly
		155	160
Gly	Gly	Ser	Glu
		165	170
Cys	Pro	Ala	Pro
		180	185
Pro	Lys	Pro	Lys
		195	200
Cys	Val	Val	Val
		210	215

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
225 230 235 240

Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
245 250 255

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
260 265 270

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
275 280 285

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
290 295 300

Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
305 310 315 320

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
325 330 335

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
340 345 350

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
355 360 365

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
370 375 380

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
385 390 395

<210> 94
<211> 395
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 94

Met Ala Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala
1 5 10 15

Leu Ala Asn Ile Asp Glu Leu Leu Met Gln Val Thr Asp Leu Ile Tyr
20 25 30

Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Ala Phe
35 40 45

Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Lys Gln
50 55 60

Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Ile
65 70 75 80

Leu Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Asp Lys Glu Asn
85 90 95

Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly
100 105 110

His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met
115 120 125

Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu
130 135 140

Glu Val Lys Arg Gly Gly Ser Gly Ser Gly Gly Ser Gly Ser Gly Ser
145 150 155 160

Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
165 170 175

Cys Pro Ala Pro Glu Leu Leu Arg Gly Pro Ser Val Phe Leu Phe Pro
180 185 190

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
195 200 205

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn

210

215

220

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
 225 230 235 240

Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
 245 250 255

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
 260 265 270

Asn Lys Ala Arg Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
 275 280 285

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
 290 295 300

Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
 305 310 315 320

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
 325 330 335

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
 340 345 350

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
 355 360 365

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
 370 375 380

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 385 390 395

<210> 95

<211> 395

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 95

Met Ala Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala
1 5 10 15

Leu Ala Asn Ile Asp Glu Leu Leu Met Gln Val Thr Asp Leu Ile Tyr
20 25 30

Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Ala Phe
35 40 45

Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Lys Gln
50 55 60

Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Ile
65 70 75 80

Leu Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Asp Lys Glu Asn
85 90 95

Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly
100 105 110

His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met
115 120 125

Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu
130 135 140

Glu Val Lys Arg Gly Gly Ser Gly Ser Gly Gly Ser Gly Ser Gly Ser
145 150 155 160

Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
165 170 175

Cys Pro Ala Pro Glu Leu Leu Ala Gly Pro Ser Val Phe Leu Phe Pro
180 185 190

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
195 200 205

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
210 215 220

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
225 230 235 240

Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
245 250 255

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
260 265 270

Asn Lys Ala Leu Pro Leu Pro Glu Glu Lys Thr Ile Ser Lys Ala Lys
275 280 285

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
290 295 300

Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
305 310 315 320

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
325 330 335

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
340 345 350

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
355 360 365

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
370 375 380

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
385 390 395

<210> 96

<211> 395

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 96

Met Ala Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala
1 5 10 15

Leu Ala Asn Ile Asp Glu Leu Leu Met Gln Val Thr Asp Leu Ile Tyr
20 25 30

Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Ala Phe
35 40 45

Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Lys Gln
50 55 60

Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Ile
65 70 75 80

Leu Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Asp Lys Glu Asn
85 90 95

Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly
100 105 110

His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met
115 120 125

Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu
130 135 140

Glu Val Lys Arg Gly Gly Ser Gly Ser Gly Gly Ser Gly Ser Gly Ser
145 150 155 160

Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
165 170 175

Cys Pro Ala Pro Glu Leu Leu Ala Gly Pro Ser Val Phe Leu Phe Pro
180 185 190

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr

195

200

205

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
 210 215 220

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
 225 230 235 240

Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
 245 250 255

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
 260 265 270

Asn Lys Ala Leu Pro Leu Pro Glu Glu Lys Thr Ile Ser Lys Ala Lys
 275 280 285

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
 290 295 300

Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
 305 310 315 320

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
 325 330 335

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
 340 345 350

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
 355 360 365

Asn Val Phe Ser Cys Ser Val Leu His Glu Ala Leu His Ser His Tyr
 370 375 380

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 385 390 395

<210> 97
 <211> 75
 <212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 97

Ala Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Pro Val Pro Ser
1 5 10 15

Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser
20 25 30

Pro Val Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr
35 40 45

Pro Ser Pro Ser Pro Val Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser
50 55 60

Thr Pro Pro Thr Pro Ser Pro Ser Ala Ser Gly
65 70 75

<210> 98

<211> 65

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 98

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Pro Val Pro Ser Thr
1 5 10 15

Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Gly
20 25 30

Gly Ser Gly Asn Ser Ser Gly Ser Gly Gly Ser Pro Val Pro Ser Thr
35 40 45

Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Ala
50 55 60

Ser

65

<210> 99
<211> 85
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 99

Gly Gly Ser Ser Gly Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr
1 5 10 15

Ile Thr Leu Glu Val Glu Pro Ser Asp Thr Ile Glu Asn Val Lys Ala
20 25 30

Lys Ile Gln Asp Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile
35 40 45

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

Ile Gln Lys Glu Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly Gly
65 70 75 80

Gly Gly Ser Ser Gly
85

<210> 100
<211> 75
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 100

Glu Leu Glu Glu Arg Val Met His Leu Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Gln Arg Ala
20 25 30

Thr His Phe Asp Lys Trp Ala Asn Glu Ala Ile Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
65 70 75

<210> 101
<211> 75
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 101

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
65 70 75

<210> 102
<211> 56
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 102

Asp Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg Leu Leu

1	5	10	15												
Asp	Glu	Leu	Gly	His	Ala	Glu	Ala	Ser	Met	Arg	Val	Ser	Asp	Leu	Ile
		20						25					30		
Tyr	Glu	Phe	Met	Lys	Lys	Gly	Asp	Glu	Arg	Leu	Leu	Glu	Glu	Ala	Glu
		35					40					45			
Arg	Leu	Leu	Glu	Glu	Val	Glu	Arg								
	50					55									

<210> 103
 <211> 56
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 103

Asp	Lys	Glu	Lys	Ile	Leu	Gln	Lys	Ile	Tyr	Glu	Ile	Met	Arg	Leu	Leu
1				5					10					15	

Asp	Glu	Leu	Gly	His	Ala	Glu	Ala	Ser	Met	Arg	Val	Ser	Asp	Leu	Ile
		20						25					30		

Tyr	Glu	Phe	Met	Lys	Lys	Gly	Asp	Glu	Arg	Leu	Leu	Glu	Glu	Ala	Glu
		35					40					45			

Arg	Leu	Leu	Glu	Glu	Val	Glu	Arg
	50					55	

<210> 104
 <211> 56
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 104

Asp	Lys	Glu	Trp	Ile	Leu	Gln	Lys	Ile	Tyr	Glu	Ile	Met	Lys	Leu	Leu
1				5					10					15	

Asp Glu Leu Gly His Ala Glu Ala Ser Met Arg Val Ser Asp Leu Ile
20 25 30

Tyr Glu Phe Met Lys Lys Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu
35 40 45

Arg Leu Leu Glu Glu Val Glu Arg
50 55

<210> 105
<211> 56
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 105

Asp Lys Glu Trp Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg Thr Leu
1 5 10 15

Asp Glu Leu Gly His Ala Glu Ala Ser Met Arg Val Ser Asp Leu Ile
20 25 30

Tyr Glu Phe Met Lys Lys Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu
35 40 45

Arg Leu Leu Glu Glu Val Glu Arg
50 55

<210> 106
<211> 56
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 106

Asp Lys Glu Trp Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg Leu Leu
1 5 10 15

Asp Gln Leu Gly His Ala Glu Ala Ser Met Arg Val Ser Asp Leu Ile

30

Arg Leu Leu Glu Glu Val Glu Arg
50 55

<220>
<223> Synthetic

Asp Lys Glu Trp Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg Leu Leu
1 5 10 15

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

Tyr Glu Phe Met Lys Lys Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu
35 40 45

Arg Leu Leu Glu Glu Val Glu Arg
50 55

<220>
<223> Synthetic

Asp Lys Glu Trp Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg Leu Leu
1 5 10 15

Asp Glu Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile
20 25 30

Tyr Glu Phe Met Lys Lys Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu
35 40 45

Arg Leu Leu Glu Glu Val Glu Arg
50 55

<210> 109
<211> 56
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 109

Asp Lys Glu Trp Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg Leu Leu
1 5 10 15

Asp Glu Leu Gly His Ala Glu Ala Ser Met Tyr Val Ser Asp Leu Ile
20 25 30

Tyr Glu Phe Met Lys Lys Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu
35 40 45

Arg Leu Leu Glu Glu Val Glu Arg
50 55

<210> 110
<211> 56
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 110

Asp Lys Glu Trp Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg Leu Leu
1 5 10 15

Glu Glu Leu Gly His Ala Glu Ala Ser Met Arg Val Ser Asp Leu Ile
20 25 30

Tyr Glu Phe Met Lys Lys Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu

35

40

45

Arg Leu Leu Glu Glu Val Glu Arg
50 55

<210> 111
<211> 56
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 111

Asp Lys Glu Trp Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg Leu Leu
1 5 10 15

Arg Glu Leu Gly His Ala Glu Ala Ser Met Arg Val Ser Asp Leu Ile
20 25 30

Tyr Glu Phe Met Lys Lys Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu
35 40 45

Arg Leu Leu Glu Glu Val Glu Arg
50 55

<210> 112
<211> 56
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 112

Asp Lys Glu Trp Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg Leu Leu
1 5 10 15

Asp Glu Leu Gly His Ala Glu Ala Ser Met Arg Val Ser Asp Leu Ile
20 25 30

Tyr Glu Phe Met Lys Lys Gly Asp Glu Asn Leu Leu Glu Glu Ala Glu
35 40 45

Arg Leu Leu Glu Glu Val Glu Arg
50 55

<210> 113
<211> 56
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 113

Asp Lys Glu Trp Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg Leu Leu
1 5 10 15

Asp Glu Leu Gly His Ala Glu Ala Ser Met Arg Val Ser Asp Leu Ile
20 25 30

Tyr Glu Phe Met Lys Lys Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu
35 40 45

Gln Leu Leu Glu Glu Val Glu Arg
50 55

<210> 114
<211> 56
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 114

Asp Lys Glu Trp Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg Leu Leu
1 5 10 15

Asp Glu Leu Gly His Ala Glu Ala Ser Met Arg Val Ser Asp Leu Ile
20 25 30

Tyr Glu Phe Met Lys Lys Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu
35 40 45

Arg Leu Leu Gln Glu Val Glu Arg

50

55

<210> 115
 <211> 56
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 115

Asp Lys Glu Trp Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg Leu Leu
 1 5 10 15

Asp Glu Leu Gly His Ala Glu Ala Ser Met Arg Val Ser Asp Leu Leu
 20 25 30

Tyr Glu Phe Met Lys Lys Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu
 35 40 45

Arg Leu Leu Glu Glu Val Glu Arg
 50 55

<210> 116
 <211> 56
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 116

Asp Lys Glu Trp Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg Leu Leu
 1 5 10 15

Asp Glu Leu Gly His Ala Glu Ala Ser Met Arg Ala Ser Asp Leu Ile
 20 25 30

Tyr Glu Phe Met Lys Lys Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu
 35 40 45

Arg Leu Leu Glu Glu Val Glu Arg
 50 55

<210> 117
<211> 56
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 117

Asp Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu
1 5 10 15

Glu Gln Leu Gly His Ala Glu Ala Ser Met Tyr Val Ser Asp Leu Ile
20 25 30

Tyr Glu Phe Met Lys Gln Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu
35 40 45

Arg Leu Leu Glu Glu Val Glu Arg
50 55

<210> 118
<211> 56
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 118

Asp Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu
1 5 10 15

Glu Gln Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile
20 25 30

Tyr Glu Phe Met Lys Gln Gly Asp Glu Asn Leu Leu Glu Glu Ala Glu
35 40 45

Arg Leu Leu Glu Glu Val Glu Arg
50 55

<210> 119

<211> 56
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 119

Asp Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu
1 5 10 15

Glu Gln Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile
20 25 30

Tyr Glu Phe Met Lys Gln Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu
35 40 45

Gln Leu Leu Glu Glu Val Glu Arg
50 55

<210> 120
<211> 56
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 120

Asp Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu
1 5 10 15

Glu Gln Leu Gly His Ala Glu Ala Ser Met Tyr Val Ser Asp Leu Ile
20 25 30

Tyr Glu Phe Met Lys Gln Gly Asp Glu Asn Leu Leu Glu Glu Ala Glu
35 40 45

Gln Leu Leu Glu Glu Val Glu Arg
50 55

<210> 121
<211> 56
<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 121

Asp Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu
1 5 10 15

Glu Gln Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile
20 25 30

Tyr Glu Phe Met Lys Gln Gly Asp Glu Asn Leu Leu Glu Glu Ala Glu
35 40 45

Gln Leu Leu Glu Glu Val Glu Arg
50 55

<210> 122

<211> 56

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 122

Asp Arg Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu
1 5 10 15

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

Tyr Glu Phe Met Gln Asp Lys Asp Glu Arg Leu Leu Glu Glu Ala Glu
35 40 45

Arg Leu Leu Glu Glu Val Lys Arg
50 55

<210> 123

<211> 56

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 123

Asp Arg Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu
1 5 10 15

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

Tyr Glu Phe Met Lys Thr Lys Asp Lys Arg Leu Leu Glu Glu Ala Glu
35 40 45

Arg Leu Leu Glu Glu Val Lys Arg
50 55

<210> 124

<211> 56

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 124

Asp Arg Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu
1 5 10 15

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

Tyr Glu Phe Met Gln Asp Lys Asp Lys Arg Leu Leu Glu Glu Ala Glu
35 40 45

Arg Leu Leu Glu Glu Val Gln Arg
50 55

<210> 125

<211> 56

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 125

Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu
1 5 10 15

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

Tyr Glu Phe Met Lys Thr Lys Asp Glu Arg Leu Leu Glu Glu Ala Glu
35 40 45

Arg Leu Leu Glu Glu Val Lys Arg
50 55

<210> 126

<211> 56

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 126

Asp Arg Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu
1 5 10 15

Glu Lys Leu Gly His Ala Glu Ala Ser Met Gln Ala Ser Asp Leu Ile
20 25 30

Tyr Glu Phe Met Lys Thr Lys Asp Glu Arg Leu Leu Glu Glu Ala Glu
35 40 45

Arg Leu Leu Glu Glu Val Gln Arg
50 55

<210> 127

<211> 56

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 127

Asp Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu
1 5 10 15

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

Tyr Glu Phe Met Gln Thr Lys Asp Glu Arg Leu Leu Glu Glu Ala Glu
35 40 45

Arg Leu Leu Glu Glu Val Lys Arg
50 55

<210> 128
<211> 56
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 128

Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu
1 5 10 15

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

Tyr Glu Phe Met Gln Thr Lys Asp Lys Arg Leu Leu Glu Glu Ala Glu
35 40 45

Arg Leu Leu Glu Glu Val Gln Arg
50 55

<210> 129
<211> 56
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 129

Asp Arg Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu

1	5	10	15												
Glu	Lys	Leu	Gly	His	Ala	Glu	Ala	Ser	Met	Gln	Val	Ser	Asp	Leu	Ile
		20						25					30		
Tyr	Glu	Phe	Met	Gln	Asp	Lys	Asp	Glu	Asn	Leu	Leu	Glu	Glu	Ala	Glu
		35					40					45			
Arg	Leu	Leu	Glu	Glu	Val	Lys	Arg								
	50					55									

<210> 130
 <211> 56
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 130

Asp	Arg	Glu	Asn	Ile	Leu	Gln	Lys	Ile	Tyr	Glu	Ile	Met	Lys	Glu	Leu
1				5					10					15	
Arg	Gln	Leu	Gly	His	Ala	Glu	Ala	Ser	Met	Gln	Val	Ser	Asp	Leu	Ile
			20					25					30		
Tyr	Glu	Phe	Met	Lys	Thr	Lys	Asp	Lys	Asn	Leu	Leu	Glu	Glu	Ala	Glu
		35					40					45			
Arg	Leu	Leu	Glu	Glu	Val	Lys	Arg								
	50					55									

<210> 131
 <211> 56
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 131

Asp	Arg	Glu	Asn	Ile	Leu	Gln	Lys	Ile	Tyr	Glu	Ile	Met	Lys	Thr	Leu
1				5					10					15	

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

Tyr Glu Phe Met Gln Asp Lys Asp Lys Asn Leu Leu Glu Glu Ala Glu
35 40 45

Arg Leu Leu Glu Glu Val Gln Arg
50 55

<210> 132
<211> 56
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 132

Asp Arg Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu
1 5 10 15

Glu Lys Leu Gly His Ala Glu Ala Ser Met Gln Ala Ser Asp Leu Ile
20 25 30

Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu
35 40 45

Arg Leu Leu Glu Glu Val Gln Arg
50 55

<210> 133
<211> 56
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 133

Asp Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu
1 5 10 15

Arg Ala Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile

20

25

30

Tyr Glu Phe Met Gln Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu
35 40 45

Arg Leu Leu Glu Glu Val Lys Arg
50 55

<210>	134
<211>	56
<212>	PRT
<213>	Artificial Sequence

<220>
<223> Synthetic

<400> 134

Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu
1 5 10 15

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

Tyr Glu Phe Met Gln Thr Lys Asp Lys Asn Leu Leu Glu Glu Ala Glu
35 40 45

Arg Leu Leu Glu Glu Val Gln Arg
50 55

<210>	135
<211>	56
<212>	PRT
<213>	Artificial Sequence

<220>
<223> Synthetic

<400> 135

Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu
1 5 10 15

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

Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu
35 40 45

Arg Leu Leu Glu Glu Val Lys Arg
50 55

<210> 136
<211> 56
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 136

Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu
1 5 10 15

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

Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu
35 40 45

Arg Leu Leu Glu Glu Val Thr Arg
50 55

<210> 137
<211> 64
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 137

Asn Asp Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Ile Lys Lys Arg Val Phe Gln Leu
20 25 30

Phe Glu Leu Ala Asp Lys Ala Tyr Lys Asn Asn Asp Arg Gln Lys Leu

35

40

45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
 50 55 60

<210> 138
 <211> 64
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 138

Asn Asp Asp Glu Leu His Met Thr Met Thr Asp Leu Val Tyr Glu Ala
 1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Ile Lys Lys Arg Val Phe Gln Leu
 20 25 30

Phe Glu Leu Ala Asp Lys Ala Tyr Lys Asn Asn Asp Arg Gln Lys Leu
 35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
 50 55 60

<210> 139
 <211> 64
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 139

Asn Asp Asp Glu Leu His Met Leu Met Thr Asp Leu Val Tyr Glu Ala
 1 5 10 15

Leu His Lys Ala Lys Asp Glu Glu Ile Lys Lys Arg Val Phe Gln Leu
 20 25 30

Phe Glu Leu Ala Asp Lys Ala Tyr Lys Asn Asn Asp Arg Gln Lys Leu
 35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

<210> 140
<211> 64
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 140

Asn Asp Asp Glu Leu His Met Leu Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Ile Ala Lys Asp Glu Glu Ile Lys Lys Arg Val Phe Gln Leu
20 25 30

Phe Glu Leu Ala Asp Lys Ala Tyr Lys Asn Asn Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

<210> 141
<211> 64
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 141

Asn Asp Asp Glu Leu His Met Leu Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Lys Lys Arg Val Phe Gln Leu
20 25 30

Phe Glu Leu Ala Asp Lys Ala Tyr Lys Asn Asn Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser

50

55

60

<210> 142
 <211> 64
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 142

Asn Asp Asp Glu Leu His Met Leu Met Thr Asp Leu Val Tyr Glu Ala
 1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Met Lys Lys Arg Val Phe Gln Leu
 20 25 30

Phe Glu Leu Ala Asp Lys Ala Tyr Lys Asn Asn Asp Arg Gln Lys Leu
 35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
 50 55 60

<210> 143
 <211> 64
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 143

Asn Asp Asp Glu Leu His Met Leu Met Thr Asp Leu Val Tyr Glu Ala
 1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Ile Gln Lys Arg Val Phe Gln Leu
 20 25 30

Phe Glu Leu Ala Asp Lys Ala Tyr Lys Asn Asn Asp Arg Gln Lys Leu
 35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
 50 55 60

<210> 144
<211> 64
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 144

Asn Asp Asp Glu Leu His Met Leu Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Ile Lys Lys His Val Phe Gln Leu
20 25 30

Phe Glu Leu Ala Asp Lys Ala Tyr Lys Asn Asn Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

<210> 145
<211> 64
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 145

Asn Asp Asp Glu Leu His Met Leu Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Ile Lys Lys Arg Val Phe Gln Leu
20 25 30

Phe Glu Lys Ala Asp Lys Ala Tyr Lys Asn Asn Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

<210> 146

<211> 64
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 146

Asn Asp Asp Glu Leu His Met Leu Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Ile Lys Lys Arg Val Phe Gln Leu
20 25 30

Phe Glu Leu Ala Thr Lys Ala Tyr Lys Asn Asn Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

<210> 147
<211> 64
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 147

Asn Asp Asp Glu Leu His Met Leu Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Ile Lys Lys Arg Val Phe Gln Leu
20 25 30

Phe Glu Leu Ala Asp Lys Ala Arg Lys Asn Asn Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

<210> 148
<211> 64
<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 148

Asn Asp Asp Glu Leu His Met Leu Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Ile Lys Lys Arg Val Phe Gln Leu
20 25 30

Phe Glu Leu Ala Asp Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

<210> 149

<211> 64

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 149

Asn Asp Asp Glu Leu His Met Leu Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Ile Lys Lys Arg Val Phe Gln Leu
20 25 30

Phe Gly Leu Ala Asp Lys Ala Tyr Lys Asn Asn Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

<210> 150

<211> 64

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 150

Asn Asp Asp Glu Leu His Met Leu Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Ile Lys Lys Arg Val Phe Gln Leu
20 25 30

Phe Tyr Leu Ala Asp Lys Ala Tyr Lys Asn Asn Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

<210> 151

<211> 64

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 151

Asn Asp Asp Glu Leu His Met Leu Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Ile Lys Lys Arg Val Phe Gln Leu
20 25 30

Phe Thr Leu Ala Asp Lys Ala Tyr Lys Asn Asn Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

<210> 152

<211> 64

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 152

Asn Asp Asp Glu Leu His Met Leu Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Ile Lys Lys Arg Val Phe Gln Leu
20 25 30

Phe Glu Leu Ala Asp Lys Ala Tyr Lys Asn Asn Asp Arg Gln Lys Leu
35 40 45

Lys Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

<210> 153

<211> 64

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 153

Asn Asp Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Ile Gln Lys His Val Phe Gln Leu
20 25 30

Phe Gly Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

<210> 154

<211> 64

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 154

Asn Asp Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Ile Gln Lys His Val Phe Gln Leu
20 25 30

Phe Tyr Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

<210> 155
<211> 64
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 155

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu
20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

<210> 156
<211> 64
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 156

Asn Asp Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala

1	5	10	15
Leu His Phe	Ala Lys Thr Glu Glu	Phe Gln Lys His Val	Phe Gln Leu
	20	25	30
Phe Glu Lys	Ala Thr Lys Ala Tyr	Lys Asn Lys Asp Arg	Gln Lys Leu
	35	40	45
Glu Lys Val	Val Glu Glu Leu Lys	Glu Leu Leu Glu	Arg Leu Leu Ser
	50	55	60

<210> 157
 <211> 64
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 157

Asn Asp Asp	Glu Leu His Met	Gln Met Thr Asp	Leu Val Tyr Glu	Ala
1	5	10	15	
Leu His Phe	Ala Lys Asp Glu Glu	Phe Gln Lys His Val	Phe Gln Leu	
	20	25	30	
Phe Glu Lys	Ala Arg Lys Ala Tyr	Lys Asn Lys Asp Arg	Gln Lys Leu	
	35	40	45	
Glu Lys Val	Val Glu Glu Leu Lys	Glu Leu Leu Glu	Arg Leu Leu Ser	
	50	55	60	

<210> 158
 <211> 64
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 158

Asn Asp Asp	Glu Leu His Met	Gln Met Thr Asp	Leu Val Trp	Glu Ala
1	5	10	15	

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu
20 25 30

Phe Glu Lys Ala Arg Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

<210> 159
<211> 64
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 159

Asn Asp Asp Glu Leu His Met Gln Met Thr Asp Leu Val Trp Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu
20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

<210> 160
<211> 64
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 160

Asn Glu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Trp Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu

30

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

<220>
<223> Synthetic

Asn Asp Asp Glu Leu His Met Gln Met Thr Asp Leu Val Trp Glu Ala
1 5 10 15

Leu His Phe Ala Lys Thr Glu Glu Phe Gln Lys His Val Phe Gln Leu
20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

<220>
<223> Synthetic

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Thr Glu Glu Phe Gln Lys His Val Phe Gln Leu
20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

<210> 163
<211> 64
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 163

Asn Ile Asp Glu Leu Leu Met Gln Val Thr Asp Leu Ile Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Ala Phe Gln Leu
20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Lys Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Ile Leu Ser
50 55 60

<210> 164
<211> 75
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 164

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys

35

40

45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Ala Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Thr
65 70 75

<210> 165
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 165

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
1 5 10 15

Gly Ser Gly Gly
20

<210> 166
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 166

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
1 5 10 15

<210> 167
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 167

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly

1

5

10

<210> 168
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 168

Gly Gly Gly Gly Ser Gly Gly Gly Gly
1 5

<210> 169
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 169

Gly Gly Gly Ser Gly Gly Gly
1 5

<210> 170
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 170

Gly Gly Ser Gly Gly
1 5

<210> 171
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 171

Gly Gly Ser Gly Ser Ser Gly
1 5

<210> 172
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 172

Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro
1 5 10 15

Ala Pro Ser Ala Pro Ala Gly Gly
20

<210> 173
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 173

Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala Gly Gly
1 5 10 15

<210> 174
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 174

Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Gly Gly
1 5 10

<210> 175
<211> 11
<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 175

Gly Gly Ala Ser Pro Ala Ala Pro Ala Gly Gly
1 5 10

<210> 176

<211> 29

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 176

Gly Gly Ser Ser Gly Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr
1 5 10 15

Pro Pro Thr Pro Ser Pro Ser Pro Gly Gly Ser Ser Gly
20 25

<210> 177

<211> 25

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 177

Gly Gly Ser Ser Ala Gly Ser Pro Thr Ser Thr Gly Thr Ser Ser Ala
1 5 10 15

Thr Pro Ser Gly Ser Gly Thr Gly Gly
20 25

<210> 178

<211> 25

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 178

Gly Gly Ser Ser Gly Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu
1 5 10 15

Ala Ala Ala Lys Gly Ser Ser Gly Gly
20 25

<210> 179

<211> 27

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 179

Gly Tyr Ile Pro Glu Ala Pro Arg Asp Gly Gln Ala Tyr Val Arg Lys
1 5 10 15

Asp Gly Glu Trp Val Leu Leu Ser Thr Phe Leu
20 25

<210> 180

<211> 85

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 180

Glu Glu Ala Glu Leu Ala Tyr Leu Leu Gly Glu Leu Ala Tyr Lys Leu
1 5 10 15

Gly Glu Tyr Arg Ile Ala Ile Arg Ala Tyr Arg Ile Ala Leu Lys Arg
20 25 30

Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr
35 40 45

Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu
50 55 60

Glu Leu Asp Pro Asn Asn Ala Glu Ala Lys Gln Asn Leu Gly Asn Ala
65 70 75 80

Lys Gln Lys Gln Gly
85

<210> 181
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 181

Glu Glu Ala Glu Leu Ala Tyr Leu Leu Gly Glu Leu Ala Tyr Lys Leu
1 5 10 15

Gly Glu Tyr Arg Ile Ala Ile Arg Ala Tyr Arg Ile Ala Leu Lys Arg
20 25 30

Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr
35 40 45

Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu
50 55 60

Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala
65 70 75 80

Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys
85 90 95

Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Lys Gln Asn Leu Gly
100 105 110

Asn Ala Lys Gln Lys Gln Gly
115

<210> 182
<211> 76
<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 182

Gly Ser Glu Tyr Glu Ile Arg Lys Ala Leu Glu Glu Leu Lys Ala Ser
1 5 10 15

Thr Ala Glu Leu Lys Arg Ala Thr Ala Ser Leu Arg Ala Ser Thr Glu
20 25 30

Glu Leu Lys Lys Asn Pro Ser Glu Asp Ala Leu Val Glu Asn Asn Arg
35 40 45

Leu Ile Val Glu His Asn Ala Ile Ile Val Glu Asn Asn Arg Ile Ile
50 55 60

Ala Ala Val Leu Glu Leu Ile Val Arg Ala Ile Lys
65 70 75

<210> 183

<211> 33

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 183

Arg Met Lys Gln Ile Glu Asp Lys Ile Glu Glu Ile Leu Ser Lys Ile
1 5 10 15

Tyr His Ile Glu Asn Glu Ile Ala Arg Ile Lys Lys Leu Ile Gly Glu
20 25 30

Arg

<210> 184

<211> 76

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 184

Gly Ser Glu Tyr Glu Ile Arg Lys Ala Leu Glu Glu Leu Lys Ala Ser
1 5 10 15

Thr Ala Glu Leu Lys Arg Ser Thr Ala Ser Leu Arg Ala Ser Thr Glu
20 25 30

Glu Leu Lys Lys Asn Pro Ser Glu Asp Ala Leu Val Glu Asn Asn Arg
35 40 45

Leu Ile Val Glu Asn Asn Ala Ile Ile Val Glu Asn Asn Arg Ile Ile
50 55 60

Ala Ala Val Leu Glu Leu Ile Val Arg Ala Ile Lys
65 70 75

<210> 185

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 185

Asn Leu Ala Glu Lys Met Tyr Lys Ala Gly Asn Ala Met Tyr Arg Lys
1 5 10 15

Gly Gln Tyr Thr Ile Ala Ile Ile Ala Tyr Thr Leu Ala Leu Leu Lys
20 25 30

Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Ala Tyr
35 40 45

Lys Lys Gly Glu Tyr Asp Glu Ala Ile Glu Ala Tyr Gln Lys Ala Leu
50 55 60

Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala
65 70 75 80

Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys
85 90 95

Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Lys Gln Asn Leu Gly
100 105 110

Asn Ala Lys Gln Lys Gln Gly
115

<210> 186
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 186

Gly Glu Ile Ala Lys Ser Leu Lys Glu Ile Ala Lys Ser Leu Lys Glu
1 5 10 15

Ile Ala Trp Ser Leu Lys Glu Ile Ala Lys Ser Leu Lys Gly
20 25 30

<210> 187
<211> 63
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 187

Ser Glu Ala Leu Glu Glu Leu Glu Lys Ala Leu Arg Glu Leu Lys Lys
1 5 10 15

Ser Thr Asp Glu Leu Glu Arg Ser Thr Glu Glu Leu Glu Lys Asn Pro
20 25 30

Ser Glu Asp Ala Leu Val Glu Asn Asn Arg Leu Ile Val Glu Asn Asn
35 40 45

Lys Ile Ile Val Glu Val Leu Arg Ile Ile Ala Lys Val Leu Lys

50

55

60

<210> 188
 <211> 57
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 188

Ser Pro Glu Leu Glu Lys Ala Leu Arg Glu Leu Lys Lys Ser Thr Asp
 1 5 10 15

Glu Leu Glu Arg Ser Thr Glu Glu Leu Glu Lys Asn Gly Ser Pro Glu
 20 25 30

Ala Leu Val Glu Asn Asn Arg Leu Ile Val Glu Asn Asn Lys Ile Ile
 35 40 45

Val Glu Val Leu Arg Ile Ile Ala Lys
 50 55

<210> 189
 <211> 50
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 189

Ser Glu Lys Ala Leu Arg Glu Leu Lys Lys Ser Thr Asp Glu Leu Glu
 1 5 10 15

Arg Ser Thr Glu Glu Leu Glu Lys Asn Gly Ser Pro Glu Ala Leu Val
 20 25 30

Glu Asn Asn Arg Leu Ile Val Glu Asn Asn Lys Ile Ile Val Glu Val
 35 40 45

Leu Arg
 50

<210> 190
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 190
atgctgcaat cgtgctacaa 20

<210> 191
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 191
gactgccgcc tctgctc 17

<210> 192
<211> 11
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 192
aacattgcca a 11

<210> 193
<211> 234
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 193

Met Glu Lys Lys Ile Gly Ser Ser Ala Trp Ser His Pro Gln Phe Glu
1 5 10 15

Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His
20 25 30

Pro Gln Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Gly Gly Gly Asp
35 40 45

Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu Asp
50 55 60

Gln Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr
65 70 75 80

Glu Phe Met Lys Gln Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg
85 90 95

Leu Leu Glu Glu Val Glu Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly
100 105 110

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
130 135 140

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
145 150 155 160

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
165 170 175

Gly Ser Asp Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys
180 185 190

Thr Leu Asp Gln Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp
195 200 205

Leu Ile Tyr Glu Phe Met Lys Gln Gly Asp Glu Arg Leu Leu Glu Glu
210 215 220

Ala Glu Arg Leu Leu Glu Glu Val Glu Arg
225 230

<210> 194

<211> 234
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 194

Met Glu Lys Lys Ile Gly Ser Ser Ala Trp Ser His Pro Gln Phe Glu
1 5 10 15

Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His
20 25 30

Pro Gln Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Gly Gly Gly Asp
35 40 45

Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu Asp
50 55 60

Gln Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr
65 70 75 80

Glu Phe Met Lys Gln Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg
85 90 95

Leu Leu Glu Glu Val Glu Arg Ala Gly Ser Gly Gly Ser Gly Gly Ser
100 105 110

Gly Gly Ser Pro Val Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr
115 120 125

Pro Pro Thr Pro Ser Pro Ser Pro Val Pro Ser Thr Pro Pro Thr Pro
130 135 140

Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Pro Val Pro Ser Thr
145 150 155 160

Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Ala
165 170 175

Ser Gly Asp Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys

180

185

190

Thr Leu Asp Gln Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp
 195 200 205

Leu Ile Tyr Glu Phe Met Lys Gln Gly Asp Glu Arg Leu Leu Glu Glu
 210 215 220

Ala Glu Arg Leu Leu Glu Glu Val Glu Arg
 225 230

<210> 195
 <211> 250
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 195

Met Glu Lys Lys Ile Gly Ser Ser Ala Trp Ser His Pro Gln Phe Glu
 1 5 10 15

Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His
 20 25 30

Pro Gln Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Gly Gly Gly Asn
 35 40 45

Asp Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu
 50 55 60

His Phe Ala Lys Asp Glu Glu Ile Gln Lys His Val Phe Gln Leu Phe
 65 70 75 80

Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu
 85 90 95

Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly
 100 105 110

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly

115

120

125

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
 130 135 140

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 145 150 155 160

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 165 170 175

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asn Asp Asp Glu Leu His
 180 185 190

Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp
 195 200 205

Glu Glu Ile Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys
 210 215 220

Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu
 225 230 235 240

Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
 245 250

<210> 196
 <211> 250
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 196

Met Glu Lys Lys Ile Gly Ser Ser Ala Trp Ser His Pro Gln Phe Glu
 1 5 10 15

Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His
 20 25 30

Pro Gln Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Gly Gly Gly Asn

35

40

45

Asp Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu
 50 55 60

His Phe Ala Lys Asp Glu Glu Ile Gln Lys His Val Phe Gln Leu Phe
 65 70 75 80

Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu
 85 90 95

Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Ala
 100 105 110

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Pro Val Pro Ser Thr
 115 120 125

Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Pro
 130 135 140

Val Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro
 145 150 155 160

Ser Pro Ser Pro Val Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr
 165 170 175

Pro Pro Thr Pro Ser Pro Ser Ala Ser Gly Asn Asp Asp Glu Leu His
 180 185 190

Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp
 195 200 205

Glu Glu Ile Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys
 210 215 220

Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu
 225 230 235 240

Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
 245 250

<210> 197
<211> 242
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 197

Met Glu Lys Lys Ile Gly Ser Ser Ala Trp Ser His Pro Gln Phe Glu
1 5 10 15

Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His
20 25 30

Pro Gln Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Gly Gly Gly Asp
35 40 45

Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu Asp
50 55 60

Gln Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr
65 70 75 80

Glu Phe Met Lys Gln Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg
85 90 95

Leu Leu Glu Glu Val Glu Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly
100 105 110

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
130 135 140

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
145 150 155 160

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
165 170 175

Gly Ser Asn Asp Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr
180 185 190

Glu Ala Leu His Phe Ala Lys Asp Glu Glu Ile Gln Lys His Val Phe
195 200 205

Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln
210 215 220

Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu
225 230 235 240

Leu Ser

<210> 198
<211> 242
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 198

Met Glu Lys Lys Ile Gly Ser Ser Ala Trp Ser His Pro Gln Phe Glu
1 5 10 15

Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His
20 25 30

Pro Gln Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Gly Gly Asn
35 40 45

Asp Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu
50 55 60

His Phe Ala Lys Asp Glu Glu Ile Gln Lys His Val Phe Gln Leu Phe
65 70 75 80

Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu
85 90 95

Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly
100 105 110

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
130 135 140

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
145 150 155 160

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
165 170 175

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Lys Glu Asn Ile Leu
180 185 190

Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu Asp Gln Leu Gly His Ala
195 200 205

Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Gln
210 215 220

Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val
225 230 235 240

Glu Arg

<210> 199
<211> 242
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 199

Met Glu Lys Lys Ile Gly Ser Ser Ala Trp Ser His Pro Gln Phe Glu
1 5 10 15

Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His
20 25 30

Pro Gln Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Gly Gly Gly Asp
35 40 45

Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu Asp
50 55 60

Gln Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr
65 70 75 80

Glu Phe Met Lys Gln Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg
85 90 95

Leu Leu Glu Glu Val Glu Arg Ala Gly Ser Gly Gly Ser Gly Gly Ser
100 105 110

Gly Gly Ser Pro Val Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr
115 120 125

Pro Pro Thr Pro Ser Pro Ser Pro Val Pro Ser Thr Pro Pro Thr Pro
130 135 140

Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Pro Val Pro Ser Thr
145 150 155 160

Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Ala
165 170 175

Ser Gly Asn Asp Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr
180 185 190

Glu Ala Leu His Phe Ala Lys Asp Glu Glu Ile Gln Lys His Val Phe
195 200 205

Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln
210 215 220

Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu

225

230

235

240

Leu Ser

<210> 200

<211> 242

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 200

Met Glu Lys Lys Ile Gly Ser Ser Ala Trp Ser His Pro Gln Phe Glu
 1 5 10 15

Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His
 20 25 30

Pro Gln Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Gly Gly Gly Asn
 35 40 45

Asp Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu
 50 55 60

His Phe Ala Lys Asp Glu Glu Ile Gln Lys His Val Phe Gln Leu Phe
 65 70 75 80

Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu
 85 90 95

Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Ala
 100 105 110

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Pro Val Pro Ser Thr
 115 120 125

Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Pro
 130 135 140

Val Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro

65		70		75		80									
Gly	Asp	Glu	Arg	Leu	Leu	Glu	Glu	Ala	Glu	Arg	Leu	Leu	Glu	Glu	Val
				85					90				95		
Glu	Arg	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly
			100					105					110		
Ser	Asp	Lys	Glu	Trp	Ile	Leu	Gln	Lys	Ile	Tyr	Glu	Ile	Met	Arg	Leu
		115					120					125			
Leu	Asp	Glu	Leu	Gly	His	Ala	Glu	Ala	Ser	Met	Arg	Val	Ser	Asp	Leu
	130					135					140				
Ile	Tyr	Glu	Phe	Met	Lys	Lys	Gly	Asp	Glu	Arg	Leu	Leu	Glu	Glu	Ala
145					150					155					160
Glu	Arg	Leu	Leu	Glu	Glu	Val	Glu	Arg							
				165											

<210> 202
 <211> 185
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 202

Met	Glu	Lys	Lys	Ile	Ser	Ala	Trp	Ser	His	Pro	Gln	Phe	Glu	Lys	Gly
1				5					10					15	
Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Ser	Ala	Trp	Ser	His	Pro	Gln
			20					25					30		
Phe	Glu	Lys	Gly	Gly	Ser	Gly	Ser	Ser	Gly	Asn	Asp	Asp	Glu	Leu	His
		35					40				45				
Met	Leu	Met	Thr	Asp	Leu	Val	Tyr	Glu	Ala	Leu	His	Phe	Ala	Lys	Asp
	50					55					60				
Glu	Glu	Ile	Lys	Lys	Arg	Val	Phe	Gln	Leu	Phe	Glu	Leu	Ala	Asp	Lys

65		70		75		80									
Ala	Tyr	Lys	Asn	Asn	Asp	Arg	Gln	Lys	Leu	Glu	Lys	Val	Val	Glu	Glu
			85						90					95	
Leu	Lys	Glu	Leu	Leu	Glu	Arg	Leu	Leu	Ser	Gly	Gly	Gly	Gly	Ser	Gly
			100					105					110		
Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Asn	Asp	Asp	Glu	Leu	His	Met
		115					120					125			
Leu	Met	Thr	Asp	Leu	Val	Tyr	Glu	Ala	Leu	His	Phe	Ala	Lys	Asp	Glu
	130					135					140				
Glu	Ile	Lys	Lys	Arg	Val	Phe	Gln	Leu	Phe	Glu	Leu	Ala	Asp	Lys	Ala
145					150					155					160
Tyr	Lys	Asn	Asn	Asp	Arg	Gln	Lys	Leu	Glu	Lys	Val	Val	Glu	Glu	Leu
				165					170					175	
Lys	Glu	Leu	Leu	Glu	Arg	Leu	Leu	Ser							
			180					185							
<210>	203														
<211>	174														
<212>	PRT														
<213>	Artificial Sequence														
<220>															
<223>	Synthetic														
<400>	203														
Met	Glu	Lys	Lys	Ile	Ser	Ala	Trp	Ser	His	Pro	Gln	Phe	Glu	Lys	Gly
1				5					10					15	
Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Ser	Ala	Trp	Ser	His	Pro	Gln
			20					25					30		
Phe	Glu	Lys	Gly	Gly	Ser	Gly	Ser	Ser	Gly	Asp	Lys	Glu	Trp	Ile	Leu
		35					40					45			
Gln	Lys	Ile	Tyr	Glu	Ile	Met	Arg	Leu	Leu	Asp	Glu	Leu	Gly	His	Ala

50

55

60

Glu Ala Ser Met Arg Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Lys
65 70 75 80

Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val
85 90 95

Glu Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
100 105 110

Ser Gly Gly Gly Gly Ser Asp Lys Glu Trp Ile Leu Gln Lys Ile Tyr
115 120 125

Glu Ile Met Arg Leu Leu Asp Glu Leu Gly His Ala Glu Ala Ser Met
130 135 140

Arg Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Lys Gly Asp Glu Arg
145 150 155 160

Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Glu Arg
165 170

<210> 204
<211> 190
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 204

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Asn Asp Asp Glu Leu His
35 40 45

Met Leu Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp

50

55

60

Glu Glu Ile Lys Lys Arg Val Phe Gln Leu Phe Glu Leu Ala Asp Lys
65 70 75 80

Ala Tyr Lys Asn Asn Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu
85 90 95

Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly Gly Gly Ser Gly
100 105 110

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asn Asp
115 120 125

Asp Glu Leu His Met Leu Met Thr Asp Leu Val Tyr Glu Ala Leu His
130 135 140

Phe Ala Lys Asp Glu Glu Ile Lys Lys Arg Val Phe Gln Leu Phe Glu
145 150 155 160

Leu Ala Asp Lys Ala Tyr Lys Asn Asn Asp Arg Gln Lys Leu Glu Lys
165 170 175

Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
180 185 190

<210> 205
<211> 230
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 205

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Ser Gly Ser Ser Gly Asp Lys Glu Trp Ile Leu Gln Lys Ile Tyr
20 25 30

Glu Ile Met Arg Leu Leu Asp Glu Leu Gly His Ala Glu Ala Ser Met

35

40

45

Arg Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Lys Gly Asp Glu Arg
 50 55 60

Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Glu Arg Gly Ser
 65 70 75 80

Ser Gly Ser Gly Ser Ser Gly Ser Gly Ser Ser Gly Ser Gly Ser Ser
 85 90 95

Gly Ser Asp Lys Glu Trp Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg
 100 105 110

Leu Leu Asp Glu Leu Gly His Ala Glu Ala Ser Met Arg Val Ser Asp
 115 120 125

Leu Ile Tyr Glu Phe Met Lys Lys Gly Asp Glu Arg Leu Leu Glu Glu
 130 135 140

Ala Glu Arg Leu Leu Glu Glu Val Glu Arg Gly Ser Ser Ser Gly Gly
 145 150 155 160

Ser Ser Ser Gly Gly Ser Ser Ser Gly Gly Ser Ser Ser Gly Asp Lys
 165 170 175

Glu Trp Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg Leu Leu Asp Glu
 180 185 190

Leu Gly His Ala Glu Ala Ser Met Arg Val Ser Asp Leu Ile Tyr Glu
 195 200 205

Phe Met Lys Lys Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu
 210 215 220

Leu Glu Glu Val Glu Arg
 225 230

<210> 206

<211> 254

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 206

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Ser Gly Ser Ser Gly Asn Asp Asp Glu Leu His Met Leu Met Thr
20 25 30

Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Ile Lys
35 40 45

Lys Arg Val Phe Gln Leu Phe Glu Leu Ala Asp Lys Ala Tyr Lys Asn
50 55 60

Asn Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu
65 70 75 80

Leu Glu Arg Leu Leu Ser Gly Ser Ser Gly Ser Gly Ser Ser Gly Ser
85 90 95

Gly Ser Ser Gly Ser Gly Ser Ser Gly Ser Asn Asp Asp Glu Leu His
100 105 110

Met Leu Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp
115 120 125

Glu Glu Ile Lys Lys Arg Val Phe Gln Leu Phe Glu Leu Ala Asp Lys
130 135 140

Ala Tyr Lys Asn Asn Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu
145 150 155 160

Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Ser Ser Ser Gly Gly
165 170 175

Ser Ser Ser Gly Gly Ser Ser Ser Gly Gly Ser Ser Ser Gly Asn Asp
180 185 190

Asp Glu Leu His Met Leu Met Thr Asp Leu Val Tyr Glu Ala Leu His
195 200 205

Phe Ala Lys Asp Glu Glu Ile Lys Lys Arg Val Phe Gln Leu Phe Glu
210 215 220

Leu Ala Asp Lys Ala Tyr Lys Asn Asn Asp Arg Gln Lys Leu Glu Lys
225 230 235 240

Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
245 250

<210> 207
<211> 174
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 207

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Asp Lys Glu Trp Ile Leu
35 40 45

Gln Lys Ile Tyr Glu Ile Met Arg Leu Leu Asp Glu Leu Gly His Ala
50 55 60

Glu Ala Ser Met Arg Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Lys
65 70 75 80

Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val
85 90 95

Glu Arg Gly Ser Ala Gly Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr
100 105 110

Gly Thr Ser Thr Ser Gly Asp Lys Glu Trp Ile Leu Gln Lys Ile Tyr
115 120 125

Glu Ile Met Arg Leu Leu Asp Glu Leu Gly His Ala Glu Ala Ser Met
130 135 140

Arg Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Lys Gly Asp Glu Arg
145 150 155 160

Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Glu Arg
165 170

<210> 208
<211> 250
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 208

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Asp Lys Glu Trp Ile Leu
35 40 45

Gln Lys Ile Tyr Glu Ile Met Arg Leu Leu Asp Glu Leu Gly His Ala
50 55 60

Glu Ala Ser Met Arg Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Lys
65 70 75 80

Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val
85 90 95

Glu Arg Gly Ser Ala Gly Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr
100 105 110

Gly Thr Ser Gly Ser Gly Asp Lys Glu Trp Ile Leu Gln Lys Ile Tyr
115 120 125

Glu Ile Met Arg Leu Leu Asp Glu Leu Gly His Ala Glu Ala Ser Met
130 135 140

Arg Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Lys Gly Asp Glu Arg
145 150 155 160

Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Glu Arg Gly Ser
165 170 175

Ala Gly Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Gly Thr Ser Gly
180 185 190

Ser Gly Asp Lys Glu Trp Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg
195 200 205

Leu Leu Asp Glu Leu Gly His Ala Glu Ala Ser Met Arg Val Ser Asp
210 215 220

Leu Ile Tyr Glu Phe Met Lys Lys Gly Asp Glu Arg Leu Leu Glu Glu
225 230 235 240

Ala Glu Arg Leu Leu Glu Glu Val Glu Arg
245 250

<210> 209
<211> 190
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 209

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Asn Asp Asp Glu Leu His
35 40 45

