# NOVEL COELENTERAZINE SUBSTRATES AND METHODS OF USE

## CROSS REFERENCE TO RELATED APPLICATIONS

**[0001]** This application claims priority to United States Provisional Application No. 61/409,422, filed November 2, 2010, which is incorporated herein by reference in its entirety.

## BACKGROUND

**[0002]** The luciferase secreted from the deep-sea shrimp *Oplophorus gracilirostris* has been shown to possess many interesting characteristics, such as high activity, high quantum yield, and broad substrate specificity (including, e.g., coelenterazine as well as various coelenterazine analogs). The bioluminescent reaction of *Oplophorus* takes place when the oxidation of coelenterazine (substrate) with molecular oxygen is catalyzed by *Oplophorus* luciferase, resulting in light of maximum intensity at 462 nm and the products $CO_2$ and coelenteramide (Shimomura *et al.*, *Biochemistry*, **17**:994 (1978)). Optimum luminescence occurs at pH 9 in the presence of 0.05-0.1 M NaCl at 40°C, and, due to the unusual resistance of this enzyme to heat, visible luminescence occurs at temperatures above 50°C when the highly purified enzyme is used or at over 70°C when partially purified enzyme is used. At pH 8.7, the native luciferase was reported by Shimomura *et al.* (1978) to have a molecular weight of approximately 130 kDa, apparently comprising four monomers of 31 kDa each; at lower pH, the native luciferase tends to polymerize.

**[0003]** Later work has shown that the *Oplophorus gracilirostris* luciferase is a complex of native 35 kDa and 19 kDa proteins, i.e., a heterotetramer consisting of two 19 kDa components and two 35 kDa components. Inouye *et al.* (2000) reported the molecular cloning of the cDNAs encoding the 35 kDa and 19 kDa proteins of *Oplophorus* luciferase, and the identification of the protein component that catalyzes the luminescence reaction. The cDNAs encoding the proteins were expressed in bacterial and mammalian cells, and the 19 kDa protein was identified as the component capable of catalyzing the luminescent oxidation of coelenterazine (Inouye *et al.*, 2000).

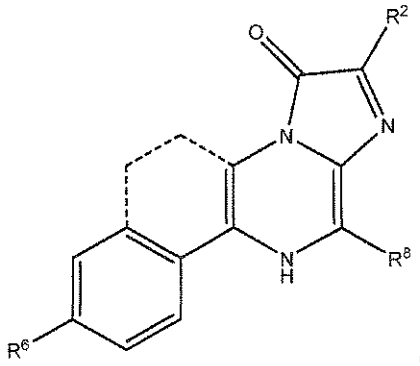
**[0004]** The 19 kDa protein of *Oplophorus* luciferase (GenBank accession BAB13776, 196 amino acids) appears to be the smallest catalytic component having luciferase function, and its primary structure has no significant similarity with any reported luciferase including imidazopyrazinone luciferases (Lorenz *et al.*, *PNAS USA*, **88**:4438 (1991); Thompson *et al.*, *PNAS USA*, **86**:6567 (1989)). Expression of the 19 kDa protein in *E. coli* resulted in the

formation of inclusion bodies (Inouye and Sasaki, *Protein Expression and Purification,* **56**:261-268 (2007)). The formation of inclusion bodies is likely due to the instability of the protein.

**[0005]** The substrate specificity of *Oplophorus* luciferase is unexpectedly broad (Inouye and Shimomura. *BBRC,* **223**:349 (1997)). For instance, bisdeoxycoelenterazine (i.e., coelenterazine-hh), an analog of coelenterazine, is an excellent substrate for *Oplophorus* luciferase comparable to coelenterazine (Nakamura *et al.*, *Tetrahedron Lett.*, **38**:6405 (1997)). Moreover, *Oplophorus* luciferase is a secreted enzyme, like the luciferase of the marine ostracod *Cypridina* (*Vargula*) *hilgendorfii* (Johnson and Shimomura, *Meth. Enzyme*, **57**:331 (1978)), which also uses an imidazopyrazinone-type luciferin to emit light.

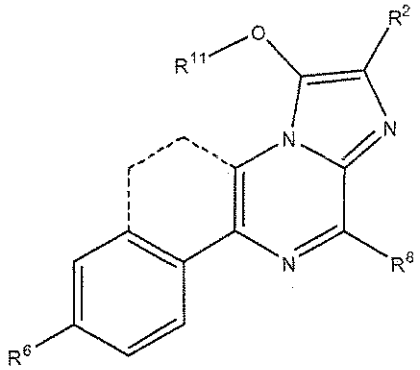
## SUMMARY

**[0006]** In an aspect, the disclosure relates to a compound of formula (Ia) or (Ib):



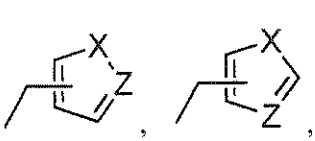
(Ia)

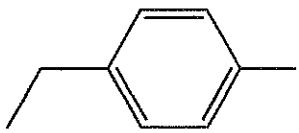
or



(Ib)

wherein $R^2$ is selected from the group consisting of

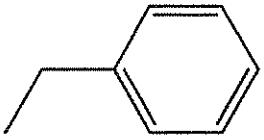
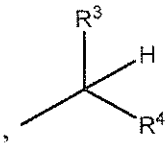




or $C_{2-5}$ straight chain alkyl;

$R^6$ is selected from the group consisting of -H, -OH, $-NH_2$, -OC(O)R or $-OCH_2OC(O)R$;

$R^8$ is selected from the group consisting of

 ,  , H or lower cycloalkyl;

wherein $R^3$ and $R^4$ are both H or both $C_{1-2}$ alkyl;

W is $-NH_2$, halo, -OH, -NHC(O)R, $-CO_2R$;

X is –S-, –O- or $-NR^{22}$-;

Y is –H, -OH, or $-OR^{11}$;

Z is –CH- or –N-;

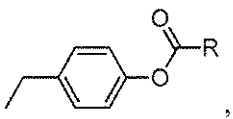
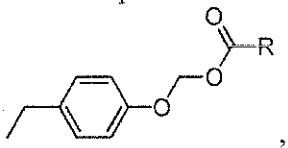
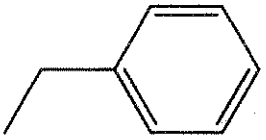
each $R^{11}$ is independently –C(O)R'' or $-CH_2OC(O)R''$;

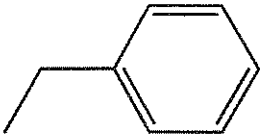
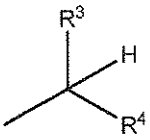
$R^{22}$ is H, $CH_3$ or $CH_2CH_3$;

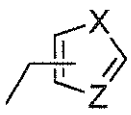
each R is independently $C_{1-7}$ straight-chain alkyl or $C_{1-7}$ branched alkyl;

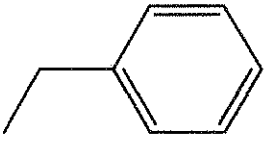
R'' is $C_{1-7}$ straight-chain alkyl or $C_{1-7}$ branched alkyl;

the dashed bonds indicate the presence of an optional ring, which may be saturated or unsaturated;

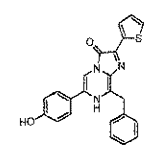
with the proviso that when $R^2$ is ,  , or  , $R^8$ is not  ;

with the proviso that when $R^2$ is  , $R^8$ is  or lower cycloalkyl; and

with the proviso that when $R^6$ is $NH_2$, $R^2$ is ,  , or $C_{2-5}$ alkyl;

or $R^8$ is not  .

**[0007]** In another aspect, the disclosure relates to a compound selected from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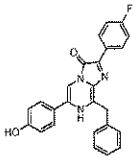
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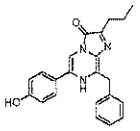
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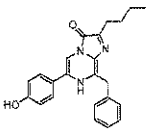
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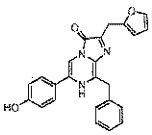
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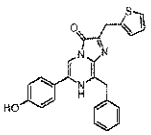
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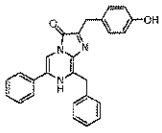
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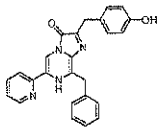
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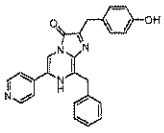
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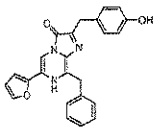
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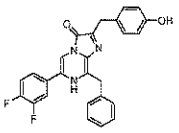
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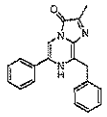
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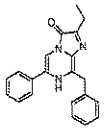
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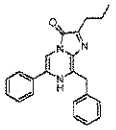
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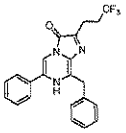
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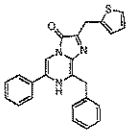
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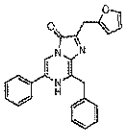
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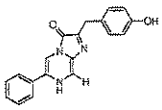
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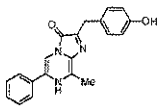
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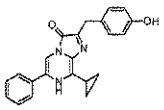
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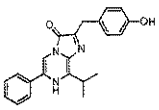
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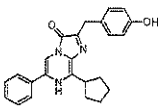
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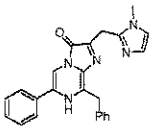
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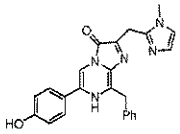
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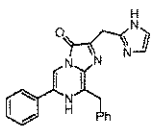
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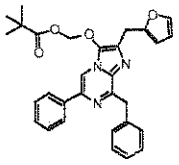
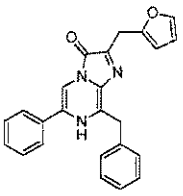


**[0008]** In an aspect, the disclosure relates to a compound of formula



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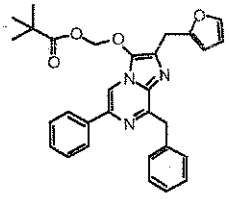


**[0009]** In an aspect, the disclosure relates to an isolated polynucleotide encoding an OgLuc variant polypeptide having at least 60% amino acid sequence identity to SEQ ID NO: 1 comprising at least one amino acid substitution at a position corresponding to an amino acid in SEQ ID NO: 1 wherein the OgLuc variant polypeptide has enhanced luminescence.

**[0010]** In an aspect, the disclosure relates to an isolated polynucleotide encoding an OgLuc variant polypeptide having at least 60% amino acid sequence identity to SEQ ID NO: 1

comprising at least one amino acid substitution at a position corresponding to an amino acid in SEQ ID NO: 1 wherein the OgLuc variant polypeptide has enhanced luminescence relative to an OgLuc polypeptide of SEQ ID NO: 3 with the proviso that the polypeptide encoded by the polynucleotide is not one of those listed in Table 47.

**[0011]** In an aspect, the disclosure relates to an isolated polynucleotide encoding an OgLuc variant polypeptide having at least 60% amino acid sequence identity to SEQ ID NO: 1 comprising at least one amino acid substitution at a position corresponding to an amino acid in SEQ ID NO: 1 wherein the OgLuc variant polypeptide has enhanced luminescence relative to a polypeptide of SEQ ID NO: 31 with the proviso that the polypeptide encoded by the polynucleotide is not SEQ ID NO: 3 or 15.

**[0012]** In an aspect, the disclosure relates to an isolated polynucleotide encoding an OgLuc variant polypeptide having at least 60% amino acid sequence identity to SEQ ID NO: 1 comprising at least one amino acid substitution at a position corresponding to an amino acid in SEQ ID NO: 1 wherein the OgLuc variant polypeptide has enhanced luminescence relative to a polypeptide of SEQ ID NO: 29 with the proviso that the polypeptide encoded by the polynucleotide is not SEQ ID NO: 3 or 15.

**[0013]** In an aspect, the disclosure relates to an isolated polynucleotide encoding an OgLuc variant polypeptide having at least 80% amino acid sequence identity to an OgLuc polypeptide of SEQ ID NO: 1 comprising amino acid substitutions A4E, Q11R, A33K, V44I, P115E, Q124K, Y138I, N166R, I90V, F54I, Q18L, F68Y, L72Q, and M75K corresponding to SEQ ID NO: 1 and the OgLuc variant polypeptide having luciferase activity.

**[0014]** In an aspect, the disclosure relates to an isolated polynucleotide encoding an OgLuc variant polypeptide having at least 80% amino acid sequence identity to an OgLuc polypeptide of SEQ ID NO: 1, wherein the amino acid at position 4 is glutamate, at position 11 is arginine, at position 18 is leucine, at position 33 is lysine, at position 44 is isoleucine, at position 54 is isoleucine, at position 68 is tyrosine, at position 72 is glutamine, at position 75 is lysine, at position 90 is valine, at position 115 is glutamate, at position 124 is lysine, at position 138 is isoleucine, and at position 166 is arginine corresponding to SEQ ID NO: 1 and the OgLuc variant polypeptide having luciferase activity.

**[0015]** In an aspect, the disclosure relates to an isolated polynucleotide encoding an OgLuc variant polypeptide having at least 80% amino acid sequence identity to an OgLuc polypeptide of SEQ ID NO: 1 comprising amino acid substitutions A4E, Q11R, A33K, V44I, P115E, Q124K,

Y138I, N166R, Q18L, F54I, L92H, and Y109F corresponding to SEQ ID NO: 1 and the OgLuc variant polypeptide having luciferase activity.

**[0016]** In an aspect, the disclosure relates to an isolated polynucleotide encoding an OgLuc variant polypeptide having at least 80% amino acid sequence identity to an OgLuc polypeptide of SEQ ID NO: 1 comprising amino acid substitutions A4E, Q11R, A33K, V44I, A54I, F77Y, I90V, P115E, Q124K, Y138I and N166R corresponding to SEQ ID NO: 1 and the OgLuc variant polypeptide having luciferase activity.

**[0017]** In an aspect, the disclosure relates to an isolated polynucleotide encoding an OgLuc variant polypeptide having at least 80% amino acid sequence identity to an OgLuc polypeptide of SEQ ID NO: 1, wherein the amino acid at position 4 is glutamate, at position 11 is arginine, at position 18 is leucine, at position 33 is lysine, at position 44 is isoleucine, at position 54 is isoleucine, at position 92 is histidine, at position 109 is phenylalanine, at position 115 is glutamate, at position 124 is lysine, at position 138 is isoleucine, and at position 166 is arginine corresponding to SEQ ID NO: 1 and the OgLuc variant polypeptide having luciferase activity.

**[0018]** In an aspect, the disclosure relates to an isolated polynucleotide encoding an OgLuc variant polypeptide having at least 80% amino acid sequence identity to an OgLuc polypeptide of SEQ ID NO: 1, wherein the amino acid at position 4 is glutamate, at position 11 is arginine, at position 33 is lysine, at position 44 is isoleucine, at position 54 is isoleucine, at position 77 is tyrosine, at position 90 is valine, at position 115 is glutamate, at position 124 is lysine, at position 138 is isoleucine, and at position 166 is arginine corresponding to SEQ ID NO: 1 and the OgLuc variant polypeptide having luciferase activity.

**[0019]** In an aspect, the disclosure relates to an isolated polynucleotide comprising the polynucleotide encoding the polypeptide of SEQ ID NO: 19.

**[0020]** In an aspect, the disclosure relates to an isolated polynucleotide comprising the polynucleotide of SEQ ID NO: 18, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 42, SEQ ID NO: 88, or SEQ ID NO: 92.

**[0021]** In an aspect, the disclosure relates to an isolated polynucleotide encoding a decapod luciferase polypeptide having at least 30% amino acid sequence identity to SEQ ID NO: 1, the polypeptide comprising a sequence pattern corresponding to the sequence pattern of Formula (VII) and including no more than 5 differences, wherein differences include differences from pattern positions 1, 2, 3, 5, 8, 10, 12, 14, 15, 17, or 18 relative to Formula (VII) according to the OgLuc pattern listed in Table 4 as well as gaps or insertions between any of the pattern positions

of Formula (VII) according to the OgLuc pattern listed in Table 4, wherein the decapod luciferase produces luminescence in the presence of a coelenterazine.

**[0022]** In an aspect, the disclosure relates to a synthetic nucleotide sequence encoding an OgLuc variant polypeptide comprising a fragment of at least 100 nucleotides having 80% or less nucleic acid sequence identity to a parent nucleic acid sequence having SEQ ID NO: 2 and having 90% or more nucleic acid sequence identity to SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, or SEQ ID NO: 25 or the complement thereof, wherein the decreased sequence identity is a result of different codons in the synthetic nucleotide sequence relative to the codons in the parent nucleic acid sequence, wherein the synthetic nucleotide sequence encodes a OgLuc variant which has at least 85% amino acid sequence identity to the corresponding luciferase encoded by the parent nucleic acid sequence, and wherein the synthetic nucleotide sequence has a reduced number of regulatory sequences relative to the parent nucleic acid sequence.

**[0023]** In an aspect, the disclosure relates to a synthetic nucleotide sequence encoding an OgLuc variant polypeptide comprising a fragment of at least 300 nucleotides having 80% or less nucleic acid sequence identity to a parent nucleic acid sequence having SEQ ID NO: 14 and having 90% or more nucleic acid sequence identity to SEQ ID NO: 22 or SEQ ID NO: 23 or the complement thereof, wherein the decreased sequence identity is a result of different codons in the synthetic nucleotide sequence relative to the codons in the parent nucleic acid sequence, wherein the synthetic nucleotide sequence encodes a firefly luciferase which has at least 85% amino acid sequence identity to the corresponding luciferase encoded by the parent nucleic acid sequence, and wherein the synthetic nucleotide sequence has a reduced number of regulatory sequences relative to the parent nucleic acid sequence.

**[0024]** In an aspect, the disclosure relates to a synthetic nucleotide sequence encoding an OgLuc variant polypeptide comprising a fragment of at least 100 nucleotides having 80% or less nucleic acid sequence identity to a parent nucleic acid sequence having SEQ ID NO: 18 and having 90% or more nucleic acid sequence identity to SEQ ID NO: 24 or SEQ ID NO: 25 or the complement thereof, wherein the decreased sequence identity is a result of different codons in the synthetic nucleotide sequence relative to the codons in the parent nucleic acid sequence, wherein the synthetic nucleotide sequence encodes a OgLuc variant which has at least 85% amino acid sequence identity to the corresponding luciferase encoded by the parent nucleic acid sequence, and wherein the synthetic nucleotide sequence has a reduced number of regulatory sequences relative to the parent nucleic acid sequence.

**[0025]** In an aspect, the disclosure relates to a fusion peptide comprising a signal peptide from *Oplophorus gracilirostris* fused to a heterologous protein, wherein said signal peptide is SEQ ID NO: 54, wherein the fusion peptide is expressed in a cell and secreted from the cell.

**[0026]** In an aspect, the disclosure relates to a method of generating a polynucleotide encoding a OgLuc variant polypeptide comprising: (a) using a parental fusion protein construct comprising a parental OgLuc polypeptide and at least one heterologous polypeptide to generate a library of variant fusion proteins; and (b) screening the library for at least one of enhanced luminescence, enhanced enzyme stability or enhanced biocompatibility relative to the parental fusion protein construct.

**[0027]** In an aspect, the disclosure relates to a method of generating codon-optimized polynucleotides encoding a luciferase for use in an organism, comprising: for each amino acid in the luciferase, randomly selecting a codon from the two most commonly used codons used in the organism to encode for the amino acid to produce a first codon-optimized polynucleotide.

**[0028]** Other aspects of the invention will become apparent by consideration of the detailed description and accompanying drawings.

## BRIEF DESCRIPTION OF THE DRAWINGS

**[0029]** FIG. 1 shows the chemical structure of native coelenterazine, known bis-coelenterazine (coelenterazine-hh), and known coelenterazine-h, where R2, R6 and R8 represent the regions of the molecule where modifications were made.

**[0030]** FIG. 2 shows the chemical structure of novel coelenterazines PBI-3939, PBI-3889, PBI-3945, PBI-4002, PBI-3841, PBI-3897, PBI-3896, PBI-3925, PBI-3894, PBI-3932, and PBI-3840.

**[0031]** FIG. 3 shows the Km determination of PBI-3939.

**[0032]** FIG. 4 shows the chemical structure of various novel coelenterazines of the present invention.

**[0033]** FIGS. 5A-G show the luminescence (RLUs) generated from lysed bacterial cells expressing C1+A4E using native, known, and novel coelenterazine as substrates. FIGS. 5A, 5C-5G show independent experiments measuring the luminescence in RLUs generated by C1+A4E with known and novel coelenterazines using native coelenterazine as a comparison. FIG. 5B

shows the fold-decrease in luminescence generated by C1+4AE using the substrates shown in FIG. 5A compared to native coelenterazine.

**[0034]** FIGS. 6A-D show the luminescence generated from lysed bacterial cells expressing various OgLuc variants using native coelenterazine ("Coelente"), known coelenterazine-h ("h"), known coelenterazine-hh ("h,h"), known 2-methyl coelenterazine ("2-me"), known coelenterazine-v ("v"), and novel coelenterazines PBI-3840, PBI-3897, PBI-3889, PBI-3899, PBI-3900, PBI-3912, PBI-3913, PBI-3925, PBI-3897, PBI-3899, PBI-3889, PBI-3939, PBI-3933, PBI-3932, PBI-3946, PBI-3897, PBI-3841, PBI-3896, PBI-3925, and PBI-3945 as substrates.

**[0035]** FIG. 7 shows the amino acid substitutions in various OgLuc variants.

**[0036]** FIGS. 8A-B show the luminescence generated from lysed bacterial cells expressing OgLuc variants listed in FIG. 7 using native coelenterazine ("Coelenterazine"), known coelenterazine-h ("H"), known coelenterazine-hh ("h,h"), and novel coelenterazines PBI-3840, PBI-3925, PBI-3912, PBI-3889, PBI-3939, PBI-3933, PBI-3932, PBI-3946, PBI-3941, and PBI-3896 as substrates.

**[0037]** FIG. 9 shows the luminescence generated from lysed bacterial cells expressing various OgLuc variants using native coelenterazine ("Coelenterazine"), known coelenterazine-hh ("h,h"), and novel coelenterazines PBI-3939, PBI-3945, PBI-3840, PBI-3932, PBI-3925, PBI-9894, and PBI-3896 as substrates.

**[0038]** FIG. 10 shows the amino acid substitutions in various OgLuc variants.

**[0039]** FIG. 11 shows the luminescence generated from lysed bacterial cells expressing OgLuc variants listed in FIG. 10 using native coelenterazine ("Coelenterazine"), known coelenterazine-hh ("h,h"), and novel coelenterazines PBI-3939, PBI-3945, PBI-3840, PBI-3932, PBI-3925, PBI-3894, and PBI-3896, as substrates.

**[0040]** FIG. 12 shows the luminescence generated from lysed bacterial cells expressing OgLuc variants using native coelenterazine ("Coelenterazine"), known coelenterazine-hh ("h,h"), and novel coelenterazines PBI-3939, PBI-3945, PBI-3889, PBI-3840, PBI-3932, PBI-3925, PBI-3894, PBI-3896, and PBI-3897 as substrates.

**[0041]** FIG. 13 shows the luminescence generated from lysed bacterial cells expressing OgLuc variants using native coelenterazine ("Coelenterazine"), known coelenterazine-hh ("H,H"), and novel coelenterazines PBI-3897, PBI-3896, and PBI-3894 as substrates.

**[0042]** FIG. 14 shows the amino acid substitutions in various OgLuc variants.

**[0043]** FIG. 15 shows the luminescence generated from lysed bacterial cells expressing OgLuc variants listed in FIG. 14 using native coelenterazine ("Coelenterazine"), known coelenterazine-hh ("h,h"), and novel coelenterazines PBI-3897, PBI-3841, PBI-3896, and PBI-3894 as substrates.

**[0044]** FIG. 16 shows the luminescence generated from lysed bacterial cells expressing OgLuc variants using native coelenterazine ("Coelenterazine"), known coelenterazine-h ("H"), known coelenterazine-hh ("HH"), and novel coelenterazines PBI-3841 and PBI-3897 as substrates.

**[0045]** FIG. 17 shows the luminescence generated from lysed bacterial cells expressing various OgLuc variants and humanized *Renilla* luciferase (hRL) using native coelenterazine ("Coel"), known coelenterazine-hh ("h,h"), and novel coelenterazines PBI-3897 and PBI-3841 as substrates.

**[0046]** FIG. 18 shows the luminescence generated from lysed bacterial cells expressing various OgLuc variants using native coelenterazine ("Coelenterazine"), known coelenterazine-hh ("h,h"), and novel coelenterazines PBI-3939, PBI-3945, PBI-3889, and PBI-4002 as substrates.

**[0047]** FIG. 19 shows the luminescence generated from lysed bacterial cells expressing various OgLuc variants using native coelenterazine ("Coelenterazine"), known coelenterazine-h ("H"), known coelenterazine-hh ("h,h"), and novel coelenterazines PBI-3939, PBI-3945, PBI-3889, and PBI-4002 as substrates.

**[0048]** FIG. 20 shows the amino acid substitutions in various OgLuc variants.

**[0049]** FIG. 21 shows the luminescence generated from lysed bacterial cells expressing OgLuc variants listed in FIG. 20 using native coelenterazine ("Coelenterazine"), known coelenterazine-h ("H"), known coelenterazine-hh ("h,h"), and novel coelenterazines PBI-3939, PBI-3945, PBI-4002, PBI-3932, and PBI-3840 as substrates.

**[0050]** FIG. 22 shows the amino acid substitutions in various OgLuc variants.

**[0051]** FIG. 23 shows the luminescence generated from lysed bacterial cells expressing OgLuc variants listed in FIG. 22 using native coelenterazine ("Coelenterazine"), known coelenterazine-h ("H"), known coelenterazine-hh ("h,h"), and novel coelenterazines PBI-3939, PBI-3945, PBI-3889, PBI-4002, PBI-3932, and PBI-3840 as substrates.

**[0052]** FIG. 24 shows the luminescence generated from lysed bacterial cells expressing various OgLuc variants and hRL ("Renilla") using native coelenterazine ("Coelenterazine"), known coelenterazine-h ("H"), known coelenterazine-hh ("H,H"), and novel coelenterazines PBI-3939 and PBI-3945 as substrates.

**[0053]** FIG. 25 shows the luminescence generated from lysed bacterial cells expressing various OgLuc variants and hRL ("Renilla") using native coelenterazine ("Coelenterazine"), known coelenterazine-hh ("h,h"), and novel coelenterazines PBI-3939, PBI-3945, PBI-3889, and PBI-4002 as substrates.

**[0054]** FIG. 26 shows the amino acid substitutions in various OgLuc variants.

**[0055]** FIG. 27 shows the luminescence generated from lysed bacterial cells expressing OgLuc variants listed in FIG. 26 using native coelenterazine ("Coelenterazine"), known coelenterazine-h ("H"), known coelenterazine-hh ("h,h"), and novel coelenterazines PBI-3939, PBI-3945, PBI-3889, and PBI-4002 as substrates.

**[0056]** FIG. 28 shows the luminescence generated from lysed bacterial cells expressing various OgLuc variants and hRL ("Renilla") using native coelenterazine ("Coel."), known coelenterazine-h ("H"), known coelenterazine-hh ("H,H"), and novel coelenterazines PBI-3939, PBI-3945, PBI-3889, and PBI-4002 as substrates.

**[0057]** FIG. 29 shows the luminescence of 9B8 opt and 9B8 opt+K33N in bacterial lysates using native coelenterazine and PBI-3939 as substrates and the relative specificity of these variants for PBI-3939 compared to native coelenterazine.

**[0058]** FIGS. 30A-D show mutational analysis at position 166 using native coelenterazine (FIG. 30A), coelenterazine-h (FIG.30B), and PBI-399 (FIG. 30C).

**[0059]** FIG. 31 shows the luminescence of various deletions in the OgLuc variant L27V where (-) is the machine background.

**[0060]** FIG. 32 shows the normalized luminescence generated from lysed HEK293 cells expressing hRL ("Renilla") using native coelenterazine as a substrate, firefly luciferase (Luc2) using luciferin (BRIGHT-GLO™ Assay Reagent) as a substrate, and various OgLuc variants using novel PBI-3939 as a substrate.

**[0061]** FIG. 33 shows the signal stability of IV and 15C1 in bacterial lysates using the novel coelenterazine PBI-3945 as a substrate and IV and 9B8 in bacterial lysates using the novel coelenterazine PBI-3889 as a substrate.

**[0062]** FIGS. 34A-B show the higher activity (FIG. 34A) and signal stability (FIG. 34B) of the OgLuc variant L27V compared to Firefly (Fluc) and Renilla (Rluc) luciferases.

**[0063]** FIG. 35 shows the Vmax (RLU/sec) and Km (μM) values for various OgLuc variants in bacterial lysates using the novel coelenterazine PBI-3939 as a substrate.

**[0064]** FIG. 36 shows the Vmax (RLU/sec) and Km (μM) values for various OgLuc variants in bacterial lysates using the novel coelenterazine PBI-3939 as a substrate.

**[0065]** FIG. 37 shows the Vmax (RLU/sec) and Km (μM) values for 9B8 opt and 9B8 opt+K33N both in bacterial lysates using the novel coelenterazine PBI-3939 as a substrate.

**[0066]** FIG. 38 shows the protein stability at 50°C of various OgLuc variants in bacterial lysates using native coelenterazine as a substrate as the luminescence at t=0 and half-life in min

**[0067]** FIGS. 39A-B show the structural integrity (determined by expression, stability, and solubility as shown by SDS-PAGE analysis) in bacterial lysates of various OgLuc variants at 25°C (FIG. 39A) and 37°C (FIG. 39B) compared to *Renilla* (hRL) and firefly luciferase (Luc2).

**[0068]** FIGS. 40A-B show the protein stability at 60°C in bacterial lysates of 9B8 opt and 9B8 opt+K33N using the novel coelenterazine PBI-3939 as a substrate as the natural log (ln) of the luminescence (in RLU) over time (FIG. 40A) and as the half-life in hrs (FIG. 40B).

**[0069]** FIG. 41 shows the percent activity of the OgLuc variants 9B8 and L27V at 60°C.

**[0070]** FIGS. 42A-B show the protein stability of the OgLuc variant L27V at various pH (FIG. 42A) and salt concentrations (FIG. 42B).

**[0071]** FIGS. 43A-B shows the gel filtration chromatographic analysis of purified C1+A4E (FIG. 43A) and 9B8 (FIG. 43B).

**[0072]** FIG. 44 shows the gel filtration chromatographic analysis demonstrating that the OgLuc variant L27V exists in a monomeric form.

**[0073]** FIGS. 45A-B show the protein expression levels of various OgLuc variant-HALOTAG® (HT7) fusion proteins in undiluted and 1:1 diluted bacterial lysate samples analyzed by SDS-PAGE (FIG.45A) and the normalized protein expression levels (FIG. 45B).

**[0074]** FIGS. 46A-B show the protein expression (FIG. 46A) and solubility of the OgLuc variants 9B8 opt, V2 and L27V (FIG. 46B).

**[0075]** FIG. 47 shows the normalized luminescence in RLUs generated from lysed HEK293 cells expressing IV, 9B8, and hRL ("Renilla") using native coelenterazine and the novel coelenterazine PBI-3939 as substrates.

**[0076]** FIG. 48 shows the normalized luminescence in RLUs generated from lysed HEK293 cells expressing pF4Ag-Ogluc-9B8-HT7, pF4Ag-Luc2-HT7 and pF4Ag-Renilla-HT7 using PBI-3939, Luciferin (BRIGHT-GLO™ Assay Reagent), and native coelenterazine, respectively, as a substrate.

**[0077]** FIG. 49 shows the luminescence generated from lysed HEK293 cells expressing 30 or 100 ng of plasmid DNA encoding either 9B8 opt or 9B8 opt+K33N ("K33N") using the novel coelenterazine PBI-3939 as a substrate.

**[0078]** FIGS. 50A-E show the luminescence of the OgLuc variant L27V compared to firefly luciferase (Luc2) in HEK 293 (FIG. 50A) and HeLa cells (non-fusion) (FIG. 50B), the luminescence of HaloTag® fusion compared to the OgLuc variant L27V (FIG. 50C) and firefly luciferase (Luc2) (FIG. 50D), and the protein expression of HaloTag®-OgLuc L27V compared to HaloTag®-Firefly luciferase (Luc2) in HEK 293 ("HEK") and HeLa cells ("HeLa").

**[0079]** FIG. 51 shows inhibition analysis of the OgLuc variants 9B8 and L27V against a LOPAC library to determine their susceptibility to off-target interactions.

**[0080]** FIGS. 52A-E show the inhibition analysis of the OgLuc variants 9B8 and L27V by Suramin and Tyr ag 835 (FIGS. 52A-C) and the chemical structures of Suramin (FIG. 52D) and Tyr ag 835 (FIG. 52E).

**[0081]** FIG. 53 shows the activity of the OgLuc variants 9B8 and L27V was analyzed in the presence of BSA to determine resistance to non-specific protein interactions.

**[0082]** FIG. 54 shows the percent activity of the OgLuc variants 9B8 and L27V to determine reactivity to plastic.

**[0083]** FIG. 55 shows the luminescence generated from lysed HEK293 cells expressing the IV cAMP transcriptional reporter compared to hRL ("Renilla") using known coelenterazine-h as a substrate with ("induced") or without ("basal") forskolin treatment and the fold induction (response) due to forskolin treatment ("fold").

**[0084]** FIG. 56 shows the normalized luminescence generated from lysed HEK293 cells expressing the 9B8, 9B8 opt, hRL ("Renilla") or firefly luciferase ("Luc2") cAMP transcriptional reporter using PBI-3939 (for 9B8 and 9B8 opt), native coelenterazine (for hRL) or luciferin (BRIGHT-GLO™ Assay Reagent; for Luc2) as a substrate with ("+FSK") or without ("-FSK") forskolin treatment and the fold induction (response) due to forskolin treatment ("FOLD").

**[0085]** FIG. 57 shows the luminescence generated from lysed HEK293 cells expressing 9B8 opt and 9B8 opt+K33N ("K33N") cAMP transcriptional reporters using the novel coelenterazine PBI-3939 as a substrate with ("Induced") or without ("Basal") forskolin treatment and the fold induction due to forskolin treatment ("Fold Induction").

**[0086]** FIGS. 58A-C show the luminescence of the OgLuc variants 9B8 and L27V lytic reporter constructs for multiple pathways in multiple cell types.

**[0087]** FIGS. 59A-C show the luminescence of the OgLuc variant L27V reporter constructs in various cell lines and with various response elements.

**[0088]** FIGS. 60A-B show the luminescence of the OgLuc variant L27V secretable reporter compared to Metridia longa luciferase with a CMV promoter (FIG. 60A) or a NFkB response element (FIG. 60B).

**[0089]** FIGS. 61A-F show the absolute luminescence (FIGS. 61A and 61B), the normalized luminescence (FIGS. 61C and 61D) and the fold response (FIGS. 61E and 61F) of optimized versions of L27V (L27V01, L27V02 and L27V03) compared to L27V (L27V00) expressed in HeLa cells.

**[0090]** FIGS. 62A-B show the luminescence of secreted OgLuc variant L27V02 (containing the IL-6 secretion signal) reporter (FIG. 62A) and L27V02 ("L27V(02)"), L27V02P ("L27V(02)P(01)") and luc2 ("Fluc") reporters (FIG. 62A) expressed in HepG2 cells treated with various doses of rhTNFα ("TNFα").

**[0091]** FIG. 63 shows the luminescence generated from media and lysate samples of HEK293 cells expressing the codon optimized variant IV opt with or without the secretion signal

sequence using the novel PBI-3939 as a substrate compared to hRL ("Renilla") with or without the secretion signal sequence using native coelenterazine as a substrate.

**[0092]** FIGS. 64A-D show the luminescence of the secreted OgLuc variants 9B8, V2 and L27V reporters expressed in CHO cells (FIGS. 64A and 64B) and HeLa (FIGS. 64C and 64D).

**[0093]** FIGS. 65A-B show a comparison of the luminescence from the secreted OgLuc variants 9B8 and V2 using PBI-3939 as a substrate to that of the secreted luciferase of *Metridia longa* using Ready-to-Glow™ as a substrate numerically (FIG. 65A) and graphically (FIG. 65B).

**[0094]** FIGS. 66A-B show the fold-increase in luminescence over background generated from HEK293 cells expressing hRL ("Ren") and 9B8 opt using the coelenterazine derivatives ENDUREN™ (FIG. 66A) and VIVIREN™ (FIG. 66B) and the novel coelenterazine PBI-3939 (FIG. 66B) as substrates.

**[0095]** FIGS. 67A-D show confocal images of U2OS cells transiently expressing L27V-HaloTag® fusion (FIG. 67A) or IL6-L27V fusion (FIGS. 67B-D). Scale bars = 20μm.

**[0096]** FIG. 68 shows the luminescence generated from lysed bacterial cells expressing various OgLuc variants and hRL ("Renilla") in the presence ("Sand") or absence of sandwich background ("pF4Ag") using native coelenterazine as a substrate.

**[0097]** FIG. 69 shows the fold-decrease in activity of various OgLuc variants and hRL ("Renilla") due to the presence of the sandwich background using native coelenterazine as a substrate.

**[0098]** FIG. 70 shows the fold-decrease in activity of 9B8 opt and 9B8 opt+K33N in bacterial lysates due to the presence of the sandwich background using the novel coelenterazine PBI-3939 as a substrate.

**[0099]** FIG. 71 shows the spectral profile of the OgLuc variant L27V.

**[00100]** FIG. 72 shows the luminescence of two circulated permuted (CP) versions of the OgLuc variant L27V, CP84 and CP95, either with no linker or with a 5, 10, or 20 amino acid linker.

**[00101]** FIGS. 73A-G show the luminescence of the various CP-TEV protease L27V constructs expressed in wheat germ extract (FIGS. 73A-D), *E. coli* (FIG. 73F-G) and HEK 293 cells (FIG. 73H). FIGS. 73A-D show the basal luminescence of the various CP-TEV protease

L27V constructs prior to TEV addition. FIG. 73E shows the response of the CP-TEV protease L27V constructs of FIGS. 73A-D.

**[00102]** FIG. 74 shows the fold response of various protein complementation L27V pairs.

**[00103]** FIGS. 75A-C show the luminescence of various protein complementation (PCA) L27V pairs: one L27V fragment of each pair was fused to either FKBP or FRB using a 1/4 configuration (FIG. 75A) or a 2/3 configuration (FIG. 75B), and the interaction of FKBP and FRB monitored in HEK 293 cells. The luminescence of various protein complementation (PCA) negative controls was also monitored (FIG. 75C).

**[00104]** FIGS. 76A-H show the luminescence of various protein complementation (PCA) L27V pairs: one L27V fragment of each pair was fused to either FKBP or FRB using a 2/3 configuration (FIGS. 76A and 76C) or a 1/4 configuration (FIGS. 76B and 76D), and the interaction of FKBP and FRB monitored in wheat germ extract (FIGS. 76A and 76B) and rabbit reticulocyte lysate (RRL) (FIGS. 76C and 76D). The luminescence of various protein complementation (PCA) negative controls was also measured (FIG. 76E) in cell free system. The 1/4 configuration was used in a cell free system (FIG. 76F), HEK293 cells (FIG. 76G) and in a lytic system (FIG. 76H).

**[00105]** FIGS. 77A-C show the luminescence of various protein complementation L27V pairs treated with FK506 and rapamycin (FIG. 77A) and the chemical structure of FK506 (FIG. 77A) and rapamycin (FIG. 77B).

**[00106]** FIG. 78 shows the activity of the OgLuc variant 9B8 cAMP biosensor with forskolin treatment.

**[00107]** FIGS. 79A-D show the luminescence of circularly permuted (FIGS. 79A and 79C) and straight split (FIG. 79B and 79D) L27V variants in rabbit reticulocyte lysate (FIGS. 79A-B) and HEK293 cells (FIGS. 79C-D).

**[00108]** FIGS. 80A-B show the subcellular distribution of the OgLuc variant L27V (FIG. 80A) and control vector pGEM3ZF (FIG. 80B) in U2OS cells for various exposure times.

**[00109]** FIGS. 81A-C show the subcellular location of the OgLuc variant L27V fused to either the transcription factor Nrf2 (FIG. 81B) or GPCR (FIG. 81C) compared to an unfused L27V control (FIG. 81A).

**[00110]** FIGS. 82A-C show the use of the OgLuc variant 9B8 opt to monitor intracellular signaling pathways using PBI-4377 (FIG. 82A). The 9B8 opt luciferase was fused to either IkB (FIG. 82B) or ODD (oxygen-dependent degradation domain of Hif-1α) (FIG. 82C), and fold response to a stimulus (TNFα for IkB and phenanthroline for ODD) was monitored via luminescence.

**[00111]** FIGS. 83A-C show the monitoring of oxidative stress signal pathways using the OgLuc variant (FIG. 83A), L27V02 (FIG. 83B), or *Renilla* luciferase (Rluc) (FIG. 83C).

**[00112]** FIGS. 84A-B show the comparison of the Nrf2-L27V02 sensor (FIG. 84A) and Nrf2(ARE)-Luc2P reporter (FIG. 84B).

**[00113]** FIGS. 85A-B show the emission spectra of IV-HT7 with and without ligand, using 1 μM TMR (FIG. 85A) or 10 μM Rhodamine 110 (FIG. 85B) as a ligand for HT7 and coelenterazine-h as a substrate for IV.

**[00114]** FIG. 86 shows the luminescence generated from lysed bacterial cells expressing 9B8 opt mixed with ("+ caspase") or without ("no caspase") caspase-3 using a pro-coelenterazine substrate.

**[00115]** FIGS. 87A-C show the luminescence generated from circularly permuted, straight split L27V variants CP84 and CP103 using PBI-3939 as a substrate with (FIG. 87B) or without (not shown) rapamycin treatment and the response (FIG. 87C) due to rapamycin treatment. The concept of the circularly permuted straight split variants is shown in FIG. 87A.

**[00116]** FIG. 88 shows percent remaining activity of the L27V variant after exposure to various amounts of urea.

**[00117]** FIG. 89 shows the effect of 3M urea on the activity of the L27V variant.

**[00118]** FIGS. 90A-B show the bioluminescence imaging of hormone-induced nuclear receptor (NR) translocation of OgLuc fusions using PBI-3939 substrate.

**[00119]** FIGS. 91A-B show the bioluminescence imaging of phorbol ester-induced Protein Kinase C alpha (PKC alpha) translocation of OgLuc fusions using PBI-3939 substrate.

**[00120]** FIGS. 92A-B show the bioluminescence imaging of autophagosomal protein translocation of OgLuc fusions using PBI-3939 substrate.

## DETAILED DESCRIPTION

**[00121]** Before any embodiments of the invention are explained in detail, it is to be understood that the invention is not limited in its application to the details of structure, synthesis, and arrangement of components set forth in the following description or illustrated in the following drawings. The invention is described with respect to specific embodiments and techniques, however, the invention is capable of other embodiments and of being practiced or of being carried out in various ways.

**[00122]** In the following description of the methods of the invention, process steps are carried out at room temperature (about 22°C) and atmospheric pressure unless otherwise specified. It also is specifically understood that any numerical range recited herein includes all values from the lower value to the upper value. For example, if a concentration range or beneficial effect range is stated as 1% to 50%, it is intended that values such as 2% to 40%, 10% to 30%, or 1% to 3%, etc. are expressly enumerated in this specification. Similarly, if a sequence identity range is given as between, e.g., 60% to <100%, it is intended that intermediate values such as 65%, 75%, 85%, 90%, 95%, etc. are expressly enumerated in this specification. These are only examples of what is specifically intended, and all possible numerical values from the lowest value to the highest value are considered expressly stated in the application.

**[00123]** Unless expressly specified otherwise, the term "comprising" is used in the context of the present application to indicate that further members may optionally be present in addition to the members of the list introduced by "comprising". It is, however, contemplated as a specific embodiment of the present invention that the term "comprising" encompasses the possibility of no further members being present, i.e., for the purpose of this embodiment "comprising" is to be understood as having the meaning of "consisting of".

**[00124]** The following detailed description discloses specific and/or preferred variants of the individual features of the invention. The present invention also contemplates, as particularly preferred embodiments, those embodiments which are generated by combining two or more of the specific and/or preferred variants described for two or more of the features of the present invention.

**[00125]** Unless expressly specified otherwise, all indications of relative amounts in the present application are made on a weight/weight basis. Indications of relative amounts of a component characterized by a generic term are meant to refer to the total amount of all specific variants or members covered by said generic term. If a certain component defined by a generic term is

specified to be present in a certain relative amount, and if this component is further characterized to be a specific variant or member covered by the generic term, it is meant that no other variants or members covered by the generic term are additionally present such that the total relative amount of components covered by the generic term exceeds the specified relative amount. More preferably, no other variants or members covered by the generic term are present at all.

*Overview*

**[00126]** In various aspects, the invention is drawn to novel compounds, novel luciferases, and combinations thereof. The invention encompasses methods, compositions, and kits including the novel compounds, novel luciferases, and/or combinations thereof.

**[00127]** The novel compounds are novel coelenterazines, which can be used as substrates by proteins that utilize coelenterazines to produce luminescence, including, but not limited to, luciferases and photoproteins found in various marine organisms such as cnidarians (e.g., *Renilla* luciferase), jellyfish (e.g., aequorin from the *Aequorea* jellyfish) and decapods luciferases (e.g., luciferase complex of *Oplophorus gracilirostris*). In various embodiments, the novel coelenterazines of the present invention have at least one of enhanced physical stability (e.g., enhanced coelenterazine stability), reduced autoluminescence, and increased biocompatibility with cells (e.g., less toxic to cells, including heterologous cell types) relative to native coelenterazine.

**[00128]** The novel luciferases disclosed herein include variants of the active subunit of a decapod luciferase. The novel luciferases can utilize various coelenterazines as substrates, including, but not limited to, native and known coelenterazines as well as the novel coelenterazines of the present invention. The novel luciferases display at least one of: enhanced luminescence (including increased brightness, enhanced signal stability and/or signal duration); enhanced enzyme stability (i.e., enhanced enzymatic activity including enhanced resistance to elevated temperature, changes in pH, inhibitors, denaturants, and/or detergents); altered substrate specificity (i.e., change in relative substrate specificity); and enhanced biocompatibility (including at least one of improved expression in cells, reduced toxicity, and/or cell stress). In various embodiments, the present invention encompasses novel luciferases that are present in solution as soluble, active monomers, chemically linked to other molecules (e.g., fusion proteins), or attached onto a solid surface (e.g., particles, capillaries, or assay tubes or plates).

**[00129]** Certain combinations of the novel coelenterazines and the novel luciferases provide significant technical advantages for bioluminescent assays including enhanced luminescence, wherein enhanced luminescence may be due to one or more factors including enhanced signal stability and enhanced coelenterazine stability. Additionally, many of the novel coelenterazines

were designed to be smaller than commercially-available and/or known coelenterazines. In some cases, the novel luciferases of the present invention preferentially utilize the novel, smaller coelenterazines over the commercially-available and/or known larger coelenterazines.

**[00130]** The invention encompasses combinations of: the novel luciferase variants with the novel coelenterazines; the novel luciferase variants with known or native coelenterazines; and the novel coelenterazines with any known or native protein (e.g., luciferases or photoproteins) that uses coelenterazine as a substrate.

**[00131]** The term "coelenterazine" refers to naturally-occurring ("native") coelenterazine as well as analogs thereof, including coelenterazine-n, coelenterazine-f, coelenterazine-h, coelenterazine-hcp, coelenterazine-cp, coelenterazine-c, coelenterazine-e, coelenterazine-fcp, bis-deoxycoelenterazine ("coelenterazine-hh"), coelenterazine-i, coelenterazine-icp, coelenterazine-v, and 2-methyl coelenterazine, in addition to those disclosed in WO 2003/040100 and U.S. Application Serial No. 12/056,073 (paragraph [0086]), the disclosures of which are incorporated by reference herein. The term "coelenterazine" also refers to the novel coelenterazines disclosed herein (see below). The term "known coelenterazine" refers to a coelenterazine analog known prior to the present invention.