Met Leu Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp
50 55 60

Glu Glu Ile Lys Lys Arg Val Phe Gln Leu Phe Glu Leu Ala Asp Lys
65 70 75 80

Ala Tyr Lys Asn Asn Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu
85 90 95

Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Ser Ala Gly Gly Ser
100 105 110

Pro Ala Gly Ser Pro Thr Ser Thr Gly Thr Ser Gly Ser Gly Asn Asp
115 120 125

Asp Glu Leu His Met Leu Met Thr Asp Leu Val Tyr Glu Ala Leu His
130 135 140

Phe Ala Lys Asp Glu Glu Ile Lys Lys Arg Val Phe Gln Leu Phe Glu
145 150 155 160

Leu Ala Asp Lys Ala Tyr Lys Asn Asn Asp Arg Gln Lys Leu Glu Lys
165 170 175

Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
180 185 190

<210> 210
<211> 274
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 210

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Asn Asp Asp Glu Leu His
35 40 45

Met Leu Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp
50 55 60

Glu Glu Ile Lys Lys Arg Val Phe Gln Leu Phe Glu Leu Ala Asp Lys
65 70 75 80

Ala Tyr Lys Asn Asn Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu
85 90 95

Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Ser Ala Gly Gly Ser
100 105 110

Pro Ala Gly Ser Pro Thr Ser Thr Gly Thr Ser Gly Ser Gly Asn Asp
115 120 125

Asp Glu Leu His Met Leu Met Thr Asp Leu Val Tyr Glu Ala Leu His
130 135 140

Phe Ala Lys Asp Glu Glu Ile Lys Lys Arg Val Phe Gln Leu Phe Glu
145 150 155 160

Leu Ala Asp Lys Ala Tyr Lys Asn Asn Asp Arg Gln Lys Leu Glu Lys
165 170 175

Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Ser
180 185 190

Ala Gly Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Gly Thr Ser Gly
195 200 205

Ser Gly Asn Asp Asp Glu Leu His Met Leu Met Thr Asp Leu Val Tyr
210 215 220

Glu Ala Leu His Phe Ala Lys Asp Glu Glu Ile Lys Lys Arg Val Phe

225		230		235		240									
Gln	Leu	Phe	Glu	Leu	Ala	Asp	Lys	Ala	Tyr	Lys	Asn	Asn	Asp	Arg	Gln
			245					250						255	

Lys	Leu	Glu	Lys	Val	Val	Glu	Glu	Leu	Lys	Glu	Leu	Leu	Glu	Arg	Leu
			260					265					270		

Leu Ser

<210> 211
 <211> 233
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 211

Met	Glu	Lys	Lys	Ile	Ser	Ser	Gly	Asp	Lys	Glu	Trp	Ile	Leu	Gln	Lys
1				5					10					15	

Ile	Tyr	Glu	Ile	Met	Arg	Leu	Leu	Asp	Glu	Leu	Gly	His	Ala	Glu	Ala
			20					25					30		

Ser	Met	Arg	Val	Ser	Asp	Leu	Ile	Tyr	Glu	Phe	Met	Lys	Lys	Gly	Asp
		35					40					45			

Glu	Arg	Leu	Leu	Glu	Glu	Ala	Glu	Arg	Leu	Leu	Glu	Glu	Val	Glu	Arg
	50					55					60				

Gly	Ser	Ser	Gly	Ser	Gly	Ser	Ser	Gly	Ser	Gly	Ser	Ser	Gly	Ser	Gly
65					70					75					80

Ser	Ser	Gly	Ser	Asp	Lys	Glu	Trp	Ile	Leu	Gln	Lys	Ile	Tyr	Glu	Ile
				85					90					95	

Met	Arg	Leu	Leu	Asp	Glu	Leu	Gly	His	Ala	Glu	Ala	Ser	Met	Arg	Val
			100					105					110		

Ser Asp Leu Ile Tyr Glu Phe Met Lys Lys Gly Asp Glu Arg Leu Leu

115

120

125

Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Glu Arg Gly Ser Ser Ser
 130 135 140

Gly Gly Ser Ser Ser Gly Gly Ser Ser Ser Gly Gly Ser Ser Ser Gly
 145 150 155 160

Asp Lys Glu Trp Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg Leu Leu
 165 170 175

Asp Glu Leu Gly His Ala Glu Ala Ser Met Arg Val Ser Asp Leu Ile
 180 185 190

Tyr Glu Phe Met Lys Lys Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu
 195 200 205

Arg Leu Leu Glu Glu Val Glu Arg Gly Gly Ser Gly Ser Ser Gly Ser
 210 215 220

Ala Trp Ser His Pro Gln Phe Glu Lys
 225 230

<210> 212
 <211> 257
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 212

Met Glu Lys Lys Ile Ser Ser Gly Asn Asp Asp Glu Leu His Met Leu
 1 5 10 15

Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu
 20 25 30

Ile Lys Lys Arg Val Phe Gln Leu Phe Glu Leu Ala Asp Lys Ala Tyr
 35 40 45

Lys Asn Asn Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys

50

55

60

Glu Leu Leu Glu Arg Leu Leu Ser Gly Ser Ser Gly Ser Gly Ser Ser
65 70 75 80

Gly Ser Gly Ser Ser Gly Ser Gly Ser Ser Gly Ser Asn Asp Asp Glu
85 90 95

Leu His Met Leu Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala
100 105 110

Lys Asp Glu Glu Ile Lys Lys Arg Val Phe Gln Leu Phe Glu Leu Ala
115 120 125

Asp Lys Ala Tyr Lys Asn Asn Asp Arg Gln Lys Leu Glu Lys Val Val
130 135 140

Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Ser Ser Ser
145 150 155 160

Gly Gly Ser Ser Ser Gly Gly Ser Ser Ser Gly Gly Ser Ser Ser Gly
165 170 175

Asn Asp Asp Glu Leu His Met Leu Met Thr Asp Leu Val Tyr Glu Ala
180 185 190

Leu His Phe Ala Lys Asp Glu Glu Ile Lys Lys Arg Val Phe Gln Leu
195 200 205

Phe Glu Leu Ala Asp Lys Ala Tyr Lys Asn Asn Asp Arg Gln Lys Leu
210 215 220

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
225 230 235 240

Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe Glu
245 250 255

Lys

<210> 213
<211> 260
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 213

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Asp Lys Glu Trp Ile Leu
35 40 45

Gln Lys Ile Tyr Glu Ile Met Arg Leu Leu Asp Glu Leu Gly His Ala
50 55 60

Glu Ala Ser Met Arg Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Lys
65 70 75 80

Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val
85 90 95

Glu Arg Gly Gly Ser Ser Ala Gly Ser Pro Thr Ser Thr Gly Thr Ser
100 105 110

Ser Ala Thr Pro Ser Gly Ser Gly Thr Gly Gly Asp Lys Glu Trp Ile
115 120 125

Leu Gln Lys Ile Tyr Glu Ile Met Arg Leu Leu Asp Glu Leu Gly His
130 135 140

Ala Glu Ala Ser Met Arg Val Ser Asp Leu Ile Tyr Glu Phe Met Lys
145 150 155 160

Lys Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu
165 170 175

Val Glu Arg Gly Gly Ser Ser Ala Gly Ser Pro Thr Ser Thr Gly Thr
180 185 190

Ser Ser Ala Thr Pro Ser Gly Ser Gly Thr Gly Gly Asp Lys Glu Trp
195 200 205

Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg Leu Leu Asp Glu Leu Gly
210 215 220

His Ala Glu Ala Ser Met Arg Val Ser Asp Leu Ile Tyr Glu Phe Met
225 230 235 240

Lys Lys Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu
245 250 255

Glu Val Glu Arg
260

<210> 214
<211> 284
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 214

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Asn Asp Asp Glu Leu His
35 40 45

Met Leu Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp
50 55 60

Glu Glu Ile Lys Lys Arg Val Phe Gln Leu Phe Glu Leu Ala Asp Lys
65 70 75 80

Ala Tyr Lys Asn Asn Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu
85 90 95

Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly Ser Ser Ala Gly
100 105 110

Ser Pro Thr Ser Thr Gly Thr Ser Ser Ala Thr Pro Ser Gly Ser Gly
115 120 125

Thr Gly Gly Asn Asp Asp Glu Leu His Met Leu Met Thr Asp Leu Val
130 135 140

Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Ile Lys Lys Arg Val
145 150 155 160

Phe Gln Leu Phe Glu Leu Ala Asp Lys Ala Tyr Lys Asn Asn Asp Arg
165 170 175

Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg
180 185 190

Leu Leu Ser Gly Gly Ser Ser Ala Gly Ser Pro Thr Ser Thr Gly Thr
195 200 205

Ser Ser Ala Thr Pro Ser Gly Ser Gly Thr Gly Gly Asn Asp Asp Glu
210 215 220

Leu His Met Leu Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala
225 230 235 240

Lys Asp Glu Glu Ile Lys Lys Arg Val Phe Gln Leu Phe Glu Leu Ala
245 250 255

Asp Lys Ala Tyr Lys Asn Asn Asp Arg Gln Lys Leu Glu Lys Val Val
260 265 270

Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
275 280

<210> 215

<211> 179
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 215

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Asp Lys Glu Asn Ile Leu
35 40 45

Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu Glu Gln Leu Gly His Ala
50 55 60

Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Gln
65 70 75 80

Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val
85 90 95

Glu Arg Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser
100 105 110

Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Asp Lys Glu Asn Ile
115 120 125

Leu Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu Glu Gln Leu Gly His
130 135 140

Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys
145 150 155 160

Gln Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu
165 170 175

Val Glu Arg

<210> 216
<211> 179
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 216

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Asp Lys Glu Asn Ile Leu
35 40 45

Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu Glu Gln Leu Gly His Ala
50 55 60

Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Gln
65 70 75 80

Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val
85 90 95

Glu Arg Gly Gly Ser Ser Ala Gly Ser Pro Thr Ser Thr Gly Thr Ser
100 105 110

Ser Ala Thr Pro Ser Gly Ser Gly Thr Gly Gly Asp Lys Glu Asn Ile
115 120 125

Leu Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu Glu Gln Leu Gly His
130 135 140

Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys
145 150 155 160

Gln Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu

165

170

175

Val Glu Arg

<210> 217

<211> 179

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 217

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
 1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
 20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Asp Lys Glu Asn Ile Leu
 35 40 45

Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu Glu Gln Leu Gly His Ala
 50 55 60

Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Gln
 65 70 75 80

Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val
 85 90 95

Glu Arg Gly Gly Ser Ser Gly Glu Ala Ala Ala Lys Glu Ala Ala Ala
 100 105 110

Lys Glu Ala Ala Ala Lys Gly Ser Ser Gly Gly Asp Lys Glu Asn Ile
 115 120 125

Leu Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu Glu Gln Leu Gly His
 130 135 140

Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys

130

135

140

Gln Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr
 145 150 155 160

Glu Phe Met Lys Gln Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg
 165 170 175

Leu Leu Glu Glu Val Glu Arg
 180

<210> 219
 <211> 239
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 219

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
 1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
 20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Asp Lys Glu Asn Ile Leu
 35 40 45

Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu Glu Gln Leu Gly His Ala
 50 55 60

Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Gln
 65 70 75 80

Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val
 85 90 95

Glu Arg Gly Gly Ser Ser Gly Gln Ile Phe Val Lys Thr Leu Thr Gly
 100 105 110

Lys Thr Ile Thr Leu Glu Val Glu Pro Ser Asp Thr Ile Glu Asn Val

115

120

125

Lys Ala Lys Ile Gln Asp Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg
 130 135 140

Leu Ile Phe Ala Gly Lys Gln Leu Glu Asp Gly Arg Thr Leu Ser Asp
 145 150 155 160

Tyr Asn Ile Gln Lys Glu Ser Thr Leu His Leu Val Leu Arg Leu Arg
 165 170 175

Gly Gly Gly Gly Ser Ser Gly Asp Lys Glu Asn Ile Leu Gln Lys Ile
 180 185 190

Tyr Glu Ile Met Lys Thr Leu Glu Gln Leu Gly His Ala Glu Ala Ser
 195 200 205

Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Gln Gly Asp Glu
 210 215 220

Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Glu Arg
 225 230 235

<210> 220
 <211> 260
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 220

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
 1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
 20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Asp Lys Glu Asn Ile Leu
 35 40 45

Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu Glu Gln Leu Gly His Ala

50

55

60

Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Gln
65 70 75 80

Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val
85 90 95

Glu Arg Gly Gly Ser Ser Ala Gly Ser Pro Thr Ser Thr Gly Thr Ser
100 105 110

Ser Ala Thr Pro Ser Gly Ser Gly Thr Gly Gly Asp Lys Glu Asn Ile
115 120 125

Leu Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu Glu Gln Leu Gly His
130 135 140

Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys
145 150 155 160

Gln Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu
165 170 175

Val Glu Arg Gly Gly Ser Ser Ala Gly Ser Pro Thr Ser Thr Gly Thr
180 185 190

Ser Ser Ala Thr Pro Ser Gly Ser Gly Thr Gly Gly Asp Lys Glu Asn
195 200 205

Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu Glu Gln Leu Gly
210 215 220

His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met
225 230 235 240

Lys Gln Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu
245 250 255

Glu Val Glu Arg
260

<210> 221
<211> 260
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 221

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Asp Lys Glu Asn Ile Leu
35 40 45

Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu Glu Gln Leu Gly His Ala
50 55 60

Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Gln
65 70 75 80

Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val
85 90 95

Glu Arg Gly Gly Ser Ser Gly Glu Ala Ala Ala Lys Glu Ala Ala Ala
100 105 110

Lys Glu Ala Ala Ala Lys Gly Ser Ser Gly Gly Asp Lys Glu Asn Ile
115 120 125

Leu Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu Glu Gln Leu Gly His
130 135 140

Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys
145 150 155 160

Gln Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu
165 170 175

Val Glu Arg Gly Gly Ser Ser Gly Glu Ala Ala Ala Lys Glu Ala Ala
180 185 190

Ala Lys Glu Ala Ala Ala Lys Gly Ser Ser Gly Gly Asp Lys Glu Asn
195 200 205

Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu Glu Gln Leu Gly
210 215 220

His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met
225 230 235 240

Lys Gln Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu
245 250 255

Glu Val Glu Arg
260

<210> 222
<211> 268
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 222

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Asp Lys Glu Asn Ile Leu
35 40 45

Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu Glu Gln Leu Gly His Ala
50 55 60

Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Gln
65 70 75 80

Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val
85 90 95

Glu Arg Gly Gly Ser Ser Gly Pro Ser Thr Pro Pro Thr Pro Ser Pro
100 105 110

Ser Thr Pro Pro Thr Pro Ser Pro Ser Pro Gly Gly Ser Ser Gly Asp
115 120 125

Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu Glu
130 135 140

Gln Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr
145 150 155 160

Glu Phe Met Lys Gln Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg
165 170 175

Leu Leu Glu Glu Val Glu Arg Gly Gly Ser Ser Gly Pro Ser Thr Pro
180 185 190

Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Pro Gly
195 200 205

Gly Ser Ser Gly Asp Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile
210 215 220

Met Lys Thr Leu Glu Gln Leu Gly His Ala Glu Ala Ser Met Gln Val
225 230 235 240

Ser Asp Leu Ile Tyr Glu Phe Met Lys Gln Gly Asp Glu Arg Leu Leu
245 250 255

Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Glu Arg
260 265

<210> 223
<211> 380
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 223

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Asp Lys Glu Asn Ile Leu
35 40 45

Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu Glu Gln Leu Gly His Ala
50 55 60

Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Gln
65 70 75 80

Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val
85 90 95

Glu Arg Gly Gly Ser Ser Gly Gln Ile Phe Val Lys Thr Leu Thr Gly
100 105 110

Lys Thr Ile Thr Leu Glu Val Glu Pro Ser Asp Thr Ile Glu Asn Val
115 120 125

Lys Ala Lys Ile Gln Asp Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg
130 135 140

Leu Ile Phe Ala Gly Lys Gln Leu Glu Asp Gly Arg Thr Leu Ser Asp
145 150 155 160

Tyr Asn Ile Gln Lys Glu Ser Thr Leu His Leu Val Leu Arg Leu Arg
165 170 175

Gly Gly Gly Gly Ser Ser Gly Asp Lys Glu Asn Ile Leu Gln Lys Ile
180 185 190

Tyr Glu Ile Met Lys Thr Leu Glu Gln Leu Gly His Ala Glu Ala Ser

195

200

205

Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Gln Gly Asp Glu
 210 215 220

Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Glu Arg Gly
 225 230 235 240

Gly Ser Ser Gly Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile
 245 250 255

Thr Leu Glu Val Glu Pro Ser Asp Thr Ile Glu Asn Val Lys Ala Lys
 260 265 270

Ile Gln Asp Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe
 275 280 285

Ala Gly Lys Gln Leu Glu Asp Gly Arg Thr Leu Ser Asp Tyr Asn Ile
 290 295 300

Gln Lys Glu Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly Gly Gly
 305 310 315 320

Gly Ser Ser Gly Asp Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile
 325 330 335

Met Lys Thr Leu Glu Gln Leu Gly His Ala Glu Ala Ser Met Gln Val
 340 345 350

Ser Asp Leu Ile Tyr Glu Phe Met Lys Gln Gly Asp Glu Arg Leu Leu
 355 360 365

Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Glu Arg
 370 375 380

<210> 224

<211> 179

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 224

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Asp Lys Glu Asn Val Leu
35 40 45

Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala
50 55 60

Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr
65 70 75 80

Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val
85 90 95

Lys Arg Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser
100 105 110

Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Asp Lys Glu Asn Val
115 120 125

Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His
130 135 140

Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys
145 150 155 160

Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu
165 170 175

Val Lys Arg

<210> 225

<211> 183

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 225

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Asp Lys Glu Asn Val Leu
35 40 45

Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala
50 55 60

Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr
65 70 75 80

Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val
85 90 95

Lys Arg Gly Gly Ser Ser Gly Pro Ser Thr Pro Pro Thr Pro Ser Pro
100 105 110

Ser Thr Pro Pro Thr Pro Ser Pro Ser Pro Gly Gly Ser Ser Gly Asp
115 120 125

Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu
130 135 140

Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr
145 150 155 160

Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg
165 170 175

Leu Leu Glu Glu Val Lys Arg
180

<210> 226
<211> 195
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 226

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Asn Leu Asp Glu Leu His
35 40 45

Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp
50 55 60

Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys
65 70 75 80

Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu
85 90 95

Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly Ser Ser Gly Gly
100 105 110

Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly
115 120 125

Ser Ser Gly Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val
130 135 140

Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val
145 150 155 160

Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg
165 170 175

Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg
180 185 190

Leu Leu Ser
195

<210> 227
<211> 199
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 227

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Asn Leu Asp Glu Leu His
35 40 45

Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp
50 55 60

Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys
65 70 75 80

Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu
85 90 95

Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly Ser Ser Gly Pro
100 105 110

Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro
115 120 125

Ser Pro Gly Gly Ser Ser Gly Asn Leu Asp Glu Leu His Met Gln Met
130 135 140

Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe
145 150 155 160

Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys
165 170 175

Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu
180 185 190

Leu Leu Glu Arg Leu Leu Ser
195

<210> 228
<211> 179
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 228

Met Glu Lys Lys Ile Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu
1 5 10 15

Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln
20 25 30

Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu
35 40 45

Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg Gly Gly Ser
50 55 60

Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser
65 70 75 80

Gly Gly Gly Ser Ser Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr
85 90 95

Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met
100 105 110

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

Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg Gly Gly
130 135 140

Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
145 150 155 160

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
165 170 175

Phe Glu Lys

<210> 229
<211> 183
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 229

Met Glu Lys Lys Ile Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu
1 5 10 15

Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln
20 25 30

Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu
35 40 45

Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg Gly Gly Ser
50 55 60

Ser Gly Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr
65 70 75 80

Pro Ser Pro Ser Pro Gly Gly Ser Ser Gly Asp Lys Glu Asn Val Leu
85 90 95

Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala
100 105 110

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

Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val
130 135 140

Lys Arg Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro Gln
145 150 155 160

Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp
165 170 175

Ser His Pro Gln Phe Glu Lys
180

<210> 230
<211> 195
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 230

Met Glu Lys Lys Ile Asn Leu Asp Glu Leu His Met Gln Met Thr Asp
1 5 10 15

Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys
20 25 30

His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys
35 40 45

Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu
50 55 60

Glu Arg Leu Leu Ser Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly
65 70 75 80

Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Asn Leu
85 90 95

Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His
100 105 110

Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu
115 120 125

Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys
130 135 140

Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly
145 150 155 160

Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
165 170 175

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
180 185 190

Phe Glu Lys
195

<210> 231
<211> 199
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 231

Met Glu Lys Lys Ile Asn Leu Asp Glu Leu His Met Gln Met Thr Asp
1 5 10 15

Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys
20 25 30

His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys
35 40 45

Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu
50 55 60

Glu Arg Leu Leu Ser Gly Gly Ser Ser Gly Pro Ser Thr Pro Pro Thr
65 70 75 80

Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Pro Gly Gly Ser
85 90 95

Ser Gly Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr
100 105 110

Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe
115 120 125

Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln
130 135 140

Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu
145 150 155 160

Leu Ser Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro Gln
165 170 175

Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp
180 185 190

Ser His Pro Gln Phe Glu Lys
195

<210> 232
<211> 240
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 232

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Ser Gly Ser Ser Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr
20 25 30

Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met
35 40 45

Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn
50 55 60

Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg Gly Gly
65 70 75 80

Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser
85 90 95

Ser Gly Gly Gly Ser Ser Gly Asp Lys Glu Asn Val Leu Gln Lys Ile
100 105 110

Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser
115 120 125

Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu
130 135 140

Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg Gly
145 150 155 160

Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly
165 170 175

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

Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala
195 200 205

Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp
210 215 220

Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg

225 230 235 240

<210> 233
 <211> 248
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 233

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
 1 5 10 15

Gly Ser Gly Ser Ser Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr
 20 25 30

Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met
 35 40 45

Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn
 50 55 60

Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg Gly Gly
 65 70 75 80

Ser Ser Gly Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro
 85 90 95

Thr Pro Ser Pro Ser Pro Gly Gly Ser Ser Gly Asp Lys Glu Asn Val
 100 105 110

Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His
 115 120 125

Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys
 130 135 140

Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu
 145 150 155 160

Val Lys Arg Gly Gly Ser Ser Gly Pro Ser Thr Pro Pro Thr Pro Ser

165

170

175

Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Pro Gly Gly Ser Ser Gly
 180 185 190

Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu
 195 200 205

Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile
 210 215 220

Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu
 225 230 235 240

Arg Leu Leu Glu Glu Val Lys Arg
 245

<210> 234
 <211> 264
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 234

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
 1 5 10 15

Gly Ser Gly Ser Ser Gly Asn Leu Asp Glu Leu His Met Gln Met Thr
 20 25 30

Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln
 35 40 45

Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn
 50 55 60

Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu
 65 70 75 80

Leu Glu Arg Leu Leu Ser Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly

85

90

95

Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Asn
 100 105 110

Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu
 115 120 125

His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe
 130 135 140

Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu
 145 150 155 160

Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly
 165 170 175

Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly
 180 185 190

Ser Ser Gly Gly Gly Ser Ser Gly Asn Leu Asp Glu Leu His Met Gln
 195 200 205

Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu
 210 215 220

Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr
 225 230 235 240

Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys
 245 250 255

Glu Leu Leu Glu Arg Leu Leu Ser
 260

<210> 235
 <211> 272
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 235

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Ser Gly Ser Ser Gly Asn Leu Asp Glu Leu His Met Gln Met Thr
20 25 30

Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln
35 40 45

Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn
50 55 60

Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu
65 70 75 80

Leu Glu Arg Leu Leu Ser Gly Gly Ser Ser Gly Pro Ser Thr Pro Pro
85 90 95

Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Pro Gly Gly
100 105 110

Ser Ser Gly Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val
115 120 125

Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val
130 135 140

Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg
145 150 155 160

Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg
165 170 175

Leu Leu Ser Gly Gly Ser Ser Gly Pro Ser Thr Pro Pro Thr Pro Ser
180 185 190

Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Pro Gly Gly Ser Ser Gly
195 200 205

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
210 215 220

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu
225 230 235 240

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
245 250 255

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
260 265 270

<210> 236
<211> 240
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 236

Met Glu Lys Lys Ile Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu
1 5 10 15

Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln
20 25 30

Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu
35 40 45

Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg Gly Gly Ser
50 55 60

Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser
65 70 75 80

Gly Gly Gly Ser Ser Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr
85 90 95

Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met
100 105 110

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

Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg Gly Gly
130 135 140

Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser
145 150 155 160

Ser Gly Gly Gly Ser Ser Gly Asp Lys Glu Asn Val Leu Gln Lys Ile
165 170 175

Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser
180 185 190

Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu
195 200 205

Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg Gly
210 215 220

Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
225 230 235 240

<210> 237
<211> 248
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 237

Met Glu Lys Lys Ile Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu
1 5 10 15

Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln
20 25 30

Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu
35 40 45

Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg Gly Gly Ser
50 55 60

Ser Gly Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr
65 70 75 80

Pro Ser Pro Ser Pro Gly Gly Ser Ser Gly Asp Lys Glu Asn Val Leu
85 90 95

Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala
100 105 110

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

Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val
130 135 140

Lys Arg Gly Gly Ser Ser Gly Pro Ser Thr Pro Pro Thr Pro Ser Pro
145 150 155 160

Ser Thr Pro Pro Thr Pro Ser Pro Ser Pro Gly Gly Ser Ser Gly Asp
165 170 175

Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu
180 185 190

Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr
195 200 205

Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg
210 215 220

Leu Leu Glu Glu Val Lys Arg Gly Gly Ser Gly Ser Ser Gly Ser Ala
225 230 235 240

Trp Ser His Pro Gln Phe Glu Lys
245

<210> 238

<211> 264
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 238

Met Glu Lys Lys Ile Asn Leu Asp Glu Leu His Met Gln Met Thr Asp
1 5 10 15

Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys
20 25 30

His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys
35 40 45

Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu
50 55 60

Glu Arg Leu Leu Ser Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly
65 70 75 80

Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Asn Leu
85 90 95

Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His
100 105 110

Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu
115 120 125

Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys
130 135 140

Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly
145 150 155 160

Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser
165 170 175

Ser Gly Gly Gly Ser Ser Gly Asn Leu Asp Glu Leu His Met Gln Met

180

185

190

Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe
 195 200 205

Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys
 210 215 220

Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu
 225 230 235 240

Leu Leu Glu Arg Leu Leu Ser Gly Gly Ser Gly Ser Ser Gly Ser Ala
 245 250 255

Trp Ser His Pro Gln Phe Glu Lys
 260

<210> 239
 <211> 272
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 239

Met Glu Lys Lys Ile Asn Leu Asp Glu Leu His Met Gln Met Thr Asp
 1 5 10 15

Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys
 20 25 30

His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys
 35 40 45

Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu
 50 55 60

Glu Arg Leu Leu Ser Gly Gly Ser Ser Gly Pro Ser Thr Pro Pro Thr
 65 70 75 80

Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Pro Gly Gly Ser

85

90

95

Ser Gly Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr
 100 105 110

Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe
 115 120 125

Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln
 130 135 140

Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu
 145 150 155 160

Leu Ser Gly Gly Ser Ser Gly Pro Ser Thr Pro Pro Thr Pro Ser Pro
 165 170 175

Ser Thr Pro Pro Thr Pro Ser Pro Ser Pro Gly Gly Ser Ser Gly Asn
 180 185 190

Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu
 195 200 205

His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe
 210 215 220

Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu
 225 230 235 240

Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly
 245 250 255

Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
 260 265 270

<210> 240

<211> 187

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 240

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Asp Lys Glu Asn Val Leu
35 40 45

Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala
50 55 60

Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr
65 70 75 80

Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val
85 90 95

Lys Arg Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser
100 105 110

Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Asn Leu Asp Glu Leu
115 120 125

His Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys
130 135 140

Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr
145 150 155 160

Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu
165 170 175

Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
180 185

<210> 241

<211> 191

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 241

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Asp Lys Glu Asn Val Leu
35 40 45

Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala
50 55 60

Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr
65 70 75 80

Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val
85 90 95

Lys Arg Gly Gly Ser Ser Gly Pro Ser Thr Pro Pro Thr Pro Ser Pro
100 105 110

Ser Thr Pro Pro Thr Pro Ser Pro Ser Pro Gly Gly Ser Ser Gly Asn
115 120 125

Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu
130 135 140

His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe
145 150 155 160

Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu
165 170 175

Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
180 185 190

<210> 242
<211> 187
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 242

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Asn Leu Asp Glu Leu His
35 40 45

Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp
50 55 60

Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys
65 70 75 80

Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu
85 90 95

Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly Ser Ser Gly Gly
100 105 110

Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly
115 120 125

Ser Ser Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met
130 135 140

Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser
145 150 155 160

Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu
165 170 175

Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
180 185

<210> 243
<211> 191
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 243

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Asn Leu Asp Glu Leu His
35 40 45

Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp
50 55 60

Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys
65 70 75 80

Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu
85 90 95

Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly Ser Ser Gly Pro
100 105 110

Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro
115 120 125

Ser Pro Gly Gly Ser Ser Gly Asp Lys Glu Asn Val Leu Gln Lys Ile
130 135 140

Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser
145 150 155 160

Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu
165 170 175

Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
180 185 190

<210> 244
<211> 187
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 244

Met Glu Lys Lys Ile Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu
1 5 10 15

Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln
20 25 30

Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu
35 40 45

Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg Gly Gly Ser
50 55 60

Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser
65 70 75 80

Gly Gly Gly Ser Ser Gly Asn Leu Asp Glu Leu His Met Gln Met Thr
85 90 95

Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln
100 105 110

Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn
115 120 125

Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu
130 135 140

Leu Glu Arg Leu Leu Ser Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp
145 150 155 160

Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly
165 170 175

Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
180 185

<210> 245
<211> 191
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 245

Met Glu Lys Lys Ile Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu
1 5 10 15

Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln
20 25 30

Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu
35 40 45

Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg Gly Gly Ser
50 55 60

Ser Gly Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr
65 70 75 80

Pro Ser Pro Ser Pro Gly Gly Ser Ser Gly Asn Leu Asp Glu Leu His
85 90 95

Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp
100 105 110

Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys
115 120 125

Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu
130 135 140

Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly Ser Gly Ser Ser
145 150 155 160

Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly
165 170 175

Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
180 185 190

<210> 246
<211> 187
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 246

Met Glu Lys Lys Ile Asn Leu Asp Glu Leu His Met Gln Met Thr Asp
1 5 10 15

Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys
20 25 30

His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys
35 40 45

Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu
50 55 60

Glu Arg Leu Leu Ser Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly
65 70 75 80

Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Asp Lys
85 90 95

Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg
100 105 110

Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu
115 120 125

Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu
130 135 140

Leu Glu Glu Val Lys Arg Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp
145 150 155 160

Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly
165 170 175

Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
180 185

<210> 247
<211> 191
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 247

Met Glu Lys Lys Ile Asn Leu Asp Glu Leu His Met Gln Met Thr Asp
1 5 10 15

Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys
20 25 30

His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys
35 40 45

Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu
50 55 60

Glu Arg Leu Leu Ser Gly Gly Ser Ser Gly Pro Ser Thr Pro Pro Thr
65 70 75 80

Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Pro Gly Gly Ser
85 90 95

Ser Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys
100 105 110

Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp
115 120 125

Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu
130 135 140

Ala Glu Arg Leu Leu Glu Glu Val Lys Arg Gly Gly Ser Gly Ser Ser
145 150 155 160

Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly
165 170 175

Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
180 185 190

<210> 248
<211> 172
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 248

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Asn Leu Asp Glu Leu His
35 40 45

Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp
50 55 60

Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys
65 70 75 80

Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu
85 90 95

Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly Gly Ser Gly Gly
100 105 110

Gly Ser Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile
115 120 125

Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val
130 135 140

Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu
145 150 155 160

Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
165 170

<210> 249
<211> 172
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 249

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Asn Leu Asp Glu Leu His
35 40 45

Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp
50 55 60

Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys
65 70 75 80

Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu
85 90 95

Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly Ser Ser Gly Gly
100 105 110

Gly Ser Ser Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile
115 120 125

Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val
130 135 140

Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu
145 150 155 160

Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
165 170

<210> 250
<211> 177
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 250

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Asn Leu Asp Glu Leu His
35 40 45

Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp
50 55 60

Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys
65 70 75 80

Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu
85 90 95

Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly Ser Ser Gly Gly
100 105 110

Gly Ser Ser Gly Gly Gly Ser Ser Gly Asp Lys Glu Asn Val Leu Gln
115 120 125

Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu
130 135 140

Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys
145 150 155 160

Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys
165 170 175

Arg

<210> 251
<211> 182
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 251

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Asn Leu Asp Glu Leu His
35 40 45

Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp
50 55 60

Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys
65 70 75 80

Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu
85 90 95

Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly Ser Ser Gly Gly
100 105 110

Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Asp Lys
115 120 125

Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg
130 135 140

Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu
145 150 155 160

Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu
165 170 175

Leu Glu Glu Val Lys Arg
180

<210> 252
<211> 164
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 252

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Asp Lys Glu Asn Val Leu
35 40 45

Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala
50 55 60

Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr
65 70 75 80

Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val
85 90 95

Lys Arg Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Asp Lys Glu Asn
100 105 110

Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly
115 120 125

His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met
130 135 140

Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu
145 150 155 160

Glu Val Lys Arg

<210> 253
<211> 169
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 253

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Asp Lys Glu Asn Val Leu
35 40 45

Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala
50 55 60

Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr
65 70 75 80

Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val
85 90 95

Lys Arg Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser
100 105 110

Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu
115 120 125

Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu
130 135 140

Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala
145 150 155 160

Glu Arg Leu Leu Glu Glu Val Lys Arg
165

<210> 254
<211> 174
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 254

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Asp Lys Glu Asn Val Leu
35 40 45

Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala
50 55 60

Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr
65 70 75 80

Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val
85 90 95

Lys Arg Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser
100 105 110

Gly Gly Gly Ser Ser Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr
115 120 125

Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met
130 135 140

Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn
145 150 155 160

Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
165 170

<210> 255
<211> 183
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 255

Met Ser Lys Ile Lys Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln Val
35 40 45

Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His
50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp
65 70 75 80

Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu
85 90 95

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu
100 105 110

Glu Leu Ala Arg Lys Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Asp
115 120 125

Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu
130 135 140

Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr
145 150 155 160

Glu Phe Met Lys Thr Lys Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg
165 170 175

Leu Leu Glu Glu Val Lys Arg
180

<210> 256
<211> 188
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 256

Met Ser Lys Ile Lys Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln Val
35 40 45

Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His
50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp
65 70 75 80

Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu
85 90 95

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu
100 105 110

Glu Leu Ala Arg Lys Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly
115 120 125

Gly Ser Ser Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile
130 135 140

Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val
145 150 155 160

Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Arg Leu Leu
165 170 175

Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
180 185

<210> 257
<211> 193
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 257

Met Ser Lys Ile Lys Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln Val
35 40 45

Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His
50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp
65 70 75 80

Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu
85 90 95

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu
100 105 110

Glu Leu Ala Arg Lys Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly
115 120 125

Gly Ser Ser Gly Gly Gly Ser Ser Gly Asp Lys Glu Asn Val Leu Gln
130 135 140

Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu
145 150 155 160

Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys
165 170 175

Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys
180 185 190

Arg

<210> 258
<211> 268
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 258

Met Ser Lys Ile Lys Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln Val
35 40 45

Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His
50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp
65 70 75 80

Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu
85 90 95

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu
100 105 110

Glu Leu Ala Arg Lys Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Glu
115 120 125

Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu Ala
130 135 140

His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala
145 150 155 160

Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser
165 170 175

Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile
180 185 190

Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Ser Gly Gly

195

200

205

Gly Ser Ser Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile
 210 215 220

Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val
 225 230 235 240

Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Arg Leu Leu
 245 250 255

Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
 260 265

<210> 259
 <211> 278
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 259

Met Ser Lys Ile Lys Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
 1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
 20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln Val
 35 40 45

Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His
 50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp
 65 70 75 80

Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu
 85 90 95

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu

100

105

110

Glu Leu Ala Arg Lys Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly
115 120 125

Gly Ser Ser Gly Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln
130 135 140

Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu
145 150 155 160

Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu
165 170 175

Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu
180 185 190

Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly
195 200 205

Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Asp Lys
210 215 220

Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg
225 230 235 240

Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu
245 250 255

Phe Met Lys Thr Lys Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu
260 265 270

Leu Glu Glu Val Lys Arg
275

<210> 260
<211> 288
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 260

Met Ser Lys Ile Lys Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln Val
35 40 45

Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His
50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp
65 70 75 80

Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu
85 90 95

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu
100 105 110

Glu Leu Ala Arg Lys Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly
115 120 125

Gly Ser Ser Gly Gly Gly Ser Ser Gly Glu Leu Glu Glu Gln Val Met
130 135 140

His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys
145 150 155 160

Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala
165 170 175

Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile
180 185 190

Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu
195 200 205

Leu Ala Arg Lys Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly
210 215 220

Ser Ser Gly Gly Gly Ser Ser Gly Asp Lys Glu Asn Val Leu Gln Lys
225 230 235 240

Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala
245 250 255

Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp
260 265 270

Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
275 280 285

<210> 261
<211> 202
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 261

Met Ser Lys Ile Lys Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln Val
35 40 45

Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His
50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp
65 70 75 80

Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu
85 90 95

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu
100 105 110

Glu Leu Ala Arg Lys Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Glu
115 120 125

Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu Ala
130 135 140

His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala
145 150 155 160

Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser
165 170 175

Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile
180 185 190

Leu Glu His Leu Glu Glu Leu Ala Arg Lys
195 200

<210> 262
<211> 207
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 262

Met Ser Lys Ile Lys Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln Val
35 40 45

Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His
50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp
65 70 75 80

Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu
85 90 95

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu
100 105 110

Glu Leu Ala Arg Lys Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly
115 120 125

Gly Ser Ser Gly Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln
130 135 140

Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu
145 150 155 160

Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu
165 170 175

Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu
180 185 190

Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
195 200 205

<210> 263
<211> 212
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 263

Met Ser Lys Ile Lys Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln Val
35 40 45

Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His
50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp
65 70 75 80

Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu
85 90 95

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu
100 105 110

Glu Leu Ala Arg Lys Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly
115 120 125

Gly Ser Ser Gly Gly Gly Ser Ser Gly Glu Leu Glu Glu Gln Val Met
130 135 140

His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys
145 150 155 160

Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala
165 170 175

Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile
180 185 190

Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu
195 200 205

Leu Ala Arg Lys
210

<210> 264
<211> 287
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 264

Met Ser Lys Ile Lys Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln Val
35 40 45

Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His
50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp
65 70 75 80

Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu
85 90 95

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu
100 105 110

Glu Leu Ala Arg Lys Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Glu
115 120 125

Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu Ala
130 135 140

His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala
145 150 155 160

Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser
165 170 175

Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile
180 185 190

Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Ser Gly Gly

195

200

205

Gly Ser Ser Gly Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln
 210 215 220

Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu
 225 230 235 240

Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu
 245 250 255

Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu
 260 265 270

Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
 275 280 285

<210> 265
 <211> 297
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 265

Met Ser Lys Ile Lys Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
 1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
 20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln Val
 35 40 45

Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His
 50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp
 65 70 75 80

Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu

85

90

95

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu
 100 105 110

Glu Leu Ala Arg Lys Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly
 115 120 125

Gly Ser Ser Gly Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln
 130 135 140

Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu
 145 150 155 160

Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu
 165 170 175

Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu
 180 185 190

Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly
 195 200 205

Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Glu Leu
 210 215 220

Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu Ala His
 225 230 235 240

Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr
 245 250 255

Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp
 260 265 270

Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu
 275 280 285

Glu His Leu Glu Glu Leu Ala Arg Lys
 290 295

<210> 266
<211> 307
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 266

Met Ser Lys Ile Lys Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln Val
35 40 45

Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His
50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp
65 70 75 80

Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu
85 90 95

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu
100 105 110

Glu Leu Ala Arg Lys Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly
115 120 125

Gly Ser Ser Gly Gly Gly Ser Ser Gly Glu Leu Glu Glu Gln Val Met
130 135 140

His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys
145 150 155 160

Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala
165 170 175

Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile
180 185 190

Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu
195 200 205

Leu Ala Arg Lys Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly
210 215 220

Ser Ser Gly Gly Gly Ser Ser Gly Glu Leu Glu Glu Gln Val Met His
225 230 235 240

Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu
245 250 255

Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr
260 265 270

Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg
275 280 285

Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu
290 295 300

Ala Arg Lys
305

<210> 267
<211> 216
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 267

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln Val
35 40 45

Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His
50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp
65 70 75 80

Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu
85 90 95

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu
100 105 110

Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala
115 120 125

Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Glu Leu Glu
130 135 140

Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu
145 150 155 160

Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe
165 170 175

Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp
180 185 190

Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu
195 200 205

His Leu Glu Glu Leu Ala Arg Lys
210 215

<210> 268
<211> 186
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 268

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Asn Leu Asp Glu Leu His
35 40 45

Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp
50 55 60

Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys
65 70 75 80

Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu
85 90 95

Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly Ala Ser Pro Ala
100 105 110

Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala
115 120 125

Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys
130 135 140

Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp
145 150 155 160

Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Arg Leu Leu Glu Glu
165 170 175

Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
180 185

<210> 269

<211> 197
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 269

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln Val
35 40 45

Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His
50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp
65 70 75 80

Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu
85 90 95

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu
100 105 110

Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala
115 120 125

Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Asp Lys Glu
130 135 140

Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu
145 150 155 160

Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe
165 170 175

Met Lys Thr Lys Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu

180

185

190

Glu Glu Val Lys Arg
195

<210> 270
<211> 315
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 270

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln Val
35 40 45

Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His
50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp
65 70 75 80

Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu
85 90 95

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu
100 105 110

Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala
115 120 125

Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Glu Leu Glu
130 135 140

Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu

145		150		155		160									
Leu	Leu	His	Lys	Leu	Thr	Gly	Glu	Glu	Leu	Glu	Arg	Ala	Ala	Tyr	Phe
				165					170					175	
Asn	Trp	Trp	Ala	Thr	Glu	Met	Met	Leu	Glu	Leu	Ile	Lys	Ser	Asp	Asp
			180					185					190		
Glu	Arg	Glu	Ile	Arg	Glu	Ile	Glu	Glu	Glu	Ala	Arg	Arg	Ile	Leu	Glu
		195					200					205			
His	Leu	Glu	Glu	Leu	Ala	Arg	Lys	Gly	Gly	Ala	Ser	Pro	Ala	Ala	Pro
	210					215					220				
Ala	Pro	Ala	Ser	Pro	Ala	Ala	Pro	Ala	Pro	Ser	Ala	Pro	Ala	Gly	Gly
225					230					235				240	
Glu	Leu	Glu	Glu	Gln	Val	Met	His	Val	Leu	Asp	Gln	Val	Ser	Glu	Leu
				245					250					255	
Ala	His	Glu	Leu	Leu	His	Lys	Leu	Thr	Gly	Glu	Glu	Leu	Glu	Arg	Ala
			260					265					270		
Ala	Tyr	Phe	Asn	Trp	Trp	Ala	Thr	Glu	Met	Met	Leu	Glu	Leu	Ile	Lys
		275					280					285			
Ser	Asp	Asp	Glu	Arg	Glu	Ile	Arg	Glu	Ile	Glu	Glu	Glu	Ala	Arg	Arg
	290					295					300				
Ile	Leu	Glu	His	Leu	Glu	Glu	Leu	Ala	Arg	Lys					
305					310					315					

<210> 271
 <211> 285
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 271

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly

1		5		10		15										
Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Ser	Ala	Trp	Ser	His	Pro	Gln	
		20					25					30				
Phe	Glu	Lys	Gly	Gly	Ser	Gly	Ser	Ser	Gly	Asn	Leu	Asp	Glu	Leu	His	
		35				40						45				
Met	Gln	Met	Thr	Asp	Leu	Val	Tyr	Glu	Ala	Leu	His	Phe	Ala	Lys	Asp	
	50					55					60					
Glu	Glu	Phe	Gln	Lys	His	Val	Phe	Gln	Leu	Phe	Glu	Lys	Ala	Thr	Lys	
65					70				75						80	
Ala	Tyr	Lys	Asn	Lys	Asp	Arg	Gln	Lys	Leu	Glu	Lys	Val	Val	Glu	Glu	
			85						90					95		
Leu	Lys	Glu	Leu	Leu	Glu	Arg	Leu	Leu	Ser	Gly	Gly	Ala	Ser	Pro	Ala	
			100					105					110			
Ala	Pro	Ala	Pro	Ala	Ser	Pro	Ala	Ala	Pro	Ala	Pro	Ser	Ala	Pro	Ala	
		115					120					125				
Gly	Gly	Glu	Leu	Glu	Glu	Gln	Val	Met	His	Val	Leu	Asp	Gln	Val	Ser	
	130					135					140					
Glu	Leu	Ala	His	Glu	Leu	Leu	His	Lys	Leu	Thr	Gly	Glu	Glu	Leu	Glu	
145					150					155					160	
Arg	Ala	Ala	Tyr	Phe	Asn	Trp	Trp	Ala	Thr	Glu	Met	Met	Leu	Glu	Leu	
				165					170					175		
Ile	Lys	Ser	Asp	Asp	Glu	Arg	Glu	Ile	Arg	Glu	Ile	Glu	Glu	Glu	Ala	
			180					185					190			
Arg	Arg	Ile	Leu	Glu	His	Leu	Glu	Glu	Leu	Ala	Arg	Lys	Gly	Gly	Ala	
		195					200					205				
Ser	Pro	Ala	Ala	Pro	Ala	Pro	Ala	Ser	Pro	Ala	Ala	Pro	Ala	Pro	Ser	
	210					215					220					

Ala Pro Ala Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu
225 230 235 240

Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln
245 250 255

Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Arg Leu
260 265 270

Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
275 280 285

<210> 272
<211> 285
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 272

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln Val
35 40 45

Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His
50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp
65 70 75 80

Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu
85 90 95

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu
100 105 110

Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala
115 120 125

Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Asn Leu Asp
130 135 140

Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe
145 150 155 160

Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys
165 170 175

Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val
180 185 190

Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly Ala
195 200 205

Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser
210 215 220

Ala Pro Ala Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu
225 230 235 240

Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln
245 250 255

Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Arg Leu
260 265 270

Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
275 280 285

<210> 273
<211> 258
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 273

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Asp Lys Glu Asn Val Leu
35 40 45

Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala
50 55 60

Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr
65 70 75 80

Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val
85 90 95

Lys Arg Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala
100 105 110

Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Asp Lys Glu Asn Val Leu
115 120 125

Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala
130 135 140

Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr
145 150 155 160

Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val
165 170 175

Lys Arg Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala
180 185 190

Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Asp Lys Glu Asn Val Leu
195 200 205

Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala

210

215

220

Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr
 225 230 235 240

Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val
 245 250 255

Lys Arg

<210> 274
 <211> 315
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 274

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
 1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
 20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln Val
 35 40 45

Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His
 50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp
 65 70 75 80

Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu
 85 90 95

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu
 100 105 110

Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala

115

120

125

Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Glu Leu Glu
 130 135 140

Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu
 145 150 155 160

Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe
 165 170 175

Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp
 180 185 190

Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu
 195 200 205

His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro Ala Ala Pro
 210 215 220

Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly
 225 230 235 240

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
 245 250 255

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
 260 265 270

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
 275 280 285

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
 290 295 300

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
 305 310 315

<210> 275

<211> 282

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 275

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Asn Leu Asp Glu Leu His
35 40 45

Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp
50 55 60

Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys
65 70 75 80

Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu
85 90 95

Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly Ala Ser Pro Ala
100 105 110

Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala
115 120 125

Gly Gly Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr
130 135 140

Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe
145 150 155 160

Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln
165 170 175

Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu
180 185 190

Leu Ser Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala
195 200 205

Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Asn Leu Asp Glu Leu His
210 215 220

Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp
225 230 235 240

Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys
245 250 255

Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu
260 265 270

Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
275 280

<210> 276
<211> 296
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 276

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln Val
35 40 45

Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His
50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp
65 70 75 80

Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu
85 90 95

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu
100 105 110

Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala
115 120 125

Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Glu Leu Glu
130 135 140

Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu
145 150 155 160

Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe
165 170 175

Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp
180 185 190

Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu
195 200 205

His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro Ala Ala Pro
210 215 220

Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly
225 230 235 240

Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu
245 250 255

Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile
260 265 270

Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu
275 280 285

Arg Leu Leu Glu Glu Val Lys Arg

290

295

<210> 277
 <211> 208
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 277

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
 1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
 20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln Val
 35 40 45

Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His
 50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp
 65 70 75 80

Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu
 85 90 95

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu
 100 105 110

Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala
 115 120 125

Ser Pro Ala Gly Gly Glu Leu Glu Glu Gln Val Met His Val Leu Asp
 130 135 140

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
 145 150 155 160

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met

165

170

175

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
 180 185 190

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
 195 200 205

<210> 278
 <211> 203
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 278

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
 1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
 20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln Val
 35 40 45

Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His
 50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp
 65 70 75 80

Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu
 85 90 95

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu
 100 105 110

Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro Ala Ala Pro Ala Gly Gly
 115 120 125

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu

130

135

140

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
 145 150 155 160

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
 165 170 175

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
 180 185 190

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
 195 200

<210> 279
 <211> 178
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 279

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
 1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
 20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Asn Leu Asp Glu Leu His
 35 40 45

Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp
 50 55 60

Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys
 65 70 75 80

Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu
 85 90 95

Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly Ala Ser Pro Ala

100

105

110

Ala Pro Ala Pro Ala Ser Pro Ala Gly Gly Asp Lys Glu Asn Val Leu
 115 120 125

Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala
 130 135 140

Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr
 145 150 155 160

Lys Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val
 165 170 175

Lys Arg

<210> 280
 <211> 173
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 280

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
 1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
 20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Asn Leu Asp Glu Leu His
 35 40 45

Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp
 50 55 60

Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys
 65 70 75 80

Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu

85

90

95

Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly Ala Ser Pro Ala
 100 105 110

Ala Pro Ala Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu
 115 120 125

Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln
 130 135 140

Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Arg Leu
 145 150 155 160

Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
 165 170

<210> 281
 <211> 189
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 281

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
 1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
 20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln Val
 35 40 45

Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His
 50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp
 65 70 75 80

Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu

85

90

95

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu
 100 105 110

Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala
 115 120 125

Ser Pro Ala Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu
 130 135 140

Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln
 145 150 155 160

Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Arg Leu
 165 170 175

Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
 180 185

<210> 282
 <211> 184
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 282

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
 1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
 20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln Val
 35 40 45

Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His
 50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp

65		70		75		80
Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu						
		85		90		95
Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu						
		100		105		110
Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro Ala Ala Pro Ala Gly Gly						
		115		120		125
Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu						
		130		135		140
Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile						
		145		150		155
Tyr Glu Phe Met Lys Thr Lys Asp Glu Arg Leu Leu Glu Glu Ala Glu						
		165		170		175
Arg Leu Leu Glu Glu Val Lys Arg						
		180				
<210> 283						
<211> 285						
<212> PRT						
<213> Artificial Sequence						
<220>						
<223> Synthetic						
<400> 283						
Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly						
1		5		10		15
Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln						
		20		25		30
Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Asn Ile Asp Glu Leu Leu						
		35		40		45
Met Gln Val Thr Asp Leu Ile Tyr Glu Ala Leu His Phe Ala Lys Asp						

50

55

60

Glu Glu Phe Gln Lys His Ala Phe Gln Leu Phe Glu Lys Ala Thr Lys
65 70 75 80

Ala Tyr Lys Asn Lys Asp Lys Gln Lys Leu Glu Lys Val Val Glu Glu
85 90 95

Leu Lys Glu Leu Leu Glu Arg Ile Leu Ser Gly Gly Ala Ser Pro Ala
100 105 110

Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala
115 120 125

Gly Gly Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser
130 135 140

Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu
145 150 155 160

Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu
165 170 175

Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala
180 185 190

Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala
195 200 205

Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser
210 215 220

Ala Pro Ala Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu
225 230 235 240

Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln
245 250 255

Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Arg Leu
260 265 270

Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
275 280 285

<210> 284
<211> 285
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 284

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln Val
35 40 45

Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His
50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp
65 70 75 80

Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu
85 90 95

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu
100 105 110

Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala
115 120 125

Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Asn Ile Asp
130 135 140

Glu Leu Leu Met Gln Val Thr Asp Leu Ile Tyr Glu Ala Leu His Phe
145 150 155 160

Ala Lys Asp Glu Glu Phe Gln Lys His Ala Phe Gln Leu Phe Glu Lys
165 170 175

Ala Thr Lys Ala Tyr Lys Asn Lys Asp Lys Gln Lys Leu Glu Lys Val
180 185 190

Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Ile Leu Ser Gly Gly Ala
195 200 205

Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser
210 215 220

Ala Pro Ala Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu
225 230 235 240

Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln
245 250 255

Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Arg Leu
260 265 270

Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
275 280 285

<210> 285
<211> 315
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 285

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln Val
35 40 45

Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His
50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp
65 70 75 80

Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu
85 90 95

Ile Arg Glu Ile Glu Glu Glu Ala Ala Arg Ile Leu Glu His Leu Glu
100 105 110

Glu Leu Ala Arg Thr Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala
115 120 125

Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Glu Leu Glu
130 135 140

Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu
145 150 155 160

Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe
165 170 175

Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp
180 185 190

Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Ala Arg Ile Leu Glu
195 200 205

His Leu Glu Glu Leu Ala Arg Thr Gly Gly Ala Ser Pro Ala Ala Pro
210 215 220

Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly
225 230 235 240

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
245 250 255

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala

260

265

270

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
 275 280 285

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Ala Arg
 290 295 300

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Thr
 305 310 315

<210> 286
 <211> 258
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 286

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
 1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
 20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Asp Lys Glu Asn Val Leu
 35 40 45

Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala
 50 55 60

Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr
 65 70 75 80

Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val
 85 90 95

Thr Arg Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala
 100 105 110

Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Asp Lys Glu Asn Val Leu

115

120

125

Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala
 130 135 140

Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr
 145 150 155 160

Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val
 165 170 175

Thr Arg Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala
 180 185 190

Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Asp Lys Glu Asn Val Leu
 195 200 205

Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala
 210 215 220

Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr
 225 230 235 240

Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val
 245 250 255

Thr Arg

<210> 287
 <211> 285
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 287

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
 1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln

20

25

30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Asn Ile Asp Glu Leu Leu
 35 40 45

Met Gln Val Thr Asp Leu Ile Tyr Glu Ala Leu His Phe Ala Lys Asp
 50 55 60

Glu Glu Phe Gln Lys His Ala Phe Gln Leu Phe Glu Lys Ala Thr Lys
 65 70 75 80

Ala Tyr Lys Asn Lys Asp Lys Gln Lys Leu Glu Lys Val Val Glu Glu
 85 90 95

Leu Lys Glu Leu Leu Glu Arg Ile Leu Ser Gly Gly Ala Ser Pro Ala
 100 105 110

Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala
 115 120 125

Gly Gly Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser
 130 135 140

Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu
 145 150 155 160

Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu
 165 170 175

Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala
 180 185 190

Ala Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Thr Gly Gly Ala
 195 200 205

Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser
 210 215 220

Ala Pro Ala Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu
 225 230 235 240

Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln
245 250 255

Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Arg Leu
260 265 270

Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
275 280 285

<210> 288
<211> 285
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 288

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln Val
35 40 45

Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His
50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp
65 70 75 80

Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu
85 90 95

Ile Arg Glu Ile Glu Glu Glu Ala Ala Arg Ile Leu Glu His Leu Glu
100 105 110

Glu Leu Ala Arg Thr Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala
115 120 125

Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Asn Ile Asp
130 135 140

Glu Leu Leu Met Gln Val Thr Asp Leu Ile Tyr Glu Ala Leu His Phe
145 150 155 160

Ala Lys Asp Glu Glu Phe Gln Lys His Ala Phe Gln Leu Phe Glu Lys
165 170 175

Ala Thr Lys Ala Tyr Lys Asn Lys Asp Lys Gln Lys Leu Glu Lys Val
180 185 190

Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Ile Leu Ser Gly Gly Ala
195 200 205

Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser
210 215 220

Ala Pro Ala Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu
225 230 235 240

Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln
245 250 255

Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Arg Leu
260 265 270

Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
275 280 285

<210> 289
<211> 285
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 289

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Asn Ile Asp Glu Leu Leu
35 40 45

Met Gln Val Thr Asp Leu Ile Tyr Glu Ala Leu His Phe Ala Lys Asp
50 55 60

Glu Glu Phe Gln Lys His Ala Phe Gln Leu Phe Glu Lys Ala Thr Lys
65 70 75 80

Ala Tyr Lys Asn Lys Asp Lys Gln Lys Leu Glu Lys Val Val Glu Glu
85 90 95

Leu Lys Glu Leu Leu Glu Arg Ile Leu Ser Gly Gly Ala Ser Pro Ala
100 105 110

Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala
115 120 125

Gly Gly Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser
130 135 140

Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu
145 150 155 160

Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu
165 170 175

Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala
180 185 190

Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala
195 200 205

Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser
210 215 220

Ala Pro Ala Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu

225		230		235		240
Ile Met Lys Glu	Leu Glu Arg Leu Gly	His Ala Glu Ala	Ser Met Gln			
	245	250	255			
Val Ser Asp Leu	Ile Tyr Glu Phe Met Lys Thr Lys Asp	Glu Asn Leu				
	260	265	270			
Leu Glu Glu Ala	Glu Arg Leu Leu Glu Glu Val Lys Arg					
	275	280	285			
<210>	290					
<211>	285					
<212>	PRT					
<213>	Artificial Sequence					
<220>						
<223>	Synthetic					
<400>	290					
Met Glu Lys Lys	Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly					
1	5	10	15			
Gly Gly Ser Gly	Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln					
	20	25	30			
Phe Glu Lys Gly	Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln Val					
	35	40	45			
Met His Val Leu	Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His					
	50	55	60			
Lys Leu Thr Gly	Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp					
65	70	75	80			
Ala Thr Glu Met	Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu					
	85	90	95			
Ile Arg Glu Ile	Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu					
	100	105	110			
Glu Leu Ala Arg	Lys Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala					

115

120

125

Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Asn Ile Asp
 130 135 140

Glu Leu Leu Met Gln Val Thr Asp Leu Ile Tyr Glu Ala Leu His Phe
 145 150 155 160

Ala Lys Asp Glu Glu Phe Gln Lys His Ala Phe Gln Leu Phe Glu Lys
 165 170 175

Ala Thr Lys Ala Tyr Lys Asn Lys Asp Lys Gln Lys Leu Glu Lys Val
 180 185 190

Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Ile Leu Ser Gly Gly Ala
 195 200 205

Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser
 210 215 220

Ala Pro Ala Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu
 225 230 235 240

Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln
 245 250 255

Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu
 260 265 270

Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
 275 280 285

<210> 291
 <211> 285
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 291

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly

Ala Pro Ala Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu
225 230 235 240

Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln
245 250 255

Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu
260 265 270

Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
275 280 285

<210> 292
<211> 285
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 292

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln Val
35 40 45

Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His
50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp
65 70 75 80

Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu
85 90 95

Ile Arg Glu Ile Glu Glu Glu Ala Ala Arg Ile Leu Glu His Leu Glu
100 105 110

Glu Leu Ala Arg Thr Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala
115 120 125

Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Asn Ile Asp
130 135 140

Glu Leu Leu Met Gln Val Thr Asp Leu Ile Tyr Glu Ala Leu His Phe
145 150 155 160

Ala Lys Asp Glu Glu Phe Gln Lys His Ala Phe Gln Leu Phe Glu Lys
165 170 175

Ala Thr Lys Ala Tyr Lys Asn Lys Asp Lys Gln Lys Leu Glu Lys Val
180 185 190

Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Ile Leu Ser Gly Gly Ala
195 200 205

Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser
210 215 220

Ala Pro Ala Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu
225 230 235 240

Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln
245 250 255

Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu
260 265 270

Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
275 280 285

<210> 293
<211> 270
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 293

Met Glu Lys Lys Ile His His His His His His Ser Gly Glu Asn Leu
1 5 10 15

Tyr Phe Gln Ser Gly Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln
20 25 30

Val Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu
35 40 45

His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp
50 55 60

Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg
65 70 75 80

Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu
85 90 95

Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro
100 105 110

Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Asn Ile
115 120 125

Asp Glu Leu Leu Met Gln Val Thr Asp Leu Ile Tyr Glu Ala Leu His
130 135 140

Phe Ala Lys Asp Glu Glu Phe Gln Lys His Ala Phe Gln Leu Phe Glu
145 150 155 160

Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Lys Gln Lys Leu Glu Lys
165 170 175

Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Ile Leu Ser Gly Gly
180 185 190

Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro
195 200 205

Ser Ala Pro Ala Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr

210

215

220

Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met
 225 230 235 240

Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn
 245 250 255

Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
 260 265 270

<210> 294
 <211> 270
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 294

Met Glu Lys Lys Ile His His His His His His Ser Gly Glu Asn Leu
 1 5 10 15

Tyr Phe Gln Ser Gly Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln
 20 25 30

Val Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu
 35 40 45

His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp
 50 55 60

Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg
 65 70 75 80

Glu Ile Arg Glu Ile Glu Glu Glu Ala Ala Arg Ile Leu Glu His Leu
 85 90 95

Glu Glu Leu Ala Arg Thr Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro
 100 105 110

Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Asn Ile

115

120

125

Asp Glu Leu Leu Met Gln Val Thr Asp Leu Ile Tyr Glu Ala Leu His
 130 135 140

Phe Ala Lys Asp Glu Glu Phe Gln Lys His Ala Phe Gln Leu Phe Glu
 145 150 155 160

Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Lys Gln Lys Leu Glu Lys
 165 170 175

Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Ile Leu Ser Gly Gly
 180 185 190

Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro
 195 200 205

Ser Ala Pro Ala Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr
 210 215 220

Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met
 225 230 235 240

Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn
 245 250 255

Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
 260 265 270

<210> 295
 <211> 297
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 295

Met Glu Lys Lys Ile Asp Tyr Lys Asp Asp Asp Asp Lys Gly Ser Gly
 1 5 10 15

Ser Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly

20

25

30

Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
 35 40 45

Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln Val Met His Val Leu
 50 55 60

Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly
 65 70 75 80

Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met
 85 90 95

Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile
 100 105 110

Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg
 115 120 125

Lys Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala
 130 135 140

Pro Ala Pro Ser Ala Pro Ala Gly Gly Asn Ile Asp Glu Leu Leu Met
 145 150 155 160

Gln Val Thr Asp Leu Ile Tyr Glu Ala Leu His Phe Ala Lys Asp Glu
 165 170 175

Glu Phe Gln Lys His Ala Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala
 180 185 190

Tyr Lys Asn Lys Asp Lys Gln Lys Leu Glu Lys Val Val Glu Glu Leu
 195 200 205

Lys Glu Leu Leu Glu Arg Ile Leu Ser Gly Gly Ala Ser Pro Ala Ala
 210 215 220

Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly
 225 230 235 240

Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu
245 250 255

Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu
260 265 270

Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala
275 280 285

Glu Arg Leu Leu Glu Glu Val Lys Arg
290 295

<210> 296
<211> 311
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 296

Met Glu Lys Lys Ile Asp Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp
1 5 10 15

His Asp Ile Asp Tyr Lys Asp Asp Asp Asp Lys Gly Ser Gly Ser Ser
20 25 30

Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly
35 40 45

Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Ser
50 55 60

Gly Ser Ser Gly Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln
65 70 75 80

Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu
85 90 95

Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu
100 105 110

Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu
115 120 125

Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly
130 135 140

Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala
145 150 155 160

Pro Ser Ala Pro Ala Gly Gly Asn Ile Asp Glu Leu Leu Met Gln Val
165 170 175

Thr Asp Leu Ile Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe
180 185 190

Gln Lys His Ala Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys
195 200 205

Asn Lys Asp Lys Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu
210 215 220

Leu Leu Glu Arg Ile Leu Ser Gly Gly Ala Ser Pro Ala Ala Pro Ala
225 230 235 240

Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Asp
245 250 255

Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu
260 265 270

Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr
275 280 285

Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg
290 295 300

Leu Leu Glu Glu Val Lys Arg
305 310

<210> 297

<211> 299
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 297

Met Glu Lys Lys Ile Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Gly
1 5 10 15

Ser Gly Ser Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly
20 25 30

Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu
35 40 45

Lys Gly Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln Val Met His
50 55 60

Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu
65 70 75 80

Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr
85 90 95

Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg
100 105 110

Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu
115 120 125

Ala Arg Lys Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro
130 135 140

Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Asn Ile Asp Glu Leu
145 150 155 160

Leu Met Gln Val Thr Asp Leu Ile Tyr Glu Ala Leu His Phe Ala Lys
165 170 175

Asp Glu Glu Phe Gln Lys His Ala Phe Gln Leu Phe Glu Lys Ala Thr

180

185

190

Lys Ala Tyr Lys Asn Lys Asp Lys Gln Lys Leu Glu Lys Val Val Glu
 195 200 205

Glu Leu Lys Glu Leu Leu Glu Arg Ile Leu Ser Gly Gly Ala Ser Pro
 210 215 220

Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro
 225 230 235 240

Ala Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met
 245 250 255

Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser
 260 265 270

Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu
 275 280 285

Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
 290 295

<210> 298
 <211> 303
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 298

Met Glu Lys Lys Ile Asp Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp
 1 5 10 15

His Asp Ile Asp Tyr Lys Asp Asp Asp Asp Lys Gly Ser Gly Ser Ser
 20 25 30

Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly
 35 40 45

Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Ser

50

55

60

Gly Ser Ser Gly Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln
65 70 75 80

Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu
85 90 95

Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu
100 105 110

Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu
115 120 125

Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly
130 135 140

Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala
145 150 155 160

Pro Ser Ala Pro Ala Gly Gly Asn Ile Asp Glu Leu Leu Met Gln Val
165 170 175

Thr Asp Leu Ile Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe
180 185 190

Gln Lys His Ala Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys
195 200 205

Asn Lys Asp Lys Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu
210 215 220

Leu Leu Glu Arg Ile Leu Ser Gly Gly Ala Ser Pro Ala Ala Pro Ala
225 230 235 240

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

Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser
260 265 270

Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu
275 280 285

Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
290 295 300

<210> 299
<211> 295
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 299

Met Glu Lys Lys Ile Asp Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp
1 5 10 15

His Asp Ile Asp Tyr Lys Asp Asp Asp Asp Lys Gly Ser Gly Ser Ser
20 25 30

Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly
35 40 45

Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Ser
50 55 60

Gly Ser Ser Gly Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln
65 70 75 80

Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu
85 90 95

Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu
100 105 110

Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu
115 120 125

Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly
130 135 140

Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala Gly Gly Asn
145 150 155 160

Ile Asp Glu Leu Leu Met Gln Val Thr Asp Leu Ile Tyr Glu Ala Leu
165 170 175

His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Ala Phe Gln Leu Phe
180 185 190

Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Lys Gln Lys Leu Glu
195 200 205

Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Ile Leu Ser Gly
210 215 220

Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala Gly Gly Asp
225 230 235 240

Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu
245 250 255

Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr
260 265 270

Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg
275 280 285

Leu Leu Glu Glu Val Lys Arg
290 295

<210> 300
<211> 290
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 300

Met Glu Lys Lys Ile Asp Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp
1 5 10 15

His Asp Ile Asp Tyr Lys Asp Asp Asp Asp Lys Gly Ser Gly Ser Ser
20 25 30

Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly
35 40 45

Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Ser
50 55 60

Gly Ser Ser Gly Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln
65 70 75 80

Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu
85 90 95

Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu
100 105 110

Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu
115 120 125

Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly
130 135 140

Gly Ala Ser Pro Ala Ala Pro Ala Gly Gly Asn Ile Asp Glu Leu Leu
145 150 155 160

Met Gln Val Thr Asp Leu Ile Tyr Glu Ala Leu His Phe Ala Lys Asp
165 170 175

Glu Glu Phe Gln Lys His Ala Phe Gln Leu Phe Glu Lys Ala Thr Lys
180 185 190

Ala Tyr Lys Asn Lys Asp Lys Gln Lys Leu Glu Lys Val Val Glu Glu
195 200 205

Leu Lys Glu Leu Leu Glu Arg Ile Leu Ser Gly Gly Ala Ser Pro Ala
210 215 220

Ala Pro Ala Pro Ala Ser Pro Ala Gly Gly Asp Lys Glu Asn Val Leu

225 230 235 240
 Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala
 245 250 255
 Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr
 260 265 270
 Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val
 275 280 285
 Lys Arg
 290

 <210> 301
 <211> 298
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Synthetic

 <400> 301

 Met Glu Lys Lys Ile Asp Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp
 1 5 10 15

 His Asp Ile Asp Tyr Lys Asp Asp Asp Asp Lys Gly Ser Gly Ser Ser
 20 25 30

 Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly
 35 40 45

 Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Ser
 50 55 60

 Gly Ser Ser Gly Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln
 65 70 75 80

 Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu
 85 90 95

 Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu

110

$\langle 210 \rangle$	302
$\langle 211 \rangle$	290
$\langle 212 \rangle$	PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 302

Met Glu Lys Lys Ile Asp Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp
1 5 10 15

His Asp Ile Asp Tyr Lys Asp Asp Asp Lys Gly Ser Gly Ser Ser
20 25 30

Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly
35 40 45

Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Ser
50 55 60

Gly Ser Ser Gly Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln
65 70 75 80

Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu
85 90 95

Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu
100 105 110

Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu
115 120 125

Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly
130 135 140

Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala Gly Gly Asn
145 150 155 160

Ile Asp Glu Leu Leu Met Gln Val Thr Asp Leu Ile Tyr Glu Ala Leu
165 170 175

His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Ala Phe Gln Leu Phe
180 185 190

Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Lys Gln Lys Leu Glu
195 200 205

Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Ile Leu Ser Gly
210 215 220

Gly Ala Ser Pro Ala Ala Pro Ala Gly Gly Asp Lys Glu Asn Val Leu
225 230 235 240

Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala
245 250 255

Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr
260 265 270

Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val
275 280 285

Lys Arg
290

<210> 303
<211> 285
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 303

Met Glu Lys Lys Ile Asp Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp
1 5 10 15

His Asp Ile Asp Tyr Lys Asp Asp Asp Asp Lys Gly Ser Gly Ser Ser
20 25 30

Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly
35 40 45

Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Ser
50 55 60

Gly Ser Ser Gly Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln
65 70 75 80

Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu
85 90 95

Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu
100 105 110

Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu
115 120 125

Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly
130 135 140

Gly Ala Ser Pro Ala Ala Pro Ala Gly Gly Asn Ile Asp Glu Leu Leu
145 150 155 160

Met Gln Val Thr Asp Leu Ile Tyr Glu Ala Leu His Phe Ala Lys Asp
165 170 175

Glu Glu Phe Gln Lys His Ala Phe Gln Leu Phe Glu Lys Ala Thr Lys
180 185 190

Ala Tyr Lys Asn Lys Asp Lys Gln Lys Leu Glu Lys Val Val Glu Glu
195 200 205

Leu Lys Glu Leu Leu Glu Arg Ile Leu Ser Gly Gly Ala Ser Pro Ala
210 215 220

Ala Pro Ala Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu
225 230 235 240

Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln
245 250 255

Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu
260 265 270

Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg

275

280

285

<210> 304
 <211> 196
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 304

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
 1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
 20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln Val
 35 40 45

Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His
 50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp
 65 70 75 80

Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu
 85 90 95

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu
 100 105 110

Glu Leu Ala Arg Lys Gly Gly Gly Gly Glu Leu Glu Glu Gln Val Met
 115 120 125

His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys
 130 135 140

Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala
 145 150 155 160

Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile

165

170

175

Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu
 180 185 190

Leu Ala Arg Lys
 195

<210> 305
 <211> 194
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 305

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
 1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
 20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln Val
 35 40 45

Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His
 50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp
 65 70 75 80

Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu
 85 90 95

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu
 100 105 110

Glu Leu Ala Arg Lys Gly Gly Glu Leu Glu Glu Gln Val Met His Val
 115 120 125

Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr

130

135

140

Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu
 145 150 155 160

Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu
 165 170 175

Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala
 180 185 190

Arg Lys

<210> 306
 <211> 205
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 306

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
 1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
 20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln Val
 35 40 45

Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His
 50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp
 65 70 75 80

Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu
 85 90 95

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu

100

105

110

Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala
 115 120 125

Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Asn Ile Asp
 130 135 140

Glu Leu Leu Met Gln Val Thr Asp Leu Ile Tyr Glu Ala Leu His Phe
 145 150 155 160

Ala Lys Asp Glu Glu Phe Gln Lys His Ala Phe Gln Leu Phe Glu Lys
 165 170 175

Ala Thr Lys Ala Tyr Lys Asn Lys Asp Lys Gln Lys Leu Glu Lys Val
 180 185 190

Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Ile Leu Ser
 195 200 205

<210> 307
 <211> 197
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 307

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
 1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
 20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln Val
 35 40 45

Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His
 50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp

65					70					75					80
Ala	Thr	Glu	Met	Met	Leu	Glu	Leu	Ile	Lys	Ser	Asp	Asp	Glu	Arg	Glu
				85					90					95	
Ile	Arg	Glu	Ile	Glu	Glu	Glu	Ala	Arg	Arg	Ile	Leu	Glu	His	Leu	Glu
			100					105					110		
Glu	Leu	Ala	Arg	Lys	Gly	Gly	Ala	Ser	Pro	Ala	Ala	Pro	Ala	Pro	Ala
		115					120					125			
Ser	Pro	Ala	Gly	Gly	Asn	Ile	Asp	Glu	Leu	Leu	Met	Gln	Val	Thr	Asp
	130					135					140				
Leu	Ile	Tyr	Glu	Ala	Leu	His	Phe	Ala	Lys	Asp	Glu	Glu	Phe	Gln	Lys
145					150					155					160
His	Ala	Phe	Gln	Leu	Phe	Glu	Lys	Ala	Thr	Lys	Ala	Tyr	Lys	Asn	Lys
				165					170					175	
Asp	Lys	Gln	Lys	Leu	Glu	Lys	Val	Val	Glu	Glu	Leu	Lys	Glu	Leu	Leu
			180					185					190		
Glu	Arg	Ile	Leu	Ser											
			195												

<210> 308
 <211> 192
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 308

Met	Glu	Lys	Lys	Ile	Ser	Ala	Trp	Ser	His	Pro	Gln	Phe	Glu	Lys	Gly
1				5					10					15	
Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Ser	Ala	Trp	Ser	His	Pro	Gln
			20					25					30		
Phe	Glu	Lys	Gly	Gly	Ser	Gly	Ser	Ser	Gly	Glu	Leu	Glu	Glu	Gln	Val

35

40

45

Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His
 50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp
 65 70 75 80

Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu
 85 90 95

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu
 100 105 110

Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro Ala Ala Pro Ala Gly Gly
 115 120 125

Asn Ile Asp Glu Leu Leu Met Gln Val Thr Asp Leu Ile Tyr Glu Ala
 130 135 140

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Ala Phe Gln Leu
 145 150 155 160

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Lys Gln Lys Leu
 165 170 175

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Ile Leu Ser
 180 185 190

<210> 309

<211> 277

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 309

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
 1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln

20

25

30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Asp Lys Glu Asn Val Leu
 35 40 45

Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala
 50 55 60

Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr
 65 70 75 80

Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val
 85 90 95

Lys Arg Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala
 100 105 110

Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Glu Leu Glu Glu Gln Val
 115 120 125

Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His
 130 135 140

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp
 145 150 155 160

Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu
 165 170 175

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu
 180 185 190

Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala
 195 200 205

Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Asp Lys Glu
 210 215 220

Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu
 225 230 235 240

Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe
245 250 255

Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu
260 265 270

Glu Glu Val Lys Arg
275

<210> 310
<211> 285
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 310

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln Val
35 40 45

Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His
50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp
65 70 75 80

Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu
85 90 95

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu
100 105 110

Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala
115 120 125

Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Asn Leu Asp
130 135 140

Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe
145 150 155 160

Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys
165 170 175

Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val
180 185 190

Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly Ala
195 200 205

Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser
210 215 220

Ala Pro Ala Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu
225 230 235 240

Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln
245 250 255

Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu
260 265 270

Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
275 280 285

<210> 311
<211> 277
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 311

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln Val
35 40 45

Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His
50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp
65 70 75 80

Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu
85 90 95

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu
100 105 110

Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala
115 120 125

Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Asn Leu Asp
130 135 140

Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe
145 150 155 160

Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys
165 170 175

Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val
180 185 190

Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly Ala
195 200 205

Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala Gly Gly Asp Lys Glu
210 215 220

Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu

225		230		235		240									
Gly	His	Ala	Glu	Ala	Ser	Met	Gln	Val	Ser	Asp	Leu	Ile	Tyr	Glu	Phe
			245						250					255	
Met	Lys	Thr	Lys	Asp	Glu	Asn	Leu	Leu	Glu	Glu	Ala	Glu	Arg	Leu	Leu
			260					265					270		
Glu	Glu	Val	Lys	Arg											
			275												
<210> 312															
<211> 277															
<212> PRT															
<213> Artificial Sequence															
<220>															
<223> Synthetic															
<400> 312															
Met	Glu	Lys	Lys	Ile	Ser	Ala	Trp	Ser	His	Pro	Gln	Phe	Glu	Lys	Gly
1				5					10					15	
Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Ser	Ala	Trp	Ser	His	Pro	Gln
			20					25					30		
Phe	Glu	Lys	Gly	Gly	Ser	Gly	Ser	Ser	Gly	Glu	Leu	Glu	Glu	Gln	Val
		35					40					45			
Met	His	Val	Leu	Asp	Gln	Val	Ser	Glu	Leu	Ala	His	Glu	Leu	Leu	His
	50					55					60				
Lys	Leu	Thr	Gly	Glu	Glu	Leu	Glu	Arg	Ala	Ala	Tyr	Phe	Asn	Trp	Trp
65					70				75					80	
Ala	Thr	Glu	Met	Met	Leu	Glu	Leu	Ile	Lys	Ser	Asp	Asp	Glu	Arg	Glu
			85						90					95	
Ile	Arg	Glu	Ile	Glu	Glu	Glu	Ala	Arg	Arg	Ile	Leu	Glu	His	Leu	Glu
			100					105					110		
Glu	Leu	Ala	Arg	Lys	Gly	Gly	Ala	Ser	Pro	Ala	Ala	Pro	Ala	Pro	Ala

115

120

125

Ser Pro Ala Gly Gly Asn Leu Asp Glu Leu His Met Gln Met Thr Asp
 130 135 140

Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys
 145 150 155 160

His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys
 165 170 175

Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu
 180 185 190

Glu Arg Leu Leu Ser Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala
 195 200 205

Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Asp Lys Glu
 210 215 220

Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu
 225 230 235 240

Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe
 245 250 255

Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu
 260 265 270

Glu Glu Val Lys Arg
 275

<210> 313
 <211> 269
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 313

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly

1		5		10		15										
Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Ser	Ala	Trp	Ser	His	Pro	Gln	
		20					25					30				
Phe	Glu	Lys	Gly	Gly	Ser	Gly	Ser	Ser	Gly	Glu	Leu	Glu	Glu	Gln	Val	
		35					40					45				
Met	His	Val	Leu	Asp	Gln	Val	Ser	Glu	Leu	Ala	His	Glu	Leu	Leu	His	
	50					55					60					
Lys	Leu	Thr	Gly	Glu	Glu	Leu	Glu	Arg	Ala	Ala	Tyr	Phe	Asn	Trp	Trp	
65					70				75						80	
Ala	Thr	Glu	Met	Met	Leu	Glu	Leu	Ile	Lys	Ser	Asp	Asp	Glu	Arg	Glu	
			85						90					95		
Ile	Arg	Glu	Ile	Glu	Glu	Glu	Ala	Arg	Arg	Ile	Leu	Glu	His	Leu	Glu	
			100					105					110			
Glu	Leu	Ala	Arg	Lys	Gly	Gly	Ala	Ser	Pro	Ala	Ala	Pro	Ala	Pro	Ala	
		115					120					125				
Ser	Pro	Ala	Gly	Gly	Asn	Leu	Asp	Glu	Leu	His	Met	Gln	Met	Thr	Asp	
	130					135					140					
Leu	Val	Tyr	Glu	Ala	Leu	His	Phe	Ala	Lys	Asp	Glu	Glu	Phe	Gln	Lys	
145					150					155					160	
His	Val	Phe	Gln	Leu	Phe	Glu	Lys	Ala	Thr	Lys	Ala	Tyr	Lys	Asn	Lys	
			165					170						175		
Asp	Arg	Gln	Lys	Leu	Glu	Lys	Val	Val	Glu	Glu	Leu	Lys	Glu	Leu	Leu	
			180					185					190			
Glu	Arg	Leu	Leu	Ser	Gly	Gly	Ala	Ser	Pro	Ala	Ala	Pro	Ala	Pro	Ala	
		195					200					205				
Ser	Pro	Ala	Gly	Gly	Asp	Lys	Glu	Asn	Val	Leu	Gln	Lys	Ile	Tyr	Glu	
	210					215					220					

Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln
225 230 235 240

Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu
245 250 255

Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
260 265

<210> 314
<211> 264
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 314

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln Val
35 40 45

Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His
50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp
65 70 75 80

Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu
85 90 95

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu
100 105 110

Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro Ala Ala Pro Ala Gly Gly
115 120 125

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
130 135 140

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu
145 150 155 160

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
165 170 175

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
180 185 190

Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala Gly Gly
195 200 205

Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu
210 215 220

Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile
225 230 235 240

Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu
245 250 255

Arg Leu Leu Glu Glu Val Lys Arg
260

<210> 315
<211> 272
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 315

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln Val
35 40 45

Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His
50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp
65 70 75 80

Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu
85 90 95

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu
100 105 110

Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala
115 120 125

Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Asn Leu Asp
130 135 140

Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe
145 150 155 160

Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys
165 170 175

Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val
180 185 190

Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly Ala
195 200 205

Ser Pro Ala Ala Pro Ala Gly Gly Asp Lys Glu Asn Val Leu Gln Lys
210 215 220

Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala
225 230 235 240

Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp

245

250

255

Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
 260 265 270

<210> 316
 <211> 264
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 316

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
 1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
 20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln Val
 35 40 45

Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His
 50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp
 65 70 75 80

Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu
 85 90 95

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu
 100 105 110

Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala
 115 120 125

Ser Pro Ala Gly Gly Asn Leu Asp Glu Leu His Met Gln Met Thr Asp
 130 135 140

Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys

145		150		155		160									
His	Val	Phe	Gln	Leu	Phe	Glu	Lys	Ala	Thr	Lys	Ala	Tyr	Lys	Asn	Lys
			165					170						175	
Asp	Arg	Gln	Lys	Leu	Glu	Lys	Val	Val	Glu	Glu	Leu	Lys	Glu	Leu	Leu
			180					185					190		
Glu	Arg	Leu	Leu	Ser	Gly	Gly	Ala	Ser	Pro	Ala	Ala	Pro	Ala	Gly	Gly
		195					200					205			
Asp	Lys	Glu	Asn	Val	Leu	Gln	Lys	Ile	Tyr	Glu	Ile	Met	Lys	Glu	Leu
	210					215					220				
Glu	Arg	Leu	Gly	His	Ala	Glu	Ala	Ser	Met	Gln	Val	Ser	Asp	Leu	Ile
225					230					235					240
Tyr	Glu	Phe	Met	Lys	Thr	Lys	Asp	Glu	Asn	Leu	Leu	Glu	Glu	Ala	Glu
				245					250					255	
Arg	Leu	Leu	Glu	Glu	Val	Lys	Arg								
			260												

<210> 317
 <211> 259
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 317

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

50

55

60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp
65 70 75 80

Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu
85 90 95

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu
100 105 110

Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro Ala Ala Pro Ala Gly Gly
115 120 125

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
130 135 140

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu
145 150 155 160

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
165 170 175

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
180 185 190

Gly Gly Ala Ser Pro Ala Ala Pro Ala Gly Gly Asp Lys Glu Asn Val
195 200 205

Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His
210 215 220

Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys
225 230 235 240

Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu
245 250 255

Val Lys Arg

<210> 318
<211> 251
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 318

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln Val
35 40 45

Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His
50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp
65 70 75 80

Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu
85 90 95

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu
100 105 110

Glu Leu Ala Arg Lys Gly Gly Ala Ser Ala Gly Gly Asn Leu Asp Glu
115 120 125

Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala
130 135 140

Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala
145 150 155 160

Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val
165 170 175

Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly Ala Ser
180 185 190

Ala Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met
195 200 205

Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser
210 215 220

Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu
225 230 235 240

Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
245 250

<210> 319
<211> 253
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 319

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln Val
35 40 45

Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His
50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp
65 70 75 80

Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu
85 90 95

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu
100 105 110

Glu Leu Ala Arg Lys Gly Gly Ser Gly Gly Ser Gly Gly Asn Leu Asp
115 120 125

Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe
130 135 140

Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys
145 150 155 160

Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val
165 170 175

Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly Ser
180 185 190

Gly Gly Ser Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu
195 200 205

Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln
210 215 220

Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu
225 230 235 240

Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
245 250

<210> 320
<211> 247
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 320

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln Val
35 40 45

Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His
50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp
65 70 75 80

Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu
85 90 95

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu
100 105 110

Glu Leu Ala Arg Lys Gly Gly Ser Gly Gly Asn Leu Asp Glu Leu His
115 120 125

Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp
130 135 140

Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys
145 150 155 160

Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu
165 170 175

Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly Ser Gly Gly Asp
180 185 190

Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu
195 200 205

Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr
210 215 220

Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg

225	230	235	240

Leu Leu Glu Glu Val Lys Arg
 245

<210> 321
 <211> 259
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 321

Met	Glu	Lys	Lys	Ile	Ser	Ala	Trp	Ser	His	Pro	Gln	Phe	Glu	Lys	Gly
1				5					10					15	

Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Ser	Ala	Trp	Ser	His	Pro	Gln
			20					25					30		

Phe	Glu	Lys	Gly	Gly	Ser	Gly	Ser	Ser	Gly	Glu	Leu	Glu	Glu	Gln	Val
		35					40					45			

Met	His	Val	Leu	Asp	Gln	Val	Ser	Glu	Leu	Ala	His	Glu	Leu	Leu	His
	50					55					60				

Lys	Leu	Thr	Gly	Glu	Glu	Leu	Glu	Arg	Ala	Ala	Tyr	Phe	Asn	Trp	Trp
65					70					75				80	

Ala	Thr	Glu	Met	Met	Leu	Glu	Leu	Ile	Lys	Ser	Asp	Asp	Glu	Arg	Glu
				85					90					95	

Ile	Arg	Glu	Ile	Glu	Glu	Glu	Ala	Arg	Arg	Ile	Leu	Glu	His	Leu	Glu
			100					105					110		

Glu	Leu	Ala	Arg	Lys	Gly	Gly	Ser	Gly	Gly	Ser	Gly	Gly	Ser	Gly	Gly
		115					120					125			

Asn	Leu	Asp	Glu	Leu	His	Met	Gln	Met	Thr	Asp	Leu	Val	Tyr	Glu	Ala
	130					135					140				

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu

50

55

60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp
65 70 75 80

Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu
85 90 95

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu
100 105 110

Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro Ala Ala Pro Ala Gly Gly
115 120 125

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
130 135 140

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
145 150 155 160

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
165 170 175

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
180 185 190

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro
195 200 205

Ala Ala Pro Ala Gly Gly Glu Leu Glu Glu Gln Val Met His Val Leu
210 215 220

Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly
225 230 235 240

Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met
245 250 255

Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile
260 265 270

Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg
275 280 285

Lys

<210> 323
<211> 289
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 323

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln Val
35 40 45

Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His
50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp
65 70 75 80

Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu
85 90 95

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu
100 105 110

Glu Leu Ala Arg Lys Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly
115 120 125

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
130 135 140

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
145 150 155 160

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
165 170 175

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
180 185 190

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Gly Gly
195 200 205

Ser Gly Gly Ser Gly Gly Glu Leu Glu Glu Gln Val Met His Val Leu
210 215 220

Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly
225 230 235 240

Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met
245 250 255

Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile
260 265 270

Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg
275 280 285

Lys

<210> 324
<211> 283
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 324

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln Val
35 40 45

Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His
50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp
65 70 75 80

Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu
85 90 95

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu
100 105 110

Glu Leu Ala Arg Lys Gly Gly Ser Gly Gly Ser Gly Gly Glu Leu Glu
115 120 125

Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu
130 135 140

Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe
145 150 155 160

Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp
165 170 175

Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu
180 185 190

His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Gly Gly Ser Gly Gly
195 200 205

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
210 215 220

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala

225		230		235		240									
Ala	Tyr	Phe	Asn	Trp	Trp	Ala	Thr	Glu	Met	Met	Leu	Glu	Leu	Ile	Lys
			245					250						255	
Ser	Asp	Asp	Glu	Arg	Glu	Ile	Arg	Glu	Ile	Glu	Glu	Glu	Ala	Arg	Arg
			260					265					270		
Ile	Leu	Glu	His	Leu	Glu	Glu	Leu	Ala	Arg	Lys					
		275					280								
<210> 325															
<211> 277															
<212> PRT															
<213> Artificial Sequence															
<220>															
<223> Synthetic															
<400> 325															
Met	Glu	Lys	Lys	Ile	Ser	Ala	Trp	Ser	His	Pro	Gln	Phe	Glu	Lys	Gly
1				5					10					15	
Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Ser	Ala	Trp	Ser	His	Pro	Gln
			20					25					30		
Phe	Glu	Lys	Gly	Gly	Ser	Gly	Ser	Ser	Gly	Glu	Leu	Glu	Glu	Gln	Val
		35					40					45			
Met	His	Val	Leu	Asp	Gln	Val	Ser	Glu	Leu	Ala	His	Glu	Leu	Leu	His
	50					55					60				
Lys	Leu	Thr	Gly	Glu	Glu	Leu	Glu	Arg	Ala	Ala	Tyr	Phe	Asn	Trp	Trp
65					70				75					80	
Ala	Thr	Glu	Met	Met	Leu	Glu	Leu	Ile	Lys	Ser	Asp	Asp	Glu	Arg	Glu
			85						90					95	
Ile	Arg	Glu	Ile	Glu	Glu	Glu	Ala	Arg	Arg	Ile	Leu	Glu	His	Leu	Glu
			100					105					110		
Glu	Leu	Ala	Arg	Lys	Gly	Gly	Ser	Gly	Gly	Glu	Leu	Glu	Glu	Gln	Val

115

120

125

Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His
 130 135 140

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp
 145 150 155 160

Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu
 165 170 175

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu
 180 185 190

Glu Leu Ala Arg Lys Gly Gly Ser Gly Gly Glu Leu Glu Glu Gln Val
 195 200 205

Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His
 210 215 220

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp
 225 230 235 240

Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu
 245 250 255

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu
 260 265 270

Glu Leu Ala Arg Lys
 275

<210> 326
 <211> 267
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 326

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly

1	5	10	15
Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln	20	25	30
Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln Val	35	40	45
Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His	50	55	60
Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp	65	70	75
Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu	85	90	95
Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu	100	105	110
Glu Leu Ala Arg Lys Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly	115	120	125
Gly Ser Gly Gly Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu	130	135	140
Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His	145	150	155
Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp	165	170	175
Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu	180	185	190
Arg Leu Leu Ser Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly	195	200	205
Ser Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met	210	215	220

Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser
225 230 235 240

Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu
245 250 255

Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
260 265

<210> 327
<211> 261
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 327

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln Val
35 40 45

Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His
50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp
65 70 75 80

Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu
85 90 95

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu
100 105 110

Glu Leu Ala Arg Lys Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu
130 135 140

Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln
145 150 155 160

Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys
165 170 175

Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu
180 185 190

Ser Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Asp Lys Glu
195 200 205

Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu
210 215 220

Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe
225 230 235 240

Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu
245 250 255

Glu Glu Val Lys Arg
260

<210> 328
<211> 255
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 328

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln Val
35 40 45

Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His
50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp
65 70 75 80

Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu
85 90 95

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu
100 105 110

Glu Leu Ala Arg Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Asn Leu
115 120 125

Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His
130 135 140

Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu
145 150 155 160

Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys
165 170 175

Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly
180 185 190

Gly Gly Ser Gly Gly Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile
195 200 205

Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser
210 215 220

Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu
225 230 235 240

Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg

245

250

255

<210> 329
 <211> 251
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 329

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
 1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
 20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln Val
 35 40 45

Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His
 50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp
 65 70 75 80

Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu
 85 90 95

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu
 100 105 110

Glu Leu Ala Arg Lys Gly Gly Gly Ser Gly Gly Gly Asn Leu Asp Glu
 115 120 125

Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala
 130 135 140

Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala
 145 150 155 160

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

165

170

175

Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly Gly Ser
 180 185 190

Gly Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met
 195 200 205

Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser
 210 215 220

Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu
 225 230 235 240

Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
 245 250

<210> 330
 <211> 182
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 330

Met Glu Lys Lys Ile Gly Gly Gly Asp Lys Glu Asn Val Leu Gln Lys
 1 5 10 15

Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala
 20 25 30

Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp
 35 40 45

Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
 50 55 60

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
 65 70 75 80

Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Lys Glu Asn Val Leu Gln

85

90

95

Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu
 100 105 110

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

Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys
 130 135 140

Arg Gly Gly Gly Ser Gly Gly Gly Ser Ala Trp Ser His Pro Gln Phe
 145 150 155 160

Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser
 165 170 175

His Pro Gln Phe Glu Lys
 180

<210> 331
 <211> 177
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 331

Met Glu Lys Lys Ile Gly Gly Gly Asp Lys Glu Asn Val Leu Gln Lys
 1 5 10 15

Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala
 20 25 30

Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp
 35 40 45

Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
 50 55 60

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg

50

55

60

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp
65 70 75 80

Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu
85 90 95

Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr
100 105 110

Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg
115 120 125

Leu Leu Glu Glu Val Lys Arg Gly Gly Gly Ser Gly Gly Gly Ser Ala
130 135 140

Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser
145 150 155 160

Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
165 170

<210> 333
<211> 167
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 333

Met Glu Lys Lys Ile Gly Gly Gly Asp Lys Glu Asn Val Leu Gln Lys
1 5 10 15

Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala
20 25 30

Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp
35 40 45

Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg

50

55

60

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

Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala
85 90 95

Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr
100 105 110

Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val
115 120 125

Lys Arg Gly Gly Gly Ser Gly Gly Gly Ser Ala Trp Ser His Pro Gln
130 135 140

Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp
145 150 155 160

Ser His Pro Gln Phe Glu Lys
165

<210> 334

<211> 186

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 334

Met Glu Lys Lys Ile Gly Gly Gly Glu Leu Glu Glu Gln Val Met His
1 5 10 15

Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu
20 25 30

Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr
35 40 45

Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg

50

55

60

Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu
65 70 75 80

Ala Arg Lys Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Lys Glu
85 90 95

Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu
100 105 110

Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe
115 120 125

Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu
130 135 140

Glu Glu Val Lys Arg Gly Gly Gly Ser Gly Gly Gly Ser Ala Trp Ser
145 150 155 160

His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
165 170 175

Ser Ala Trp Ser His Pro Gln Phe Glu Lys
180 185

<210> 335

<211> 175

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 335

Met Glu Lys Lys Ile Gly Gly Gly Asn Leu Asp Glu Leu His Met Gln
1 5 10 15

Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu
20 25 30

Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr

35

40

45

Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys
 50 55 60

Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly Ser Gly Gly Gly Gly Ser
 65 70 75 80

Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys
 85 90 95

Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp
 100 105 110

Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu
 115 120 125

Ala Glu Arg Leu Leu Glu Glu Val Lys Arg Gly Gly Gly Ser Gly Gly
 130 135 140

Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly
 145 150 155 160

Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
 165 170 175

<210> 336

<211> 194

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 336

Met Glu Lys Lys Ile Gly Gly Gly Glu Leu Glu Glu Gln Val Met His
 1 5 10 15

Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu
 20 25 30

Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr

35

40

45

Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg
 50 55 60

Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu
 65 70 75 80

Ala Arg Lys Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Asn Leu Asp
 85 90 95

Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe
 100 105 110

Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys
 115 120 125

Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val
 130 135 140

Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly Gly
 145 150 155 160

Ser Gly Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly
 165 170 175

Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe
 180 185 190

Glu Lys

<210> 337
 <211> 194
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 337

Met Glu Lys Lys Ile Gly Gly Gly Asn Leu Asp Glu Leu His Met Gln

1	5	10	15
Met Thr Asp	Leu Val Tyr	Glu Ala Leu His Phe Ala Lys	Asp Glu Glu
	20	25	30
Phe Gln Lys	His Val Phe Gln	Leu Phe Glu Lys Ala Thr Lys	Ala Tyr
	35	40	45
Lys Asn Lys	Asp Arg Gln Lys	Leu Glu Lys Val Val Glu Glu	Leu Lys
	50	55	60
Glu Leu Leu	Glu Arg Leu Leu Ser	Gly Gly Ser Gly Gly Gly Gly	Ser
65	70	75	80
Gly Gly Glu	Leu Glu Glu Gln Val Met	His Val Leu Asp Gln Val Ser	
	85	90	95
Glu Leu Ala	His Glu Leu Leu His	Lys Leu Thr Gly Glu Glu Leu Glu	
	100	105	110
Arg Ala Ala	Tyr Phe Asn Trp Trp Ala Thr	Glu Met Met Leu Glu Leu	
	115	120	125
Ile Lys Ser	Asp Asp Glu Arg Glu Ile Arg Glu	Ile Glu Glu Glu Ala	
	130	135	140
Arg Arg Ile	Leu Glu His Leu Glu Glu Leu Ala Arg	Lys Gly Gly Gly	
145	150	155	160
Ser Gly Gly	Gly Ser Ala Trp Ser His Pro Gln Phe	Glu Lys Gly Gly	
	165	170	175
Gly Ser Gly	Gly Gly Ser Gly Gly Ser Ala Trp Ser His	Pro Gln Phe	
	180	185	190
Glu Lys			