**[00132]** The term "OgLuc" refers to a decapod luciferase protein, or a variant of such a protein, which generates light in the presence of a coelenterazine. The OgLuc protein may, in its naturally-occurring form, be a monomer or may be a subunit of a protein complex. The OgLuc used in the exemplary embodiments disclosed herein is the 19 kDa subunit from the luciferase complex of *Oplophorus gracilirostris*, although comparable polypeptides from other decapod species (including other *Oplophorus* species) could also be employed and are encompassed within the invention (see R.D. Dennell, Observations on the luminescence of bathypelagic Crustacea decapoda of the Bermuda area, *Zool. J. Linn. Soc., Lond.* **42** (1955), pp. 393–406; see also Poupin et al. Sept 1999. Inventaire documenté des espèces et bilan des formes les plus communes de la mer d'Iroise. *Rapport Scientifique du Laboratoire d'Océanographie de l'École Navale (LOEN),* Brest (83pgs), each of which is incorporated by reference herein); examples include, without limitation, luciferases of the Aristeidae family, including *Plesiopenaeus coruscans*; the Pandalidea family, including *Heterocarpus* and *Parapandalus richardi*, the Solenoceridae family, including *Hymenopenaeus debilis* and *Mesopenaeus tropicalis*; the Luciferidae family, including *Lucifer typus*; the Sergestidae family, including *Sergestes atlanticus, Sergestes arcticus, Sergestes armatus, Sergestes pediformis, Sergestes cornutus, Sergestes edwardsi, Sergestes henseni, Sergestes pectinatus, Sergestes sargassi, Sergestes similis, Sergestes vigilax, Sergia challengeri, Sergia grandis, Sergia lucens, Sergia prehensilis,*

*Sergia potens, Sergia robusta, Sergia scintillans,* and *Sergia splendens*; the Pasiphaeidae family, including *Glyphus marsupialis, Leptochela bermudensis, Parapasiphae sulcatifrons,* and *Pasiphea tarda*; the Oplophoridae family, including *Acanthephyra acanthitelsonis, Acanthephyra acutifrons, Acanthephyra brevirostris, Acanthephyra cucullata, Acanthephyra curtirostris, Acanthephyra eximia, Acanthephyra gracilipes, Acanthephyra kingsleyi, Acanthephyra media, Acanthephyra microphthalma, Acanthephyra pelagica, Acanthephyra prionota, Acanthephyra purpurea, Acanthephyra sanguinea, Acanthephyra sibogae, Acanthephyra stylorostratis, Ephyrina bifida, Ephyrina figueirai, Ephyrina koskynii, Ephyrina ombango, Hymenodora glacialis, Hymenodora gracilis, Meningodora miccyla, Meningodora mollis, Meningodora vesca, Notostomus gibbosus, Notostomus auriculatus, Oplophorus gracilirostris, Oplophorus grimaldii, Oplophorus novaezealandiae, Oplophorus spinicauda, Oplophorus foliaceus, Oplophorus spinosus, Oplophorus typus, Systellaspis braueri, Systellaspis cristata, Systellaspis debilis,* and *Systellaspis pellucida*; and the Thalassocaridae family, including *Chlorotocoides spinicauda, Thalassocaris crinita,* and *Thalassocaris lucida*.

**[00133]** The polypeptide sequence of the mature (i.e., with no signal sequence) 19 kDa subunit of the naturally-occurring form of the *Oplophorus gracilirostris* luciferase (i.e., 169 amino acids, residues 28 to 196 of BAB 13776) is given in SEQ ID NO: 1. In various embodiments, a methionine residue and a valine residue are inserted at the beginning of the synthetic OgLuc sequence (e.g., as indicated in the C1+A4E polypeptide sequence, SEQ ID NO: 3) to facilitate cloning and expression in heterologous systems. Nevertheless, for consistency, the position numbers of the various amino acid substitutions referred to herein are specified "relative to" SEQ ID NO: 1, i.e., the polypeptide sequence of the mature (with no signal sequence), native 19 kDa subunit of the *Oplophorus gracilirostris* luciferase protein complex.

**[00134]** Specifically, a protein is a decapod luciferase if, upon alignment of its amino acid sequence with SEQ ID NO: 1, the sequence identity is > 30%, preferably > 40%, and most preferably > 50%, and the protein can utilize coelenterazine as a substrate to catalyze the emission of luminescence, and the amino acid sequence beginning at the position corresponding to position 8 of SEQ ID NO: 1 is:

**[00135]** [GSAIVK]-{FE}-[FYW]-x-[LIVMFSYQ]-x-x-{K}-x-[NHGK]-x-[DE]-x-[LIVMFY]-[LIVMWF]-x-{G}-[LIVMAKRG] (SEQ ID NO. 330) (VII),

**[00136]** with no more than 5 differences, or more preferably no more than 4, 3, 2, or 1 difference, or most preferably no differences, wherein the differences occur in positions corresponding to pattern position 1, 2, 3, 5, 8, 10, 12, 14, 15, 17, or 18 of Formula (VII)

according to Table 4. Differences may also include gaps or insertions between the pattern positions of Table 4.

**[00137]** The term "variant" refers to a modified version of a starting polypeptide or polynucleotide sequence. The term "parental" is a relative term that refers to a starting sequence which is then modified. The parental sequence is generally used as a reference for the protein encoded by the resulting modified sequence, e.g., to compare the activity levels or other properties of the proteins encoded by the parental and the modified sequences. The starting sequence can be a naturally-occurring (i.e., native or wild-type) sequence. The starting sequence can also be a variant sequence which is then further modified. A polypeptide sequence is "modified" when one or more amino acids (which may be naturally-occurring or synthetic) are substituted, deleted, and/or added at the beginning, middle, and/or end of the sequence. A polynucleotide sequence is "modified" when one or more nucleotides are substituted, deleted, and/or added at the beginning, middle, and/or end of the sequence, but which may or may not alter the amino acid encoded by the sequence. In some embodiments, the modifications produce a variant that is a functional fragment of a particular OgLuc or OgLuc variant. A functional fragment is a fragment which is less than a full-length parental sequence which has the same functional activity as the full-length parental sequence. Functional activity is the ability to exhibit luminescence. In some embodiments, the modifications produce a variant that is a permuted sequence of the parental sequence, such as a circularly permuted sequence and permuted sequences comprising deletions and/or insertions.

**[00138]** Several of the OgLuc variants disclosed herein have been assigned shorthand names to facilitate discussion. The term "C1+A4E" (also referred to as "C1A4E") refers to a particular OgLuc variant with the amino acid substitutions A4E, Q11R, A33K, V44I, A54F, P115E, Q124K, Y138I, and N166R relative to SEQ ID NO: 1 (SEQ ID NOs: 2 and 3) (where the format "*x#y*" indicates a parent amino acid '*x*' at a position '#' that is changed to variant amino acid '*y*'). Variants of the C1+A4E OgLuc variant which are presented herein contain at least the amino acid substitutions found in C1+A4E, unless otherwise indicated. The term "IVY" refers to a variant of the C1+A4E OgLuc variant having additional amino acid substitutions F54I, I90V, and F77Y relative to SEQ ID NO: 1 (SEQ ID NOs: 8 and 9). The term "IV" refers to another variant of the C1+A4E OgLuc variant having additional amino acid substitutions F54I and I90V relative to SEQ ID NO: 1 (SEQ ID NOs: 14 and 15). The term "QC27" refers to yet another variant of the C1+A4E OgLuc variant having additional amino acid substitutions Q18L, F54I, L92H, and Y109F relative to SEQ ID NO: 1 (SEQ ID NOs: 4 and 5). The term "QC27-9a" refers to a variant of the QC27 OgLuc variant with additional amino acid substitutions V21L, F68Y, L72Q,

M75K, H92R, and V158F relative to SEQ ID NO: 1 (SEQ ID NOs: 6 and 7). The term "9B8" refers to a variant of the IV OgLuc variant with additional amino acid substitutions Q18L, F68Y, L72Q, and M75K relative to SEQ ID NO: 1 (SEQ ID NOs: 18 and 19). The term "9B8 opt" refers to the codon optimized version of the 9B8 variant (SEQ ID NO: 24). The term "9B8 opt+K33N" refers to a variant of the 9B8 opt variant with additional amino acid substitution K33N relative to SEQ ID NO: 1 (SEQ ID NOs: 42 and 43). The term "9B8 opt+K33N+170G" refers to a variant of the "9B8 opt+K33N" variant with an additional glycine appended to the C-terminus of the variant, i.e., 170G relative to SEQ ID NO: 1 (SEQ ID NO: 68 and 69). The terms "L27V+T39T+K43R+Y68D" and "L27V" refers to a variant of the 9B8 opt+K33N" variant with additional amino acid substitutions L27V, T39T, K43R, and Y68D relative to SEQ ID NO: 1 (SEQ ID NOs: 88 and 89). The terms "T39T+K43R+Y68D" and "V2" refers to a variant of the "9B8 opt+K33N" variant with additional amino acid substitutions T39T, K43R, and Y68D relative to SEQ ID NO: 1 (SEQ ID NOs: 92 and 93).

**[00139]** In general, "enhanced" means that the particular property (e.g., luminescence, signal stability, biocompatibility, protein stability (e.g., enzyme stability), or protein expression) is increased relative to that of the reference luciferase plus coelenterazine combination or luciferase under consideration, where the increase is at least 1%, at least 5%, at least 10%, at least 20%, at least 25%, at least 50%, at least 75%, at least 90%, at least 100%, at least 200%, at least 500%, or at least 1000% greater than the reference luciferase plus coelenterazine combination or luciferase under consideration.

**[00140]** The term "luminescence" refers to the light output of the OgLuc variant under appropriate conditions, e.g., in the presence of a suitable substrate such as a coelenterazine. The light output may be measured as an instantaneous or near-instantaneous measure of light output (which is sometimes referred to as "T=0" luminescence or "flash") at the start of the luminescence reaction, which may be initiated upon addition of the coelenterazine substrate. The luminescence reaction in various embodiments is carried out in a solution. In other embodiments, the luminescence reaction is carried out on a solid support. The solution may contain a lysate, for example from the cells in a prokaryotic or eukaryotic expression system. In other embodiments, expression occurs in a cell-free system, or the luciferase protein is secreted into an extracellular medium, such that, in the latter case, it is not necessary to produce a lysate. In some embodiments, the reaction is started by injecting appropriate materials, e.g., coelenterazine, buffer, etc., into a reaction chamber (e.g., a well of a multiwell plate such as a 96-well plate) containing the luminescent protein. In still other embodiments, the OgLuc variant and/or novel coelenterazine are introduced into a host and measurements of luminescence are

made on the host or a portion thereof, which can include a whole organism or cells, tissues, explants, or extracts thereof. The reaction chamber may be situated in a reading device which can measure the light output, e.g., using a luminometer or photomultiplier. The light output or luminescence may also be measured over time, for example in the same reaction chamber for a period of seconds, minutes, hours, etc. The light output or luminescence may be reported as the average over time, the half-life of decay of signal, the sum of the signal over a period of time, or the peak output. Luminescence may be measured in Relative Light Units (RLUs).

**[00141]** The "enhanced luminescence" of an OgLuc variant may be due to one or more of the following characteristics: enhanced light output (i.e., brightness), enhanced substrate specificity, enhanced signal stability, and/or enhanced signal duration. Enhanced signal stability includes an increase in how long the signal from a luciferase continues to luminesce, for example, as measured by the half-life of decay of the signal in a time-course. Enhanced luminescence may be determined relative to the comparable property of a luciferase such as wild-type OgLuc, an OgLuc variant protein, *Renilla* luciferase (e.g., hRluc), or firefly luciferase (e.g., Luc2 luciferase from *Photinus pyralis*) combined with a native, known, or novel substrate, as shown in the Examples below. For example, the luminescence of a given OgLuc variant in combination with a particular coelenterazine (including native, known, or novel coelenterazines) may be compared to the properties of one of OgLuc variants C1+A4E, IV, or IVY combined with any of a native, known, or novel coelenterazine disclosed herein, using one or more of the assays disclosed in the Examples below. In particular, enhanced luminescence may be determined by measuring the luminescence signal (RLU) resulting from the incubation of bacterial lysates containing OgLuc variants in question with the substrate, PBI-3939. Measurements are taken in a reagent which may contain TERGITOL™ to provide Glo-like kinetics, e.g., in which enzyme inactivation is slowed and the luminescence signal is stabilized, which is described elsewhere in the application. In some embodiments, some luciferase variants, e.g., L27V, with certain compounds, e.g., PBI-3939, provide extended duration of the luminescent emission, or glow-like kinetics, in the absence of TERGITOL™. The luminescence signal may be compared to that of a reference point such as the C1+A4E variant with coelenterazine or coelenterazine-h or *Renilla* luciferase with native coelenterazine.

**[00142]** "Enzyme stability" refers to the stability of enzyme activity (i.e., tolerance of enzymatic activity to reaction conditions). Enhanced enzyme stability refers to enhanced stability of enzyme activity (i.e., enhanced tolerance to reaction conditions). Enhanced enzyme stability includes enhanced thermal stability (e.g., stability at elevated temperatures) and chemical stability (e.g., stability in the presence of inhibitors or denaturants such as detergents,

including, e.g., TRITON™ X-100). Enzyme stability can be used as a measure of protein stability, particularly under conditions known to be disruptive of protein structure, such as high temperatures or the presence of chemical denaturants. In particular, enhanced protein stability may be determined using thermal analysis as described elsewhere in the application (e.g., in Example 28). The luminescence signal may be compared to the reference point of C1+A4E variant with coelenterazine or coelenterazine-h or *Renilla* luciferase with native coelenterazine.

**[00143]** "Biocompatibility" refers to the tolerance of a cell (e.g., prokaryotic or eukaryotic) to a luciferase and/or coelenterazine compound. Biocompatibility of a luciferase and/or coelenterazine compound is related to the stress it causes on the host cell. For example, a luciferase that is not tolerated by the cell (i.e., one that stresses a cell) may not be expressed efficiently within the cell, for example, the luciferase may be expressed within the cell, but exhibit reduced activity due to the formation of inclusion bodies by the expressed protein. Biocompatibility of a luciferase is related to the ability of the cells to tolerate the insertion of the foreign gene, i.e., a transgene containing the gene encoding the luciferase or fragment thereof, whereby the cells with the transgene do not exhibit manifestations of stress, including induction of stress response pathways, reduced rate of growth, and/or reduced viability (e.g., reduced number of living cells, reduced membrane integrity, or increased rates of apoptosis). Other indications of cell stress may include changes in gene expression, signaling pathways, and/or regulatory pathways. Enhanced biocompatibility of an OgLuc variant may be due to factors such as enhanced protein expression and/or reduced cell stress. Enhanced expression of luminescence for a particular polynucleotide encoding an OgLuc variant may be determined relative to luminescence expression levels for a polynucleotide encoding wild-type OgLuc or an OgLuc variant protein, including codon-optimized polynucleotides, where luminescence activity can be used as a means to monitor protein expression levels.

**[00144]** In particular, enhanced biocompatibility of the OgLuc variant, novel coelenterazine compound and/or a combination thereof, may be determined by measuring cell viability and/or growth rate of cells. For example, enhanced biocompatibility of the OgLuc variants may be determined by measuring cell viability and/or growth rate of cells containing the OgLuc variants compared to cells containing firefly or *Renilla* luciferase or no luciferase, in the absence of any coelenterazine compound to determine how compatible and/or toxic the luciferase is to the cells. Enhanced biocompatibility of the novel coelenterazine compounds may be determined by measuring cell viability in the absence of luciferase expression of cells exposed to the novel coelenterazine compound compared to native or known coelenterazines to determine how compatible and/or toxic the coelenterazine compound is to the cells. Enhanced biocompatibility

of a combination of an OgLuc variant with a novel coelenterazine compound may be determined by measuring cell viability and/or growth rate of cells containing the OgLuc variant and exposed to the novel coelenterazine and compared to cells containing firefly or *Renilla* luciferase or no luciferase and exposed to native or known coelenterazines.

**[00145]** In particular, enhanced biocompatibility may be determined using cell viability analysis as described elsewhere in the application (e.g., using a CELLTITER-GLO® assay as described in Example 18 or an apoptosis assay such as one using CASPASE-GLO® technology according to the manufacturer's instructions) or one known in the art. The effect of an OgLuc variant on cell viability or apoptosis may be compared to the effect of a reference luciferase, such as the C1+A4E variant, a firefly luciferase or *Renilla* luciferase. The effect of the novel coelenterazine compound on cell viability or apoptosis may be compared to the effect of native or known coelenterazine compounds on cell viability or apoptosis.

**[00146]** Enhanced biocompatibility may also be determined by measuring the effect of the OgLuc variant and/or novel coelenterazine compound on cell growth or gene expression. For examples, enhanced biocompatibility of the OgLuc variant may be determined by measuring the cell number after a period of time or by determining the expression of stress response genes in a sample of cells that contain the OgLuc variant compared to cells that contain another luciferase or no luciferase. Enhanced biocompatibility of the novel coelenterazine compound may be determined by measuring the cell number after a period of time or by determining the expression of stress response genes in a sample of cells that are exposed to the novel coelenterazine compound compared to cells exposed to native or known coelenterazines or no coelenterazines. The effect of the OgLuc variant on cell growth or gene expression may be compared to a reference luciferase, such as C1+A4E variant, a firefly luciferase or *Renilla* luciferase. The effect of the novel coelenterazine on cell growth or gene expression may be compared to native or known coelenterazines.

**[00147]** The identification of robust, stable cell lines expressing an OgLuc variant of the present invention, either in the cytoplasm or as a secreted form, can be facilitated by the bright signal of the luciferase and the small size of the OgLuc gene. The relatively small gene sequence is expected to reduce the likelihood of genetic instability resulting from the integration of the foreign DNA into a cell's genome. As a result of the increased brightness of the OgLuc variants and/or the novel coelenterazines of the present invention, less protein expression, and thereby less DNA needed for transfection, may produce a given level of brightness compared to other known luciferases such as native OgLuc, firefly, or *Renilla* luciferase, which contributes to an enhanced biocompatibility for the OgLuc variants and/or novel coelenterazines. Enhanced

biocompatibility of the OgLuc variants may be measured by the amount of DNA or reagents, e.g., transfection chemicals, needed in transient transfections to generate cells with the same level of luminescence as cells transfected with other luciferases, e.g., native OgLuc, firefly or *Renilla* luciferase. In some embodiments, the amount of OgLuc variant DNA or reagents needed for transfection is less than the amount needed for another luciferase, e.g., native OgLuc, firefly, or *Renilla* luciferase, to generate transfected cells with the same level of luminescence obtained with the other luciferase. Enhanced biocompatibility of the OgLuc variants may be measured by the recovery time of the cells after transfection. In some embodiments, the amount of time needed for recovery after transfection with the OgLuc variant is less than the time needed for another luciferase, e.g., native OgLuc, firefly or *Renilla* luciferase.

**[00148]** "Relative substrate specificity" is determined by dividing the luminescence of a luciferase in the presence of a test coelenterazine substrate by the luminescence of the luciferase in the presence of a reference coelenterazine substrate. For example, relative specificity may be determined by dividing the luminescence of a luciferase with a novel coelenterazine of the present invention by the luminescence of the luciferase with a different coelenterazine (e.g., native or known coelenterazine, see FIG. 1 for examples, or a different novel coelenterazine of the present invention). The test coelenterazine substrate and the reference coelenterazine substrate that are compared are considered a comparison substrate pair for determining relative substrate specificity.

**[00149]** A "change in relative substrate specificity" is determined by dividing the relative substrate specificity of a test luciferase using a comparison substrate pair by the relative substrate specificity of a reference luciferase using the same comparison substrate pair. For example, a change in relative specificity may be determined by dividing the relative substrate specificity of a test luciferase with a novel coelenterazine of the present invention compared to a different coelenterazine (e.g., native or known coelenterazine or a different novel coelenterazine of the present invention), by the relative substrate specificity of a reference luciferase with the same novel coelenterazine of the present invention compared to the same different coelenterazine used for the test luciferase.

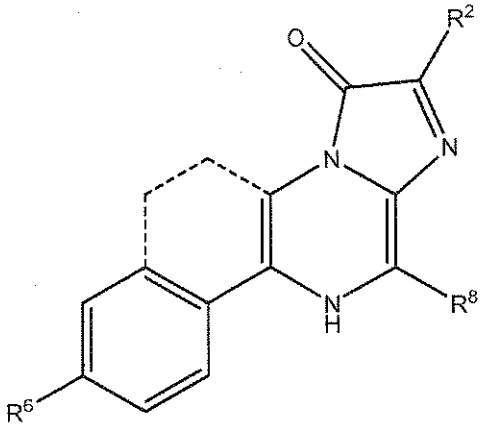
**[00150]** In some embodiments, the luminescence with one novel coelenterazine is compared to the luminescence with a different novel coelenterazine. In some embodiments, the luminescence with one native or known coelenterazine is compared to the luminescence with another native or known coelenterazine. In still other embodiments, the luminescence with one native or known coelenterazine is compared to the luminescence with a novel coelenterazine.

**[00151]** The novel coelenterazines of the present invention include properties such as enhanced physical stability (e.g., enhanced coelenterazine stability) or reduced autoluminescence. The physical stability of the coelenterazine refers to how stable the coelenterazine is in certain conditions such that it maintains the ability to luminesce when used as a substrate by a luciferase. Luminescence that is not dependent on the activity of a luciferase or photoprotein is termed autoluminescence. Autoluminescence is the luminescence of a substance produced by energy released in the form of light during decay or decomposition. For example, autoluminescence can be caused by spontaneous oxidation of the luminogenic substrate coelenterazine.

**[00152]** As used herein, "pure" or "purified" means an object species is the predominant species present (i.e., on a molar and/or mass basis, it is more abundant than any other individual species, apart from water, solvents, buffers, or other common components of an aequeous system in the composition), and, in some embodiments, a purified fraction is a composition wherein the object species comprises at least about 50% (on a molar basis) of all macromolecular species present. Generally, a "substantially pure" composition will comprise more than about 80% of all macromolecular species present in the composition, in some embodiments more than about 85%, more than about 90%, more than about 95%, or more than about 99%. In some embodiments, the object species is purified to essential homogeneity (contaminant species cannot be detected in the composition by conventional detection methods) wherein the composition consists essentially of a single macromolecular species.

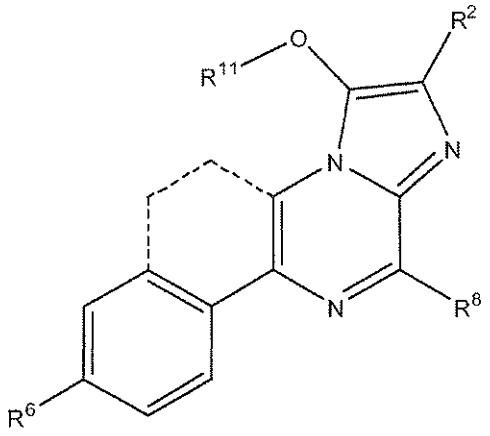
***Coelenterazine Derivatives***

**[00153]** In some embodiments, the present invention provides novel coelenterazine derivatives of formula (Ia) or (Ib):



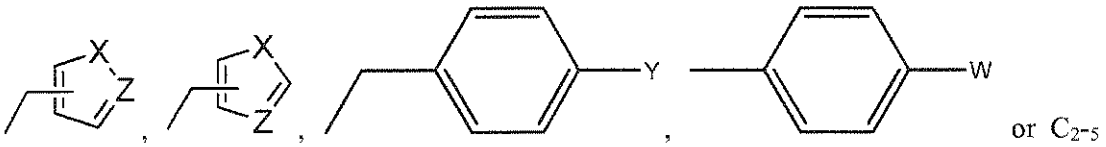

(Ia)

or



(Ib)

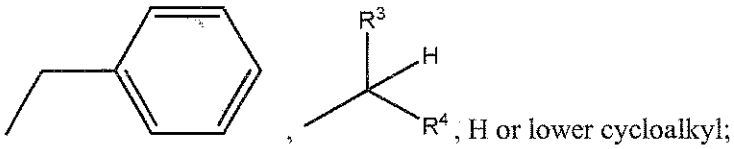
wherein $R^2$ is selected from the group consisting of



straight chain alkyl;

$R^6$ is selected from the group consisting of -H, -OH, $-NH_2$, -OC(O)R or $-OCH_2OC(O)R$;

$R^8$ is selected from the group consisting of



, H or lower cycloalkyl;

wherein $R^3$ and $R^4$ are both H or both $C_{1-2}$ alkyl;

W is $-NH_2$, halo, -OH, -NHC(O)R, $-CO_2R$;

X is –S-, –O- or $–NR^{22}$-;

Y is –H, -OH, or $–OR^{11}$;

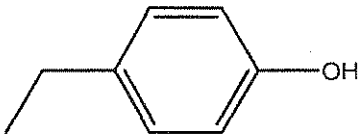
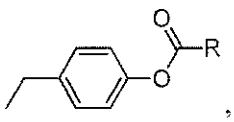
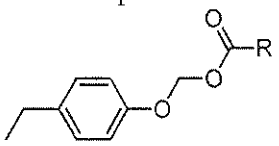
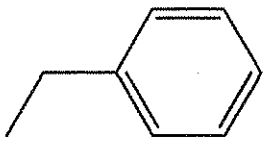
Z is –CH- or –N-;

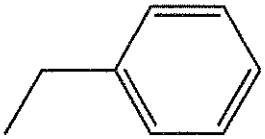
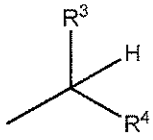
each $R^{11}$ is independently –C(O)R'' or $–CH_2OC(O)R''$;

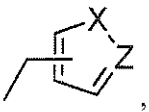
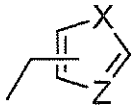
$R^{22}$ is H, $CH_3$, or $CH_2CH_3$
each R is independently $C_{1-7}$ straight-chain alkyl or $C_{1-7}$ branched alkyl;

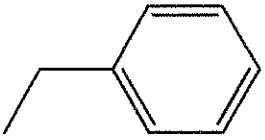
R'' is $C_{1-7}$ straight-chain alkyl or $C_{1-7}$ branched alkyl;

the dashed bonds indicate the presence of an optional ring, which may be saturated or unsaturated;

with the proviso that when $R^2$ is  ,  , or  , $R^8$ is not  ;

with the proviso that when $R^2$ is  , $R^8$ is  or lower cycloalkyl; and

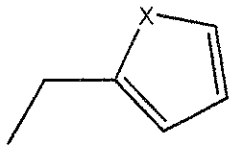
with the proviso that when $R^6$ is $NH_2$, $R^2$ is  ,  , or $C_{2-5}$ alkyl;

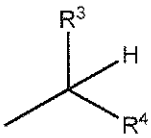
or $R^8$ is not  .

**[00154]** The term "alkyl", as used herein, pertains to a monovalent moiety obtained by removing a hydrogen atom from a hydrocarbon compound, and which may be saturated, partially unsaturated, or fully unsaturated. The alkyl group may be a straight-chain or branched. An alkyl group may be optionally substituted with, for example, halo. Examples of straight-chain alkyl groups include, but are not limited to, ethyl, n-propyl, n-butyl, and n-propyl, n-hexyl and n-heptyl. Examples of unsaturated alkyl groups which have one or more carbon-carbon double bonds include, but are not limited to, ethenyl (vinyl,-CH=$CH_2$), 2-propenyl (allyl, -CH-CH=$CH_2$), and butenyl. Examples of unsaturated alkyl which have one or more carbon-carbon triple bonds include, but are not limited to, ethynyl and 2-propynyl (propargyl). Examples of branched alkyl groups included isopropyl, iso-butyl, sec-butyl, t-butyl and iso-pentyl.

**[00155]** The term "lower cycloalkyl", as used herein, pertains to a monovalent moiety obtained by removing a hydrogen atom from a hydrocarbon compound having from 3 to 5 carbon atoms. Examples of saturated lower cycloalkyl groups include, but are not limited to, groups such as cyclopropyl, cyclobutyl and cyclopentyl. Examples of unsaturated lower cycloalkyl groups which have one or more carbon-carbon double bonds include, but are not limited to, groups such as cyclopropenyl, cyclobutenyl and cyclopentenyl.

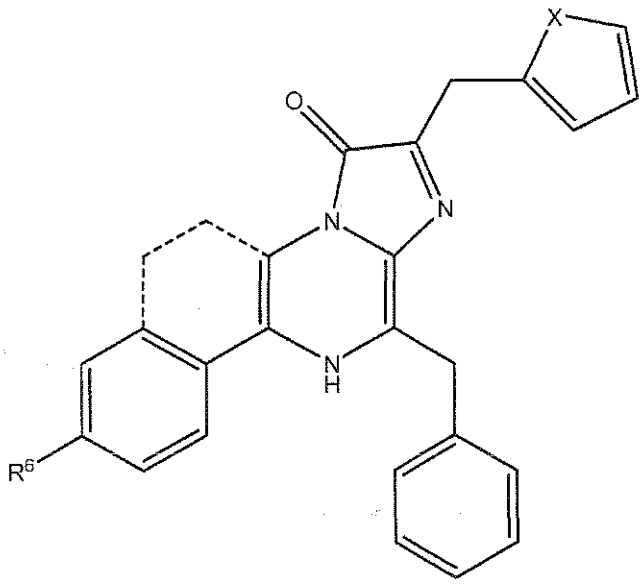
**[00156]** The term "halo", as used herein, pertains to a halogen, such as Cl, F, Br or I.

**[00157]** In some embodiments, $R^2$ is 

; and X is O or S. In other embodiments, $R^2$ is $C_{2\text{-}5}$ straight chain alkyl. In certain embodiments, $R^8$ is 

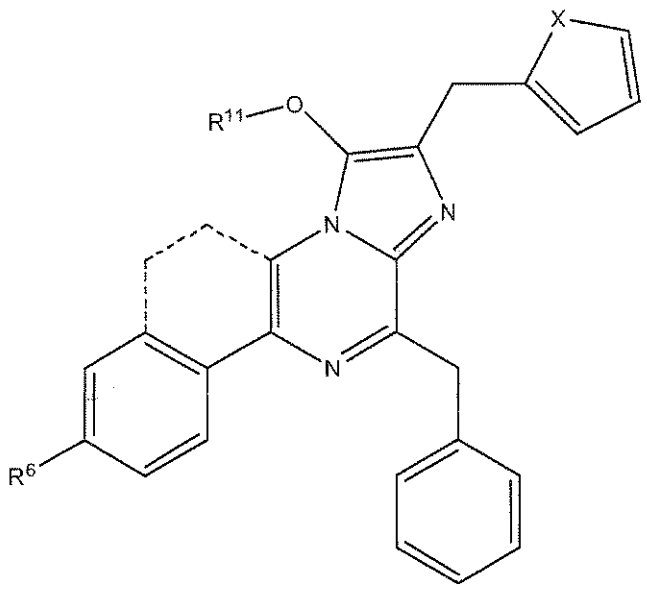
, lower cycloalkyl or H. In other embodiments, $R^8$ is benzyl. In some embodiments, R'' is $-C(CH_3)_3$, $-CH(CH_3)_2$, $-CH_2C(CH_3)_3$, or $-CH_2CH(CH_3)_2$.

**[00158]** In some embodiments, the present invention provides compounds according to Formula (IIa) or (IIb):




(IIa)

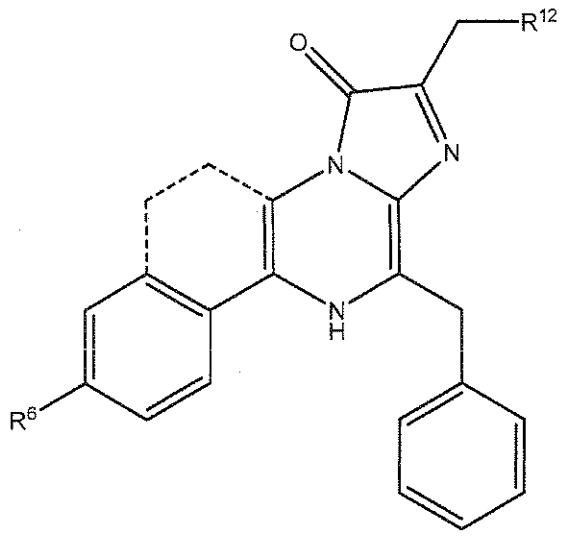
or



(IIb)

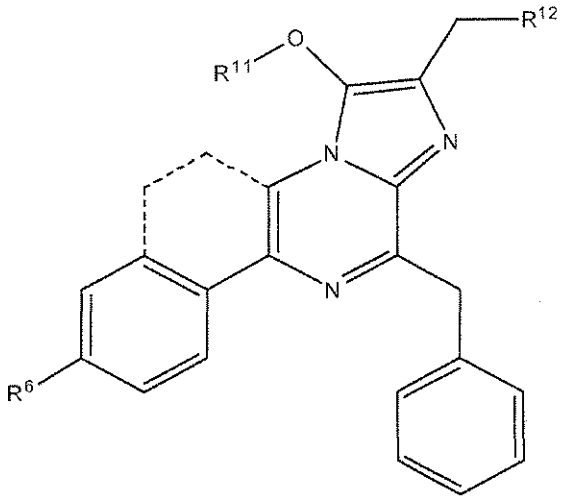
wherein X is O or S, $R^6$ is H or OH, $R^{11}$ is as defined above, and the dashed bonds indicate the presence of an optional ring.

**[00159]** In some embodiments, the invention provides compounds according to Formula (IIIa) or (IIIb):



(IIIa)

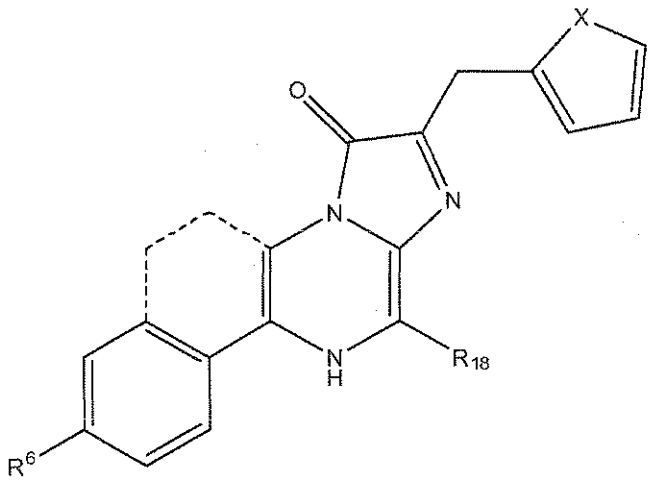
or



(IIIb)

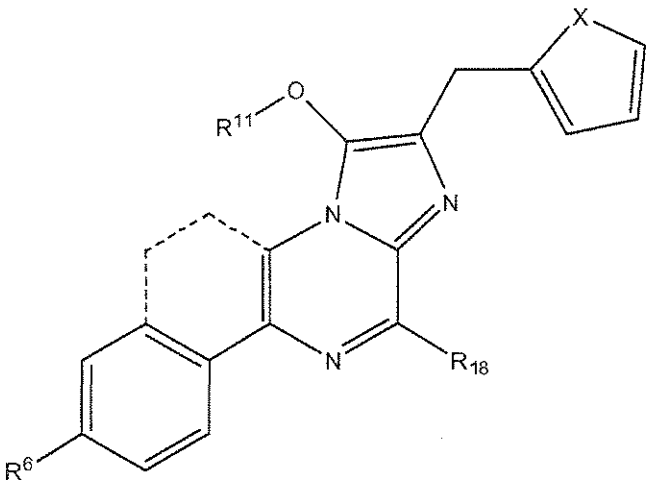
wherein $R^{12}$ is $C_{2-5}$ straight-chain alkyl, furyl or thienyl, $R^6$ is H or OH, $R^{11}$ is as defined above, and the dashed bonds indicate the presence of an optional ring.

**[00160]** In some embodiments, the invention provides compounds according to Formula (IVa) or (IVb):

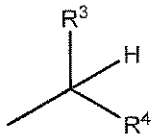


(IVa)

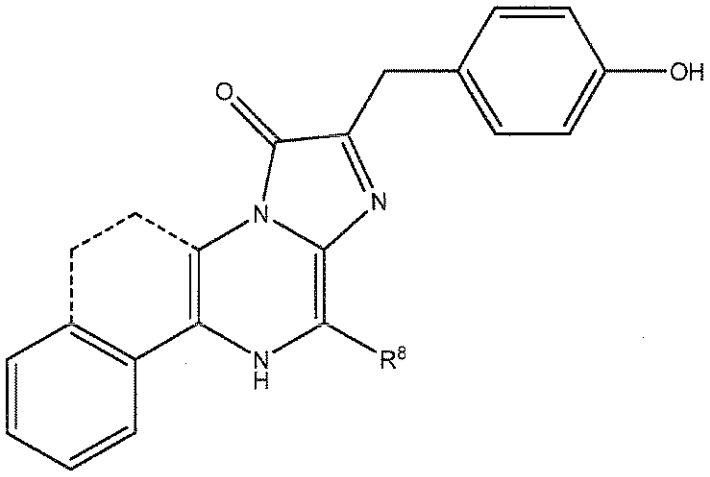
or



(IVb)

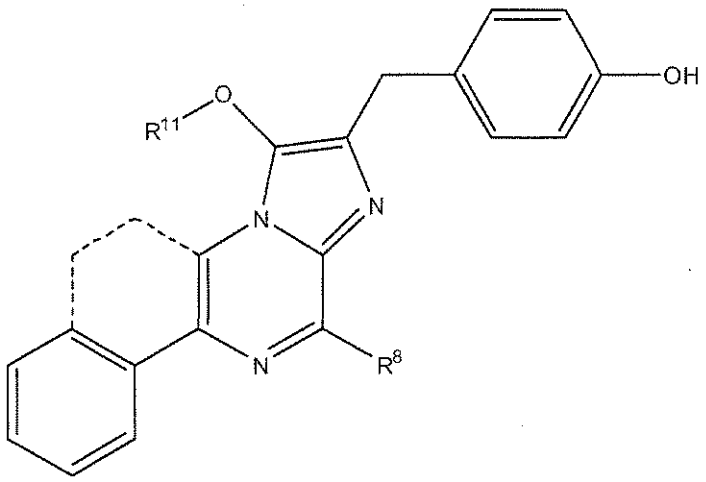
wherein X is O or S, $R^6$ is H or OH, $R^{18}$ is H,  or lower cycloalkyl, $R^3$, $R^4$ and $R^{11}$ are as defined above, and the dashed bonds indicate the presence of an optional ring.

**[00161]** In some embodiments, the invention provides a compound according to Formula (Va) or (Vb):



(Va)

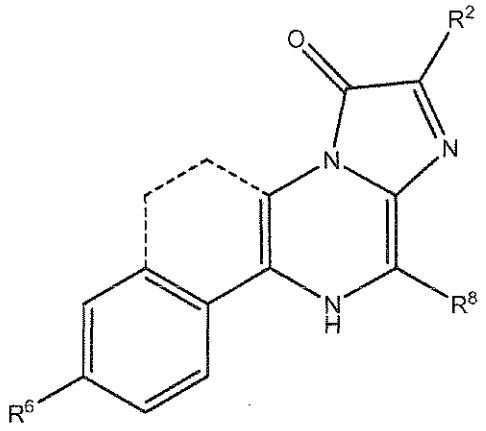
or




(Vb)

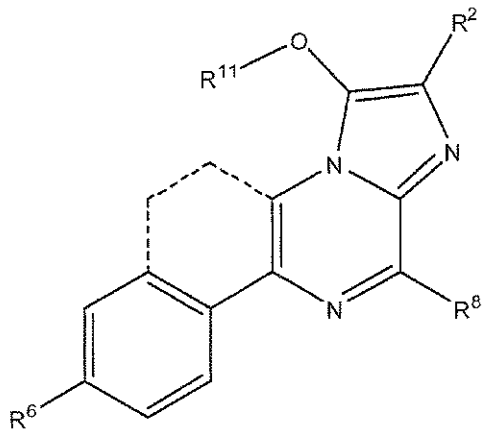
wherein $R^8$ is benzyl, $R^{11}$ is as defined above, and the dashed bonds indicate the presence of an optional ring.

**[00162]** In some embodiments, the present invention provides novel coelenterazine derivatives of formula (VIa) or (VIb):



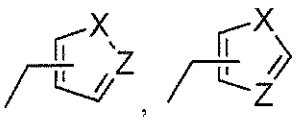

(VIa)

or

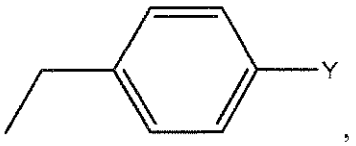


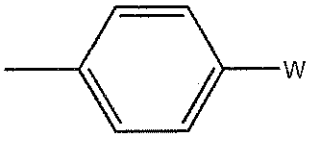

(VIb)

wherein $R^2$ is selected from the group consisting of



, 

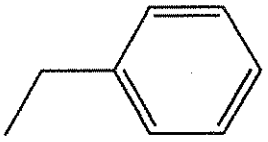
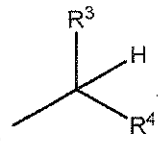
, 

, 

or $C_{2-5}$ straight chain alkyl;

$R^6$ is selected from the group consisting of -H, -OH, $-NH_2$, -OC(O)R or $-OCH_2OC(O)R$;

$R^8$ is selected from the group consisting of


, 

, H or lower cycloalkyl;

wherein $R^3$ and $R^4$ are both H or both $C_{1-2}$ alkyl;

W is $-NH_2$, halo, -OH, -NHC(O)R, $-CO_2R$;

X is –S-, –O- or –NH-;

Y is –H, -OH, or $–OR^{11}$;

Z is –CH- or –N-;

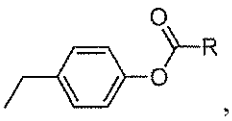
each $R^{11}$ is independently –C(O)R'' or $–CH_2OC(O)R''$;

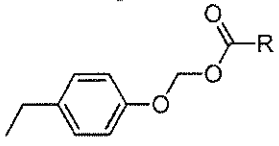
each R is independently $C_{1-7}$ straight-chain alkyl or $C_{1-7}$ branched alkyl;

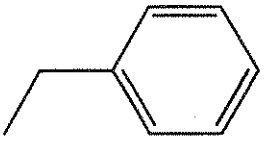
R'' is $C_{1-7}$ straight-chain alkyl or $C_{1-7}$ branched alkyl;

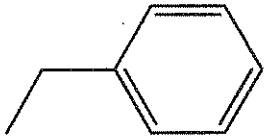
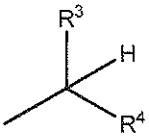
the dashed bonds indicate the presence of an optional ring, which may be saturated or unsaturated;

with the proviso that when $R^2$ is

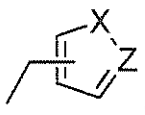
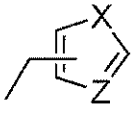
, 

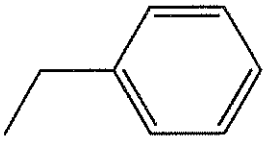
, or 

, $R^8$ is not 
;

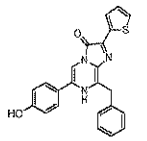
with the proviso that when $R^2$ is 
, $R^8$ is 

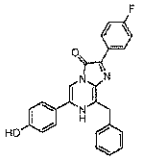
or lower cycloalkyl; and

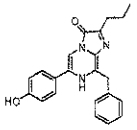
with the proviso that when $R^6$ is $NH_2$, $R^2$ is  ,  , or $C_{2-5}$ alkyl;

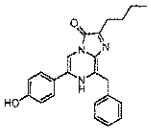
or $R^8$ is not  .

**[00163]** Suitable compounds according to the present invention include


3882


3881


3899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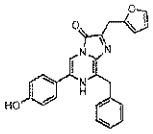
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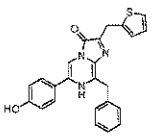
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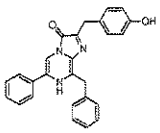
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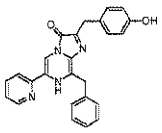
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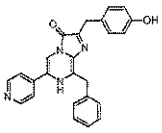
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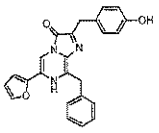
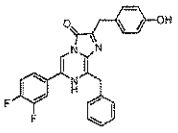

3887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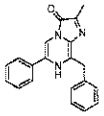
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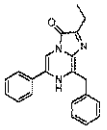
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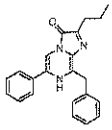
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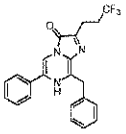
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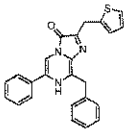
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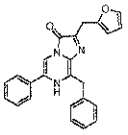
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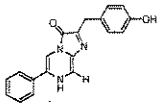
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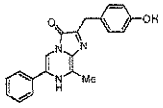
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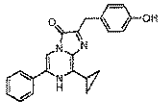
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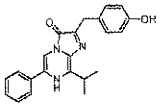
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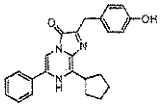
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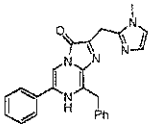
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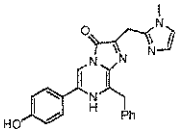
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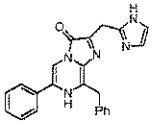
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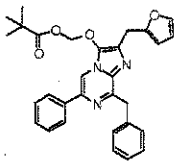


*Isomers, Salts and Protected Forms*

**[00164]** Certain compounds may exist in one or more particular geometric, optical, enantiomeric, diasteriomeric, epimeric, stereoisomeric, tautomeric, conformational, or anomeric forms, including but not limited to, cis- and trans-forms; E- and Z-forms; c-, t-, and r- forms; endo and exo-forms; R-, S-, and meso-forms; D- and L-forms; d- and l-forms; (+) and (-) forms; keto-, enol-, and enolate- forms; syn- and anti-forms; synclinal- and anticlinal-forms; α- and β-

forms; axial and equatorial forms; boat-, chair-, twist-, envelope-, and half-chair forms; and combinations thereof, hereinafter collectively referred to as "isomers" (or "isomeric forms").

**[00165]** Note that, except as discussed below for tautomeric forms, specifically excluded from the term "isomers", as used herein, are structural (or constitutional) isomers (i.e., isomers which differ in the connections between atoms rather than merely by the position of atoms in space). For example, a reference to a methoxy group, $-OCH_3$, is not to be construed as a reference to its structural isomer, a hydroxymethyl group, $-CH_2OH$. Similarly, a reference to ortho-chlorophenyl is not to be construed as a reference to its structural isomer, meta-chlorophenyl. However, a reference to a class of structures may well include structurally isomeric forms falling within that class (e.g., $C_{1-7}$ alkyl includes n-propyl and iso-propyl; butyl includes n-, iso-, sec-, and tert-butyl; methoxyphenyl includes ortho-, meta-, and paramethoxyphenyl).

**[00166]** Note that specifically included in the term "isomer" are compounds with one or more isotopic substitutions. For example, H may be in any isotopic form, including $^{1}H$, $^{2}H$ (D), and $^{3}H$ (T); C may be in any isotopic form, including $^{12}C$, $^{13}C$, and $^{14}C$; O may be in any isotopic form, including $^{16}O$ and $^{18}O$; and the like.

**[00167]** Unless otherwise specified, a reference to a particular compound includes all such isomeric forms, including (wholly or partially) racemic and other mixtures thereof. Methods for the preparation (e.g., asymmetric synthesis) and separation (e.g., fractional crystallization and chromatographic means) of such isomeric forms are either known in the art or are readily obtained by adapting the methods taught herein, or known methods, in a known manner.

**[00168]** Unless otherwise specified, a reference to a particular compound also includes ionic, salt, solvate, and protected forms of thereof, for example, as discussed below. It may be convenient or desirable to prepare, purify, and/or handle a corresponding salt of the active compound, for example, a pharmaceutically-acceptable salt. Examples of pharmaceutically acceptable salts are discussed in Berge *et al.*, *J. Pharm. Sci.*, **66**:1-19 (1977).

**[00169]** For example, if the compound is anionic, or has a functional group which may be anionic (e.g., -COOH may be -COO-), then a salt may be formed with a suitable cation. Examples of suitable inorganic cations include, but are not limited to, alkali metal ions such as $Na^+$ and $K^+$, alkaline earth cations such as $Ca^{2+}$ and $Mg^{2+}$, and other cations such as $Al^{3+}$. Examples of suitable organic cations include, but are not limited to, ammonium ion (i.e., $NH^{4+}$) and substituted ammonium ions (e.g., $NH_3R^+$, $NH_2R_2^+$, $NHR_3^+$, $NR_4^+$). Examples of some suitable substituted ammonium ions are those derived from: ethylamine, diethylamine,

dicyclohexylamine, triethylamine, butylamine, ethylenediamine, ethanolamine, diethanolamine, piperazine, benzylamine, phenylbenzylamine, choline, meglumine, and tromethamine, as well as amino acids, such as lysine and arginine. An example of a common quaternary ammonium ion is $N(CH_3)_4^+$.

**[00170]** If the compound is cationic, or has a functional group which may be cationic (e.g., -$NH_2$ may be -$NH_3^+$), then a salt may be formed with a suitable anion. Examples of suitable inorganic anions include, but are not limited to, those derived from the following inorganic acids: hydrochloric, hydrobromic, hydroiodic, sulfuric, sulfurous, nitric, nitrous, phosphoric, and phosphorous. Examples of suitable organic anions include, but are not limited to, those derived from the following organic acids: acetic, propionic, succinic, glycolic, stearic, palmitic, lactic, malic, pamoic, tartaric, citric, gluconic, ascorbic, maleic, hydroxymaleic, phenylacetic, glutamic, aspartic, benzoic, cinnamic, pyruvic, salicyclic, sulfanilic, 2-acetyoxybenzoic, fumaric, phenylsulfonic, toluenesulfonic, methanesulfonic, ethanesulfonic, ethane disulfonic, oxalic, pantothenic, isethionic, valeric, lactobionic, and gluconic. Examples of suitable polymeric anions include, but are not limited to, those derived from the following polymeric acids: tannic acid, carboxymethyl cellulose.