<210> 338
 <211> 260
 <212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 338

Met Glu Lys Lys Ile Gly Gly Gly Glu Leu Glu Glu Gln Val Met His
1 5 10 15

Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu
20 25 30

Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr
35 40 45

Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg
50 55 60

Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu
65 70 75 80

Ala Arg Lys Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Asn Leu Asp
85 90 95

Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe
100 105 110

Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys
115 120 125

Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val
130 135 140

Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly Ser
145 150 155 160

Gly Gly Gly Gly Ser Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile
165 170 175

Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser
180 185 190

Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu
195 200 205

Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg Gly
210 215 220

Gly Gly Ser Gly Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
225 230 235 240

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro
245 250 255

Gln Phe Glu Lys
260

<210> 339
<211> 260
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 339

Met Glu Lys Lys Ile Gly Gly Gly Asn Leu Asp Glu Leu His Met Gln
1 5 10 15

Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu
20 25 30

Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr
35 40 45

Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys
50 55 60

Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly Ser Gly Gly Gly Gly Ser
65 70 75 80

Gly Gly Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser
85 90 95

Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu
100 105 110

Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu
115 120 125

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

Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser
145 150 155 160

Gly Gly Gly Gly Ser Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile
165 170 175

Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser
180 185 190

Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu
195 200 205

Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg Gly
210 215 220

Gly Gly Ser Gly Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
225 230 235 240

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro
245 250 255

Gln Phe Glu Lys
260

<210> 340
<211> 270
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 340

Met Glu Lys Lys Ile Gly Gly Gly Glu Leu Glu Glu Gln Val Met His
1 5 10 15

Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu
20 25 30

Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr
35 40 45

Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg
50 55 60

Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu
65 70 75 80

Ala Arg Lys Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
85 90 95

Gly Gly Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr
100 105 110

Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe
115 120 125

Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln
130 135 140

Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu
145 150 155 160

Leu Ser Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
165 170 175

Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu
180 185 190

Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu
195 200 205

Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala

210

215

220

Glu Arg Leu Leu Glu Glu Val Lys Arg Gly Gly Gly Ser Gly Gly Gly
 225 230 235 240

Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly
 245 250 255

Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
 260 265 270

<210> 341

<211> 270

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 341

Met Glu Lys Lys Ile Gly Gly Gly Asn Leu Asp Glu Leu His Met Gln
 1 5 10 15

Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu
 20 25 30

Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr
 35 40 45

Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys
 50 55 60

Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly Ser Gly Gly Gly Gly Ser
 65 70 75 80

Gly Gly Gly Gly Ser Gly Gly Glu Leu Glu Glu Gln Val Met His Val
 85 90 95

Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr
 100 105 110

Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu

115

120

125

Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu
 130 135 140

Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala
 145 150 155 160

Arg Lys Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 165 170 175

Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu
 180 185 190

Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu
 195 200 205

Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala
 210 215 220

Glu Arg Leu Leu Glu Glu Val Lys Arg Gly Gly Gly Ser Gly Gly Gly
 225 230 235 240

Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly
 245 250 255

Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
 260 265 270

<210> 342

<211> 174

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 342

Met Glu Lys Lys Ile Asn Leu Asp Glu Leu His Met Gln Met Thr Asp
 1 5 10 15

Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys

20

25

30

His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys
 35 40 45

Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu
 50 55 60

Glu Arg Leu Leu Ser Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Gly
 65 70 75 80

Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu
 85 90 95

Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu
 100 105 110

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

Glu Arg Leu Leu Glu Glu Val Lys Arg Gly Gly Ser Gly Ser Ser Gly
 130 135 140

Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly
 145 150 155 160

Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
 165 170

<210> 343
 <211> 185
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 343

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
 1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu

20

25

30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
 35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
 50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
 65 70 75 80

Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Gly Gly Asp Lys Glu Asn
 85 90 95

Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly
 100 105 110

His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met
 115 120 125

Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu
 130 135 140

Glu Val Lys Arg Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His
 145 150 155 160

Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser
 165 170 175

Ala Trp Ser His Pro Gln Phe Glu Lys
 180 185

<210> 344
 <211> 193
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 344

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp

1	5	10	15
Gln Val Ser	Glu Leu Ala His	Glu Leu Leu His Lys	Leu Thr Gly Glu
	20	25	30
Glu Leu Glu	Arg Ala Ala Tyr	Phe Asn Trp Trp Ala	Thr Glu Met Met
	35	40	45
Leu Glu Leu	Ile Lys Ser Asp	Asp Glu Arg Glu	Ile Arg Glu Ile Glu
	50	55	60
Glu Glu Ala	Arg Arg Ile Leu	Glu His Leu Glu	Glu Leu Ala Arg Lys
65	70	75	80
Gly Gly Ala	Ser Pro Ala Ala	Pro Ala Pro Gly	Gly Asn Leu Asp Glu
	85	90	95
Leu His Met	Gln Met Thr Asp	Leu Val Tyr Glu	Ala Leu His Phe Ala
	100	105	110
Lys Asp Glu	Glu Phe Gln Lys	His Val Phe Gln	Leu Phe Glu Lys Ala
	115	120	125
Thr Lys Ala	Tyr Lys Asn Lys	Asp Arg Gln Lys	Leu Glu Lys Val Val
	130	135	140
Glu Glu Leu	Lys Glu Leu Leu	Glu Arg Leu Leu	Ser Gly Gly Ser Gly
145	150	155	160
Ser Ser Gly	Ser Ala Trp Ser	His Pro Gln Phe	Glu Lys Gly Gly Gly
	165	170	175
Ser Gly Gly	Gly Ser Gly Gly	Ser Ala Trp Ser	His Pro Gln Phe Glu
	180	185	190

Lys

<210> 345
 <211> 193
 <212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 345

Met Glu Lys Lys Ile Asn Leu Asp Glu Leu His Met Gln Met Thr Asp
1 5 10 15

Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys
20 25 30

His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys
35 40 45

Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu
50 55 60

Glu Arg Leu Leu Ser Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Gly
65 70 75 80

Gly Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu
85 90 95

Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg
100 105 110

Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile
115 120 125

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

Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Gly
145 150 155 160

Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly
165 170 175

Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu
180 185 190

Lys

<210> 346
<211> 261
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 346

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
65 70 75 80

Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Gly Gly Asn Leu Asp Glu
85 90 95

Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala
100 105 110

Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala
115 120 125

Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val
130 135 140

Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly Ala Ser
145 150 155 160

Pro Ala Ala Pro Ala Pro Gly Gly Asp Lys Glu Asn Val Leu Gln Lys
165 170 175

Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala
180 185 190

Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp
195 200 205

Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
210 215 220

Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe Glu
225 230 235 240

Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His
245 250 255

Pro Gln Phe Glu Lys
260

<210> 347
<211> 261
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 347

Met Glu Lys Lys Ile Asn Leu Asp Glu Leu His Met Gln Met Thr Asp
1 5 10 15

Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys
20 25 30

His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys
35 40 45

Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu
50 55 60

Glu Arg Leu Leu Ser Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Gly
65 70 75 80

Gly Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu
85 90 95

Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg
100 105 110

Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile
115 120 125

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

Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser
145 150 155 160

Pro Ala Ala Pro Ala Pro Gly Gly Asp Lys Glu Asn Val Leu Gln Lys
165 170 175

Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala
180 185 190

Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp
195 200 205

Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
210 215 220

Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe Glu
225 230 235 240

Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His
245 250 255

Pro Gln Phe Glu Lys
260

<210> 348

<211> 285
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 348

Met Glu Lys Lys Ile Asn Leu Asp Glu Leu His Met Gln Met Thr Asp
1 5 10 15

Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys
20 25 30

His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys
35 40 45

Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu
50 55 60

Glu Arg Leu Leu Ser Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala
65 70 75 80

Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Glu Leu Glu
85 90 95

Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu
100 105 110

Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe
115 120 125

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

Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu
145 150 155 160

His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro Ala Ala Pro
165 170 175

Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly

180

185

190

Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu
 195 200 205

Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile
 210 215 220

Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu
 225 230 235 240

Arg Leu Leu Glu Glu Val Lys Arg Gly Gly Ser Gly Ser Ser Gly Ser
 245 250 255

Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly
 260 265 270

Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
 275 280 285

<210> 349

<211> 185

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 349

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
 1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
 20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
 35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
 50 55 60

Glu Glu Ala Ala Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Thr

65					70						75				80
Gly	Gly	Ala	Ser	Pro	Ala	Ala	Pro	Ala	Pro	Gly	Gly	Asp	Lys	Glu	Asn
				85					90					95	
Val	Leu	Gln	Lys	Ile	Tyr	Glu	Ile	Met	Lys	Glu	Leu	Glu	Arg	Leu	Gly
			100					105					110		
His	Ala	Glu	Ala	Ser	Met	Gln	Val	Ser	Asp	Leu	Ile	Tyr	Glu	Phe	Met
		115					120					125			
Lys	Thr	Lys	Asp	Glu	Asn	Leu	Leu	Glu	Glu	Ala	Glu	Arg	Leu	Leu	Glu
	130					135					140				
Glu	Val	Lys	Arg	Gly	Gly	Ser	Gly	Ser	Ser	Gly	Ser	Ala	Trp	Ser	His
145					150					155					160
Pro	Gln	Phe	Glu	Lys	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Ser
				165					170					175	
Ala	Trp	Ser	His	Pro	Gln	Phe	Glu	Lys							
			180					185							

<210> 350
 <211> 193
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 350

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

50

55

60

Glu Glu Ala Ala Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Thr
65 70 75 80

Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Gly Gly Asn Leu Asp Glu
85 90 95

Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala
100 105 110

Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala
115 120 125

Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val
130 135 140

Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly Ser Gly
145 150 155 160

Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly
165 170 175

Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu
180 185 190

Lys

<210> 351
<211> 193
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 351

Met Glu Lys Lys Ile Asn Leu Asp Glu Leu His Met Gln Met Thr Asp
1 5 10 15

Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys

20

25

30

His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys
 35 40 45

Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu
 50 55 60

Glu Arg Leu Leu Ser Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Gly
 65 70 75 80

Gly Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu
 85 90 95

Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg
 100 105 110

Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile
 115 120 125

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

Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Thr Gly Gly Ser Gly
 145 150 155 160

Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly
 165 170 175

Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu
 180 185 190

Lys

<210> 352
 <211> 261
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 352

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
50 55 60

Glu Glu Ala Ala Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Thr
65 70 75 80

Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Gly Gly Asn Leu Asp Glu
85 90 95

Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala
100 105 110

Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala
115 120 125

Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val
130 135 140

Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly Ala Ser
145 150 155 160

Pro Ala Ala Pro Ala Pro Gly Gly Asp Lys Glu Asn Val Leu Gln Lys
165 170 175

Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala
180 185 190

Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp
195 200 205

Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
210 215 220

Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe Glu
225 230 235 240

Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His
245 250 255

Pro Gln Phe Glu Lys
260

<210> 353
<211> 261
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 353

Met Glu Lys Lys Ile Asn Leu Asp Glu Leu His Met Gln Met Thr Asp
1 5 10 15

Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys
20 25 30

His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys
35 40 45

Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu
50 55 60

Glu Arg Leu Leu Ser Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Gly
65 70 75 80

Gly Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu
85 90 95

Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg
100 105 110

Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile
115 120 125

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

Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Thr Gly Gly Ala Ser
145 150 155 160

Pro Ala Ala Pro Ala Pro Gly Gly Asp Lys Glu Asn Val Leu Gln Lys
165 170 175

Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala
180 185 190

Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp
195 200 205

Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
210 215 220

Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe Glu
225 230 235 240

Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His
245 250 255

Pro Gln Phe Glu Lys
260

<210> 354
<211> 285
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 354

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln Val
35 40 45

Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His
50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp
65 70 75 80

Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu
85 90 95

Ile Arg Glu Ile Glu Glu Glu Ala Ala Arg Ile Leu Glu His Leu Glu
100 105 110

Glu Leu Ala Arg Thr Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala
115 120 125

Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Asn Leu Asp
130 135 140

Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe
145 150 155 160

Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys
165 170 175

Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val
180 185 190

Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly Ala
195 200 205

Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser
210 215 220

Ala Pro Ala Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu

225		230		235		240
Ile Met Lys Glu	Leu Glu Arg Leu Gly	His Ala Glu Ala	Ser Met Gln			
	245	250	255			
Val Ser Asp Leu	Ile Tyr Glu Phe Met Lys Thr Lys Asp	Glu Asn Leu				
	260	265	270			
Leu Glu Glu Ala	Glu Arg Leu Leu Glu Glu Val Lys Arg					
	275	280	285			
<210> 355						
<211> 285						
<212> PRT						
<213> Artificial Sequence						
<220>						
<223> Synthetic						
<400> 355						
Met Glu Lys Lys	Ile Asn Leu Asp Glu Leu His Met Gln Met Thr Asp					
1	5	10	15			
Leu Val Tyr Glu	Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys					
	20	25	30			
His Val Phe Gln	Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys					
	35	40	45			
Asp Arg Gln Lys	Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu					
	50	55	60			
Glu Arg Leu Leu	Ser Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala					
65	70	75	80			
Ser Pro Ala Ala	Pro Ala Pro Ser Ala Pro Ala Gly Gly Glu Leu Glu					
	85	90	95			
Glu Gln Val Met	His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu					
	100	105	110			
Leu Leu His Lys	Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe					

115

120

125

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

Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Ala Arg Ile Leu Glu
 145 150 155 160

His Leu Glu Glu Leu Ala Arg Thr Gly Gly Ala Ser Pro Ala Ala Pro
 165 170 175

Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly
 180 185 190

Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu
 195 200 205

Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile
 210 215 220

Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu
 225 230 235 240

Arg Leu Leu Glu Glu Val Lys Arg Gly Gly Ser Gly Ser Ser Gly Ser
 245 250 255

Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly
 260 265 270

Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
 275 280 285

<210> 356

<211> 150

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 356

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp

1	5	10	15
Gln Val Ser	Glu Leu Ala His	Glu Leu Leu His Lys	Leu Thr Gly Glu
	20	25	30
Glu Leu Glu	Arg Ala Ala Tyr	Phe Asn Trp Trp Ala	Thr Glu Met Met
	35	40	45
Leu Glu Leu	Ile Lys Ser Asp	Asp Glu Arg Glu	Ile Arg Glu Ile Glu
	50	55	60
Glu Glu Ala	Arg Arg Ile Leu	Glu His Leu Glu	Glu Leu Ala Arg Lys
65	70	75	80
Gly Ser Gly	Ser Gly Tyr Ile	Pro Glu Ala Pro	Arg Asp Gly
	85	90	95
Gln Ala Tyr	Val Arg Lys Asp	Gly Glu Trp Val	Leu Leu Ser Thr Phe
	100	105	110
Leu Gly Gly	Ser Gly Ser Ser	Gly Ser Ala Trp	Ser His Pro Gln Phe
	115	120	125
Glu Lys Gly	Gly Gly Ser Gly	Gly Gly Ser Gly	Gly Ser Ala Trp Ser
	130	135	140
His Pro Gln	Phe Glu Lys		
145	150		

<210> 357
 <211> 253
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 357

Met Glu Lys	Lys Ile Glu Leu	Glu Glu Gln Val	Met His Val	Leu Asp
1	5	10	15	

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu

20

25

30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
 35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
 50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
 65 70 75 80

Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser
 85 90 95

Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Glu Leu Glu Glu
 100 105 110

Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu
 115 120 125

Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn
 130 135 140

Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu
 145 150 155 160

Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His
 165 170 175

Leu Glu Glu Leu Ala Arg Lys Gly Ser Gly Ser Gly Ser Gly Tyr Ile
 180 185 190

Pro Glu Ala Pro Arg Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu
 195 200 205

Trp Val Leu Leu Ser Thr Phe Leu Gly Gly Ser Gly Ser Ser Gly Ser
 210 215 220

Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly
 225 230 235 240

Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
245 250

<210> 358
<211> 149
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 358

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
65 70 75 80

Gly Ser Gly Ser Gly Gly Tyr Ile Pro Glu Ala Pro Arg Asp Gly Gln
85 90 95

Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu Leu Ser Thr Phe Leu
100 105 110

Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe Glu
115 120 125

Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His
130 135 140

Pro Gln Phe Glu Lys
145

<210> 359
<211> 148
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 359

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
65 70 75 80

Gly Ser Gly Ser Gly Tyr Ile Pro Glu Ala Pro Arg Asp Gly Gln Ala
85 90 95

Tyr Val Arg Lys Asp Gly Glu Trp Val Leu Leu Ser Thr Phe Leu Gly
100 105 110

Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
115 120 125

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro
130 135 140

Gln Phe Glu Lys
145

<210> 360
<211> 147
<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 360

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
65 70 75 80

Gly Ser Gly Gly Tyr Ile Pro Glu Ala Pro Arg Asp Gly Gln Ala Tyr
85 90 95

Val Arg Lys Asp Gly Glu Trp Val Leu Leu Ser Thr Phe Leu Gly Gly
100 105 110

Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
115 120 125

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
130 135 140

Phe Glu Lys
145

<210> 361

<211> 250

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 361

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
65 70 75 80

Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser
85 90 95

Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Glu Leu Glu Glu
100 105 110

Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu
115 120 125

Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn
130 135 140

Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu
145 150 155 160

Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His
165 170 175

Leu Glu Glu Leu Ala Arg Lys Gly Ser Gly Gly Tyr Ile Pro Glu Ala
180 185 190

Pro Arg Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu
195 200 205

Leu Ser Thr Phe Leu Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser
210 215 220

His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
225 230 235 240

Ser Ala Trp Ser His Pro Gln Phe Glu Lys
245 250

<210> 362
<211> 206
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 362

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
65 70 75 80

Gly Ser Gly Ser Ser Glu Glu Leu Arg Ala Val Ala Asp Leu Gln Arg
85 90 95

Leu Asn Ile Glu Leu Ala Arg Lys Leu Leu Glu Ala Val Ala Arg Leu
100 105 110

Gln Glu Leu Asn Ile Asp Leu Val Arg Lys Thr Ser Glu Leu Thr Asp
115 120 125

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

Arg Ile Val Glu Glu Ala Glu Glu Glu Ile Arg Arg Ala Lys Glu Glu
145 150 155 160

Ser Arg Lys Ile Ala Asp Glu Ser Arg Gly Gly Ser Gly Ser Ser Gly
165 170 175

Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly
180 185 190

Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
195 200 205

<210> 363
<211> 207
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 363

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
65 70 75 80

Gly Ser Gly Ser Gly Ser Glu Glu Leu Arg Ala Val Ala Asp Leu Gln
85 90 95

Arg Leu Asn Ile Glu Leu Ala Arg Lys Leu Leu Glu Ala Val Ala Arg
100 105 110

Leu Gln Glu Leu Asn Ile Asp Leu Val Arg Lys Thr Ser Glu Leu Thr
115 120 125

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

Lys Arg Ile Val Glu Glu Ala Glu Glu Glu Ile Arg Arg Ala Lys Glu
145 150 155 160

Glu Ser Arg Lys Ile Ala Asp Glu Ser Arg Gly Gly Ser Gly Ser Ser
165 170 175

Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly
180 185 190

Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
195 200 205

<210> 364
<211> 309
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 364

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
65 70 75 80

Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser
85 90 95

Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Glu Leu Glu Glu
100 105 110

Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu
115 120 125

Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn
130 135 140

Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu
145 150 155 160

Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His
165 170 175

Leu Glu Glu Leu Ala Arg Lys Gly Ser Gly Ser Ser Glu Glu Leu Arg
180 185 190

Ala Val Ala Asp Leu Gln Arg Leu Asn Ile Glu Leu Ala Arg Lys Leu
195 200 205

Leu Glu Ala Val Ala Arg Leu Gln Glu Leu Asn Ile Asp Leu Val Arg
210 215 220

Lys Thr Ser Glu Leu Thr Asp Glu Lys Thr Ile Arg Glu Glu Ile Arg
225 230 235 240

Lys Val Lys Glu Glu Ser Lys Arg Ile Val Glu Glu Ala Glu Glu Glu
245 250 255

Ile Arg Arg Ala Lys Glu Glu Ser Arg Lys Ile Ala Asp Glu Ser Arg
260 265 270

Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe Glu

275

280

285

Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His
 290 295 300

Pro Gln Phe Glu Lys
 305

<210> 365
 <211> 310
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 365

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
 1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
 20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
 35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
 50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
 65 70 75 80

Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser
 85 90 95

Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Glu Leu Glu Glu
 100 105 110

Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu
 115 120 125

Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn

130

135

140

Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu
145 150 155 160

Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His
165 170 175

Leu Glu Glu Leu Ala Arg Lys Gly Ser Gly Ser Gly Ser Glu Glu Leu
180 185 190

Arg Ala Val Ala Asp Leu Gln Arg Leu Asn Ile Glu Leu Ala Arg Lys
195 200 205

Leu Leu Glu Ala Val Ala Arg Leu Gln Glu Leu Asn Ile Asp Leu Val
210 215 220

Arg Lys Thr Ser Glu Leu Thr Asp Glu Lys Thr Ile Arg Glu Glu Ile
225 230 235 240

Arg Lys Val Lys Glu Glu Ser Lys Arg Ile Val Glu Glu Ala Glu Glu
245 250 255

Glu Ile Arg Arg Ala Lys Glu Glu Ser Arg Lys Ile Ala Asp Glu Ser
260 265 270

Arg Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe
275 280 285

Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser
290 295 300

His Pro Gln Phe Glu Lys
305 310

<210> 366
<211> 139
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 366

Met Glu Lys Lys Ile Asn Leu Asp Glu Leu His Met Gln Met Thr Asp
1 5 10 15

Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys
20 25 30

His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys
35 40 45

Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu
50 55 60

Glu Arg Leu Leu Ser Gly Ser Gly Ser Gly Ser Gly Tyr Ile Pro Glu
65 70 75 80

Ala Pro Arg Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val
85 90 95

Leu Leu Ser Thr Phe Leu Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp
100 105 110

Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly
115 120 125

Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
130 135

<210> 367

<211> 138

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 367

Met Glu Lys Lys Ile Asn Leu Asp Glu Leu His Met Gln Met Thr Asp
1 5 10 15

Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys

20

25

30

His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys
 35 40 45

Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu
 50 55 60

Glu Arg Leu Leu Ser Gly Ser Gly Ser Gly Gly Tyr Ile Pro Glu Ala
 65 70 75 80

Pro Arg Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu
 85 90 95

Leu Ser Thr Phe Leu Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser
 100 105 110

His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
 115 120 125

Ser Ala Trp Ser His Pro Gln Phe Glu Lys
 130 135

<210> 368
 <211> 137
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 368

Met Glu Lys Lys Ile Asn Leu Asp Glu Leu His Met Gln Met Thr Asp
 1 5 10 15

Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys
 20 25 30

His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys
 35 40 45

Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu

50

55

60

Glu Arg Leu Leu Ser Gly Ser Gly Ser Gly Tyr Ile Pro Glu Ala Pro
65 70 75 80

Arg Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu Leu
85 90 95

Ser Thr Phe Leu Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His
100 105 110

Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser
115 120 125

Ala Trp Ser His Pro Gln Phe Glu Lys
130 135

<210> 369
<211> 196
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 369

Met Glu Lys Lys Ile Asn Leu Asp Glu Leu His Met Gln Met Thr Asp
1 5 10 15

Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys
20 25 30

His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys
35 40 45

Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu
50 55 60

Glu Arg Leu Leu Ser Gly Ser Gly Ser Gly Ser Glu Glu Leu Arg Ala
65 70 75 80

Val Ala Asp Leu Gln Arg Leu Asn Ile Glu Leu Ala Arg Lys Leu Leu

85

90

95

Glu Ala Val Ala Arg Leu Gln Glu Leu Asn Ile Asp Leu Val Arg Lys
 100 105 110

Thr Ser Glu Leu Thr Asp Glu Lys Thr Ile Arg Glu Glu Ile Arg Lys
 115 120 125

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

Arg Arg Ala Lys Glu Glu Ser Arg Lys Ile Ala Asp Glu Ser Arg Gly
 145 150 155 160

Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
 165 170 175

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro
 180 185 190

Gln Phe Glu Lys
 195

<210> 370
 <211> 287
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 370

Met Glu Lys Lys Ile Asn Leu Asp Glu Leu His Met Gln Met Thr Asp
 1 5 10 15

Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys
 20 25 30

His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys
 35 40 45

Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu

50

55

60

Glu Arg Leu Leu Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly
65 70 75 80

Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly
85 90 95

Ser Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu
100 105 110

Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln
115 120 125

Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys
130 135 140

Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu
145 150 155 160

Ser Gly Ser Gly Ser Ser Glu Glu Leu Arg Ala Val Ala Asp Leu Gln
165 170 175

Arg Leu Asn Ile Glu Leu Ala Arg Lys Leu Leu Glu Ala Val Ala Arg
180 185 190

Leu Gln Glu Leu Asn Ile Asp Leu Val Arg Lys Thr Ser Glu Leu Thr
195 200 205

Asp Glu Lys Thr Ile Arg Glu Glu Ile Arg Lys Val Lys Glu Glu Ser
210 215 220

Lys Arg Ile Val Glu Glu Ala Glu Glu Glu Ile Arg Arg Ala Lys Glu
225 230 235 240

Glu Ser Arg Lys Ile Ala Asp Glu Ser Arg Gly Gly Ser Gly Ser Ser
245 250 255

Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly
260 265 270

Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
275 280 285

<210> 371
<211> 288
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 371

Met Glu Lys Lys Ile Asn Leu Asp Glu Leu His Met Gln Met Thr Asp
1 5 10 15

Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys
20 25 30

His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys
35 40 45

Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu
50 55 60

Glu Arg Leu Leu Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly
65 70 75 80

Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly
85 90 95

Ser Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu
100 105 110

Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln
115 120 125

Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys
130 135 140

Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu
145 150 155 160

Ser Gly Ser Gly Ser Gly Ser Glu Glu Leu Arg Ala Val Ala Asp Leu
165 170 175

Gln Arg Leu Asn Ile Glu Leu Ala Arg Lys Leu Leu Glu Ala Val Ala
180 185 190

Arg Leu Gln Glu Leu Asn Ile Asp Leu Val Arg Lys Thr Ser Glu Leu
195 200 205

Thr Asp Glu Lys Thr Ile Arg Glu Glu Ile Arg Lys Val Lys Glu Glu
210 215 220

Ser Lys Arg Ile Val Glu Glu Ala Glu Glu Glu Ile Arg Arg Ala Lys
225 230 235 240

Glu Glu Ser Arg Lys Ile Ala Asp Glu Ser Arg Gly Gly Ser Gly Ser
245 250 255

Ser Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser
260 265 270

Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
275 280 285

<210> 372
<211> 238
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 372

Met Glu Lys Lys Ile Glu Glu Ala Glu Leu Ala Tyr Leu Leu Gly Glu
1 5 10 15

Leu Ala Tyr Lys Leu Gly Glu Tyr Arg Ile Ala Ile Arg Ala Tyr Arg
20 25 30

Ile Ala Leu Lys Arg Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu
35 40 45

Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr
50 55 60

Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr
65 70 75 80

Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile
85 90 95

Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala
100 105 110

Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu
115 120 125

Ala Ile Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Gly Ser Gly Ser Gly
130 135 140

Ser Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu
145 150 155 160

Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu
165 170 175

Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala
180 185 190

Glu Arg Leu Leu Glu Glu Val Lys Arg Gly Gly Ser Gly Ser Ser Gly
195 200 205

Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly
210 215 220

Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
225 230 235

<210> 373
<211> 236
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 373

Met Glu Lys Lys Ile Glu Glu Ala Glu Leu Ala Tyr Leu Leu Gly Glu
1 5 10 15

Leu Ala Tyr Lys Leu Gly Glu Tyr Arg Ile Ala Ile Arg Ala Tyr Arg
20 25 30

Ile Ala Leu Lys Arg Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu
35 40 45

Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr
50 55 60

Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr
65 70 75 80

Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile
85 90 95

Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala
100 105 110

Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu
115 120 125

Ala Ile Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Gly Ser Gly Ser Asp
130 135 140

Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu
145 150 155 160

Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr
165 170 175

Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg
180 185 190

Leu Leu Glu Glu Val Lys Arg Gly Gly Ser Gly Ser Ser Gly Ser Ala

195

200

205

Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser
 210 215 220

Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
 225 230 235

<210> 374
 <211> 234
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 374

Met Glu Lys Lys Ile Glu Glu Ala Glu Leu Ala Tyr Leu Leu Gly Glu
 1 5 10 15

Leu Ala Tyr Lys Leu Gly Glu Tyr Arg Ile Ala Ile Arg Ala Tyr Arg
 20 25 30

Ile Ala Leu Lys Arg Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu
 35 40 45

Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr
 50 55 60

Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr
 65 70 75 80

Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile
 85 90 95

Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala
 100 105 110

Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu
 115 120 125

Ala Ile Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Gly Ser Asp Lys Glu

130

135

140

Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu
 145 150 155 160

Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe
 165 170 175

Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu
 180 185 190

Glu Glu Val Lys Arg Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser
 195 200 205

His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
 210 215 220

Ser Ala Trp Ser His Pro Gln Phe Glu Lys
 225 230

<210> 375
 <211> 283
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 375

Met Glu Lys Lys Ile Asn Leu Asp Glu Leu His Met Gln Met Thr Asp
 1 5 10 15

Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys
 20 25 30

His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys
 35 40 45

Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu
 50 55 60

Glu Arg Leu Leu Ser Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala

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

<210> 376
<211> 284
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 376

Met Glu Lys Lys Ile Asn Leu Asp Glu Leu His Met Gln Met Thr Asp
1 5 10 15

Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys
20 25 30

His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys
35 40 45

Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu
50 55 60

Glu Arg Leu Leu Ser Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala
65 70 75 80

Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Asn Leu Asp
85 90 95

Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe
100 105 110

Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys
115 120 125

Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val
130 135 140

Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Ser Gly
145 150 155 160

Ser Gly Ser Glu Glu Leu Arg Ala Val Ala Asp Leu Gln Arg Leu Asn
165 170 175

Ile Glu Leu Ala Arg Lys Leu Leu Glu Ala Val Ala Arg Leu Gln Glu
180 185 190

Leu Asn Ile Asp Leu Val Arg Lys Thr Ser Glu Leu Thr Asp Glu Lys
195 200 205

Thr Ile Arg Glu Glu Ile Arg Lys Val Lys Glu Glu Ser Lys Arg Ile
210 215 220

Val Glu Glu Ala Glu Glu Glu Ile Arg Arg Ala Lys Glu Glu Ser Arg
225 230 235 240

Lys Ile Ala Asp Glu Ser Arg Gly Gly Ser Gly Ser Ser Gly Ser Ala
245 250 255

Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser
260 265 270

Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
275 280

<210> 377
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 377

Met Glu Lys Lys Ile Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu
1 5 10 15

Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln
20 25 30

Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu
35 40 45

Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg Gly Gly Gly
50 55 60

Ser Gly Gly Gly Ser Gly Gly Glu Leu Glu Glu Gln Val Met His Val
65 70 75 80

Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr
85 90 95

Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu
100 105 110

Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu
115 120 125

Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala
130 135 140

Arg Lys Gly Ser Gly Ser Gly Tyr Ile Pro Glu Ala Pro Arg Asp Gly
145 150 155 160

Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu Leu Ser Thr Phe
165 170 175

Leu Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe
180 185 190

Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser
195 200 205

His Pro Gln Phe Glu Lys
210

<210> 378
<211> 232
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 378

Met Glu Lys Lys Ile Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu
1 5 10 15

Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln
20 25 30

Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu
35 40 45

Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg Gly Ser Gly
50 55 60

Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly
65 70 75 80

Ser Gly Ser Gly Ser Gly Ser Gly Ser Glu Leu Glu Glu Gln Val Met
85 90 95

His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys
100 105 110

Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala
115 120 125

Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile
130 135 140

Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu
145 150 155 160

Leu Ala Arg Lys Gly Ser Gly Ser Gly Tyr Ile Pro Glu Ala Pro Arg
165 170 175

Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu Leu Ser
180 185 190

Thr Phe Leu Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro
195 200 205

Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala
210 215 220

Trp Ser His Pro Gln Phe Glu Lys

225

230

<210> 379

<211> 222

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 379

Met Glu Lys Lys Ile Asn Leu Asp Glu Leu His Met Gln Met Thr Asp
 1 5 10 15

Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys
 20 25 30

His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys
 35 40 45

Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu
 50 55 60

Glu Arg Leu Leu Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Glu
 65 70 75 80

Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu Ala
 85 90 95

His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala
 100 105 110

Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser
 115 120 125

Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile
 130 135 140

Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Ser Gly Ser Gly Tyr
 145 150 155 160

Ile Pro Glu Ala Pro Arg Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly

165

170

175

Glu Trp Val Leu Leu Ser Thr Phe Leu Gly Gly Ser Gly Ser Ser Gly
 180 185 190

Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly
 195 200 205

Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
 210 215 220

<210> 380

<211> 228

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 380

Met Glu Lys Lys Ile Asn Leu Asp Glu Leu His Met Gln Met Thr Asp
 1 5 10 15

Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys
 20 25 30

His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys
 35 40 45

Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu
 50 55 60

Glu Arg Leu Leu Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly
 65 70 75 80

Ser Gly Ser Gly Ser Glu Leu Glu Glu Gln Val Met His Val Leu Asp
 85 90 95

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
 100 105 110

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met

115

120

125

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
 130 135 140

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
 145 150 155 160

Gly Ser Gly Ser Gly Tyr Ile Pro Glu Ala Pro Arg Asp Gly Gln Ala
 165 170 175

Tyr Val Arg Lys Asp Gly Glu Trp Val Leu Leu Ser Thr Phe Leu Gly
 180 185 190

Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
 195 200 205

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro
 210 215 220

Gln Phe Glu Lys
 225

<210> 381
 <211> 331
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 381

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
 1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
 20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Met Glu Glu Ala Glu Leu
 35 40 45

Ala Tyr Leu Leu Gly Glu Leu Ala Tyr Lys Leu Gly Glu Tyr Arg Ile

50

55

60

Ala Ile Arg Ala Tyr Arg Ile Ala Leu Lys Arg Asp Pro Asn Asn Ala
65 70 75 80

Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr
85 90 95

Asp Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn
100 105 110

Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly
115 120 125

Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Asp
130 135 140

Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr Lys
145 150 155 160

Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu Glu
165 170 175

Leu Gly Ser Gly Ser Gly Ser Asp Lys Glu Asn Val Leu Gln Lys Ile
180 185 190

Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser
195 200 205

Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu
210 215 220

Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg Gly
225 230 235 240

Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly
245 250 255

Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Asn Leu Asp Glu Leu
260 265 270

His Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys
275 280 285

Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr
290 295 300

Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu
305 310 315 320

Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
325 330

<210> 382
<211> 312
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 382

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Met Glu Glu Ala Glu Leu
35 40 45

Ala Tyr Leu Leu Gly Glu Leu Ala Tyr Lys Leu Gly Glu Tyr Arg Ile
50 55 60

Ala Ile Arg Ala Tyr Arg Ile Ala Leu Lys Arg Asp Pro Asn Asn Ala
65 70 75 80

Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr
85 90 95

Asp Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn
100 105 110

Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly
115 120 125

Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Asp
130 135 140

Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr Lys
145 150 155 160

Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu Glu
165 170 175

Leu Gly Ser Gly Ser Gly Ser Asp Lys Glu Asn Val Leu Gln Lys Ile
180 185 190

Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser
195 200 205

Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu
210 215 220

Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg Gly
225 230 235 240

Ser Gly Ser Gly Ser Gly Ser Gly Asn Leu Asp Glu Leu His Met Gln
245 250 255

Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu
260 265 270

Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr
275 280 285

Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys
290 295 300

Glu Leu Leu Glu Arg Leu Leu Ser
305 310

<210> 383

<211> 342
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 383

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Met Glu Glu Ala Glu Leu
35 40 45

Ala Tyr Leu Leu Gly Glu Leu Ala Tyr Lys Leu Gly Glu Tyr Arg Ile
50 55 60

Ala Ile Arg Ala Tyr Arg Ile Ala Leu Lys Arg Asp Pro Asn Asn Ala
65 70 75 80

Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr
85 90 95

Asp Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn
100 105 110

Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly
115 120 125

Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Asp
130 135 140

Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr Lys
145 150 155 160

Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu Glu
165 170 175

Leu Gly Ser Gly Ser Gly Ser Asp Lys Glu Asn Val Leu Gln Lys Ile

180

185

190

Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser
 195 200 205

Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu
 210 215 220

Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg Gly
 225 230 235 240

Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly
 245 250 255

Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Glu Leu Glu Glu Gln
 260 265 270

Val Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu
 275 280 285

His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp
 290 295 300

Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg
 305 310 315 320

Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu
 325 330 335

Glu Glu Leu Ala Arg Lys
 340

<210> 384
 <211> 323
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 384

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly

1	5	10	15
Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln	20	25	30
Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Met Glu Glu Ala Glu Leu	35	40	45
Ala Tyr Leu Leu Gly Glu Leu Ala Tyr Lys Leu Gly Glu Tyr Arg Ile	50	55	60
Ala Ile Arg Ala Tyr Arg Ile Ala Leu Lys Arg Asp Pro Asn Asn Ala	65	70	75
Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr	85	90	95
Asp Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn	100	105	110
Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly	115	120	125
Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Asp	130	135	140
Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr Lys	145	150	155
Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu Glu	165	170	175
Leu Gly Ser Gly Ser Gly Ser Asp Lys Glu Asn Val Leu Gln Lys Ile	180	185	190
Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser	195	200	205
Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu	210	215	220

Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg Gly
225 230 235 240

Ser Gly Ser Gly Ser Gly Ser Gly Glu Leu Glu Glu Gln Val Met His
245 250 255

Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu
260 265 270

Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr
275 280 285

Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg
290 295 300

Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu
305 310 315 320

Ala Arg Lys

<210> 385
<211> 203
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 385

Met Glu Lys Lys Ile Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu
1 5 10 15

Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln
20 25 30

Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu
35 40 45

Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg Gly Gly Gly
50 55 60

Ser Gly Gly Gly Ser Gly Gly Asn Leu Asp Glu Leu His Met Gln Met
65 70 75 80

Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe
85 90 95

Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys
100 105 110

Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu
115 120 125

Leu Leu Glu Arg Leu Leu Ser Gly Ser Gly Ser Gly Tyr Ile Pro Glu
130 135 140

Ala Pro Arg Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val
145 150 155 160

Leu Leu Ser Thr Phe Leu Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp
165 170 175

Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly
180 185 190

Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
195 200

<210> 386
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 386

Met Glu Lys Lys Ile Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu
1 5 10 15

Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln
20 25 30

Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu
35 40 45

Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg Gly Ser Gly
50 55 60

Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly
65 70 75 80

Ser Gly Ser Gly Ser Gly Ser Gly Ser Asn Leu Asp Glu Leu His Met
85 90 95

Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu
100 105 110

Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala
115 120 125

Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu
130 135 140

Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Ser Gly Ser Gly Tyr Ile
145 150 155 160

Pro Glu Ala Pro Arg Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu
165 170 175

Trp Val Leu Leu Ser Thr Phe Leu Gly Gly Ser Gly Ser Ser Gly Ser
180 185 190

Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly
195 200 205

Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
210 215 220

<210> 387
<211> 222
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 387

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
65 70 75 80

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Asn Leu Asp Glu Leu His
85 90 95

Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp
100 105 110

Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys
115 120 125

Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu
130 135 140

Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Ser Gly Ser Gly Tyr
145 150 155 160

Ile Pro Glu Ala Pro Arg Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly
165 170 175

Glu Trp Val Leu Leu Ser Thr Phe Leu Gly Gly Ser Gly Ser Ser Gly
180 185 190

Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly

195

200

205

Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
 210 215 220

<210> 388
 <211> 228
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 388

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
 1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
 20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
 35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
 50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
 65 70 75 80

Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser
 85 90 95

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
 100 105 110

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu
 115 120 125

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
 130 135 140

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser

145 150 155 160
 Gly Ser Gly Ser Gly Tyr Ile Pro Glu Ala Pro Arg Asp Gly Gln Ala
 165 170 175
 Tyr Val Arg Lys Asp Gly Glu Trp Val Leu Leu Ser Thr Phe Leu Gly
 180 185 190
 Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
 195 200 205
 Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro
 210 215 220
 Gln Phe Glu Lys
 225
 <210> 389
 <211> 261
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 389
 Met Glu Lys Lys Ile Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu
 1 5 10 15
 Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln
 20 25 30
 Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu
 35 40 45
 Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg Gly Ser Gly
 50 55 60
 Ser Gly Ser Gly Ser Gly Asn Leu Asp Glu Leu His Met Gln Met Thr
 65 70 75 80
 Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln

85

90

95

Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn
 100 105 110

Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu
 115 120 125

Leu Glu Arg Leu Leu Ser Gly Ser Gly Ser Gly Ser Glu Glu Leu Arg
 130 135 140

Ala Val Ala Asp Leu Gln Arg Leu Asn Ile Glu Leu Ala Arg Lys Leu
 145 150 155 160

Leu Glu Ala Val Ala Arg Leu Gln Glu Leu Asn Ile Asp Leu Val Arg
 165 170 175

Lys Thr Ser Glu Leu Thr Asp Glu Lys Thr Ile Arg Glu Glu Ile Arg
 180 185 190

Lys Val Lys Glu Glu Ser Lys Arg Ile Val Glu Glu Ala Glu Glu Glu
 195 200 205

Ile Arg Arg Ala Lys Glu Glu Ser Arg Lys Ile Ala Asp Glu Ser Arg
 210 215 220

Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe Glu
 225 230 235 240

Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His
 245 250 255

Pro Gln Phe Glu Lys
 260

<210> 390
 <211> 280
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 390

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
65 70 75 80

Gly Ser Gly Ser Gly Ser Gly Ser Gly Asn Leu Asp Glu Leu His Met
85 90 95

Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu
100 105 110

Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala
115 120 125

Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu
130 135 140

Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Ser Gly Ser Gly Ser Glu
145 150 155 160

Glu Leu Arg Ala Val Ala Asp Leu Gln Arg Leu Asn Ile Glu Leu Ala
165 170 175

Arg Lys Leu Leu Glu Ala Val Ala Arg Leu Gln Glu Leu Asn Ile Asp
180 185 190

Leu Val Arg Lys Thr Ser Glu Leu Thr Asp Glu Lys Thr Ile Arg Glu
195 200 205

Glu Ile Arg Lys Val Lys Glu Glu Ser Lys Arg Ile Val Glu Glu Ala
210 215 220

Glu Glu Glu Ile Arg Arg Ala Lys Glu Glu Ser Arg Lys Ile Ala Asp
225 230 235 240

Glu Ser Arg Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro
245 250 255

Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala
260 265 270

Trp Ser His Pro Gln Phe Glu Lys
275 280

<210> 391
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 391

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
65 70 75 80

Gly Ser Gly Ser Glu Glu Ala Glu Leu Ala Tyr Leu Leu Gly Glu Leu
85 90 95

Ala Tyr Lys Leu Gly Glu Tyr Arg Ile Ala Ile Arg Ala Tyr Arg Ile
100 105 110

Ala Leu Lys Arg Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly
115 120 125

Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Tyr Tyr Gln
130 135 140

Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Lys Gln Asn Leu
145 150 155 160

Gly Asn Ala Lys Gln Lys Gln Gly Gly Gly Ser Gly Ser Ser Gly Ser
165 170 175

Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly
180 185 190

Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
195 200 205

<210> 392
<211> 207
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 392

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
65 70 75 80

Gly Ser Gly Ser Gly Ser Glu Glu Ala Glu Leu Ala Tyr Leu Leu Gly
85 90 95

Glu Leu Ala Tyr Lys Leu Gly Glu Tyr Arg Ile Ala Ile Arg Ala Tyr
100 105 110

Arg Ile Ala Leu Lys Arg Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn
115 120 125

Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ile Glu Tyr
130 135 140

Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Lys Gln
145 150 155 160

Asn Leu Gly Asn Ala Lys Gln Lys Gln Gly Gly Gly Ser Gly Ser Ser
165 170 175

Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly
180 185 190

Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
195 200 205

<210> 393
<211> 238
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 393

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
65 70 75 80

Gly Ser Gly Ser Glu Glu Ala Glu Leu Ala Tyr Leu Leu Gly Glu Leu
85 90 95

Ala Tyr Lys Leu Gly Glu Tyr Arg Ile Ala Ile Arg Ala Tyr Arg Ile
100 105 110

Ala Leu Lys Arg Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly
115 120 125

Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Tyr Tyr Gln
130 135 140

Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu
145 150 155 160

Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr
165 170 175

Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Lys Gln
180 185 190

Asn Leu Gly Asn Lys Gln Lys Gln Gly Gly Gly Ser Gly Ser Ser Gly
195 200 205

Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly
210 215 220

Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
225 230 235

<210> 394

<211> 240
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 394

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
65 70 75 80

Gly Ser Gly Ser Gly Ser Glu Glu Ala Glu Leu Ala Tyr Leu Leu Gly
85 90 95

Glu Leu Ala Tyr Lys Leu Gly Glu Tyr Arg Ile Ala Ile Arg Ala Tyr
100 105 110

Arg Ile Ala Leu Lys Arg Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn
115 120 125

Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Tyr
130 135 140

Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr
145 150 155 160

Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile
165 170 175

Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala

180

185

190

Lys Gln Asn Leu Gly Asn Lys Gln Lys Gln Gly Gly Gly Ser Gly Ser
 195 200 205

Ser Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser
 210 215 220

Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
 225 230 235 240

<210> 395
 <211> 196
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 395

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
 1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
 20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
 35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
 50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
 65 70 75 80

Gly Ser Gly Ser Gly Ser Glu Tyr Glu Ile Arg Lys Ala Leu Glu Glu
 85 90 95

Leu Lys Ala Ser Thr Ala Glu Leu Lys Arg Ala Thr Ala Ser Leu Arg
 100 105 110

Ala Ser Thr Glu Glu Leu Lys Lys Asn Pro Ser Glu Asp Ala Leu Val

115

120

125

Glu Asn Asn Arg Leu Ile Val Glu His Asn Ala Ile Ile Val Glu Asn
 130 135 140

Arg Ile Ile Ala Ala Val Leu Glu Leu Ile Val Arg Ala Ile Lys Gly
 145 150 155 160

Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
 165 170 175

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro
 180 185 190

Gln Phe Glu Lys
 195

<210> 396
 <211> 198
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 396

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
 1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
 20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
 35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
 50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
 65 70 75 80

Gly Ser Gly Ser Gly Ser Gly Ser Glu Tyr Glu Ile Arg Lys Ala Leu

85

90

95

Glu Glu Leu Lys Ala Ser Thr Ala Glu Leu Lys Arg Ala Thr Ala Ser
 100 105 110

Leu Arg Ala Ser Thr Glu Glu Leu Lys Lys Asn Pro Ser Glu Asp Ala
 115 120 125

Leu Val Glu Asn Asn Arg Leu Ile Val Glu His Asn Ala Ile Ile Val
 130 135 140

Glu Asn Arg Ile Ile Ala Ala Val Leu Glu Leu Ile Val Arg Ala Ile
 145 150 155 160

Lys Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe
 165 170 175

Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser
 180 185 190

His Pro Gln Phe Glu Lys
 195

<210> 397
 <211> 238
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 397

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
 1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
 20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Glu Ala Glu Leu Ala
 35 40 45

Tyr Leu Leu Gly Glu Leu Ala Tyr Lys Leu Gly Glu Tyr Arg Ile Ala

50

55

60

Ile Arg Ala Tyr Arg Ile Ala Leu Lys Arg Asp Pro Asn Asn Ala Glu
65 70 75 80

Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp
85 90 95

Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn
100 105 110

Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp
115 120 125

Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Asp Pro
130 135 140

Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr Lys Gln
145 150 155 160

Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu Glu Leu
165 170 175

Gly Ser Gly Ser Gly Ser Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr
180 185 190

Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met
195 200 205

Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn
210 215 220

Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
225 230 235

<210> 398

<211> 236

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 398

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Glu Ala Glu Leu Ala
35 40 45

Tyr Leu Leu Gly Glu Leu Ala Tyr Lys Leu Gly Glu Tyr Arg Ile Ala
50 55 60

Ile Arg Ala Tyr Arg Ile Ala Leu Lys Arg Asp Pro Asn Asn Ala Glu
65 70 75 80

Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp
85 90 95

Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn
100 105 110

Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp
115 120 125

Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Asp Pro
130 135 140

Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr Lys Gln
145 150 155 160

Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu Glu Leu
165 170 175

Gly Ser Gly Ser Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile
180 185 190

Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val
195 200 205

Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu
210 215 220

Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
225 230 235

<210> 399
<211> 234
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 399

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Glu Ala Glu Leu Ala
35 40 45

Tyr Leu Leu Gly Glu Leu Ala Tyr Lys Leu Gly Glu Tyr Arg Ile Ala
50 55 60

Ile Arg Ala Tyr Arg Ile Ala Leu Lys Arg Asp Pro Asn Asn Ala Glu
65 70 75 80

Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp
85 90 95

Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn
100 105 110

Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp
115 120 125

Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Asp Pro
130 135 140

Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr Lys Gln
145 150 155 160

Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu Glu Leu
165 170 175

Gly Ser Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys
180 185 190

Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp
195 200 205

Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu
210 215 220

Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
225 230

<210> 400
<211> 210
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 400

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
65 70 75 80

Gly Ser Gly Ser Gly Ser Gly Ser Glu Glu Ala Glu Leu Ala Tyr Leu
85 90 95

Leu Gly Glu Leu Ala Tyr Lys Leu Gly Glu Tyr Arg Ile Ala Ile Arg
100 105 110

Ala Tyr Arg Ile Ala Leu Lys Arg Asp Pro Asn Asn Ala Glu Ala Trp
115 120 125

Tyr Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala
130 135 140

Ile Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu
145 150 155 160

Ala Lys Gln Asn Leu Gly Asn Ala Lys Gln Lys Gln Gly Gly Gly Ser
165 170 175

Gly Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly
180 185 190

Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe
195 200 205

Glu Lys
210

<210> 401
<211> 244
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 401

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
65 70 75 80

Gly Ser Gly Ser Gly Ser Gly Ser Glu Glu Ala Glu Leu Ala Tyr Leu
85 90 95

Leu Gly Glu Leu Ala Tyr Lys Leu Gly Glu Tyr Arg Ile Ala Ile Arg
100 105 110

Ala Tyr Arg Ile Ala Leu Lys Arg Asp Pro Asn Asn Ala Glu Ala Trp
115 120 125

Tyr Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala
130 135 140

Ile Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu
145 150 155 160

Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp
165 170 175

Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn
180 185 190

Ala Glu Ala Lys Gln Asn Leu Gly Asn Ala Lys Gln Lys Gln Gly Gly
195 200 205

Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
210 215 220

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro
225 230 235 240

Gln Phe Glu Lys

<210> 402
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 402

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
65 70 75 80

Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Glu Tyr Glu Ile Arg Lys
85 90 95

Ala Leu Glu Glu Leu Lys Ala Ser Thr Ala Glu Leu Lys Arg Ala Thr
100 105 110

Ala Ser Leu Arg Ala Ser Thr Glu Glu Leu Lys Lys Asn Pro Ser Glu
115 120 125

Asp Ala Leu Val Glu Asn Asn Arg Leu Ile Val Glu His Asn Ala Ile
130 135 140

Ile Val Glu Asn Asn Arg Ile Ile Ala Ala Val Leu Glu Leu Ile Val
145 150 155 160

Arg Ala Ile Lys Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His

165

170

175

Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser
 180 185 190

Ala Trp Ser His Pro Gln Phe Glu Lys
 195 200

<210> 403

<211> 203

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 403

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
 1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
 20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
 35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
 50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
 65 70 75 80

Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Glu Tyr Glu Ile
 85 90 95

Arg Lys Ala Leu Glu Glu Leu Lys Ala Ser Thr Ala Glu Leu Lys Arg
 100 105 110

Ala Thr Ala Ser Leu Arg Ala Ser Thr Glu Glu Leu Lys Lys Asn Pro
 115 120 125

Ser Glu Asp Ala Leu Val Glu Asn Asn Arg Leu Ile Val Glu His Asn

130

135

140

Ala Ile Ile Val Glu Asn Asn Arg Ile Ile Ala Ala Val Leu Glu Leu
 145 150 155 160

Ile Val Arg Ala Ile Lys Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp
 165 170 175

Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly
 180 185 190

Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
 195 200

<210> 404
 <211> 212
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 404

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
 1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
 20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
 35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
 50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
 65 70 75 80

Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Glu Glu Ala Glu Leu Ala
 85 90 95

Tyr Leu Leu Gly Glu Leu Ala Tyr Lys Leu Gly Glu Tyr Arg Ile Ala

100

105

110

Ile Arg Ala Tyr Arg Ile Ala Leu Lys Arg Asp Pro Asn Asn Ala Glu
 115 120 125

Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp
 130 135 140

Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn
 145 150 155 160

Ala Glu Ala Lys Gln Asn Leu Gly Asn Ala Lys Gln Lys Gln Gly Gly
 165 170 175

Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
 180 185 190

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro
 195 200 205

Gln Phe Glu Lys
 210

<210> 405
 <211> 246
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 405

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
 1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
 20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
 35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu

50

55

60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
65 70 75 80

Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Glu Glu Ala Glu Leu Ala
85 90 95

Tyr Leu Leu Gly Glu Leu Ala Tyr Lys Leu Gly Glu Tyr Arg Ile Ala
100 105 110

Ile Arg Ala Tyr Arg Ile Ala Leu Lys Arg Asp Pro Asn Asn Ala Glu
115 120 125

Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp
130 135 140

Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn
145 150 155 160

Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp
165 170 175

Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Asp Pro
180 185 190

Asn Asn Ala Glu Ala Lys Gln Asn Leu Gly Asn Ala Lys Gln Lys Gln
195 200 205

Gly Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe
210 215 220

Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser
225 230 235 240

His Pro Gln Phe Glu Lys
245

<210> 406

<211> 154

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 406

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
65 70 75 80

Gly Ser Gly Ser Arg Met Lys Gln Ile Glu Asp Lys Ile Glu Glu Ile
85 90 95

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

Leu Ile Gly Glu Arg Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser
115 120 125

His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
130 135 140

Ser Ala Trp Ser His Pro Gln Phe Glu Lys
145 150

<210> 407

<211> 158

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 407

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
65 70 75 80

Gly Ser Gly Ser Gly Ser Gly Ser Arg Met Lys Gln Ile Glu Asp Lys
85 90 95

Ile Glu Glu Ile Leu Ser Lys Ile Tyr His Ile Glu Asn Glu Ile Ala
100 105 110

Arg Ile Lys Lys Leu Ile Gly Glu Arg Gly Gly Ser Gly Ser Ser Gly
115 120 125

Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly
130 135 140

Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
145 150 155

<210> 408

<211> 197

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 408

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp

1	5	10	15
Gln Val Ser	Glu Leu Ala His	Glu Leu Leu His Lys	Leu Thr Gly Glu
	20	25	30
Glu Leu Glu	Arg Ala Ala Tyr	Phe Asn Trp Trp Ala	Thr Glu Met Met
	35	40	45
Leu Glu Leu	Ile Lys Ser Asp Asp	Glu Arg Glu Ile Arg	Glu Ile Glu
	50	55	60
Glu Glu Ala	Arg Arg Ile Leu Glu	His Leu Glu Glu Leu	Ala Arg Lys
65	70	75	80
Gly Ser Gly	Ser Gly Ser Glu Tyr	Glu Ile Arg Lys Ala	Leu Glu Glu
	85	90	95
Leu Lys Ala	Ser Thr Ala Glu Leu	Lys Arg Ser Thr Ala	Ser Leu Arg
	100	105	110
Ala Ser Thr	Glu Glu Leu Lys Lys	Asn Pro Ser Glu Asp	Ala Leu Val
	115	120	125
Glu Asn Asn	Arg Leu Ile Val Glu	Asn Asn Ala Ile Ile	Val Glu Asn
	130	135	140
Asn Arg Ile	Ile Ala Ala Val Leu	Glu Leu Ile Val Arg	Ala Ile Lys
145	150	155	160
Gly Gly Ser	Gly Ser Ser Gly Ser	Ala Trp Ser His Pro	Gln Phe Glu
	165	170	175
Lys Gly Gly	Gly Ser Gly Gly Gly	Ser Gly Gly Ser Ala	Trp Ser His
	180	185	190
Pro Gln Phe	Glu Lys		
	195		
<210>	409		
<211>	201		
<212>	PRT		

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 409

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
65 70 75 80

Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Glu Tyr Glu Ile Arg Lys
85 90 95

Ala Leu Glu Glu Leu Lys Ala Ser Thr Ala Glu Leu Lys Arg Ser Thr
100 105 110

Ala Ser Leu Arg Ala Ser Thr Glu Glu Leu Lys Lys Asn Pro Ser Glu
115 120 125

Asp Ala Leu Val Glu Asn Asn Arg Leu Ile Val Glu Asn Asn Ala Ile
130 135 140

Ile Val Glu Asn Asn Arg Ile Ile Ala Ala Val Leu Glu Leu Ile Val
145 150 155 160

Arg Ala Ile Lys Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His
165 170 175

Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser
180 185 190

Ala Trp Ser His Pro Gln Phe Glu Lys
195 200

<210> 410
<211> 242
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 410

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
65 70 75 80

Gly Ser Gly Ser Gly Ser Asn Leu Ala Glu Lys Met Tyr Lys Ala Gly
85 90 95

Asn Ala Met Tyr Arg Lys Gly Gln Tyr Thr Ile Ala Ile Ile Ala Tyr
100 105 110

Thr Leu Ala Leu Leu Lys Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn
115 120 125

Leu Gly Asn Ala Ala Tyr Lys Lys Gly Glu Tyr Asp Glu Ala Ile Glu
130 135 140

Ala Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp
145 150 155 160

Tyr Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala
165 170 175

Ile Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu
180 185 190

Ala Lys Gln Asn Leu Gly Asn Ala Lys Gln Lys Gln Gly Gly Gly Ser
195 200 205

Gly Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly
210 215 220

Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe
225 230 235 240

Glu Lys

<210> 411
<211> 246
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 411

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
65 70 75 80

Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Asn Leu Ala Glu Lys Met
85 90 95

Tyr Lys Ala Gly Asn Ala Met Tyr Arg Lys Gly Gln Tyr Thr Ile Ala
100 105 110

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

Ala Trp Tyr Asn Leu Gly Asn Ala Ala Tyr Lys Lys Gly Glu Tyr Asp
130 135 140

Glu Ala Ile Glu Ala Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn
145 150 155 160

Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp
165 170 175

Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Asp Pro
180 185 190

Asn Asn Ala Glu Ala Lys Gln Asn Leu Gly Asn Ala Lys Gln Lys Gln
195 200 205

Gly Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe
210 215 220

Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser
225 230 235 240

His Pro Gln Phe Glu Lys
245

<210> 412
<211> 153
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 412

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
65 70 75 80

Gly Ser Gly Ser Gly Ser Gly Glu Ile Ala Lys Ser Leu Lys Glu Ile
85 90 95

Ala Lys Ser Leu Lys Glu Ile Ala Trp Ser Leu Lys Glu Ile Ala Lys
100 105 110

Ser Leu Lys Gly Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His
115 120 125

Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser
130 135 140

Ala Trp Ser His Pro Gln Phe Glu Lys
145 150

<210> 413
<211> 157
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 413

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
65 70 75 80

Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Glu Ile Ala Lys Ser
85 90 95

Leu Lys Glu Ile Ala Lys Ser Leu Lys Glu Ile Ala Trp Ser Leu Lys
100 105 110

Glu Ile Ala Lys Ser Leu Lys Gly Gly Gly Ser Gly Ser Ser Gly Ser
115 120 125

Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly
130 135 140

Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
145 150 155

<210> 414
<211> 207
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 414

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
65 70 75 80

Gly Gly Ser Gly Gly Glu Glu Ala Glu Leu Ala Tyr Leu Leu Gly Glu
85 90 95

Leu Ala Tyr Lys Leu Gly Glu Tyr Arg Ile Ala Ile Arg Ala Tyr Arg
100 105 110

Ile Ala Leu Lys Arg Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu
115 120 125

Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr
130 135 140

Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Lys Gln
145 150 155 160

Asn Leu Gly Asn Ala Lys Gln Lys Gln Gly Gly Gly Ser Gly Ser Ser
165 170 175

Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly
180 185 190

Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
195 200 205

<210> 415
<211> 209
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 415

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
65 70 75 80

Gly Gly Gly Ser Gly Gly Gly Glu Glu Ala Glu Leu Ala Tyr Leu Leu
85 90 95

Gly Glu Leu Ala Tyr Lys Leu Gly Glu Tyr Arg Ile Ala Ile Arg Ala
100 105 110

Tyr Arg Ile Ala Leu Lys Arg Asp Pro Asn Asn Ala Glu Ala Trp Tyr
115 120 125

Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile
130 135 140

Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala
145 150 155 160

Lys Gln Asn Leu Gly Asn Ala Lys Gln Lys Gln Gly Gly Gly Ser Gly
165 170 175

Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly
180 185 190

Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu
195 200 205

Lys

<210> 416
<211> 211
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 416

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
65 70 75 80

Gly Gly Gly Gly Ser Gly Gly Gly Gly Glu Glu Ala Glu Leu Ala Tyr
85 90 95

Leu Leu Gly Glu Leu Ala Tyr Lys Leu Gly Glu Tyr Arg Ile Ala Ile
100 105 110

Arg Ala Tyr Arg Ile Ala Leu Lys Arg Asp Pro Asn Asn Ala Glu Ala
115 120 125

Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu
130 135 140

Ala Ile Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala
145 150 155 160

Glu Ala Lys Gln Asn Leu Gly Asn Ala Lys Gln Lys Gln Gly Gly Gly

165

170

175

Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
 180 185 190

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
 195 200 205

Phe Glu Lys
 210

<210> 417
 <211> 241
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 417

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
 1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
 20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
 35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
 50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
 65 70 75 80

Gly Gly Ser Gly Gly Glu Glu Ala Glu Leu Ala Tyr Leu Leu Gly Glu
 85 90 95

Leu Ala Tyr Lys Leu Gly Glu Tyr Arg Ile Ala Ile Arg Ala Tyr Arg
 100 105 110

Ile Ala Leu Lys Arg Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu

115

120

125

Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr
 130 135 140

Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr
 145 150 155 160

Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile
 165 170 175

Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala
 180 185 190

Lys Gln Asn Leu Gly Asn Ala Lys Gln Lys Gln Gly Gly Gly Ser Gly
 195 200 205

Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly
 210 215 220

Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu
 225 230 235 240

Lys

<210> 418
 <211> 243
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 418

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
 1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
 20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met

35

40

45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
 50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
 65 70 75 80

Gly Gly Gly Ser Gly Gly Gly Glu Glu Ala Glu Leu Ala Tyr Leu Leu
 85 90 95

Gly Glu Leu Ala Tyr Lys Leu Gly Glu Tyr Arg Ile Ala Ile Arg Ala
 100 105 110

Tyr Arg Ile Ala Leu Lys Arg Asp Pro Asn Asn Ala Glu Ala Trp Tyr
 115 120 125

Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile
 130 135 140

Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala
 145 150 155 160

Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu
 165 170 175

Ala Ile Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala
 180 185 190

Glu Ala Lys Gln Asn Leu Gly Asn Ala Lys Gln Lys Gln Gly Gly Gly
 195 200 205

Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
 210 215 220

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
 225 230 235 240

Phe Glu Lys

<210> 419
<211> 245
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 419

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
65 70 75 80

Gly Gly Gly Gly Ser Gly Gly Gly Gly Glu Glu Ala Glu Leu Ala Tyr
85 90 95

Leu Leu Gly Glu Leu Ala Tyr Lys Leu Gly Glu Tyr Arg Ile Ala Ile
100 105 110

Arg Ala Tyr Arg Ile Ala Leu Lys Arg Asp Pro Asn Asn Ala Glu Ala
115 120 125

Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu
130 135 140

Ala Ile Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala
145 150 155 160

Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr
165 170 175

Asp Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn
180 185 190

Asn Ala Glu Ala Lys Gln Asn Leu Gly Asn Ala Lys Gln Lys Gln Gly
195 200 205

Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe Glu
210 215 220

Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His
225 230 235 240

Pro Gln Phe Glu Lys
245

<210> 420
<211> 198
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 420

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
65 70 75 80

Gly Gly Ser Gly Gly Gly Ser Glu Tyr Glu Ile Arg Lys Ala Leu Glu
85 90 95

Glu Leu Lys Ala Ser Thr Ala Glu Leu Lys Arg Ala Thr Ala Ser Leu
100 105 110

Arg Ala Ser Thr Glu Glu Leu Lys Lys Asn Pro Ser Glu Asp Ala Leu
115 120 125

Val Glu Asn Asn Arg Leu Ile Val Glu His Asn Ala Ile Ile Val Glu
130 135 140

Asn Asn Arg Ile Ile Ala Ala Val Leu Glu Leu Ile Val Arg Ala Ile
145 150 155 160

Lys Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe
165 170 175

Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser
180 185 190

His Pro Gln Phe Glu Lys
195

<210> 421
<211> 200
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 421

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
65 70 75 80

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Tyr Glu Ile Arg Lys Ala
85 90 95

Leu Glu Glu Leu Lys Ala Ser Thr Ala Glu Leu Lys Arg Ala Thr Ala
100 105 110

Ser Leu Arg Ala Ser Thr Glu Glu Leu Lys Lys Asn Pro Ser Glu Asp
115 120 125

Ala Leu Val Glu Asn Asn Arg Leu Ile Val Glu His Asn Ala Ile Ile
130 135 140

Val Glu Asn Asn Arg Ile Ile Ala Ala Val Leu Glu Leu Ile Val Arg
145 150 155 160

Ala Ile Lys Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro
165 170 175

Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala
180 185 190

Trp Ser His Pro Gln Phe Glu Lys
195 200

<210> 422
<211> 202
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 422

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
65 70 75 80

Gly Gly Gly Gly Ser Gly Gly Gly Gly Gly Ser Glu Tyr Glu Ile Arg
85 90 95

Lys Ala Leu Glu Glu Leu Lys Ala Ser Thr Ala Glu Leu Lys Arg Ala
100 105 110

Thr Ala Ser Leu Arg Ala Ser Thr Glu Glu Leu Lys Lys Asn Pro Ser
115 120 125

Glu Asp Ala Leu Val Glu Asn Asn Arg Leu Ile Val Glu His Asn Ala
130 135 140

Ile Ile Val Glu Asn Asn Arg Ile Ile Ala Ala Val Leu Glu Leu Ile
145 150 155 160

Val Arg Ala Ile Lys Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser
165 170 175

His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
180 185 190

Ser Ala Trp Ser His Pro Gln Phe Glu Lys
195 200

<210> 423
<211> 155
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 423

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
65 70 75 80

Gly Gly Ser Gly Gly Arg Met Lys Gln Ile Glu Asp Lys Ile Glu Glu
85 90 95

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

Lys Leu Ile Gly Glu Arg Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp
115 120 125

Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly
130 135 140

Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
145 150 155

<210> 424
<211> 157
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 424

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
65 70 75 80

Gly Gly Gly Ser Gly Gly Gly Arg Met Lys Gln Ile Glu Asp Lys Ile
85 90 95

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

Ile Lys Lys Leu Ile Gly Glu Arg Gly Gly Ser Gly Ser Ser Gly Ser
115 120 125

Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly
130 135 140

Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
145 150 155

<210> 425
<211> 159
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 425

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
65 70 75 80

Gly Gly Gly Gly Ser Gly Gly Gly Gly Arg Met Lys Gln Ile Glu Asp
85 90 95

Lys Ile Glu Glu Ile Leu Ser Lys Ile Tyr His Ile Glu Asn Glu Ile
100 105 110

Ala Arg Ile Lys Lys Leu Ile Gly Glu Arg Gly Gly Ser Gly Ser Ser
115 120 125

Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly
130 135 140

Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
145 150 155

<210> 426
<211> 198
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 426

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
65 70 75 80

Gly Gly Ser Gly Gly Gly Ser Glu Tyr Glu Ile Arg Lys Ala Leu Glu
85 90 95

Glu Leu Lys Ala Ser Thr Ala Glu Leu Lys Arg Ser Thr Ala Ser Leu
100 105 110

Arg Ala Ser Thr Glu Glu Leu Lys Lys Asn Pro Ser Glu Asp Ala Leu
115 120 125

Val Glu Asn Asn Arg Leu Ile Val Glu Asn Asn Ala Ile Ile Val Glu
130 135 140

Asn Asn Arg Ile Ile Ala Ala Val Leu Glu Leu Ile Val Arg Ala Ile
145 150 155 160

Lys Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe
165 170 175

Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser
180 185 190

His Pro Gln Phe Glu Lys
195

<210> 427
<211> 200
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 427

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
65 70 75 80

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Tyr Glu Ile Arg Lys Ala
85 90 95

Leu Glu Glu Leu Lys Ala Ser Thr Ala Glu Leu Lys Arg Ser Thr Ala
100 105 110

Ser Leu Arg Ala Ser Thr Glu Glu Leu Lys Lys Asn Pro Ser Glu Asp
115 120 125

Ala Leu Val Glu Asn Asn Arg Leu Ile Val Glu Asn Asn Ala Ile Ile
130 135 140

Val Glu Asn Asn Arg Ile Ile Ala Ala Val Leu Glu Leu Ile Val Arg
145 150 155 160

Ala Ile Lys Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro
165 170 175

Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala
180 185 190

Trp Ser His Pro Gln Phe Glu Lys
195 200

<210> 428

<211> 202

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 428

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
65 70 75 80

Gly Gly Gly Gly Ser Gly Gly Gly Gly Gly Ser Glu Tyr Glu Ile Arg
85 90 95

Lys Ala Leu Glu Glu Leu Lys Ala Ser Thr Ala Glu Leu Lys Arg Ser
100 105 110

Thr Ala Ser Leu Arg Ala Ser Thr Glu Glu Leu Lys Lys Asn Pro Ser
115 120 125

Glu Asp Ala Leu Val Glu Asn Asn Arg Leu Ile Val Glu Asn Asn Ala
130 135 140

Ile Ile Val Glu Asn Asn Arg Ile Ile Ala Ala Val Leu Glu Leu Ile
145 150 155 160

Val Arg Ala Ile Lys Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser
165 170 175

His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
180 185 190

Ser Ala Trp Ser His Pro Gln Phe Glu Lys

195

200

<210> 429
 <211> 241
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 429

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
 1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
 20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
 35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
 50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
 65 70 75 80

Gly Gly Ser Gly Gly Asn Leu Ala Glu Lys Met Tyr Lys Ala Gly Asn
 85 90 95

Ala Met Tyr Arg Lys Gly Gln Tyr Thr Ile Ala Ile Ile Ala Tyr Thr
 100 105 110

Leu Ala Leu Leu Lys Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu
 115 120 125

Gly Asn Ala Ala Tyr Lys Lys Gly Glu Tyr Asp Glu Ala Ile Glu Ala
 130 135 140

Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr
 145 150 155 160

Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile

165

170

175

Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala
 180 185 190

Lys Gln Asn Leu Gly Asn Ala Lys Gln Lys Gln Gly Gly Gly Ser Gly
 195 200 205

Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly
 210 215 220

Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu
 225 230 235 240

Lys

<210> 430
 <211> 243
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 430

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
 1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
 20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
 35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
 50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
 65 70 75 80

Gly Gly Gly Ser Gly Gly Gly Asn Leu Ala Glu Lys Met Tyr Lys Ala

85

90

95

Gly Asn Ala Met Tyr Arg Lys Gly Gln Tyr Thr Ile Ala Ile Ile Ala
 100 105 110

Tyr Thr Leu Ala Leu Leu Lys Asp Pro Asn Asn Ala Glu Ala Trp Tyr
 115 120 125

Asn Leu Gly Asn Ala Ala Tyr Lys Lys Gly Glu Tyr Asp Glu Ala Ile
 130 135 140

Glu Ala Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala
 145 150 155 160

Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu
 165 170 175

Ala Ile Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala
 180 185 190

Glu Ala Lys Gln Asn Leu Gly Asn Ala Lys Gln Lys Gln Gly Gly Gly
 195 200 205

Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
 210 215 220

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
 225 230 235 240

Phe Glu Lys

<210> 431
 <211> 245
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 431

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp

1	5	10	15
Gln Val Ser	Glu Leu Ala His	Glu Leu Leu His Lys	Leu Thr Gly Glu
	20	25	30
Glu Leu Glu	Arg Ala Ala Tyr	Phe Asn Trp Trp Ala	Thr Glu Met Met
	35	40	45
Leu Glu Leu	Ile Lys Ser Asp	Asp Glu Arg Glu	Ile Arg Glu Ile Glu
	50	55	60
Glu Glu Ala	Arg Arg Ile Leu	Glu His Leu Glu Glu	Leu Ala Arg Lys
65	70	75	80
Gly Gly Gly	Gly Ser Gly Gly	Gly Gly Asn Leu	Ala Glu Lys Met Tyr
	85	90	95
Lys Ala Gly	Asn Ala Met Tyr	Arg Lys Gly Gln	Tyr Thr Ile Ala Ile
	100	105	110
Ile Ala Tyr	Thr Leu Ala Leu	Leu Lys Asp Pro	Asn Asn Ala Glu Ala
	115	120	125
Trp Tyr Asn	Leu Gly Asn Ala	Ala Tyr Lys Lys	Gly Glu Tyr Asp Glu
	130	135	140
Ala Ile Glu	Ala Tyr Gln Lys	Ala Leu Glu Leu	Asp Pro Asn Asn Ala
145	150	155	160
Glu Ala Trp	Tyr Asn Leu Gly	Asn Ala Tyr Tyr	Lys Gln Gly Asp Tyr
	165	170	175
Asp Glu Ala	Ile Glu Tyr Tyr	Gln Lys Ala Leu	Glu Leu Asp Pro Asn
	180	185	190
Asn Ala Glu	Ala Lys Gln Asn	Leu Gly Asn Ala	Lys Gln Lys Gln Gly
	195	200	205
Gly Gly Ser	Gly Ser Ser Gly	Ser Ala Trp Ser	His Pro Gln Phe Glu
	210	215	220

Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His
225 230 235 240

Pro Gln Phe Glu Lys
245

<210> 432
<211> 152
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 432

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
65 70 75 80

Gly Gly Ser Gly Gly Gly Glu Ile Ala Lys Ser Leu Lys Glu Ile Ala
85 90 95

Lys Ser Leu Lys Glu Ile Ala Trp Ser Leu Lys Glu Ile Ala Lys Ser
100 105 110

Leu Lys Gly Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro
115 120 125

Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala
130 135 140

Trp Ser His Pro Gln Phe Glu Lys
145 150

<210> 433
<211> 154
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 433

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
65 70 75 80

Gly Gly Gly Ser Gly Gly Gly Gly Glu Ile Ala Lys Ser Leu Lys Glu
85 90 95

Ile Ala Lys Ser Leu Lys Glu Ile Ala Trp Ser Leu Lys Glu Ile Ala
100 105 110

Lys Ser Leu Lys Gly Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser
115 120 125

His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
130 135 140

Ser Ala Trp Ser His Pro Gln Phe Glu Lys
145 150

<210> 434
<211> 156
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 434

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
65 70 75 80

Gly Gly Gly Gly Ser Gly Gly Gly Gly Gly Glu Ile Ala Lys Ser Leu
85 90 95

Lys Glu Ile Ala Lys Ser Leu Lys Glu Ile Ala Trp Ser Leu Lys Glu
100 105 110

Ile Ala Lys Ser Leu Lys Gly Gly Gly Ser Gly Ser Ser Gly Ser Ala
115 120 125

Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser
130 135 140

Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
145 150 155

<210> 435
<211> 182
<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 435

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
65 70 75 80

Gly Gly Ser Glu Ala Leu Glu Glu Leu Glu Lys Ala Leu Arg Glu Leu
85 90 95

Lys Lys Ser Thr Asp Glu Leu Glu Arg Ser Thr Glu Glu Leu Glu Lys
100 105 110

Asn Pro Ser Glu Asp Ala Leu Val Glu Asn Asn Arg Leu Ile Val Glu
115 120 125

Asn Asn Lys Ile Ile Val Glu Val Leu Arg Ile Ile Ala Lys Val Leu
130 135 140

Lys Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe
145 150 155 160

Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser
165 170 175

His Pro Gln Phe Glu Lys
180

<210> 436
<211> 184
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 436

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
65 70 75 80

Gly Gly Gly Ser Ser Glu Ala Leu Glu Glu Leu Glu Lys Ala Leu Arg
85 90 95

Glu Leu Lys Lys Ser Thr Asp Glu Leu Glu Arg Ser Thr Glu Glu Leu
100 105 110

Glu Lys Asn Pro Ser Glu Asp Ala Leu Val Glu Asn Asn Arg Leu Ile
115 120 125

Val Glu Asn Asn Lys Ile Ile Val Glu Val Leu Arg Ile Ile Ala Lys
130 135 140

Val Leu Lys Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro
145 150 155 160

Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala
165 170 175

Trp Ser His Pro Gln Phe Glu Lys
180

<210> 437
<211> 186
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 437

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
65 70 75 80

Gly Gly Gly Gly Ser Gly Ser Glu Ala Leu Glu Glu Leu Glu Lys Ala
85 90 95

Leu Arg Glu Leu Lys Lys Ser Thr Asp Glu Leu Glu Arg Ser Thr Glu
100 105 110

Glu Leu Glu Lys Asn Pro Ser Glu Asp Ala Leu Val Glu Asn Asn Arg
115 120 125

Leu Ile Val Glu Asn Asn Lys Ile Ile Val Glu Val Leu Arg Ile Ile
130 135 140

Ala Lys Val Leu Lys Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser
145 150 155 160

His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
165 170 175

Ser Ala Trp Ser His Pro Gln Phe Glu Lys
180 185

<210> 438
<211> 176
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 438

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
65 70 75 80

Gly Gly Ser Pro Glu Leu Glu Lys Ala Leu Arg Glu Leu Lys Lys Ser
85 90 95

Thr Asp Glu Leu Glu Arg Ser Thr Glu Glu Leu Glu Lys Asn Gly Ser
100 105 110

Pro Glu Ala Leu Val Glu Asn Asn Arg Leu Ile Val Glu Asn Asn Lys
115 120 125

Ile Ile Val Glu Val Leu Arg Ile Ile Ala Lys Gly Gly Ser Gly Ser
130 135 140

Ser Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser
145 150 155 160

Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
165 170 175

<210> 439
<211> 178
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 439

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
65 70 75 80

Gly Gly Gly Ser Ser Pro Glu Leu Glu Lys Ala Leu Arg Glu Leu Lys
85 90 95

Lys Ser Thr Asp Glu Leu Glu Arg Ser Thr Glu Glu Leu Glu Lys Asn
100 105 110

Gly Ser Pro Glu Ala Leu Val Glu Asn Asn Arg Leu Ile Val Glu Asn
115 120 125

Asn Lys Ile Ile Val Glu Val Leu Arg Ile Ile Ala Lys Gly Gly Ser
130 135 140

Gly Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly
145 150 155 160

Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe
165 170 175

Glu Lys

<210> 440
<211> 180
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 440

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
65 70 75 80

Gly Gly Gly Gly Ser Gly Ser Pro Glu Leu Glu Lys Ala Leu Arg Glu
85 90 95

Leu Lys Lys Ser Thr Asp Glu Leu Glu Arg Ser Thr Glu Glu Leu Glu
100 105 110

Lys Asn Gly Ser Pro Glu Ala Leu Val Glu Asn Asn Arg Leu Ile Val
115 120 125

Glu Asn Asn Lys Ile Ile Val Glu Val Leu Arg Ile Ile Ala Lys Gly
130 135 140

Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
145 150 155 160

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro
165 170 175

Gln Phe Glu Lys
180

<210> 441
<211> 169
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 441

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
65 70 75 80

Gly Gly Ser Glu Lys Ala Leu Arg Glu Leu Lys Lys Ser Thr Asp Glu
85 90 95

Leu Glu Arg Ser Thr Glu Glu Leu Glu Lys Asn Gly Ser Pro Glu Ala
100 105 110

Leu Val Glu Asn Asn Arg Leu Ile Val Glu Asn Asn Lys Ile Ile Val
115 120 125

Glu Val Leu Arg Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His
130 135 140

Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser
145 150 155 160

Ala Trp Ser His Pro Gln Phe Glu Lys
165

<210> 442
<211> 171
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 442

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
65 70 75 80

Gly Gly Gly Ser Ser Glu Lys Ala Leu Arg Glu Leu Lys Lys Ser Thr
85 90 95

Asp Glu Leu Glu Arg Ser Thr Glu Glu Leu Glu Lys Asn Gly Ser Pro
100 105 110

Glu Ala Leu Val Glu Asn Asn Arg Leu Ile Val Glu Asn Asn Lys Ile
115 120 125

Ile Val Glu Val Leu Arg Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp
130 135 140

Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly
145 150 155 160

Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
165 170

<210> 443
<211> 173
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 443

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
65 70 75 80

Gly Gly Gly Gly Ser Gly Ser Glu Lys Ala Leu Arg Glu Leu Lys Lys
85 90 95

Ser Thr Asp Glu Leu Glu Arg Ser Thr Glu Glu Leu Glu Lys Asn Gly
100 105 110

Ser Pro Glu Ala Leu Val Glu Asn Asn Arg Leu Ile Val Glu Asn Asn
115 120 125

Lys Ile Ile Val Glu Val Leu Arg Gly Gly Ser Gly Ser Ser Gly Ser
130 135 140

Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly
145 150 155 160

Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
165 170

<210> 444
<211> 167
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 444

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Ser Glu Ala Leu Glu Glu
35 40 45

Leu Glu Lys Ala Leu Arg Glu Leu Lys Lys Ser Thr Asp Glu Leu Glu
50 55 60

Arg Ser Thr Glu Glu Leu Glu Lys Asn Pro Ser Glu Asp Ala Leu Val
65 70 75 80

Glu Asn Asn Arg Leu Ile Val Glu Asn Asn Lys Ile Ile Val Glu Val
85 90 95

Leu Arg Ile Ile Ala Lys Val Leu Lys Gly Gly Gly Gly Ser Gly Asp
100 105 110

Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu
115 120 125

Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr
130 135 140

Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg
145 150 155 160

Leu Leu Glu Glu Val Lys Arg
165

<210> 445
<211> 171
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 445

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Ser Glu Ala Leu Glu Glu
35 40 45

Leu Glu Lys Ala Leu Arg Glu Leu Lys Lys Ser Thr Asp Glu Leu Glu
50 55 60

Arg Ser Thr Glu Glu Leu Glu Lys Asn Pro Ser Glu Asp Ala Leu Val
65 70 75 80

Glu Asn Asn Arg Leu Ile Val Glu Asn Asn Lys Ile Ile Val Glu Val
85 90 95

Leu Arg Ile Ile Ala Lys Val Leu Lys Gly Gly Gly Gly Ser Gly Gly
100 105 110

Gly Gly Ser Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met
115 120 125

Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser
130 135 140

Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu
145 150 155 160

Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
165 170

<210> 446
<211> 161
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 446

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Ser Pro Glu Leu Glu Lys
35 40 45

Ala Leu Arg Glu Leu Lys Lys Ser Thr Asp Glu Leu Glu Arg Ser Thr
50 55 60

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

Arg Leu Ile Val Glu Asn Asn Lys Ile Ile Val Glu Val Leu Arg Ile
85 90 95

Ile Ala Lys Gly Gly Gly Gly Ser Gly Asp Lys Glu Asn Val Leu Gln
100 105 110

Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu
115 120 125

Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys
130 135 140

Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys
145 150 155 160

Arg

<210> 447
<211> 165
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 447

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Ser Pro Glu Leu Glu Lys
35 40 45

Ala Leu Arg Glu Leu Lys Lys Ser Thr Asp Glu Leu Glu Arg Ser Thr
50 55 60

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

Arg Leu Ile Val Glu Asn Asn Lys Ile Ile Val Glu Val Leu Arg Ile
85 90 95

Ile Ala Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Lys Glu
100 105 110

Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu
115 120 125

Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe
130 135 140

Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu
145 150 155 160

Glu Glu Val Lys Arg
165

<210> 448
<211> 181
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 448

Met Glu Lys Lys Ile Asn Leu Asp Glu Leu His Met Gln Met Thr Asp
1 5 10 15

Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys
20 25 30

His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys
35 40 45

Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu
50 55 60

Glu Arg Leu Leu Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Glu Ala
65 70 75 80

Leu Glu Glu Leu Glu Lys Ala Leu Arg Glu Leu Lys Lys Ser Thr Asp
85 90 95

Glu Leu Glu Arg Ser Thr Glu Glu Leu Glu Lys Asn Pro Ser Glu Asp
100 105 110

Ala Leu Val Glu Asn Asn Arg Leu Ile Val Glu Asn Asn Lys Ile Ile
115 120 125

Val Glu Val Leu Arg Ile Ile Ala Lys Val Leu Lys Gly Gly Ala Ser
130 135 140

Pro Ala Ala Pro Ala Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu
145 150 155 160

Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His
165 170 175

Pro Gln Phe Glu Lys
180

<210> 449
<211> 179
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 449

Met Glu Lys Lys Ile Asn Leu Asp Glu Leu His Met Gln Met Thr Asp
1 5 10 15

Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys
20 25 30

His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys
35 40 45

Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu
50 55 60

Glu Arg Leu Leu Ser Gly Gly Gly Gly Ser Gly Ser Glu Ala Leu Glu
65 70 75 80

Glu Leu Glu Lys Ala Leu Arg Glu Leu Lys Lys Ser Thr Asp Glu Leu
85 90 95

Glu Arg Ser Thr Glu Glu Leu Glu Lys Asn Pro Ser Glu Asp Ala Leu
100 105 110

Val Glu Asn Asn Arg Leu Ile Val Glu Asn Asn Lys Ile Ile Val Glu
115 120 125

Val Leu Arg Ile Ile Ala Lys Val Leu Lys Gly Gly Ala Ser Pro Ala
130 135 140

Ala Pro Ala Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
145 150 155 160

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
165 170 175

Phe Glu Lys

<210> 450
<211> 177
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 450

Met Glu Lys Lys Ile Asn Leu Asp Glu Leu His Met Gln Met Thr Asp
1 5 10 15

Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys
20 25 30

His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys
35 40 45

Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu
50 55 60

Glu Arg Leu Leu Ser Gly Gly Gly Ser Ser Glu Ala Leu Glu Glu Leu
65 70 75 80

Glu Lys Ala Leu Arg Glu Leu Lys Lys Ser Thr Asp Glu Leu Glu Arg
85 90 95

Ser Thr Glu Glu Leu Glu Lys Asn Pro Ser Glu Asp Ala Leu Val Glu
100 105 110

Asn Asn Arg Leu Ile Val Glu Asn Asn Lys Ile Ile Val Glu Val Leu
115 120 125

Arg Ile Ile Ala Lys Val Leu Lys Gly Gly Ala Ser Pro Ala Ala Pro
130 135 140

Ala Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly
145 150 155 160

Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu
165 170 175

Lys

<210> 451
<211> 175
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 451

Met Glu Lys Lys Ile Asn Leu Asp Glu Leu His Met Gln Met Thr Asp
1 5 10 15

Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys
20 25 30

His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys
35 40 45

Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu
50 55 60

Glu Arg Leu Leu Ser Gly Gly Ser Glu Ala Leu Glu Glu Leu Glu Lys
65 70 75 80

Ala Leu Arg Glu Leu Lys Lys Ser Thr Asp Glu Leu Glu Arg Ser Thr
85 90 95

Glu Glu Leu Glu Lys Asn Pro Ser Glu Asp Ala Leu Val Glu Asn Asn
100 105 110

Arg Leu Ile Val Glu Asn Asn Lys Ile Ile Val Glu Val Leu Arg Ile
115 120 125

Ile Ala Lys Val Leu Lys Gly Gly Ala Ser Pro Ala Ala Pro Ala Gly
130 135 140

Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly
145 150 155 160

Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
165 170 175

<210> 452
<211> 182
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 452

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
65 70 75 80

Gly Gly Ser Glu Ala Leu Glu Glu Leu Glu Lys Ala Leu Arg Glu Leu
85 90 95

Lys Lys Ser Thr Asp Glu Leu Glu Arg Ser Thr Glu Glu Leu Glu Lys
100 105 110

Asn Pro Ser Glu Asp Ala Leu Val Glu Asn Asn Arg Leu Ile Val Glu
115 120 125

Asn Asn Lys Ile Ile Val Glu Val Leu Arg Ile Ile Ala Lys Val Leu
130 135 140

Lys Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe
145 150 155 160

Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser
165 170 175

His Pro Gln Phe Glu Lys
180

<210> 453
<211> 182
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 453

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
50 55 60

Glu Glu Ala Ala Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Thr
65 70 75 80

Gly Gly Ser Glu Ala Leu Glu Glu Leu Glu Lys Ala Leu Arg Glu Leu
85 90 95

Lys Lys Ser Thr Asp Glu Leu Glu Arg Ser Thr Glu Glu Leu Glu Lys
100 105 110

Asn Pro Ser Glu Asp Ala Leu Val Glu Asn Asn Arg Leu Ile Val Glu
115 120 125

Asn Asn Lys Ile Ile Val Glu Val Leu Arg Ile Ile Ala Lys Val Leu
130 135 140

Lys Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe
145 150 155 160

Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser
165 170 175

His Pro Gln Phe Glu Lys
180

<210> 454
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 454

Asp Lys Glu Trp Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg Leu Leu
1 5 10 15

Asp Glu Leu Gly His Ala Glu Ala Ser Met Arg Val Ser Asp Leu Ile
20 25 30

Tyr Glu Phe Met Lys Lys Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu
35 40 45

Arg Leu Leu Glu Glu Val Glu Arg Gly Gly Gly Gly Ser Gly Gly Gly
50 55 60

Gly Ser Gly Gly Gly Gly Ser Asp Lys Glu Trp Ile Leu Gln Lys Ile
65 70 75 80

Tyr Glu Ile Met Arg Leu Leu Asp Glu Leu Gly His Ala Glu Ala Ser
85 90 95

Met Arg Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Lys Gly Asp Glu
100 105 110

Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Glu Arg
115 120 125

<210> 455
<211> 143
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 455

Asn Asp Asp Glu Leu His Met Leu Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Ile Lys Lys Arg Val Phe Gln Leu
20 25 30

Phe Glu Leu Ala Asp Lys Ala Tyr Lys Asn Asn Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asn
65 70 75 80

Asp Asp Glu Leu His Met Leu Met Thr Asp Leu Val Tyr Glu Ala Leu
85 90 95

His Phe Ala Lys Asp Glu Glu Ile Lys Lys Arg Val Phe Gln Leu Phe
100 105 110

Glu Leu Ala Asp Lys Ala Tyr Lys Asn Asn Asp Arg Gln Lys Leu Glu
115 120 125

Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
130 135 140

<210> 456
<211> 132
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 456

Asp Lys Glu Trp Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg Leu Leu
1 5 10 15

Asp Glu Leu Gly His Ala Glu Ala Ser Met Arg Val Ser Asp Leu Ile
20 25 30

Tyr Glu Phe Met Lys Lys Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu
35 40 45

Arg Leu Leu Glu Glu Val Glu Arg Gly Gly Gly Gly Ser Gly Gly Gly
50 55 60

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Lys Glu Trp
65 70 75 80

Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg Leu Leu Asp Glu Leu Gly
85 90 95

His Ala Glu Ala Ser Met Arg Val Ser Asp Leu Ile Tyr Glu Phe Met
100 105 110

Lys Lys Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu
115 120 125

Glu Val Glu Arg
130

<210> 457
<211> 148
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 457

Asn Asp Asp Glu Leu His Met Leu Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Ile Lys Lys Arg Val Phe Gln Leu
20 25 30

Phe Glu Leu Ala Asp Lys Ala Tyr Lys Asn Asn Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
65 70 75 80

Gly Gly Gly Ser Asn Asp Asp Glu Leu His Met Leu Met Thr Asp Leu
85 90 95

Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Ile Lys Lys Arg
100 105 110

Val Phe Gln Leu Phe Glu Leu Ala Asp Lys Ala Tyr Lys Asn Asn Asp
115 120 125

Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu
130 135 140

Arg Leu Leu Ser
145

<210> 458
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 458

Asp Lys Glu Trp Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg Leu Leu
1 5 10 15

Asp Glu Leu Gly His Ala Glu Ala Ser Met Arg Val Ser Asp Leu Ile
20 25 30

Tyr Glu Phe Met Lys Lys Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu
35 40 45

Arg Leu Leu Glu Glu Val Glu Arg Gly Ser Ser Gly Ser Gly Ser Ser
50 55 60

Gly Ser Gly Ser Ser Gly Ser Gly Ser Ser Gly Ser Asp Lys Glu Trp
65 70 75 80

Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg Leu Leu Asp Glu Leu Gly
85 90 95

His Ala Glu Ala Ser Met Arg Val Ser Asp Leu Ile Tyr Glu Phe Met
100 105 110

Lys Lys Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu
115 120 125

Glu Val Glu Arg Gly Ser Ser Ser Gly Gly Ser Ser Ser Gly Gly Ser
130 135 140

Ser Ser Gly Gly Ser Ser Ser Gly Asp Lys Glu Trp Ile Leu Gln Lys
145 150 155 160

Ile Tyr Glu Ile Met Arg Leu Leu Asp Glu Leu Gly His Ala Glu Ala
165 170 175

Ser Met Arg Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Lys Gly Asp
180 185 190

Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Glu Arg
195 200 205

<210> 459
<211> 232
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 459

Asn Asp Asp Glu Leu His Met Leu Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Ile Lys Lys Arg Val Phe Gln Leu
20 25 30

Phe Glu Leu Ala Asp Lys Ala Tyr Lys Asn Asn Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

Gly Ser Ser Gly Ser Gly Ser Ser Gly Ser Gly Ser Ser Gly Ser Gly
65 70 75 80

Ser Ser Gly Ser Asn Asp Asp Glu Leu His Met Leu Met Thr Asp Leu
85 90 95

Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Ile Lys Lys Arg
100 105 110

Val Phe Gln Leu Phe Glu Leu Ala Asp Lys Ala Tyr Lys Asn Asn Asp
115 120 125

Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu
130 135 140

Arg Leu Leu Ser Gly Ser Ser Ser Gly Gly Ser Ser Ser Gly Gly Ser
145 150 155 160

Ser Ser Gly Gly Ser Ser Ser Gly Asn Asp Asp Glu Leu His Met Leu
165 170 175

Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu
180 185 190

Ile Lys Lys Arg Val Phe Gln Leu Phe Glu Leu Ala Asp Lys Ala Tyr
195 200 205

Lys Asn Asn Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys
210 215 220

Glu Leu Leu Glu Arg Leu Leu Ser
225 230

<210> 460
<211> 132
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 460

Asp Lys Glu Trp Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg Leu Leu
1 5 10 15

Asp Glu Leu Gly His Ala Glu Ala Ser Met Arg Val Ser Asp Leu Ile
20 25 30

Tyr Glu Phe Met Lys Lys Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu
35 40 45

Arg Leu Leu Glu Glu Val Glu Arg Gly Ser Ala Gly Gly Ser Pro Ala
50 55 60

Gly Ser Pro Thr Ser Thr Gly Thr Ser Thr Ser Gly Asp Lys Glu Trp
65 70 75 80

Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg Leu Leu Asp Glu Leu Gly
85 90 95

His Ala Glu Ala Ser Met Arg Val Ser Asp Leu Ile Tyr Glu Phe Met
100 105 110

Lys Lys Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu
115 120 125

Glu Val Glu Arg
130

<210> 461
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 461

Asp Lys Glu Trp Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg Leu Leu
1 5 10 15

Asp Glu Leu Gly His Ala Glu Ala Ser Met Arg Val Ser Asp Leu Ile
20 25 30

Tyr Glu Phe Met Lys Lys Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu
35 40 45

Arg Leu Leu Glu Glu Val Glu Arg Gly Ser Ala Gly Gly Ser Pro Ala
50 55 60

Gly Ser Pro Thr Ser Thr Gly Thr Ser Gly Ser Gly Asp Lys Glu Trp
65 70 75 80

Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg Leu Leu Asp Glu Leu Gly
85 90 95