**[00171]** It may be convenient or desirable to prepare, purify, and/or handle a corresponding solvate of the active compound. The term "solvate" is used herein in the conventional sense to refer to a complex of solute (e.g., active compound, salt of active compound) and solvent. If the solvent is water, the solvate may be conveniently referred to as a hydrate, for example, a mono-hydrate, a di-hydrate, a tri-hydrate, etc.

**[00172]** It may be convenient or desirable to prepare, purify, and/or handle the active compound in a chemically protected form. The term "chemically protected form", as used herein, pertains to a compound in which one or more reactive functional groups are protected from undesirable chemical reactions, that is, are in the form of a protected or protecting group (also known as a masked or masking group or a blocked or blocking group). By protecting a reactive functional group, reactions involving other unprotected reactive functional groups can be performed, without affecting the protected group; the protecting group may be removed, usually in a subsequent step, without substantially affecting the remainder of the molecule. See, for example, Protective Groups in Organic Synthesis (T. Green and P. Wuts, Wiley, 1999).

**[00173]** For example, a hydroxy group may be protected as an ether (-OR) or an ester (-OC(=O)R), for example, as: a t-butyl ether; a benzyl, benzhydryl (diphenylmethyl), or trityl (triphenylmethyl) ether; a trimethylsilyl or t-butyldimethylsilyl ether; or an acetyl ester (-

$OC(=O)CH_3$, -OAc). For example, an aldehyde or ketone group may be protected as an acetal or ketal, respectively, in which the carbonyl group (>C=O) is converted to a diether ($>C(OR)_2$), by reaction with, for example, a primary alcohol. The aldehyde or ketone group is readily regenerated by hydrolysis using a large excess of water in the presence of acid. For example, an amine group may be protected, for example, as an amide or a urethane, for example, as: a methyl amide (-NHCO-$CH_3$); a benzyloxy amide (-NHCO-$OCH_2C_6H_5$, -NHCbz); as a t-butoxy amide (-NHCO-$OC(CH_3)_3$, -NH-Boc); a 2-biphenyl-2-propoxy amide (-NHCO-$OC(CH_3)_2C_6H_4C_6H_5$, -NH-Bpoc), as a 9-fluorenylmethoxy amide (-NH-Fmoc), as a 6-nitroveratryloxy amide (-NH-Nvoc), as a 2-trimethylsilylethyloxy amide (-NH-Teoc), as a 2,2,2-trichloroethyloxy amide (-NH-Troc), as an allyloxy amide (-NH-Alloc), as a 2(-phenylsulphonyl)ethyloxy amide (-NH-Psec); or, in suitable cases, as an N-oxide.

**[00174]** For example, a carboxylic acid group may be protected as an ester for example, as: an $C_{1-7}$ alkyl ester (e.g., a methyl ester; a t-butyl ester); a $C_{1-7}$ haloalkyl ester (e.g., a $C_{1-7}$ trihaloalkylester); a tri$C_{1-7}$ alkylsilyl-$C_{1-7}$ alkyl ester; or a $C_{5-20}$ aryl-$C_{1-7}$ alkyl ester (e.g., a benzyl ester; a nitrobenzyl ester); or as an amide, for example, as a methyl amide.

**[00175]** For example, a thiol group may be protected as a thioether (-SR), for example, as: a benzyl thioether; an acetamidomethyl ether (-S-$CH_2NHC(=O)CH_3$).

***Synthesis of Coelenterazine Derivatives***

**[00176]** Coelenterazine derivatives according to the present invention may be synthesized according those methods detailed in Examples 1-16.

***Mutant Oplophorus Luciferases***

**[00177]** In embodiments of the present invention, various techniques as described herein were used to identify sites for amino acid substitution to produce an improved synthetic OgLuc polypeptide. Additional techniques were used to optimize codons of the polynucleotides encoding the various polypeptides in order to enhance expression of the polypeptides. It was found that making one or more amino acid substitutions, either alone or in various combinations, produced synthetic OgLuc-type polypeptides having enhanced luminescence (e.g., enhanced brightness, enhanced signal stability, enhanced enzyme stability, and/or change in relative substrate specificity). Furthermore, including one or more codon-optimizing substitutions in the polynucleotides which encode for the various synthetic OgLuc variant polypeptides produced enhanced expression of the polypeptides in various eukaryotic and prokaryotic expression

systems. One embodiment of the present invention is a polynucleotide that encodes a synthetic OgLuc variant polypeptide which is soluble and active in the monomeric form when expressed in prokaryotic and/or eukaryotic cells.

**[00178]** The OgLuc variants of the present invention may be coupled to any protein of interest or molecule of interest. In some embodiments, the variants are fusion proteins, for example some variants are coupled to a HaloTag® polypeptide attached at either the N-terminus or the C-terminus. Unless otherwise noted, the variants that are HaloTag® fusions include 'HT7' as part of the name, e.g., 'IVY-HT7'. In some embodiments, a signal sequence (e.g., the naturally-occurring *Oplophorus gracilirostris* signal sequence) is attached to the N-terminus of the fusion protein to facilitate the secretion of the fusion protein from the cell. Signal sequences, other than the naturally-occuring signal sequence of OgLuc luciferase, are known in the art to facilitate protein secretion in mammalian cells or other cell types. Signal sequences, in combination with membrane anchoring sequences, may be used to position or display OgLuc variants on the outer surface of the cellular membrane. Other methods, known in the art may also be used to position OgLuc variants to the membrane or other locations within the cell.

**[00179]** In some embodiments, the invention provides a modified decapod luciferase which has enhanced luminescence relative to a corresponding parental variant decapod luciferase. For example, the parental, variant OgLuc is C1+A4E, IVY, IV, QC27, QC27-9a, 9B8, 9B8 opt+K33N, 9B8 opt+K33N+170G, V2 or "L27V". In another embodiment, the invention provides a modified decapod luciferase which utilizes a novel coelenterazine. In one embodiment, the modified decapod luciferase has a change in relative specificity for native, known or novel coelenterazines. In one embodiment, the modified decapod luciferase has a change in relative specificity relative to a corresponding parental, variant decapod luciferase.

**[00180]** In some embodiments, the corresponding parental, variant decapod luciferase is a decapod species, including various species from families within the decapod order including, without limitation, luciferases of the Aristeidae family, including *Plesiopenaeus coruscans*; the Pandalidea family, including *Heterocarpus* and *Parapandalus richardi*, the Solenoceridae family, including *Hymenopenaeus debilis* and *Mesopenaeus tropicalis*; the Luciferidae family, including *Lucifer typus*; the Sergestidae family, including *Sergestes atlanticus, Sergestes arcticus, Sergestes armatus, Sergestes pediformis, Sergestes cornutus, Sergestes edwardsi, Sergestes henseni, Sergestes pectinatus, Sergestes sargassi, Sergestes similis, Sergestes vigilax, Sergia challengeri, Sergia grandis, Sergia lucens, Sergia prehensilis, Sergia potens, Sergia robusta, Sergia scintillans,* and *Sergia splendens*; the Pasiphaeidae family, including *Glyphus marsupialis, Leptochela bermudensis, Parapasiphae sulcatifrons,* and *Pasiphea tarda*; the

Oplophoridae family, including *Acanthephyra acanthitelsonis, Acanthephyra acutifrons, Acanthephyra brevirostris, Acanthephyra cucullata, Acanthephyra curtirostris, Acanthephyra eximia, Acanthephyra gracilipes, Acanthephyra kingsleyi, Acanthephyra media, Acanthephyra microphthalma, Acanthephyra pelagica, Acanthephyra prionota, Acanthephyra purpurea, Acanthephyra sanguinea, Acanthephyra sibogae, Acanthephyra stylorostratis, Ephyrina bifida, Ephyrina figueirai, Ephyrina koskynii, Ephyrina ombango, Hymenodora glacialis, Hymenodora gracilis, Meningodora miccyla, Meningodora mollis, Meningodora vesca, Notostomus gibbosus, Notostomus auriculatus, Oplophorus gracilirostris, Oplophorus grimaldii, Oplophorus novaezealandiae, Oplophorus spinicauda, Oplophorus foliaceus, Oplophorus spinosus, Oplophorus typus, Systellaspis braueri, Systellaspis cristata, Systellaspis debilis,* and *Systellaspis pellucida*; and the Thalassocaridae family, including *Chlorotocoides spinicauda, Thalassocaris crinita,* and *Thalassocaris lucida*. In certain embodiments, the modified luciferase has increased luminescence emission, e.g., at least 1.3-fold, at least 2-fold, or at least 4-fold, in a prokaryotic cell and/or a eukaryotic cell relative to the corresponding wild-type luciferase. In some embodiments, one or more properties of the modified decapod luciferase is compared to comparable properties of a luciferase from another species, e.g., a firefly luciferase or a *Renilla* luciferase.

**[00181]** In some embodiments, the OgLuc variant has at least 60%, e.g., at least 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99%, or 100%, amino acid sequence identity to SEQ ID NOs: 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 27, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 56, 58, 60, 62, 64, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, or 95. In some embodiments, the OgLuc variant, or a functional fragment thereof, has no more than 5 differences, or more preferably, no more than 4, 3, 2, or 1 difference, or most preferably no differences, wherein the differences occur in positions corresponding to pattern position 1, 2, 3, 5, 8, 10, 12, 14, 15, 17, or 18 of Formula (VII) according to Table 4. Differences may also include gaps or insertions between the pattern positions of Table 4.

**[00182]** In some embodiments, the OgLuc variant of the invention has one or more heterologous amino acid sequences at the N-terminus, C-terminus, or both (a fusion polypeptide such as one with an epitope or fusion tag), which optionally directly or indirectly interact with a molecule of interest. In some embodiments, the presence of the heterologous sequence(s) does not substantially alter the luminescence of the OgLuc variant either before or after the interaction with the molecule of interest. In some embodiments, the heterologous amino acid sequence is an epitope tag. In some embodiments, the heterologous amino acid sequence is one which, during or after interaction with a molecule of interest, undergoes a conformational change, which in turn

alters the activity of the OgLuc variant e.g., an OgLuc variant with such an amino acid sequence is useful to detect allosteric interactions. The OgLuc variant or a fusion with the OgLuc variant or a fragment thereof may be employed as a reporter.

**[00183]** In some embodiments, a fragment of an OgLuc variant of the invention is fused to a heterologous amino acid sequence, the fusion thereby forming a beta-barrel, which fusion protein is capable of generating luminescence from a naturally-occurring coelenterazine or an analog thereof including the various known coelenterazines discussed herein, or a novel coelenterazine of the present invention.

**[00184]** Also provided is a polynucleotide encoding an OgLuc variant of the invention or a fusion thereof, an isolated host cell having the polynucleotide or the OgLuc variant or a fusion thereof, and methods of using the polynucleotide, OgLuc variant or a fusion thereof or host cell of the invention.

**[00185]** The term "identity," in the context of two or more nucleic acids or polypeptide sequences, refers to two or more sequences or subsequences that are the same or have a specified percentage of amino acid residues or nucleotides that are the same when compared and aligned for maximum correspondence over a comparison window or designated region as measured using any number of sequence comparison algorithms or by manual alignment and visual inspection. Methods of alignment of sequence for comparison are well-known in the art. Optimal alignment of sequences for comparison can be conducted by the algorithm of Smith *et al.*, (*J. Mol. Biol.* **147**:195-197 (1981)), by the homology alignment algorithm of Needleman and Wunsch, (*J. Mol. Biol.*, **48**:443-453 (1970)), by the search for similarity method of Pearson and Lipman, (*Proc. Natl. Acad. Sci. USA*, **85**:2444-2448 (1988)), by computerized implementations of algorithms e.g., FASTA, SSEARCH, GGSEARCH (available at the University of Virginia FASTA server by William R. Pearson http://fasta.bioch.virginia.edu/fasta_www2/fasta_intro.shtml), the Clustal series of programs (Chenna *et al.*, *Nucl. Acids Res.* **31(13)**:3497-3500 (2003); available examples at http://www.ebi.ac.uk or http://www.ch.embnet.org), or other sequence analysis software. It is known in the art that generating alignments with maximum correspondence between polypeptide sequences with significant sequence alterations (e.g., altered domain order, missing/added domains, repeated domains, shuffled domains, circular permutation) may involve the use of specialized methods, such as the ABA method (Raphael *et al.*, *Genome Res.* **14(11)**:2336-2346 (2004)), other suitable methods, or performing the alignment with two concatenated identical copies of the polypeptide sequences.

**[00186]** The term "nucleic acid molecule," "polynucleotide" or "nucleic acid sequence" as used herein, refers to nucleic acid, including DNA or RNA, that comprises coding sequences necessary for the production of a polypeptide or protein precursor. The encoded polypeptide may be a full-length polypeptide, a fragment thereof (less than full-length), or a fusion of either the full-length polypeptide or fragment thereof with another polypeptide, yielding a fusion polypeptide.

**[00187]** A polynucleotide encoding a protein or polypeptide means a nucleic acid sequence comprising the coding region of a gene, or in other words, the nucleic acid sequence encoding a gene product. The coding region may be present in a cDNA, genomic DNA or RNA form. When present in a DNA form, the oligonucleotide may be single stranded (e.g., the sense strand) or double stranded. Suitable control elements such as enhancers/promoters, splice junctions, polyadenylation signals, etc. may be placed in close proximity to the coding region of the gene if needed to permit proper initiation of transcription and/or correct processing of the primary RNA transcript. Other control or regulatory elements include, but are not limited to, transcription factor binding sites, splicing signals, polyadenylation signals, termination signals and enhancer elements.

**[00188]** By "peptide," "protein" and "polypeptide" is meant amino acid chains of varying lengths, regardless of post-translational modification (e.g., glycosylation or phosphorylation). The nucleic acid molecules of the invention encode a variant of a man made (i.e., synthetic) variant protein or polypeptide fragment thereof, which has an amino acid sequence that is at least 60%, e.g., at least 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100%, amino acid sequence identity to the amino acid sequence of the parental protein from which it is derived, where the parental protein can be a naturally-occurring (native or wild-type) sequence or a variant sequence which is subsequently modified further. The term "fusion polypeptide" or "fusion protein" refers to a chimeric protein containing a reference protein (e.g., OgLuc variant) joined at the N- and/or C-terminus to one or more heterologous sequences (e.g., a non-OgLuc polypeptide). The heterologous sequence can include, but is not limited to, reporter proteins such as the HALOTAG® fusion protein (Promega Corp.), FlAsH (fluorescein arsenical helix binder), and ReAsH (red arsenical helix binder) (e.g., LUMIO™ tag recognition sequence (Invitrogen)), chloramphenicol acetyltransferase (CAT), β-galactosidase (β-Gal), lactamase (P-gal), neomycin resistance (Neo), GUS, galactopyranoside, green fluorescent protein (GFP), luciferase (e.g., a *Renilla reniformis* luciferase, a firefly luciferase (e.g., *Photinus pyralis* or *Photuris pennsylvanica*), or a click beetle luciferase (e.g., *Pyrophorus plagiophthalamus or Pyrearinus termitilluminans*) or a glowworm luciferase (e.g., *Phrixothrix hirtus*), xylosidase, thymidine

kinase, arabinosidase and SNAP-tag, CLIP-tag, ACP-tag and MCP-tag (New England Biolabs). In one embodiment, a chimeric protein contains an OgLuc variant joined at the N-terminus to a HALOTAG® fusion protein (Promega Corp.). In another embodiment, a chimeric protein contains an OgLuc variant joined at the C-terminus to a HALOTAG® fusion protein.

**[00189]** Nucleic acids are known to contain different types of "mutations", which refers to an alteration in the sequence of a nucleotide at a particular base position relative to the wild-type sequence. Mutations may also refer to insertion or deletion of one or more bases so that the nucleic acid sequence differs from a reference, e.g., a wild-type sequence, or replacement with a stop codon. A "substitution" refers to a change in an amino acid at a particular position in a sequence, e.g., a change from A to E at position 4.

**[00190]** The term "vector" refers to nucleic acid molecules into which fragments of DNA may be inserted or cloned and can be used to transfer DNA segment(s) into a cell and capable of replication in a cell. Vectors may be derived from plasmids, bacteriophages, viruses, cosmids, and the like.

**[00191]** The term "wild-type" or "native" as used herein, refers to a gene or gene product that has the characteristics of that gene or gene product isolated from a naturally occurring source. A wild-type gene is that which is most frequently observed in a population and is thus arbitrarily designated the "wild-type" form of the gene. In contrast, the term "mutant" refers to a gene or gene product that displays modifications in sequence and/or functional properties (i.e., altered characteristics) when compared to the wild-type gene or gene product. It is noted that naturally occurring mutants can be isolated; these are identified by the fact that they have altered characteristics when compared to the wild-type gene or gene product.

***Exemplary Polynucleotides and Proteins***

**[00192]** The invention includes an OgLuc variant or protein fragments thereof, e.g., those with deletions, for instance a deletion of 1 to about 5 residues, and chimeras (fusions) thereof (see U.S. Patent Publication No. 2009/0253131 and WIPO Publication No. WO 2007/120522, the disclosures of which are incorporated by reference herein) having at least one amino acid substitution relative to a wild-type OgLuc, which substitution results in the OgLuc variant having enhanced stability, enhanced luminescence, e.g., increased luminescence emission, greater stability of the luminescence kinetics, and/or altered luminescence color. The sequences of an OgLuc variant are substantially the same as the amino acid sequence of a corresponding wild-type OgLuc. A polypeptide or peptide having substantially the same sequence means that an

amino acid sequence is largely, but is not entirely, the same and retains the functional activity of the sequence to which it is related. In general, two amino acid sequences are substantially the same if they are at least 60%, e.g., at least 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99%, but less than 100%, amino acid sequence identity. In some embodiments, the OgLuc variant is encoded by a recombinant polynucleotide. In some embodiments, the OgLuc variant, or a functional fragment thereof, has no more than 5 differences, or more preferably no more than 4, 3, 2, or 1 difference, or most preferably no differences, wherein the differences occur in positions corresponding to pattern position 1, 2, 3, 5, 8, 10, 12, 14, 15, 17, or 18 of Formula (VII) according to Table 4. Differences may also include gaps, insertions, or permutations between the pattern positions of Table 4.

**[00193]** The OgLuc variant proteins or fusion proteins of the invention may be prepared by recombinant methods or by solid phase chemical peptide synthesis methods. Such methods are known in the art.

***Methods of Use and Kits***

**[00194]** The compounds and proteins of the invention may be used in any way that luciferases and luciferase substrates, e.g., coelenterazines, have been used. For example, they may be used in a bioluminogenic method which employs an analog of coelenterazine to detect one or more molecules in a sample, e.g., an enzyme, a cofactor for an enzymatic reaction, an enzyme substrate, an enzyme inhibitor, an enzyme activator, or OH radicals, or one or more conditions, e.g., redox conditions. The sample may include an animal (e.g., a vertebrate), a plant, a fungus, physiological fluid (e.g., blood, plasma, urine, mucous secretions and the like), a cell, a cell lysate, a cell supernatant, or a purified fraction of a cell (e.g., a subcellular fraction). The presence, amount, spectral distribution, emission kinetics, or specific activity of such a molecule may be detected or quantified. The molecule may be detected or quantified in solution, including multiphasic solutions (e.g., emulsions or suspensions), or on solid supports (e.g., particles, capillaries, or assay vessels). In some embodiments the OgLuc variant can be used in luminescence-based assays to detect an enzyme of interest, e.g., CYP450 enzyme, MAO A or B enzyme, a caspase, etc. The novel coelenterazines could be used with photoproteins such as aequorin, obelin, or iPhotina. In some embodiment, the OgLuc variant can be used as an energy donor to another molecule (e.g., to a fluorophore, a chromophore, or a nanoparticle).

**[00195]** The invention also provides a polynucleotide encoding a transcriptional reporter. In some embodiments, the OgLuc variant or fragment thereof could be operably linked to transcription regulatory sequences, e.g., one or more enhancer, a promoter, a transcription

termination sequence or a combination thereof, to form an expression cassette. For example, the OgLuc variant could be operably linked to a minimal promoter and a cAMP-response element (CRE).

**[00196]** The proteins of the invention may be used as biosensors, e.g., an OgLuc variant, which, in the presence of another molecule (e.g, one or more molecules of interest), or under certain conditions, has one or more altered activities. Upon interacting with a molecule of interest or being subject to certain conditions, the biosensor undergoes a conformational change or is chemically altered which causes an alteration of the enzyme activity or luminescence, e.g., specific activity, spectral distribution, or emission kinetics. For example, the OgLuc variant of the present invention, for example a circularly permuted variant, can comprise an interaction domain for a molecule of interest. Alternatively, for example, the OgLuc variant may be coupled to an energy acceptor, for example a fluorescent protein, and comprise an interaction domain that alters the efficiency of energy transfer from the enzyme to the energy acceptor. For example, the biosensor could be generated to detect proteases, kinases, a ligand, a binding protein such as an antibody, cyclic nucleotides such as cAMP or cGMP, or a metal such as calcium, by insertion of a suitable sensor region into the OgLuc variant sequence. One or more sensor region can be inserted at the C-terminus, the N-terminus, and/or at one or more suitable location in the polypeptide sequence, where the sensor region comprises one or more amino acids. In the case of a circularly-permuted OgLuc variant, the sensor region may be inserted between the N- and C-termini of the parent OgLuc variant. In addition, one or all of the inserted sensor regions may include linker amino acids to couple the sensor to the remainder of the OgLuc variant polypeptide. Examples of luciferase biosensors are disclosed in U.S. Pat. Appl. Publ. Nos. 2005/0153310 and 2009/0305280 and PCT Publ. No. WO 2007/120522 A2, each of which is incorporated by reference herein.

**[00197]** In various embodiments, the OgLuc variants disclosed herein may be used to transfer energy to an energy acceptor, for example in Bioluminescence Resonance Energy Transfer (BRET) analysis. For example, the OgLuc variants used in BRET analysis can be used to determine if two molecules are capable of binding each other or co-localize in a cell. For example, an OgLuc variant can be used as a bioluminescence donor molecule which is combined with a molecule or protein of interest to create a first fusion protein. In various embodiments, the first fusion protein contains an OgLuc variant and a protein of interest. In various embodiments, the first fusion proteins containing the OgLuc variant can be used in BRET analysis to detect protein/protein interaction in systems including but not limited to cell lysates, intact cells, and living animals. In various embodiments, HALOTAG® can be used as a fluorescent acceptor

molecule. In some embodiments, HALOTAG® can be fused to a second protein of interest or to an OgLuc variant. For example, an OgLuc variant can be fused to HALOTAG®, expressed in cells or animals, and labeled with a fluorescent HALOTAG® ligand such as HALOTAG® TMR ligand. The fusion can subsequently be excited to fluoresce in the presence of a cell-permeant OgLuc substrate. In some embodiments, BRET may be performed using OgLuc variants in combination with fluorescent proteins, including but not limited to Green Fluorescent Protein (GFP) or Red Fluorescent Protein (RFP) or fluorescent labels including fluorescein, rhodamine green, Oregon green, or Alexa 488, to name a few non-limiting examples.

**[00198]** In various embodiments, the OgLuc variants and/or the novel coelenterazines of the present invention may be used in protein complementation assays (PCA) to detect the interaction of two biomolecules, e.g., polypeptides. For example, an OgLuc variant of the present invention can be separated into two fragments at a site(s) tolerant to separation and each fragment of the separated OgLuc variant can be fused to one of a pair of polypeptides of interest believed to interact, e.g., FKBP and FRB. If the two polypeptides of interest do in fact interact, the OgLuc fragments then come into close proximity with each other to reconstitute the functional, active OgLuc variant. In some embodiments, the activity of the reconstituted OgLuc variant can then be detected and measured using a native or known coelenterazine or a novel coelenterazine of the present invention. In some embodiments, the split OgLuc variant can be used in a more general complementation system similar to lac-Z (Langley *et al., PNAS* 72:1254-1257 (1975)) or ribonuclease S (Levit and Berger, *J. Biol. Chem.* **251**:1333 –1339 (1976)). In some embodiments, an OgLuc variant fragment (designated "A") known to complement with another OgLuc variant fragment ("B") can be fused to a target protein, and the resulting fusion can be monitored via luminescence in a cell or cell lysate containing fragment B. In some embodiments, the source of fragment B could be the same cell (e.g., if the gene for fragment B is integrated into the genome of the cell or is contained on another plasmid within the cell) or it could be a lysate or purified protein derived from another cell. In some embodiments, this same fusion protein (fragment A) could be captured or immobilized using a fusion between fragment B and a polypeptide such as HALOTAG® capable of attachment to a solid support. In some embodiments, luminescence can be used to demonstrate successful capture or to quantify the amount of material captured.

**[00199]** In various embodiments, the OgLuc variants and/or the novel coelenterazines of the present invention may be used to quantify coelenterazine. In some embodiments, a coelenterazine (e.g., a native or known coelenterazine, or a novel coelenterazine of the present invention) can be used as a probe of a specific biochemical activity, e.g., apoptosis and drug

metabolism. In some embodiments, the coelenterazine concentration is coupled to a specific enzyme activity by a "pro-coelenterazine" or "pro-substrate" that can be acted on by the specific enzyme of interest. In some embodiments, the pro-coelenterazine is a molecule that cannot support luminescence directly when combined with luciferase, but can be converted into coelenterazine through catalytic processing by a specific enzyme of interest. In some embodiments, the approach can be used for enzymes such as those used in drug metabolism, e.g., cytochrome P450 enzymes, monoamine oxidase, and glutathione S-transferase; and apoptosis, e.g., caspases. For example, coelenterazine (e.g., a native or known coelenterazine, or a novel coelenterazine of the present invention) can be modified to contain a cleavable group, such as 6'-O-methyl. In some embodiments, when incubated with a specific cytochrome P450 enzyme, the 6'O-methyl is cleaved, and the pro-coelenterazine converted to coelenterazine which can be detected with an OgLuc variant of the present invention. In some embodiments, the pro-coelenterazine can be combined with other components necessary to support luminescence, e.g., luminescent protein such as an OgLuc variant of the present invention, to provide a single reagent and a homogeneous assay. For example, when the reagent is added to a sample, luminescence is generated as pro-coelenterazine is converted to coelenterazine. In various embodiments, similar assays can be developed for other enzymes, small molecules, or other cellular processes that can be linked to the generation of coelenterazines from pro-coelenterazines.

**[00200]** In various embodiments, the OgLuc variants and/or the novel coelenterazines of the present invention may be used as genetic transcriptional reporter systems. In some embodiments, the OgLuc variants can be multiplexed with a luciferase that emits light at a different wavelength, e.g., red click beetle luciferase (CHROMA-LUC™; Promega Corp.). For example, if an OgLuc variant of the present invention is used as a functional reporter, then the red CHROMA-LUC™ luciferase could be used to control for non-specific effects on genetic regulation or to normalize for transfection efficiency. In some embodiments, luminescence generated from the OgLuc variant (approximately 460 nm) and red CHROMA-LUC™ (approximately 610 nm) can be easily resolved using a luminometer with wavelength-discriminating filters, enabling the measurement of both signals from the same sample. In another example, an OgLuc variant of the present invention could be used as a transcriptional reporter and paired with a luciferase that emits light at a different wavelength contained in an assay reagent. For example, an OgLuc variant of the present invention could be used as transcriptional reporter and paired with either aequorin or a cAMP circularly-permuted firefly luciferase biosensor, or both simultaneously, to detect multiple pathways in a single sample. In such a system, for example, aequorin could be used for the detection and/or measurement of calcium, the biosensor for the detection and/or

measurement of cAMP, and an OgLuc variant for monitoring of downstream gene expression. In another example, an OgLuc variant may be used with one or more additional luciferases, where the luminescence of each luciferase may be separately measured through the use of selective enzyme inhibitors. For example, the luminescence of a first luciferase may be measured upon addition of appropriate substrates and buffers, followed by measurement of a second luciferase upon a subsequent addition of appropriate substrates and buffers and one or more inhibitors selective for the first luciferase. In another example, the luciferase contained in an assay reagent may be used for measuring a specific aspect of cellular physiology, for example ATP to estimate cell viability, or caspase activity to estimate cellular apoptosis.

**[00201]** In various embodiments, the OgLuc variants of the present invention may be used as reporters in difficult to transfect cell lines or perhaps even in non-dividing primary cells, e.g., stem cells or HepG2 cells. Due to their high signal intensity, the OgLuc variants of the present invention will enable detectable luminescence when transfection efficiency is low. In some embodiments, the OgLuc variants can be used as reporters in cells that are especially sensitive to conditions associated with transfection, e.g., which are sensitive to elevated DNA concentrations or the addition of transfection reagent. Thus, in various embodiments, due to the enhanced luminescence of the OgLuc variants of the present invention, an adequate level of luminescence can be achieved using lower DNA concentrations, less transfection reagent, and/or shorter post-transfection times prior to beginning an assay so that there is a reduced toxicity burden on sensitive cells. In various embodiments, the enhanced luminescence of the OgLuc variants will also allow for a signal to be detected at much later time points. In still other embodiments, the OgLuc variants could be used as reporters for single-copy native promoters.

**[00202]** In various embodiments, the OgLuc variants of the present invention may be used as fusion tags for a target protein of interest as a way to monitor intracellular levels of the target protein. In some embodiments, the OgLuc variants can be used to monitor specific proteins involved in stress response pathways (e.g., DNA damage, oxidative stress, inflammation) in cells as a way to probe the role various types of stimuli may play in these pathways. In some embodiments, the OgLuc variants can also be used as a means to monitor cellular trafficking of a target protein. For example, the OgLuc variants can also be fused to viral genomes (e.g., HIV, HCV) so that titer levels, i.e., infectivity, can be monitored in cells following treatment with potential antiviral agents. In some embodiments, the variants can also be fused to green fluorescent protein (GFP) or HALOTAG® (in addition to a target protein) for fluorescence activated cell sorting (FACS) to identify high expression clones.

**[00203]** In various embodiments, identification of robust, stable cell lines expressing an OgLuc variant of the present invention, either in the cytoplasm or as a secreted form, can be facilitated by the enhanced signal of the OgLuc variant and the small size of the OgLuc gene. The relatively small gene sequence should reduce the likelihood of genetic instability resulting from the integration of the foreign DNA into a cell's genome.

**[00204]** In various embodiments, the OgLuc variants of the present invention can be integrated into a variety of different immunoassay concepts. For example, an OgLuc variant can be fused to a primary or secondary antibody to provide a method of detection for a particular analyte. As another example, an OgLuc variant can be fused to protein A or protein G, and the fusion could then be used to detect a specific antibody bound to a particular analyte. As another example, an OgLuc variant can be fused to streptavidin and used to detect a specific biotinylated antibody bound to a particular analyte. As yet another example, complementary fragments of an OgLuc variant can be fused to primary and secondary antibodies, where the primary antibody recognizes a particular analyte, and the secondary antibody recognizes the primary antibody. In some embodiments, the OgLuc variant activity would be reconstituted in the presence of analyte. As still another example, an OgLuc variant can be conjugated to an analyte (e.g., prostaglandins) and used in a competitive sandwich ELISA format. The OgLuc variant conjugated to an analyte may also be used to detect antibodies capable of binding the analyte, where the binding activity allows the OgLuc variant to be selectively linked to the antibody. An example using Renilla luciferase for quantitatively measuring patient antibody titers to an antigenic target is the Luciferase Immunoprecipitation System (Burbelo *et al.*, Expert Review of Vaccines **9(6)**:567-578 (2010))

**[00205]** In various embodiments, the OgLuc variants and novel substrates of the present invention can be used for detecting luminescence in live cells. In some embodiments, an OgLuc variant can be expressed in cells (as a reporter or otherwise), and the cells treated with a coelenterazine, e.g., a novel coelenterazine such as PBI-3939, which will permeate cells in culture, react with the OgLuc variant and generate luminescence. In addition to being cell permeant, PBI-3939 shows comparable biocompatibility to native coelenterazine in terms of cell viability. In some embodiments, a version of PBI-3939 containing chemical modifications known to increase the stability of native coelenterazine in media can be synthesized and used for more robust, live cell OgLuc variant-based reporter assays. In still other embodiments, a sample (including cells, tissues, animals, etc.) containing an OgLuc variant and/or a novel coelenterazine of the present invention may be assayed using various microscopy and imaging techniques. In

still other embodiments, a secretable OgLuc variant is expressed in cells as part of a live-cell reporter system.

**[00206]** In various embodiments, the OgLuc variants and/or novel coelenterazines disclosed herein may be provided as part of a kit. The kit may include one or more OgLuc variants as disclosed herein (in the form of a polypeptide, a polynucleotide, or both) and/or a coelenterazine, along with suitable reagents and instructions to enable a user to perform assays such as those disclosed herein. The coelenterazine may be any of the native, known, or novel coelenterazines disclosed herein. The kit may also include one or more buffers, such as those disclosed herein.

***Vectors and Host Cells Encoding the Modified Luciferase or Fusions Thereof***

**[00207]** Once a desirable nucleic acid molecule encoding an OgLuc variant or a fragment thereof, such as one with luminescence activity or which may be complemented by another molecule to result in luminescence activity, or a fusion thereof with luminescence activity, is prepared, an expression cassette encoding the OgLuc variant or a fragment thereof, e.g., one for complementation, or a fusion thereof with luminescence activity, may be prepared. For example, a nucleic acid molecule comprising a nucleic acid sequence encoding an OgLuc variant is optionally operably linked to transcription regulatory sequences, e.g., one or more enhancers, a promoter, a transcription termination sequence or a combination thereof, to form an expression cassette. The nucleic acid molecule or expression cassette may be introduced to a vector, e.g., a plasmid or viral vector, which optionally includes a selectable marker gene, and the vector introduced to a cell of interest, for example, a prokaryotic cell such as *E. coli, Streptomyces* spp., *Bacillus* spp., *Staphylococcus* spp. and the like, as well as eukaryotic cells including a plant (dicot or monocot), fungus (including yeast, e.g., *Pichia*, *Saccharomyces* or *Schizosaccharomyces*), or a mammalian cell, lysates thereof, or to an *in vitro* transcription/translation mixture. Mammalian cells include but are not limited to bovine, caprine, ovine, canine, feline, non-human primate, e.g., simian, and human cells. Mammalian cell lines include, but are not limited to, CHO, COS, HEK293, HeLa, CV-1, SH-SY5Y, and NIH 3T3 cells, although numerous other cell lines can also be used as well.

**[00208]** The expression of an encoded OgLuc variant may be controlled by any promoter capable of expression in prokaryotic cells or eukaryotic cells including synthetic promoters. Prokaryotic promoters include, but are not limited to, SP6, T7, T5, *tac*, *bla*, *trp*, *gal*, *lac* or maltose promoters, including any fragment that has promoter activity. Eukaryotic promoters include, but are not limited to, constitutive promoters, e.g., viral promoters such as CMV, SV40 and RSV promoters, as well as regulatable promoters, e.g., an inducible or repressible promoter

such as the tet promoter, the hsp70 promoter and a synthetic promoter regulated by CRE, including any fragment that has promoter activity. The expression of an encoded OgLuc variant may also be controlled by post-transcriptional processes, such as by regulation of RNA processing or regulation of translation, for example by RNAi, miRNA, shRNA, siRNA, or by RNA or protein degradation. The nucleic acid molecule, expression cassette and/or vector of the invention may be introduced to a cell by any method including, but not limited to, calcium-mediated transformation, electroporation, microinjection, lipofection, and the like.

***Optimized Sequences, and Vectors and Host Cells Encoding the OgLuc Variants***

**[00209]** Also provided is an isolated nucleic acid molecule (polynucleotide) comprising a nucleic acid sequence encoding an OgLuc variant of the invention, a functional fragment thereof or a fusion protein thereof. In some embodiments, the isolated nucleic acid molecule comprises a nucleic acid sequence which is optimized for expression in at least one selected host. Optimized sequences include sequences which are codon optimized, i.e., codons which are employed more frequently in one organism relative to another organism, e.g., a distantly related organism, as well as modifications to add or modify Kozak sequences and/or introns, and/or to remove undesirable sequences, for instance, potential transcription factor binding sites. Such optimized sequences can provide enhanced expression, e.g., increased levels of protein expression, when introduced into a host cell. Examples of optimized sequences are disclosed in U.S. Pat. No. 7,728,118 and U.S. Pat. Appl. Publ. Nos. 2008/0070299, 2008/0090291, and 2006/0068395, each of which is incorporated by reference herein.

**[00210]** In some embodiments, the polynucleotide includes a nucleic acid sequence encoding an OgLuc variant of the invention, which nucleic acid sequence is optimized for expression in a mammalian host cell. In some embodiments, an optimized polynucleotide no longer hybridizes to the corresponding non-optimized sequence, e.g., does not hybridize to the non-optimized sequence under medium or high stringency conditions. The term "stringency" is used in reference to the conditions of temperature, ionic strength, and the presence of other compounds, under which nucleic acid hybridizations are conducted. With "high stringency" conditions, nucleic acid base pairing will occur only between nucleic acid fragments that have a high frequency of complementary base sequences. Thus, conditions of "medium" or "low" stringency are often used when it is desired that nucleic acids that are not completely complementary to one another be hybridized or annealed together. The art knows well that numerous equivalent conditions can be employed to comprise medium or low stringency conditions.

**[00211]** In some embodiments, the polynucleotide has less than 90%, e.g., less than 80%, nucleic acid sequence identity to the corresponding non-optimized sequence and optionally encodes a polypeptide having at least 60%, e.g., at least 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100%, amino acid sequence identity with the polypeptide encoded by the non-optimized sequence. Constructs, e.g., expression cassettes, and vectors comprising the isolated nucleic acid molecule, e.g., with optimized nucleic acid sequence, as well as kits comprising the isolated nucleic acid molecule, construct or vector are also provided.

**[00212]** A nucleic acid molecule comprising a nucleic acid sequence encoding an OgLuc variant of the invention, a fragment thereof or a fusion thereof is optionally optimized for expression in a particular host cell and also optionally operably linked to transcription regulatory sequences, e.g., one or more enhancers, a promoter, a transcription termination sequence or a combination thereof, to form an expression cassette.

**[00213]** In some embodiments, a nucleic acid sequence encoding an OgLuc variant of the invention, a fragment thereof or a fusion thereof is optimized by replacing codons, e.g., at least 25% of the codons in a parental OgLuc sequence with codons which are preferentially employed in a particular (selected) cell. Preferred codons have a relatively high codon usage frequency in a selected cell, and preferably their introduction results in the introduction of relatively few transcription factor binding sites for transcription factors present in the selected host cell, and relatively few other undesirable structural attributes. Examples of undesirable structural attributes include, but not limited to, restriction enzyme sites, eukaryotic sequence elements, vertebrate promoter modules and transcription factor binding sites, response elements, *E. coli* sequence elements, mRNA secondary structure. Thus, the optimized nucleic acid product may have an improved level of expression due to improved codon usage frequency, and a reduced risk of inappropriate transcriptional behavior due to a reduced number of undesirable transcription regulatory sequences.

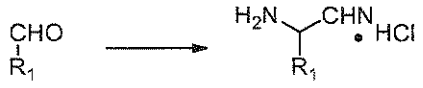
**[00214]** An isolated and optimized nucleic acid molecule may have a codon composition that differs from that of the corresponding wild-type nucleic acid sequence at more than 30%, 35%, 40% or more than 45%, e.g., 50%, 55%, 60% or more of the codons. Exemplary codons for use in the invention are those which are employed more frequently than at least one other codon for the same amino acid in a particular organism and, in some embodiments, are also not low-usage codons in that organism and are not low-usage codons in the organism used to clone or screen for the expression of the nucleic acid molecule. Moreover, codons for certain amino acids (i.e., those amino acids that have three or more codons), may include two or more codons that are employed more frequently than the other (non-preferred) codon(s). The presence of codons in

the nucleic acid molecule that are employed more frequently in one organism than in another organism results in a nucleic acid molecule which, when introduced into the cells of the organism that employs those codons more frequently, is expressed in those cells at a level that is greater than the expression of the wild-type or parent nucleic acid sequence in those cells.

**[00215]** In some embodiments of the invention, the codons that are different are those employed more frequently in a mammal, while in still other embodiments, the codons that are different are those employed more frequently in a plant. Preferred codons for different organisms are known to the art, e.g., see http://www.kazusa.or.jp./codon/. A particular type of mammal, e.g., a human, may have a different set of preferred codons than another type of mammal. Likewise, a particular type of plant may have a different set of preferred codons than another type of plant. In one embodiment of the invention, the majority of the codons that differ are ones that are preferred codons in a desired host cell. Preferred codons for organisms including mammals (e.g., humans) and plants are known to the art (e.g., Wada *et al.*, *Nucl. Acids Res.*, **18**:2367 (1990); Murray *et al.*, *Nucl. Acids Res.*, 17:477 (1989)).

**EXAMPLES**

**Reference Example 1 – Synthesis of α-Aminonitrile (Compound 1)**:

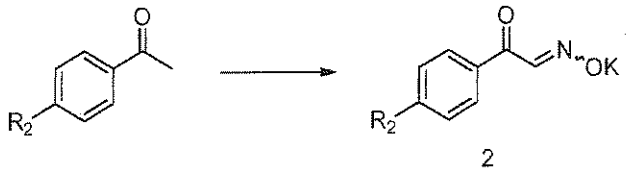



1

**[00216]** A flask was charged with sodium bisulfite (71.4 mmol) and 17 mL of water. To this, a solution of aldehyde (69.3 mmol) in 14 mL of tetrahydrofuran (THF) was added dropwise at a rate that kept the internal temperature below 60°C. The resulting suspension was stirred at ambient temperature for 40 min, and ammonium hydroxide solution (4.85 mL) added over 2 min. The resulting solution was magnetically stirred while being heated in an oil bath at 60°C for 1 hr and then left at ambient temperature overnight. The solution was cooled in an ice/saltwater bath until the internal temperature measured below 5°C. To this, a solution of sodium cyanide (71.4 mmol) in 14 mL of water was added dropwise over 30 min. The resulting mixture was stirred at approximately 10°C for 20 min, 30°C for 2 hrs, and at ambient temperature for 18 hrs. The reaction mixture was extracted into three 200 mL portions of diethyl ether, and the combined extracts dried over anhydrous sodium sulfate. The mixture was filtered, and the solution cooled in an ice bath for 20 min. To the stirred solution, hydrogen chloride gas was added until precipitation ceased, and the suspension stirred for 1 hr. The solid was isolated by filtration and

rinsed with three 50 mL portions of diethyl ether. The material was dried under vacuum, and 6.4 g (47.5 mmol) of a white solid was obtained (69%). Procedure was adapted from: Freifelder and Hasbrouck, "Synthesis of Primary 1,2-Diamines by Hydrogenation of alpha-Aminonitriles," *Journal of the American Chemical Society,* 82(3):696-698 (1960).

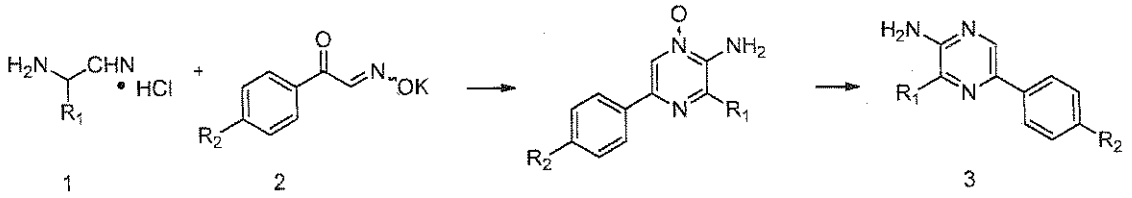
**Reference Example 2 – Synthesis of 2-oxo-2-phenylacetaldehyde oxime (Compound 2):**




2

**[00217]** A flask was charged with potassium tert-butoxide (58 mmol) and 63 mL of tert-butyl alcohol. The mixture was stirred until a solution was formed, and a solution of the appropriate benzophenone (50 mmol) in 35 mL of tert-butyl alcohol added dropwise over 15 min. The reaction mixture was stirred for 1 hr, and the neat isoamyl nitrite (75 mmol) added over five min. The reaction mixture was monitored for completion and then diluted with 100 mL of heptanes. The resulting solid (38 mmol) was collected via suction filtration and dried to a constant weight under vacuum. Procedure was adapted from: Hagedorn *et al.*, *Chem. Ber.*, 98:193 (1965).

**Reference Example 3 – Synthesis of Pyrazine derivatives (Compound 3)**



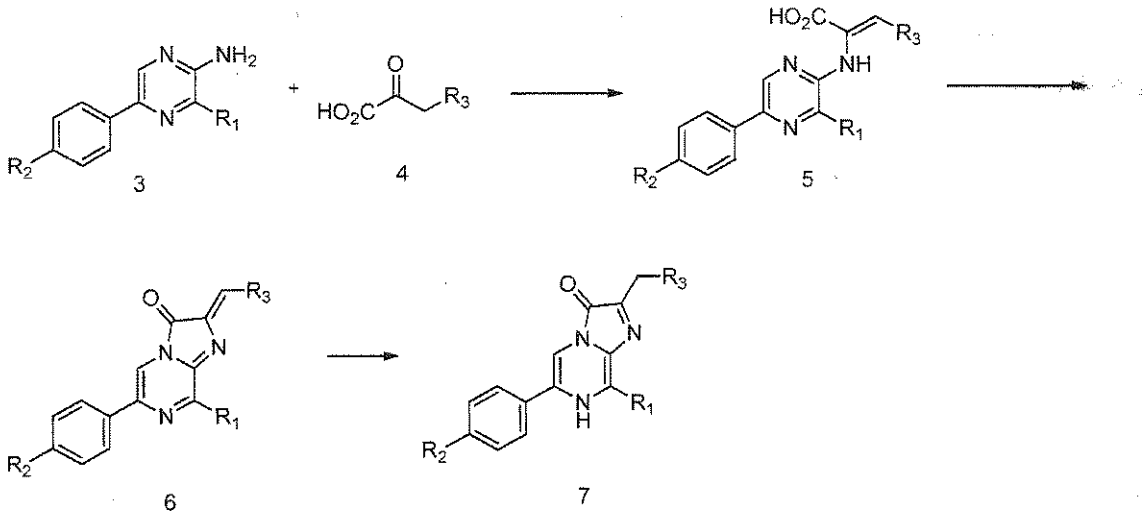

1 2 3

**[00218]** A 3-neck flask was fitted with a thermometer, septum, and argon line. To this, aminonitrile (47.5 mmol), dry pyridine (190 mL), and oxime (61.75 mmol) was added. The mixture was well stirred for 15 min, and tetra-chloro(bis-pyridyl)titanium complex (94.9 mmol) added in five portions over 35 min making sure the internal temperature remained below 40°C. After the addition was complete, the reaction mixture was stirred overnight at ambient temperature. The reaction mixture was slowly added to a solution of sodium bicarbonate (21.75 g in 174 mL water) in small portions. The resulting mixture was well stirred for 15 min and 80 g of celite was added. The suspension was stirred for 30 min and filtered through a Buchner funnel. The filtrate was removed to a separatory funnel, and the filter cake was suspended in 400 mL of methanol. The mixture was stirred for 30 min and filtered again. This process was repeated a total of four times. The methanolic filtrates were combined and concentrated, and the

residue dissolved in 200 mL of ethyl acetate (EtOAc). The solution was added to the separatory funnel containing the original filtrate, and the mixture further extracted with three 100 mL portions of EtOAc. The combined extracts were washed with two 100 mL portions of saturated sodium carbonate and two 100 mL portions of brine solution. The organic solvent was evaporated, and the crude pyazine-oxide obtained as a brown oil. The material was dissolved in 3 mL of methanol, and 89 mL of dichloromethane (DCM) was added. To this solution, zinc dust (80.7 mmol) was added, and the mixture cooled in an ice bath until an internal temperature of 15°C was reached. The mixture was treated with glacial acetic acid (3 mL) and warmed to an internal temperature of 30°C in an oil bath for 40 min. The reaction mixture was cooled to room temperature and filtered through a pad of celite. The filter cake was rinsed with DCM, and the combined filtrates washed with an aqueous solution of saturated sodium bicarbonate. The crude product was purified by chromatography over silica gel using a heptane/EtOAc gradient. This gave 2.9 g (29%) of the pyrazine as a brown solid. Procedure was adapted from: Kishi *et al.,* "The structure confirmation of the light-emitting moiety of bioluminescent jellyfish." *Tetrahedron Lett.,* 13(27):2747 (1972).