His Ala Glu Ala Ser Met Arg Val Ser Asp Leu Ile Tyr Glu Phe Met
100 105 110

Lys Lys Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu
115 120 125

Glu Val Glu Arg Gly Ser Ala Gly Gly Ser Pro Ala Gly Ser Pro Thr
130 135 140

Ser Thr Gly Thr Ser Gly Ser Gly Asp Lys Glu Trp Ile Leu Gln Lys
145 150 155 160

Ile Tyr Glu Ile Met Arg Leu Leu Asp Glu Leu Gly His Ala Glu Ala
165 170 175

Ser Met Arg Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Lys Gly Asp
180 185 190

Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Glu Arg
195 200 205

<210> 462
<211> 148
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 462

Asn Asp Asp Glu Leu His Met Leu Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Ile Lys Lys Arg Val Phe Gln Leu
20 25 30

Phe Glu Leu Ala Asp Lys Ala Tyr Lys Asn Asn Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

Gly Ser Ala Gly Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Gly Thr
65 70 75 80

Ser Gly Ser Gly Asn Asp Asp Glu Leu His Met Leu Met Thr Asp Leu
85 90 95

Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Ile Lys Lys Arg
100 105 110

Val Phe Gln Leu Phe Glu Leu Ala Asp Lys Ala Tyr Lys Asn Asn Asp
115 120 125

Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu
130 135 140

Arg Leu Leu Ser
145

<210> 463
<211> 232
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 463

Asn Asp Asp Glu Leu His Met Leu Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Ile Lys Lys Arg Val Phe Gln Leu
20 25 30

Phe Glu Leu Ala Asp Lys Ala Tyr Lys Asn Asn Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

Gly Ser Ala Gly Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Gly Thr
65 70 75 80

Ser Gly Ser Gly Asn Asp Asp Glu Leu His Met Leu Met Thr Asp Leu
85 90 95

Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Ile Lys Lys Arg
100 105 110

Val Phe Gln Leu Phe Glu Leu Ala Asp Lys Ala Tyr Lys Asn Asn Asp
115 120 125

Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu
130 135 140

Arg Leu Leu Ser Gly Ser Ala Gly Gly Ser Pro Ala Gly Ser Pro Thr
145 150 155 160

Ser Thr Gly Thr Ser Gly Ser Gly Asn Asp Asp Glu Leu His Met Leu
165 170 175

Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu
180 185 190

Ile Lys Lys Arg Val Phe Gln Leu Phe Glu Leu Ala Asp Lys Ala Tyr
195 200 205

Lys Asn Asn Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys
210 215 220

Glu Leu Leu Glu Arg Leu Leu Ser
225 230

<210> 464
<211> 218
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 464

Asp Lys Glu Trp Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg Leu Leu
1 5 10 15

Asp Glu Leu Gly His Ala Glu Ala Ser Met Arg Val Ser Asp Leu Ile
20 25 30

Tyr Glu Phe Met Lys Lys Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu
35 40 45

Arg Leu Leu Glu Glu Val Glu Arg Gly Gly Ser Ser Ala Gly Ser Pro
50 55 60

Thr Ser Thr Gly Thr Ser Ser Ala Thr Pro Ser Gly Ser Gly Thr Gly
65 70 75 80

Gly Asp Lys Glu Trp Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg Leu
85 90 95

Leu Asp Glu Leu Gly His Ala Glu Ala Ser Met Arg Val Ser Asp Leu
100 105 110

Ile Tyr Glu Phe Met Lys Lys Gly Asp Glu Arg Leu Leu Glu Glu Ala
115 120 125

Glu Arg Leu Leu Glu Glu Val Glu Arg Gly Gly Ser Ser Ala Gly Ser
130 135 140

Pro Thr Ser Thr Gly Thr Ser Ser Ala Thr Pro Ser Gly Ser Gly Thr
145 150 155 160

Gly Gly Asp Lys Glu Trp Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg
165 170 175

Leu Leu Asp Glu Leu Gly His Ala Glu Ala Ser Met Arg Val Ser Asp
180 185 190

Leu Ile Tyr Glu Phe Met Lys Lys Gly Asp Glu Arg Leu Leu Glu Glu
195 200 205

Ala Glu Arg Leu Leu Glu Glu Val Glu Arg
210 215

<210> 465

<211> 242
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 465

Asn Asp Asp Glu Leu His Met Leu Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Ile Lys Lys Arg Val Phe Gln Leu
20 25 30

Phe Glu Leu Ala Asp Lys Ala Tyr Lys Asn Asn Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

Gly Gly Ser Ser Ala Gly Ser Pro Thr Ser Thr Gly Thr Ser Ser Ala
65 70 75 80

Thr Pro Ser Gly Ser Gly Thr Gly Gly Asn Asp Asp Glu Leu His Met
85 90 95

Leu Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu
100 105 110

Glu Ile Lys Lys Arg Val Phe Gln Leu Phe Glu Leu Ala Asp Lys Ala
115 120 125

Tyr Lys Asn Asn Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu
130 135 140

Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly Ser Ser Ala Gly Ser
145 150 155 160

Pro Thr Ser Thr Gly Thr Ser Ser Ala Thr Pro Ser Gly Ser Gly Thr
165 170 175

Gly Gly Asn Asp Asp Glu Leu His Met Leu Met Thr Asp Leu Val Tyr

180

185

190

Glu Ala Leu His Phe Ala Lys Asp Glu Glu Ile Lys Lys Arg Val Phe
 195 200 205

Gln Leu Phe Glu Leu Ala Asp Lys Ala Tyr Lys Asn Asn Asp Arg Gln
 210 215 220

Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu
 225 230 235 240

Leu Ser

<210> 466
 <211> 137
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 466

Asp Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu
 1 5 10 15

Glu Gln Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile
 20 25 30

Tyr Glu Phe Met Lys Gln Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu
 35 40 45

Arg Leu Leu Glu Glu Val Glu Arg Gly Gly Ser Ser Gly Gly Gly Ser
 50 55 60

Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser
 65 70 75 80

Gly Asp Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys Thr
 85 90 95

Leu Glu Gln Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu

100

105

110

Ile Tyr Glu Phe Met Lys Gln Gly Asp Glu Arg Leu Leu Glu Glu Ala
 115 120 125

Glu Arg Leu Leu Glu Glu Val Glu Arg
 130 135

<210> 467

<211> 137

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 467

Asp Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu
 1 5 10 15

Glu Gln Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile
 20 25 30

Tyr Glu Phe Met Lys Gln Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu
 35 40 45

Arg Leu Leu Glu Glu Val Glu Arg Gly Gly Ser Ser Ala Gly Ser Pro
 50 55 60

Thr Ser Thr Gly Thr Ser Ser Ala Thr Pro Ser Gly Ser Gly Thr Gly
 65 70 75 80

Gly Asp Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys Thr
 85 90 95

Leu Glu Gln Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu
 100 105 110

Ile Tyr Glu Phe Met Lys Gln Gly Asp Glu Arg Leu Leu Glu Glu Ala
 115 120 125

Glu Arg Leu Leu Glu Glu Val Glu Arg

130

135

<210> 468
 <211> 137
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 468

Asp Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu
 1 5 10 15

Glu Gln Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile
 20 25 30

Tyr Glu Phe Met Lys Gln Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu
 35 40 45

Arg Leu Leu Glu Glu Val Glu Arg Gly Gly Ser Ser Gly Glu Ala Ala
 50 55 60

Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Gly Ser Ser Gly
 65 70 75 80

Gly Asp Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys Thr
 85 90 95

Leu Glu Gln Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu
 100 105 110

Ile Tyr Glu Phe Met Lys Gln Gly Asp Glu Arg Leu Leu Glu Glu Ala
 115 120 125

Glu Arg Leu Leu Glu Glu Val Glu Arg
 130 135

<210> 469
 <211> 141
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Synthetic

<400> 469

Asp Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu
1 5 10 15

Glu Gln Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile
20 25 30

Tyr Glu Phe Met Lys Gln Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu
35 40 45

Arg Leu Leu Glu Glu Val Glu Arg Gly Gly Ser Ser Gly Pro Ser Thr
50 55 60

Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Pro
65 70 75 80

Gly Gly Ser Ser Gly Asp Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu
85 90 95

Ile Met Lys Thr Leu Glu Gln Leu Gly His Ala Glu Ala Ser Met Gln
100 105 110

Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Gln Gly Asp Glu Arg Leu
115 120 125

Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Glu Arg
130 135 140

<210> 470

<211> 197

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 470

Asp Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu
1 5 10 15

Glu Gln Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile
20 25 30

Tyr Glu Phe Met Lys Gln Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu
35 40 45

Arg Leu Leu Glu Glu Val Glu Arg Gly Gly Ser Ser Gly Gln Ile Phe
50 55 60

Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu Val Glu Pro Ser
65 70 75 80

Asp Thr Ile Glu Asn Val Lys Ala Lys Ile Gln Asp Lys Glu Gly Ile
85 90 95

Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys Gln Leu Glu Asp
100 105 110

Gly Arg Thr Leu Ser Asp Tyr Asn Ile Gln Lys Glu Ser Thr Leu His
115 120 125

Leu Val Leu Arg Leu Arg Gly Gly Gly Gly Ser Ser Gly Asp Lys Glu
130 135 140

Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu Glu Gln Leu
145 150 155 160

Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe
165 170 175

Met Lys Gln Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu
180 185 190

Glu Glu Val Glu Arg
195

<210> 471
<211> 218
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 471

Asp Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu
1 5 10 15

Glu Gln Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile
20 25 30

Tyr Glu Phe Met Lys Gln Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu
35 40 45

Arg Leu Leu Glu Glu Val Glu Arg Gly Gly Ser Ser Ala Gly Ser Pro
50 55 60

Thr Ser Thr Gly Thr Ser Ser Ala Thr Pro Ser Gly Ser Gly Thr Gly
65 70 75 80

Gly Asp Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys Thr
85 90 95

Leu Glu Gln Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu
100 105 110

Ile Tyr Glu Phe Met Lys Gln Gly Asp Glu Arg Leu Leu Glu Glu Ala
115 120 125

Glu Arg Leu Leu Glu Glu Val Glu Arg Gly Gly Ser Ser Ala Gly Ser
130 135 140

Pro Thr Ser Thr Gly Thr Ser Ser Ala Thr Pro Ser Gly Ser Gly Thr
145 150 155 160

Gly Gly Asp Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys
165 170 175

Thr Leu Glu Gln Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp
180 185 190

Leu Ile Tyr Glu Phe Met Lys Gln Gly Asp Glu Arg Leu Leu Glu Glu

195

200

205

Ala Glu Arg Leu Leu Glu Glu Val Glu Arg
 210 215

<210> 472
 <211> 218
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 472

Asp Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu
 1 5 10 15

Glu Gln Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile
 20 25 30

Tyr Glu Phe Met Lys Gln Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu
 35 40 45

Arg Leu Leu Glu Glu Val Glu Arg Gly Gly Ser Ser Gly Glu Ala Ala
 50 55 60

Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Gly Ser Ser Gly
 65 70 75 80

Gly Asp Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys Thr
 85 90 95

Leu Glu Gln Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu
 100 105 110

Ile Tyr Glu Phe Met Lys Gln Gly Asp Glu Arg Leu Leu Glu Glu Ala
 115 120 125

Glu Arg Leu Leu Glu Glu Val Glu Arg Gly Gly Ser Ser Gly Glu Ala
 130 135 140

Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Gly Ser Ser

145		150		155		160									
Gly	Gly	Asp	Lys	Glu	Asn	Ile	Leu	Gln	Lys	Ile	Tyr	Glu	Ile	Met	Lys
				165					170					175	
Thr	Leu	Glu	Gln	Leu	Gly	His	Ala	Glu	Ala	Ser	Met	Gln	Val	Ser	Asp
			180					185					190		
Leu	Ile	Tyr	Glu	Phe	Met	Lys	Gln	Gly	Asp	Glu	Arg	Leu	Leu	Glu	Glu
		195					200					205			
Ala	Glu	Arg	Leu	Leu	Glu	Glu	Val	Glu	Arg						
	210					215									
<210> 473															
<211> 226															
<212> PRT															
<213> Artificial Sequence															
<220>															
<223> Synthetic															
<400> 473															
Asp	Lys	Glu	Asn	Ile	Leu	Gln	Lys	Ile	Tyr	Glu	Ile	Met	Lys	Thr	Leu
1				5					10					15	
Glu	Gln	Leu	Gly	His	Ala	Glu	Ala	Ser	Met	Gln	Val	Ser	Asp	Leu	Ile
			20					25					30		
Tyr	Glu	Phe	Met	Lys	Gln	Gly	Asp	Glu	Arg	Leu	Leu	Glu	Glu	Ala	Glu
		35					40					45			
Arg	Leu	Leu	Glu	Glu	Val	Glu	Arg	Gly	Gly	Ser	Ser	Gly	Pro	Ser	Thr
	50					55					60				
Pro	Pro	Thr	Pro	Ser	Pro	Ser	Thr	Pro	Pro	Thr	Pro	Ser	Pro	Ser	Pro
65					70					75					80
Gly	Gly	Ser	Ser	Gly	Asp	Lys	Glu	Asn	Ile	Leu	Gln	Lys	Ile	Tyr	Glu
				85					90					95	
Ile	Met	Lys	Thr	Leu	Glu	Gln	Leu	Gly	His	Ala	Glu	Ala	Ser	Met	Gln

100

105

110

Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Gln Gly Asp Glu Arg Leu
 115 120 125

Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Glu Arg Gly Gly Ser
 130 135 140

Ser Gly Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr
 145 150 155 160

Pro Ser Pro Ser Pro Gly Gly Ser Ser Gly Asp Lys Glu Asn Ile Leu
 165 170 175

Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu Glu Gln Leu Gly His Ala
 180 185 190

Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Gln
 195 200 205

Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val
 210 215 220

Glu Arg
 225

<210> 474
 <211> 338
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 474

Asp Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu
 1 5 10 15

Glu Gln Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile
 20 25 30

Tyr Glu Phe Met Lys Gln Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu

35

40

45

Arg Leu Leu Glu Glu Val Glu Arg Gly Gly Ser Ser Gly Gln Ile Phe
 50 55 60

Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu Val Glu Pro Ser
 65 70 75 80

Asp Thr Ile Glu Asn Val Lys Ala Lys Ile Gln Asp Lys Glu Gly Ile
 85 90 95

Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys Gln Leu Glu Asp
 100 105 110

Gly Arg Thr Leu Ser Asp Tyr Asn Ile Gln Lys Glu Ser Thr Leu His
 115 120 125

Leu Val Leu Arg Leu Arg Gly Gly Gly Gly Ser Ser Gly Asp Lys Glu
 130 135 140

Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu Glu Gln Leu
 145 150 155 160

Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe
 165 170 175

Met Lys Gln Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu
 180 185 190

Glu Glu Val Glu Arg Gly Gly Ser Ser Gly Gln Ile Phe Val Lys Thr
 195 200 205

Leu Thr Gly Lys Thr Ile Thr Leu Glu Val Glu Pro Ser Asp Thr Ile
 210 215 220

Glu Asn Val Lys Ala Lys Ile Gln Asp Lys Glu Gly Ile Pro Pro Asp
 225 230 235 240

Gln Gln Arg Leu Ile Phe Ala Gly Lys Gln Leu Glu Asp Gly Arg Thr
 245 250 255

Leu Ser Asp Tyr Asn Ile Gln Lys Glu Ser Thr Leu His Leu Val Leu
260 265 270

Arg Leu Arg Gly Gly Gly Gly Ser Ser Gly Asp Lys Glu Asn Ile Leu
275 280 285

Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu Glu Gln Leu Gly His Ala
290 295 300

Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Gln
305 310 315 320

Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val
325 330 335

Glu Arg

<210> 475
<211> 137
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 475

Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu
1 5 10 15

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

Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu
35 40 45

Arg Leu Leu Glu Glu Val Lys Arg Gly Gly Ser Ser Gly Gly Gly Ser
50 55 60

Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser
65 70 75 80

Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu
85 90 95

Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu
100 105 110

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

Glu Arg Leu Leu Glu Glu Val Lys Arg
130 135

<210> 476
<211> 141
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 476

Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu
1 5 10 15

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

Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu
35 40 45

Arg Leu Leu Glu Glu Val Lys Arg Gly Gly Ser Ser Gly Pro Ser Thr
50 55 60

Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Pro
65 70 75 80

Gly Gly Ser Ser Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu
85 90 95

Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln
100 105 110

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

Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
130 135 140

<210> 477
<211> 153
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 477

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu
20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly
65 70 75 80

Gly Ser Ser Gly Gly Gly Ser Ser Gly Asn Leu Asp Glu Leu His Met
85 90 95

Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu
100 105 110

Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala
115 120 125

Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu
130 135 140

Lys Glu Leu Leu Glu Arg Leu Leu Ser
145 150

<210> 478
<211> 157
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 478

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu
20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

Gly Gly Ser Ser Gly Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr
65 70 75 80

Pro Pro Thr Pro Ser Pro Ser Pro Gly Gly Ser Ser Gly Asn Leu Asp
85 90 95

Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe
100 105 110

Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys
115 120 125

Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val
130 135 140

Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
145 150 155

<210> 479
<211> 218
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 479

Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu
1 5 10 15

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

Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu
35 40 45

Arg Leu Leu Glu Glu Val Lys Arg Gly Gly Ser Ser Gly Gly Gly Ser
50 55 60

Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser
65 70 75 80

Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu
85 90 95

Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu
100 105 110

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

Glu Arg Leu Leu Glu Glu Val Lys Arg Gly Gly Ser Ser Gly Gly Gly
130 135 140

Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser
145 150 155 160

Ser Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys
165 170 175

Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp
180 185 190

Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu
195 200 205

Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
210 215

<210> 480
<211> 226
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 480

Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu
1 5 10 15

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

Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu
35 40 45

Arg Leu Leu Glu Glu Val Lys Arg Gly Gly Ser Ser Gly Pro Ser Thr
50 55 60

Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Pro
65 70 75 80

Gly Gly Ser Ser Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu
85 90 95

Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln
100 105 110

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

Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg Gly Gly Ser
130 135 140

Ser Gly Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr
145 150 155 160

Pro Ser Pro Ser Pro Gly Gly Ser Ser Gly Asp Lys Glu Asn Val Leu
165 170 175

Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala
180 185 190

Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr
195 200 205

Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val
210 215 220

Lys Arg
225

<210> 481
<211> 242
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 481

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu
20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly
65 70 75 80

Gly Ser Ser Gly Gly Gly Ser Ser Gly Asn Leu Asp Glu Leu His Met
85 90 95

Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu
100 105 110

Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala
115 120 125

Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu
130 135 140

Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly Ser Ser Gly Gly Gly
145 150 155 160

Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser
165 170 175

Ser Gly Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr
180 185 190

Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe
195 200 205

Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln
210 215 220

Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu
225 230 235 240

Leu Ser

<210> 482
<211> 250
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 482

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu
20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

Gly Gly Ser Ser Gly Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr
65 70 75 80

Pro Pro Thr Pro Ser Pro Ser Pro Gly Gly Ser Ser Gly Asn Leu Asp
85 90 95

Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe
100 105 110

Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys
115 120 125

Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val
130 135 140

Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly Ser
145 150 155 160

Ser Gly Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr
165 170 175

Pro Ser Pro Ser Pro Gly Gly Ser Ser Gly Asn Leu Asp Glu Leu His
180 185 190

Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp

195

200

205

Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys
 210 215 220

Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu
 225 230 235 240

Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
 245 250

<210> 483
 <211> 145
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 483

Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu
 1 5 10 15

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

Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu
 35 40 45

Arg Leu Leu Glu Glu Val Lys Arg Gly Gly Ser Ser Gly Gly Gly Ser
 50 55 60

Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser
 65 70 75 80

Gly Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu
 85 90 95

Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln
 100 105 110

Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys

115

120

125

Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu
 130 135 140

Ser
 145

<210> 484
 <211> 149
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 484

Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu
 1 5 10 15

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

Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu
 35 40 45

Arg Leu Leu Glu Glu Val Lys Arg Gly Gly Ser Ser Gly Pro Ser Thr
 50 55 60

Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Pro
 65 70 75 80

Gly Gly Ser Ser Gly Asn Leu Asp Glu Leu His Met Gln Met Thr Asp
 85 90 95

Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys
 100 105 110

His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys
 115 120 125

Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu

130

135

140

Glu Arg Leu Leu Ser
145

<210> 485
<211> 145
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 485

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu
20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly
65 70 75 80

Gly Ser Ser Gly Gly Gly Ser Ser Gly Asp Lys Glu Asn Val Leu Gln
85 90 95

Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu
100 105 110

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

Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys
130 135 140

Arg

145

<210> 486
<211> 149
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 486

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu
20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

Gly Gly Ser Ser Gly Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr
65 70 75 80

Pro Pro Thr Pro Ser Pro Ser Pro Gly Gly Ser Ser Gly Asp Lys Glu
85 90 95

Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu
100 105 110

Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe
115 120 125

Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu
130 135 140

Glu Glu Val Lys Arg
145

<210> 487

<211> 130
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 487

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu
20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

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

Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala
85 90 95

Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr
100 105 110

Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val
115 120 125

Lys Arg
130

<210> 488
<211> 130
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 488

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu
20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

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

Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala
85 90 95

Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr
100 105 110

Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val
115 120 125

Lys Arg
130

<210> 489
<211> 135
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 489

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu
20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Asp
65 70 75 80

Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu
85 90 95

Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr
100 105 110

Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg
115 120 125

Leu Leu Glu Glu Val Lys Arg
130 135

<210> 490
<211> 140
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 490

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu
20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly
65 70 75 80

Gly Ser Ser Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile
85 90 95

Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val
100 105 110

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

Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
130 135 140

<210> 491
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 491

Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu
1 5 10 15

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

Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu
35 40 45

Arg Leu Leu Glu Glu Val Lys Arg Gly Gly Ser Ser Gly Gly Gly Ser
50 55 60

Ser Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys
65 70 75 80

Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp
85 90 95

Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu
100 105 110

Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
115 120

<210> 492
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 492

Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu
1 5 10 15

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

Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu
35 40 45

Arg Leu Leu Glu Glu Val Lys Arg Gly Gly Ser Ser Gly Gly Gly Ser
50 55 60

Ser Gly Gly Gly Ser Ser Gly Asp Lys Glu Asn Val Leu Gln Lys Ile
65 70 75 80

Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser
85 90 95

Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu
100 105 110

Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
115 120 125

<210> 493
<211> 132
<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 493

Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu
1 5 10 15

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

Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu
35 40 45

Arg Leu Leu Glu Glu Val Lys Arg Gly Gly Ser Ser Gly Gly Gly Ser
50 55 60

Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Asp Lys Glu Asn
65 70 75 80

Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly
85 90 95

His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met
100 105 110

Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu
115 120 125

Glu Val Lys Arg
130

<210> 494

<211> 141

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 494

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu

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

<210> 495
 <211> 146
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 495

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

35

40

45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
 50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Ser Gly
 65 70 75 80

Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Asp Lys Glu Asn Val Leu
 85 90 95

Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala
 100 105 110

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

Lys Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val
 130 135 140

Lys Arg
 145

<210> 496
 <211> 151
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 496

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
 1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
 20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
 35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg

50

55

60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Ser Gly
65 70 75 80

Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Asp
85 90 95

Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu
100 105 110

Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr
115 120 125

Glu Phe Met Lys Thr Lys Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg
130 135 140

Leu Leu Glu Glu Val Lys Arg
145 150

<210> 497
<211> 226
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 497

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Ser Gly

65		70		75		80
Gly Gly Ser Ser	Gly Glu Leu Glu Glu Gln Val Met His Val Leu Asp	85		90		95
Gln Val Ser	Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu	100		105		110
Glu Leu	Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met	115		120		125
Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu		130		135		140
Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys		145		150		155
Gly Gly Ser Ser	Gly Gly Gly Ser Ser Gly Asp Lys Glu Asn Val Leu	165		170		175
Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala		180		185		190
Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr		195		200		205
Lys Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val		210		215		220
Lys Arg		225				

<210> 498
 <211> 236
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 498

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu

1	5	10	15
Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala	20	25	30
Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys	35	40	45
Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg	50	55	60
Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Ser Gly	65	70	75
Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Glu Leu Glu Glu Gln Val	85	90	95
Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His	100	105	110
Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp	115	120	125
Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu	130	135	140
Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu	145	150	155
Glu Leu Ala Arg Lys Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly	165	170	175
Gly Ser Ser Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile	180	185	190
Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val	195	200	205
Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Arg Leu Leu	210	215	220

Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
225 230 235

<210> 499
<211> 246
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 499

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Ser Gly
65 70 75 80

Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Glu
85 90 95

Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu Ala
100 105 110

His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala
115 120 125

Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser
130 135 140

Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile
145 150 155 160

Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Ser Gly Gly
165 170 175

Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Asp Lys
180 185 190

Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg
195 200 205

Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu
210 215 220

Phe Met Lys Thr Lys Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu
225 230 235 240

Leu Glu Glu Val Lys Arg
245

<210> 500
<211> 160
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 500

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Ser Gly
65 70 75 80

Gly Gly Ser Ser Gly Glu Leu Glu Glu Gln Val Met His Val Leu Asp
85 90 95

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
100 105 110

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
115 120 125

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
130 135 140

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
145 150 155 160

<210> 501
<211> 165
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 501

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Ser Gly
65 70 75 80

Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Glu Leu Glu Glu Gln Val
85 90 95

Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His
100 105 110

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp
115 120 125

Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu
130 135 140

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu
145 150 155 160

Glu Leu Ala Arg Lys
165

<210> 502
<211> 170
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 502

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Ser Gly
65 70 75 80

Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Glu
85 90 95

Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu Ala
100 105 110

His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala
115 120 125

Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser
130 135 140

Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile
145 150 155 160

Leu Glu His Leu Glu Glu Leu Ala Arg Lys
165 170

<210> 503
<211> 245
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 503

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Ser Gly
65 70 75 80

Gly Gly Ser Ser Gly Glu Leu Glu Glu Gln Val Met His Val Leu Asp
85 90 95

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
100 105 110

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
115 120 125

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
130 135 140

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
145 150 155 160

Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Glu Leu Glu Glu Gln Val
165 170 175

Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His
180 185 190

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp
195 200 205

Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu
210 215 220

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu
225 230 235 240

Glu Leu Ala Arg Lys
245

<210> 504
<211> 255
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 504

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Ser Gly
65 70 75 80

Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Glu Leu Glu Glu Gln Val
85 90 95

Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His
100 105 110

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp
115 120 125

Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu
130 135 140

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu
145 150 155 160

Glu Leu Ala Arg Lys Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly
165 170 175

Gly Ser Ser Gly Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln
180 185 190

Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu
195 200 205

Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu
210 215 220

Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu

225					230					235					240
Glu	Ala	Arg	Arg	Ile	Leu	Glu	His	Leu	Glu	Glu	Leu	Ala	Arg	Lys	
				245					250					255	
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<211>	265														
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Glu	Leu	Glu	Glu	Gln	Val	Met	His	Val	Leu	Asp	Gln	Val	Ser	Glu	Leu
1				5					10					15	
Ala	His	Glu	Leu	Leu	His	Lys	Leu	Thr	Gly	Glu	Glu	Leu	Glu	Arg	Ala
			20					25					30		
Ala	Tyr	Phe	Asn	Trp	Trp	Ala	Thr	Glu	Met	Met	Leu	Glu	Leu	Ile	Lys
		35					40					45			
Ser	Asp	Asp	Glu	Arg	Glu	Ile	Arg	Glu	Ile	Glu	Glu	Glu	Ala	Arg	Arg
	50					55					60				
Ile	Leu	Glu	His	Leu	Glu	Glu	Leu	Ala	Arg	Lys	Gly	Gly	Ser	Ser	Gly
65				70						75					80
Gly	Gly	Ser	Ser	Gly	Gly	Gly	Ser	Ser	Gly	Gly	Gly	Ser	Ser	Gly	Glu
				85					90					95	
Leu	Glu	Glu	Gln	Val	Met	His	Val	Leu	Asp	Gln	Val	Ser	Glu	Leu	Ala
			100					105					110		
His	Glu	Leu	Leu	His	Lys	Leu	Thr	Gly	Glu	Glu	Leu	Glu	Arg	Ala	Ala
		115					120					125			
Tyr	Phe	Asn	Trp	Trp	Ala	Thr	Glu	Met	Met	Leu	Glu	Leu	Ile	Lys	Ser
	130					135					140				
Asp	Asp	Glu	Arg	Glu	Ile	Arg	Glu	Ile	Glu	Glu	Glu	Ala	Arg	Arg	Ile

145		150		155		160									
Leu	Glu	His	Leu	Glu	Glu	Leu	Ala	Arg	Lys	Gly	Gly	Ser	Ser	Gly	Gly
			165						170					175	
Gly	Ser	Ser	Gly	Gly	Gly	Ser	Ser	Gly	Gly	Gly	Ser	Ser	Gly	Glu	Leu
			180					185					190		
Glu	Glu	Gln	Val	Met	His	Val	Leu	Asp	Gln	Val	Ser	Glu	Leu	Ala	His
		195					200					205			
Glu	Leu	Leu	His	Lys	Leu	Thr	Gly	Glu	Glu	Leu	Glu	Arg	Ala	Ala	Tyr
	210					215					220				
Phe	Asn	Trp	Trp	Ala	Thr	Glu	Met	Met	Leu	Glu	Leu	Ile	Lys	Ser	Asp
225					230					235					240
Asp	Glu	Arg	Glu	Ile	Arg	Glu	Ile	Glu	Glu	Glu	Ala	Arg	Arg	Ile	Leu
			245					250						255	
Glu	His	Leu	Glu	Glu	Leu	Ala	Arg	Lys							
		260					265								

<210> 506
 <211> 174
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Synthetic

 <400> 506

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

50

55

60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro
65 70 75 80

Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro
85 90 95

Ala Gly Gly Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val
100 105 110

Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu
115 120 125

Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu
130 135 140

Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu
145 150 155 160

Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
165 170

<210> 507
<211> 144
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 507

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu
20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser

50

55

60

Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro
65 70 75 80

Ala Pro Ser Ala Pro Ala Gly Gly Asp Lys Glu Asn Val Leu Gln Lys
85 90 95

Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala
100 105 110

Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp
115 120 125

Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
130 135 140

<210> 508

<211> 155

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 508

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro
65 70 75 80

Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro

85

90

95

Ala Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met
 100 105 110

Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser
 115 120 125

Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Arg Leu Leu Glu
 130 135 140

Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
 145 150 155

<210> 509
 <211> 273
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 509

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
 1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
 20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
 35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
 50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro
 65 70 75 80

Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro
 85 90 95

Ala Gly Gly Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val

100

105

110

Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu
 115 120 125

Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu
 130 135 140

Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu
 145 150 155 160

Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly
 165 170 175

Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro
 180 185 190

Ser Ala Pro Ala Gly Gly Glu Leu Glu Glu Gln Val Met His Val Leu
 195 200 205

Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly
 210 215 220

Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met
 225 230 235 240

Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile
 245 250 255

Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg
 260 265 270

Lys

<210> 510
 <211> 243
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 510

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu
20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro
65 70 75 80

Ala Pro Ser Ala Pro Ala Gly Gly Glu Leu Glu Glu Gln Val Met His
85 90 95

Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu
100 105 110

Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr
115 120 125

Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg
130 135 140

Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu
145 150 155 160

Ala Arg Lys Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro
165 170 175

Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Asp Lys Glu Asn Val
180 185 190

Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His
195 200 205

Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys
210 215 220

Thr Lys Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu
225 230 235 240

Val Lys Arg

<210> 511
<211> 243
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 511

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro
65 70 75 80

Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro
85 90 95

Ala Gly Gly Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val
100 105 110

Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val
115 120 125

Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg
130 135 140

Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg
145 150 155 160

Leu Leu Ser Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro
165 170 175

Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Asp Lys Glu Asn Val
180 185 190

Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His
195 200 205

Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys
210 215 220

Thr Lys Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu
225 230 235 240

Val Lys Arg

<210> 512
<211> 216
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 512

Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu
1 5 10 15

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

Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu
35 40 45

Arg Leu Leu Glu Glu Val Lys Arg Gly Gly Ala Ser Pro Ala Ala Pro
50 55 60

Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly
65 70 75 80

Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu
85 90 95

Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile
100 105 110

Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu
115 120 125

Arg Leu Leu Glu Glu Val Lys Arg Gly Gly Ala Ser Pro Ala Ala Pro
130 135 140

Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly
145 150 155 160

Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu
165 170 175

Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile
180 185 190

Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu
195 200 205

Arg Leu Leu Glu Glu Val Lys Arg
210 215

<210> 513
<211> 240
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 513

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu
20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro
65 70 75 80

Ala Pro Ser Ala Pro Ala Gly Gly Asn Leu Asp Glu Leu His Met Gln
85 90 95

Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu
100 105 110

Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr
115 120 125

Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys
130 135 140

Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly Ala Ser Pro Ala Ala Pro
145 150 155 160

Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly
165 170 175

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
180 185 190

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu
195 200 205

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu

210

215

220

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
 225 230 235 240

<210> 514
 <211> 254
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 514

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
 1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
 20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
 35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
 50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro
 65 70 75 80

Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro
 85 90 95

Ala Gly Gly Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val
 100 105 110

Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu
 115 120 125

Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu
 130 135 140

Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu

145		150		155		160									
Ala	Arg	Arg	Ile	Leu	Glu	His	Leu	Glu	Glu	Leu	Ala	Arg	Lys	Gly	Gly
			165					170						175	
Ala	Ser	Pro	Ala	Ala	Pro	Ala	Pro	Ala	Ser	Pro	Ala	Ala	Pro	Ala	Pro
			180					185					190		
Ser	Ala	Pro	Ala	Gly	Gly	Asp	Lys	Glu	Asn	Val	Leu	Gln	Lys	Ile	Tyr
		195					200					205			
Glu	Ile	Met	Lys	Glu	Leu	Glu	Arg	Leu	Gly	His	Ala	Glu	Ala	Ser	Met
	210					215					220				
Gln	Val	Ser	Asp	Leu	Ile	Tyr	Glu	Phe	Met	Lys	Thr	Lys	Asp	Glu	Asn
225					230					235					240
Leu	Leu	Glu	Glu	Ala	Glu	Arg	Leu	Leu	Glu	Glu	Val	Lys	Arg		
				245					250						
<210>	515														
<211>	166														
<212>	PRT														
<213>	Artificial Sequence														
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<223>	Synthetic														
<400>	515														
Glu	Leu	Glu	Glu	Gln	Val	Met	His	Val	Leu	Asp	Gln	Val	Ser	Glu	Leu
1				5					10					15	
Ala	His	Glu	Leu	Leu	His	Lys	Leu	Thr	Gly	Glu	Glu	Leu	Glu	Arg	Ala
			20					25						30	
Ala	Tyr	Phe	Asn	Trp	Trp	Ala	Thr	Glu	Met	Met	Leu	Glu	Leu	Ile	Lys
		35					40					45			
Ser	Asp	Asp	Glu	Arg	Glu	Ile	Arg	Glu	Ile	Glu	Glu	Glu	Ala	Arg	Arg
	50					55					60				
Ile	Leu	Glu	His	Leu	Glu	Glu	Leu	Ala	Arg	Lys	Gly	Gly	Ala	Ser	Pro

65		70		75		80									
Ala	Ala	Pro	Ala	Pro	Ala	Ser	Pro	Ala	Gly	Gly	Glu	Leu	Glu	Glu	Gln
			85						90				95		
Val	Met	His	Val	Leu	Asp	Gln	Val	Ser	Glu	Leu	Ala	His	Glu	Leu	Leu
			100					105					110		
His	Lys	Leu	Thr	Gly	Glu	Glu	Leu	Glu	Arg	Ala	Ala	Tyr	Phe	Asn	Trp
		115					120					125			
Trp	Ala	Thr	Glu	Met	Met	Leu	Glu	Leu	Ile	Lys	Ser	Asp	Asp	Glu	Arg
	130					135					140				
Glu	Ile	Arg	Glu	Ile	Glu	Glu	Glu	Ala	Arg	Arg	Ile	Leu	Glu	His	Leu
145					150					155					160
Glu	Glu	Leu	Ala	Arg	Lys										
				165											
<210>	516														
<211>	161														
<212>	PRT														
<213>	Artificial Sequence														
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<223>	Synthetic														
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Glu	Leu	Glu	Glu	Gln	Val	Met	His	Val	Leu	Asp	Gln	Val	Ser	Glu	Leu
1				5					10				15		
Ala	His	Glu	Leu	Leu	His	Lys	Leu	Thr	Gly	Glu	Glu	Leu	Glu	Arg	Ala
		20						25					30		
Ala	Tyr	Phe	Asn	Trp	Trp	Ala	Thr	Glu	Met	Met	Leu	Glu	Leu	Ile	Lys
	35					40					45				
Ser	Asp	Asp	Glu	Arg	Glu	Ile	Arg	Glu	Ile	Glu	Glu	Glu	Ala	Arg	Arg
	50					55				60					
Ile	Leu	Glu	His	Leu	Glu	Glu	Leu	Ala	Arg	Lys	Gly	Gly	Ala	Ser	Pro

65		70		75		80									
Asp	Lys	Glu	Asn	Val	Leu	Gln	Lys	Ile	Tyr	Glu	Ile	Met	Lys	Glu	Leu
			85					90					95		
Glu	Arg	Leu	Gly	His	Ala	Glu	Ala	Ser	Met	Gln	Val	Ser	Asp	Leu	Ile
		100						105					110		
Tyr	Glu	Phe	Met	Lys	Thr	Lys	Asp	Glu	Arg	Leu	Leu	Glu	Glu	Ala	Glu
		115					120					125			
Arg	Leu	Leu	Glu	Glu	Val	Lys	Arg								
	130					135									
<210> 518															
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<212> PRT															
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<400> 518															
Asn	Leu	Asp	Glu	Leu	His	Met	Gln	Met	Thr	Asp	Leu	Val	Tyr	Glu	Ala
1				5					10					15	
Leu	His	Phe	Ala	Lys	Asp	Glu	Glu	Phe	Gln	Lys	His	Val	Phe	Gln	Leu
			20					25					30		
Phe	Glu	Lys	Ala	Thr	Lys	Ala	Tyr	Lys	Asn	Lys	Asp	Arg	Gln	Lys	Leu
		35					40					45			
Glu	Lys	Val	Val	Glu	Glu	Leu	Lys	Glu	Leu	Leu	Glu	Arg	Leu	Leu	Ser
	50					55					60				
Gly	Gly	Ala	Ser	Pro	Ala	Ala	Pro	Ala	Gly	Gly	Asp	Lys	Glu	Asn	Val
65					70				75					80	
Leu	Gln	Lys	Ile	Tyr	Glu	Ile	Met	Lys	Glu	Leu	Glu	Arg	Leu	Gly	His
			85						90					95	
Ala	Glu	Ala	Ser	Met	Gln	Val	Ser	Asp	Leu	Ile	Tyr	Glu	Phe	Met	Lys

100

105

110

Thr Lys Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu
 115 120 125

Val Lys Arg
 130

<210> 519
 <211> 147
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 519

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
 1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
 20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
 35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
 50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro
 65 70 75 80

Ala Ala Pro Ala Pro Ala Ser Pro Ala Gly Gly Asp Lys Glu Asn Val
 85 90 95

Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His
 100 105 110

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

Thr Lys Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu

130

135

140

Val Lys Arg
145

<210> 520
<211> 142
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 520

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro
65 70 75 80

Ala Ala Pro Ala Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr
85 90 95

Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met
100 105 110

Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Arg
115 120 125

Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
130 135 140

<210> 521

<211> 243
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 521

Asn Ile Asp Glu Leu Leu Met Gln Val Thr Asp Leu Ile Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Ala Phe Gln Leu
20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Lys Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Ile Leu Ser
50 55 60

Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro
65 70 75 80

Ala Pro Ser Ala Pro Ala Gly Gly Glu Leu Glu Glu Gln Val Met His
85 90 95

Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu
100 105 110

Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr
115 120 125

Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg
130 135 140

Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu
145 150 155 160

Ala Arg Lys Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro
165 170 175

Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Asp Lys Glu Asn Val

180

185

190

Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His
 195 200 205

Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys
 210 215 220

Thr Lys Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu
 225 230 235 240

Val Lys Arg

<210> 522
 <211> 243
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 522

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
 1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
 20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
 35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
 50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro
 65 70 75 80

Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro
 85 90 95

Ala Gly Gly Asn Ile Asp Glu Leu Leu Met Gln Val Thr Asp Leu Ile

100

105

110

Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Ala
 115 120 125

Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Lys
 130 135 140

Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg
 145 150 155 160

Ile Leu Ser Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro
 165 170 175

Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Asp Lys Glu Asn Val
 180 185 190

Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His
 195 200 205

Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys
 210 215 220

Thr Lys Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu
 225 230 235 240

Val Lys Arg

<210> 523
 <211> 273
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 523

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
 1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala

20

25

30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
 35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Ala Arg
 50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Thr Gly Gly Ala Ser Pro
 65 70 75 80

Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro
 85 90 95

Ala Gly Gly Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val
 100 105 110

Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu
 115 120 125

Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu
 130 135 140

Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu
 145 150 155 160

Ala Ala Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Thr Gly Gly
 165 170 175

Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro
 180 185 190

Ser Ala Pro Ala Gly Gly Glu Leu Glu Glu Gln Val Met His Val Leu
 195 200 205

Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly
 210 215 220

Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met
 225 230 235 240

Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile
245 250 255

Glu Glu Glu Ala Ala Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg
260 265 270

Thr

<210> 524
<211> 216
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 524

Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu
1 5 10 15

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

Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu
35 40 45

Arg Leu Leu Glu Glu Val Thr Arg Gly Gly Ala Ser Pro Ala Ala Pro
50 55 60

Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly
65 70 75 80

Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu
85 90 95

Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile
100 105 110

Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu
115 120 125

Arg Leu Leu Glu Glu Val Thr Arg Gly Gly Ala Ser Pro Ala Ala Pro
130 135 140

Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly
145 150 155 160

Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu
165 170 175

Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile
180 185 190

Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu
195 200 205

Arg Leu Leu Glu Glu Val Thr Arg
210 215

<210> 525
<211> 243
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 525

Asn Ile Asp Glu Leu Leu Met Gln Val Thr Asp Leu Ile Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Ala Phe Gln Leu
20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Lys Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Ile Leu Ser
50 55 60

Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro
65 70 75 80

Ala Pro Ser Ala Pro Ala Gly Gly Glu Leu Glu Glu Gln Val Met His
85 90 95

Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu
100 105 110

Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr
115 120 125

Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg
130 135 140

Glu Ile Glu Glu Glu Ala Ala Arg Ile Leu Glu His Leu Glu Glu Leu
145 150 155 160

Ala Arg Thr Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro
165 170 175

Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Asp Lys Glu Asn Val
180 185 190

Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His
195 200 205

Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys
210 215 220

Thr Lys Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu
225 230 235 240

Val Lys Arg

<210> 526
<211> 243
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 526

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Ala Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Thr Gly Gly Ala Ser Pro
65 70 75 80

Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro
85 90 95

Ala Gly Gly Asn Ile Asp Glu Leu Leu Met Gln Val Thr Asp Leu Ile
100 105 110

Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Ala
115 120 125

Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Lys
130 135 140

Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg
145 150 155 160

Ile Leu Ser Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro
165 170 175

Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Asp Lys Glu Asn Val
180 185 190

Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His
195 200 205

Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys

210

215

220

Thr Lys Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu
 225 230 235 240

Val Lys Arg

<210> 527
 <211> 243
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 527

Asn Ile Asp Glu Leu Leu Met Gln Val Thr Asp Leu Ile Tyr Glu Ala
 1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Ala Phe Gln Leu
 20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Lys Gln Lys Leu
 35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Ile Leu Ser
 50 55 60

Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro
 65 70 75 80

Ala Pro Ser Ala Pro Ala Gly Gly Glu Leu Glu Glu Gln Val Met His
 85 90 95

Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu
 100 105 110

Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr
 115 120 125

Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg

130

135

140

Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu
145 150 155 160

Ala Arg Lys Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro
165 170 175

Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Asp Lys Glu Asn Val
180 185 190

Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His
195 200 205

Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys
210 215 220

Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu
225 230 235 240

Val Lys Arg

<210> 528
<211> 243
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 528

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg

50

55

60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro
65 70 75 80

Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro
85 90 95

Ala Gly Gly Asn Ile Asp Glu Leu Leu Met Gln Val Thr Asp Leu Ile
100 105 110

Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Ala
115 120 125

Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Lys
130 135 140

Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg
145 150 155 160

Ile Leu Ser Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro
165 170 175

Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Asp Lys Glu Asn Val
180 185 190

Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His
195 200 205

Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys
210 215 220

Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu
225 230 235 240

Val Lys Arg

<210> 529

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 529

Asn Ile Asp Glu Leu Leu Met Gln Val Thr Asp Leu Ile Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Ala Phe Gln Leu
20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Lys Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Ile Leu Ser
50 55 60

Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro
65 70 75 80

Ala Pro Ser Ala Pro Ala Gly Gly Glu Leu Glu Glu Gln Val Met His
85 90 95

Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu
100 105 110

Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr
115 120 125

Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg
130 135 140

Glu Ile Glu Glu Glu Ala Ala Arg Ile Leu Glu His Leu Glu Glu Leu
145 150 155 160

Ala Arg Thr Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro
165 170 175

Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Asp Lys Glu Asn Val
180 185 190

Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His
195 200 205

Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys
210 215 220

Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu
225 230 235 240

Val Lys Arg

<210> 530
<211> 243
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 530

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Ala Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Thr Gly Gly Ala Ser Pro
65 70 75 80

Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro
85 90 95

Ala Gly Gly Asn Ile Asp Glu Leu Leu Met Gln Val Thr Asp Leu Ile
100 105 110

Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Ala
115 120 125

Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Lys
130 135 140

Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg
145 150 155 160

Ile Leu Ser Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro
165 170 175

Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Asp Lys Glu Asn Val
180 185 190

Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His
195 200 205

Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys
210 215 220

Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu
225 230 235 240

Val Lys Arg

<210> 531
<211> 243
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 531

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro
65 70 75 80

Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro
85 90 95

Ala Gly Gly Asn Ile Asp Glu Leu Leu Met Gln Val Thr Asp Leu Ile
100 105 110

Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Ala
115 120 125

Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Lys
130 135 140

Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg
145 150 155 160

Ile Leu Ser Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro
165 170 175

Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Asp Lys Glu Asn Val
180 185 190

Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His
195 200 205

Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys
210 215 220

Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu
225 230 235 240

Val Lys Arg

<210> 532
<211> 235
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 532

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro
65 70 75 80

Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro
85 90 95

Ala Gly Gly Asn Ile Asp Glu Leu Leu Met Gln Val Thr Asp Leu Ile
100 105 110

Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Ala
115 120 125

Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Lys
130 135 140

Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg
145 150 155 160

Ile Leu Ser Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro

165

170

175

Ala Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met
 180 185 190

Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser
 195 200 205

Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu
 210 215 220

Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
 225 230 235

<210> 533
 <211> 227
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 533

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
 1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
 20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
 35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
 50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro
 65 70 75 80

Ala Ala Pro Ala Pro Ala Ser Pro Ala Gly Gly Asn Ile Asp Glu Leu
 85 90 95

Leu Met Gln Val Thr Asp Leu Ile Tyr Glu Ala Leu His Phe Ala Lys

100

105

110

Asp Glu Glu Phe Gln Lys His Ala Phe Gln Leu Phe Glu Lys Ala Thr
 115 120 125

Lys Ala Tyr Lys Asn Lys Asp Lys Gln Lys Leu Glu Lys Val Val Glu
 130 135 140

Glu Leu Lys Glu Leu Leu Glu Arg Ile Leu Ser Gly Gly Ala Ser Pro
 145 150 155 160

Ala Ala Pro Ala Pro Ala Ser Pro Ala Gly Gly Asp Lys Glu Asn Val
 165 170 175

Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His
 180 185 190

Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys
 195 200 205

Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu
 210 215 220

Val Lys Arg
 225

<210> 534
 <211> 222
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 534

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
 1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
 20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys

35

40

45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro
65 70 75 80

Ala Ala Pro Ala Gly Gly Asn Ile Asp Glu Leu Leu Met Gln Val Thr
85 90 95

Asp Leu Ile Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln
100 105 110

Lys His Ala Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn
115 120 125

Lys Asp Lys Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu
130 135 140

Leu Glu Arg Ile Leu Ser Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro
145 150 155 160

Ala Ser Pro Ala Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr
165 170 175

Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met
180 185 190

Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn
195 200 205

Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
210 215 220

<210> 535

<211> 230

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 535

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro
65 70 75 80

Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro
85 90 95

Ala Gly Gly Asn Ile Asp Glu Leu Leu Met Gln Val Thr Asp Leu Ile
100 105 110

Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Ala
115 120 125

Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Lys
130 135 140

Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg
145 150 155 160

Ile Leu Ser Gly Gly Ala Ser Pro Ala Ala Pro Ala Gly Gly Asp Lys
165 170 175

Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg
180 185 190

Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu
195 200 205

Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu
210 215 220

Leu Glu Glu Val Lys Arg
225 230

<210> 536
<211> 222
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 536

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro
65 70 75 80

Ala Ala Pro Ala Pro Ala Ser Pro Ala Gly Gly Asn Ile Asp Glu Leu
85 90 95

Leu Met Gln Val Thr Asp Leu Ile Tyr Glu Ala Leu His Phe Ala Lys
100 105 110

Asp Glu Glu Phe Gln Lys His Ala Phe Gln Leu Phe Glu Lys Ala Thr
115 120 125

Lys Ala Tyr Lys Asn Lys Asp Lys Gln Lys Leu Glu Lys Val Val Glu
130 135 140

Glu Leu Lys Glu Leu Leu Glu Arg Ile Leu Ser Gly Gly Ala Ser Pro
145 150 155 160

Ala Ala Pro Ala Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr
165 170 175

Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met
180 185 190

Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn
195 200 205

Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
210 215 220

<210> 537
<211> 217
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 537

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro
65 70 75 80

Ala Ala Pro Ala Gly Gly Asn Ile Asp Glu Leu Leu Met Gln Val Thr
85 90 95

Asp Leu Ile Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln
100 105 110

Lys His Ala Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn
115 120 125

Lys Asp Lys Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu
130 135 140

Leu Glu Arg Ile Leu Ser Gly Gly Ala Ser Pro Ala Ala Pro Ala Gly
145 150 155 160

Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu
165 170 175

Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu
180 185 190

Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala
195 200 205

Glu Arg Leu Leu Glu Glu Val Lys Arg
210 215

<210> 538
<211> 154
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 538

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Gly Gly Glu
65 70 75 80

Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu Ala
85 90 95

His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala
100 105 110

Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser
115 120 125

Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile
130 135 140

Leu Glu His Leu Glu Glu Leu Ala Arg Lys
145 150

<210> 539
<211> 152
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 539

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Glu Leu Glu
65 70 75 80

Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu
85 90 95

Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe
100 105 110

Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp
115 120 125

Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu
130 135 140

His Leu Glu Glu Leu Ala Arg Lys
145 150

<210> 540
<211> 163
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 540

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro
65 70 75 80

Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro
85 90 95

Ala Gly Gly Asn Ile Asp Glu Leu Leu Met Gln Val Thr Asp Leu Ile
100 105 110

Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Ala
115 120 125

Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Lys
130 135 140

Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg
145 150 155 160

Ile Leu Ser

<210> 541
<211> 155
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 541

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro
65 70 75 80

Ala Ala Pro Ala Pro Ala Ser Pro Ala Gly Gly Asn Ile Asp Glu Leu
85 90 95

Leu Met Gln Val Thr Asp Leu Ile Tyr Glu Ala Leu His Phe Ala Lys
100 105 110

Asp Glu Glu Phe Gln Lys His Ala Phe Gln Leu Phe Glu Lys Ala Thr
115 120 125

Lys Ala Tyr Lys Asn Lys Asp Lys Gln Lys Leu Glu Lys Val Val Glu
130 135 140

Glu Leu Lys Glu Leu Leu Glu Arg Ile Leu Ser
145 150 155

<210> 542
<211> 150
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 542

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro
65 70 75 80

Ala Ala Pro Ala Gly Gly Asn Ile Asp Glu Leu Leu Met Gln Val Thr
85 90 95

Asp Leu Ile Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln
100 105 110

Lys His Ala Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn
115 120 125

Lys Asp Lys Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu
130 135 140

Leu Glu Arg Ile Leu Ser
145 150

<210> 543
<211> 235
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 543

Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu
1 5 10 15

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

Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu
35 40 45

Arg Leu Leu Glu Glu Val Lys Arg Gly Gly Ala Ser Pro Ala Ala Pro
50 55 60

Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly
65 70 75 80

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
85 90 95

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
100 105 110

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
115 120 125

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
130 135 140

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro
145 150 155 160

Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro
165 170 175

Ala Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met
180 185 190

Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser
195 200 205

Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu
210 215 220

Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
225 230 235

<210> 544
<211> 243
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 544

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro
65 70 75 80

Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro
85 90 95

Ala Gly Gly Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val
100 105 110

Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val
115 120 125

Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg
130 135 140

Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg
145 150 155 160

Leu Leu Ser Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro
165 170 175

Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Asp Lys Glu Asn Val
180 185 190

Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His
195 200 205

Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys
210 215 220

Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu
225 230 235 240

Val Lys Arg

<210> 545

<211> 235
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 545

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro
65 70 75 80

Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro
85 90 95

Ala Gly Gly Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val
100 105 110

Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val
115 120 125

Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg
130 135 140

Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg
145 150 155 160

Leu Leu Ser Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro
165 170 175

Ala Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met

180

185

190

Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser
 195 200 205

Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu
 210 215 220

Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
 225 230 235

<210> 546
 <211> 235
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 546

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
 1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
 20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
 35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
 50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro
 65 70 75 80

Ala Ala Pro Ala Pro Ala Ser Pro Ala Gly Gly Asn Leu Asp Glu Leu
 85 90 95

His Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys
 100 105 110

Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr

115

120

125

Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu
130 135 140

Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly Ala Ser Pro
145 150 155 160

Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro
165 170 175

Ala Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met
180 185 190

Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser
195 200 205

Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu
210 215 220

Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
225 230 235

<210> 547
<211> 227
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 547

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg

50

55

60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro
 65 70 75 80

Ala Ala Pro Ala Pro Ala Ser Pro Ala Gly Gly Asn Leu Asp Glu Leu
 85 90 95

His Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys
 100 105 110

Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr
 115 120 125

Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu
 130 135 140

Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly Ala Ser Pro
 145 150 155 160

Ala Ala Pro Ala Pro Ala Ser Pro Ala Gly Gly Asp Lys Glu Asn Val
 165 170 175

Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His
 180 185 190

Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys
 195 200 205

Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu
 210 215 220

Val Lys Arg
 225

<210> 548
 <211> 222
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 548

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro
65 70 75 80

Ala Ala Pro Ala Gly Gly Asn Leu Asp Glu Leu His Met Gln Met Thr
85 90 95

Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln
100 105 110

Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn
115 120 125

Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu
130 135 140

Leu Glu Arg Leu Leu Ser Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro
145 150 155 160

Ala Ser Pro Ala Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr
165 170 175

Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met
180 185 190

Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn
195 200 205

Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
210 215 220

<210> 549
<211> 230
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 549

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro
65 70 75 80

Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro
85 90 95

Ala Gly Gly Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val
100 105 110

Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val
115 120 125

Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg
130 135 140

Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg
145 150 155 160

Leu Leu Ser Gly Gly Ala Ser Pro Ala Ala Pro Ala Gly Gly Asp Lys
165 170 175

Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg
180 185 190

Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu
195 200 205

Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu
210 215 220

Leu Glu Glu Val Lys Arg
225 230

<210> 550
<211> 222
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 550

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro
65 70 75 80

Ala Ala Pro Ala Pro Ala Ser Pro Ala Gly Gly Asn Leu Asp Glu Leu
85 90 95

His Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys
100 105 110

Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr
115 120 125

Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu
130 135 140

Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly Ala Ser Pro
145 150 155 160

Ala Ala Pro Ala Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr
165 170 175

Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met
180 185 190

Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn
195 200 205

Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
210 215 220

<210> 551
<211> 217
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 551

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro
65 70 75 80

Ala Ala Pro Ala Gly Gly Asn Leu Asp Glu Leu His Met Gln Met Thr
85 90 95

Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln
100 105 110

Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn
115 120 125

Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu
130 135 140

Leu Glu Arg Leu Leu Ser Gly Gly Ala Ser Pro Ala Ala Pro Ala Gly
145 150 155 160

Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu
165 170 175

Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu
180 185 190

Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala
195 200 205

Glu Arg Leu Leu Glu Glu Val Lys Arg
210 215

<210> 552
<211> 209
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 552

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Ala
65 70 75 80

Gly Gly Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr
85 90 95

Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe
100 105 110

Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln
115 120 125

Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu
130 135 140

Leu Ser Gly Gly Ala Ser Ala Gly Gly Asp Lys Glu Asn Val Leu Gln
145 150 155 160

Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu
165 170 175

Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys
180 185 190

Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys
195 200 205

Arg

<210> 553
<211> 211
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 553

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Gly Gly
65 70 75 80

Ser Gly Gly Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val
85 90 95

Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val
100 105 110

Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg
115 120 125

Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg
130 135 140

Leu Leu Ser Gly Gly Ser Gly Gly Ser Gly Gly Asp Lys Glu Asn Val
145 150 155 160

Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His

165

170

175

Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys
 180 185 190

Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu
 195 200 205

Val Lys Arg
 210

<210> 554
 <211> 204
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 554

Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu Ala
 1 5 10 15

His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala
 20 25 30

Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser
 35 40 45

Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile
 50 55 60

Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Gly Gly Asn
 65 70 75 80

Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu
 85 90 95

His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe
 100 105 110

Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu

115

120

125

Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly
 130 135 140

Gly Ser Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile
 145 150 155 160

Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val
 165 170 175

Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu
 180 185 190

Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
 195 200

<210> 555
 <211> 217
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 555

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
 1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
 20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
 35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
 50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Gly Gly
 65 70 75 80

Ser Gly Gly Ser Gly Gly Asn Leu Asp Glu Leu His Met Gln Met Thr

85

90

95

Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln
 100 105 110

Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn
 115 120 125

Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu
 130 135 140

Leu Glu Arg Leu Leu Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly
 145 150 155 160

Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu
 165 170 175

Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu
 180 185 190

Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala
 195 200 205

Glu Arg Leu Leu Glu Glu Val Lys Arg
 210 215

<210> 556
 <211> 247
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 556

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
 1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
 20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys

35

40

45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
 50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro
 65 70 75 80

Ala Ala Pro Ala Gly Gly Glu Leu Glu Glu Gln Val Met His Val Leu
 85 90 95

Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly
 100 105 110

Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met
 115 120 125

Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile
 130 135 140

Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg
 145 150 155 160

Lys Gly Gly Ala Ser Pro Ala Ala Pro Ala Gly Gly Glu Leu Glu Glu
 165 170 175

Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu
 180 185 190

Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn
 195 200 205

Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu
 210 215 220

Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His
 225 230 235 240

Leu Glu Glu Leu Ala Arg Lys
 245

<210> 557
<211> 247
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 557

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Gly Gly
65 70 75 80

Ser Gly Gly Ser Gly Gly Glu Leu Glu Glu Gln Val Met His Val Leu
85 90 95

Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly
100 105 110

Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met
115 120 125

Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile
130 135 140

Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg
145 150 155 160

Lys Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Glu Leu Glu Glu
165 170 175

Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu
180 185 190

Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn
195 200 205

Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu
210 215 220

Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His
225 230 235 240

Leu Glu Glu Leu Ala Arg Lys
245

<210> 558
<211> 241
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 558

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Gly Gly
65 70 75 80

Ser Gly Gly Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val
85 90 95

Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu
100 105 110

Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu
115 120 125

Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu
130 135 140

Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly
145 150 155 160

Ser Gly Gly Ser Gly Gly Glu Leu Glu Glu Gln Val Met His Val Leu
165 170 175

Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly
180 185 190

Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met
195 200 205

Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile
210 215 220

Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg
225 230 235 240

Lys

<210> 559
<211> 235
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 559

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Gly Gly
65 70 75 80

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
85 90 95

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
100 105 110

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
115 120 125

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
130 135 140

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Gly Gly
145 150 155 160

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
165 170 175

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
180 185 190

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
195 200 205

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
210 215 220

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys

225

230

235

<210> 560
 <211> 225
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 560

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
 1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
 20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
 35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
 50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Gly Gly
 65 70 75 80

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Asn Leu Asp Glu Leu His
 85 90 95

Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp
 100 105 110

Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys
 115 120 125

Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu
 130 135 140

Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly Ser Gly Gly Gly
 145 150 155 160

Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Lys Glu Asn Val Leu Gln

165

170

175

Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu
 180 185 190

Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys
 195 200 205

Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys
 210 215 220

Arg
 225

<210> 561
 <211> 219
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 561

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
 1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
 20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
 35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
 50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Gly Gly
 65 70 75 80

Gly Gly Ser Gly Gly Gly Gly Asn Leu Asp Glu Leu His Met Gln Met
 85 90 95

Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe

100

105

110

Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys
 115 120 125

Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu
 130 135 140

Leu Leu Glu Arg Leu Leu Ser Gly Gly Ser Gly Gly Gly Gly Ser Gly
 145 150 155 160

Gly Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met
 165 170 175

Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser
 180 185 190

Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu
 195 200 205

Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
 210 215

<210> 562
 <211> 213
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 562

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
 1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
 20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
 35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg

50

55

60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Gly Gly Ser
65 70 75 80

Gly Gly Gly Gly Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu
85 90 95

Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His
100 105 110

Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp
115 120 125

Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu
130 135 140

Arg Leu Leu Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Asp Lys Glu
145 150 155 160

Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu
165 170 175

Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe
180 185 190

Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu
195 200 205

Glu Glu Val Lys Arg
210

<210> 563
<211> 209
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 563

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu

[illegible]

<210> 564
<211> 137
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 564

Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu
1 5 10 15

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

Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu
35 40 45

Arg Leu Leu Glu Glu Val Lys Arg Gly Gly Ser Gly Gly Gly Gly Ser
50 55 60

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
65 70 75 80

Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu
85 90 95

Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu
100 105 110

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

Glu Arg Leu Leu Glu Glu Val Lys Arg
130 135

<210> 565
<211> 132
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 565

Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu
1 5 10 15

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

Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu
35 40 45

Arg Leu Leu Glu Glu Val Lys Arg Gly Gly Ser Gly Gly Gly Gly Ser
50 55 60

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Lys Glu Asn
65 70 75 80

Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly
85 90 95

His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met
100 105 110

Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu
115 120 125

Glu Val Lys Arg
130

<210> 566

<211> 127

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 566

Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu
1 5 10 15

Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile

20

25

30

Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu
 35 40 45

Arg Leu Leu Glu Glu Val Lys Arg Gly Gly Ser Gly Gly Gly Gly Ser
 50 55 60

Gly Gly Gly Gly Ser Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile
 65 70 75 80

Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser
 85 90 95

Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu
 100 105 110

Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
 115 120 125

<210> 567
 <211> 122
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 567

Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu
 1 5 10 15

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

Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu
 35 40 45

Arg Leu Leu Glu Glu Val Lys Arg Gly Gly Ser Gly Gly Gly Gly Ser
 50 55 60

Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys

65		70		75		80									
Glu	Leu	Glu	Arg	Leu	Gly	His	Ala	Glu	Ala	Ser	Met	Gln	Val	Ser	Asp
				85					90					95	
Leu	Ile	Tyr	Glu	Phe	Met	Lys	Thr	Lys	Asp	Glu	Asn	Leu	Leu	Glu	Glu
			100					105					110		
Ala	Glu	Arg	Leu	Leu	Glu	Glu	Val	Lys	Arg						
		115					120								
<210> 568															
<211> 141															
<212> PRT															
<213> Artificial Sequence															
<220>															
<223> Synthetic															
<400> 568															
Glu	Leu	Glu	Glu	Gln	Val	Met	His	Val	Leu	Asp	Gln	Val	Ser	Glu	Leu
1				5					10					15	
Ala	His	Glu	Leu	Leu	His	Lys	Leu	Thr	Gly	Glu	Glu	Leu	Glu	Arg	Ala
			20					25						30	
Ala	Tyr	Phe	Asn	Trp	Trp	Ala	Thr	Glu	Met	Met	Leu	Glu	Leu	Ile	Lys
		35					40					45			
Ser	Asp	Asp	Glu	Arg	Glu	Ile	Arg	Glu	Ile	Glu	Glu	Glu	Ala	Arg	Arg
	50					55					60				
Ile	Leu	Glu	His	Leu	Glu	Glu	Leu	Ala	Arg	Lys	Gly	Gly	Ser	Gly	Gly
65					70					75					80
Gly	Gly	Ser	Gly	Gly	Asp	Lys	Glu	Asn	Val	Leu	Gln	Lys	Ile	Tyr	Glu
				85					90					95	
Ile	Met	Lys	Glu	Leu	Glu	Arg	Leu	Gly	His	Ala	Glu	Ala	Ser	Met	Gln
			100					105						110	
Val	Ser	Asp	Leu	Ile	Tyr	Glu	Phe	Met	Lys	Thr	Lys	Asp	Glu	Asn	Leu

115

120

125

Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
 130 135 140

<210> 569
 <211> 130
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 569

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
 1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu
 20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
 35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
 50 55 60

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

Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala
 85 90 95

Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr
 100 105 110

Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val
 115 120 125

Lys Arg
 130

<210> 570

<211> 149
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 570

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Gly Gly
65 70 75 80

Gly Gly Ser Gly Gly Asn Leu Asp Glu Leu His Met Gln Met Thr Asp
85 90 95

Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys
100 105 110

His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys
115 120 125

Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu
130 135 140

Glu Arg Leu Leu Ser
145

<210> 571
<211> 149
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 571

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu
20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Glu Leu Glu Glu Gln Val
65 70 75 80

Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His
85 90 95

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp
100 105 110

Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu
115 120 125

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu
130 135 140

Glu Leu Ala Arg Lys
145

<210> 572

<211> 215

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 572

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Gly Gly
65 70 75 80

Gly Gly Ser Gly Gly Asn Leu Asp Glu Leu His Met Gln Met Thr Asp
85 90 95

Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys
100 105 110

His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys
115 120 125

Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu
130 135 140

Glu Arg Leu Leu Ser Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp
145 150 155 160

Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu
165 170 175

Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr
180 185 190

Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg
195 200 205

Leu Leu Glu Glu Val Lys Arg

210

215

<210> 573
 <211> 215
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 573

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
 1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu
 20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
 35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
 50 55 60

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Glu Leu Glu Glu Gln Val
 65 70 75 80

Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His
 85 90 95

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp
 100 105 110

Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu
 115 120 125

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu
 130 135 140

Glu Leu Ala Arg Lys Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp
 145 150 155 160

Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu

165

170

175

Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr
 180 185 190

Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg
 195 200 205

Leu Leu Glu Glu Val Lys Arg
 210 215

<210> 574
 <211> 225
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 574

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
 1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu
 20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
 35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
 50 55 60

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Glu
 65 70 75 80

Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu Ala
 85 90 95

His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala
 100 105 110

Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser

115

120

125

Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile
 130 135 140

Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Gly Gly Gly
 145 150 155 160

Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Lys Glu Asn Val Leu Gln
 165 170 175

Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu
 180 185 190

Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys
 195 200 205

Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys
 210 215 220

Arg
 225

<210> 575
 <211> 132
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 575

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
 1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu
 20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
 35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser

50

55

60

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

Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly
85 90 95

His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met
100 105 110

Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu
115 120 125

Glu Val Lys Arg
130

<210> 576
<211> 143
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 576

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro
65 70 75 80

Ala Ala Pro Ala Pro Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile

85

90

95

Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser
 100 105 110

Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu
 115 120 125

Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
 130 135 140

<210> 577

<211> 151

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 577

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
 1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
 20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
 35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
 50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro
 65 70 75 80

Ala Ala Pro Ala Pro Gly Gly Asn Leu Asp Glu Leu His Met Gln Met
 85 90 95

Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe
 100 105 110

Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys

115

120

125

Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu
 130 135 140

Leu Leu Glu Arg Leu Leu Ser
 145 150

<210> 578
 <211> 151
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 578

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
 1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu
 20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
 35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
 50 55 60

Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Gly Gly Glu Leu Glu Glu
 65 70 75 80

Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu
 85 90 95

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

Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu
 115 120 125

Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His

130

135

140

Leu Glu Glu Leu Ala Arg Lys
145 150

<210> 579
<211> 219
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 579

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro
65 70 75 80

Ala Ala Pro Ala Pro Gly Gly Asn Leu Asp Glu Leu His Met Gln Met
85 90 95

Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe
100 105 110

Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys
115 120 125

Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu
130 135 140

Leu Leu Glu Arg Leu Leu Ser Gly Gly Ala Ser Pro Ala Ala Pro Ala

145		150		155		160									
Pro	Gly	Gly	Asp	Lys	Glu	Asn	Val	Leu	Gln	Lys	Ile	Tyr	Glu	Ile	Met
				165					170					175	
Lys	Glu	Leu	Glu	Arg	Leu	Gly	His	Ala	Glu	Ala	Ser	Met	Gln	Val	Ser
			180					185					190		
Asp	Leu	Ile	Tyr	Glu	Phe	Met	Lys	Thr	Lys	Asp	Glu	Asn	Leu	Leu	Glu
		195					200					205			
Glu	Ala	Glu	Arg	Leu	Leu	Glu	Glu	Val	Lys	Arg					
	210					215									
<210> 580															
<211> 219															
<212> PRT															
<213> Artificial Sequence															
<220>															
<223> Synthetic															
<400> 580															
Asn	Leu	Asp	Glu	Leu	His	Met	Gln	Met	Thr	Asp	Leu	Val	Tyr	Glu	Ala
1				5					10					15	
Leu	His	Phe	Ala	Lys	Asp	Glu	Glu	Phe	Gln	Lys	His	Val	Phe	Gln	Leu
			20					25					30		
Phe	Glu	Lys	Ala	Thr	Lys	Ala	Tyr	Lys	Asn	Lys	Asp	Arg	Gln	Lys	Leu
		35					40					45			
Glu	Lys	Val	Val	Glu	Glu	Leu	Lys	Glu	Leu	Leu	Glu	Arg	Leu	Leu	Ser
	50					55					60				
Gly	Gly	Ala	Ser	Pro	Ala	Ala	Pro	Ala	Pro	Gly	Gly	Glu	Leu	Glu	Glu
65					70					75				80	
Gln	Val	Met	His	Val	Leu	Asp	Gln	Val	Ser	Glu	Leu	Ala	His	Glu	Leu
			85						90					95	
Leu	His	Lys	Leu	Thr	Gly	Glu	Glu	Leu	Glu	Arg	Ala	Ala	Tyr	Phe	Asn

100

105

110

Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu
 115 120 125

Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His
 130 135 140

Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro Ala Ala Pro Ala
 145 150 155 160

Pro Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met
 165 170 175

Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser
 180 185 190

Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu
 195 200 205

Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
 210 215

<210> 581
 <211> 243
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 581

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
 1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu
 20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
 35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser

50

55

60

Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro
65 70 75 80

Ala Pro Ser Ala Pro Ala Gly Gly Glu Leu Glu Glu Gln Val Met His
85 90 95

Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu
100 105 110

Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr
115 120 125

Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg
130 135 140

Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu
145 150 155 160

Ala Arg Lys Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro
165 170 175

Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Asp Lys Glu Asn Val
180 185 190

Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His
195 200 205

Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys
210 215 220

Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu
225 230 235 240

Val Lys Arg

<210> 582

<211> 143

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 582

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Ala Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Thr Gly Gly Ala Ser Pro
65 70 75 80

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

Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser
100 105 110

Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu
115 120 125

Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
130 135 140

<210> 583

<211> 151

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 583

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu

1	5	10	15
Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala	20	25	30
Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys	35	40	45
Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Ala Arg	50	55	60
Ile Leu Glu His Leu Glu Glu Leu Ala Arg Thr Gly Gly Ala Ser Pro	65	70	75
Ala Ala Pro Ala Pro Gly Gly Asn Leu Asp Glu Leu His Met Gln Met	85	90	95
Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe	100	105	110
Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys	115	120	125
Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu	130	135	140
Leu Leu Glu Arg Leu Leu Ser	145	150	

<210> 584
 <211> 151
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 584

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala	5	10	15
1			

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu

20

25

30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
 35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
 50 55 60

Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Gly Gly Glu Leu Glu Glu
 65 70 75 80

Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu
 85 90 95

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

Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu
 115 120 125

Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Ala Arg Ile Leu Glu His
 130 135 140

Leu Glu Glu Leu Ala Arg Thr
 145 150

<210> 585
 <211> 219
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 585

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
 1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
 20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys

35

40

45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Ala Arg
 50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Thr Gly Gly Ala Ser Pro
 65 70 75 80

Ala Ala Pro Ala Pro Gly Gly Asn Leu Asp Glu Leu His Met Gln Met
 85 90 95

Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe
 100 105 110

Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys
 115 120 125

Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu
 130 135 140

Leu Leu Glu Arg Leu Leu Ser Gly Gly Ala Ser Pro Ala Ala Pro Ala
 145 150 155 160

Pro Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met
 165 170 175

Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser
 180 185 190

Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu
 195 200 205

Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
 210 215

<210> 586

<211> 219

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 586

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu
20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Gly Gly Glu Leu Glu Glu
65 70 75 80

Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu
85 90 95

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

Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu
115 120 125

Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Ala Arg Ile Leu Glu His
130 135 140

Leu Glu Glu Leu Ala Arg Thr Gly Gly Ala Ser Pro Ala Ala Pro Ala
145 150 155 160

Pro Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met
165 170 175

Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser
180 185 190

Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu
195 200 205

Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
210 215

<210> 587
<211> 243
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 587

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Ala Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Thr Gly Gly Ala Ser Pro
65 70 75 80

Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro
85 90 95

Ala Gly Gly Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val
100 105 110

Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val
115 120 125

Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg
130 135 140

Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg
145 150 155 160

Leu Leu Ser Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro
165 170 175

Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Asp Lys Glu Asn Val
180 185 190

Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His
195 200 205

Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys
210 215 220

Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu
225 230 235 240

Val Lys Arg

<210> 588
<211> 243
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 588

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu
20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro
65 70 75 80

Ala Pro Ser Ala Pro Ala Gly Gly Glu Leu Glu Glu Gln Val Met His
85 90 95

Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu
100 105 110

Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr
115 120 125

Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg
130 135 140

Glu Ile Glu Glu Glu Ala Ala Arg Ile Leu Glu His Leu Glu Glu Leu
145 150 155 160

Ala Arg Thr Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro
165 170 175

Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Asp Lys Glu Asn Val
180 185 190

Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His
195 200 205

Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys
210 215 220

Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu
225 230 235 240

Val Lys Arg

<210> 589
<211> 85
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 589

Ser Glu Glu Leu Arg Ala Val Ala Asp Leu Gln Arg Leu Asn Ile Glu
1 5 10 15

Leu Ala Arg Lys Leu Leu Glu Ala Val Ala Arg Leu Gln Glu Leu Asn
20 25 30

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

Arg Glu Glu Ile Arg Lys Val Lys Glu Glu Ser Lys Arg Ile Val Glu
50 55 60

Glu Ala Glu Glu Glu Ile Arg Arg Ala Lys Glu Glu Ser Arg Lys Ile
65 70 75 80

Ala Asp Glu Ser Arg
85

<210> 590
<211> 134
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 590

Glu Glu Ala Glu Leu Ala Tyr Leu Leu Gly Glu Leu Ala Tyr Lys Leu
1 5 10 15

Gly Glu Tyr Arg Ile Ala Ile Arg Ala Tyr Arg Ile Ala Leu Lys Arg
20 25 30

Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr
35 40 45

Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu
50 55 60

Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala
65 70 75 80

Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys
85 90 95

Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly
100 105 110

Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr
115 120 125

Gln Lys Ala Leu Glu Leu
130

<210> 591
<211> 83
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 591

Glu Glu Ala Glu Leu Ala Tyr Leu Leu Gly Glu Leu Ala Tyr Lys Leu
1 5 10 15

Gly Glu Tyr Arg Ile Ala Ile Arg Ala Tyr Arg Ile Ala Leu Lys Arg
20 25 30

Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr
35 40 45

Lys Gln Gly Asp Tyr Asp Glu Ala Ile Tyr Tyr Gln Lys Ala Leu Glu
50 55 60

Leu Asp Pro Asn Asn Ala Glu Ala Lys Gln Asn Leu Gly Asn Ala Lys
65 70 75 80

Gln Lys Gln

<210> 592
<211> 83
<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 592

Glu Glu Ala Glu Leu Ala Tyr Leu Leu Gly Glu Leu Ala Tyr Lys Leu
1 5 10 15

Gly Glu Tyr Arg Ile Ala Ile Arg Ala Tyr Arg Ile Ala Leu Lys Arg
20 25 30

Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr
35 40 45

Lys Gln Gly Asp Tyr Asp Glu Ile Glu Tyr Tyr Gln Lys Ala Leu Glu
50 55 60

Leu Asp Pro Asn Asn Ala Glu Ala Lys Gln Asn Leu Gly Asn Ala Lys
65 70 75 80

Gln Lys Gln

<210> 593

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 593

Glu Glu Ala Glu Leu Ala Tyr Leu Leu Gly Glu Leu Ala Tyr Lys Leu
1 5 10 15

Gly Glu Tyr Arg Ile Ala Ile Arg Ala Tyr Arg Ile Ala Leu Lys Arg
20 25 30

Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr
35 40 45

Lys Gln Gly Asp Tyr Asp Glu Ala Ile Tyr Tyr Gln Lys Ala Leu Glu

50

55

60

Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr
65 70 75 80

Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys Ala
85 90 95

Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Lys Gln Asn Leu Gly Asn
100 105 110

Lys Gln Lys Gln
115

<210> 594
<211> 73
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 594

Glu Tyr Glu Ile Arg Lys Ala Leu Glu Glu Leu Lys Ala Ser Thr Ala
1 5 10 15

Glu Leu Lys Arg Ala Thr Ala Ser Leu Arg Ala Ser Thr Glu Glu Leu
20 25 30

Lys Lys Asn Pro Ser Glu Asp Ala Leu Val Glu Asn Asn Arg Leu Ile
35 40 45

Val Glu His Asn Ala Ile Ile Val Glu Asn Arg Ile Ile Ala Ala Val
50 55 60

Leu Glu Leu Ile Val Arg Ala Ile Lys
65 70

<210> 595
<211> 108
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 595

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Ser Gly Ser Gly
65 70 75 80

Ser Gly Tyr Ile Pro Glu Ala Pro Arg Asp Gly Gln Ala Tyr Val Arg
85 90 95

Lys Asp Gly Glu Trp Val Leu Leu Ser Thr Phe Leu
100 105

<210> 596

<211> 211

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 596

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Ser Gly Ser Gly
65 70 75 80

Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly
85 90 95

Ser Gly Ser Gly Ser Gly Ser Glu Leu Glu Glu Gln Val Met His Val
100 105 110

Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr
115 120 125

Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu
130 135 140

Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu
145 150 155 160

Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala
165 170 175

Arg Lys Gly Ser Gly Ser Gly Ser Gly Tyr Ile Pro Glu Ala Pro Arg
180 185 190

Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu Leu Ser
195 200 205

Thr Phe Leu
210

<210> 597
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 597

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Ser Gly Ser Gly
65 70 75 80

Gly Tyr Ile Pro Glu Ala Pro Arg Asp Gly Gln Ala Tyr Val Arg Lys
85 90 95

Asp Gly Glu Trp Val Leu Leu Ser Thr Phe Leu
100 105

<210> 598
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 598

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Ser Gly Ser Gly
65 70 75 80

Tyr Ile Pro Glu Ala Pro Arg Asp Gly Gln Ala Tyr Val Arg Lys Asp
85 90 95

Gly Glu Trp Val Leu Leu Ser Thr Phe Leu
100 105

<210> 599
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 599

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Ser Gly Gly Tyr
65 70 75 80

Ile Pro Glu Ala Pro Arg Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly
85 90 95

Glu Trp Val Leu Leu Ser Thr Phe Leu
100 105

<210> 600
<211> 208
<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 600

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Ser Gly Ser Gly
65 70 75 80

Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly
85 90 95

Ser Gly Ser Gly Ser Gly Ser Glu Leu Glu Glu Gln Val Met His Val
100 105 110

Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr
115 120 125

Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu
130 135 140

Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu
145 150 155 160

Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala
165 170 175

Arg Lys Gly Ser Gly Gly Tyr Ile Pro Glu Ala Pro Arg Asp Gly Gln
180 185 190

Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu Leu Ser Thr Phe Leu
195 200 205

<210> 601
<211> 164
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 601

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Ser Gly Ser Ser
65 70 75 80

Glu Glu Leu Arg Ala Val Ala Asp Leu Gln Arg Leu Asn Ile Glu Leu
85 90 95

Ala Arg Lys Leu Leu Glu Ala Val Ala Arg Leu Gln Glu Leu Asn Ile
100 105 110

Asp Leu Val Arg Lys Thr Ser Glu Leu Thr Asp Glu Lys Thr Ile Arg
115 120 125

Glu Glu Ile Arg Lys Val Lys Glu Glu Ser Lys Arg Ile Val Glu Glu
130 135 140

Ala Glu Glu Glu Ile Arg Arg Ala Lys Glu Glu Ser Arg Lys Ile Ala
145 150 155 160

Asp Glu Ser Arg

<210> 602
<211> 165
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 602

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Ser Gly Ser Gly
65 70 75 80

Ser Glu Glu Leu Arg Ala Val Ala Asp Leu Gln Arg Leu Asn Ile Glu
85 90 95

Leu Ala Arg Lys Leu Leu Glu Ala Val Ala Arg Leu Gln Glu Leu Asn
100 105 110

Ile Asp Leu Val Arg Lys Thr Ser Glu Leu Thr Asp Glu Lys Thr Ile
115 120 125

Arg Glu Glu Ile Arg Lys Val Lys Glu Glu Ser Lys Arg Ile Val Glu
130 135 140

Glu Ala Glu Glu Glu Ile Arg Arg Ala Lys Glu Glu Ser Arg Lys Ile
145 150 155 160

Ala Asp Glu Ser Arg
165

<210> 603
<211> 267
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 603

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Ser Gly Ser Gly
65 70 75 80

Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly
85 90 95

Ser Gly Ser Gly Ser Gly Ser Glu Leu Glu Glu Gln Val Met His Val
100 105 110

Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr
115 120 125

Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu
130 135 140

Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu
145 150 155 160

Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala
165 170 175

Arg Lys Gly Ser Gly Ser Ser Glu Glu Leu Arg Ala Val Ala Asp Leu
180 185 190

Gln Arg Leu Asn Ile Glu Leu Ala Arg Lys Leu Leu Glu Ala Val Ala
195 200 205

Arg Leu Gln Glu Leu Asn Ile Asp Leu Val Arg Lys Thr Ser Glu Leu
210 215 220

Thr Asp Glu Lys Thr Ile Arg Glu Glu Ile Arg Lys Val Lys Glu Glu
225 230 235 240

Ser Lys Arg Ile Val Glu Glu Ala Glu Glu Glu Ile Arg Arg Ala Lys
245 250 255

Glu Glu Ser Arg Lys Ile Ala Asp Glu Ser Arg
260 265

<210> 604
<211> 268
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 604

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Ser Gly Ser Gly
65 70 75 80

Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly
85 90 95

Ser Gly Ser Gly Ser Gly Ser Glu Leu Glu Glu Gln Val Met His Val
100 105 110

Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr
115 120 125

Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu
130 135 140

Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu
145 150 155 160

Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala
165 170 175

Arg Lys Gly Ser Gly Ser Gly Ser Glu Glu Leu Arg Ala Val Ala Asp
180 185 190

Leu Gln Arg Leu Asn Ile Glu Leu Ala Arg Lys Leu Leu Glu Ala Val
195 200 205

Ala Arg Leu Gln Glu Leu Asn Ile Asp Leu Val Arg Lys Thr Ser Glu
210 215 220

Leu Thr Asp Glu Lys Thr Ile Arg Glu Glu Ile Arg Lys Val Lys Glu
225 230 235 240

Glu Ser Lys Arg Ile Val Glu Glu Ala Glu Glu Glu Ile Arg Arg Ala
245 250 255

Lys Glu Glu Ser Arg Lys Ile Ala Asp Glu Ser Arg
260 265

<210> 605

<211> 97
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 605

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu
20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

Gly Ser Gly Ser Gly Ser Gly Tyr Ile Pro Glu Ala Pro Arg Asp Gly
65 70 75 80

Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu Leu Ser Thr Phe
85 90 95

Leu

<210> 606
<211> 96
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 606

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu
20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

Gly Ser Gly Ser Gly Gly Tyr Ile Pro Glu Ala Pro Arg Asp Gly Gln
65 70 75 80

Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu Leu Ser Thr Phe Leu
85 90 95

<210> 607
<211> 95
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 607

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu
20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

Gly Ser Gly Ser Gly Tyr Ile Pro Glu Ala Pro Arg Asp Gly Gln Ala
65 70 75 80

Tyr Val Arg Lys Asp Gly Glu Trp Val Leu Leu Ser Thr Phe Leu
85 90 95

<210> 608
<211> 154
<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 608

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu
20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

Gly Ser Gly Ser Gly Ser Glu Glu Leu Arg Ala Val Ala Asp Leu Gln
65 70 75 80

Arg Leu Asn Ile Glu Leu Ala Arg Lys Leu Leu Glu Ala Val Ala Arg
85 90 95

Leu Gln Glu Leu Asn Ile Asp Leu Val Arg Lys Thr Ser Glu Leu Thr
100 105 110

Asp Glu Lys Thr Ile Arg Glu Glu Ile Arg Lys Val Lys Glu Glu Ser
115 120 125

Lys Arg Ile Val Glu Glu Ala Glu Glu Glu Ile Arg Arg Ala Lys Glu
130 135 140

Glu Ser Arg Lys Ile Ala Asp Glu Ser Arg
145 150

<210> 609

<211> 245

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 609

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu
20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser
65 70 75 80

Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Asn Leu Asp Glu
85 90 95

Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala
100 105 110

Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala
115 120 125

Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val
130 135 140

Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Ser Gly Ser
145 150 155 160

Ser Glu Glu Leu Arg Ala Val Ala Asp Leu Gln Arg Leu Asn Ile Glu
165 170 175

Leu Ala Arg Lys Leu Leu Glu Ala Val Ala Arg Leu Gln Glu Leu Asn
180 185 190

Ile Asp Leu Val Arg Lys Thr Ser Glu Leu Thr Asp Glu Lys Thr Ile
195 200 205

Arg Glu Glu Ile Arg Lys Val Lys Glu Glu Ser Lys Arg Ile Val Glu
210 215 220

Glu Ala Glu Glu Glu Ile Arg Arg Ala Lys Glu Glu Ser Arg Lys Ile
225 230 235 240

Ala Asp Glu Ser Arg
245

<210> 610
<211> 246
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 610

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu
20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser
65 70 75 80

Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Asn Leu Asp Glu
85 90 95

Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala
100 105 110

Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala
115 120 125

Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val
130 135 140

Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Ser Gly Ser
145 150 155 160

Gly Ser Glu Glu Leu Arg Ala Val Ala Asp Leu Gln Arg Leu Asn Ile
165 170 175

Glu Leu Ala Arg Lys Leu Leu Glu Ala Val Ala Arg Leu Gln Glu Leu
180 185 190

Asn Ile Asp Leu Val Arg Lys Thr Ser Glu Leu Thr Asp Glu Lys Thr
195 200 205

Ile Arg Glu Glu Ile Arg Lys Val Lys Glu Glu Ser Lys Arg Ile Val
210 215 220

Glu Glu Ala Glu Glu Glu Ile Arg Arg Ala Lys Glu Glu Ser Arg Lys
225 230 235 240

Ile Ala Asp Glu Ser Arg
245

<210> 611
<211> 196
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 611

Glu Glu Ala Glu Leu Ala Tyr Leu Leu Gly Glu Leu Ala Tyr Lys Leu
1 5 10 15

Gly Glu Tyr Arg Ile Ala Ile Arg Ala Tyr Arg Ile Ala Leu Lys Arg
20 25 30

Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr
35 40 45

Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu
50 55 60

Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala
65 70 75 80

Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys
85 90 95

Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly
100 105 110

Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr
115 120 125

Gln Lys Ala Leu Glu Leu Gly Ser Gly Ser Gly Ser Asp Lys Glu Asn
130 135 140

Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly
145 150 155 160

His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met
165 170 175

Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu
180 185 190

Glu Val Lys Arg
195

<210> 612
<211> 194
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 612

Glu Glu Ala Glu Leu Ala Tyr Leu Leu Gly Glu Leu Ala Tyr Lys Leu
1 5 10 15

Gly Glu Tyr Arg Ile Ala Ile Arg Ala Tyr Arg Ile Ala Leu Lys Arg
20 25 30

Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr
35 40 45

Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu
50 55 60

Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala
65 70 75 80

Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys
85 90 95

Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly
100 105 110

Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr
115 120 125

Gln Lys Ala Leu Glu Leu Gly Ser Gly Ser Asp Lys Glu Asn Val Leu
130 135 140

Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala
145 150 155 160

Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr
165 170 175

Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val
180 185 190

Lys Arg

<210> 613
<211> 192
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 613

Glu Glu Ala Glu Leu Ala Tyr Leu Leu Gly Glu Leu Ala Tyr Lys Leu
1 5 10 15

Gly Glu Tyr Arg Ile Ala Ile Arg Ala Tyr Arg Ile Ala Leu Lys Arg
20 25 30

Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr
35 40 45

Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu
50 55 60

Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala
65 70 75 80

Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys
85 90 95

Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly
100 105 110

Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr
115 120 125

Gln Lys Ala Leu Glu Leu Gly Ser Asp Lys Glu Asn Val Leu Gln Lys
130 135 140

Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala
145 150 155 160

Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp
165 170 175

Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
180 185 190

<210> 614

<211> 241
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 614

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu
20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro
65 70 75 80

Ala Pro Ser Ala Pro Ala Gly Gly Asn Leu Asp Glu Leu His Met Gln
85 90 95

Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu
100 105 110

Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr
115 120 125

Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys
130 135 140

Glu Leu Leu Glu Arg Leu Leu Ser Gly Ser Gly Ser Ser Glu Glu Leu
145 150 155 160

Arg Ala Val Ala Asp Leu Gln Arg Leu Asn Ile Glu Leu Ala Arg Lys
165 170 175

Leu Leu Glu Ala Val Ala Arg Leu Gln Glu Leu Asn Ile Asp Leu Val

180

185

190

Arg Lys Thr Ser Glu Leu Thr Asp Glu Lys Thr Ile Arg Glu Glu Ile
 195 200 205

Arg Lys Val Lys Glu Glu Ser Lys Arg Ile Val Glu Glu Ala Glu Glu
 210 215 220

Glu Ile Arg Arg Ala Lys Glu Glu Ser Arg Lys Ile Ala Asp Glu Ser
 225 230 235 240

Arg

<210> 615
 <211> 242
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 615

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
 1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu
 20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
 35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
 50 55 60

Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro
 65 70 75 80

Ala Pro Ser Ala Pro Ala Gly Gly Asn Leu Asp Glu Leu His Met Gln
 85 90 95

Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu

100

105

110

Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr
 115 120 125

Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys
 130 135 140

Glu Leu Leu Glu Arg Leu Leu Ser Gly Ser Gly Ser Gly Ser Glu Glu
 145 150 155 160

Leu Arg Ala Val Ala Asp Leu Gln Arg Leu Asn Ile Glu Leu Ala Arg
 165 170 175

Lys Leu Leu Glu Ala Val Ala Arg Leu Gln Glu Leu Asn Ile Asp Leu
 180 185 190

Val Arg Lys Thr Ser Glu Leu Thr Asp Glu Lys Thr Ile Arg Glu Glu
 195 200 205

Ile Arg Lys Val Lys Glu Glu Ser Lys Arg Ile Val Glu Glu Ala Glu
 210 215 220

Glu Glu Ile Arg Arg Ala Lys Glu Glu Ser Arg Lys Ile Ala Asp Glu
 225 230 235 240

Ser Arg

<210> 616
 <211> 172
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 616

Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu
 1 5 10 15

Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile

20

25

30

Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu
 35 40 45

Arg Leu Leu Glu Glu Val Lys Arg Gly Gly Gly Ser Gly Gly Gly Ser
 50 55 60

Gly Gly Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser
 65 70 75 80

Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu
 85 90 95

Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu
 100 105 110

Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala
 115 120 125

Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Ser Gly
 130 135 140

Ser Gly Tyr Ile Pro Glu Ala Pro Arg Asp Gly Gln Ala Tyr Val Arg
 145 150 155 160

Lys Asp Gly Glu Trp Val Leu Leu Ser Thr Phe Leu
 165 170

<210> 617
 <211> 190
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 617

Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu
 1 5 10 15

Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile

20

25

30

Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu
 35 40 45

Arg Leu Leu Glu Glu Val Lys Arg Gly Ser Gly Ser Gly Ser Gly Ser
 50 55 60

Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser
 65 70 75 80

Gly Ser Gly Ser Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln
 85 90 95

Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu
 100 105 110

Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu
 115 120 125

Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu
 130 135 140

Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly
 145 150 155 160

Ser Gly Ser Gly Tyr Ile Pro Glu Ala Pro Arg Asp Gly Gln Ala Tyr
 165 170 175

Val Arg Lys Asp Gly Glu Trp Val Leu Leu Ser Thr Phe Leu
 180 185 190

<210> 618

<211> 180

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 618

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala

1	5	10	15
Leu His Phe	Ala Lys Asp Glu Glu Phe Gln Lys His Val	Phe Gln Leu	
	20	25	30
Phe Glu Lys	Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu		
	35	40	45
Glu Lys Val	Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser		
	50	55	60
Gly Gly Gly	Ser Gly Gly Gly Ser Gly Gly Glu Leu Glu Glu Gln Val		
65	70	75	80
Met His Val	Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His		
	85	90	95
Lys Leu Thr	Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp		
	100	105	110
Ala Thr Glu	Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu		
	115	120	125
Ile Arg Glu	Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu		
	130	135	140
Glu Leu Ala	Arg Lys Gly Ser Gly Ser Gly Tyr Ile Pro Glu Ala Pro		
145	150	155	160
Arg Asp Gly	Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu Leu		
	165	170	175
Ser Thr Phe	Leu		
	180		

<210> 619
 <211> 186
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Synthetic

<400> 619

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu
20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser
65 70 75 80

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
85 90 95

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
100 105 110

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
115 120 125

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
130 135 140

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Ser Gly Ser Gly
145 150 155 160

Tyr Ile Pro Glu Ala Pro Arg Asp Gly Gln Ala Tyr Val Arg Lys Asp
165 170 175

Gly Glu Trp Val Leu Leu Ser Thr Phe Leu
180 185

<210> 620

<211> 288

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 620

Glu Glu Ala Glu Leu Ala Tyr Leu Leu Gly Glu Leu Ala Tyr Lys Leu
1 5 10 15

Gly Glu Tyr Arg Ile Ala Ile Arg Ala Tyr Arg Ile Ala Leu Lys Arg
20 25 30

Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr
35 40 45

Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu
50 55 60

Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala
65 70 75 80

Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys
85 90 95

Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly
100 105 110

Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr
115 120 125

Gln Lys Ala Leu Glu Leu Gly Ser Gly Ser Gly Ser Asp Lys Glu Asn
130 135 140

Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly
145 150 155 160

His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met
165 170 175

Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu
180 185 190

Glu Val Lys Arg Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser
195 200 205

Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser
210 215 220

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
225 230 235 240

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu
245 250 255

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
260 265 270

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
275 280 285

<210> 621
<211> 269
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 621

Glu Glu Ala Glu Leu Ala Tyr Leu Leu Gly Glu Leu Ala Tyr Lys Leu
1 5 10 15

Gly Glu Tyr Arg Ile Ala Ile Arg Ala Tyr Arg Ile Ala Leu Lys Arg
20 25 30

Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr
35 40 45

Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu
50 55 60

Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala
65 70 75 80

Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys
85 90 95

Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly
100 105 110

Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr
115 120 125

Gln Lys Ala Leu Glu Leu Gly Ser Gly Ser Gly Ser Asp Lys Glu Asn
130 135 140

Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly
145 150 155 160

His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met
165 170 175

Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu
180 185 190

Glu Val Lys Arg Gly Ser Gly Ser Gly Ser Gly Ser Gly Asn Leu Asp
195 200 205

Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe
210 215 220

Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys
225 230 235 240

Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val
245 250 255

Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
260 265

<210> 622
<211> 299
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 622

Glu Glu Ala Glu Leu Ala Tyr Leu Leu Gly Glu Leu Ala Tyr Lys Leu
1 5 10 15

Gly Glu Tyr Arg Ile Ala Ile Arg Ala Tyr Arg Ile Ala Leu Lys Arg
20 25 30

Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr
35 40 45

Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu
50 55 60

Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala
65 70 75 80

Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys
85 90 95

Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly
100 105 110

Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr
115 120 125

Gln Lys Ala Leu Glu Leu Gly Ser Gly Ser Gly Ser Asp Lys Glu Asn
130 135 140

Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly
145 150 155 160

His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met
165 170 175

Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu
180 185 190

Glu Val Lys Arg Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser

195

200

205

Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser
 210 215 220

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
 225 230 235 240

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
 245 250 255

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
 260 265 270

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
 275 280 285

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
 290 295

<210> 623
 <211> 280
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 623

Glu Glu Ala Glu Leu Ala Tyr Leu Leu Gly Glu Leu Ala Tyr Lys Leu
 1 5 10 15

Gly Glu Tyr Arg Ile Ala Ile Arg Ala Tyr Arg Ile Ala Leu Lys Arg
 20 25 30

Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr
 35 40 45

Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu
 50 55 60

Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala

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

<210> 624
<211> 161
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 624

Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu
1 5 10 15

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

Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu
35 40 45

Arg Leu Leu Glu Glu Val Lys Arg Gly Gly Gly Ser Gly Gly Gly Ser
50 55 60

Gly Gly Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr
65 70 75 80

Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe
85 90 95

Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln
100 105 110

Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu
115 120 125

Leu Ser Gly Ser Gly Ser Gly Tyr Ile Pro Glu Ala Pro Arg Asp Gly
130 135 140

Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu Leu Ser Thr Phe
145 150 155 160