**Reference Example 4 – Synthesis of Coelenterazines**

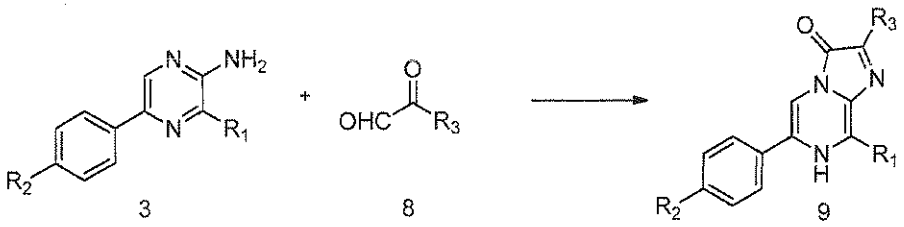
**[00219]** *Method A*: (the following compounds can be synthesized by Method A: compounds PBI-3840, PBI-3886, PBI-3857, PBI-3887, PBI-3913, PBI-3894, PBI-3896, PBI-3897, PBI-3841 and PBI-3842)




**[00220]** A flask was charged with pyrazine (8.25 mmol), pyruvic acid (14.0 mmol), camphor sulfonic acid (0.8 mmol), and anhydrous 2-methyl THF (150 mL). The flask was equipped with a condenser and soxhlet extractor charged with 4-angstrom molecular sieves, and the reaction mixture heated in an oil bath at 110°C for 18 hrs. The sieves were replaced with fresh ones, and

reflux continued for 24 hrs. The reaction mixture was filtered and concentrated, and the residue dissolved in EtOAc (200 mL). This solution was washed with three 25 mL portions of saturated sodium bicarbonate solution, 100 mL of 0.1 M sodium acetate buffer, pH 5, and 100 mL of brine solution. The solution was dried over magnesium sulfate, filtered, and concentrated to give 2.3 g (6.2 mmol, 75%) of the crude enamine/acid. This material was dissolved in anhydrous THF (30 mL), and the solution cooled in an ice/water bath for 10 min. To this, the carbodiimide (9.0 mmol) and neat diisopropylethyl amine (14.9 mmol) was added. The cold bath was removed after 10 min, and the reaction mixture stirred at ambient temperature for 3 hrs. To the reaction mixture, 50 mL of 0.1 M sodium acetate buffer, pH 5 was added, and the mixture well stirred for 10 min. The biphasic mixture was extracted with three 100 mL portions of EtOAc, and the combined extracts washed with brine solution. The organic solution was concentrated, and the residue purified by chromatography over silica gel using a DCM/methanol gradient. This gave 336 mg (0.94 mmol, 16%) of the dehydrocoelenterazine as a red solid. This material was suspended in 10 mL of methanol, and the mixture cooled in an ice bath. To this, sodium borohydride (100 mg, 2.6 mmol) was added in three portions over 1 hr. The reaction mixture was stirred for an additional 30 min, and neat glacial acetic acid added drop wise until a pH of 5 was reached. The solution was concentrated, and the residue triturated with 15 mL of water. The solid was isolated via suction filtration and dried under vacuum for several hours to give 318 mg (94%) of the crude coelenterazine as a yellow solid. Procedure was adapted from: Kakoi and Inoue, *Chem. Lett.* 11(3):299-300 (1980).

**[00221]** *Method B*: (the following compounds can be synthesized by method B: compounds PBI-3882, PBI-3932, PBI-3881)




**[00222]** A flask was charged with the glyoxal (2.2 mmol), aminopyrazine (1.1 mmol), ethanol (20 mL), 12N HCl (0.6 mL), and water (1 mL). The reaction mixture was heated at reflux for 24 hrs and concentrated. The residue was purified by column chromatography over silica gel using a DCM/methanol gradient. This gave 100 mg (0.25 mmol, 23%) of the coelenterazine product as a dark solid. Procedure was adapted from: Inoue *et al.* "Squid bioluminescence. II. Isolation from *Watasenia scintillans* and synthesis of 2-(p-hydroxybenzyl)-6-(p-hydroxyphenyl)-3,7-dihydroimidazo[1,2-a]pyrazin-3-one." *Chem. Lett.*, 4(2):141-4 (1975).

*Method C*: Synthesis of novel coelenterazines (the following compounds can be synthesized by method C: PBI-3939, PBI-3945, PBI-3889, PBI-4002)

**[00223]** The compound 4-(5-amino-6-benzylpyrazin-2-yl)phenol can be prepared according to previously described methods (Kishi *et al.*, *Tetrahedron Lett.*, 13:2747 (1972); Mosrin *et al.*, *Organic Letters*, 11:3406 (2009); Kakoi, *Chem. Pharm. Bull.*, 50:301 (2002)).

**[00224]** *Synthesis of 2-amino-3-benzyl-5-phenylpyrazine.* A round bottomed flask was charged with 5 g (33.5 mmol) of 2-isonitrosoacetophenone, 6.7 g (36.8 mmol) of 2-amino-3-phenylpropanenitrile hydrochloride and 100 mL of dry pyridine. The mixture was cooled to -20°C and 4.6 mL (40.0 mmol) of $TiCl_4$ was added dropwise. The reaction was kept at -20°C for 30 min and heated to 80°C for 2.5 hrs. The solvent was evaporated, and the residue taken up in 1 L of DCM. This solution was washed with saturated $NaHCO_3$ and brine. All volatiles were evaporated, and the residue redissolved in ethanol (400 mL). Raney Ni (2.0 g, aqueous suspension) was added, and the reaction allowed to stir for 5 days under 1 atm of hydrogen. The mixture was passed through celite, and volatiles removed. The residue was chromatographed on silica gel (heptanes/DCM) to give 2.5 g (29%) of 2-amino-3-benzyl-5-phenylpyrazine.

**[00225]** *Synthesis of 2-amino-3-phenylpropanenitrile hydrochloride.* A round bottomed flask was charged with 65 g (0.624 mol) of sodium hydrogensulfite and 150 mL of water. A solution of 75 g (0.624 mol) of phenylacetaldehyde in 150 mL of THF was added dropwise. After stirring for 20 min, 37 mL of 14 M ammonium hydroxide was added in one portion, and the mixture heated to 60°C for 60 min. After cooling to 0°C, the mix was diluted with 150 mL of water, and a solution of sodium cyanide (27.5 g, 0.560 mol) in 100 mL of water added dropwise keeping internal temperature below 10°C. Upon addition, the mixture was heated to 30°C for 2 hrs and extracted with ether. After drying with sodium sulfate, all volatiles were evaporated, and the residue dissolved in 3.5 L of ether and treated with 400 mL of 3.3 M ethanolic HCl. The resulting precipitate was filtered and dried in vacuum to give 55 g (60%) of product.

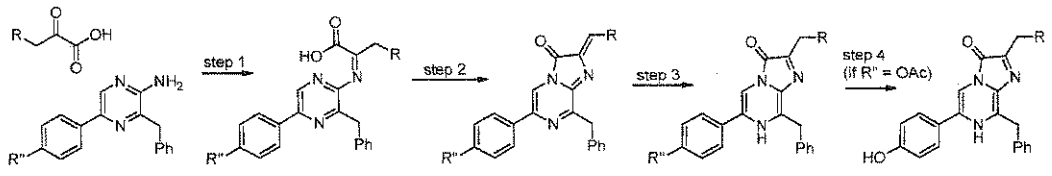
**[00226]** *Synthesis of 3-(furan-2-yl)-2-oxopropanoic acid.* To a 100 mL flask, 3-(furan-2-yl)-2-oxopropanoate (940 mg) along with 23 mL cold 6N NaOH was added. The insoluble mixture was stirred in a 90°C bath for 5 min until dissolved. Cold 1N HCl was added until solution was acidic (approx 120 mL). Solution was extracted 2 x 50 mL EtOAc. Combined organic layers were washed with 40 mL brine and dried with $Na_2SO_4$. Solution was evaporated to yield 540 mg brown solid. Solid was further purified by reversed-phase high-performance liquid chromatography (HPLC) ramping from 97% aqueous trifluoroacetic acid (TFA) to acetonitrile (ACN).

**[00227]** *Synthesis of ethyl 3-(furan-2-yl)-2-oxopropanoate.* To a 500 mL flask containing the mixture of isomers (E/Z)-ethyl 2-formamido-3-(furan-2-yl)acrylate (5.0 g), a chilled solution of 220 mL 1.4M (5%) HCl in 50/50 ethanol/water was added. After 5 hrs, the reaction was partitioned between 200 mL of EtOAc and 30 mL brine. The aqueous layer was extracted 2 x 50 mL EtOAc. Combined organic layers were washed with 1 x 50 mL water, and 1 x 50 mL brine and dried over $Na_2SO_4$. Organic layers were co-evaporated with 26 g celite and eluted over 80 g silica gold ramping from heptane to EtOAc. The appropriate combined fractions were evaporated to yield 2.1 g.

**[00228]** *Synthesis of (E/Z)-ethyl 2-formamido-3-(furan-2-yl)acrylate.* To a 500 mL flask, 50 mL diethyl ether, $Cu_2O$ (320 mg), and furyl aldehyde (5.2 mL) was added. The flasked was cooled in an ice bath, and ethyl 2-isocyanoacetate (5.3 mL) added. After 1.5 hrs, potassium tert-butoxide (5 g) was added to the reaction. After 4 hrs, the heterogeneous reaction was filtered. 60 mL 30% citric acid and 20 mL EtOAc was added and stirred for 10 min. Aqueous layer was extracted with 50 mL EtOAc. Combined organic layers were dried over anhydrous sodium sulfate. EtOAc layers were co-evaporated with 24 g celite and eluted over 80 g silica gold ramping from heptane to EtOAc. Yellow syrup was used without further purification.

**[00229]** *Synthesis of 2-oxo-3-(thiophen-2-yl)propanoic acid.* To a 250 mL flask, (E/Z)-5-(thiophen-2-ylmethylene)imidazolidine-2,4-dione (5.0 g) and 100 mL of cold 6N NaOH were added. The mixture was heated to 100°C for 1 hr. Concentrated HCl was added to the cooled solution until acidic (pH=1). The mixture was extracted 8 x 50 mL diethylether. The combined ether layers were washed with 50 mL brine, dried over $Na_2SO_4$ and evaporated to yield 3.36 g solid. Sample was further purified by recrystalization with α,α,α-trifluorotoluene to yield 1.63 g.

**[00230]** *Synthesis of (E/Z)-5-(thiophen-2-ylmethylene)imidazolidine-2,4-dione.* To a 250 mL flask, hydantoin (9.8 g) and thiophene-2-carbaldehyde (10 g) were added. To the mixture was dripped piperidine (9.6 mL). The mixture was heated to 100°C for 1 hr and then poured into 300 mL of 1N HCl. The solid was filtered, washed with water and dried in vacuo to yield 4.9 g solid.




**[00231]** *Steps 1-* To a microwave vial (10 mL), the appropriate phenylpyrazin-2-amine (100 mg), the appropriate pyruvic acid (2 Equivalents), DCM (1 mL), and 1,1,1-trifluoroethanol (1 mL) were heated with stirring for 30 min at 80°C. Reaction was co-adsorbed on 2 grams of

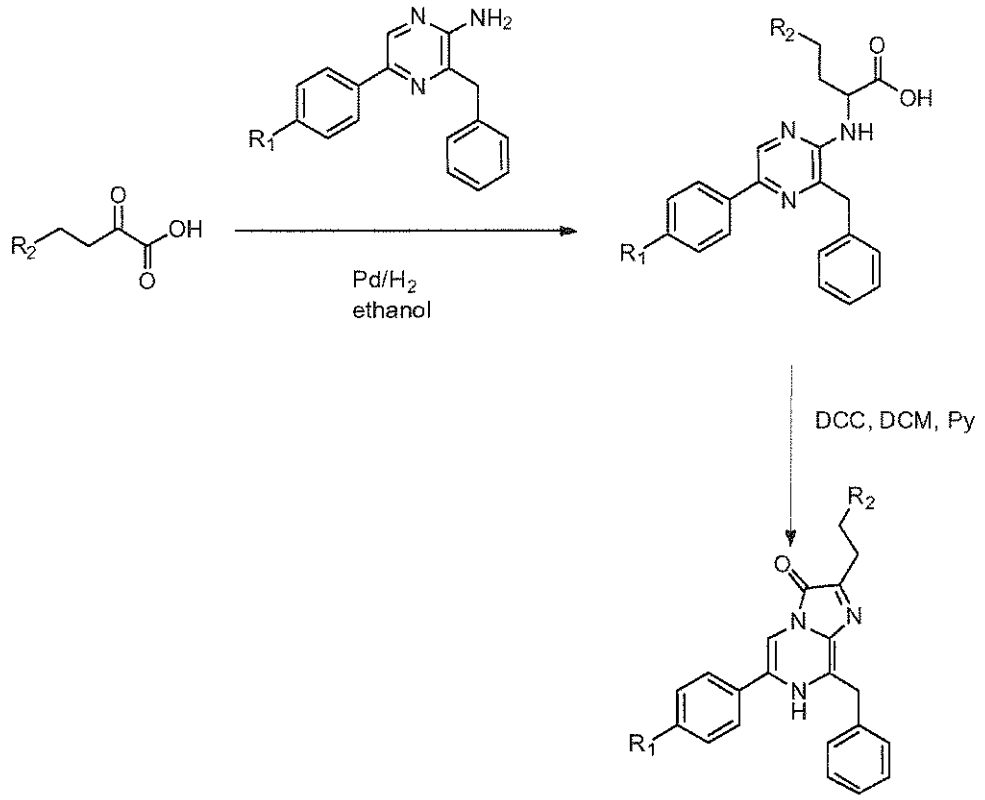
celite, and solvents removed in vacuo. The celite was loaded on 24 g of spherical silica gel and eluted with a ramp of heptanes to ethylacetate. Appropriate fractions were combined and evaporated.

**[00232]** *Step 2* – The material isolated in step 1 dissolved in THF (0.5 mL) was chilled in an ice bath. Acetic anhydride (25 μL), dimethylaminopyridine (8.5 mg), and triethylamine (25 μL) were added. After 2 hrs, the majority of THF was removed in vacuo. The product was precipitated with an aqueous solution of 30% citric acid (2 mL). The solid was washed with water (2 mL) and then dissolved in 3 mL DCM. The DCM was washed 1 x 2 mL water followed by 1 x 2 mL brine. The DCM layer was co-adsorbed on 2 grams of celite, and solvent removed in vacuo. The celite was loaded on 12 g of spherical silica gel and eluted with a ramp of heptanes to DCM. Appropriate fractions were combined and evaporated.

**[00233]** *Step 3* - The material from step 2 dissolved in DCM (1 mL) was chilled in an ice bath. To the solution, methanol (0.5 mL) and sodium borohydride solution in diglyme (325 μL of 0.5 M) were added. After 2 hrs, acetic acid (10 μL) was added, and the solution quickly partitioned between an aqueous solution of 30% citric acid (1 mL) and DCM (2 mL). The DCM layer was co-adsorbed on 1 gram of celite, and solvent removed in vacuo. The celite was loaded on 4 g of spherical silica gel and eluted with a ramp of DCM to EtOAc. Appropriate fractions were combined and evaporated.

**[00234]** *Step 4* (only if R" = OAc) – The material in step 3 was dissolved in THF (200 μL) and chilled in an ice bath. 1 equivalent of 1.35 M potassium methoxide in THF was added to the solution. After 30 min, the reaction was partitioned between DCM (1 mL) and 30% citric acid (1 mL). The DCM layer was co-adsorbed on 0.5 g celite, and solvent removed in vacuo. The celite was loaded on 4 g of spherical silica gel and eluted with a ramp of DCM to EtOAc. Appropriate fractions were combined and evaporated.

**[00235]** *Method D*: (the following compounds can be synthesized by method D: compounds PBI-3899, PBI-3900, PBI-3925, PBI-3933, PBI-3946) - In general, an aminopyrazine was condensed with 2 equivalents of a 2-oxoacid under an atmosphere of hydrogen in the presence of palladium catalyst. The alpha-amino acid produced was purified and subsequently activated for intramolecular condensation giving rise to the corresponding imidazopyrazinone.




**Example 5 – Synthesis of 8-benzyl-6-(4-hydroxyphenyl)-2-propylimidazo[1,2-a]pyrazin-3(7H)-one**

**[00236]** *2-((3-benzyl-5-(4-hydroxyphenyl)pyrazin-2-yl)amino)pentanoic acid.* 4-(5-amino-6-benzylpyrazin-2-yl)phenol (100 mg, 0.36 mmol) was mixed with 2-Oxovaleric acid (84 mg, 0.72 mmol) in ethanol (20 mL). Pd/C (10% Palladium in active carbon, 40 mg) was added, and the reaction mixture heated to 65°C. Air was bubbled out by $N_2$ gas, and a hydrogen balloon applied to the reaction flask. The reaction was continuously stirred for 4 hrs. After cooling down, it was filtered, and the resulting solution purified by flash chromatography (eluting solvent: 50% EtOAc in heptanes) to give the product as a yellow powder (70 mg, 52%). $^1$H NMR (300 MHz, $CD_2Cl_2$, δ): 8.31 (s, 1H), 7.82 (d, 2H, J = 9.0Hz), 7.31 (m, 5H), 6.92 (d, 2H, J = 9.0Hz), 5.34 (s, 2H), 4.20 (m, 1H), 1.10 (m, 2H), 0.98 (m, 2H), 0.87 (t, 3H); MS (ESI) m/z 378.3 (M+1).

**[00237]** *8-benzyl-6-(4-hydroxyphenyl)-2-propylimidazo[1,2-a]pyrazin-3(7H)-one.* 2-((3-benzyl-5-(4-hydroxyphenyl)pyrazin-2-yl)amino)pentanoic acid (49 mg, 0.13 mmol) was dissolved in DCM (10 mL). Pyridine (0.5 mL) was added followed by N,N'-Dicyclohexylcarbodiimide (54 mg, 0.26 mmol). The reaction mixture was slowly stirred at room temperature for 1 hr. The solvent was evaporated, and the residue purified by flash chromatography (eluting solvent: EtOAc to DCM to 10% methanol in DCM) to give the product

as a yellow powder (40 mg, 86%). $^1$H NMR (300 MHz, $CD_3OD$, δ): 7.35 (m, 8H), 6.88 (d, J = 9.0Hz, 2H), 4.40 (s, 2H), 2.81 (t, J = 7.5Hz, 2H), 1.81 (m, 2H), 1.02 (t, J = 7.5Hz, 3H); MS (ESI) m/z 359.0.

**Example 6 – Synthesis of 8-benzyl-2-butyl-6-(4-hydroxyphenyl)imidazo[1,2-a]pyrazin-3(7H)-one**

**[00238]** *2-((3-benzyl-5-(4-hydroxyphenyl)pyrazin-2-yl)amino)hexanoic acid.* 4-(5-amino-6-benzylpyrazin-2-yl)phenol (200 mg, 0.72 mmol) was mixed with 2-Ketohexanoic acid sodium salt (220 mg, 1.44 mmol) in ethanol (20 mL). Pd/C (10% Palladium in active carbon, 100 mg) was added with a few drops of acetic acid, and the reaction mixture heated to 65°C. Air was bubbled out by $N_2$ gas, and a hydrogen balloon applied to the reaction flask. The reaction was continuously stirred for 4 hrs. After cooling down, it was filtered and the resulting solution was purified by flash chromatography (eluting solvent: 50% EtOAc in heptanes) to give the product as a yellow powder (130 mg, 46%). MS (ESI): m/z 392.2 (M+1).

**[00239]** *8-benzyl-2-butyl-6-(4-hydroxyphenyl)imidazo[1,2-a]pyrazin-3(7H)-one.* 2-((3-benzyl-5-(4-hydroxyphenyl)pyrazin-2-yl)amino)hexanoic acid (130 mg, 0.33 mmol) was dissolved in DCM (10 mL). Pyridine (0.5 mL) was added followed by N,N'-Dicyclohexylcarbodiimide (137 mg, 0.67 mmol). The reaction mixture was slowly stirred at room temperature for 1 hr. The solvent was evaporated, and the residue purified by flash chromatography (eluting solvent: EtOAc to DCM to 10% methanol in DCM) to give the product as a yellow powder (110 mg, 89%). $^1$H NMR (300 MHz, $CD_3OD$, δ): 7.30 (m, 8H), 6.88 (d, 2H), 4.40 (s, 2H), 2.84 (t, 2H), 1.77 (m, 2H), 1.51 (m, 2H), 0.89 (m, 3H); MS (ESI) m/z 374.3 (M + 1).

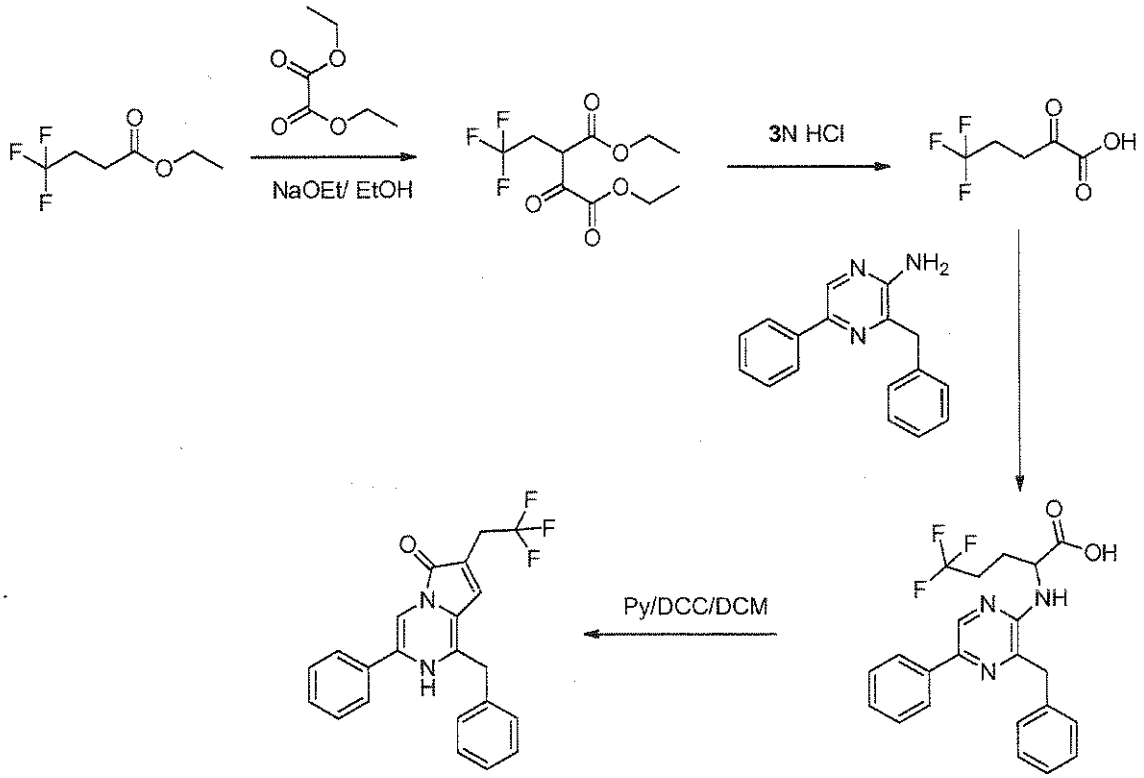
**Example 7 – Synthesis of 8-benzyl-2-ethyl-6-phenylimidazo[1,2-a]pyrazin-3(7H)-one (PBI-3925)**

**[00240]** *2-((3-benzyl-5-phenylpyrazin-2-yl)amino)butanoic acid.* 3-benzyl-5-phenylpyrazin-2-amine (200 mg, 0.77 mmol) was mixed with 2-Oxobutyric acid (157 mg, 1.54 mmol) in ethanol (20 mL). Pd/C (10% Palladium in active carbon, 100 mg) was added, and the reaction mixture heated to 65°C. Air was bubbled out by $N_2$ gas, and a hydrogen balloon applied to the reaction flask. The reaction was continuously stirred for 4 hrs. After cooling down, it was filtered, and the resulting solution purified by flash chromatography (eluting solvent: 50% EtOAc in heptanes) to give the product as a yellow powder (90 mg, 34%). $^1$H NMR (300 MHz, $CD_2Cl_2$, δ): 7.72 (s,

1H), 7.32-7.48 (m, 10H), 4.46 (s, 2H), 4.20 (m, 2H), 2.25 (q, 2H), 0.99 (t, 3H); MS (ESI): m/z 348.3 (M+1).

**[00241]** 2-((3-benzyl-5-phenylpyrazin-2-yl)amino)butanoic acid was dissolved in DCM (10 mL). Pyridine (0.5 mL) was added followed by N,N'-Dicyclohexylcarbodiimide (137 mg, 0.67 mmol). The reaction mixture was slowly stirred at room temperature for 1 hr. The solvent was evaporated, and the residue purified by flash chromatography (eluting solvent: EtOAc to DCM to 10% methanol in DCM) to give the product as a yellow powder (110 mg, 89%). $^1$H NMR (300 MHz, $CD_3OD$, δ): 7.26 (m, 3H), 6.84-7.07 (m, 8H), 4.03 (s, 2H), 2.47 (q, J = 9.0Hz, 2H), 0.96 (t, J = 9.0Hz, 3H); MS (ESI): m/z 330.2 (M+1).

**Example 8 – Synthesis of 8-benzyl-6-phenyl-2-(3,3,3-trifluoropropyl)imidazo[1,2-a]pyrazin-3(7H)-one**



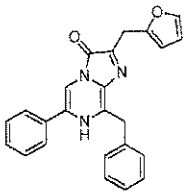

**[00242]** *5,5,5-trifluoro-2-oxopentanoic acid.* Ethyl 4,4,4-trifluorobutyrate (1 g, 5.88 mmol) and diethyl oxalate (3.87 g, 26.5 mmol) was dissolved in ethanol. Sodium ethoxide (21% in ethanol, 2.09 g) was added to the solution, and the reaction mixture stirred for 0.5 hrs. Solvent was distilled, and the residue extracted with EtOAc/water. The organic layers were collected and dried over sodium sulfate. After filtration, solvent was removed to give a clear liquid. MS (ESI): m/z 269.1 (M-1). The liquid was then dissolved in 3N HCl (20 mL), and the reaction mixture

refluxed for 4 hrs. After cooling down, the reaction mixture was extracted with EtOAc. The organic layers were collected and dried over sodium sulfate. After filtration, solvent was removed, and the residue used directly in the next step. MS (ESI): m/z 169.7 (M-1).

**[00243]** *5,5,5-trifluoro-2-((3-benzyl-5-phenylpyrazin-2-yl)amino)butanoic acid.* 3-benzyl-5-phenylpyrazin-2-amine (240 mg, 0.92 mmol) was mixed with 5,5,5-trifluoro-2-oxopentanoic acid (150 mg, 0.88 mmol) in ethanol (20 mL). Pd/C (10% Palladium in active carbon, 100 mg) was added, and the reaction mixture heated to 65°C. Air was bubbled out by $N_2$ gas, and a hydrogen balloon applied to the reaction flask. The reaction was continuously stirred for 4 hrs. After cooling down, it was filtered, and the resulting solution purified by flash chromatography (eluting solvent: 50% EtOAc in heptanes) to give the product as a yellow powder (200 mg, 54%). $^1$H NMR (300 MHz, $CD_2Cl_2$, δ): 11.45 (s, 1H), 10.20 (s, 1H), 7.94 (s, 1H), 7.34 (m, 10H), 5.34 (s, 2H), 3.96-4.23 (m, 2H), 3.02-3.28 (m, 2H); FNMR: -76.3; MS (ESI): m/z 416.1 (M+1).

**[00244]** *Coelenterazine ($R_1$ = H, $R_2$ = $-CH_2CH_2CF_3$).* 5,5,5-trifluoro-2-((3-benzyl-5-phenylpyrazin-2-yl)amino)butanoic acid (100 mg, 0.24 mmol) was dissolved in DCM (10 mL). Pyridine (0.5 mL) was added followed by N,N'-Dicyclohexylcarbodiimide (100 mg, 0.48 mmol). The reaction mixture was slowly stirred at room temperature for 1 hr. The solvent was evaporated, and the residue purified by flash chromatography (eluting solvent: EtOAc to DCM to 10% methanol in DCM) to give the product as a yellow powder (80 mg, 87%). $^1$H NMR (300 MHz, $CD_2Cl_2$, δ): 7.36 (m, 11H), 3.43 (s, 2H), 1.60-1.92 (m, 4H); FNMR: 67.4 (t, J = 18Hz); MS (ESI): m/z 398.2 (M+1).

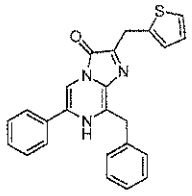
**Example 9 – Synthesis of 8-benzyl-2-(furan-2-ylmethyl)-6-phenylimidazo[1,2-a]pyrazin-3(7H)-one (PBI-3939)**



PBI-3939

**[00245]** *8-benzyl-2-(furan-2-ylmethyl)-6-phenylimidazo[1,2-a]pyrazin-3(7H)-one*: Synthesized from method C using 3-(furan-2-yl)-2-oxopropanoic acid and 3-benzyl-5-phenylpyrazin-2-amine as starting materials. $^1$H NMR (300 MHz, dmso) δ 8.88 (s, 1H), 8.02 (d, *J* = 7.9, 2H), 7.61 – 7.38 (m, 6H), 7.37 – 7.14 (m, 3H), 6.38 (s, 1H), 6.26 (d, *J* = 3.2, 1H), 4.64 (s, 3H), 4.40 (s, 3H); exact mass calculated for $C_{24}H_{20}N_3O_2^-$ *m/z*+ 382.16, found *m/z*+ 382.

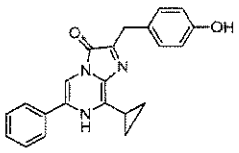
**Example 10 – Synthesis of 8-benzyl-6-phenyl-2-(thiophen-2-ylmethyl)imidazo[1,2-a]pyrazin-3(7H)-one (PBI-3889)**



PBI-3889

**[00246]** *8-benzyl-6-phenyl-2-(thiophen-2-ylmethyl)imidazo[1,2-a]pyrazin-3(7H)-one*: Synthesized from method C using 2-oxo-3-(thiophen-2-yl)propanoic acid and 3-benzyl-5-phenylpyrazin-2-amine as starting materials. $^1$H NMR (300 MHz, dmso) δ 8.85 (s, 1H), 7.99 (d, $J$ = 6.8, 2H), 7.63 – 7.02 (m, 10H), 6.94 (dd, $J$ = 3.5, 5.1, 1H), 4.62 (s, 2H), 4.58 (s, 2H), 2.69 (contaminate); exact mass calculated for $C_{24}H_{20}N_3OS^+$ *m/z*+ 398.13, found *m/z*+ 398.

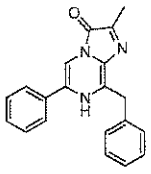
**Example 11 – Synthesis of 8-cyclopropyl-2-(4-hydroxybenzyl)-6-phenylimidazo[1,2-a]pyrazin-3(7H)-one (PBI-3897)**



PBI-3897

**[00247]** *8-cyclopropyl-2-(4-hydroxybenzyl)-6-phenylimidazo[1,2-a]pyrazin-3(7H)-one:* Synthesized using method A with 3-cyclopropyl-5-phenylpyrazin-2-amine and 3-(4-hydroxyphenyl)-2-oxopropanoic acid as starting materials. Exact mass calculated for $C_{22}H_{18}N_3O_2^-$ *m/z*- 356.14, found *m/z*- 356.

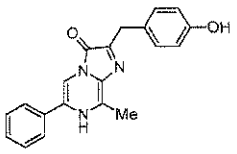
**Example 12 – Synthesis of 8-benzyl-2-methyl-6-phenylimidazo[1,2-a]pyrazin-3(7H)-one (PBI-3932)**



PBI-3932

**[00248]** *8-benzyl-2-methyl-6-phenylimidazo[1,2-a]pyrazin-3(7H)-one:* Synthesized using method B with 1,1-dimethoxypropan-2-one and 3-benzyl-5-phenylpyrazin-2-amine as starting materials. Exact mass calculated for $C_{20}H_{18}N_3O^+$ *m/z*+ 316.14, found *m/z*+ 316.

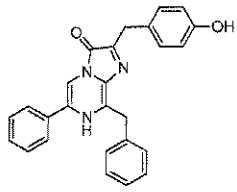
**Example 13 – Synthesis of 2-(4-hydroxybenzyl)-8-methyl-6-phenylimidazo[1,2-a]pyrazin-3(7H)-one (PBI-3896)**




PBI-3896

**[00249]** *2-(4-hydroxybenzyl)-8-methyl-6-phenylimidazo[1,2-a]pyrazin-3(7H)-one:* Synthesized using method A with 3-methyl-5-phenylpyrazin-2-amine and 3-(4-hydroxyphenyl)-2-oxopropanoic acid as starting materials. $^1$H NMR (300 MHz, dmso) δ 8.84 (s, 1H), 8.00 (d, $J$ = 7.6, 2H), 7.47 (dd, $J$ = 8.6, 16.2, 3H), 7.17 (d, $J$ = 7.3, 2H), 6.69 (d, $J$ = 8.4, 2H), 6.26 (s, 4H), 4.17 (s, 2H), 2.86 (s, 3H), 2.48 (s, 1H).

**Example 14 – Synthesis of 8-benzyl-2-(4-hydroxybenzyl)-6-phenylimidazo[1,2-a]pyrazin-3(7H)-one (PBI-3840)**



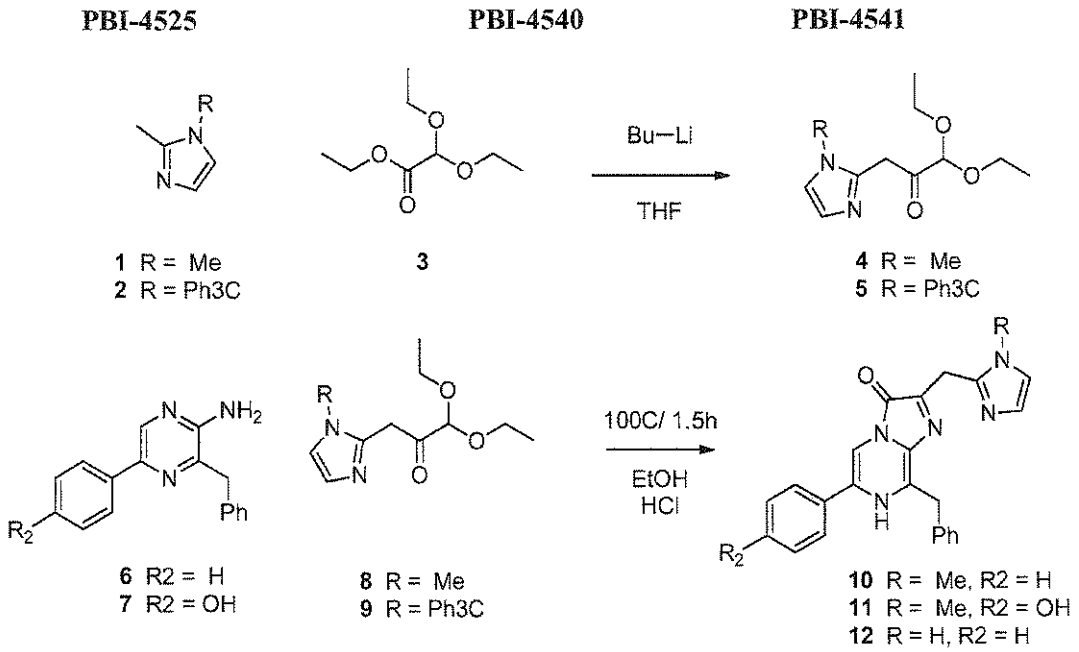

PBI-3840

**[00250]** *8-benzyl-2-(4-hydroxybenzyl)-6-phenylimidazo[1,2-a]pyrazin-3(7H)-one:* Synthesized using method A with 3-(4-hydroxyphenyl)-2-oxopropanoic acid and 3-benzyl-5-phenylpyrazin-2-amine as starting materials. Exact mass calculated for $C_{26}H_{22}N_3O_2^+$ *m/z*+ 408.17, found *m/z*+ 408.

**Example 15 - Synthesis of Protected Coelenterazine (Stabilized) (PBI-4377)**

**[00251]** To a mixture of PBI-3939, potassium carbonate (1.1 equiv) and potassium iodide (1.1 equiv) in dimethylformamide (DMF), under an argon atmosphere, was added one equivalent of chloromethyl pivalate at room temperature. Reaction progress was monitored by thin layer chromatography, and upon completion, the reaction mixture was cooled in an ice bath for several minutes before addition of a volume of water equal to the reaction volume. The resulting mixture was extracted with a suitable organic solvent (e.g., EtOAc), and the extract was concentrated to give the crude product. The material was further purified by chromatography over silica gel.

**Example 16 – Synthesis of 8-benzyl-2-((1-methyl-1H-imidazol-2-yl)methyl)-6-phenylimidazo[1,2-a]pyrazin-3(7H)-one (PBI-4525), 8-benzyl-6-(4-hydroxyphenyl)-2-((1-methyl-1H-imidazol-2-yl)methyl)-6-phenylimidazo[1,2-a]pyrazin-3(7H)-one (PBI-4540) and 2-((1H-imidazol-2-yl)methyl)-8-benzyl-6-phenylimidazo[1,2-a]pyrazin-3(7H)-one (PBI-4541)**




**[00252]** To a flask containing 10 mmol of 2-methyl imidazole derivative 1 or 2 under an argon atmosphere, 20 mL of dry THF was added, and the solution was cooled in a dry ice/acetone bath to approximately -78°C. To the cold mixture, 9.3 mmol of a solution of n-butyllithium (2.46 M in Hexanes) was added dropwise over several minutes. The resulting solution was stirred at approximately -78°C for 30 min, and 6.7 mmol of compound 3 was added via syringe. The reaction mixture was stirred for 3 hrs and quenched with the addition of 20 mL saturated ammonium chloride solution and 20 mL of saturated sodium bicarbonate solution. The cold bath was removed, and after warming to room temperature, the mixture was extracted with 3 x 100 mL of EtOAc. The combined extracts were dried ($MgSO_4$), concentrated in vacuo, and the crude compounds 4 or 5 were purified by column chromatography using silica gel (EtOAc/Heptane).

**[00253]** A microwave vial was charged with 100 mg (1 eq) of compound 6 or 7 and 2 equivalents of compound 8 or 9. To the mixture, 4.5 mL of ethanol and 0.25 mL of concentrated HCl was added. The reaction mixture was heated in a microwave at 100°C for 1.5 hr. The resulting mixture was added to 50 mL of EtOAc and washed sequentially with 20 mL of saturated sodium bicarbonate solution and 20 mL of brine. The organic phase was concentrated

in vacuo, and the residue purified by column chromatography using silica gel (methanol/dichloromethane) to give compounds 10-12.

**Example 17 – Stability and Auto-Luminescence Characterization of Novel Coelenterazines**

**[00254]** The stability and auto-luminescence characterization of the novel coelenterazines PBI-3939, PBI-3889, PBI-3945, PBI-4002, or PBI-3896 were determined. Higher stability and less auto-luminescence is an attractive technical feature in a substrate/reagent.

**[00255]** To determine stability, 20 μM of novel coelenterazines PBI-3939, PBI-3889, PBI-3945, PBI-4002, or PBI-3896, 30 μM native coelenterazine, or 22 μM of known coelenterazine-h or known coelenterazine-hh, were placed in a reporter reagent buffer containing 50 mM CDTA, 150 mM KCl, 50 mM DTT, 35 mM thiourea, 1% TERGITOL® NP-9 (v/v), and 0.1% MAZU® DF 204. Replicate samples were incubated at room temperature (i.e., 22-24°C) for various lengths of time and then transferred to -70°C. After all the samples were collected and frozen, they were thawed and mixed with 10 μL of bacterial cell lysate containing the OgLuc variant IV in 40 μL of DMEM without phenol red + 0.1% PRIONEX®. The luminescence of the sample was read at 5 min after IV addition.

**[00256]** "$T_{90}$" indicates the amount of time for the luminescent signal to decay by 10% (i.e., loss in activity by 10%) at ambient temperature, i.e., 22°C. The rate of decay of the luminescent signal ("$T_{90}$") was determined from the slope of the linear fit of the data plotted as ln RLU vs. time, which was calculated from the following equation: $t = \ln (A/A_0) \div (-k)$, where A = intensity at time t, $A_0$ = intensity at time 0, and k = the rate of decay. As shown in Table 1, the $T_{90}$ values for known coelenterazines-h and -hh, novel coelenterazines PBI-3939, PBI-3889, PBI-3945, PBI-4002, and PBI-3896 were higher than for native coelenterazine, indicating that these coelenterazines were more stable compounds than native coelenterazine.

**[00257]** To determine the auto-luminescence characterization, HEK293 cells were grown overnight at 15,000 cells per well in DMEM + 10% FBS + pyruvate. Media was removed and replaced with 20 μM each of the novel coelenterazines shown in FIG. 2, i.e., PBI-3939, PBI-3889, PBI-3945, PBI-4002, PBI-3841, PBI-3897, PBI-3896, PBI-3925, PBI-3894, PBI-3932, and PBI-3840, native coelenterazine and known coelenterazines, coelenterazine-h and coelenterazine-hh, diluted into $CO_2$ independent media plus 10% FBS. Luminescence was measured shortly after substrate addition on the GLOMAX® Luminometer (1 sec/well). Background luminescence was 154±15 RLU. Table 1 shows the auto-luminescence characterization normalized to native coelenterazine ("Autolum (norm to coel)"). While coelenterazine-h had

more auto-luminescence than native coelenterazine, all of the other coelenterazines tested had less auto-luminescence.

**Table 1: Stability Experiments and Autoluminescence Characterization of IV with Various Coelenterazines.**

| Substrate ID | Stability (pH 8) ($T_{90}$ in hrs) | Autolum (norm to coel) |
|---|---|---|
| Coel | 1.7 | 1 |
| Coel h | 2.1 | 1.2 |
| Coel hh | 2.0 | 0.3 |
| 3939 | 4.1 | 0.2 |
| 3889 | 2.9 | 0.2 |
| 3945 | 3.3 | 0.5 |
| 4002 | 3.5 | 0.6 |
| 3841 | | 0.1 |
| 3897 | | 0.1 |
| 3896 | 2.8 | 0.1 |
| 3894 | | 0.2 |
| 3932 | | 0.1 |
| 3840 | | 0.2 |
| 3925 | | 0.2 |

**Example 18 – Toxicity of Novel Coelenterazines**

**[00258]** The toxicity of the novel coelenterazines were investigated in HEK293 cells. HEK293 cells were grown overnight at 15,000/well in DMEM + 10% FBS + pyruvate. The media was removed and replaced with the novel coelenterazine compounds (or DMSO control) diluted into $CO_2$ independent media plus 10% FBS. Cell viability was measured 24 hrs after compound addition using CELLTITER-GLO® assay reagent (Promega Corp.) according to the manufacturer's instructions, and luminescence was measured on the GLOMAX® Luminometer (1 sec/well). Table 2 shows the toxicity of the native coelenterazine, known coelenterazine-h and coelenterazine-hh, and the novel coelenterazines PBI-3939, PBI-3889, PBI-3841, PBI-3897, PBI-3945, PBI-4002, and PBI-3840 in HEK293 cells. With the exception of PBI-3840, the novel

coelenterazines had at least the same toxicity as coelenterazine-hh. Some of the novel coelenterazines had the same toxicity as native coelenterazine and coelenterazine-h.

**Table 2: Toxicity of Various Coelenterazines in HEK293 Cells Based on CELLTITER-GLO®**

| Substrate | Viability (normalized to vehicle (DMSO) control) (%) |
|---|---|
| Native coelenterazine | 100 |
| Coelenterazine h | 100 |
| Coelenterazine hh | 87 |
| PBI-3939 | 89 |
| PBI-3889 | 90 |
| PBI-3841 | 100 |
| PBI-3897 | 100 |
| PBI-3945 | 100 |
| PBI-4002 | 100 |
| PBI-3840 | 60 |

**Example 19 - Km of PBI-3939**

**[00259]** To determine the Km of PBI-3939, the OgLuc variant L27V (described in Example 26) was purified via HALOTAG® fusion using the HALOTAG® Protein Purification System according to the manufacturer's instructions and diluted in DMEM without Phenol Red and 0.1% PRIONEX®. 50 µL assay buffer (100 mM MES pH 6, 35 mM Thiourea, 0.5% TERGITOL® NP-9 (v/v), 1 mM CDTA, 2 mM DTT and 150 mM KCl) with varying amounts of PBI-3939 was added to 50 µL diluted enzyme (approximately 20 pM final enzyme concentration), and luminescence measured at 3 min at 22°C. As the data in FIG. 3 demonstrates, the Km of PBI-3939 is approximately 10 µM.

**Example 20 – Characterization of compounds PBI-4525, PBI-4540 and PBI-4541**

**[00260]** Compounds PBI-4525, PBI-4540 and PBI-4541 were screened for their ability to detect luminescence. For analysis, 20 µM of each compound was added to assay buffer (100 mM MES pH 6, 35 mM Thiourea, 0.5% TERGITOL® NP-9 (v/v), 1 mM CDTA, 2 mM DTT and 150 mM KCl) which was adjusted to pH 7 with 100 mM HEPES pH 7 to create an assay reagent. The assay reagent was then mixed with 36 pM purified L27V02 enzyme (described in

Example 25B), in DMEM without Phenol Red and 0.1% PRIONEX®. As a control, assay buffer with 20 μM PBI-3939 or PBI-4528 was used. Luminescence was measured as previously described 3 min after the assay reagent was added to the enzyme mixture. Table 3 demonstrates that compounds PBI-4525, PBI-4540 and PBI-4541 can be used to detect luminescence from a coelenterazine-utilizing luciferase.

**Table 3**

| cmpd | RLU | +/- |
|---|---|---|
| 4525 | 20,655 | 1,006 |
| 4528 | 202,080 | 5,688 |
| 3939 | 9,808,880 | 307,565 |
| 4540 | 909 | 7 |
| 4541 | 5,676 | 80 |

**Example 21 – OgLuc Pattern Sequence**

**[00261]** Enzyme families, including different classes of luciferases, can be recognized by having common three-dimensional structures and defined catalytic activity. Because enzyme families share evolutionary histories with other enzyme families, they will also exhibit similarities in their three-dimensional structures. Through various means of structural and functional analysis, the inventors have determined that OgLuc, as a representative of decapod luciferases, has a strikingly similar three-dimensional structure to Fatty Acid Binding Proteins (FABPs), indicating commonality of evolutionary history. Thus, decapod luciferase may be defined as having a characteristic three-dimensional structure similar to FABPs and utilizing coelenterazine as a substrate to catalyze the emission of luminescence. Other luciferases, e.g., firefly luciferase, *Renilla* luciferase, bacterial luciferase, and so forth, have clearly distinct three-dimensional structures, indicating that they belong to different enzyme families and do not share evolutionary histories. Dinoflagellate luciferase has a three-dimensional structure exhibiting some similarities to FABPs, suggesting a shared evolutionary history, but does not utilize coelenterazine as a substrate, and thus does not belong to the same enzyme family as decapod luciferases.

**[00262]** Because amino acid sequences are not as well conserved as three-dimensional structures, defining enzyme families based only on sequence comparisons can be difficult. For example, even though FABPs all have a characteristic barrel-shaped three-dimensional shape, comparisons of their amino acid sequences often reveal very low levels of sequence identity. Nonetheless, sequence identity can be used to demonstrate commonality of three-dimensional structures. Two proteins will have analogous three-dimensional structures if their amino acid

sequences can be aligned to reveal > 30% sequence identity, preferably > 40% sequence identity, and most preferably > 50% sequence identity (Chothia and Lesk, *EMBO J.* 5(4):823-826 (1986); Tramontano, *Genomics,* 4:402–405 (2003)). Thus, a protein is a decapod luciferase if, upon alignment of its amino acid sequence with the sequence of OgLuc, the sequence identity is > 30%, preferably > 40%, and most preferably > 50%, and the protein can utilize coelenterazine as a substrate to catalyze the emission of luminescence.

**[00263]** Because of structural constraints necessary to sustain the characteristic three-dimensional structure of an enzyme family, some portions of the amino acid sequences in an enzyme family exhibit greater amounts of conservation (i.e., a greater level of sequence identity). Thus, these conserved regions can serve as further evidence of a common three-dimensional structure shared between two proteins. A conserved sequence pattern, also called a signature, motif, or fingerprint, can be generated by manual or computational methods that are known in the art. Patterns can be found in public databases such as PROSITE (http://expasy.org/prosite; Sigrist *et al.*, *Nucleic Acids Res.* 38(suppl 1):D161-D166 (2010)).

**[00264]** For example, a pattern of conserved amino acids can be found upon examination of a large number of known FABPs. PROSITE (Release 20.67, of 05-Oct-2010) contains an FABP pattern (accession number PS00214, created Apr-1990, data updated Apr-2006). This FABP pattern spans 18 amino acid positions and is defined as:

**[00265]** [GSAIVK]-{FE}-[FYW]-x-[LIVMF]-x-x-{K}-x-[NHG]-[FY]-[DE]-x-[LIVMFY]-[LIVM]-{N}-{G}-[LIVMAKR] (SEQ ID NO: 329) (VI),

**[00266]** where:

- the standard IUPAC one-letter codes for the amino acids are used.
- the symbol 'x' is used for a position where any amino acid is accepted.
- alternative amino acids at a site are indicated by listing the amino acids between square parentheses '[ ]' (for example: [ALT] represents the possibility of an Ala, Leu, or Thr at the position).
- the absence of particular amino acids at a site is indicated by curly brackets '{ }' (for example: {AM} represents any amino acid at a position except Ala and Met).
- each sequence position (or element in the pattern) is separated from its neighbor by '-'.

- each sequence position is referred to as a "pattern position", for example the [GSAIVK] would be considered pattern position 1 of Formula (VI), {FE} is considered pattern position 2 of Formula (VI), etc.

**[00267]** Although a conserved sequence pattern results from a common underlying three-dimensional structure, some changes to the sequence pattern may be allowed without disruption to the three-dimensional structure. For example, for some members of the FABP family, differences are found at four sites in the PROSITE pattern. These additional members of the FABP family include five proteins listed in PROSITE as false negative hits, i.e., FABP protein family members not picked up by the FABP pattern (UniProt database accession numbers FBP12_HUMAN, FABP1_FASGI, FABP2_FASHE, FABPL_SCHBI, RET5_BOVIN) and one protein known to have an FABP fold (Protein Data Bank accession number 2A02). Although OgLuc shares a closely similar three-dimensional structure with FABPs, the sequence patterns of the native and variant amino acid sequences also differ slightly, having differences at 5 positions from the PROSITE pattern. In various embodiments, the pattern in OgLuc begins at a position corresponding to position 8 of SEQ ID NO: 1. An amino acid substitution, deletion, or insertion the sequence pattern is counted as a difference.

**[00268]** Combining the sequence information from these additional FABPs and the OgLuc variants, an improved sequence pattern can be derived:

**[00269]** [GSAIVK]-{FE}-[FYW]-x-[LIVMFSYQ]-x-x-{K}-x-[NHGK]-x-[DE]-x-[LIVMFY]-[LIVMWF]-x-{G}-[LIVMAKRG] (SEQ ID NO: 330) (VII).

**[00270]** The sequence information used to derive this pattern is shown in Table 4. Column 1 identifies the pattern position (listed N- to C-terminus; pattern length is 18 amino acids), and column 6 identifies the corresponding sequence position in OgLuc (numbering according to SEQ ID NO: 1). Column 2 shows the PROSITE FABP pattern (Formula (VI)) element for each pattern position. Column 3 lists amino acids present in six FABP family members that are not represented by the PROSITE FABP pattern. Column 4 lists amino acids present in OgLuc (SEQ ID NO: 1) or OgLuc variants that are not represented by the PROSITE pattern. Column 5 lists the improved pattern ("OgLuc pattern") (Formula (VII)) created by merging pattern information from columns 2, 3, and 4. Column 7 lists the amino acids in OgLuc (SEQ ID NO: 1) corresponding to the PROSITE FABP pattern positions. Column 8 lists the amino acids found in dinoflagellate luciferase sequences (8 different species) at positions corresponding to the improved pattern (GenBank accession numbers 2021262A, AAA68491, AAC36472,

AAV35379, AAV35380, AAL40676, AAL40677, AAV35378, AAV35377, AAV35381, and Protein Data Bank accession number 1VPR).

**[00271]** The improved pattern (Formula (VII)) serves as an indication (i.e., a fingerprint) of the three-dimensional protein structure shared between FABPs and OgLuc. However, strict agreement with this pattern is not needed to indicate commonality of the three-dimensional structure. From the examples given here, a common three-dimensional structure may exist even with as many as 5 changes in the pattern. Also, for example, although the dinoflagellate luciferase has a similar three-dimensional structure to FABPs and OgLuc, it has 4 differences from the improved pattern.

**[00272]** Thus, although a protein may be recognized as being a decapod luciferase based on sequence similarity and utilization of coelenterazine for luminescence, it can be further recognized by also having the improved sequence pattern. Specifically, a protein is a decapod luciferase if, upon alignment of its amino acid sequence with SEQ ID NO: 1 or variants thereof, the sequence identity is > 30%, preferably > 40%, and most preferably > 50%, and the protein can utilize coelenterazine as a substrate to catalyze the emission of luminescence, and the amino acid sequence beginning at the position corresponding to position 8 of SEQ ID NO: 1 is:

**[00273]** [GSAIVK]-{FE}-[FYW]-x-[LIVMFSYQ]-x-x-{K}-x-[NHGK]-x-[DE]-x-[LIVMFY]-[LIVMWF]-x-{G}-[LIVMAKRG] (SEQ ID NO: 330) (VII),

**[00274]** with no more than 5 differences, or more preferably no more than 4, 3, 2, or 1 difference, or most preferably no differences, wherein the differences occur in positions corresponding to pattern position 1, 2, 3, 5, 8, 10, 12, 14, 15, 17, or 18 of Formula (VII) according to Table 4. Differences may also include gaps or insertions between the pattern positions of Table 4.

**Table 4: Protein sequence patterns**

| Pattern position | PROSITE FABP pattern PS00214 | Other FABPs | OgLuc wt & variants | OgLuc pattern | OgLuc position | OgLuc wt sequence | Dinofl. Luc |
|---|---|---|---|---|---|---|---|
| 1 | [GSAIVK] (SEQ ID NO: 427) | | | [GSAIVK] (SEQ ID NO: 579) | 8 | G | G |
| 2 | {FE} | | | {FE} | 9 | D | R |
| 3 | [FYW] | | | [FYW] | 10 | W | W |
| 4 | x | | | x | 11 | Q | I |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 5 | [LIVMF] (SEQ ID NO: 590) | SY | Q | [LIVMFSYQ] (SEQ ID NO: 591) | 12 | Q | *T* |
| 6 | x | | | x | 13 | T | [VI] |
| 7 | x | | | x | 14 | A | S |
| 8 | {K} | | | {K} | 15 | G | G |
| 9 | x | | | x | 16 | Y | G |
| 10 | [NHG] | K | | [NHGK] (SEQ ID NO: 580) | 17 | N | *Q* |
| 11 | [FY] | SILM (SEQ ID NO: 581) | {FY} | x | 18 | Q | [AVTK] (SEQ ID NO: 582) |
| 12 | [DE] | | | [DE] | 19 | D | [*A*E] |
| 13 | x | | | x | 20 | Q | F |
| 14 | [LIVMFY] (SEQ ID NO: 583) | | | [LIVMFY] (SEQ ID NO: 584) | 21 | V | I |
| 15 | [LIVM] (SEQ ID NO: 585) | W | F | [LIVMWF] (SEQ ID NO: 586) | 22 | L | *K* |
| 16 | {K} | | K | x | 23 | E | [EKTQ] (SEQ ID NO: 587) |
| 17 | {G} | | | {G} | 24 | Q | [AV] |
| 18 | [LIVMAKR] (SEQ ID NO: 588) | | G | [LIVMAKRG] (SEQ ID NO: 589) | 25 | G | [VI] |

**Example 22 - Generation of OgLuc Variants**

**[00275]** *Experimental Details*

**[00276]** Unless otherwise stated, further variants of a starting OgLuc variant sequence with random substitutions were generated using the error-prone, mutagenic PCR-based system GeneMorph II Random Mutagenesis Kit (Stratagene; Daughtery, *PNAS USA*, 97(5):2029 (2000)), according to manufacturer's instructions, and NNK site saturation (Zheng *et al.*, *Nucleic Acids Research*, 32:e115 (2004)).

**[00277]** Further variants of a starting OgLuc variant having specific mutations were generated using the oligo-based site-directed mutagenesis kit QuikChange Site-Directed Mutagenesis Kit (Stratagene; Kunkel, *PNAS USA*, 82(2):488 (1985)), according to the manufacturer's instructions.

**[00278]** The resulting variants were constructed in the context of pF1K FLEXI® vector for T7 promoter-based expression (Promega Corp.). Alternatively, the resulting variants were

constructed in the context of pF4Ag vector (a version of the commercially-available pF4A (Promega Corp.), which contained T7 and CMV promoters modified to contain an *E. coli* ribosome-binding site with or without a C-terminal HALOTAG® (Promega Corp.; referred herein as "HT7") (Ohana *et al.*, *Protein Expression and Purification,* 68:110-120 (2009)) to generate a fusion protein. For example, to obtain C1+A4E variants, NNK saturation mutagenesis experiments were performed in a pF1K vector background. The C1+A4E library was generated in a pF4Ag vector background with no HT7. The QC27, QC27-9a, and IVY libraries were generated in a pF4Ag vector background with a C-terminal HT7. The IV-based variants were generated in a pF4Ag vector background without HT7. The resulting vectors were used to transform KRX *E. coli* using techniques known in the art.

**[00279]** Generated OgLuc variants are named for the amino acid substitutions identified in the variant and/or for the *E. coli* clone that contained the variant, e.g., FIG. 6A shows, among other results, that *E. coli* clone 16C5 has the substitution Q20R.

**[00280]** *Screening Details*

**[00281]** Resulting libraries were expressed in *E. coli* and primarily screened with a robotic system for OgLuc variants having increased light output (i.e., increased luminescence, increased brightness, or increased light emission) or a change in relative specificity compared to the corresponding starting OgLuc variant. The robotic primary screen was conducted as follows: individual colonies from the generated library were used to inoculate minimal media in 96-well plates and grown at 37°C for 17 to 20 hrs ("M1 culture"). The M1 culture was diluted 1:20 with fresh minimal media and grown at 37°C for 17 – 20 hrs ("M2 culture"). The M2 culture was diluted 1:20 into induction media and grown 17-20 hrs at 25°C with walk-away induction, i.e., autoinduction (Schagat *et al.*, "KRX Autoinduction Protocol: A Convenient Method for Protein Expression." *Promega Notes,* 98:16-18 (2008)). The induction media contained rhamnose and glucose when novel coelenterazines PBI-3841, PBI-3842, PBI-3857, PBI-3880, PBI-3881, PBI-3886, PBI-3887, PBI-3897, PBI-3896, or PBI-3894 were used as substrates in the primary screen. The induction media did not contain rhamnose or glucose when native coelenterazine, known coelenterazine-h, or novel coelenterazines PBI-3840, PBI-3889, PBI-3899, or PBI-3900 were used as substrates in the primary screen. The use of the different induction media was determined based on the luminescence generated between C1+A4E and the novel coelenterazines, i.e., the induction media containing rhamnose and glucose were used with novel coelenterazines that generated less luminescence with C1+A4E compared to the other novel coelenterazines with C1+A4E.

**[00282]** Ten µL of induced cells were lysed using 60 µL lysis buffer containing 300 mM HEPES pH 8.0, 300 mM thiourea, 0.3X Passive Lysis Buffer ("PLB"; Promega Corp. Cat. No. E194A), 0.3 mg/mL lysozyme, and 0.003 U/µL RQ1 DNase and measured for luminescence with 50 µL assay buffer containing 150 mM KCl, 1 mM CDTA, 10 mM DTT, 0.5% TERGITOL® NP-9 (v/v), and 20 µM of a native, known, or novel coelenterazine as a substrate. Luminescence measurements for each variant were taken 3 min after reagent addition and relative luminescence unit (RLU) values were normalized to an average of 8 control wells of the corresponding starting OgLuc variant for each plate. Assay was completed on a TECAN® robotic system.

**[00283]** OgLuc variants of interest were sequenced using standard sequencing techniques known in the art to identify any additional amino acid substitutions in each such variant. A secondary screen using a non-robotic (manual) system was performed on the variant clones of interest. The manual screen was conducted as follows: Variant clones were grown, in triplicate, in 96-well plates and expressed and assayed as described for the automated assay except the assay buffer was added manually with a multichannel pipette. For each variant, luminescence was measured, averaged, and normalized to the corresponding starting OgLuc variant. Luminescence measurements were made using a TECAN® INFINITE® F500 luminometer.

**[00284]** *Determining Change in Relative Specificity*

**[00285]** Relative substrate specificity was determined by dividing the luminescence of a luciferase in the presence of a test coelenterazine substrate by the luminescence of the luciferase in the presence of a reference coelenterazine substrate. For example, relative specificity was determined by dividing the luminescence of a luciferase with a novel coelenterazine of the present invention by the luminescence of the luciferase with a different coelenterazine (e.g., native or known coelenterazine, or a different novel coelenterazine of the present invention). The test coelenterazine substrate and the reference coelenterazine substrate that were compared were considered a comparison substrate pair for determining relative substrate specificity.

**[00286]** A change in relative substrate specificity was determined by dividing the relative substrate specificity of a test luciferase using a comparison substrate pair by the relative substrate specificity of a reference luciferase using the same comparison substrate pair. For example, a change in relative specificity was determined by dividing the relative substrate specificity of a test luciferase with a novel coelenterazine of the present invention compared to a different coelenterazine (e.g., native or known coelenterazine or a different novel coelenterazine of the present invention), by the relative substrate specificity of a reference luciferase with the same

novel coelenterazine of the present invention compared to the same different coelenterazine used for the test luciferase.

**[00287]** The luminescence with one novel coelenterazine was compared to the luminescence with a different novel coelenterazine. The luminescence with one native or known coelenterazine was compared to the luminescence with another native or known coelenterazine. The luminescence with one native or known coelenterazine was compared to the luminescence with a novel coelenterazine.

**[00288]** An increase in luminescence (RLUs) for the OgLuc variant compared to the corresponding starting OgLuc template for novel coelenterazine and a decrease or no change in luminescence for a reference coelenterazine was indicative of a change in relative specificity. A decrease in luminescence of an OgLuc variant for both the novel and reference coelenterazines compared to the corresponding starting OgLuc, but the luminescence of the OgLuc variant with the novel coelenterazine decreasing more, was also indicative of a change in relative specificity. An increase in luminescence of the OgLuc variant compared to the corresponding starting OgLuc for the novel and reference coelenterazines indicated an improvement in activity/stability/expression. If the luminescence of the OgLuc variant with both the novel and the reference coelenterazines increased, but the increase in luminescence with the novel coelenterazine was greater, it indicated an increase in relative specificity and an improvement in activity/stability/expression of the OgLuc variant.

**[00289]** *A. C1+A4E Variants*

**[00290]** C1+A4E (SEQ ID NOs: 2 and 3), previously described in U.S. Serial Application No. 12/773,002 (U.S. Published Application No. 2010/0281552), was used as a primary starting sequence (i.e., the parental sequence) for generating additional, synthetic OgLuc variants. C1+A4E has the following amino acid substitutions: A4E, Q11R, A33K, V44I, A54F, P115E, Q124K, Y138I, and N166R, relative to SEQ ID NO: 1. Luminescence of C1+A4E containing bacterial lysates, using the novel coelenterazines described in Examples 1-14 (see FIG. 4 for examples) as substrates, was measured as described previously and compared to the luminescence using native and known coelenterazines as substrates (FIGS. 5A-G). FIG. 5A shows the luminescence of C1+A4E using native coelenterazine ("coelenterazine"), known PBI-3880, and novel coelenterazines PBI-3842, PBI-3857, PBI-3881, PBI-3882, PBI-3886, and PBI-3887 as substrates. The luminescence measurements using known and novel coelenterazines were normalized to the luminescence of C1+A4E using native coelenterazine and the fold-decrease compared to native coelenterazine (FIG. 5B). FIGS. 5C-E show the luminescence of

C1+A4E using native coelenterazine and novel coelenterazines PBI-3945, PBI-3894, and PBI-4002, respectively. FIG. 5F shows the luminescence of C1+A4E using native coelenterazine and novel coelenterazines PBI-3840, PBI-3897, PBI-3889, PBI-3899, and PBI-3900. FIG. 5G shows the luminescence of C1+A4E using native coelenterazine, known coelenterazine PBI-3912 and novel coelenterazines PBI-3913, PBI-3925, PBI-3939, PBI-3933, PBI-3932, PBI-3946, PBI-3841, and PBI-3896. The data indicates the C1+A4E variant can use each of the novel coelenterazines as substrates.

**[00291]** C1+A4E variants were generated that had at least the amino acid substitutions identified in C1+A4E, unless otherwise indicated. A library (Library 1) of 4400 variant clones of C1+A4E was generated by random mutagenesis as described previously and screened as described previously for improvement in relative specificity change and/or activity change, e.g., brightness. The variants were primarily screened with native coelenterazine, known coelenterazine-h, known PBI-3880, and novel coelenterazines PBI-3840, PBI-3841, PBI-3842, PBI-3857, PBI-3881, PBI-3886, PBI-3887, PBI-3889, PBI-3897, and PBI-3900 as substrates. In addition, half of the variants were screened with novel coelenterazines PBI-3896 and PBI-3894 as substrates. Plates containing variants having known mutations of interest identified from screening previous novel compounds were selected. Variants that showed improvement (either relative specificity change or activity change) for one or more of the novel coelenterazines tested in the primary screen were isolated, sequenced, and screened in a secondary screen.

**[00292]** In the secondary manual screen, the variants were tested with known coelenterazines PBI-3912, coelenterazine-h, coelenterazine-hh, 2-methyl coelenterazine, and coelenterazine v; and novel coelenterazines PBI-3840, PBI-3897, PBI-3889, PBI-3899, PBI-3900, PBI-3925, PBI-3944, PBI-3932, PBI-3945, PBI-3913, and PBI-3896 as substrates. FIGS. 6A-D summarize the average luminescence normalized to C1+A4E for the variants ("Clone"). FIGS. 6A-D summarize the substitutions in these variants ("AA sequence"), which had at least one of the following additional amino acid substitutions: A14V, G15R, Q18L, Q20R, L22I, E23K, L27V, L27M, K33N, T39I, E49K, F54S, F54I, D55G, I56V, V58I, V58L, I59T, S66T, G67S, F68S, L72Q, M75K, I76N, F77T, F77C, K89E, I90V, I90T, L92H, H93R, M106K, Y109F, P113T, I117F, T126R, V127A, L136M, D139G, P145L, S148T, C164S, or A169V.

**[00293]** Amino acid substitutions at position 54, 92, and 109 were of interest as substitutions at these positions provided greater light output or improved relative specificity, i.e., specificity away from native coelenterazine and towards at least one novel coelenterazine, as shown in FIGS. 6A-C. The amino acid substitution F54I in clone 29H7 provided greater light output with native coelenterazine and several of the novel coelenterazines. The amino acid substitution

Q18L in clone 40H11, the amino acid substitution L92H in clone 04A12, and the amino acid substitution Y109F in clone 43F9 provided improved relative specificity.

**[00294]** Table 5 lists C1+A4E variants with an additional amino acid substitution at position 77, 92, or 109 ("AA change"), generated as described previously. These variants were analyzed for increased light output as described previously, i.e., screened for variants that were at least 1.3x brighter than C1+A4E, using native coelenterazine, known coelenterazine-hh, and novel coelenterazines PBI-3939, PBI-3894, PBI-3896, PBI-3897, PBI-3932, or PBI-3925 as a substrate. The following additional substitutions yielded a variant that was at least 1.3x brighter than C1+A4E: L92G, L92Q, L92S, L92A, L92M, L92H, L92Y, F77W, F77Y, F77S, F77T, F77V,, F77A, F77G, F77C, F77D, F77M, and Y109F. As shown in Table 5, L92H, F77W and F77A substitutions had the most dramatic improvements with PBI-3897, PBI-3896, and PBI - 3932.

**Table 5: Site Saturation of Positions 77, 92 and 109**

| AA Change | native | hh | PBI-3939 | PBI-3894 | PBI-3896 | PBI-3897 | PBI-3932 | PBI-3925 |
|---|---|---|---|---|---|---|---|---|
| L92G | 2.2 | | | | | | | |
| L92Q | 2 | 1.8 | 1.6 | 1.3 | 1.4 | 2.8 | 1.4 | 3.4 |
| L92S | 2.9 | | | | 1.5 | 2.9 | 2.7 | 6 |
| L92A | 2.5 | 1.3 | | | | | | |
| L92M | | 1.3 | | | | | | |
| L92H | | | | 2.2 | 21 | 9.1 | 3.4 | 5.9 |
| L92Y | | | | | | | | 2.5 |
| F77W | 1.4 | | 1.4 | 1.4 | 8.3 | 3.2 | 1.7 | 2.3 |
| F77Y | | | | | 1.6 | 1.3 | 4.9 | 6.5 |
| F77S | | | | | | | 2.6 | |
| F77T | | | | | | | 2.3 | |
| F77V | | | | | | | 2.3 | |
| F77A | | | | | | | 7.9 | 2.5 |
| F77G | | | | | | | 3.1 | |
| F77C | | | | | | | 2.3 | |
| F77D | | | | | | | 1.5 | |
| F77M | | | | | | | 1.5 | 1.6 |
| Y109F | | | | | 1.34 | 14 | | |

**[00295]** Additional C1+A4E variants (Group A) were generated by site-directed mutagenesis as described previously to have an additional substitution in at least one of the following amino acid positions relative to SEQ ID NO: 1: 18, 20, 54, 59, 72, 77, 89, 92, 109, 113, 127, 136, or 164. These amino acid positions were chosen because, based on the primary and secondary screens of Library 1, substitutions at these positions had increased total light output compared to C1+A4E using at least one of the following as a substrate: novel coelenterazines PBI-3841, PBI-3896, PBI-3897, PBI-3894, PBI-3925, or PBI-3932, or known coelenterazines 2-methyl coelenterazine or PBI-3912. FIG. 7 lists the variants ("Clone") and the additional amino acid substitutions contained in each variant. Variant clones were assayed in triplicate as described for the secondary manual screen as described previously and normalized to C1+A4E. FIGS. 8A-B and 9 show the normalized average luminescence of the variants listed in FIG. 7 with various coelenterazines as substrates. FIGS. 8A-B and 9 show variants with either large increases in luminescence for the listed novel compounds compared to C1+A4E or no change or a decrease in luminescence for the known coelenterazine compared to C1+A4E. Clone QC27, which has additional amino acid substitutions Q18L, F54I, L92H, and Y109F, had a 561.32-fold-increase in luminescence with PBI-3896, a 392.98-fold-increase with PBI-3894, and a 283.85-fold-increase with PBI-3896 compared to C1+A4E. This data shows that Q18L, L92H, and Y109F can be combined with each other and with additional substitutions to result in variants with improved relative specificity.

**[00296]** Other substitutions of interest identified from Library 1 were combined to generate additional variants (Group B) (FIG. 10). Additional amino acid substitutions were made in at least one of the following amino acid positions relative to SEQ ID NO: 1: 18, 20, 54, 71, 77, 90, 92, 109, or 127. These substitutions showed improvement with at least one of the following novel coelenterazines as a substrate: PBI-3841, PBI-3896, PBI-3897, PBI-3894, PBI-3925, or PBI-3932. These variants were assayed as described for Group A variants using native coelenterazine, known coelenterazine-hh, and novel coelenterazines PBI-3939, PBI-3945, PBI-3840, PBI-3932, PBI-3925, PBI-3894, and PBI-3896. Variant clones were assayed in triplicate as described for the secondary manual screen as described previously and normalized to C1+A4E. FIG. 11 shows the normalized average luminescence of the variants listed in FIG. 10 with the various coelenterazines as substrates. FIG. 11 shows variants with either large increases in luminescence for the listed novel coelenterazines compared to C1+A4E or no change or a decrease in luminescence for the native and known coelenterazine compared to C1+A4E.

**[00297]** Additional variants were generated with the additional amino acid substitution I90V and/or Y109F (Group C) and compared to variants generated from Group A or B (see FIG. 12). Clones containing variants with an I90V substitution ("I90V"), a Y109F substitution ("Y109F"), or both substitutions ("LE2") were compared to clones QC #27, QC#2 E7, QC#2 F4, and QC#1 A11 using assays as described for Group A recombinants with native coelenterazine, known coelenterazine-hh, and novel coelenterazines PBI-3939, PBI-3945, PBI-3889, PBI-3840, PBI-3925, PBI-3932, PBI-3894, PBI-3896, and PBI-3897 as substrates (FIG. 12). Variant clones were assayed in triplicate as described for the secondary manual screen as previously described and normalized to C1+A4E (FIG. 12). FIG. 12 shows variants with either large increases in luminescence for the listed novel coelenterazines compared to C1+A4E and no change or a decrease in luminescence for the native or known coelenterazine compared to C1+A4E. FIG. 12 shows that I90V provided greater light output for native coelenterazine and several of the novel substrates.

**[00298]** *B. QC27 Variants*

**[00299]** The variant QC27 (SEQ ID NOs: 4 and 5) from A, which has additional amino acid substitutions Q18L, F54I, L92H, and Y109F, was cloned into a pF4A modified vector as described previously to create a C-terminal HT7 (Promega Corp.) fusion protein ("QC27-HT7") (SEQ ID NOs: 44 and 45). 4400 variants of QC27-HT7 (Library 2) were generated by random mutagenesis as described previously, and primarily screened for increased relative specificity change as described previously using native coelenterazine and novel coelenterazines PBI-3896 and PBI-3897 as substrates. Variant clones were selected, sequenced, and assayed in a secondary manual screen as described previously using native coelenterazine, known coelenterazine-hh, and novel coelenterazines PBI-3897, PBI-3896, and PBI-3894 as substrates.

**[00300]** FIG. 13 lists the additional amino acid substitutions ("Sequence") identified in these variants ("Sample"), and the luminescence of the variants using native coelenterazine, known coelenterazine-hh, and novel coelenterazines PBI-3897, PBI-3896, and PBI-3894 as substrates in the secondary screen normalized to the corresponding starting QC27-HT7. The variants in FIG. 14, had at least one of the following additional amino acid substitutions: F1I, R11Q, L18I, L18Q, V21L, V21M, L22F, F31I, Q32H, V45E, L46Q, S47P, G48R, E49D, G51E, D55E, G67S, F68Y, F68L, Q69H, L72Q, E74K, E74I, M75K, I76F, I76V, H86R, I90T, H92Q, H92R, T96A, V98F, I99V, I99T, V102M, M106I, F109Y, L142V, V158I, T159S, L168F, or G170R (the G170R is located in the linker region between HT7 and the OgLuc variant).

**[00301]** The amino acid substitutions F68Y in variant 24B12, L72Q in variant 29C4, and M75K in variant 3H11 each provided greater light output for native coelenterazine and several of the novel substrates. The amino acid substitutions V21L in variant 25A11 and H92R in variant 1B6 provided improved relative specificity. Both of these substitutions were cases where luminescence signals were down using the novel coelenterazines as substrates, but were down more using native and known coelenterazines as substrates.

**[00302]** Additional QC27-HT7 variants were generated to have specific amino acid substitutions (FIG. 14) using site-directed mutagenesis as described previously. Additional substitutions were made in at least one of the following amino acid positions relative to SEQ ID NO: 1: 21, 68, 72, 75, 76, 90, 92, and 158, as these positions showed improvement in relative specificity change as shown in FIG. 14. FIG. 15 shows the luminescence of the QC27-HT7 variants using native coelenterazine, known coelenterazine-hh, and novel coelenterazines PBI-3897, PBI-3841, PBI-3896, and PBI-3894 as substrates normalized to the corresponding starting QC27-HT7. As seen in FIG. 15, combining the three amino acid substitutions F68Y, L72Q, and M75K with V158I, as for example in variant QC27#1, provided greater light output for each coelenterazine tested.

**[00303]** *C. QC27-9a Variants*

**[00304]** The variant QC27-9a (SEQ ID NOs: 6 and 7) from B, a QC27-HT7 fusion protein with additional amino acid substitutions V21L, H29R, F68Y, L72Q, M75K, and V158I, was used as a starting sequence to generate a library. 4400 variants of QC27-9a (Library 3) were generated by random mutagenesis as described previously and screened for increased relative specificity change using native coelenterazine and novel coelenterazines PBI-3841 and PBI-3897. Variant clones were selected, sequenced, and assayed in a secondary manual screen as described previously using native coelenterazine, known coelenterazine-hh, known coelenterazine-h, and novel coelenterazines PBI-3841 and PBI-3897 as substrates. FIG. 16 lists the additional substitutions ("AA change") identified in the variants ("Sample"), and the average luminescence of the variants using native coelenterazine, known coelenterazine-hh, known coelenterazine-h, and novel coelenterazines PBI-3841 and PBI-3897 as substrates in the secondary screen normalized to the corresponding starting QC27-9a. The increase in relative specificity represents cases where there was a decrease in luminescence for the variant with the novel, native, and known coelenterazines compared to the starting template, but luminescence with the native and known coelenterazines decreased more. For example, the variant 30D12 with the amino acid substitution L22F had an approximately three-fold loss in activity with the novel coelenterazines PBI-3841 and PBI-3897. However, with native coelenterazine, known

coelenterazine-h, and known coelenterazine-hh, the luminescence of the variant 30D12 was down by ten-fold or more.

**[00305]** FIG. 17 shows a comparison of the luminescence of C1+A4E, QC27-HT7 and QC27-9a compared to humanized *Renilla* luciferase (referred herein as "hRL") (SEQ ID NOs: 30 and 31) using native coelenterazine, known coelenterazine-hh, and novel coelenterazines PBI-3841 and PBI-3897 as substrates. Although the reaction of QC27-9a with PBI-3897 was brighter than QC27-9a with PBI-3841 (see FIG. 17), the evolution trend, i.e., magnitude of improvement in luminescence, was greatest for PBI-3841 (Table 6). Combining the improvement in luminescence (440-fold) with the decrease in luminescence for native coelenterazine (800-fold) indicated a change in relative specificity (350,000-fold) of QC27-9a using PBI-3841 compared to native coelenterazine.

**Table 6: The Change in Relative Specificity of the OgLuc Variants for PBI-3897 and PBI-3841 Compared to Native Coelenterazine and coelenterazine-hh.**

| Compound | Evolution trend: C1A4E to QC27 #9a | Change in relative specificity (novel coelenterazine/native coelenterazine) |
|---|---|---|
| coelenterazine | DOWN 800X | |
| coelenterazine-hh | DOWN 300X | |
| PBI-3897 | UP 100X | 80,000X |
| PBI-3841 | UP 440X | 350,000X |

**[00306]** *D. IVY Variants*

**[00307]** IVY (SEQ ID NOs: 8 and 9), a C1+A4E variant with additional amino acid substitutions F54I, I90V, and F77Y, was cloned into a pF4A modified vector as described previously to create a C-terminal HT7 fusion protein ("IVY-HT7"). 4400 variants of IVY-HT7 (Library 4) were generated by random mutagenesis and screened for increased light output (i.e., increased brightness) and increased relative specificity using native coelenterazine, known coelenterazine-hh, and novel coelenterazines PBI-3840, PBI-3889, PBI-3925, PBI-3932, and PBI-3945 as substrates. Variant clones were selected, sequenced, and assayed in triplicate in a secondary screen as described previously using native coelenterazine, known coelenterazine-hh, and novel coelenterazines PBI-3889, PBI-3939, PBI-3945, and PBI-4002 as substrates. FIGS. 18 and 19 lists the additional substitutions ("AA change") identified in the variants ("Sample") and

the average luminescence of the variants normalized to IVY-HT7 using native coelenterazine, known coelenterazine-hh, and novel coelenterazines PBI-3889, PBI-3939, PBI-3945, and PBI-4002 as substrates in the secondary screen. FIG. 18 lists those variants chosen based on performance with PBI-3945 (Group A), which had at least one of the following amino acid substitutions: Q18H, D19N, Q20P, Q32P, K33N, V38I, V38F, K43N, I44F, E49G, I60V, Q69H, I76N, Y77N, Y94F, G95S, G95D, F110I, V119M, K124M, L149I, or R152S. FIG. 19 lists those variants chosen based on performance with PBI-3889 (Group B), which had at least one of the following amino acid substitutions: F6Y, Q18L, L27V, S28Y, Q32L, K33N, V36E, P40T, Q42H, N50K, G51R, H86L, N135D, or I155T.

**[00308]** Additional IVY-HT7 variants were generated to have additional specific amino acid substitutions using site-directed mutagenesis as described previously. FIG. 20 lists variants with at least one of the following additional amino acid positions relative to SEQ ID NO: 1: 19, 20, 27, 32, 38, 43, 49, 58, 77, 95, 110, and 149, as these substitutions were identified in the variants of FIG. 18, which showed specificity towards PBI-3945 and PBI-4002. FIG. 21 shows the luminescence of the variants listed in FIG. 20 normalized to IVY-HT7 using native coelenterazine, known coelenterazine-h, known coelenterazine-hh, and novel coelenterazines PBI-3939, PBI-3945, PBI-4002, PBI-3932 and PBI-3840 as substrates. None of the variants showed an improvement over IVY-HT7, but there were instances, such as variant C5.19 (SEQ ID NOs: 12 and 13) where luminescence with native or a known coelenterazine decreased about 3-4 logs, but luminescence with PBI-3945 and PBI-4002 decreased only two-fold. Variant C5.19 has additional amino acid substitutions L27V, V38I, and L149I.

**[00309]** FIG. 22 lists variants with at least one of the following additional amino acid positions relative to SEQ ID NO: 1: 6, 18, 27, 28, 33, 34, 36, 40, 50, 51, 135, and 155, as these substitutions were identified in the variants of FIG. 19, which showed specificity towards PBI-3889 and PBI-3939. FIG. 23 shows the luminescence of the variants listed in FIG. 21 using native coelenterazine, known coelenterazine-h, known coelenterazine-hh, and novel coelenterazines PBI-3939, PBI-3945, PBI-3889, PBI-4002, PBI-3932, and PBI-3840 as substrates normalized to IVY-HT7. Luminescence decreased for each of the variants compared to IVY-HT7. Variant C1.3 (SEQ ID NOs: 10 and 11) had about 2000-fold more luminescence with PBI-3939 than with native or known coelenterazine. Variant C1.3 has additional amino acid substitutions F6Y, K33N, N135D, and I155T.

**[00310]** The best IVY-HT7 variants for relative specificity change compared to hRL and IVY-HT7 were C5.19, which had the best luminescence with PBI-3945, and C1.3, which had the best luminescence with PBI-3889. FIG. 24 shows the luminescence of hRL, IVY-HT7, C5.19 (a C-

terminal HT7 fusion), and C1.3 (a C-terminal HT7 fusion) with native coelenterazine, known coelenterazine-h, known coelenterazine-hh, and novel coelenterazines PBI-3939 and PBI-3945.

**[00311]** *E. IV Variants*

**[00312]** IV (SEQ ID NOs: 14 and 15), a C1+A4E variant with additional amino acid substitutions F54I and I90V, was generated as previously described. To determine the brightest variant for use as a transcriptional reporter, luminescence was measured as described previously provided for C1+A4E (SEQ ID NOs: 2 and 3), IVY (SEQ ID NOs: 8 and 9), and IV (SEQ ID NOs: 14 and 15) using native coelenterazine, known coelenterazine-hh, and novel coelenterazines PBI-3939, PBI-3945, PBI-3889, and PBI-4002 as substrates. hRL was used as a control. As seen in FIG. 25, IV was brighter than both C1+A4E and IVY. The amino acid substitution F54I in IV provided greater light output for native coelenterazine and several of the novel substrates. All three variants were brighter than hRL with the tested coelenterazines.

**[00313]** The data from A, B and D (i.e., screenings of the libraries generated from C1+A4E, IVY, and QC27 as the starting sequences) were reviewed to determine those additional amino acid substitutions with increased light output (i.e., increased brightness) with a variety of coelenterazines. IV variants were generated as described previously to have additional substitutions which had reduced specificity for native coelenterazine by two- to ten-fold. As listed in FIG. 26, the IV variants ("clone") had an additional amino acid substitution ("Sequence") of at least one of the following amino acid substitutions: F1I, E4K, Q18L, L27V, K33N, V38I, F68Y, M70V, L72Q, M75K, or V102E.

**[00314]** Sixteen plates of variant clones for all combinations of amino acid substitutions were primarily screened and assayed using the automated robot method described previously with native coelenterazine, known coelenterazine-h, known coelenterazine-hh, and novel coelenterazines PBI-3889 and PBI-3945 as substrates. Variants with improved luminescence were selected, sequenced, and assayed in triplicate using the manual screen as described previously. Luminescence was measured using native coelenterazine, known coelenterazine-h, known coelenterazine-hh, and novel coelenterazines PBI-3889, PBI-3939, PBI-3945, and PBI-4002 as substrates. Corresponding starting sequences IV and hRL were used as controls.

**[00315]** FIG. 26 lists the variants, and the additional amino acid substitutions identified in the variants. FIG. 27 shows the average luminescence of the variants in the secondary screen normalized to IV. Variant 8A3 (SEQ ID NOs: 26 and 27), which has additional amino acid substitutions F1I, L27V, and V38I, had improved relative specificity with novel coelenterazines,

but was not brighter than IV. Variant 8F2 (SEQ ID NOs: 46 and 47), which has additional amino acid substitution L27V, offered improved relative specificity and brightness with 3 of the 4 novel coelenterazines used. Variant 9B8 (SEQ ID NOs: 18 and 19), which has additional amino acid substitutions Q18L, F68Y, L72Q, and M75K, was brighter for all substrates and offered some relative specificity advantage over native coelenterazine as well. Variant 9F6 (SEQ ID NOs: 20 and 21), which has additional amino acid substitutions Q18L, L27V, V38I, F68Y, L72Q, and M75K, showed similar improvements as was seen with 8F2. Variant 15C1 (SEQ ID NOs: 16 and 17), which has additional amino acid substitutions E4K, K33N, F68Y, L72Q, and M75K, was brighter for all novel coelenterazines, but did not have any improved relative specificity benefit. The amino acid substitution Q18L in variant 1D6 provided improved relative specificity, i.e., away from native coelenterazine and towards novel substrates, in the context of IV. In general, the amino acid substitution L27V provided improved relative specificity in the context of IV.

**[00316]** FIG. 28 shows the luminescence of the 8A3, 9B8, 9F6, and 15C1 variants in the secondary screen using native coelenterazine, known coelenterazine-hh, known coelenterazine-h, and novel coelenterazines PBI-3939, PBI-3945, PBI-3889, and PBI-4002 as substrates compared to IV and hRL. Variant 8A3 had 2 logs decrease in brightness with native coelenterazine compared to IV. Variant 9F6 had 1 log decrease in brightness with native coelenterazine compared to IV. Variant 15C1 with PBI-3945 was the brightest, but the signal half-life was short (see Example 27).

**[00317]** *F. 9B8 Variants*

**[00318]** The 9B8 variant from E was further modified to generate additional variants with increased light emission and/or improved relative specificity for PBI-3939. Amino acid substitution L72Q appeared to be a beneficial amino acid substitution for increased light emission (i.e., brightness) as this substitution was identified in the variants 9B8, 9F6, and 15C1, all of which showed improved light emission. To determine if other amino acid substitutions at position 72 would provide similar increases in brightness, additional variants of 9B8 were generated as described previously by saturating position 72 with alternative residues. Four replicates of *E. coli* lysates were prepared and analyzed for brightness as described previously using PBI-3939 as a substrate except the assay buffer contained 10 mM CDTA, 150 mM KCl, 10 mM DTT, 100 mM HEPES, pH 7.0, 35 mM thiourea, and 0.5% TERGITOL® NP-9 (v/v). Table 7 lists 9B8 variants ("Variant") with similar or improved luminescence compared to 9B8 as indicated by luminescence normalized to 9B8 ("RLU (normalized to 9B8)"), i.e., fold

improvement. The amino acid substitutions of A, G, N, R, and M at position 72 provided at least the same brightness benefit as amino acid Q, i.e., 1-fold.

**Table 7: Variants with Similar Luminescence Compared to Variant 9B8.**

| Variant | RLU (normalized to 9B8) |
|---|---|
| 9B8 + Q72A | 1.1 |
| 9B8 + Q72G | 1 |
| 9B8 + Q72N | 1 |
| 9B8 + Q72R | 1 |
| 9B8 + Q72M | 1 |

**[00319]** Additional variants with improved relative specificity to novel PBI-3939 were generated as described previously by saturating amino acid positions 18, 68, 72, 75, and 90 in variant 9B8. *E. coli* lysates were prepared and analyzed for brightness as described previously using native coelenterazine and novel PBI-3939 as substrates. Relative specificity was determined from the ratio of the luminescence of the variant with PBI-3939 to the luminescence of the variant with native coelenterazine, normalized to the ratio of corresponding luminescence of 9B8. Table 8 lists 9B8 variants ("Variant") with at least 1.1X fold-increase in relative specificity for PBI-3939. The results demonstrate that at least one additional change at each of the sites provided improved relative specificity for PBI-3939 versus native coelenterazine. 9B8 variants with amino acid substitutions K, D, F, G, Y, W, and H at position 18 had the highest fold improvement in relative specificity.

**Table 8: Variants with Improved Relative Specificity for PBI-3939**

| Variant | Relative specificity<br>(PBI-3939 RLU/native coelenterazine RLU; normalized to 9B8) |
|---|---|
| 9B8 + L18K | 40.7 |
| 9B8 + L18D | 25.8 |
| 9B8 + L18F | 25.6 |
| 9B8 + L18G | 18.2 |
| 9B8 + L18Y | 17.8 |

| | |
|---|---|
| 9B8 + L18W | 11.2 |
| 9B8 + L18H | 9.1 |
| 9B8 + L18R | 3.5 |
| 9B8 + L18M | 3.4 |
| 9B8 + L18N | 2.9 |
| 9B8 + L18P | 2.6 |
| 9B8 + L18S | 2.3 |
| 9B8 + Y68W | 1.1 |
| 9B8 + Q72W | 6.1 |
| 9B8 + Q72Y | 2.5 |
| 9B8 + Q72F | 2.2 |
| 9B8 + Q72V | 2.2 |
| 9B8 + Q72I | 2.1 |
| 9B8 + Q72T | 1.9 |
| 9B8 + Q72N | 1.8 |
| 9B8 + Q72R | 1.7 |
| 9B8 + Q72P | 1.6 |
| 9B8 + Q72G | 1.5 |
| 9B8 + Q72A | 1.4 |
| 9B8 + Q72M | 1.3 |
| 9B8 + Q72C | 1.3 |
| 9B8 + Q72H | 1.2 |
| 9B8 + Q72S | 1.2 |
| 9B8 + M75F | 1.2 |
| 9B8 + V90R | 2.4 |
| 9B8 + V90Y | 1.6 |
| 9B8 + V90D | 1.4 |
| 9B8 + V90P | 1.4 |
| 9B8 + V90K | 1.3 |
| 9B8 + V90Q | 1.2 |

**[00320]** *G. 9B8 + K33N Variants*

**[00321]** An additional variant, 9B8 opt+K33N (SEQ ID NOs: 42 and 43) was generated to investigate the benefits of amino acid substitution K33N for brightness, relative specificity, and thermal stability. 9B8 opt+K33N was examined and compared to 9B8 opt (described in Example 25A) in various applications.

**[00322]** *E. coli* lysates containing the variant 9B8 opt or 9B8 opt+K33N were prepared and analyzed as described previously except the assay buffer contained 0.1% TERGITOL® NP-9 (v/v). Luminescence generated from the lysates was measured using the novel PBI-3939 and native coelenterazine as substrates. The relative specificity of the variants for PBI-3939 and native coelenterazine was calculated as described previously. 9B8 opt+K33N ("K33N") had greater light output (RLU) and a higher relative specificity for PBI-3939 than native coelenterazine compared to 9B8 opt (FIG. 29), indicating that the K33N substitution provided greater light output and improved relative specificity.

**[00323]** A new OgLuc library was created using 9B8opt+K33N as a starting template. The random library was created using DIVERSIFY® PCR Random Mutagenesis Kit (ClonTech; Catalog # 630703). Condition 5 (as listed in the user manual) was used to generate additional variants, and the average mutation rate was calculated to be 2.6 mutations per gene by compiling sequence data from 83 randomly selected clones. This PCR library was cloned into the pF4Ag-based, non-fusion vector background described previously and the sandwich background, i.e., Id-OgLuc-HT7 (described in Example 45). Variants in the pF4Ag-base non-fusion vector background are designated with (NF). Variants in the sandwich vector background are designated with (F). In order to clone the PCR product into both vectors, an amino acid, i.e., a glycine, was appended to the variant sequence in pF4Ag, generating a new position 170 in the OgLuc variant ("170G"). The 170G is present in the sandwich construct, but in this case is considered part of the linker between OgLuc and HT7. For each library, 4,400 *E. coli* clones were assayed as described previously with the following exceptions. The lysis buffer contained 300 mM MES pH 6.0 instead of HEPES, and 0.5% TERGITOL® NP-9 (v/v), but did not contain thiourea. The assay buffer contained 100 mM MES pH 6.0 instead of HEPES, and 35 mM thiourea. The assay volumes were as follows: 10 µL cells, 40 µL lysis buffer, and 50 µL assay buffer.

**[00324]** The PCR library in the pF4Ag-based non-fusion background was screened for additional variants with increased luminescence compared to 9B8 opt+K33N+170G (SEQ ID NOs: 68 and 69). Selected variants were then assayed in HEK293 and NIH3T3 cells. For each

cell type, 15,000 cells were plated and grown overnight at 37°C. The next day, the cells were transfected as described in Example 25 with 10 ng pGL4.13 (Promega Corp.) as a transfection control and 100 ng of the OgLuc test DNA. The media was removed, and the cells were lysed with 100 µL of lysis buffer as described in Example 25 except the lysis buffer contained 100 mM MES pH 6.0 instead of HEPES, and luminescence measured using a GLOMAX® Luminometer. For each sample, 10 µL of lysate was assayed with 50 µL of lysis buffer containing 20 µM PBI-3939. For the transfection control, 10 µL of lysate was assayed with 50 µL of BRIGHT-GLO™ Assay Reagent.

**[00325]** Table 9 shows the fold-increase in luminescence of variants in *E. coli,* HEK293, and NIH3T3 cells and the amino acid substitutions found in the variants. The variants 27A5 (NF) (SEQ ID NOs: 70 and 71), 23D4 (NF) (SEQ ID NOs: 72 and 73) and 24C2 (NF) (SEQ ID NOs: 74 and 75) had at least 1.3 fold-increase in luminescence in *E. coli* and HEK293 cells.

**Table 9: Increase in Luminescence Generated by OgLuc Variants Compared to 9B8 opt+K33N+170G in *E. coli,* HEK293 and NIH3T3 Cells**

| Sample | Sequence | Fold over 9B8 opt+K33N + 170G | | |
|---|---|---|---|---|
| | | *E. coli* | HEK293 | NIH3T3 |
| 27A5 (NF) | T39T, 170G | 1.3 | 1.5 | 1.3 |
| 23D4 (NF) | G26G, M106L, R112R, 170G | 1.5 | 1.6 | 1.2 |
| 24C2 (NF) | R11Q, T39T, 170G | 1.5 | 1.5 | 1.1 |

**[00326]** Based on the above data, further combination variants were designed and generated (see Table 10) in the context of the pF4Ag-based non-fusion vector background without the 170G. The variants were analyzed in *E. coli,* HEK293 and NIH3T3 cells as described above and compared to 9B8 opt+K33N. The variants were also examined for luminescence with native coelenterazine. Table 10 shows the fold-increase in luminescence of the variants in *E. coli,* HEK293, and NIH3T3 cells, and the amino acid substitutions found in the variants ("Sample"). The variants were named by adding the additional amino acid substitutions in the variant to the prefix "9B8 opt+K33N." Table 11 shows the relative specificity of the different variants for PBI-3939 compared to native coelenterazine in *E. coli,* NIH3T3, and HEK293 cells. As shown in Table 10, the variant 9B8 opt+K33N+T39T+K43R+Y68D ("V2"; SEQ ID NOs: 92 and 93) had improved luminescence in *E. coli* and a slight improvement in luminescence in NIH3T3 cells. The variant 9B8 opt+K33N+L27V+K43R+Y68D ("L27V, K43R, Y68D") had a neutral

improvement in luminescence (Table 10) and 5X fold-increase in relative specificity over 9B8 opt+K33N (Table 11) in the three cell types examined.