Leu

<210> 625
<211> 179
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 625

Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu
1 5 10 15

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

Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu
35 40 45

Arg Leu Leu Glu Glu Val Lys Arg Gly Ser Gly Ser Gly Ser Gly Ser
50 55 60

Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser
65 70 75 80

Gly Ser Gly Ser Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu
85 90 95

Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His
100 105 110

Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp
115 120 125

Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu
130 135 140

Arg Leu Leu Ser Gly Ser Gly Ser Gly Tyr Ile Pro Glu Ala Pro Arg
145 150 155 160

Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu Leu Ser
165 170 175

Thr Phe Leu

<210> 626
<211> 180
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 626

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Gly Ser Gly
65 70 75 80

Gly Gly Ser Gly Gly Asn Leu Asp Glu Leu His Met Gln Met Thr Asp
85 90 95

Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys
100 105 110

His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys
115 120 125

Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu
130 135 140

Glu Arg Leu Leu Ser Gly Ser Gly Ser Gly Tyr Ile Pro Glu Ala Pro
145 150 155 160

Arg Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu Leu
165 170 175

Ser Thr Phe Leu
180

<210> 627
<211> 186
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 627

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Ser Gly Ser Gly
65 70 75 80

Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Asn Leu Asp Glu Leu
85 90 95

His Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys
100 105 110

Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr
115 120 125

Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu
130 135 140

Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Ser Gly Ser Gly
145 150 155 160

Tyr Ile Pro Glu Ala Pro Arg Asp Gly Gln Ala Tyr Val Arg Lys Asp
165 170 175

Gly Glu Trp Val Leu Leu Ser Thr Phe Leu
180 185

<210> 628
<211> 219
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 628

Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu
1 5 10 15

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

Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu
35 40 45

Arg Leu Leu Glu Glu Val Lys Arg Gly Ser Gly Ser Gly Ser Gly Ser
50 55 60

Gly Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu
65 70 75 80

Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln
85 90 95

Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys
100 105 110

Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu
115 120 125

Ser Gly Ser Gly Ser Gly Ser Glu Glu Leu Arg Ala Val Ala Asp Leu
130 135 140

Gln Arg Leu Asn Ile Glu Leu Ala Arg Lys Leu Leu Glu Ala Val Ala
145 150 155 160

Arg Leu Gln Glu Leu Asn Ile Asp Leu Val Arg Lys Thr Ser Glu Leu
165 170 175

Thr Asp Glu Lys Thr Ile Arg Glu Glu Ile Arg Lys Val Lys Glu Glu
180 185 190

Ser Lys Arg Ile Val Glu Glu Ala Glu Glu Glu Ile Arg Arg Ala Lys
195 200 205

Glu Glu Ser Arg Lys Ile Ala Asp Glu Ser Arg
210 215

<210> 629
<211> 238
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 629

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Ser Gly Ser Gly
65 70 75 80

Ser Gly Ser Gly Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu
85 90 95

Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His
100 105 110

Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp
115 120 125

Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu
130 135 140

Arg Leu Leu Ser Gly Ser Gly Ser Gly Ser Glu Glu Leu Arg Ala Val
145 150 155 160

Ala Asp Leu Gln Arg Leu Asn Ile Glu Leu Ala Arg Lys Leu Leu Glu
165 170 175

Ala Val Ala Arg Leu Gln Glu Leu Asn Ile Asp Leu Val Arg Lys Thr
180 185 190

Ser Glu Leu Thr Asp Glu Lys Thr Ile Arg Glu Glu Ile Arg Lys Val
195 200 205

Lys Glu Glu Ser Lys Arg Ile Val Glu Glu Ala Glu Glu Glu Ile Arg
210 215 220

Arg Ala Lys Glu Glu Ser Arg Lys Ile Ala Asp Glu Ser Arg
225 230 235

<210> 630
<211> 162
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 630

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Ser Gly Ser Glu
65 70 75 80

Glu Ala Glu Leu Ala Tyr Leu Leu Gly Glu Leu Ala Tyr Lys Leu Gly
85 90 95

Glu Tyr Arg Ile Ala Ile Arg Ala Tyr Arg Ile Ala Leu Lys Arg Asp
100 105 110

Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr Lys
115 120 125

Gln Gly Asp Tyr Asp Glu Ala Ile Tyr Tyr Gln Lys Ala Leu Glu Leu
130 135 140

Asp Pro Asn Asn Ala Glu Ala Lys Gln Asn Leu Gly Asn Ala Lys Gln
145 150 155 160

Lys Gln

<210> 631
<211> 164
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 631

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Ser Gly Ser Gly
65 70 75 80

Ser Glu Glu Ala Glu Leu Ala Tyr Leu Leu Gly Glu Leu Ala Tyr Lys
85 90 95

Leu Gly Glu Tyr Arg Ile Ala Ile Arg Ala Tyr Arg Ile Ala Leu Lys
100 105 110

Arg Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr
115 120 125

Tyr Lys Gln Gly Asp Tyr Asp Glu Ile Glu Tyr Tyr Gln Lys Ala Leu
130 135 140

Glu Leu Asp Pro Asn Asn Ala Glu Ala Lys Gln Asn Leu Gly Asn Ala
145 150 155 160

Lys Gln Lys Gln

<210> 632
<211> 195
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 632

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Ser Gly Ser Glu
65 70 75 80

Glu Ala Glu Leu Ala Tyr Leu Leu Gly Glu Leu Ala Tyr Lys Leu Gly
85 90 95

Glu Tyr Arg Ile Ala Ile Arg Ala Tyr Arg Ile Ala Leu Lys Arg Asp
100 105 110

Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr Lys
115 120 125

Gln Gly Asp Tyr Asp Glu Ala Ile Tyr Tyr Gln Lys Ala Leu Glu Leu
130 135 140

Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr
145 150 155 160

Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu
165 170 175

Glu Leu Asp Pro Asn Asn Ala Glu Ala Lys Gln Asn Leu Gly Asn Lys
180 185 190

Gln Lys Gln
195

<210> 633
<211> 197
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 633

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Ser Gly Ser Gly
65 70 75 80

Ser Glu Glu Ala Glu Leu Ala Tyr Leu Leu Gly Glu Leu Ala Tyr Lys
85 90 95

Leu Gly Glu Tyr Arg Ile Ala Ile Arg Ala Tyr Arg Ile Ala Leu Lys
100 105 110

Arg Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr
115 120 125

Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Tyr Tyr Gln Lys Ala Leu
130 135 140

Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala
145 150 155 160

Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys
165 170 175

Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Lys Gln Asn Leu Gly
180 185 190

Asn Lys Gln Lys Gln

195

<210> 634
<211> 154
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 634

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Ser Gly Ser Gly
65 70 75 80

Ser Glu Tyr Glu Ile Arg Lys Ala Leu Glu Glu Leu Lys Ala Ser Thr
85 90 95

Ala Glu Leu Lys Arg Ala Thr Ala Ser Leu Arg Ala Ser Thr Glu Glu
100 105 110

Leu Lys Lys Asn Pro Ser Glu Asp Ala Leu Val Glu Asn Asn Arg Leu
115 120 125

Ile Val Glu His Asn Ala Ile Ile Val Glu Asn Arg Ile Ile Ala Ala
130 135 140

Val Leu Glu Leu Ile Val Arg Ala Ile Lys
145 150

<210> 635

<211> 156
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 635

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Ser Gly Ser Gly
65 70 75 80

Ser Gly Ser Glu Tyr Glu Ile Arg Lys Ala Leu Glu Glu Leu Lys Ala
85 90 95

Ser Thr Ala Glu Leu Lys Arg Ala Thr Ala Ser Leu Arg Ala Ser Thr
100 105 110

Glu Glu Leu Lys Lys Asn Pro Ser Glu Asp Ala Leu Val Glu Asn Asn
115 120 125

Arg Leu Ile Val Glu His Asn Ala Ile Ile Val Glu Asn Arg Ile Ile
130 135 140

Ala Ala Val Leu Glu Leu Ile Val Arg Ala Ile Lys
145 150 155

<210> 636
<211> 196
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 636

Glu Glu Ala Glu Leu Ala Tyr Leu Leu Gly Glu Leu Ala Tyr Lys Leu
1 5 10 15

Gly Glu Tyr Arg Ile Ala Ile Arg Ala Tyr Arg Ile Ala Leu Lys Arg
20 25 30

Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr
35 40 45

Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu
50 55 60

Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala
65 70 75 80

Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys
85 90 95

Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly
100 105 110

Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr
115 120 125

Gln Lys Ala Leu Glu Leu Gly Ser Gly Ser Gly Ser Asp Lys Glu Asn
130 135 140

Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly
145 150 155 160

His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met
165 170 175

Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu
180 185 190

Glu Val Lys Arg

<210> 637
 <211> 194
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 637

Glu Glu Ala Glu Leu Ala Tyr Leu Leu Gly Glu Leu Ala Tyr Lys Leu
 1 5 10 15

Gly Glu Tyr Arg Ile Ala Ile Arg Ala Tyr Arg Ile Ala Leu Lys Arg
 20 25 30

Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr
 35 40 45

Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu
 50 55 60

Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala
 65 70 75 80

Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys
 85 90 95

Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly
 100 105 110

Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr
 115 120 125

Gln Lys Ala Leu Glu Leu Gly Ser Gly Ser Asp Lys Glu Asn Val Leu
 130 135 140

Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala
 145 150 155 160

Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr

165

170

175

Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val
 180 185 190

Lys Arg

<210> 638
 <211> 192
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 638

Glu Glu Ala Glu Leu Ala Tyr Leu Leu Gly Glu Leu Ala Tyr Lys Leu
 1 5 10 15

Gly Glu Tyr Arg Ile Ala Ile Arg Ala Tyr Arg Ile Ala Leu Lys Arg
 20 25 30

Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr
 35 40 45

Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu
 50 55 60

Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala
 65 70 75 80

Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys
 85 90 95

Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly
 100 105 110

Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr
 115 120 125

Gln Lys Ala Leu Glu Leu Gly Ser Asp Lys Glu Asn Val Leu Gln Lys

130

135

140

Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala
 145 150 155 160

Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp
 165 170 175

Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
 180 185 190

<210> 639
 <211> 168
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 639

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
 1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
 20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
 35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
 50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Ser Gly Ser Gly
 65 70 75 80

Ser Gly Ser Glu Glu Ala Glu Leu Ala Tyr Leu Leu Gly Glu Leu Ala
 85 90 95

Tyr Lys Leu Gly Glu Tyr Arg Ile Ala Ile Arg Ala Tyr Arg Ile Ala
 100 105 110

Leu Lys Arg Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn

115

120

125

Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln
 130 135 140

Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Lys Gln Asn Leu
 145 150 155 160

Gly Asn Ala Lys Gln Lys Gln Gly
 165

<210> 640
 <211> 202
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 640

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
 1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
 20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
 35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
 50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Ser Gly Ser Gly
 65 70 75 80

Ser Gly Ser Glu Glu Ala Glu Leu Ala Tyr Leu Leu Gly Glu Leu Ala
 85 90 95

Tyr Lys Leu Gly Glu Tyr Arg Ile Ala Ile Arg Ala Tyr Arg Ile Ala
 100 105 110

Leu Lys Arg Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn

115

120

125

Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln
 130 135 140

Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu
 145 150 155 160

Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr
 165 170 175

Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Lys Gln
 180 185 190

Asn Leu Gly Asn Ala Lys Gln Lys Gln Gly
 195 200

<210> 641
 <211> 159
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 641

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
 1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
 20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
 35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
 50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Ser Gly Ser Gly
 65 70 75 80

Ser Gly Ser Gly Ser Glu Tyr Glu Ile Arg Lys Ala Leu Glu Glu Leu

85

90

95

Lys Ala Ser Thr Ala Glu Leu Lys Arg Ala Thr Ala Ser Leu Arg Ala
 100 105 110

Ser Thr Glu Glu Leu Lys Lys Asn Pro Ser Glu Asp Ala Leu Val Glu
 115 120 125

Asn Asn Arg Leu Ile Val Glu His Asn Ala Ile Ile Val Glu Asn Asn
 130 135 140

Arg Ile Ile Ala Ala Val Leu Glu Leu Ile Val Arg Ala Ile Lys
 145 150 155

<210> 642
 <211> 161
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 642

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
 1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
 20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
 35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
 50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Ser Gly Ser Gly
 65 70 75 80

Ser Gly Ser Gly Ser Gly Ser Glu Tyr Glu Ile Arg Lys Ala Leu Glu
 85 90 95

Glu Leu Lys Ala Ser Thr Ala Glu Leu Lys Arg Ala Thr Ala Ser Leu

100

105

110

Arg Ala Ser Thr Glu Glu Leu Lys Lys Asn Pro Ser Glu Asp Ala Leu
 115 120 125

Val Glu Asn Asn Arg Leu Ile Val Glu His Asn Ala Ile Ile Val Glu
 130 135 140

Asn Asn Arg Ile Ile Ala Ala Val Leu Glu Leu Ile Val Arg Ala Ile
 145 150 155 160

Lys

<210> 643
 <211> 170
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 643

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
 1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
 20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
 35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
 50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Ser Gly Ser Gly
 65 70 75 80

Ser Gly Ser Gly Ser Glu Glu Ala Glu Leu Ala Tyr Leu Leu Gly Glu
 85 90 95

Leu Ala Tyr Lys Leu Gly Glu Tyr Arg Ile Ala Ile Arg Ala Tyr Arg

100

105

110

Ile Ala Leu Lys Arg Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu
 115 120 125

Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr
 130 135 140

Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Lys Gln
 145 150 155 160

Asn Leu Gly Asn Ala Lys Gln Lys Gln Gly
 165 170

<210> 644
 <211> 204
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 644

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
 1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
 20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
 35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
 50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Ser Gly Ser Gly
 65 70 75 80

Ser Gly Ser Gly Ser Glu Glu Ala Glu Leu Ala Tyr Leu Leu Gly Glu
 85 90 95

Leu Ala Tyr Lys Leu Gly Glu Tyr Arg Ile Ala Ile Arg Ala Tyr Arg

100

105

110

Ile Ala Leu Lys Arg Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu
 115 120 125

Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr
 130 135 140

Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr
 145 150 155 160

Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile
 165 170 175

Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala
 180 185 190

Lys Gln Asn Leu Gly Asn Ala Lys Gln Lys Gln Gly
 195 200

<210> 645
 <211> 112
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 645

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
 1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
 20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
 35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
 50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Ser Gly Ser Arg

65

70

75

80

Met Lys Gln Ile Glu Asp Lys Ile Glu Glu Ile Leu Ser Lys Ile Tyr
 85 90 95

His Ile Glu Asn Glu Ile Ala Arg Ile Lys Lys Leu Ile Gly Glu Arg
 100 105 110

<210> 646

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 646

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
 1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
 20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
 35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
 50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Ser Gly Ser Gly
 65 70 75 80

Ser Gly Ser Arg Met Lys Gln Ile Glu Asp Lys Ile Glu Glu Ile Leu
 85 90 95

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

Ile Gly Glu Arg
 115

<210> 647

<211> 155
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 647

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Ser Gly Ser Gly
65 70 75 80

Ser Glu Tyr Glu Ile Arg Lys Ala Leu Glu Glu Leu Lys Ala Ser Thr
85 90 95

Ala Glu Leu Lys Arg Ser Thr Ala Ser Leu Arg Ala Ser Thr Glu Glu
100 105 110

Leu Lys Lys Asn Pro Ser Glu Asp Ala Leu Val Glu Asn Asn Arg Leu
115 120 125

Ile Val Glu Asn Asn Ala Ile Ile Val Glu Asn Asn Arg Ile Ile Ala
130 135 140

Ala Val Leu Glu Leu Ile Val Arg Ala Ile Lys
145 150 155

<210> 648
<211> 159
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 648

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Ser Gly Ser Gly
65 70 75 80

Ser Gly Ser Gly Ser Glu Tyr Glu Ile Arg Lys Ala Leu Glu Glu Leu
85 90 95

Lys Ala Ser Thr Ala Glu Leu Lys Arg Ser Thr Ala Ser Leu Arg Ala
100 105 110

Ser Thr Glu Glu Leu Lys Lys Asn Pro Ser Glu Asp Ala Leu Val Glu
115 120 125

Asn Asn Arg Leu Ile Val Glu Asn Asn Ala Ile Ile Val Glu Asn Asn
130 135 140

Arg Ile Ile Ala Ala Val Leu Glu Leu Ile Val Arg Ala Ile Lys
145 150 155

<210> 649

<211> 200

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 649

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Ser Gly Ser Gly
65 70 75 80

Ser Asn Leu Ala Glu Lys Met Tyr Lys Ala Gly Asn Ala Met Tyr Arg
85 90 95

Lys Gly Gln Tyr Thr Ile Ala Ile Ile Ala Tyr Thr Leu Ala Leu Leu
100 105 110

Lys Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Ala
115 120 125

Tyr Lys Lys Gly Glu Tyr Asp Glu Ala Ile Glu Ala Tyr Gln Lys Ala
130 135 140

Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn
145 150 155 160

Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln
165 170 175

Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Lys Gln Asn Leu
180 185 190

Gly Asn Ala Lys Gln Lys Gln Gly
195 200

<210> 650

<211> 204
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 650

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Ser Gly Ser Gly
65 70 75 80

Ser Gly Ser Gly Ser Asn Leu Ala Glu Lys Met Tyr Lys Ala Gly Asn
85 90 95

Ala Met Tyr Arg Lys Gly Gln Tyr Thr Ile Ala Ile Ile Ala Tyr Thr
100 105 110

Leu Ala Leu Leu Lys Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu
115 120 125

Gly Asn Ala Ala Tyr Lys Lys Gly Glu Tyr Asp Glu Ala Ile Glu Ala
130 135 140

Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr
145 150 155 160

Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile
165 170 175

Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala

180

185

190

Lys Gln Asn Leu Gly Asn Ala Lys Gln Lys Gln Gly
 195 200

<210> 651
 <211> 111
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 651

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
 1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
 20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
 35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
 50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Ser Gly Ser Gly
 65 70 75 80

Ser Gly Glu Ile Ala Lys Ser Leu Lys Glu Ile Ala Lys Ser Leu Lys
 85 90 95

Glu Ile Ala Trp Ser Leu Lys Glu Ile Ala Lys Ser Leu Lys Gly
 100 105 110

<210> 652
 <211> 115
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 652

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Ser Gly Ser Gly
65 70 75 80

Ser Gly Ser Gly Ser Gly Glu Ile Ala Lys Ser Leu Lys Glu Ile Ala
85 90 95

Lys Ser Leu Lys Glu Ile Ala Trp Ser Leu Lys Glu Ile Ala Lys Ser
100 105 110

Leu Lys Gly
115

<210> 653
<211> 165
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 653

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Gly Gly
65 70 75 80

Glu Glu Ala Glu Leu Ala Tyr Leu Leu Gly Glu Leu Ala Tyr Lys Leu
85 90 95

Gly Glu Tyr Arg Ile Ala Ile Arg Ala Tyr Arg Ile Ala Leu Lys Arg
100 105 110

Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr
115 120 125

Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu
130 135 140

Glu Leu Asp Pro Asn Asn Ala Glu Ala Lys Gln Asn Leu Gly Asn Ala
145 150 155 160

Lys Gln Lys Gln Gly
165

<210> 654
<211> 167
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 654

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Gly Ser Gly
65 70 75 80

Gly Gly Glu Glu Ala Glu Leu Ala Tyr Leu Leu Gly Glu Leu Ala Tyr
85 90 95

Lys Leu Gly Glu Tyr Arg Ile Ala Ile Arg Ala Tyr Arg Ile Ala Leu
100 105 110

Lys Arg Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala
115 120 125

Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys
130 135 140

Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Lys Gln Asn Leu Gly
145 150 155 160

Asn Ala Lys Gln Lys Gln Gly
165

<210> 655
<211> 169
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 655

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Gly Gly Ser
65 70 75 80

Gly Gly Gly Gly Glu Glu Ala Glu Leu Ala Tyr Leu Leu Gly Glu Leu
85 90 95

Ala Tyr Lys Leu Gly Glu Tyr Arg Ile Ala Ile Arg Ala Tyr Arg Ile
100 105 110

Ala Leu Lys Arg Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly
115 120 125

Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr
130 135 140

Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Lys Gln Asn
145 150 155 160

Leu Gly Asn Ala Lys Gln Lys Gln Gly
165

<210> 656
<211> 199
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 656

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Gly Gly
65 70 75 80

Glu Glu Ala Glu Leu Ala Tyr Leu Leu Gly Glu Leu Ala Tyr Lys Leu
85 90 95

Gly Glu Tyr Arg Ile Ala Ile Arg Ala Tyr Arg Ile Ala Leu Lys Arg
100 105 110

Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr
115 120 125

Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu
130 135 140

Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala
145 150 155 160

Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys
165 170 175

Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Lys Gln Asn Leu Gly
180 185 190

Asn Ala Lys Gln Lys Gln Gly
195

<210> 657
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 657

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Gly Ser Gly
65 70 75 80

Gly Gly Glu Glu Ala Glu Leu Ala Tyr Leu Leu Gly Glu Leu Ala Tyr
85 90 95

Lys Leu Gly Glu Tyr Arg Ile Ala Ile Arg Ala Tyr Arg Ile Ala Leu
100 105 110

Lys Arg Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala
115 120 125

Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys
130 135 140

Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly
145 150 155 160

Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr
165 170 175

Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Lys Gln Asn
180 185 190

Leu Gly Asn Ala Lys Gln Lys Gln Gly
195 200

<210> 658

<211> 203

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 658

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Gly Gly Ser
65 70 75 80

Gly Gly Gly Gly Glu Glu Ala Glu Leu Ala Tyr Leu Leu Gly Glu Leu
85 90 95

Ala Tyr Lys Leu Gly Glu Tyr Arg Ile Ala Ile Arg Ala Tyr Arg Ile
100 105 110

Ala Leu Lys Arg Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly
115 120 125

Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr
130 135 140

Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn
145 150 155 160

Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu
165 170 175

Tyr Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Lys
180 185 190

Gln Asn Leu Gly Asn Ala Lys Gln Lys Gln Gly

195

200

<210> 659
 <211> 156
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 659

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
 1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
 20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
 35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
 50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Gly Gly
 65 70 75 80

Gly Ser Glu Tyr Glu Ile Arg Lys Ala Leu Glu Glu Leu Lys Ala Ser
 85 90 95

Thr Ala Glu Leu Lys Arg Ala Thr Ala Ser Leu Arg Ala Ser Thr Glu
 100 105 110

Glu Leu Lys Lys Asn Pro Ser Glu Asp Ala Leu Val Glu Asn Asn Arg
 115 120 125

Leu Ile Val Glu His Asn Ala Ile Ile Val Glu Asn Asn Arg Ile Ile
 130 135 140

Ala Ala Val Leu Glu Leu Ile Val Arg Ala Ile Lys
 145 150 155

<210> 660

<211> 158
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 660

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Gly Ser Gly
65 70 75 80

Gly Gly Gly Ser Glu Tyr Glu Ile Arg Lys Ala Leu Glu Glu Leu Lys
85 90 95

Ala Ser Thr Ala Glu Leu Lys Arg Ala Thr Ala Ser Leu Arg Ala Ser
100 105 110

Thr Glu Glu Leu Lys Lys Asn Pro Ser Glu Asp Ala Leu Val Glu Asn
115 120 125

Asn Arg Leu Ile Val Glu His Asn Ala Ile Ile Val Glu Asn Asn Arg
130 135 140

Ile Ile Ala Ala Val Leu Glu Leu Ile Val Arg Ala Ile Lys
145 150 155

<210> 661
<211> 160
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 661

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Gly Gly Ser
65 70 75 80

Gly Gly Gly Gly Gly Ser Glu Tyr Glu Ile Arg Lys Ala Leu Glu Glu
85 90 95

Leu Lys Ala Ser Thr Ala Glu Leu Lys Arg Ala Thr Ala Ser Leu Arg
100 105 110

Ala Ser Thr Glu Glu Leu Lys Lys Asn Pro Ser Glu Asp Ala Leu Val
115 120 125

Glu Asn Asn Arg Leu Ile Val Glu His Asn Ala Ile Ile Val Glu Asn
130 135 140

Asn Arg Ile Ile Ala Ala Val Leu Glu Leu Ile Val Arg Ala Ile Lys
145 150 155 160

<210> 662

<211> 113

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 662

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Gly Gly
65 70 75 80

Arg Met Lys Gln Ile Glu Asp Lys Ile Glu Glu Ile Leu Ser Lys Ile
85 90 95

Tyr His Ile Glu Asn Glu Ile Ala Arg Ile Lys Lys Leu Ile Gly Glu
100 105 110

Arg

<210> 663
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 663

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Gly Ser Gly
65 70 75 80

Gly Gly Arg Met Lys Gln Ile Glu Asp Lys Ile Glu Glu Ile Leu Ser
85 90 95

Lys Ile Tyr His Ile Glu Asn Glu Ile Ala Arg Ile Lys Lys Leu Ile
100 105 110

Gly Glu Arg
115

<210> 664
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 664

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Gly Gly Ser
65 70 75 80

Gly Gly Gly Gly Arg Met Lys Gln Ile Glu Asp Lys Ile Glu Glu Ile
85 90 95

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

Leu Ile Gly Glu Arg
115

<210> 665
<211> 156
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 665

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Gly Gly
65 70 75 80

Gly Ser Glu Tyr Glu Ile Arg Lys Ala Leu Glu Glu Leu Lys Ala Ser
85 90 95

Thr Ala Glu Leu Lys Arg Ser Thr Ala Ser Leu Arg Ala Ser Thr Glu
100 105 110

Glu Leu Lys Lys Asn Pro Ser Glu Asp Ala Leu Val Glu Asn Asn Arg
115 120 125

Leu Ile Val Glu Asn Asn Ala Ile Ile Val Glu Asn Asn Arg Ile Ile
130 135 140

Ala Ala Val Leu Glu Leu Ile Val Arg Ala Ile Lys
145 150 155

<210> 666
<211> 158
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 666

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Gly Ser Gly
65 70 75 80

Gly Gly Gly Ser Glu Tyr Glu Ile Arg Lys Ala Leu Glu Glu Leu Lys
85 90 95

Ala Ser Thr Ala Glu Leu Lys Arg Ser Thr Ala Ser Leu Arg Ala Ser
100 105 110

Thr Glu Glu Leu Lys Lys Asn Pro Ser Glu Asp Ala Leu Val Glu Asn
115 120 125

Asn Arg Leu Ile Val Glu Asn Asn Ala Ile Ile Val Glu Asn Asn Arg
130 135 140

Ile Ile Ala Ala Val Leu Glu Leu Ile Val Arg Ala Ile Lys
145 150 155

<210> 667
<211> 160
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 667

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Gly Gly Ser
65 70 75 80

Gly Gly Gly Gly Gly Ser Glu Tyr Glu Ile Arg Lys Ala Leu Glu Glu
85 90 95

Leu Lys Ala Ser Thr Ala Glu Leu Lys Arg Ser Thr Ala Ser Leu Arg
100 105 110

Ala Ser Thr Glu Glu Leu Lys Lys Asn Pro Ser Glu Asp Ala Leu Val
115 120 125

Glu Asn Asn Arg Leu Ile Val Glu Asn Asn Ala Ile Ile Val Glu Asn
130 135 140

Asn Arg Ile Ile Ala Ala Val Leu Glu Leu Ile Val Arg Ala Ile Lys
145 150 155 160

<210> 668
<211> 199
<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 668

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Gly Gly
65 70 75 80

Asn Leu Ala Glu Lys Met Tyr Lys Ala Gly Asn Ala Met Tyr Arg Lys
85 90 95

Gly Gln Tyr Thr Ile Ala Ile Ile Ala Tyr Thr Leu Ala Leu Leu Lys
100 105 110

Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Ala Tyr
115 120 125

Lys Lys Gly Glu Tyr Asp Glu Ala Ile Glu Ala Tyr Gln Lys Ala Leu
130 135 140

Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala
145 150 155 160

Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys
165 170 175

Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Lys Gln Asn Leu Gly
180 185 190

Asn Ala Lys Gln Lys Gln Gly
195

<210> 669

<211> 201

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 669

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Gly Ser Gly
65 70 75 80

Gly Gly Asn Leu Ala Glu Lys Met Tyr Lys Ala Gly Asn Ala Met Tyr
85 90 95

Arg Lys Gly Gln Tyr Thr Ile Ala Ile Ile Ala Tyr Thr Leu Ala Leu
100 105 110

Leu Lys Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala
115 120 125

Ala Tyr Lys Lys Gly Glu Tyr Asp Glu Ala Ile Glu Ala Tyr Gln Lys
130 135 140

Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly
145 150 155 160

Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr
165 170 175

Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Lys Gln Asn
180 185 190

Leu Gly Asn Ala Lys Gln Lys Gln Gly
195 200

<210> 670
<211> 203
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 670

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Gly Gly Ser
65 70 75 80

Gly Gly Gly Gly Asn Leu Ala Glu Lys Met Tyr Lys Ala Gly Asn Ala
85 90 95

Met Tyr Arg Lys Gly Gln Tyr Thr Ile Ala Ile Ile Ala Tyr Thr Leu
100 105 110

Ala Leu Leu Lys Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly
115 120 125

Asn Ala Ala Tyr Lys Lys Gly Glu Tyr Asp Glu Ala Ile Glu Ala Tyr
130 135 140

Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn
145 150 155 160

Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu
165 170 175

Tyr Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Lys
180 185 190

Gln Asn Leu Gly Asn Ala Lys Gln Lys Gln Gly
195 200

<210> 671
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 671

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Gly Gly
65 70 75 80

Gly Glu Ile Ala Lys Ser Leu Lys Glu Ile Ala Lys Ser Leu Lys Glu
85 90 95

Ile Ala Trp Ser Leu Lys Glu Ile Ala Lys Ser Leu Lys Gly
100 105 110

<210> 672
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 672

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Gly Ser Gly
65 70 75 80

Gly Gly Gly Glu Ile Ala Lys Ser Leu Lys Glu Ile Ala Lys Ser Leu
85 90 95

Lys Glu Ile Ala Trp Ser Leu Lys Glu Ile Ala Lys Ser Leu Lys Gly
100 105 110

<210> 673
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 673

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu

1	5	10	15
Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala	20	25	30
Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys	35	40	45
Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg	50	55	60
Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Gly Gly Ser	65	70	75
Gly Gly Gly Gly Gly Glu Ile Ala Lys Ser Leu Lys Glu Ile Ala Lys	85	90	95
Ser Leu Lys Glu Ile Ala Trp Ser Leu Lys Glu Ile Ala Lys Ser Leu	100	105	110

Lys Gly

<210> 674
 <211> 140
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 674

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

50

55

60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Glu Ala
65 70 75 80

Leu Glu Glu Leu Glu Lys Ala Leu Arg Glu Leu Lys Lys Ser Thr Asp
85 90 95

Glu Leu Glu Arg Ser Thr Glu Glu Leu Glu Lys Asn Pro Ser Glu Asp
100 105 110

Ala Leu Val Glu Asn Asn Arg Leu Ile Val Glu Asn Asn Lys Ile Ile
115 120 125

Val Glu Val Leu Arg Ile Ile Ala Lys Val Leu Lys
130 135 140

<210> 675
<211> 142
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 675

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Gly Ser Ser
65 70 75 80

Glu Ala Leu Glu Glu Leu Glu Lys Ala Leu Arg Glu Leu Lys Lys Ser

85

90

95

Thr Asp Glu Leu Glu Arg Ser Thr Glu Glu Leu Glu Lys Asn Pro Ser
 100 105 110

Glu Asp Ala Leu Val Glu Asn Asn Arg Leu Ile Val Glu Asn Asn Lys
 115 120 125

Ile Ile Val Glu Val Leu Arg Ile Ile Ala Lys Val Leu Lys
 130 135 140

<210> 676

<211> 144

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 676

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
 1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
 20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
 35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
 50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Gly Gly Ser
 65 70 75 80

Gly Ser Glu Ala Leu Glu Glu Leu Glu Lys Ala Leu Arg Glu Leu Lys
 85 90 95

Lys Ser Thr Asp Glu Leu Glu Arg Ser Thr Glu Glu Leu Glu Lys Asn
 100 105 110

Pro Ser Glu Asp Ala Leu Val Glu Asn Asn Arg Leu Ile Val Glu Asn

115

120

125

Asn Lys Ile Ile Val Glu Val Leu Arg Ile Ile Ala Lys Val Leu Lys
 130 135 140

<210> 677
 <211> 134
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 677

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
 1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
 20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
 35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
 50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Pro Glu
 65 70 75 80

Leu Glu Lys Ala Leu Arg Glu Leu Lys Lys Ser Thr Asp Glu Leu Glu
 85 90 95

Arg Ser Thr Glu Glu Leu Glu Lys Asn Gly Ser Pro Glu Ala Leu Val
 100 105 110

Glu Asn Asn Arg Leu Ile Val Glu Asn Asn Lys Ile Ile Val Glu Val
 115 120 125

Leu Arg Ile Ile Ala Lys
 130

<210> 678

<211> 136
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 678

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Gly Ser Ser
65 70 75 80

Pro Glu Leu Glu Lys Ala Leu Arg Glu Leu Lys Lys Ser Thr Asp Glu
85 90 95

Leu Glu Arg Ser Thr Glu Glu Leu Glu Lys Asn Gly Ser Pro Glu Ala
100 105 110

Leu Val Glu Asn Asn Arg Leu Ile Val Glu Asn Asn Lys Ile Ile Val
115 120 125

Glu Val Leu Arg Ile Ile Ala Lys
130 135

<210> 679
<211> 138
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 679

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Gly Gly Ser
65 70 75 80

Gly Ser Pro Glu Leu Glu Lys Ala Leu Arg Glu Leu Lys Lys Ser Thr
85 90 95

Asp Glu Leu Glu Arg Ser Thr Glu Glu Leu Glu Lys Asn Gly Ser Pro
100 105 110

Glu Ala Leu Val Glu Asn Asn Arg Leu Ile Val Glu Asn Asn Lys Ile
115 120 125

Ile Val Glu Val Leu Arg Ile Ile Ala Lys
130 135

<210> 680
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 680

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Glu Lys
65 70 75 80

Ala Leu Arg Glu Leu Lys Lys Ser Thr Asp Glu Leu Glu Arg Ser Thr
85 90 95

Glu Glu Leu Glu Lys Asn Gly Ser Pro Glu Ala Leu Val Glu Asn Asn
100 105 110

Arg Leu Ile Val Glu Asn Asn Lys Ile Ile Val Glu Val Leu Arg
115 120 125

<210> 681
<211> 129
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 681

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Gly Ser Ser
65 70 75 80

Glu Lys Ala Leu Arg Glu Leu Lys Lys Ser Thr Asp Glu Leu Glu Arg
85 90 95

Ser Thr Glu Glu Leu Glu Lys Asn Gly Ser Pro Glu Ala Leu Val Glu
100 105 110

Asn Asn Arg Leu Ile Val Glu Asn Asn Lys Ile Ile Val Glu Val Leu
115 120 125

Arg

<210> 682
<211> 131
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 682

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Gly Gly Ser
65 70 75 80

Gly Ser Glu Lys Ala Leu Arg Glu Leu Lys Lys Ser Thr Asp Glu Leu
85 90 95

Glu Arg Ser Thr Glu Glu Leu Glu Lys Asn Gly Ser Pro Glu Ala Leu
100 105 110

Val Glu Asn Asn Arg Leu Ile Val Glu Asn Asn Lys Ile Ile Val Glu
115 120 125

Val Leu Arg
130

<210> 683
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 683

Ser Glu Ala Leu Glu Glu Leu Glu Lys Ala Leu Arg Glu Leu Lys Lys
1 5 10 15

Ser Thr Asp Glu Leu Glu Arg Ser Thr Glu Glu Leu Glu Lys Asn Pro
20 25 30

Ser Glu Asp Ala Leu Val Glu Asn Asn Arg Leu Ile Val Glu Asn Asn
35 40 45

Lys Ile Ile Val Glu Val Leu Arg Ile Ile Ala Lys Val Leu Lys Gly
50 55 60

Gly Gly Gly Ser Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu
65 70 75 80

Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln
85 90 95

Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu
100 105 110

Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
115 120 125

<210> 684
<211> 129
<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 684

Ser Glu Ala Leu Glu Glu Leu Glu Lys Ala Leu Arg Glu Leu Lys Lys
1 5 10 15

Ser Thr Asp Glu Leu Glu Arg Ser Thr Glu Glu Leu Glu Lys Asn Pro
20 25 30

Ser Glu Asp Ala Leu Val Glu Asn Asn Arg Leu Ile Val Glu Asn Asn
35 40 45

Lys Ile Ile Val Glu Val Leu Arg Ile Ile Ala Lys Val Leu Lys Gly
50 55 60

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Lys Glu Asn Val Leu Gln
65 70 75 80

Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu
85 90 95

Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys
100 105 110

Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys
115 120 125

Arg

<210> 685

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 685

Ser Pro Glu Leu Glu Lys Ala Leu Arg Glu Leu Lys Lys Ser Thr Asp

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

<210> 686
 <211> 123
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 686

Ser Pro Glu Leu Glu Lys Ala Leu Arg Glu Leu Lys Lys Ser Thr Asp	1	5	10	15
Glu Leu Glu Arg Ser Thr Glu Glu Leu Glu Lys Asn Gly Ser Pro Glu	20	25	30	
Ala Leu Val Glu Asn Asn Arg Leu Ile Val Glu Asn Asn Lys Ile Ile	35	40	45	
Val Glu Val Leu Arg Ile Ile Ala Lys Gly Gly Gly Gly Ser Gly Gly				

50

55

60

Gly Gly Ser Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met
65 70 75 80

Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser
85 90 95

Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu
100 105 110

Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
115 120

<210> 687
<211> 135
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 687

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu
20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

Gly Gly Gly Gly Ser Gly Gly Gly Ser Glu Ala Leu Glu Glu Leu Glu
65 70 75 80

Lys Ala Leu Arg Glu Leu Lys Lys Ser Thr Asp Glu Leu Glu Arg Ser
85 90 95

Thr Glu Glu Leu Glu Lys Asn Pro Ser Glu Asp Ala Leu Val Glu Asn

100

105

110

Asn Arg Leu Ile Val Glu Asn Asn Lys Ile Ile Val Glu Val Leu Arg
 115 120 125

Ile Ile Ala Lys Val Leu Lys
 130 135

<210> 688

<211> 133

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 688

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
 1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu
 20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
 35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
 50 55 60

Gly Gly Gly Gly Ser Gly Ser Glu Ala Leu Glu Glu Leu Glu Lys Ala
 65 70 75 80

Leu Arg Glu Leu Lys Lys Ser Thr Asp Glu Leu Glu Arg Ser Thr Glu
 85 90 95

Glu Leu Glu Lys Asn Pro Ser Glu Asp Ala Leu Val Glu Asn Asn Arg
 100 105 110

Leu Ile Val Glu Asn Asn Lys Ile Ile Val Glu Val Leu Arg Ile Ile
 115 120 125

Ala Lys Val Leu Lys

130

<210> 689
<211> 131
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 689

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu
20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

Gly Gly Gly Ser Ser Glu Ala Leu Glu Glu Leu Glu Lys Ala Leu Arg
65 70 75 80

Glu Leu Lys Lys Ser Thr Asp Glu Leu Glu Arg Ser Thr Glu Glu Leu
85 90 95

Glu Lys Asn Pro Ser Glu Asp Ala Leu Val Glu Asn Asn Arg Leu Ile
100 105 110

Val Glu Asn Asn Lys Ile Ile Val Glu Val Leu Arg Ile Ile Ala Lys
115 120 125

Val Leu Lys
130

<210> 690
<211> 129
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 690

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu
20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

Gly Gly Ser Glu Ala Leu Glu Glu Leu Glu Lys Ala Leu Arg Glu Leu
65 70 75 80

Lys Lys Ser Thr Asp Glu Leu Glu Arg Ser Thr Glu Glu Leu Glu Lys
85 90 95

Asn Pro Ser Glu Asp Ala Leu Val Glu Asn Asn Arg Leu Ile Val Glu
100 105 110

Asn Asn Lys Ile Ile Val Glu Val Leu Arg Ile Ile Ala Lys Val Leu
115 120 125

Lys

<210> 691

<211> 140

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 691

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Glu Ala
65 70 75 80

Leu Glu Glu Leu Glu Lys Ala Leu Arg Glu Leu Lys Lys Ser Thr Asp
85 90 95

Glu Leu Glu Arg Ser Thr Glu Glu Leu Glu Lys Asn Pro Ser Glu Asp
100 105 110

Ala Leu Val Glu Asn Asn Arg Leu Ile Val Glu Asn Asn Lys Ile Ile
115 120 125

Val Glu Val Leu Arg Ile Ile Ala Lys Val Leu Lys
130 135 140

<210> 692
<211> 140
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 692

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Ala Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Thr Gly Gly Ser Glu Ala
65 70 75 80

Leu Glu Glu Leu Glu Lys Ala Leu Arg Glu Leu Lys Lys Ser Thr Asp
85 90 95

Glu Leu Glu Arg Ser Thr Glu Glu Leu Glu Lys Asn Pro Ser Glu Asp
100 105 110

Ala Leu Val Glu Asn Asn Arg Leu Ile Val Glu Asn Asn Lys Ile Ile
115 120 125

Val Glu Val Leu Arg Ile Ile Ala Lys Val Leu Lys
130 135 140

<210> 693
<211> 141
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 693

Met Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu
1 5 10 15

Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg
20 25 30

Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile
35 40 45

Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg
50 55 60

Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Glu
65 70 75 80

Ala Leu Glu Glu Leu Glu Lys Ala Leu Arg Glu Leu Lys Lys Ser Thr
85 90 95

Asp Glu Leu Glu Arg Ser Thr Glu Glu Leu Glu Lys Asn Pro Ser Glu
100 105 110

Asp Ala Leu Val Glu Asn Asn Arg Leu Ile Val Glu Asn Asn Lys Ile
115 120 125

Ile Val Glu Val Leu Arg Ile Ile Ala Lys Val Leu Lys
130 135 140

<210> 694
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 694

Met Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu
1 5 10 15

Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg
20 25 30

Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile
35 40 45

Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Ala
50 55 60

Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Thr Gly Gly Ala Ser
65 70 75 80

Pro Ala Ala Pro Ala Pro Gly Gly Asn Leu Asp Glu Leu His Met Gln
85 90 95

Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu
100 105 110

Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr
115 120 125

Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys
130 135 140

Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly Ala Ser Pro Ala Ala Pro
145 150 155 160

Ala Pro Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile
165 170 175

Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val
180 185 190

Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu
195 200 205

Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
210 215 220

<210> 695
<211> 244
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 695

Met Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu
1 5 10 15

Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg
20 25 30

Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile
35 40 45

Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Ala
50 55 60

Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Thr Gly Gly Ala Ser
65 70 75 80

Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala
85 90 95

Pro Ala Gly Gly Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu
100 105 110

Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His
115 120 125

Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp
130 135 140

Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu
145 150 155 160

Arg Leu Leu Ser Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser
165 170 175

Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Asp Lys Glu Asn
180 185 190

Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly
195 200 205

His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met
210 215 220

Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu
225 230 235 240

Glu Val Lys Arg

<210> 696
<211> 143
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 696

Met Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu
1 5 10 15

Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg
20 25 30

Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile
35 40 45

Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg
50 55 60

Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Gly Ser
65 70 75 80

Ser Glu Ala Leu Glu Glu Leu Glu Lys Ala Leu Arg Glu Leu Lys Lys
85 90 95

Ser Thr Asp Glu Leu Glu Arg Ser Thr Glu Glu Leu Glu Lys Asn Pro
100 105 110

Ser Glu Asp Ala Leu Val Glu Asn Asn Arg Leu Ile Val Glu Asn Asn
115 120 125

Lys Ile Ile Val Glu Val Leu Arg Ile Ile Ala Lys Val Leu Lys
130 135 140

<210> 697

<211> 216

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 697

Met Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu
1 5 10 15

Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg
20 25 30

Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile
35 40 45

Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg
50 55 60

Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Gly Ser
65 70 75 80

Gly Gly Gly Ser Gly Gly Asn Leu Asp Glu Leu His Met Gln Met Thr
85 90 95

Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln
100 105 110

Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn
115 120 125

Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu
130 135 140

Leu Glu Arg Leu Leu Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
145 150 155 160

Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu
165 170 175

Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile
180 185 190

Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu
195 200 205

Arg Leu Leu Glu Glu Val Lys Arg
210 215

<210> 698

<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 698

Met Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu
1 5 10 15

Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg
20 25 30

Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile
35 40 45

Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg
50 55 60

Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Ser Gly Ser
65 70 75 80

Gly Tyr Ile Pro Glu Ala Pro Arg Asp Gly Gln Ala Tyr Val Arg Lys
85 90 95

Asp Gly Glu Trp Val Leu Leu Ser Thr Phe Leu
100 105

<210> 699
<211> 235
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> MISC_FEATURE
<222> (1)..(20)
<223> optionally absent

<400> 699

Met Ser His His His His His His His Ser Glu Asn Leu Tyr Phe

1	5	10	15
Gln Ser Gly Gly Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln	20	25	30
Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu	35	40	45
Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu	50	55	60
Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu	65	70	75
Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly	85	90	95
Gly Gly Ser Gly Gly Gly Ser Gly Gly Asn Ile Asp Glu Leu Leu Met	100	105	110
Gln Val Thr Asp Leu Ile Tyr Glu Ala Leu His Phe Ala Lys Asp Glu	115	120	125
Glu Phe Gln Lys His Ala Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala	130	135	140
Tyr Lys Asn Lys Asp Lys Gln Lys Leu Glu Lys Val Val Glu Glu Leu	145	150	155
Lys Glu Leu Leu Glu Arg Ile Leu Ser Gly Gly Gly Ser Gly Gly Gly	165	170	175
Ser Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met	180	185	190
Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser	195	200	205
Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu	210	215	220

Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
225 230 235

<210> 700
<211> 77
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> MISC_FEATURE
<222> (1)..(21)
<223> optionally absent

<400> 700

Met Ser His His His His His His His Ser Glu Asn Leu Tyr Phe
1 5 10 15

Gln Ser Gly Gly Gly Asp Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu
20 25 30

Ile Met Lys Thr Leu Glu Gln Leu Gly His Ala Glu Ala Ser Met Gln
35 40 45

Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Gln Gly Asp Glu Arg Leu
50 55 60

Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Glu Arg
65 70 75

<210> 701
<211> 303
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 701

Asp Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu
1 5 10 15

Asp Gln Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile
20 25 30

Tyr Glu Phe Met Lys Gln Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu
35 40 45

Arg Leu Leu Glu Glu Val Glu Arg Gly Gly Ser Gly Ser Gly Gly Ser
50 55 60

Gly Ser Gly Ser Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys Thr His
65 70 75 80

Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
85 90 95

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
100 105 110

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
115 120 125

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
130 135 140

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
145 150 155 160

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
165 170 175

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
180 185 190

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
195 200 205

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
210 215 220

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn

225					230					235				240	
Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser
				245					250					255	
Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg
			260					265					270		
Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu
		275					280					285			
His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys	
	290					295					300				