**Table 10: Increase in Luminescence Generated by OgLuc Combination Variants Compared to 9B8 opt+K33N in *E. coli*, NIH3T3 and HEK293 Cells**

| Sample | Fold over 9B8 opt +K33N | | |
|---|---|---|---|
| | *E. coli* | NIH3T3 | HEK293 |
| T39T | 1.8 | 1.1 | 1.1 |
| K43R | 1.2 | 1.1 | 1.1 |
| T39T, K43R | 1.3 | 0.9 | 1.1 |
| Y68D | 1.0 | 1.0 | 1.2 |
| K43R, Y68D | 1.2 | 1.2 | 1.2 |
| T39T, K43R, Y68D ("V2") | 1.8 | 1.1 | 1.3 |
| L27V | 0.9 | 0.7 | 0.8 |
| L27V, K43R | 0.7 | 0.6 | 0.6 |
| L27V, K43R, Y68D | 1.2 | 0.8 | 0.9 |
| L27V, Y68D | 1.2 | 0.8 | 0.7 |
| S66N, K43R | 0.9 | 1.1 | 1.1 |
| L27V, K43R, S66N | 1.0 | 0.6 | 0.7 |
| 9B8 opt + K33N | 1.0 | 1.0 | 1.0 |

**Table 11: Change in Relative Specificity of OgLuc Combination Variants for PBI-3939 Compared to Native Coelenterazine in *E. coli*, NIH3T3 and HEK293 Cells**

| Sample | Fold over Native Coelenterazine | | |
|---|---|---|---|
| | *E. coli* | NIH3T3 | HEK293 |
| T39T | 18.2 | 18 | 20 |
| K43R | 29.5 | 31 | 32 |
| T39T, K43R | 29.4 | 30 | 32 |
| Y68D | 11.4 | 10 | 12 |
| K43R, Y68D | 18.6 | 19 | 21 |
| T39T, K43R, Y68D ("V2") | 18.5 | 18 | 21 |
| L27V | 85.2 | 85 | 97 |

| | | | |
|---|---|---|---|
| L27V, K43R | 120.1 | 131 | 147 |
| L27V, K43R, Y68D | 98.3 | 98 | 101 |
| L27V, Y68D | 59.9 | 61 | 64 |
| S66N, K43R | 22.9 | 23 | 25 |
| L27V, K43R, S66N | 100.4 | 97 | 106 |
| 9B8 opt + K33N | 19.0 | 19 | 19 |

**[00327]** Additional OgLuc variants were generated from 9B8 opt+K33N to contain at least one of the following additional amino acid substitutions relative to SEQ ID NO: 1: L27V, T39T, K43R, Y68D, or S66N (see "Sample" in Table 12 for the amino acid substitutions in the variants). The variants were named by adding the additional amino acid substitutions in the variant after the prefix "9B8 opt+K33N." These additional variants and the variants 9B8 opt+K33N+L27V+Y68D ("L27V, Y68D"), 9B8 opt+K33N+L27V+K43R+Y68D ("L27V, K43R, Y68D"), 9B8 opt+K33N+L27V+K43R+S66N ("L27V, K43R, S66N"), and 9B8 opt+K33N+T39T+K43R+Y68D ("T39T, K43R, Y68D"; also known as "V2") from above, were examined for brightness, relative specificity, signal stability and thermal stability. The variants were compared to the variants 9B8 opt ("9B8") and 9B8 opt+K33N ("K33N").

**[00328]** *E. coli* lysates containing the variants were prepared and analyzed as described previously. Luminescence generated from the lysates was measured using the novel PBI-3939 and native coelenterazine as substrates. The luminescence of the variants was normalized to the luminescence generated by 9B8 opt (Table 12). The relative specificity of the variants for PBI-3939 and native coelenterazine was calculated by dividing the luminescence of the variants using PBI-3939 as a substrate with the luminescence of the variants using native coelenterazine as a substrate (Table 12). This data indicates that the amino acid substitution L27V lowers specificity for native coelenterazine.

**Table 12: Increase in Luminescence Generated by OgLuc Variants Compared to 9B8 and Change in Specificity of OgLuc Variants for PBI-3939 Compared to Native Coelenterazine in Bacterial Lysates**

| Sample | Fold over 9B8 | Fold over coelenterazine |
|---|---|---|
| 9B8 | 1.0 | 7 |
| K33N | 1.1 | 21 |
| T39T, Y68D | 0.9 | 12 |
| T39T, L27V, K43R | 1.2 | 149 |
| L27V, T39T, K43R, Y68D | 1.8 | 110 |
| T39T, K43R, Y68D | 1.6 | 21 |
| L27V, T39T, K43R, S66N | 1.3 | 114 |
| L27V,K43R, Y68D | 1.3 | 110 |
| L27V, Y68D | 1.0 | 63 |
| L27V, K43R, S66N | 1.1 | 114 |

**[00329]** *H. V2 Variants*

**[00330]** A set of additional variants were designed using V2 (9B8opt with the additional amino acid substitutions K33N+T39T+K43R+Y68D) as a template. The substitutions shown in Table 13 were designed based on either 1) the known diversity according to the structure-based alignment of 28 fatty acid binding proteins (1VYF, 1FDQ, 2A0A, 1O8V, 1BWY, 2ANS, 1VIV, 1PMP, 1FTP, 2HNX, 1JJJ, 1CBR, 2CBS, 1LPJ, 1KQW, 2RCQ, 1EII, 1CRB, 1IFC, 2PYI, 2JU3, 1MVG, 2QO4, 1P6P, 2FT9, 1MDC, 1O1U, 1EIO; See U.S. Published Application No. 2010/0281552), or 2) the probing of alternative residues at positions previously identified to play a role in substrate specificity. Changes listed under "Consensus" in Table 13 relate to residues identified in at least 50% of the aligned, above-mentioned fatty acid binding proteins. Changes listed under "Predominant Minority" relate to residues identified in many of the fatty acid binding proteins mentioned above, but found in fewer than 50% of the aligned sequences. Changes listed under "Other" relate to residues were identified less frequently than the predominant minority residue at a given position in the aligned sequences. Finally, changes listed under "Specificity" relate to positions suspected to be involved in determining a variant's specificity for coelenterazine or a coelenterazine analog. For example, the designed specificity changes at position 27 (leucine residue in the parental sequence, i.e., V2) were changed to other hydrophobic residues or amino acids representing alternative chemistries (e.g., other hydrophobic residues containing rings, residues containing uncharged polar side chains, or residues containing charged side chains); and the designed specificity changes at position 40 (proline in the parental sequence), were to a sampling of different chemistries (chemistries (e.g., other hydrophobic residues containing rings, residues containing uncharged polar side chains, or residues containing charged side chains); note that glycine, glutamine, isoleucine, and leucine are identified at this position the aligned fatty acid binding proteins).

**Table 13**

| Consensus | Predominant minority | Other | Specificity |
|---|---|---|---|
| 9 T | 9 K | 9 R | 27 A, I, M, G, S |
| 14 S | 10 Y | 40 G | 40 T, S, F, D, Y |
| 16 E | 23 R | | |
| 22 M | 32 I | | |
| 23 K | 63 T | | |
| 24 A | 87 T | | |
| 25 L | 100 I | | |
| 32 R | 111 N, D | | |
| 35 A | 118 I | | |
| 39 K | 134 K | | |
| 46 Q | 142 K, W | | |
| 57 F | 147 N | | |
| 63 S | 149 M | | |
| 87 N | 152 E | | |
| 97 E | 162 Q | | |
| 98 F | | | |
| 100 E | | | |
| 102 T | | | |
| 110 D | | | |
| 113 K | | | |
| 118 V | | | |
| 125 L | | | |
| 126 V | | | |
| 129 Q | | | |
| 130 K | | | |
| 142 E | | | |
| 146 G | | | |
| 147 D | | | |
| 150 V | | | |
| 152 T | | | |
| 165 K | | | |

**[00331]** The variants were constructed using standard site-directed mutagenesis protocols (see previous examples), and the resulting plasmids transformed into *E. coli* for analysis. Cultures were grown per standard walk away induction in minimal media as described previously. To 10 µL of the cultured, transformed *E. coli* cells, 40 µL of lysis buffer (100 mM MES pH 6.0, 0.3X PLB, 0.3 mg/mL Lysozyme, 0.003 U/µL RQ1 DNaseI and 0.25% TERGITOL® NP-9 (v/v)) was added followed by the additional of an equal volume (50 µL) of assay reagent (1 mM CDTA, 150 mM KCl, 2 mM DTT, 20 µM PBI-3939 or native coelenterazine, 100 mM MES pH 6.0, 35 mM thiourea, and 0.5% TERGITOL® NP-9 (v/v)). Luminescence was measured on a GLOMAX® 96 Microplate Luminometer (Promega Corp.).

**[00332]** Table 14 summarizes the different amino acid substitutions identified in the analysis. The data is presented as normalized to the parental clone (V2) with regards to the luminescence measured for both PBI-3939 and native coelenterazine. The relative change in specificity to PBI-3939 with respect to native coelenterazine is also shown.

**Table 14**

| Substitution | PBI-3939 NORMALIZED | COELENTERAZINE NORMALIZED | RELATIVE CHANGE IN SPECIFICITY FOR PBI-3939 |
|---|---|---|---|
| 10 Y | 0.7 | 0.2 | 3.5 |
| 14 S | 1.3 | 1.2 | 1.1 |
| 16 E | 0.5 | 0.2 | 2.5 |
| 23 K | 1.3 | 4 | 0.3 |
| 24 A | 0.4 | 0.2 | 2.0 |
| 25 L | 0.0001 | 0.000023 | 4.3 |
| 27 A | 0.8 | 0.1 | 8.0 |
| 27 D | 0.006 | 0.001 | 6.0 |
| 27 G | 0.088 | 0.005 | 17.6 |
| 27 I | 0.2 | 0.024 | 8.3 |
| 27 M | 2.2 | 0.9 | 2.4 |
| 40 I | 0.0017 | 0.0002 | 8.5 |
| 40 L | 0.0007 | 0.0001 | 7.0 |
| 40 Q | 0.0001 | 0.000026 | 3.8 |
| 87 H | 1.2 | 1.5 | 0.8 |
| 87 T | 1.3 | 1.6 | 0.8 |
| 97 E | 0.014 | 0.01 | 1.4 |
| 100 I | 0.002 | 0.002 | 1.0 |
| 102 T | 1.1 | 1.1 | 1.0 |
| 111 H | 0.6 | 0.6 | 1.0 |
| 113 K | 1.2 | 0.6 | 2.0 |
| 125 L | 0.6 | 0.4 | 1.5 |
| 129 Q | 0.0003 | 0.0001 | 3.0 |
| 130 K | 1.1 | 0.9 | 1.2 |
| 142 E | 0.9 | 0.3 | 3.0 |
| 142 K | 0.9 | 0.3 | 3.0 |
| 142 W | 0.8 | 0.4 | 2.0 |
| 146 G | 0.9 | 0.8 | 1.1 |
| 147 H | 0.4 | 0.4 | 1.0 |
| 149 M | 0.7 | 0.4 | 1.8 |
| 150 V | 0.9 | 0.4 | 2.3 |
| 152 E | 0.9 | 0.5 | 1.8 |
| 152 T | 0.9 | 0.3 | 3.0 |

**[00333]** *I. L27V Variants*

**[00334]** Using the OgLuc variant L27V as a starting template, i.e., starting sequence or parental sequence, additional variants were made in which some of the amino acids (Table 15) in the L27V variant were reverted to the amino acids found in the native OgLuc luciferase of SEQ ID NO: 1. The variants were constructed by site-directed mutagenesis as previously described. The variants were then screened as previously described for relative activity with either native coelenterazine or PBI-3939. Luminescence was measured on a TECAN® INFINITE® F500 5 min after substrate/assay reagent (as described in H) was added and normalized to the L27V variant starting template. SDS-PAGE analysis of the lysates indicates comparable expression levels (data not shown).

**[00335]** Table 15 shows the relative activities of the L27V variants with native coelenterazine or PBI-3939. Relative activities <1 indicate the reversion is detrimental compared to the residue

at that site in the L27V variant. Relative activities >1 indicate the reversion is favorable for activity compared to the residue at that site in the L27V variant. Some additional data on these mutants indicated the following: 166K, 54F, 54A and L27V were tested for thermal stability. The $T_{1/2}$ 60°C for 166K, 54F, and 54A were 87, 74, and 33%, respectively, indicating these substitutions cause a reduction in thermal stability. The Km values for these same 4 variants were the following: for native coelenterazine, L27V was 16 μM, 54A was 23 μM, 54F was 40 μM, and 166K was 21 μM; for PBI-3939, L27V was 18 μM, 54A was 62 μM, 54F was 163 μM, and 166K was 23 μM. This indicates higher substrate affinity for L27V, particularly for the position 54 substitutions.

**Table 15**

| Native coelenterazine (50 mM) | | PBI-3939 (50 mM) | |
|---|---|---|---|
| AA substitution | Relative activity (5 min) | AA substitution | Relative activity (5 min) |
| 72L | 0.2 | 72L | 0.6 |
| 4A | 1.0 | 4A | 1.0 |
| 124Q | 1.6 | 124Q | 1.0 |
| 43K | 1.9 | 43K | 1.1 |
| 115P | 0.6 | 115P | 0.9 |
| 166N | 2 | 166N | 2.0 |
| 75M | 1.1 | 75M | 1.2 |
| 54F | 0.1 | 54F | 0.4 |
| 68F | 0.5 | 68F | 0.9 |
| 33A | 1.7 | 33A | 1.0 |
| 138Y | 1.0 | 138Y | 1.0 |
| 54A | 0.6 | 54A | 1.6 |
| 90I | 0.8 | 90I | 0.6 |
| 33K | 4.2 | 33K | 0.8 |
| 44V | 0.7 | 44V | 1 |
| 166K | 2.1 | 166K | 2 |
| 11Q | 1.6 | 11Q | 1.3 |
| 166F | 0.3 | 166F | 0.4 |
| 18Q | 4.1 | 18Q | 0.6 |

**Example 23 - Mutational Analysis of Position 166**

**[00336]** A. To assess the effect of different amino acids at position 166 on the luciferase activity, the arginine (R) residue at position 166 was substituted to each of the other 19 amino acids using site-directed mutagenesis as previously described in the context of a pF4Ag vector (i.e., in the context of the wild-type OgLuc sequence SEQ ID NO: 1). These position 166 variants were then expressed in *E. coli* as previously described.

**[00337]** To create lysates, 50 µL 0.5X FASTBREAK™ Cell Lysis Reagent (Promega Corp.) was added to 950 µl of induced cultures, and the mixtures incubated for 30 min at 22°C. For the analysis, 50 µL of lysate was assayed in 50 µL of assay reagent (as previously described in Example 22H) with either 100 µM PBI-3939, 30 µM native coelenterazine, or 22 µM coelenterazine-h). Luminescence was measured as previously described (FIGS. 30A-C). FIGS. 30A-C show the relative activity of the N166 mutants. Western analysis confirmed comparable expression of all variants (data not shown).

**[00338]** B. The specific single amino acid substitutions, L27V, A33N, K43R, M75K, T39T, L72Q and F68D were assessed in the wild-type OgLuc or N166R background. The single amino acid substitutions were generated via site-directed mutagenesis as previously described, expressed in *E. coli* as previously described, and luminescence measured using the assay reagent (previously described in Example 22H) with 22 µM native coelenterazine (FIG. 30D). Western analysis confirmed comparable expression of all variants (data not shown).

**Example 24 - Deletion Variants**

**[00339]** Deletions to the L27V variant were made as follows:

**Table 16**

| Deletion # | Deletion Made |
|---|---|
| 27 | Residues 1-27 and Val -1 |
| 52 | Residues 1-52 and Val -1 |
| 64 | Residues 1-64 and Val -1 |
| 84 | Residues 1-84 and Val -1 |
| 19 | Residues 65-83 |
| 23 | Residues 65-87 |
| 23A1 | Residues 65-87 + G64D |

**[00340]** The N-terminus of the OgLuc variant L27V is methionine, valine and phenylalanine, i.e., MVF. For numbering purposes, the phenylalanine was considered the first amino acid. "Val-1" indicates that the Valine in "MVF" was deleted. The methionine of "MVF" was included in these deletions. The L27 deletion variants were cloned in the pF4Ag vector and expressed in *E. coli* KRX cells as previously described. Inductions and lysate preparations were performed as described Lysates were analyzed using the assay reagent (previously described; 100 μM PBI-3939), and luminescence measured as previously described (FIG. 31). The data demonstrates that smaller fragments of the OgLuc variants can also generate luminescence.

**Example 25 – Codon Optimization of OgLuc Variants**

**[00341]** A. *IV and 9B8*

**[00342]** The IV and 9B8 OgLuc variants were used as templates for codon optimization. The goals, as understood by those skilled in the art, were two-fold: 1) to remove known transcription factor binding sites, or other regulatory sequences, e.g., promoter modules, splice donor/acceptor sites, splice silencers, Kozak sequences, and poly-A signals, that could potentially interfere with the regulation or expression of the OgLuc variants, and 2) to alter the DNA sequence (via silent mutations that do not alter protein sequence) to eliminate rarely used codons, and favor the most commonly used codons in cells of *E. coli,* human, other mammalian, or other eukaryotic organisms (Wada *et al.*, *Nucleic Acids Res.*, 18:2367 (1990)).

**[00343]** Two different optimized sequences for IV and 9B8, referred to as opt (aka optA) and optB, were designed for each variant. The first optimized sequence, i.e., opt/optA for each variant, was designed by identifying the two best, i.e., most common, human codons for each site (see Table 17) and then randomly picking one of the two for incorporation at each site. For the optB versions, the previous, codon-usage, optimized version, i.e., opt/optA, was used as a starting template, and each codon replaced with the other of the two best human codons identified for this codon-optimization strategy. As an example, the leucine at position 3 in either the IV or 9B8 sequence is encoded by the codon TTG. TTG is not one of the two most common codons for leucine in a human cell, and therefore the codon was changed to the alternative, more common codons for leucine, CTC (opt/optA) or CTG (optB). This same process was repeated for all leucines in the sequence, and due to the random nature of the approach, a CTC codon could end up in optB and the CTG could end up in optA. Because of this two codon-usage approach to optimization, sequences opt/optA and opt B were maximally codon-distinct.

**Table 17: Codons used in Codon Optimization**

| Amino acid | Choice#1 | Choice#2 |
|---|---|---|
| Gly | GGC | GGG |
| Glu | GAG | GAA |
| Asp | GAC | GAT |
| Val | GTG | GTC |
| Ala | GCC | GCT |
| Ser | AGC | TTC |
| Lys | AAG | AAA |
| Asn | AAC | AAT |
| Met | ATG | |
| Ile | ATC | ATT |
| Thr | ACC | ACA |
| Trp | TGG | |
| Cys | TGC | TGT |
| Tyr | TAC | TAT |
| Phe | TTC | TTT |
| Arg | CGG | CGC |
| Gln | CAG | CAA |
| His | CAC | CAT |
| Leu | CTG | CTC |
| Pro | CCC | CCT |

**[00344]** Each of the 4 sequences (IV opt, IV optB; 9B8 opt, 9B8 optB) were then analyzed (Genomatix Software, Germany) for the presence of transcription factor binding sites or other regulatory sequences as described above, and these undesirable sequences were disrupted via silent nucleotide changes. In some cases, where there were other non-rare codons for both human and *E. coli,* the transcription factor binding sites or other regulatory elements was removed by changing to one of these codons, even though they are not choice#1 or choice#2 (see Table 18). In cases, where removing a transcription factor binding site or other regulatory element would have involved introducing a rare codon, the transcription binding site (or other regulatory element) was usually not changed.

**Table 18: Additional Codons used to Remove Transcription Factor Binding Sites and Other Regulatory Elements**

| Amino Acid | Choice #3 | Choice #4 |
|---|---|---|
| Gly | GGA | GGT |
| Val | GTA | GTT |
| Ala | GCG | GCA |
| Ser | AGT | TCA |
| Thr | ACG | ACT |
| Leu | TTG | CTT |
| Pro | CCG | CCA |

**[00345]** Codon optimized versions of IV ("IV opt" (SEQ ID NO: 22) and "IV optB" (SEQ ID NO: 23)) and 9B8 ("9B8 opt" (SEQ ID NO: 24) and "9B8 optB" (SEQ ID NO: 25)) were generated and cloned into pF4Ag by methods known in the art. HEK293 cells were plated in 96-well plates at 15,000 cells/well and grown overnight at 37°C. The following day, the cells were transiently transfected in 6 well replicates using TRANSIT®-LT1 Transfection Reagent (Mirus Bio) with 100 ng of plasmid DNA encoding the codon optimized versions in pF4Ag and grown overnight at 37°C. HEK293 cells were also transfected with either pGL4.13 (Luc2/SV40) (Paguio *et al.*, "pGL4 Vectors: A New Generation of Luciferase Reporter Vectors" *Promega Notes,* 89:7-10 (2005)) or pGL4.73 (hRL/SV40) (*Id.*) to normalize for differences in transfection efficiency. Ten ng/transfection or 10% of the total DNA transfected was used. Media was removed, and cells were lysed with 100 µL lysis buffer which contained 10 mM CDTA, 150 mM KCl, 10 mM DTT, 100 mM HEPES, pH 7.0, 35 mM thiourea, and 0.5% TERGITOL® NP-9 (v/v) to create a lysate sample. Luminescence of the lysate sample was measured on a TECAN® INFINITE® F500 luminometer as follows: for hRL and the OgLuc variants, 10 µL of the lysate sample was assayed for luminescence with 50 µL of lysis buffer containing 20 µM of substrate (native coelenterazine for hRL and PBI-3939 for the OgLuc variants). For Luc2 (SEQ ID NOs: 28 and 29), a firefly luciferase, 10 µL of lysate sample was assayed for luminescence with 50 µL of BRIGHT-GLO™ Luciferase Assay Reagent (Promega Corp.).

**[00346]** FIG. 32 shows a comparison of the luminescence measured for the lysates containing the codon optimized versions of the OgLuc variants compared to hRL and Luc2. hRL and the OgLuc variants were normalized to pGL4.13 and Luc2 was normalized to pGL4.73 using methods known in the art. As shown in FIG. 32, Luc2 had approximately 14 fold higher luminescence than hRL. The OgLuc variants had higher luminescence compared to Luc2 and hRL. The codon optimized versions of IV ("IV opt" and "IV optB") and 9B8 ("9B8 opt") showed increased luminescence compared to the non-optimized versions.

**[00347]** As a result of this optimization, the "opt/optA" versions expressed better in human HEK293 cells than their parental sequence, while the "optB" versions did not express as well in HEK293 cells compared to the parental sequence.

**[00348]** *B. L27V*

**[00349]** The L27V variant (SEQ ID NO: 88) was optimized to minimize the occurrence of common vertebrate response elements (any transcription factor binding site (TFBS) in the Genomatix database). Three different optimized versions of the L27V variant were created:

**[00350]** 1. L27V01 - version 1 (SEQ ID NO: 319) - Promoter modules and all other undesired sequence elements (additional details below) were removed by nucleotide substitutions except for individual TFBSs.

**[00351]** 2. L27V02 - version 2 - L27V01 was used as the starting, i.e., parental, sequence, and as many TFBSs were removed as possible using high stringency match criteria (A higher stringency involves a better match to the binding site and will thus find fewer matches than a lower stringency). There were two versions, A (SEQ ID NO: 322) & B ((SEQ ID NO: 318)), created for L27V02. These two versions were created by selecting different codons for each version to remove undesired sequence elements. Both versions were analyzed by searching for TFBSs with lower stringency.

**[00352]** 3. L27V03 - version 3 (SEQ ID NO: 325) - L27V02B (SEQ ID NO: 318) was used as the starting sequence. Lower stringency TFBS matches were removed where possible. L27V03 was created to be very codon distinct from L27V02A.

**[00353]** The following criteria were used to create the L27V optimized variants:

**[00354]** 1. Codon usage: Preferably, the best two human codons were used for each amino acid (as was done for the IV variant), and the use of rare human codons (HS; coding for <10% of amino acids) was avoided (Table 19). The use of rare *E. coli* codons (EC) was used, if necessary, to remove undesired sequence elements.

**Table 19**

| Amino acid | Best Codons | Avoid Codons |
|---|---|---|
| A | GCT | |
| A | GCC | |

| Amino acid | Best Codons | Avoid Codons |
|---|---|---|
| N | AAT | |
| N | AAC | |

| | | |
|---|---|---|
| C | TGT | |
| C | TGC | |
| D | GAT | |
| D | GAC | |
| E | GAG | |
| E | GAA | |
| F | TTT | |
| F | TTC | |
| G | GGG | |
| G | GGC | |
| H | CAT | |
| H | CAC | |
| I | ATT | ~~ATA~~ ~~[*EC*]~~ |
| I | ATC | |
| K | AAG | |
| K | AAA | |
| L | CTG | TTA [*HS*] CTA |
| L | CTC | [*HS,EC* ] |
| M | ATG | |

| | | |
|---|---|---|
| P | CCT | |
| P | CCC | |
| Q | CAG | |
| Q | CAA | |
| R | CGG | ~~AGG~~ ~~[*EC*]~~ ~~AGA~~ ~~[*EC*]~~ ~~CGA~~ |
| R | CGC | ~~[*EC*]~~ CGT [*HS*] |
| S | AGC | TCG [*HS*] |
| S | TCC | |
| T | ACA | |
| T | ACC | |
| V | GTG | |
| V | GTC | |
| W | TGG | |
| Y | TAT | |
| Y | TAC | |

**[00355]** 2. Undesired sequence elements that were removed where possible

**[00356]** A. Restriction Enzyme (RE) Sites: RE sites were removed that would be useful for cloning and should otherwise not be present in open reading frame (ORF).

**[00357]** B. Eukaryotic Sequence Elements: Splice donor and acceptor sites, splice silencers, Kozak sequence and PolyA sequences in the (+) mRNA strand were removed.

**[00358]** C. Vertebrate Promoter Modules (PM) (in Genomatix category: Vertebrate) were removed.

**[00359]** D. Vertebrate TFBS (in Genomatix categories: Vertebrate, general Core Promoter Elements, and miscellaneous other sequences) were removed where possible. This applied only to L27V optimized versions 2 and 3, but not to version 1.

**[00360]** E. *E. coli* Sequence Elements: *E. coli* promoters were removed.

**[00361]** F. mRNA Secondary Structure: Strong secondary structures (high mRNA folding energy) near the 5'end (Zuker, *Nucleic Acid Res.* 31(13): 3406-3415 (2003)) and other strong hairpin structures were removed.

**[00362]** A sequence comparison, percent pair-wise sequence identity is provided in Table 20 ("()" indicate number of nucleotide differences).

**Table 20**

| | L27V01 | L27V02A | L27V02B | L27V03 |
|---|---|---|---|---|
| L27V00 | 99% (3) | 97% | 97% | 94% |
| L27V01 | | 98% (12) | 98% | 94% (32) |
| L27V02A | | | 99% (4) | 95% (26) |
| L27V02B | | | | 96% |

**Example 26 - Signal Stability of OgLuc Variants**

**[00363]** *A. 15C1, 9B and IV*

**[00364]** The signal stability of 15C1 with PBI-3945 and 9B8 with PBI-3889 was measured and compared to IV. *E. coli* containing plasmid DNA encoding 15C1, 9B8, or IV were grown and induced as described previously in 8-well replicates. Cells were lysed using a lysis buffer containing of 300 mM HEPES pH 8.0, 0.3X Passive Lysis Buffer ("PLB"; Promega Corp. Cat. No. E194A), 0.3 mg/mL lysozyme, and 0.003 U/μL RQ1 DNase. Lysates were diluted 1:1000 in lysis buffer and measured for luminescence using a TECAN® INFINITE® F500 luminometer. Measurements were taken immediately after the addition to 10 μL of diluted lysate sample of 50 μL of "Glo" 0.5% TERGITOL assay buffer ("0.5% TERGITOL"), which contained 150 mM

KCl, 1 mM CDTA, 10 mM DTT, 100 mM thiourea, 0.5% TERGITOL® NP-9 (v/v), and 20 μM of either novel coelenterazines PBI-3945 or PBI 3889.

**[00365]** The signal stability of the variants was determined by re-reading the plate every 30 seconds for a length of time after the addition of the assay buffer to the sample. The signal half-life was determined from these measurements using methods known in the art. The average signal half-life was compared between the variants and IV. Both 15C1 and 9B8 had a signal half-life of at least 30 min (FIG. 33). Although 15C1, assayed with PBI-3945 had a higher luminescence at t=0, the signal decayed more rapidly than variant 9B8 assayed with PBI-3889. At t=10 min, luminescence for 15C1 with PBI-3945 and 9B8 with PBI-3889 were equivalent.

**[00366]** *B. 9B8 opt + K33N*

**[00367]** The signal stability of the 9B8 opt + K33N variants was examined. *E. coli* lysates containing the variants were prepared and analyzed as described previously except the assay buffer contained 0.25% TERGITOL® NP-9 (v/v), 100 mM MES pH 6.0, 1 mM CDTA, 150 mM KCl, 35 mM thiourea, 2 mM DTT, and 20 μM PBI-3939. Table 22 shows the signal half-life in min of the variants and indicates that the amino acid substitution L27V improves signal stability.

**Table 22: Signal stability of OgLuc variants in bacterial lysates**

| sample | signal half life (min) |
|---|---|
| 9B8 | 74 |
| K33N | 55 |
| T39T, Y68D | 87 |
| T39T, L27V, K43R | 139 |
| L27V, T39T, K43R, Y68D | 114 |
| T39T, K43R, Y68D | 61 |
| L27V, T39T, K43R, S66N | 124 |
| L27V,K43R, Y68D | 122 |
| L27V, Y68D | 139 |
| L27V, K43R, S66N | 124 |

**[00368]** The signal activity and stability of the L27V variant (9B8+K33N+L27V+T39T+K43R+Y68D; SEQ ID NO: 88 and 89) was measured and compared to that of firefly (Luc2) and *Renilla* luciferases. The L27V variant, Luc2 and *Renilla* luciferases were fused to HALOTAG® and expressed in *E. coli*. The luciferases were purified using HALOTAG® as a purification tag according to the manufacturer's protocol (pFN18A; HALOTAG® Protein Purification System). 10 pM of each purified luciferase (diluted in DMEM without phenol red containing 0.01% PRIONEX®) was then mixed with an equal volume of an

assay reagent (100 mM MES pH 6, 35 mM thiourea, 0.5% TERGITOL® NP-9 (v/v), 1 mM CDTA, 2 mM DTT, 150 mM KCl, and 100 μM PBI-3939 for the L27V variant; ONE-GLO™ Luciferase Assay System (Promega Corp.) for firefly luciferase; and RENILLA-GLO™ Luciferase Assay System (Promega Corp.) for *Renilla* luciferase), and luminescence was monitored over time (3, 10, 20, 30, 45 and 60 min). FIGS. 34A-B demonstrates the high specific activity (FIG. 34A) and signal stability (FIG. 34B) of the L27V variant when compared to firefly and *Renilla* luciferase.

**Example 27 – Enzyme Kinetics of OgLuc Variants**

**[00369]** *A. IV, 15C1, 9B8, 9F6 and 9A3*

**[00370]** Using methods known in the art, enzyme kinetic assays measuring luminescence were performed with the lysates of *E. coli* containing IV and the IV variants 15C1, 9B8, 9F6, and 9A3. Cells were induced, lysed, and diluted as described in Example 26 except the lysis buffer had a pH of 7.5. Two fold serial dilutions of PBI-3939 in the assay buffer described previously in Example 26 were assayed with the diluted lysates. FIG. 35 shows the Km and Vmax values calculated using a hyperbolic fit for IV and the variants 15C1, 9B8, 9F6, and 9A3. Variants 9B8 and 9F6 had higher Km values compared to IV while Km values for the other variants were unchanged. Variants 15C1, 9B8, and 9F6 all had higher Vmax values, while 8A3 had a lower Vmax value compared to IV.

**[00371]** 15C1, which had the highest luminescence with PBI-3945 contained the amino acid substitution K33N, indicating that K33N provided increased luminescence. A 9B8 variant was generated to have this additional substitution to provide improvement in luminescence for this variant. Additional variants of 9B8 and 9F6 were generated to have at least one of amino acid substitutions K33N or V38I ("9B8+K33N+V38I" and "9F6+K33N"). Variant 1D6 was used to highlight the importance of amino acid substitutions at positions 68, 72, and 75 for increasing light output and stability. FIG. 36 shows the Km and Vmax values calculated using a hyperbolic fit for IV and the variants 9B8, 9B8+K33N+V38I, 9F6, 9F6+K33N, and 1D6. While the actual Km values were different between FIGS. 35 and 36 for 9B8 and 9F6, the general trend between the variants was consistent.

**[00372]** The enzyme kinetics, i.e., Vmax and Km values, were determined and compared for the variants 9B8 opt and 9B8 opt+K33N as described above except the *E. coli* lysates were assayed with a buffer containing 1 mM CTDA, 150 mM KCl, 2 mM DTT, 100 mM MES pH 6.0, 35 mM thiourea, 0.25% TERGITOL® NP-9 (v/v), 10 mg/mL 2-hydroxypropyl-β-cyclodextrin,

and 20 μM PBI-3939. Luminescence was measured on a TECAN® INFINITE® F500 luminometer. As shown in FIG. 37, the Vmax and Km values for 9B8 opt+K33N were higher than 9B8 opt, indicating that this clone is brighter and has a lower affinity for substrate.

**[00373]** *B. 9B8 OPT+K33N VARIANTS*

**[00374]** The enzyme kinetics values were determined for the OgLuc variants as described previously, except luminescence was measured using a GLOMAX® luminometer. Three replicates were used for each variant. Table 23 shows the average Km and Vmax values with the standard deviation ("Km(+/-)" and "Vmax(+/-)" respectively) calculated using HYPER.EXE, Version 1.0.

**Table 23: Vmax (RLU/0.5 sec) and Km (μM) values for OgLuc Variants**

| sample | Km | Km (+/-) | Vmax | Vmax (+/-) |
|---|---|---|---|---|
| 9B8 | 7.7 | 2.0 | 86,000,000 | 14,000,000 |
| K33N | 12.5 | 3.0 | 110,000,000 | 17,000,000 |
| T39T, Y68D | 7.9 | 1.8 | 74,000,000 | 10,000,000 |
| T39T, L27V, K43R | 21.4 | 5.4 | 150,000,000 | 28,000,000 |
| L27V, T39T, K43R, Y68D | 13.9 | 2.9 | 190,000,000 | 28,000,000 |
| T39T, K43R, Y68D | 10.5 | 2.8 | 140,000,000 | 25,000,000 |
| L27V, T39T, K43R, S66N | 16.3 | 4.8 | 130,000,000 | 28,000,000 |
| L27V,K43R, Y68D | 13.7 | 4.3 | 130,000,000 | 28,000,000 |
| L27V, Y68D | 10.2 | 3.0 | 97,000,000 | 19,000,000 |
| L27V K43R, S66N | 20.0 | 6.2 | 130,000,000 | 30,000,000 |

**Example 28 - Protein Stability of OgLuc variants**

**[00375]** As stability of the luciferase protein is another factor affecting luminescence, protein stability, i.e., thermal stability, of the variants was determined.

**[00376]** *A. 15C1, 9B8, 9F6, 8A3 and IV*

**[00377]** Lysates of *E. coli* containing 15C1, 9B8, 9F6, 8A3 or IV and *E. coli* expressing hRL (SEQ ID NO: 30 and 31) were prepared from induced cultures as described previously. Lysate samples were diluted 1:1000 with a buffer containing 10 mM HEPES pH 7.5 with 0.1% gelatin. Diluted lysate (100 μL) samples, in replicate 96-well plates, were incubated at 50°C. At different time points, plates were placed at -70°C (minus seventy degrees Celsius). Prior to measuring the luminescence as described previously, each plate was thawed at room temperature, i.e., 22°C, for 10 min. Samples (10 μL of each thawed sample) were assayed using native coelenterazine as a substrate. Luminescence was measured immediately after addition of assay buffer for each time

point plate. The half-life of the protein, which indicated protein stability, was calculated from the luminescence data for each time point using methods known in the art.

**[00378]** Table 24 shows the protein stability of variants 15C1, 9B8, 9F6, and 8A3 having half-lives in min (hrs) of 630.1 (10.5), 346.6 (5.8), 770.2 (12.8) and 65.4 (1.1), respectively. In comparison, hRL had a half-life of 9.6 min, while IV had a half-life of 27.2 min. Table 24 also shows that at 4 hrs, 79%, 61%, and 80% of 15C1, 9B8, and 9F6, respectively, remained active.

**Table 24: Protein Stability of OgLuc Variants at 50°C**

| Sample | ½ life (min) | ½ life (hrs) | % remaining at t = 4 hrs |
|---|---|---|---|
| Renilla | 9.6 | | |
| IV | 27.2 | | |
| 15C1 | 630.1 | 10.5 | 79% |
| 9B8 | 346.6 | 5.8 | 61% |
| 9F6 | 770.2 | 12.8 | 80% |
| 8A3 | 65.4 | 1.1 | |

**[00379]** *B. 1D6, 9B8, 9B8+K33N+V38I, 9F6, 9F6+K33N, and IV*

**[00380]** Lysates of *E. coli* containing 1D6, 9B8, 9B8+K33N+V38I, 9F6, 9F6+K33N, or IV were prepared from induced cultures and assayed for luminescence as described previously. Protein stability, i.e., thermal stability of the lysates, was assayed as described above in this Example. FIG. 38 shows the half-life in minutes (min) of the variants at 50°C, and the luminescence of the sample measured at the start of the incubation period, i.e., t=0, using native coelenterazine as a substrate. The difference between variant 9B8+33+38 and 9F6 was one amino acid substitution, L27V, indicating that this amino acid substitution increased stability. The addition of "activity/expression" substitutions in positions 68, 72, and 75 increased stability. FIG. 38 shows K33N provided greater thermal stability to variant 9F6 and that variant 9B8 had greater light output and stability than variant 1D6. The difference between these two variants, i.e., 9B8 contains additional amino acid substitutions F68Y, L72Q, and M75K, indicated the importance of these three substitutions.

**[00381]** In addition to thermal stability, structural integrity determined by expression, stability, and solubility can also affect luminescence. As a way to further test the structural integrity of the

improved variants, KRX *E. coli* harboring pF4Ag-based (i.e., no HT7) OgLuc variants N166R (previously described in U.S. Serial Application No. 12/773,002 (U.S. Published Application No. 2010/0281552)), C1+A4E, IV, 9B8, and 9F6 were grown at 37°C in Luria broth (LB) to an $OD_{600}$=0.6 and then induced for overexpression by the addition of rhamnose (0.2% final concentration). Duplicate induced cultures were then grown at either 25 or 37°C for 17 hrs at which time total (T) and soluble (S) fractions were prepared and analyzed by SDS-PAGE using SIMPLYBLUE™ SafeStain (Invitrogen) to stain the gels (FIGS. 39A-B). hRL and Luc2 were used as controls.

**[00382]** The OgLuc variants, hRL and Luc2 expressed well and were soluble when the induction occurred at 25°C (FIG. 39A; note the approximately 19 kDa dark band in the "soluble" fraction for the OgLuc variants, excluding the N166R variant, and the approximately 36 and 64 kDa bands in the "soluble" fraction for hRL and Luc2, respectively). In contrast, although C1+A4E, IV, 9B8, and 9F6 expressed well at 37°C (significantly better than hRL or Luc2, as shown in the "total" fraction), only the 9B8 and 9F6 variants were soluble when the elevated induction temperature was employed (see FIG. 39B; note the approximately 19 kDa dark band in the "soluble" fraction for 9B8 and 9F6). These results tracked with the thermal stability data shown in Table 24 and FIG. 38.

**[00383]** *C. 9B8 OPT AND 9B8 OPT + K33N*

**[00384]** The thermal stability of the variants 9B8 opt and 9B8 opt+K33N was compared. *E. coli* lysates containing the variant 9B8 opt or 9B8 opt+K33N were prepared and analyzed as described previously with the following exceptions: Lysates were diluted 1:100 in the lysis buffer described previously and replicate diluted lysates were incubated at 60°C in a thermocycler. Aliquots were removed at different time-points and placed on dry ice to freeze the samples. Frozen lysates were thawed at 22°C and assayed with a buffer containing 20 mM CDTA, 150 mM KCl, 10 mM DTT, 20 μM PBI-3939, 100 mM HEPES pH 7.0, 35 mM thiourea, and 0.1% TERGITOL® NP-9 (v/v). Luminescence was measured on a GLOMAX® luminometer (Promega Corp.). FIG. 40A shows the light output time course of the natural logarithm (ln) value of luminescence measured in RLU over time in min. As shown in FIG. 40B, 9B8 opt+K33N had a half-life at 60°C of 6.8 hrs, which was longer than the 5.7 hrs half-life of 9B8 opt.

**[00385]** Table 25 shows the thermal stability at 60°C ("$T_{1/2}$ (60°C)") of 9B8 opt and 9B8 opt+K33N, and the luminescence ("RLU") data at the start of the incubation period (i.e., t=0). 9B8 opt+K33N was more stable and approximately 1.8-fold brighter than 9B8 opt, indicating

that the amino acid substitution K33N provided both greater light output and higher thermal stability.

**Table 25: Thermal Stability and Luminescence Data for 9B8 opt and 9B8 opt+K33N**

| Variant | $T_{1/2}$ (60°C) | RLU |
|---|---|---|
| 9B8 opt | 5.7 hrs | 23,283,252,000 |
| 9B8 opt+K33N | 6.8 hrs | 42,278,732,000 |

**[00386]** *D. 9B8 + K33N Variants*

**[00387]** The thermal stability of the variants at 60°C was examined as described above, except the assay buffer contained 100 mM MES pH 6.0 instead of HEPES. Table 26 and FIG. 41 shows the half-life in hrs of the variants at 60°C. The data indicates that the amino acid substitution L27V improves thermal stability.

**Table 26: Thermal stability of OgLuc variants at 60°C**

| Sample | 1/2 life hours |
|---|---|
| 9B8 | 5.1 |
| K33N | 6.7 |
| T39T, Y68D | 16.3 |
| T39T, L27V, K43R | 11.8 |
| L27V, T39T, K43R, Y68D | 21.7 |
| T39T, K43R, Y68D | 15.2 |
| L27V, T39T, K43R, S66N | 11.8 |
| L27V,K43R, Y68D | 23.2 |
| L27V, Y68D | 28.5 |
| L27V, K43R, S66N | 10.7 |

**[00388]** The variants 9B8 and V2 (9B8+K33N+T39T+K43R+Y68D) were also screened in HEK293 cells to determine their stability. The variants were cloned into pF4Ag and transfected into HEK293 cells (15,000 cells/well) as previously described. After transfection, the cells were lysed in assay reagent (as previously described; no PBI-3939), and luminescence measured using the assay reagent with 20 μM PBI-3939. 9B8 had a half-life of 5.2 hrs while V2 had a half-life of 16.8 hrs. This is consistent with the half-life seen for these variants in *E. coli* (Table 26).

**[00389]** *E. L27V variant*

**[00390]** The activity of the L27V variant (9B8+K33N+L27V+T39T+K43R+Y68D) was assessed at various pHs and different salt conditions. 9B8 and 9B8+K33N were previously shown to have similar stability at pH 6 and pH 7 (data not shown). For assessing activity at various salt conditions, 50 µL of assay buffer with 20 µM PBI-3939 and varying amounts of KCl or NaCl was mixed with 50 µL of HEK293 cells transiently transfected with L27V (pF4Ag). Luminescence was measured, and the percent activity (the ratio of luminescence to no salt) determined (FIG. 42B). For assessing activity in various pHs, a reagent was made containing 100 mM citrate, 100 mM MES, 100 mM PIPES, 100 mM HEPES, 100 mM TAPS, 0.5% TERGITOL® NP-9 (v/v), 0.05 % MAZU® DF 204, 1 mM CDTA, and 1 mM DTT titrated to various pH values. 362 pM L27V in assay reagent was mixed with substrate 100 µM PBI-3939 and luminescence was measured. (FIG. 42A).

**Example 29 - Gel filtration Chromatographic Analysis of OgLuc Variants**

**[00391]** *A. C1+A4E and 9B8*

**[00392]** Gel filtration analysis was used to verify the expected molecular weight of the purified OgLuc proteins based on the theoretical values and consequently to determine their oligomeric state. A comparison between the relative hydrodynamic volume of the OgLuc variants C1+A4E and 9B8 was made by gel filtration chromatography. For this analysis, the nucleotide sequence for the OgLuc variants, C1+A4E and 9B8, were cloned into a HQ-Tagged FLEXI® Vector (Promega Corp.) to create a HQHQHQ N-terminally tagged protein that was overexpressed in *E. coli* KRX cells. The overexpressed proteins were purified using the HISLINK™ Protein Purification System (Promega Corp.) according to manufacturer's instructions. Samples of each individual standard and sample protein were analyzed by gel filtration chromatography, which was performed at 24°C on an Agilent 1200 HPLC, using a Superdex 200 5/150 GL column (GE Healthcare) with a flow rate of 0.25 mL/min (FIGS. 43A-B). The mobile phase (i.e., running buffer) consisted of 50 mM Tris and 150 mM NaCl, pH 7.5. Protein elution was monitored at 214 and 280 nm. A standard calibration curve was generated using: 1) Ovalbumin, 43 kDa (GE Healthcare), 2) Carbonic Anhydrase, 29 kDa (Sigma) and 3) Myoglobin, 17 kDa (Horse Heart, Sigma). The molecular weights of the purified proteins were calculated directly from the calibration curve.

**[00393]** The relative elution of the proteins observed with this column was Ovalbumin at 7.98 min, Carbonic Anhydrase at 8.65 min, 9B8 at 8.97 min, and Myoglobin at 9.06 min (FIGS. 43A-B). As shown in FIG. 43B, 9B8 eluted as a 21 kDa protein (predicted MW is approximately 19 kDa) indicating that the 9B8 variant existed as a monomer, whereas C1+A4E eluted at

approximately 4.3 min (FIG. 43A), indicating that C1+A4E was expressed and exists as multimer, e.g., possibly as a tetrameric complex or something larger.

**[00394]** *B. L27V variant*

**[00395]** To demonstrate that the OgLuc variant L27V exists in a monomeric state, gel filtration analysis was used to verify the expected molecular weight of the purified L27V protein based on the theoretical value, and consequently to determine its oligomeric state. The relative hydrodynamic volume of the L27V variant was made by gel filtration chromatography. For this analysis, the nucleotide sequence for the L27V variant was cloned into a HaloTag® vector pFN18A (Promega Corp.) to create a HaloTag®-terminally tagged protein that was overexpressed in *E. coli* KRX cells (Promega Corp.). The overexpressed protein was purified using the HaloTag® Protein Purification System (Promega Corp.) according to manufacturer's instructions. Samples of each individual standard and sample protein were analyzed by gel filtration chromatography performed at 24°C on an Agilent 1200 HPLC using a Superdex 200 5/150 GL column (GE Healthcare) with a flow rate of 0.25 mL/min (FIG. 56). The mobile phase (i.e., running buffer) consisted of 50 mM Tris and 150 mM NaCl, pH 7.5. Protein elution was monitored at 214 and 280 nm. A standard calibration curve was generated using: 1) Ovalbumin, 43 kDa (GE Healthcare), 2) Myoglobin, 17 kDa (Horse Heart, Sigma), and 3) Ribonuclease, 14 kDa (Bovine pancreas, GE Healthcare). As shown in FIG. 44, the L27V variant eluted as a 24 kDa protein (predicted MW is approximately 19 kDa) indicating that it existed as a monomer.

**Example 30 – Protein Expression Levels of OgLuc variants**

**[00396]** *A. IV, 8A3, 8F2, 9B8, 9F6 and 15C1*

**[00397]** Normalizing for protein expression provides information about potential differences in specific activity. To provide a means for quantifying protein expression, OgLuc variants were cloned into a pF4Ag vector containing a C-terminal HT7 to generate OgLuc variant-HT7 fusion proteins as described previously. The following fusion proteins were generated: IV-HT7 (SEQ ID NOs: 48 and 49), 8A3-HT7 (SEQ ID NOs: 34 and 35), 8F2-HT7 (SEQ ID NOs: 50 and 51), 9B8-HT7 (SEQ ID NOs: 36 and 37), 9F6-HT7 (SEQ ID NOs: 38 and 39), and 15C1-HT7 (SEQ ID NOs: 52 and 53). *E. coli* containing the OgLuc variant-HT7 fusions were grown and induced as described previously. 900 µL of cell culture was lysed with 100 µL of 10X FASTBREAK™ Cell Lysis Reagent (Promega Corp.). HALOTAG® TMR-ligand (Promega Corp.) was added to each bacterial lysate sample to obtain a final concentration of 0.5 µM. Bacterial lysates were incubated with the HALOTAG® TMR-ligand for 30 min at room temperature according to

manufacture's instructions. 10 µL of each sample was diluted 1:1 with 1X FASTBREAK™, i.e., 10 µL sample to 10 µL 1X FASTBREAK™. 15 µL of the lysate and 15 µL of the 1:1 dilution for each sample were analyzed by SDS PAGE. The labeled fusion proteins were resolved by SDS-PAGE, stained with SIMPLYBLUE™ SafeStain (FIG. 45A) and fluorimaged (GE Healthcare Typhoon). Bands were quantitated using Imagequant software (GE Healthcare). FIG. 45B shows the band volume measured from FIG. 45A for IV-HT7 ("IV"), 15C1-HT7 ("15C1"), 9B8-HT7 ("9B8"), 9F6-HT7 ("9F6"), and 8F2-HT7 ("8F2"), normalized to IV-HT7. The data shows that the IV variants expressed well compared to IV.

**[00398]** *B. 9B8 opt, V2 and L27V*

**[00399]** The expression levels and solubility of 9B8 opt, V2 and L27V were compared. These three variants, in the context of a pF4Ag background, were used to transform *E. coli* KRX cells. The resulting clones were used for an expression experiment where single colonies were grown overnight at 30°C, diluted 1:100 in LB, grown to an $OD_{600}$ approximately 0.5, and then induced with 0.2% rhamnose for 18 hrs at 25°C. Cells were then incubated for 30 min at room temperature in the presence of 0.5X FASTBREAK™ Lysis Reagent (Promega Corp.), and the resulting lysates stored at -20°C. Following a slow-thaw on ice, soluble fractions were prepared by high-speed centrifugation for 10 min at 4°C. Crude total (T) and soluble (S) fractions were then analyzed for expression levels using SDS-PAGE + Simply blue staining (FIG. 46A) as well as by measuring luminescence (FIG. 46B). For luminescence measurement, 50 µL of soluble lysates in 96-well microtiter plates were mixed with 50 µL assay reagent (previously described; 40 µM PBI-3939), and luminescence measured using a TECAN® INFINITE® F500 multi-detection plate reader. These results indicate that the ranking for these three variants, in terms of their expression levels and solubility, is L27V > V2 > 9B8opt.

**Example 31 – Brightness of OgLuc Variants Expressed in Mammalian Cells**

**[00400]** *A. IV and 9B8*

**[00401]** The IV and 9B8 variant in pF4Ag vector (i.e., no HT7) were evaluated for brightness in HEK293 cells. hRL was used as a control. Briefly, HEK293 cells, plated at 15,000 cells/well in a 96-well plate, were transiently transfected using TRANSIT®-LT1 with plasmid DNAs encoding the various variants and/or control sequences. Cells were grown, lysed, and treated as described in Example 25. Cells were co-transfected with pGL4.13 (Promega Corp.) as a transfection control (10 ng/transfection or 10% of the total DNA transfected was used). Luminescence was measured as described previously using native coelenterazine as a substrate

for hRL or PBI-3939 as a substrate for the OgLuc variants. The OgLuc variant data was corrected for transfection efficiency using Luc2 luminescence (i.e., measuring luminescence after the addition of luciferin substrate). The OgLuc variants IV and 9B8 had greater luminescence compared to hRL ("Renilla") (FIG. 47).

**[00402]** For comparison of brightness on a per mole basis in mammalian cells, the C-terminal HT7 fusion protein of variant 9B8 ("pF4Ag-OgLuc-9B8-HT7") described in Example 30 was analyzed and compared with C-terminal HT7-hRL fusion protein ("pF4Ag-Renilla-HT7") and C-terminal HT7- Luc2 fusion protein ("pF4Ag-Luc2-HT7"). HEK293 cells (15,000) were plated and grown overnight at 37°C. These cells were transfected with 100 ng of DNA from pF4Ag-Renilla-HT7, pF4Ag-Luc2-HT7, or pF4Ag-OgLuc-9B8-HT7 and grown overnight at 37°C. Media was removed and cells were lysed as described previously. 10 µL of each sample was assayed for luminescence (RLU) with 50 µL BRIGHT-GLO™ for Luc2, 50 µL of 20 µM native coelenterazine for hRL, and 50 µL of 20 µM PBI-3939 for variant 9B8.

**[00403]** The lysates from 6 wells were pooled and labeled with HALOTAG® TMR-ligand as described in Example 30. The labeled fusion proteins were resolved by SDS-PAGE and fluorimaged (GE Healthcare Typhoon). The band densities were determined to quantitate the relative number of moles present for each luciferase enzyme and the RLU value for each sample was normalized by the calculated band density to normalize expression levels of each protein, i.e., RLUs normalized using TMR label quantitation (FIG. 48). On a mole-to-mole basis, the 9B8 variant was approximately 15-fold brighter than Luc2 and >100-fold brighter than hRL. This data represented differences in specific activity.

**[00404]** *B. 9B8 opt and 9B8 opt+K33N*

The brightness of the variants 9B8 opt and 9B8 opt+K33N expressed in HEK293 cells was measured and compared as described for the variants without the HT7 in Example 31. 30 and 100 ng of plasmid DNA containing the variant DNA was used to transfect HEK293 cells. Cells were grown and induced as described in Example 31 except the cells were lysed with a lysis buffer containing 1 mM CTDA, 150 mM KCl, 2 mM DTT, 100 mM MES pH 6.0, 35 mM thiourea, 0.25% TERGITOL® NP-9 (v/v), and 10 mg/mL 2-hydroxypropyl-β-cyclodextrin. The lysates were assayed with lysis buffer containing 20 µM PBI-3939 and luminescence was measured on a TECAN® GENIOS™ Pro luminometer. As shown in FIG. 49, 9B8 opt+K33N had greater luminescence compared to 9B8 opt in HEK293 cells, which tracks with the bacterial expression data in Table 25 and FIG. 29.

**[00405]** *C. 9B8+K33N Variants*

**[00406]** The brightness of the variants expressed in HEK293 and NIH3T3 cells was measured as described previously. The luminescence of the variants was normalized to the luminescence generated by 9B8 opt (Table 27).

**Table 27: Increase in Luminescence generated by OgLuc combination variants in NIH3T3 and HEK293 cells**

| Sample | HEK293 | NIH3T3 |
|---|---|---|
| 9B8 | 1.0 | 1.0 |
| K33N | 1.8 | 1.5 |
| T39T, Y68D | 1.9 | 1.5 |
| T39T, L27V, K43R | 1.3 | 0.9 |
| L27V, T39T, K43R, Y68D | 1.6 | 1.6 |
| T39T, K43R, Y68D | 1.9 | 1.9 |
| L27V, T39T, K43R, S66N | 1.3 | 1.2 |
| L27V, K43R, Y68D | 1.6 | 1.5 |
| L27V, Y68D | 1.7 | 1.4 |
| L27V, K43R, S66N | 1.2 | 1.0 |

**[00407]** *D. L27V*

**[00408]** A comparison of the luminescence of the L27V variant to firefly luciferase alone and as a fusion was performed. HEK293 and HeLa cells were plated at 15,000 and 10,000 cells/well, respectively, into wells of 12-well plates and incubated overnight at 37°C, 5% $CO_2$. The cells were then transfected with serial dilutions of pF4Ag containing L27V or Luc2. 20 ng of pGL4.13 (Promega Corp.) was co-transfected with L27V, and 20 ng of pGL4.73 (Promega Corp.) was co-transfected with Luc2 to act as carrier DNA for lower dilutions of the L27V or Luc2 plasmid DNA. The plasmid DNA was then transfected into the cells (6 replicates for each dilution for each cell type) using TRANSIT®-LTI transfection reagent according to the manufacturer's instructions. The cells were then incubated for 24 hrs at 37°C, 5% $CO_2$.

**[00409]** After transfection, the media was removed from the cells, and 100 µL PBS with 0.5% TERGITOL® NP-9 (v/v) added and shaken for 10 min at room temperature. 10 µL of each cell lysate was assayed using ONE-GLO™ Luciferase Assay System (Promega Corp.; Luc2) or assay

reagent (Example 22H with 20μM PBI-3939; OgLuc). Luminescence was measured as previously described for the HEK293 (FIG. 50A) and HeLa cells (FIG. 50B).

**[00410]** Comparison of L27V and Luc2 as fusion partners was performed as described above. L27V and Luc2 were fused to HALOTAG® protein in pF4Ag. FIGS. 50C-D show the luminescence measured with the different fusions in HEK293 (FIG. 50C) and HeLa cells (FIG. 50D).

**[00411]** In addition to measuring luminescence, protein expression was also analyzed. The transfection was performed as described above. After transfection, the media was removed from the cells, and the cells washed in 1X PBS. 100 μL 0.1X Mammalian Lysis Buffer (Promega Corp.) containing 1 μM HALOTAG®TMR ligand (Promega Corp.) and 20 U DNase I was added, and the cells incubated with slow shaking for 45 min at room temperature. The cell samples were then frozen at -20°C. For protein analysis, 32.5 μL 4X SDS loading dye was added to each sample, and the samples heated at 95°C for 2 min. 10 μL of sample was then loaded onto an SDS-PAGE gel and imaged on a Typhoon Scanner as previously described (FIG. 50E).

**Example 32 – Brightness of Purified OgLuc Variant Compared to Firefly Luciferase**

**[00412]** The 9B8 OgLuc variant was overexpressed and purified as described in Example 33. Reactions between diluted enzyme and substrate were performed using the following 2X buffer/assay reagent: 100 mM MES pH 6.0, 1 mM CDTA, 150 mM KCl, 35 mM thiourea, 2 mM DTT, 0.25% TERGITOL® NP-9 (v/v), 0.025% MAZU® DF 204, 10 mg/mL 2-hydroxy-β-cyclodextrin, and 20 μM PBI-3939. The final assay concentrations of purified enzyme and substrate were 0.5 pM and 10 μM, respectively. In parallel, reactions between diluted purified firefly luciferase (i.e., QUANTILUM® Recombinant Luciferase (Promega Corp.)) and luciferin were analyzed. The assay buffer/reagent for the firefly luciferase reaction was BRIGHT-GLO™, and the final assay concentrations were 0.5 pM enzyme and 500 μM luciferin. As the buffers/reagents for each reaction were known to provide "glow" kinetics, a 15 min time point was used to collect luminescence data. The results from this experiment showed that 9B8 opt using PBI-3939 (19,200 RLU) was approximately 8-fold brighter than QUANTILUM® Recombinant Luciferase with BRIGHT-GLO™ (2,300 RLU).

**Example 33 - Inhibition Analysis**

**[00413]** To determine the susceptibility of the OgLuc variants to off-target interactions, the activity of the 9B8 and L27V variants was screened against a LOPAC (library of

pharmacologically active compounds) library. A LOPAC 1280 library (Sigma) was prepared by diluting the compounds to 1 mM in DMSO. On the day of the assay, the compounds were diluted to 20 μM in 1X PBS, and 10 μL transferred to a 96-well, white plate. To each well, 10 μL of purified 9B8, L27V or firefly luciferase (Luc2) enzyme diluted $10^{-4}$ in Glo Lysis Buffer (Promega Corp.) was added and incubated at room temperature for 2 min. To the samples, 20 μL assay reagent (1 mM CDTA, 150 mM KCl, 2 mM DTT, 100 mM MES pH 6.0, 35 mM Thiourea, 0.5% TERGITOL® NP-9 (v/v) and 60 μM PBI-3939) was added, incubated for 3 min, and luminescence measured on a TECAN® GENIOS™ Pro Luminometer. For assaying firefly luciferase, the BRIGHT-GLO™ Assay reagent (Promega Corp.) was used according to the manufacturer's protocol. As a negative control, 8 wells of each plate contained 1X PBS + 2% glycerol. As a positive control, 8 wells of each plate contained 2 mM Suramin in 2% DMSO or 2 mM luciferase inhibitor 1 in 2% DMSO (Calbiochem). Suramin was identified in the preliminary screen of the LOPAC library (i.e., the LOPAC library was screened using the 9B8 variant with a lower substrate concentration of 20 μM) to be an inhibitor of OgLuc.

**[00414]** The results in FIG. 51 indicate a general low frequency of off-target interactions between the compounds in the LOPAC library and L27V. This suggests a potential use for L27V as a screening tool for large libraries of diverse chemicals and therapeutic candidates, including live cell-based formats (e.g., high-throughput screening).

**[00415]** To further examine inhibition resistance, purified 9B8 and L27V were screened against various concentrations of Suramin (Sigma S-2671) and Tyrphostin AG 835 ("Tyr ag 835") (Sigma T-5568) (FIGS. 52A-C). FIGS. 52E-D show the chemical structures for Suramin and Tyr ag 835, respectively. Purified 9B8 and L27V were prepared as described above. Serial dilutions (0, 2 μM, 6 μM, 20 μM, 60 μM, 200 μM and 2 mM) of the inhibitors were prepared in 1X PBS with 2% DMSO. To wells of a 96-well, white assay plate, 10 μL of diluted enzyme and 10 μL of diluted inhibitor were added and incubated at room temperature for 2 min. 20 μL assay reagent (described above) was added, and luminescence measured on a GLOMAX®-96 luminometer (FIGS. 52A-C). FIGS. 52A-B show the dose response curves of 9B8 and L27V to Suramin (FIGS. 52A) and Tyr ag 835 (FIGS. 52B). FIG. 52C shows the half maximal inhibitory concentration ($IC_{50}$) of Suramin and Tyr ag 835 for 9B8 and L27V. The data indicates that L27V is a robust reporter that could be used as a screening tool for large libraries of diverse chemicals and/or therapeutic candidates.

**Example 34 - Resistance to Non-specific Protein Interactions**

**[00416]** 1. Purified 9B8 and L27V enzyme were serial diluted in 1:10 in buffer (1X PBS, 1 mM DTT, and 0.005% IGEPAL® CA-630) with or without 0.5 mg/mL BSA (4 sets of each dilution) to 200 µL into PCR strip tubes. The samples were incubated at 60°C wherein at 0, 2, 4, and 6 hrs one set of dilutions for each variant was transferred to -70°C.

**[00417]** To analyze activity, the samples were thawed to room temperature in a water bath. 50 µL assay reagent (as previously described with 100 µM PBI-3939) was added, and luminescence measured for each minute for 30 min on a TECAN® INFINITE® F500 plate reader. Activity was calculated using the average luminescence of the $1x10^6$ and $1x10^7$ dilutions (FIG. 53).

**[00418]** 2. To demonstrate the reactivity of the OgLuc variants to plastic, purified 9B8 and L27V were exposed to polystyrene plates, and their activity measured.

**[00419]** 50 µL purified 9B8 (45.3 pM) and L27V (85.9 pM) in DMEM without phenol red with 0.1% PRIONEX® was placed into wells of a 96-well, polystyrene microtiter plate at 60, 40, 20 and 0 min. To the samples, 50 µL assay reagent (described above) containing 20 µM PBI-3939 was added and incubated for 5 min at room temperature. Luminescence was measured as previously described, and percent activity determined (FIG. 54; ratio of luminescence to time 0).

**Example 35 - Post Translational Modification**

**[00420]** To determine if the OgLuc variants undergo any post translation modifications when expressed in mammalian cells, the 9B8 and L27V variants were expressed in both mammalian cells and *E. coli* and analyzed via mass spectrometry (MS).

**[00421]** 9B8 and L27V variants were expressed as N-terminal HALOTAG® fusions (pFN18K for *E. coli*; pFN21K for HEK293 cells) in HEK293 and *E. coli* KRX (Promega Corp.) cells and purified using the HALOTAG® Protein Purification System (Promega Corp.) according to the manufacture's instructions. Approximately 5 pmols of purified enzyme was analyzed via LC/MS using a C4 column (Waters Xbridge BEH300, 3.5µm) interfaced to an LTQ Orbitrap Velos mass spectrometer (Thermo Scientific). Data was acquired from 600-2000 *m/z* using the LTQ for detection and processed using the MagTran v1.03 software (Zhang *et al., J. Am. Soc. Mass Spectrom.*, *9*:225–233 (1998)). Both purified enzymes had an experimentally determined mass of 19,666 Da, compared to a calculated mass of an un-modified OgLuc variant, i.e., absent of any post translational modifications, of 19,665 Da.

**Example 36 – Evaluation of OgLuc Variants as a Transcriptional Reporter**

**[00422]** *A. IV*

**[00423]** The use of the OgLuc variants as a transcriptional reporter was examined. To generate a transcriptional reporter of cAMP, hRL and IV were sub-cloned using methods known in the art into a modified pGL4 vector (Promega Corp.) containing a barnase sequence, which was replaced by the DNA fragment of interest. The leader sequence of the modified pGL4 contained a minimal promoter and a cAMP-response element (CRE; SEQ ID NO: 96), so that upon stimulation with a cAMP agonist such as forskolin (FSK), cells accumulating cAMP activated the reporter and generated luminescence. In this experiment, 2 ng DNA of either the hRL or IV transcriptional reporter construct was used to transfect HEK293 cells as described in Example 25. At 24 hrs post transfection, the cells were treated with 100 μM FSK. Cells that were not treated with FSK were used as a control. After 6 hrs, a reporter reagent was added to treated and control cells. For hRL, the reporter reagent was Renilla-Glo™ reagent (Promega Corp.). For IV, the reporter reagent contained 1 mM CDTA pH 5.5, 150 mM KCl, 10 mM DTT, 0.5% TERGITOL® NP-9 (v/v), 20 μM coelenterazine-h, and 150 mM thiourea. After 10 min, luminescence was read on a Varioskan® Flash (Thermo Scientific).

**[00424]** FIG. 55 shows the normalized luminescence of HEK293 cells containing the hRL ("Renilla") or IV transcriptional reporter treated ("+FSK") or not treated ("-FSK") with FSK. The response, i.e., fold-induction or fold-increase ("FOLD") in luminescence was determined by dividing the luminescence from the treated cells (+FSK) with the luminescence from the control cells (-FSK). As shown in FIG. 55, the response for hRL was <50, while for IV it was >300, demonstrating the use of IV as a transcriptional reporter.

**[00425]** *B. 9B8 and 9B8 opt*

**[00426]** The use of variants 9B8 and 9B8 opt as a transcriptional reporter was also examined and compared to hRL and Luc2 transcriptional reporters as previously described for the IV transcriptional reporter with the following modifications. Transcriptional reporters of cAMP containing either variants 9B8 or 9B8 opt were generated as described above. After 6 hrs of FSK induction, the media was removed from the cells and replaced with 100 μL of the lysis buffer described in Example 25 creating a lysate. The lysate of transfected cells treated with or without FSK were assayed for luminescence as described in Example 25. 10 μL of the Luc2 lysate was assayed with 50 μL of BRIGHT-GLO™ Luciferase Assay Reagent. 10 μL of the hRL lysate was assayed with 50 μL of lysis buffer containing 20 μM native coelenterazine. 10 μL of the variants 9B8 and 9B8 opt lysates were assayed with 50 μL of lysis buffer containing 20 μM PBI-3939.

**[00427]** FIG. 56 shows the normalized luminescence of HEK293 cells containing the 9B8, 9B8 opt, hRL, or Luc2 transcriptional reporter treated ("induced") or not treated ("basal") with

FSK. The response, i.e., fold-induction or fold-increase ("fold") in luminescence, was determined by dividing the induced luminescence by the basal luminescence (FIG. 56). Although the fold induction values are similar for each of the reporters except Luc2, the luminescence generated by the induced 9B8 opt transcriptional reporter was approximately 2.5 logs higher than the induced *Renilla* transcriptional reporter and approximately 1.5 logs higher than the Luc2 transcriptional reporter. FIG. 56 demonstrated the use of 9B8 and 9B8 opt as transcriptional reporters.

**[00428]** *C. 9B8 opt and 9B8 opt+K33N*

**[00429]** The variants 9B8 opt and 9B8 opt+K33N were compared in a lytic transcriptional reporter assay. The variant 9B8 opt+K33N was cloned using methods known in the art into a pGL4.29 vector (Promega Corp.), which contains a cyclic AMP response element (CRE). The 9B8 opt+K33N transcriptional reporter was tested and compared to the 9B8 opt transcriptional reporter as described above in HEK293 cells. 30 and 100 ng of plasmid DNA containing the transcriptional reporter versions of the variants were used to transfect HEK293 cells. The cells were induced with FSK for 5 hrs prior to measurement for luminescence. Cells were lysed with a lysis buffer containing 1 mM CTDA, 150 mM KCl, 2 mM DTT, 100 mM MES pH 6.0, 35 mM thiourea, 0.25% TERGITOL® NP-9 (v/v), and 10 mg/mL 2-hydroxypropyl-β-cyclodextrin. Luminescence was measured on a TECAN® GENIOS™ Pro luminometer. The lysate was assayed with the lysis buffer containing 20 μM PBI-3939. FIG. 57 shows the normalized luminescence (transfection corrected) of HEK293 cells expressing the 9B8 opt or 9B8 opt+K33N transcriptional reporter construct treated ("Induced") or not treated ("Basal") with FSK. As shown in FIG. 57, the fold-induction for 9B8 opt was 360 when 30 ng of DNA was used for transfection and 109 when 100 ng was used for transfection, while the fold-induction for 9B8 opt+K33N was 275 and 147, respectively. When higher amounts of DNA were used for transfection, K33N provided a greater response.

**[00430]** *D. L27V*

**[00431]** 1. L27V was cloned into a reporter vector as described in C of this Example containing a CRE, NFkB or HSE (Heat shock element) response element. Reporter constructs were then transfected into HEK293 cells or HeLa cells as previously described. The cells were then induced using FSK for CRE, TNFα for NFkB or 17-AAG for HSE. Luminescence was measured as previously described using the assay reagent with 20 μM PBI-3939 (FIGS. 58A-C). The reporter constructs were all validated in HEK293, HeLa, NIH3T3, U2OS and Jurkat cell lines (data not shown).

**[00432]** 2. L27V02 and L27V02P (containing a PEST sequence; SEQ ID NO: 323) were cloned into a reporter vector (pGL4.32 based) as described in C of this Example. Other OgLuc variants containing a PEST sequence include L27V01-PEST00 and L27V03-PEST02 (SEQ ID NOs: 320 and 326, respectively). The reporter construct was then transfected into HEK293 cells as previously described. The cells were then induced using FSK, and luminescence was measured as previously described using the assay reagent with 20 μM PBI-3939 (FIGS. 59A-B). Various other reporter constructs were also created and tested in various cell lines (FIGS. 59C). FIG. 59A shows the full dose response for the CRE system in HEK293 cells. FIG. 59B summarizes FIG. 59B. FIG. 59C summarizes the data in FIGS. 59A-B and shows the same type of data for the NFkB response element. Both CRE and NFkB report constructs were examined in HEK293, HeLa, HepG2, Jurkat, ME180, HCT116, and U2OS cell lines.

**[00433]** 3. HEK293 cells ($0.9x10^6$ cells in a T25 flask) were transfected with pNFkB-L27V secretion construct (SEQ ID NOS: 463 & 464; wherein the IL-6 secretion sequence (SEQ ID NOs: 461 and 462) replaced the native OgLuc secretion sequence SEQ ID NO: 54), Metridia longa (Clontech), pNFkB-L27V (native secretion sequence; SEQ ID NOs: 465 and 466) or firefly luciferase (Luc2; pGL4.32-based) plasmid DNA using FUGENE® HD (Promega Corp.) according to the manufacturer's instructions. Cells were incubated at 37°C, 5% $CO_2$ for 8 hrs, then trypsinized in 0.5 mL TrypLE (Invitrogen). The lysates were then resuspended in 8 mL DMEM with 10% FBS, 1X NEAA and 1X sodium pyruvate. 100 μL of the resuspended sample was then added to wells of a 96-well plate and incubated for 16 hrs at 37°C, 5% $CO_2$.

**[00434]** Following incubation, the media was removed from the cells and replaced with 100 μL fresh media with our without TNFα (serially diluted). To assay for secretion, at 3 and 6 hrs, 5 μL of media (in triplicate) was removed from the cells, brought to 50 μL with PBS and mixed with 50 μL assay reagent (as previously described with 100 μM PBI-3939). Luminescence was measured at 0 and 10 min as previously described (FIG. 60).

**[00435]** For measuring *Metridia longa* luciferase activity, the Ready-To-Glow™ Secreted Luciferase System (Clontech) was used according to the manufacturer's protocol. Briefly, 5 μL Ready-to-Glow™ reagent was added to 5 μL of sample and 45 μL of PBS. Luminescence was measured immediately after reagent addition (FIG. 60).

**[00436]** *E. L27V optimized variants.*

**[00437]** Plasmid DNAs (pGL4.32-L27V00, pGL4.32-L27V01, pGL4.32-L27V02, pGL4.32-L27V03, and pGL4.13) were prepared for transfection using FUGENE® HD according to the

manufacturer's protocol. The pGL4.32 vector (Promega Corp.) contains the NF-κB response element. The L27V codon optimized sequences replaced the Luc2P sequence in the vector. pGL4.13 vector (Promega Corp.) contains the Luc2 gene driven by the SV40 promoter.

**[00438]** 300 µL of DNA transfection mixture was then mixed with 6 mL of HeLa cell suspension ($2x10^5$ cells/mL), homogenized, and 100 µL plated into wells of a 96-well plate. The cells were then incubated overnight at 37°C, 5% $CO_2$. Following incubation, 10 µL of 10X rhTNFα in DPBS with BSA was added to the wells and incubated for 4.5 hrs at 37°C, 5% $CO_2$. Six wells were given vehicle only. The cells were then allowed to equilibrate at room temperature for 20 min, and then 100 µL assay reagent (as previously described with 100 µM PBI-3939) was added. To cells expressing Luc2 or receiving vehicle only treatment, 100 µL of the ONE-GLO™ Luciferase Assay Reagent was added. Luminescence was measured 12 min post-assay reagent addition as previously described. FIGS. 61A-B shows the absolute luminescence, FIGS. 61C-D shows normalized luminescence and FIGS. 61E-F shows fold response.

**Example 37 - OgLuc Variants in a Transcription Reporter Assay**

**[00439]** To demonstrate the ability of the OgLuc variants of the present invention to be used as transcription reporters, the OgLuc variant 9B8 opt was used as a transcriptional reporter in a forward, reverse, and bulk transfection. These methods of transfection were chosen because they are representative of the approaches commonly used for the transient expression of genetic transcriptional reporters.

**[00440]** *Forward Transfection*

**[00441]** Transcriptional reporters containing the cAMP response element (CRE) and 9B8 opt or 9B8 opt further comprising the PEST protein degradation sequence (9B8 opt-P) were prepared in the pGL4.29 (Promega Corp.) backbone, i.e., the luc2P gene of the pGL4.29 vector was replaced with 9B9 opt (SEQ ID NO: 24) or 9B8 opt-P (SEQ ID NO: 65). pGL4.29 was used as a control/benchmark.

**[00442]** HEK293 cells were plated at 15,000 cells/well in six 96-well tissue culture plates. Cells were grown in 100 µL of DMEM + 10% FBS + 1X non-essential amino acids (NEAA) and incubated overnight at 37°C. The cells were transiently transfected with either 10 ng or 100 ng plasmid DNA/well of pGL4.29 9B8 opt, pGL4.29 9B8 opt-P, or pGL4.29. Plasmid DNA was mixed with 850 µL of OPTI-MEM® (Invitrogen) and 32.4 µL of FUGENE® HD transfection reagent (Promega Corp.) and incubated at room temperature for 10 min. Eight µL of the

transfection/reporter DNA mixture was added to the appropriate wells (2 constructs/plate). Cells were incubated for 4 hrs at 37°C. The medium was replaced with OPTI-MEM® + 0.5% dialyzed FBS + 1X NEAA + 1X sodium pyruvate + 1X Penn-Strep and incubated overnight at 37°C.

**[00443]** Following incubation, 10 nM or 10 μM FSK (from a 10X stock) in OPTI-MEM® was added to the cells and incubated for 3 hrs at 37°C. A lytic reagent containing 100 mM MES pH 6.1, 1 mM CDTA, 150 mM KCl, 35 mM thiourea, 2 mM DTT, 0.25% TERGITOL® NP-9 (v/v), 0.025% MAZU® DF 204, and 20 μM PBI-3939 was added to the cells containing pGL4.29 9B8 opt or pGL4.29 9B8 opt-P and allowed to incubated for 10 min at room temperature (100 μL lytic reagent added to 100 μL cells). ONE-GLO™ assay reagent (Promega Corp.) was added to cells containing pGL4.29 and used according to the manufacturer's protocol (100 μL reagent added to 100 μL cells). Luminescence was measured on a GLOMAX® Luminometer. Table 26 shows the luminescence of the HEK293 cells expressing the transcriptional reporters containing CRE treated with 10 nM ("baseline") or 10 mM FSK, and the response to FSK (i.e., the luminescence generated by the 10 mM FSK treated cells divided by the luminescence generated of the 10 nM FSK treated cells.)

**[00444]** The results shown in Table 28 indicate that 9B8 opt and 9B8 opt-P were brighter than luc2P, and that all the luciferase reporters responded to FSK when 100 ng of DNA was used for the transfection. However, when only 10 ng of DNA was used for the transfection, the luminescence for the luc2P reporter was below the detection level for the luminometer.

**Table 28: Transcriptional Reporters Containing CRE in HEK293 Cells (3 h timepoint)**

| Reporter construct | 100 ng DNA for transfection | | | 10 ng DNA for transfection | | |
|---|---|---|---|---|---|---|
| | baseline | RLU (10 mM FSK) | Response | baseline | RLU (10 mM FSK) | Response |
| 9B8 opt | 3,078,418 | 104,687,723 | 34 | 192810 | 12,926,465 | 67 |
| 9B8 opt-P | 122,071 | 20,544,753 | 168 | 11179 | 1,353,459 | 121 |
| luc2P | 356 | 5,293 | 15 | 0 | 0 | - |

**[00445]** *Reverse Transfection*

**[00446]** Transcriptional reporters containing the antioxidant response element (ARE) and 9B8 opt or 9B8 opt-P were prepared in the pGL4.29 (Promega Corp.) backbone, i.e., the luc2P gene of the pGL4.29 vector was replaced with 9B9 opt or 9B8 opt-P, and CRE was replaced with 2X ARE (SEQ ID NO: 66) using methods known in the arts.

**[00447]** HEK293 cells were trypsinized (T75 flask, 3 mL trypsin) and resuspended in $1x10^5$ cells/mL (approximately $8.9x10^6$ total cells) in medium containing DMEM + 10% FBS + 1X NEAA. Each transcriptional reporter was prepared for transfection by mixing 1.2 mL OPTI-MEM®, 12 µL transcription reporter DNA (100 ng) and 36 µL FUGENE® HD transfection reagent together and incubated at room temperature for 35 min. Following incubation, 624µL of the transfection/reporter DNA mixture was added to 12 mL of cell suspension and mixed by inversion. After mixing, 100 µL of the cell/DNA mixture was added to wells of a 96-well plate (2 constructs/plate). The cells were incubated at 37°C for 22 hrs. Tert-butylhydroquinone (a Nrf2 stabilizer; tBHQ; 1 µM ("baseline") or 20 µM) or sulphoraphane, (an organosulfer antioxidant known to activate Nrf2; 1 µM ("baseline") or 20 µM) in OPTI-MEM® was added to each well and incubated at 37°C for 24 hrs. Cells were lysed with 100 µL lytic reagent as described above for the forward transfection. Luminescence was measured on a GLOMAX® Luminometer.

**[00448]** Table 29 shows the luminescence of the HEK293 cells expressing the transcriptional reporters containing ARE treated with 1 µM ("baseline") or 20 µM sulphoraphane and the response to sulphoraphane (i.e., the luminescence generated by the 1 µM sulphoraphane treated cells divided by the luminescence generated of the 20 µM sulphoraphane treated cells). Table 30 shows the luminescence of the HEK293 cells expressing the transcriptional reporters containing ARE treated with 1 µM ("baseline") or 20 µM tBHQ, and the response to tBHQ (i.e., the luminescence generated by the 1 µM tBHQ treated cells divided by the luminescence generated of the 20 µM tBHQ treated cells). Tables 29 and 30 show that 9B8 opt and 9B8 opt-P could report the presences of two different known stimuli for ARE.

**Table 29: Transcriptional Reporters Containing ARE in HEK293 Cells (24 h time point)**

| Reporter construct | 100 ng DNA for transfection | | |
|---|---|---|---|
| | baseline | RLU (20 mM sulphoraphane) | Response |
| 9B8 opt | 15,600,000 | 89,600,000 | 5.8 |
| 9B8 opt-P | 258,406 | 3,940,000 | 15 |

**Table 30: Transcriptional Reporters Containing ARE in HEK293 Cells (24 h time point)**

| Reporter construct | 100 ng DNA for transfection | | |
|---|---|---|---|
| | baseline | RLU (20 mM tBHQ) | Response |
| 9B8 opt | 15,100,000 | 120,000,000 | 8 |

| | | | |
|---|---|---|---|
| 9B8 opt-P | 317,238 | 8,460,000 | 27 |

**[00449]** *Bulk Transfection*

**[00450]** The transcriptional reporters containing CRE and 9B8 opt or 9B8 opt-P described in the forward transfection were used in the bulk transfection of HEK293 and NIH3T3 cells. Transcriptional reporters containing the heat shock response element (HRE; SEQ ID NO: 67) and 9B8 opt or 9B8 opt-P were prepared in the pGL4.29 (Promega Corp.) backbone, i.e., the luc2P gene of the pGL4.29 vector was replaced with 9B9 opt or 9B8 opt-P, and the CRE was replaced with HRE. The transcriptional reporter containing HRE and 9B8 opt-P was used in the bulk transfection of HeLa cells

**[00451]** HEK293, NIH3T3, or HeLa cells were plated to a single well of a 6-well tissue culture plate the day before transfection at a density of $4.5x10^5$ cells/well in 3 mL complete medium (DMEM + 10% FBS + 1X NEAA + 1X sodium pyruvate) for HEK293 cells, $3x10^5$ cells/well in 3 mL complete medium (DMEM + 10% fetal calf serum (FCS) + 1X NEAA+1X sodium pyruvate) for NIH3T3 cells, or $9.9x10^5$ cells/well in 3 mL complete medium (DMEM + 10% FBS + 1X NEAA) for HeLa cells. Cells were grown overnight at 37°C.

**[00452]** 3,300 ng of reporter plasmid DNA in 155 µL OPTI-MEM® was mixed with 9.9 µL FUGENE® HD transfection reagent, vortexed briefly, and incubated at room temperature for 10 min. The CRE transcriptional reporters were used to transfect HEK293 and NIH3T3 cells. The HRE transcriptional reporters were used to transfect HeLa cells. The reporter mixture was added to cells and mixed by gentle rocking followed by incubation at 37°C for 6 hrs (HEK293 and NIH3T3) or 3 hrs (HeLa). Cells were then trypsinized and resuspended in medium (DMEM + 10% FBS + 1X NEAA + 1X sodium pyruvate for HEK293 cells, DMEM + 10% FCS + 1X NEAA + 1X sodium pyruvate for NIH3T3 cells, or DMEM + 10% FBS + 1X NEAA for HeLa cells), followed by plating to the individual wells of a 96-well plate (20,000 cells/100 µL for HEK293, 10,000 cells/100 µL for NIH3T3, or 13,000 cells/µL for HeLa) and incubated at 37°C overnight.

**[00453]** FSK (CRE stimulator) or 17-AAG (HRE stimulator; 17-Allylamino-demethoxy geldanamycin) in OPTI-MEM® was added to the cells (10 nM or 10 µM final concentration for FSK; 1 nM or 1 µM final concentration for 17-AAG) and incubated at 37°C for 4 hrs (FSK) or 6 hrs (17-AAG). Plates were removed from the incubator and allowed to equilibrate to room

temperature for 25 min. Cells were lysed with 100 µL lytic reagent as described above for the forward transfection. Luminescence was measured on a GLOMAX® Luminometer.

**[00454]** Table 31 shows the luminescence of the HEK293 cells expressing the transcriptional reporters containing CRE treated with 10 nM ("baseline") or 10 mM FSK and the response to FSK. Table 32 shows the luminescence of the NIH3T3 cells expressing the transcriptional reporters containing CRE treated with 10 nM ("baseline") or 10 mM FSK and the response to FSK. Table 33 shows the luminescence of the HeLa cells expressing the transcriptional reporters containing HRE treated with 10 nM ("baseline") or 10 mM 17-AAG and the response to 17-AAG.

**[00455]** Tables 29-31 show that 1) both versions of the 9B8opt OgLuc variant can report the presence and stimulatory effects of FSK on CRE in the context of two different cell lines, HEK293 and NIH3T3, and 2) 9B8 optP can report the presence and stimulatory effects of 17-AAG on HRE in the context of HeLa cells.

**Table 31: Transcriptional Reporters Containing CRE in HEK293 Cells (4 h time point)**

| Reporter construct | 100 ng DNA for transfection | | |
|---|---|---|---|
| | baseline | RLU (10 mM FSK) | Response |
| 9B8 opt | 39,700,000 | 654,000,000 | 16 |
| 9B8 opt-P | 3,960,000 | 460,000,000 | 116 |

**Table 32: Transcriptional Reporters Containing CRE in NIH3T3 Cells (4 h time point)**

| Reporter construct | 100 ng DNA for transfection | | |
|---|---|---|---|
| | baseline | RLU (10 mM FSK) | Response |
| 9B8 opt | 9,187,000 | 23,600,000 | 2.6 |
| 9B8 opt-P | 410,461 | 3,720,000 | 9 |

**Table 33: Transcriptional Reporters Containing HRE in HeLa Cells (6 h time point)**

| Reporter construct | 100 ng DNA for transfection | | |
|---|---|---|---|
| | baseline | RLU (1 mM 17-AAG) | Response |
| 9B8 opt-P | 278,118 | 3,204,000 | 12 |

**Example 38 - Lytic and Secretable Reporter in Difficult to Express Cells**

**[00456]** HepG2 cells, $1x10^5$ cells/mL in a cell suspension, were reverse transfected with plasmid DNA (pGL4.32 backbone; Promega Corp.) containing L27V02, luc2P (Promega Corp.), luc2 (Promega Corp.) or L27V02-IL6 (L27V02 with the native secretion sequence replaced with the IL-6 secretion sequence; ("IL601-L27V02A"; SEQ ID NO: 324) using FUGENE® HD according to the manufacturer's instructions (1:20 DNA-transfection mixture to cells). 100 µL cell suspension was then plated into wells of a 96-well plate and incubated for 22 hrs at 37°C, 5% $CO_2$. Other OgLuc constructs which have the native secretion sequence replaced by the IL-6 secretion sequence include IL601-L27V01 and IL602-L27V03 (SEQ ID NOs: 321 and 327, respectively).

**[00457]** For secretion analysis, the media was removed from the cells, and the cells washed in 100 µL DPBS. 100 µL complete media (DMEM + 10% FBS+ 1X NEAA) was added along with varying doses (1 pg/mL – 100 ng/mL) of rhTNFα ("TNFα") for 4.5 h. 10 µL of the media was then removed, added to 90 µL complete media, and 100 µL assay reagent (as previously described; 100 µM PBI-3939) added. Luminescence was measured as previously described (FIG. 62A).

**[00458]** For lytic analysis, following plating, the cells were incubated for 4.5 hrs at 37°C, 5% $CO_2$. The cells were then allowed to equilibrate to room temperature for 20 min. Assay reagent (as previously described; 100 µM PBI-3939) was added to the cells, and luminescence measured as previously described (FIG. 62B).

**Example 39 - Additional lytic reporter features**

**[00459]** The OgLuc variants of the present invention in the context of a cell-based, lytic transcriptional reporter should offer a luminescent signal of a magnitude such that the signal appears sooner than it might with other luciferases. The bright luminescence should also allow for weak promoters to be examined.

**Example 40 - Mammalian cell transfections**

**[00460]** The OgLuc variants of the present invention were used as reporters in difficult to transfect cell lines, e.g., Jurkat, HepG2, primary cells, non-dividing primary cells, or stem cells. (*See* e.g., FIG. 59C) Due to their high signal intensity, the OgLuc variants enable detectable luminescence when transfection efficiency is low. The OgLuc variants can also be used as reporters in cells that are especially sensitive to conditions associated with transfection, i.e., DNA concentration, transfection reagent addition. Due to the brightness of the OgLuc variants, an adequate level of luminescence can be achieved using lower DNA concentrations, less

transfection reagent, and perhaps shorter post-transfection times prior to beginning an assay. This will place less of a toxicity burden on what would otherwise be sensitive cells. The bright luminescence of the OgLuc variants should also allow for a signal to be detected at very long time points in the event such an output is desirable. As another example, the OgLuc variants could be used as reporters for single copy native promoters, e.g., HSB thymidylate kinase (TK) promoter, HOX genes, or LIN28.

**Example 41 - Stable cell lines**

**[00461]** The identification of robust, stable cell lines expressing an OgLuc variant of the present invention, either in the cytoplasm or as a secreted form, can be facilitated by the bright signal of the luciferase and the small size of the OgLuc gene. The relatively small gene sequence should reduce the likelihood of genetic instability resulting from the integration of the foreign DNA.

**[00462]** To generate stable cell lines using an OgLuc variant of the present invention, plasmid DNA comprising a nucleotide sequence for an OgLuc variant and a selectable marker gene, e.g., neomycin, hygromycin, or puromycin, is used to transfect a cell line of interest, e.g., HEK293 cells. Cells of an early passage number, e.g., less than 10 passages, are plated into T25 ($1x10^6$) or T75 ($3x10^6$) tissue culture flasks and allowed to grow overnight to approximately 75% confluency. Cells are then transfected using the above plasmid DNA and an appropriate transfection reagent, e.g., TRANSIT®-LT1 or FUGENE® HD. Forty-eight hrs post-transfection, the media is replaced on the cells with selection media containing the selection drug, e.g., G418, hygromycin or puromycin, at a concentration previously determined to kill untransfected cells. Selection of cells containing the plasmid DNA occurs over 2-4 weeks. During this time, the cells are re-plated in selection media at various concentrations into either T25 or T75 tissue culture flasks. The media on the re-plated cells is replaced every 3-4 days for 2-3 weeks with fresh selection media. The flasks are monitored for the formation of live cell colonies. Eventually, the flasks will contain many large colonies and few dead cells.

**[00463]** From the pool of stable colonies in the flasks, single colonies are isolated and expanded into a single 24-well tissue culture plate. Briefly, cells are harvested using the trypsin/EDTA method, i.e., cells are harvested by removing media, rinsing with $Ca^{2+}$ and $Mg^{2+}$ free PBS and detached by treatment with Trypsin/EDTA. The cells are counted using a hemocytometer and diluted $1x10^5$ in complete media. The cells are then diluted to 100 cells/mL, 33 cells/mL, 10 cells/mL, and 3.3 cells/mL in complete media. 100 µL of each dilution is plated into all wells of 96-well tissue culture plate (1 plate for each dilution) and allowed to grow 4-5

days after which 50 µL of selection media is added to the cells. Approximately a week after plating, cells are visually screened for colony growth and another 50 µL of selection media is added. The cells continue to be monitored until a single colony covers 40-60% of the well area. When a colony is ready for expansion and screening, colonies are harvested using the trypsin/EDTA method. Each colony is transferred to selection media as follows: 1) Dilute 1:10 into 6 wells of a 96-well assay plate for functional assay, e.g., luminescence detection; 2) Dilute 1:10 into 3 wells of a clear bottom 96-well assay plate for cell viability assay, e.g., CELLTITER-GLO® Luminescent Cell Viability Assay (Promega Corp.); and 3) Dilute 1:10 into a 24-well tissue culture plate for expansion. Cells in the plates for the functional and cell viability assay are then grown 2-3 days and the functional and cell viability assays performed. Positive clones in the 24-well plate are further tested with the functional and cell viability assays as well as for stability of expression and response for at least 20 passages, normal growth rate morphology, and frozen for future use at the earliest possible passage.

**Example 42 – OgLuc Secretion Signal Analysis**

**[00464]** *A. IV opt*

**[00465]** The wild-type OgLuc is processed after synthesis into a mature protein with the secretion signal sequence cleaved off. To determine if the secretion signal sequence would facilitate secretion of the OgLuc variant, the IV opt variant of Example 25 and hRL were cloned into pF4Ag containing an N-terminal OgLuc secretion signal (SEQ ID NO: 54). HEK293 cells (15,000) in 100 µL Dulbecco's Modified Eagle's medium ("DMEM") with 10% fetal bovine serum (FBS) were transfected as described in Example 25 with 100 ng of plasmid DNA, i.e., hRL or IV opt with or without the secretion signal and grown overnight at 37°C. 50 µL of media was removed to a new plate and saved for a later assay generating a "media" sample. The rest of the media was removed, and the cells were lysed with 100 µL of lysis buffer described in Example 25 to generate a "lysate" sample. 10 µL of media sample and 10 µL of lysate sample were assayed for luminescence (FIG. 63). Samples for hRL with ("Renilla sig") or without ("Renilla") the OgLuc secretion signal sequence were measured using 50 µL of lysis buffer containing 20 µM native coelenterazine. Samples for IV opt with ("IV opt sig") or without ("IV opt") the OgLuc secretion signal sequence were measured using 50 µL of lysis buffer containing 20 µM PBI-3939.

**[00466]** In FIG. 63, the filled bars represent the amount of light that was detected from the media in the absence of any lytic reagent. The open bars represent the total light (secreted + non-secreted) that was detected upon addition of a lytic reagent. FIG. 63 shows that IV opt was

secreted from HEK293 cells into the growth media and that the secretion signal sequence was functional in mammalian cells. "IV opt sig" represents the only situation where a significant amount of luciferase was detected in the media. The results also indicate that this particular signal peptide did not facilitate secretion of hRL.

**[00467]** *B. 9B8, V2 and L27V*

**[00468]** To determine if the secretion signal sequence of OgLuc facilitates its secretion, the OgLuc variants 9B8, V2 and L27V were cloned into pF4Ag containing an N-terminal OgLuc secretion signal sequence. The variants were also cloned into vectors without the secretion signal sequence. CHO or HeLa cells were then plates at 100,000 cells/well in 1 mL F12 media with 10% FBS and 1X sodium pyruvate (CHO cells) or DMEM with 10% FBS and 1X sodium pyruvate (HeLa cells) into 12-well plates and incubated overnight at 37°C, 5% $CO_2$.

**[00469]** After the overnight incubation, the cells were transfected with 1μg plasmid DNA containing 9B8, V2, or L27V with or without the secretion signal sequence using the TRANSIT®-LT1 transfection reagent (Mirus Bio) and OPTI-MEM® media (Invitrogen). The cells were again incubated overnight at 37°C, 5% $CO_2$.

**[00470]** After the second overnight incubation, the media was removed and saved for analysis. To the cells, 1 mL of assay buffer (1 mM CDTA, 150 mM KCl, 2 mM DTT, 100 mM MES pH 6.0, 35 mM Thiourea and 0.5% TERGITOL® NP-9 (v/v)) was added to create a cell lysate. To 10 μL of cell lysate or saved media from each sample, 50 μL assay buffer with 40 μM PBI-3939 was added, and luminescence measured as described above. FIGS. 64A-D demonstrates that 9B8, V2 and L27V variants can be used in a secretable system.

**[00471]** To determine the stability of the secreted variants, 150 μL aliquots of the saved media from each sample was placed at 37°C or 50°C. The aliquots were then removed at different time points (0, 1, 2, 3, 5, 6, and 7 min), frozen on dry ice, and kept at -20°C until assayed. To assay for stability, the media aliquots were thawed to room temperature, and 10 μL of each aliquot was mixed with assay buffer with PBI-3939 (pH 6.0) as described above. Luminescence was measured as above, and the half-life ($t_{50}$) determined (Table 34).

**Table 34**

| sample | 1/2 life 37C (days) |
|---|---|
| 9B8 | 8 |
| V2 | 10 |
| L27V | 17 |
| | |
| sample | 1/2 life 50C (hours) |
| 9B8 | 3 |
| V2 | 7 |
| L27V | 11 |

**[00472]** *C. 9B8 and V2 comparison to secreted luciferase of Metridia longa*

**[00473]** The secretion of the OgLuc variants 9B8 and V2 was compared to that of the secreted luciferase from *Metridia longa*. CHO cells were plated at 300,000 cells/well in 3 mL F12 media with 10% FBS into wells of 6-well plates and incubated overnight at 37°C, 5% $CO_2$. The cells were then transfected with either 10 or 100 ng of each variant or *Metridia* luciferase (Clontech) plasmid DNA using TRANSIT®-LTI according to the manufacturer's instructions and incubated for 20 hrs at 37°C, 5% $CO_2$. After transfection, the media was removed from the cells and assayed. For the OgLuc variants, 50 µL of media was assayed with 50 µL of assay reagent (previously described; 40 µM PBI-3939). For *Metridia* luciferase, the media was assayed using the Ready-to-Glo™ Secreted Luciferase Reporter System (Clontech) according to the manufacture's protocol. Briefly, 5 µL of the 1X substrate/reaction buffer was added to 50 µL of media sample. Luminescence was then measured as previously described (FIGS. 65A-B).

**Example 43 – Evaluation of OgLuc Variants and Novel Coelenterazine in Live Cells**

**[00474]** A. The use of OgLuc variants and PBI-3939 in live cells was examined. HEK293 cells were plated in 96-well plates at 15,000 cells/well and grown overnight at 37°C. The following day, the cells were transiently transfected using TRANSIT®-LT1 in 3 replicates with 100 ng of hRL or 9B8 opt in pF4Ag and grown overnight at 37°C. The following day the growth media was removed and replaced with media containing 60 µM VIVIREN™ Live Cell Substrate (Promega Corp.), 60 µM ENDUREN™ Live Cell Substrate (Promega Corp.), or 60 µM PBI-3939 for both hRL and 9B8 opt transfected cells. Non-transfected cells were used as background control. The plate was incubated at 37°C during the course of one day and periodically measured on a TECAN® GENIOS™ Pro luminometer, i.e., 11 times over the course of 24 hrs. FIGS. 66A-B shows the luminescence of the transfected cells divided by the luminescence of the non-transfected cells for each of the substrates, i.e., the signal to background ratio. The data shows that 9B8 opt generated luminescence in a live cell setting (i.e., no lysis) by incubating cells with

VIVIREN™, ENDUREN™, or PBI-3939. The data also demonstrated that PBI-3939 can permeate cells in culture, react with the OgLuc variant, and generate luminescence, thus making it compatible with use in a live cell assay.

**[00475]** B. To demonstrate live cell analysis using the OgLuc variants, L27V was fused to HALOTAG® and expressed and monitored in live cells. U2OS cells were plated at 40,000 cells/mL into imaging chamber wells and incubated overnight at 37°C, 5% $CO_2$. Cells were than transfected using FUGENE® HD according to the manufacturer's protocol with the plasmids pFC14K, pFN21K or pF4Ag (all Promega Corp.) containing L27V or pF4Ag containing L27V with the native or IL-6 secretion sequence. Cells were then incubated for 24 hrs at 37°C, 5% $CO_2$.

**[00476]** Following incubation, the cells were exposed to HALOTAG® TMR ligand (Promega Corp.), imaged, and fixed. Immunocytochemistry (ICC) was then performed according to the ICC protocol in the HALOTAG® Technology: Focus on Imaging technical manual (Promega Corp.; TM260). The primary antibody used was a polyclonal rabbit, anti-OgLuc 9B8 antibody (1:1000). The secondary antibody used was an Alexa 488 conjugated secondary antibody (green) (FIG. 67A). FIG. 67A shows green fluorescent channel and FIG. 67B shows the differential interference contrast (DIC). Images were acquired using an Olympus Fluoview FV500 confocal microscope (Olympus, USA) outfitted with a 37°C + CO2 environmental chamber (Solent Scientific Ltd., UK).

**[00477]** FIGS. 67B-D shows the ICC images with native or IL-6 secretion sequence. Both signal sequences dramatically decrease the amount of enzyme in the nucleus. The punctuate nature of the labeling in the cytoplasm is indicative of vesicle formation expected to occur during the secretion process. The data demonstrates that the presence of a signal peptide reduces the amount of luciferase in the nucleus.

**[00478]** C. As shown above, the OgLuc variants and novel substrates of the present invention are biocompatible. A reporter system is envisioned where the OgLuc variant is cloned into an expression vector with a promoter of interest and expressed in cells as a reporter protein. The cells are then treated with PBI-3939 which will permeate cells in culture, react with the OgLuc variant, and generate luminescence.

**[00479]** In addition to being cell permeant, PBI-3939 shows comparable biocompatibility to native coelenterazine in terms of cell viability. A version of compound 3939 containing chemical modifications known to increase the stability of native coelenterazine in media can be

synthesized and used for more robust, live cell OgLuc variant-based reporter assays. Another example of live cell reporting includes the use of a secretable OgLuc variant as a reporter. The native secretion signal peptide (or other known secretion signal peptides) can be fused to the N-terminus of an OgLuc variant so that when the fusion is expressed in mammalian cells, a portion of it will be secreted through the cell membrane into the culture media. Upon addition of substrate luminescence is generated.

**Example 44 - Protein fusion reporters**

**[00480]** The OgLuc variants of the present invention can be used as fusion tags for a target protein of interest as a way to monitor intracellular levels of that target protein. Specific proteins involved in stress response pathways, e.g., DNA damage, oxidative stress, inflammation, can be monitored in cells as a way to probe the role various types of stimuli may play in these pathways. The variants can also be used as a means to monitor cellular trafficking of a target protein. The variants can also be fused to viral genomes (e.g., HIV, HCV) so that titer levels, i.e., infectivity, can be monitored in cells following treatment with potential antiviral agents. The variants can also be fused to green fluorescent protein (GFP) or HALOTAG® (in addition to a target protein) so that FACS could be used to identify high expression clones and to provide localization information.

**Example 45 - Evaluation of OgLuc Variant in 3-Component Fusion Protein ("Sandwich")**

**[00481]** 3-component fusion proteins, or "sandwich" fusions, can be used to place bioluminescent and fluorescent proteins close to one another for optimization of a biosensor based on BRET.

**[00482]** *A. C1+4AE, IV, 9B8 and 9F6*

**[00483]** The OgLuc variants C1+4AE (SEQ ID NOs: 55 and 56), IV (SEQ ID NOs: 57 and 58), 9B8 (SEQ ID NOs: 61 and 62), and 9F6 (SEQ ID NOs: 63 and 64), and hRL (SEQ ID NOs: 32 and 33) were cloned into a pF4Ag fusion vector with an N-terminal Id (Benezra *et al.*, *Cell,* 61(1):49-59 (1990)), known to be a poor fusion partner, and a C-terminal HT7, which was used for normalization. The gene of interest was "sandwiched" between Id and HT7, i.e., Id-Luciferase-HT7. *E. coli* lysates, containing the variant constructs in pF4Ag or pF4Ag sandwich background, were prepared as described in Example 26 and then assayed with 20 μM native coelenterazine in the buffer described in Example 25.

**[00484]** FIG. 68 shows the luminescence for each variant in either pF4Ag or pF4Ag sandwich background ("Sand"). FIG. 69 shows the fold-decrease in luminescence due to the presence of Id and HT7 and determined by dividing the luminescence of the variant in pF4Ag by the luminescence of the variant in the pF4Ag-sandwich. Samples with the largest values showed the most sensitivity to the poor fusion partner Id. The variant 9B8 was the brightest in the sandwich context.

**[00485]** *B. 9B8 OPT AND 9B8 OPT+K33N*

**[00486]** The variants 9B8 opt and 9B8 opt+K33N were analyzed in a sandwich background as described above. Sandwich constructs for 9B8 opt (SEQ ID NOs: 40 and 41) and 9B8 opt+K33N (SEQ ID NOs: 59 and 60) were generated as described above. *E. coli* lysates were assayed and measured using the same assay buffer and luminometer as used for generating FIG. 40. FIG. 70 shows the fold-decrease in the presence of a sandwich background indicating that 9B8 opt+K33N is less sensitive to the poor fusion partner Id than 9B8 opt.

**[00487]** *C. 23D2 and 24C2*

**[00488]** Variants 23D4 (NF) and 24C2 (NF) were subcloned into the Id-OgLuc-HT7 sandwich background and assayed in *E. coli*. The sandwich variants, 23D4 (F) (SEQ ID NOs: 76 and 77) and 24C2 (F) (SEQ ID NOs: 78 and 79) were compared to 9B8 opt+K33N in the sandwich background (SEQ ID NO: 59 and 60). Table 35 shows the variants had at least the same luminescence as 9B8 opt+K33N in the sandwich background context.

**Table 35: Increase in Luminescence Generated by OgLuc Variants Compared to 9B8 opt+K33N+170G in Sandwich Background**

| Sample | Sequence | Fold over 9B8 opt+K33N sandwich (*E. coli*) |
|---|---|---|
| 23D4 (F) | G26G, M106L, R112R, 170G | 1.0 |
| 24C2 (F) | R11Q, T39T, 170G | 1.0 |

**[00489]** *D. 1F7 and 15H1*

**[00490]** The PCR library in the Id-OgLuc-HT7 sandwich background was screened for additional variants with increased luminescence compared to 9B8 opt+K33N in sandwich background. Selected variants were then assayed in HEK293 and NIH3T3 cells. Table 36 shows the fold-increase in luminescence of the sandwich variants in *E. coli*, HEK293 and NIH3T3 cells,

and the amino acid substitutions found in the variants. 1F7 (F) (SEQ ID NOs: 84 and 85) and 15H1 (F) (SEQ ID NOs: 86 and 87) had at least 1.3 fold-increase in luminescence in *E. coli*. 1F7 (F) was brighter than 9B8 opt+K33N in the sandwich background in HEK293 and NIH3T3 cells.

**Table 36: Increase in Luminescence Generated by OgLuc Variants Compared to 9B8 opt+K33N in Sandwich Background**

| Sample | Sequence | Fold over 9B8 opt+K33N sandwich | | |
|---|---|---|---|---|
| | | *E. coli* | HEK293 | NIH3T3 |
| 1F7 (F) | K43R, Y68D | 1.9 | 2.4 | 1.4 |
| 15H1 (F) | D19D, S66N | 1.5 | 0.9 | 1.2 |

**[00491]** The sandwich variants were subcloned into the pF4Ag-based non-fusion background vector to generate 1F7 (NF) (SEQ ID NOs: 80 and 81) and 15H1 (NF) (SEQ ID NOs: 82 and 83) and were analyzed as described above and compared to 9B8 opt+K33N. Table 37 shows the fold-increase in luminescence of the variants in *E. coli,* HEK293 and NIH3T3 cells. 1F7 (NF) and 15H1 (F) had at least 1.3 fold-increase in luminescence in *E. coli* and HEK293 cells.

**Table 37: Increase in Luminescence Generated by OgLuc Variants Compared to 9B8 opt+K33N +170G**

| Sample | Sequence | Fold over 9B8 opt+K33N + 170G | | |
|---|---|---|---|---|
| | | *E. coli* | HEK293 | NIH3T3 |
| 1F7 (NF) | K43R, Y68D | 1.5 | 1.5 | 1.1 |
| 15H1 (NF) | D19D, S66N | 1.7 | 1.7 | 1.2 |

**[00492]** *E. V2, 9B8 opt+K33N+L27V+K43R+Y68D, 9B8 opt+K33N+L27V+T39T+K43R+S66N and L27V*

**[00493]** The variants 9B8 opt+K33N+T39T+K43R+Y68D ("V2"; SEQ ID NOs: 92 and 93), 9B8 opt+K33N+L27V+K43R+Y68D (SEQ ID NOs: 339 and 340), 9B8 opt+K33N+L27V+T39T+K43R+S66N (SEQ ID NOs: 341 and 342), and 9B8 opt+K33N+L27V+T39T+K43R+Y68D ("L27V"; SEQ ID NOs: 88 and 89) were subcloned into the Id-OgLuc-HT7 sandwich background as described above and assayed in HEK293 and NIH3T3 cells as described above. The luminescence generated by the sandwiched variants were compared to the luminescence generated by the 9B9 opt+K33N sandwich (SEQ ID NOs: 59 and

60) (Table 38). The L27V sandwich (SEQ ID NOs: 90 and 91) and V2 sandwich (SEQ ID NOs: 94 and 95) had at least 1.3X fold-increase in luminescence in HEK293 and NIH3T3 cells.

**Table 38: Increase in Luminescence Generated by OgLuc variants in sandwich background compared to 9B8 opt+K33N in sandwich background**

| Sample | NIH 3T3 cells | HEK 293 |
|---|---|---|
| K33N Sand | 1.0 | 1.0 |
| T39T, K43R, Y68D Sand | 1.6 | 2.3 |
| L27V, K43R, Y68D Sand | 1.4 | 1.7 |
| L27V, T39T, K43R, S66N Sand | 0.7 | 0.7 |
| L27V, T39T, K43R, Y68D Sand | 1.4 | 1.7 |

**[00494]** The sandwich and non-sandwich versions of the variants V2, 9B8 opt+K33N+L27V+K43R+Y68D, 9B8 opt+K33N+L27V+T39T+K43R+S66N, and L27V were assayed in HEK293 and NIH3T3 cells as described in Example 37. The luminescence generated by the non-sandwiched variants was compared to the luminescence generated by the sandwiched variants (Table 39). The data shown in Table 39 indicates that the fold-decrease in luminescence for the 9B8 opt+K33N sandwich was less in mammalian cells than in *E. coli* cells as shown in FIG. 70.

**Table 39: Fold-Decrease in Luminescence of the OgLuc Variants in the Presence of Sandwich Background**

| Sample | NIH 3T3 cells | HEK 293 |
|---|---|---|
| K33N | 29 | 15 |
| T39T, K43R, Y68D | 20 | 6 |
| L27V, K43R, Y68D | 22 | 8 |
| L27V, T39T, K43R, S66N | 25 | 12 |
| L27V, T39T, K43R, Y68D | 18 | 6 |

**Example 46 - Multiplexing**

**[00495]** A. Lysates of *E. coli* expressing the variant 9B8 opt were prepared as previously described in Example 27 and diluted 1000-fold in DMEM without phenol red + 0.1% PRIONEX®. Luminescence from a sample containing 6.3 µg/mL of purified red click beetle luciferase and *E. coli* lysate expressing the variant 9B8 opt was detected using a modified DUAL-GLO® Luciferase Assay System (Promega Corp.). DUAL-GLO® STOP&GLO® Reagent containing 20 µM coelenterazine-h and DUAL-GLO® STOP&GLO® Reagent containing 20 µM PBI 3939 were used, according to the manufacturer's protocol, to detect the

red click beetle luciferase and OgLuc variant 9B8 luciferase from a single sample. Three replicates were performed.

**[00496]** Luminescence was detected on a Turner MODULUS™ luminometer. Table 40 shows the average luminescence generated by the red click beetle luciferase ("click beetle"), and the luminescence generated by 9B8 opt ("Ogluc") with coelenterazine-h ("coel h") or PBI-3939 ("3939"). The standard deviation ("+/-") and coefficient of variance ("CV") are also shown. A "no coelenterazine" control was performed to illustrate the amount of quenching of the red click beetle signal by the DUAL-GLO® STOP&GLO® Reagent of the DUAL-GLO® Luciferase Assay System in the absence of coelenterazine. The "no coelenterazine" control yielded a 349-fold quench. Table 40 shows that large luminescent signals from both the red click beetle and OgLuc variant 9B8 was detected in a single sample. This demonstrates that each signal can be read sequentially in a two-step assay, and the signal from the first enzyme can be quenched enough to not contribute significantly to the signal from the second enzyme.

**Table 40: Average Luminescence Generated by the Red Click Beetle and 9B8 opt Luciferases Using a Modified DUAL-LUCIFERASE™ Reporter Assay**

| | click beetle | +/- | CV | Ogluc | +/- | CV | fold-quench | +/- coel |
|---|---|---|---|---|---|---|---|---|
| no coel | 5,081,163 | 147,145 | 2.9% | 14,504 | 214 | 1.5% | 349 | |
| coel h | 5,082,100 | 152,254 | 3.0% | 921,440 | 47,623 | 5.2% | | 64 |
| 3939 | 5,078,547 | 41,753 | 0.8% | 2,996,940 | 187,300 | 6.2% | | 207 |

**[00497]** B. To demonstrate that the multiplex reporter assay described above could be done in reverse, i.e., OgLuc luminescence detected first, quenched and a second luminescence detected, e.g., red click beetle or firefly luciferase, various *Renilla* luciferase inhibitors (see U.S. Published Application No. 2008/0248511) were screened for their ability to also inhibit OgLuc. Two different, previously identified, *Renilla* inhibitors, PBI-3077 and 1424, were added at various concentrations (*see* Table 41) to *E. coli* lysate samples expressing the variant 9B8 (diluted as above) and a buffer containing 100 mM MES pH 6.0, 1 mM CDTA, 150 mM KCl, 35 mM Thiourea, 2 mM DTT, 0.25% TERGITOL® NP-9 (v/v), 0.025% MAZU® DF 204, and 20 µM PBI-3939. Luminescence was measured as described previously except luminescence was measured using the GLOMAX®-Multi Microplate luminometer (Promega Corp.; also known as Turner MODULUS™). As shown in Table 41, both compounds were able to inhibit OgLuc luminescence. This demonstrates that an OgLuc variant can be multiplexed in a reporter assay with another luciferase wherein luminescence from an OgLuc variant is detected first in the reporter assay.

**Table 41: The effect of PBI-3077 and PBI-1424 on Luminescence Generated by Bacterial Lysates Expressing 9B8 opt Using PBI-3939 as a Substrate**

| | (mM or %) | RLU | +/- | % |
|---|---|---|---|---|
| | control | 27,794,600 | 626,862 | 100% |
| AI (3077) | 3 | 15,473,100 | 209,567 | 56% |
| mM | 0.3 | 22,210,433 | 102,888 | 80% |
| | 0.03 | 22,484,933 | 927,459 | 81% |
| AC (1424) | 0.4 | 176,868 | 9,579 | 0.64% |
| % | 0.04 | 24,267,533 | 363,861 | 87% |
| | 0.004 | 25,126,900 | 1,569,453 | 90% |

**[00498]** C. The spectral resolution between OgLuc Variant L27V and firefly luciferase (Fluc) was analyzed. Purified L27V (previously described; 9.54 pM) in DMEM without phenol red + 0.1% PRIONEX® was mixed with assay reagent (previously described) containing 20 μM PBI-3939. Purified firefly luciferase enzyme (QUANTILUM® Recombinant Luciferase; Promega Corp.; 271 ng/mL) in the same media was mixed with a test reagent (100 mM HEPES, pH 7.4, 1 mM CDTA, 16 mM MgSO4, 1% TERGITOL® NP-9 (v/v), 0.1% MAZU® DF 204, 5 mM ATP, 50 mM DTT, 333 μM luciferin). Purified *Renilla* luciferase (5 ng/mL GST-Renilla) in 1X Renilla Luciferase Assay Lysis Buffer (Promega Corp.) was mixed with 10.5 μM native coelenterazine in Renilla Luciferase Assay Buffer. Luminescence was measured after 3 min for L27V and Fluc and after 10 min for *Renilla* luciferase (FIG. 71)

**[00499]** D. As another example, an OgLuc variant of the present invention could be used as transcriptional reporter and paired with either aequorin or a cAMP circularly permuted firefly luciferase biosensor (or both simultaneously) to detect multiple pathways in a single sample, e.g., aequorin for the detection and/or measurement of calcium, the biosensor for the detection and/or measurement of cAMP, and an OgLuc variant for monitoring of downstream gene expression.

**[00500]** E. Other examples for multiplexing with the OgLuc variants of the present invention include:

**[00501]** i) Transfecting cells with constructs containing an OgLuc variant of the present invention and Firefly luciferase. After transfection, a first reagent could be added to lyse the cells as well as provide the substrate to generate luminescence for the first luciferase. Luminescence from the first luciferase would then be measured. A second reagent would then be added to quench luminescence from the first luciferase as well as provide the substrate to generate luminescence from the second luciferase. Luminescence from the second luciferase

would then be measured. The choice of which luciferase to measure first would only depend on the ability to quench the luminescence from the first luciferase with the second reagent. For this example, luminescence from the OgLuc variant could be measured first as high concentrations of luciferin (substrate for firefly luciferase) has been shown to inhibit OgLuc variant activity.

**[00502]** ii) Transfecting cells with constructs containing an OgLuc variant of the present invention and Firefly luciferase. After transfection, a first reagent could be added which contained a live cell substrate to generate luminescence for the first luciferase. Luminescence from the first luciferase would then be measured. A second reagent would then be added to lyse the cells, quench luminescence from the first luciferase and provide the substrate to generate luminescence from the second luciferase. Luminescence from the second luciferase would then be measured. This is similar to i) except cell lysis will further limit usage of the live cell substrate and contribute to the quenching of luminescence from the first luciferase.

**[00503]** iii) Transfecting cells with constructs containing an OgLuc variant of the present invention and Firefly luciferase. After transfection, one reagent could be added which contained substrates to generate luminescence from both luciferases, but the luminescence from each luciferase is spectrally different. The emission max of the OgLuc variants is approximately 460 nm, and certain substrates for Firefly luciferase, for example 5'-chloroluciferin and 5'-methylluciferin, can yield an emission max of approximately 610 nm. Therefore, although there may be some overlap from the blue emission into the red emission, there would be no overlap of the red emission into the blue emission suggesting that little to no mathematical correction would be involved.

**[00504]** iv) Transfecting cells with constructs containing an OgLuc variant of the present invention and Firefly luciferase. After transfection, one reagent could be added which contained live cell substrates to generate luminescence from both luciferases. The unique feature of this example is that firefly luminescence tends to shift to red at live cell assay temperatures, e.g., 37°C, therefore, a number of different luciferin derivatives could be chosen as a live cell substrate for firefly luciferase to generate luminescence which is spectrally different from that of the OgLuc variant.

**[00505]** v) Transfecting cells with constructs containing an OgLuc variant of the present invention and *Renilla* luciferase. After transfection, a first reagent could be added to lyse the cells as well as provide the substrate to generate luminescence for the first luciferase. Luminescence from the first luciferase would then be measured. A second reagent would then be added to quench luminescence from the first luciferase as well as provide the substrate to

generate luminescence from the second luciferase. Luminescence from the second luciferase would then be measured. The choice of which luciferase to measure first would only depend on the ability to quench the luminescence from the first luciferase with the second reagent. For this example, inhibitors to quench either the OgLuc variant or *Renilla* luciferase luminescence would need to be used.

**[00506]** vi) Transfecting cells with constructs containing an OgLuc variant of the present invention and click beetle luciferase. After transfection, one reagent could be added which contained substrates to generate luminescence from both luciferases, but the luminescence from each luciferase is spectrally different as click beetle luciferase generates red-shifted luminescence with native luciferin.

**Example 47 - Circular Permutation**

**[00507]** Two circularly permuted (CP) versions of the L27V variant were made: CP84 and CP95. The number designation refers to the N-terminal residue (e.g., "84" indicates the new N-terminus of the CP version).

**[00508]** To create the circular permutations, the prior N- and C-termini are fused together with no linker ("CP84 no linker" (SEQ ID NOs: 97 and 98) and "CP95 no linker" (SEQ ID NOs: 105 and 106)) or a 5 ("CP84 5AA linker" (SEQ ID NOs: 99 and 100) and "CP95 5AA linker" (SEQ ID NOs: 107 and 108), 10 ("CP84 10AA linker" (SEQ ID NOs: 101 and 102) and "CP95 10AA linker" (SEQ ID NOs: 109 and 110), or 20 ("CP84 20AA linker" (SEQ ID NOs: 103 and 104) and "CP95 20AA linker" (SEQ ID NOs: 111 and 112) amino acid linker, (GSSGG)n (SEQ ID NO: 113) in between the N- and C-termini ends. (Note: L27V starts with the phenylalanine at the N-terminus, i.e., MVF. The "MV" is present in the "no linker" construct, but not in the "linker" constructs). Once circularly permuted, the CP L27V variants were cloned into the pF1K vector. *E. coli* cells were transformed with the CP vectors and grown in minimal media using the standard walk away induction protocol previously described. For each CP construct, cells were grown in 8 wells of a 96-well plate. After induction, the 8 wells from each sample were pooled, and 10 µL lysed in 40 µL lysis buffer (100 mM MES pH 6.0, 0.3X PLB, 0.3 mg/mL lysozyme, 0.003 U/µL DNase I, and 0.25% TERGITOL® NP-9 (v/v)). The lysates were then diluted 1:100 (CP versions with linker) or 1:1000 (non-CP versions) in lysis buffer. The CP version without linker was not diluted. The lysates or lysate dilutions were assayed in triplicate in 50 µL assay reagent (previously described). Luminescence was measured as previously described (FIG. 72).

**Example 48 - Identifying Additional Sites for Circular Permutation**

**[00509]** To identify additional CP sites, determine the impact of the CP sites on luciferase activity and investigate the use of a "tether" between fragments, CP constructs were made with a circular permutation made at approximately every 3rd site (i.e., amino acid) of the L27V variant (*See* FIG. 73E). One skilled in the art would understand that other sites, e.g., the 1st and 2nd site, could also be tested and used in circular permuted OgLuc variants described herein using the methods described here. For example, the L27V variant has been found to be particularly tolerant to circular permutation, particularly situations in which a relatively large binding domain is placed in between the permuted fragments (e.g. cAMP/RIIbB-based sensors). At each site, the linker GSSGG-GSSGG-EPTT-ENLYFQS-DN-GSSGG-GSSGG (SEQ ID NO: 328) was added. The underscored sequence refers to a TEV protease recognition site. The purpose of the linker is to provide a long enough tether between the two variant fragments so they can associate in a way that produces a functional luciferase enzyme. The TEV protease recognition site was used to provide a means to disrupt the tether (in the presence of TEV protease) so that its importance to maintaining activity could be investigated. The use of the TEV protease recognition site created a mode to predict which CP sites would be useful for protein complementation assays (PCA) or for biosensor applications (e.g., insertion of a response element between the CP sites).

**[00510]** The activity that is seen prior to TEV cleavage represents how the two halves of the variant enzyme behaves in a tethered state. TEV binding to the recognition site causes cleavage, thereby separating the two halves of the variant enzyme. Samples that have been cleaved with TEV would represent the un-induced state and provide an indication of how much background could be expected. Lower activity after TEV cleavage indicates that the two halves cannot come together without induction. Samples that show a large loss in activity after TEV cleavage indicate sites that would function in PCA and biosensor applications. In the case of PCA, the two halves of the variant enzyme would be fused to binding partners that are able to come together (tether) after an induced binding event. In the case of a biosensor, the two halves would "tether" after a binding-induced conformational change occurs. One example for PCA would be to fuse one half of L27V to FRB and the other half to FKBP. The two halves would be brought into proximity with exposure to rapamycin (Banaszynski *et al.*, *J. Am. Chem. Soc*, **127(13)**:4715–4721(2005)). One example of a biosensor application would be to insert a Cyclic AMP binding domain (e.g., RIIbB) between the CP sites and induce a conformational change by binding of Cyclic AMP to the binding domain.

**[00511]** Once each CP L27V construct was made, the CP enzyme was expressed in wheat germ, *E. coli* and mammalian cells and digested with TEV protease to investigate luciferase activity.

**[00512]** 1. For analysis in wheat germ, the CP constructs were expressed using the TnT® T7 Coupled Wheat Germ Extract System (Promega Corp.) according to the manufacture's instructions. The TnT® reactions were then diluted 1:100 in 1X PBS + 0.1% gelatin, and 20 µL added to 25 µL of TEV reaction reagent (5 µL 20X ProTEV buffer (Promega Corp.), 1 µL 100 mM DTT, and 2 µL 10 U ProTEV Plus (Promega Corp.)). The volume of the digestion reactions was the brought to 100 µL with water and incubated at 30°C for 60 min. Control samples without TEV protease were also prepared. 10 µL of the digested samples were then added to 40 µl DMEM to a final volume of 50 µL and assayed in 50 µL assay reagent (as previously described; 100 µM PBI-3939). Luminescence was measured as previously described (FIGS. 73A-D).

**[00513]** 2. For analysis in mammalian cells, HEK293 cells were transfected with the CP L27V variants using a reverse transfection protocol. Briefly, 1 ng CP L27V plasmid DNA was mixed with 1 µg carrier DNA and added to cells in a well of a 12-well plate. Cells were then incubated for 16 hrs at 37°C, 5% $CO_2$. Cell lysates were then prepared by removing the media from the cells, washing them in 1X PBS, and adding 1 mL 1X PLB. Lysates were then diluted 1:10 in 1X PBS with 0.1% gelatin. 40 µL of the diluted lysate was then used in a TEV protease digestion as described above. 10 µL of the digestion was mixed with 40 µL DMEM without phenol red, and 50 µL assay reagent (previously described; 100 µM PBI-3939) added. Luminescence was measured as previously described (FIG. 73H).

**[00514]** 3. For analysis in *E. coli*, *E. coli* cultures expressing the CP L27V variants were grown overnight at 30°C. These cultures were used (1:100 diluted in LB + antibiotic) to make new starter cultures for eventual induction. The starter cultures were incubated at 37°C with shaking for 2.5 hrs ($OD_{600}$ is approximately 0.5). Rhamnose (final concentration of 0.2%) was added, the cultures moved to 25°C, and incubated with shaking for 18 hrs.

**[00515]** To create lysates, 50 µL 0.5X FASTBREAK™ Cell Lysis Reagent (Promega Corp.) was added to 950 µL of induced cultures, and the mixtures incubated for 30 min at 22°C. 50 µL of the lysed culture was then digested with TEV protease as described above and incubated at room temperature for 2 hrs.

**[00516]** For analysis, lysates were diluted 1:10,000 in HaloTag® Mammalian Purification Buffer (Promega Corp.), and 50 µL assayed in 50 µL of assay reagent (as previously described; 100 µM PBI-3939). Basal and TEV induced luminescence was measured at 5 min time points (FIG. 73F) and the response (FIG. 73G) was determined as previously described.

**[00517]** FIGS. 73A-D show the basal luminescence of various CP-TEV protease L27V constructs expressed in wheat germ extract. FIG. 73E summarizes the derived CP variants that responded to TEV protease (response is fold decreased), indicating that the CP variants can be used as TEV sensors, i.e., they are indicative of "tether dependence." Variants showing at least a 1.2-fold change were further validated as signification using Student's Test (unpaired *p* values; confidence level of 0.03). These results indicate that each CP variant is capable of generating luminescence.

**[00518]** Various CP-TEV protease L27V constructs were expressed in HEK293 cells. The reverse transfection protocol, previously described was used to transfect 1 ng DNA /well with 1 μg of carrier DNA. Each cell sample was grown in 1 mL of media in a 12 well plate. Cell lysates were prepared by removing media and adding 1 mL of 1X PLB. Samples were diluted 1:10 in 1X PBS+0.1% gelatin. 40 μL of the dilution sample was set up for TEV digestion. 10 μL of the digestion reaction was added to 40 μL of DMEM without phenol red and 50 μL of PBI-3939 as previously described. FIG. 73H shows the luminescence of the various CP-TEV protease L27V constructs expressed in HEK293 cells.

**[00519]** The data in FIGS. 73A-H demonstrates that the L27V variant can be circularly permuted at various sites, and different sites have different dependencies regarding tether length. The mammalian cell data and Wheat Germ data show similar fold reduction with TEV cleavage. The CP L27V variants that are more dependent on the tether, i.e., are more sensitive to TEV protease cleavage, are potential candidates for PCA. CP L27V variants that are less dependent on the tether may be potential candidates for self-complementation/dimerization assays.

## EXAMPLE 49 - PROTEIN COMPLEMENTATION ASSAYS

**[00520]** Protein complementation assays (PCA) provide a means to detect the interaction of two biomolecules, e.g., polypeptides. PCA utilizes two fragments of the same protein, e.g., enzyme, that when brought into close proximity with each other can reconstitute into a functional, active protein. An OgLuc variant of the present invention can be separated into two fragments at a site(s) tolerant to separation. Then, each fragment of the separated OgLuc variant can be fused to one of a pair of polypeptides of interest believed to interact, e.g., FKBP and FRB. If the two polypeptides of interest do in fact interact, the OgLuc fragments then come into close proximity with each other to reconstitute the functional, active OgLuc variant. The activity of the reconstituted OgLuc variant can then be detected and measured using a native or known coelenterazine or a novel coelenterazine of the present invention. In another example, the split OgLuc variant can be used in a more general complementation system similar to lac-Z (Langley

*et al., PNAS,* 72:1254-1257 (1975)) or ribonuclease S (Levit and Berger, *J. Biol. Chem.,* 251:1333 –1339 (1976)). Specifically, an OgLuc variant fragment (designated "A") known to complement with another OgLuc variant fragment ("B") can be fused to a target protein, and the resulting fusion can be monitored via luminescence in a cell or a cell lysate containing fragment B. The source of fragment B could be the same cell (either in the chromosome or on another plasmid), or it could be a lysate or purified protein derived from another cell. This same fusion protein (fragment A) could be captured or immobilized using a fusion between fragment B and a polypeptide such as HALOTAG® capable of attachment to a solid support. Luminescence can then be used to demonstrate successful capture or to quantitate the amount of material captured. Methods for protein complementation can be carried out according to U.S. Published Application No. 2005/0153310, incorporated herein by reference.

**[00521]** 1. 9B8 opt PCA constructs were made as follows:

**[00522]** -p9B8PCA 1/4 = pF5A/Met-[9B8 opt (51-169)]-GGGGSGGGSS-FRB (SEQ ID NOs: 331 and 332) & pF5A/FKBP-GGGSSGGGSG-[9B8 opt (1-50)] (SEQ ID NOs: 337 and 338)

**[00523]** -p9B8PCA 1/2 = pF5A/Met-[9B8 opt (51-169)]-GGGGSGGGSS-FRB (SEQ ID NOs: 331 and 332) & pF5A/[9B8 opt (1-50)]-GGGGSGGGSS-FRB (SEQ ID NOs: 333 and 334)

**[00524]** -p9B8PCA 2/3 = pF5A/[9B8 opt (1-50)]-GGGGSGGGSS-FRB (SEQ ID NOs: 333 and 334) & pF5A/FKBP-GGGSSGGGSG-[9B8 opt (51-169)] (SEQ ID NOs: 335 and 336)

**[00525]** -p9B8PCA 3/4 = pF5A/FKBP-GGGSSGGGSG-[9B8 opt (51-169)] (SEQ ID NOs: 335 and 336) & pF5A/FKBP-GGGSSGGGSG-[9B8 opt (1-50)] (SEQ ID NOs: 337 and 338)

**[00526]** The PCA constructs were transfected into HEK293 cells (15,000cells/well) into a 96-well plate using FUGENE® HD according to the manufacturer's instructions. The cells were then incubated overnight at 37°C, 5% $CO_2$. After transfection, the media on the cells was replaced with $CO_2$-independent media with 10% FBS. Assay reagent with 20 μM PBI-3939 was then added, and luminescence measured on a Varioskan Flash at 28°C. 100 μM rapamycin was then added to the wells, and luminescence continuously measured for 1 hr. Fold response was calculated by dividing all luminescence of a given well by the pre-rapamycin treatment luminescence for the same well (FIG. 74).

**[00527]** 2. To demonstrate the use of the OgLuc variants in PCA, the L27V02A variant fragments were complementated with FKBP or FRB, and the interaction between FKBP and FRB measured.

**[00528]** Table 42 lists the various protein complementation (PCA) constructs made and tested. "2/3" designates the variant complementation pairs where 1) the "old" C-terminus of L27V02A ("old"=original C-terminus of L27V02A) is the C-terminal partner of FKBP; and 2) the "old" N-terminus of L27V02A is the N-terminal partner of FRB. "1/4" designates the variant pairs where 1) the "old" N-terminus of L27V02A is the C-terminal partner of FKBP; and 2) the "old" C-terminus of L27V02A is the N-terminal partner of FRB. For all constructs, FKBP was located at the N-terminus of the L27V02A fragment, and FRB was located at the C-terminus of the L27V02A fragment. For example, PCA constructs were made with split sites at position 157 (*see* Table 42, "2/3" and "1/4" #s 11 and 12 (SEQ ID NOs: 288-295)), 103 (*see* Table 42, "2/3" and "1/4" #s 9 and 10 (SEQ ID NOs: 296-303)), and 84 (*see* Table 42, "2/3" and "1/4" #s 7 and 8 (SEQ ID NOs: 304-315)). Other PCA constructs were made (SEQ ID NOs: 343-426 and 428-440) (*See* Table 21)

**Table 42**

| *"2/3"* | *"1/4"* |
|---|---|
| 1. FKBP—L27V **6**-169 | 1. FKBP—L27V 1-5 |
| 2. L27V 1-5—FRB | 2. L27V **6**-169—FRB |
| 3. FKBP—L27V **12**-169 | 3. FKBP—L27V 1-11 |
| 4. L27V 1-11—FRB | 4. L27V **12**-169—FRB |
| 5. FKBP—L27V **55**-169 | 5. FKBP—L27V 1-54 |
| 6. L27V 1-54—FRB | 6. L27V **55**-169—FRB |
| 7. FKBP—L27V **84**-169 | 7. FKBP—L27V 1-83 |
| 8. L27V 1-83—FRB | 8. L27V **84**-169—FRB |
| 9. FKBP—L27V **103**-169 | 9. FKBP—L27V 1-102 |
| 10. L27V 1-102—FRB | 10. L27V **103**-169—FRB |
| 11. FKBP—L27V **157**-169 | 11. FKBP—L27V 1-156 |
| 12. L27V 1-156—FRB | 12. L27V **157**-169—FRB |

| *"2/3"* | *"1/4"* |
|---|---|
| 1. FKBP—L27V **6**-169 | 1. FKBP—L27V 1-5 |
| 2. L27V 1-5—FRB | 2. L27V **6**-169—FRB |
| 3. FKBP—L27V **12**-169 | 3. FKBP—L27V 1-11 |
| 4. L27V 1-11—FRB | 4. L27V **12**-169—FRB |
| 5. FKBP—L27V **55**-169 | 5. FKBP—L27V 1-54 |
| 6. L27V 1-54—FRB | 6. L27V **55**-169—FRB |
| 7. FKBP—L27V **84**-169 | 7. FKBP—L27V 1-83 |
| 8. L27V 1-83—FRB | 8. L27V **84**-169—FRB |
| 9. FKBP—L27V **103**-169 | 9. FKBP—L27V 1-102 |
| 10. L27V 1-102—FRB | 10. L27V **103**-169—FRB |
| 11. FKBP—L27V **157**-169 | 11. FKBP—L27V 1-156 |
| 12. L27V 1-156—FRB | 12. L27V **157**-169—FRB |

**Table 21**

| pCA constructs |
|---|
| SEQ ID NO:343 (pCA 31 pCA L27V02A 45-169 FRB) |
| SEQ ID NO:344 (pCA 31 pCA L27V02A 45-169 FRB) |
| SEQ ID NO:345 (pCA 32 FKBP L27V02A 1-44) |
| SEQ ID NO:346 (pCA 32 FKBP L27V02A 1-44) |
| SEQ ID NO:347 (pCA 33 pCA L27V02A 46-169 FRB) |
| SEQ ID NO:348 (pCA 33 pCA L27V02A 46-169 FRB) |
| SEQ ID NO:349 (pCA 34 pCA FKBP 1-45 L27V02A) |
| SEQ ID NO:350 (pCA 34 pCA FKBP 1-45 L27V02A) |
| SEQ ID NO:351 (pCA 35 pCA L27V02A 100-169 FRB) |
| SEQ ID NO:352 (pCA 35 pCA L27V02A 100-169 FRB) |
| SEQ ID NO:353 (pCA 36 FKBP L27V02A 1-99) |
| SEQ ID NO:354 (pCA 36 FKBP L27V02A 1-99) |
| SEQ ID NO:355 (pCA 37 L27V02A 101-169 FRB) |
| SEQ ID NO:356 (pCA 37 L27V02A 101-169 FRB) |
| SEQ ID NO:357 (pCA 38 FKBP 1-100 L27V02A) |
| SEQ ID NO:358 (pCA 38 FKBP 1-100 L27V02A) |
| SEQ ID NO:359 (pCA 39 L27V02A 102-169 FRB) |
| SEQ ID NO:360 (pCA 39 L27V02A 102-169 FRB) |
| SEQ ID NO:361 (pCA 40 FKBP L27V02A 1-101) |
| SEQ ID NO:362 (pCA 40 FKBP L27V02A 1-101) |
| SEQ ID NO:363 (pCA 41 L27V02A 143-169 FRB) |
| SEQ ID NO:364 (pCA 41 L27V02A 143-169 FRB) |
| SEQ ID NO:365 (pCA 42 FKBP 1-142 L27V02A) |
| SEQ ID NO:366 (pCA 42 FKBP 1-142 L27V02A) |
| SEQ ID NO:367 (pCA 43 L27V02A 145-169 FRB) |
| SEQ ID NO:368 (pCA 43 L27V02A 145-169 FRB) |
| SEQ ID NO:369 (pCA 44 FKBP 1-144 L27V02A) |
| SEQ ID NO:370 (pCA 44 FKBP 1-144 L27V02A) |
| SEQ ID NO:371 (pCA 45 L27V02A 147-169 FRB) |
| SEQ ID NO:372 (pCA 45 L27V02A 147-169 FRB) |
| SEQ ID NO:373 (pCA 46 FKBP- L27V02A 1-146) |
| SEQ ID NO:374 (pCA 46 L27V02A-FKBP 1-146) |
| SEQ ID NO:375 (pCA 47 L27V02A 148-169 FRB) |
| SEQ ID NO:376 (pCA 47 L27V02A 148-169 FRB) |
| SEQ ID NO:377 (pCA 48 FKBP- L27V02A 1-147) |
| SEQ ID NO:378 (pCA 48 FKBP- L27V02A 1-147) |

| |
|---|
| SEQ ID NO:379 (pCA 49 L27V02A 156-169 FRB) |
| SEQ ID NO:380 (pCA 49 L27V02A 156-169 FRB) |
| SEQ ID NO:381 (pCA 50 FKBP-L27V02A 1-155) |
| SEQ ID NO:382 (pCA 50 FKBP-L27V02A 1-155) |
| SEQ ID NO:383 (pCA 51 L27V02A 158-169 FRB) |
| SEQ ID NO:384 (pCA 51 L27V02A 158-169 FRB) |
| SEQ ID NO:385 (pCA 52 FKBP 1-157 L27V02A) |
| SEQ ID NO:386 (pCA 52 FKBP 1-157 L27V02A) |
| SEQ ID NO:387 (pCA 53 L27V02A 166-169 FRB) |
| SEQ ID NO:388 (pCA 53 L27V02A 166-169 FRB) |
| SEQ ID NO:389 (pCA 54 FKBP L27V02A 1-165) |
| SEQ ID NO:390 (pCA 54 FKBP L27V02A 1-165) |
| SEQ ID NO:391 (pCA 55 FKBP L27V02A 1-47) |
| SEQ ID NO:392 (pCA 55 FKBP L27V02A 1-47) |
| SEQ ID NO:393 (pCA 56 L27V02A 48-169-FRB) |
| SEQ ID NO:394 (pCA 56 L27V02A 48-169-FRB) |
| SEQ ID NO:395 (pCA 57 FKBP L27V02A 1-49) |
| SEQ ID NO:396 (pCA 57 FKBP L27V02A 1-49) |
| SEQ ID NO:397 (pCA 58 pCA L27V02A 50-169 FRB) |
| SEQ ID NO:398 (pCA 58 pCA L27V02A 50-169 FRB) |
| SEQ ID NO:399 (pCA 59 FKBP L27V02A 1-82) |
| SEQ ID NO:400 (pCA 59 FKBP L27V02A 1-82) |
| SEQ ID NO:401 (pCA 60 L27V02A 83-169-FRB) |
| SEQ ID NO:402 (pCA 60 L27V02A 83-16-FRB) |
| SEQ ID NO:403 (pCA 61 FKBP L27V02A 1-84) |
| SEQ ID NO:404 (pCA 61 FKBP L27V02A 1-84) |
| SEQ ID NO:405 (pCA 62 L27V02A 85-169-FRB) |
| SEQ ID NO:406 (pCA 62 L27V02A 85-169-FRB) |
| SEQ ID NO:407 (pCA 63 FKBP L27V02A 1-122) |
| SEQ ID NO:408 (pCA 63 FKBP L27V02A 1-122) |
| SEQ ID NO:409 (pCA 64 L27V02A 123-169-FRB) |
| SEQ ID NO:410 (pCA 64 L27V02A 123-169-FRB) |
| SEQ ID NO:411 (pCA 65 FKBP L27V02A 1-123) |
| SEQ ID NO:412 (pCA 65 FKBP L27V02A 1-123) |
| SEQ ID NO:413 (pCA 66 L27V02A 124-169 FRB) |
| SEQ ID NO:414 (pCA 66 L27V02A 124-169 FRB) |
| SEQ ID NO:415 (pCA 67 L27V02A 1-168) |
| SEQ ID NO:416 (pCA 67 L27V02A 1-168) |

| |
|---|
| SEQ ID NO:417 (pCA 67 L27V02A 1-168) |
| SEQ ID NO:418 (*pCA 68 L27V02A 169 FRB) |
| SEQ ID NO:419 (*pCA 68 L27V02A 169 FRB) |
| SEQ ID NO:420 (pCA 69 FKBP L27V02A 1-166) |
| SEQ ID NO:421 (pCA 69 FKBP L27V02A 1-166) |
| SEQ ID NO:422 (*pCA 70 L27V02A 167-169 FRB) |
| SEQ ID NO:423 (*pCA 70 L27V02A 167-169 FRB) |
| SEQ ID NO:424 (pCA 71 FKBP L27V02A 1-164) |
| SEQ ID NO:425 (pCA 71 FKBP L27V02A 1-164) |
| SEQ ID NO:426 (pCA 72 L27V02A 165-169 FRB) |
| SEQ ID NO:428 (pCA 72 L27V02A 165-169 FRB) |
| SEQ ID NO:429 (pCA 73 FKBP L27V02A 1-162) |
| SEQ ID NO:430 (pCA 73 FKBP L27V02A 1-162) |
| SEQ ID NO:431 (pCA 74 L27V02A 163-169 FRB) |
| SEQ ID NO:432 (pCA 74 L27V02A 163-169 FRB) |
| SEQ ID NO:433 (pCA 75 FKBP L27V02A 1-160) |
| SEQ ID NO:434 (pCA 75 FKBP L27V02A 1-160) |
| SEQ ID NO:435 (pCA 76 L27V02A 161-169 FRB) |
| SEQ ID NO:436 (pCA 76 L27V02A 161-169 FRB) |
| SEQ ID NO:437 (pCA 77 FKBP L27V02A 1-158) |
| SEQ ID NO:438 (pCA 77 FKBP L27V02A 1-158) |
| SEQ ID NO:439 (pCA 78 L27V02A 159-169 FRB) |
| SEQ ID NO:440 (pCA 78 L27V02A 159-169 FRB) |

**[00529]** The complementation pairs described in Table 42 were cloned into the pF4Ag vector as previously described. The PCA constructs (900 μL) were then expressed in rabbit reticulocyte lysate (RRL; Promega Corp.) or wheat germ extract (Promega Corp.) following the manufacture's instructions. 1.25 μL of the expression reactions for each PCA pair were mixed with 10 μL of 2X Binding Buffer (100 mM HEPES, 200 mM NaCl, 0.2% CHAPS, 2 mM EDTA, 20% glycerol, 20 mM DTT, pH 7.5) and 7.5 μL water, and 18 μL transferred to wells of a 96-well plate. 2 μL of 5 μM Rapamycin (final concentration 0.5 μM) was added and incubated for 10 min at room temperature.

**[00530]** Following incubation, 100 μL of PBI-3939 (50X stock diluted to 1X in assay buffer) and incubate for 3 min at room temperature. Luminescence was measured as previously described (FIG. 76A-B: wheat germ; FIG. 76C-D: rabbit reticulocyte; FIG. 76E-F: cell free system [which system? WG or RRL?]; FIG. 76G: HEK293 cells).

**[00531]** FIG. 76A-G show the luminescence of various protein complementation (PCA) L27V pairs: one L27V fragment of each pair was fused to either FKBP or FRB using a 2/3 configuration (FIGS. 76A and 76C) or a 1/4 configuration (FIGS. 76B and 76D) as described, and the interaction of FKBP and FRB monitored in wheat germ extract (FIGS. 76A and 76B) and rabbit reticulocyte lysate (RRL) (FIGS. 76C and 76D); and the luminescence of various protein complementation (PCA) negative controls (FIG. 76E). The luminescence of various protein complementation L27V using a 1/4 configuration in a cell free system (RRL) (FIG. 76F) and HEK293 cells (FIG. 76G) was measured. The data in FIGS. 76A-G demonstrates that a variety of different deletions, i.e., small fragments of the L27V variant, are functional.

**[00532]** 3. To demonstrate the use of the PCA constructs for cell-based PCA, the constructs were transfected into HEK293 cells and assayed with PBI-4377. Plasmid DNA (5 ng) from each PCA pair (6, 12, 55, 84, and 103) were mixed with 40 ng carrier DNA (pGEM-3fz) and 5 μL OPTI-MEM® and incubated at room temperature for 5 min. FUGENE® HD (0.15 μL) was then added and again incubated at room temperature for 15 min. The DNA transfection mixtures were added to 100 μL HEK293 cells ($1.5x10^5$ cells/mL) in DMEM with 10% FBS (no antibiotics), transferred to wells of a 96-well plate, and incubated overnight at 37°C, 5% $CO_2$.

**[00533]** After transfection, the media was removed and replaced with $CO_2$-independent media with 20 μM or 50X PBI-4377 and incubated at 37°C without $CO_2$ regulation for 2 hrs. Luminescence was measured, 10 μL rapamycin added, and luminescence measured again every 2 min for 2 hrs (FIGS. 76A-C).

**[00534]** 4. To demonstrate the use of the PCA constructs to identify inhibitors of protein-protein interactions, the constructs described in #2 of this example were used.

**[00535]** The complementation pairs, 103 "2/3", 157 "2/3", 103 "1/4" and 157 "1/4" described in Table 42 were cloned into the pF4Ag vector as previously described. The PCA constructs (25 μL) were then expressed in rabbit reticulocyte lysate (RRL; Promega Corp.) following the manufacture's instructions. 1.25 μL of the expression reactions for each PCA pair were mixed with 10 μL of 2X Binding Buffer (100 mM HEPES, 200 mM NaCl, 0.2% CHAPS, 2 mM EDTA, 20% glycerol, 20 mM DTT, pH 7.5) and 7.5 μL water, and 16.2 μL transferred to wells of a 96-well plate. Rapamycin was examined with various amounts of FK506. To the reactions, the FRB-FKBP binding inhibitor, FK506 (10X) was added, and the reactions incubated at room temperature for 10 min. 15 nM rapamycin (10X stock solution) was added to get a final concentration of 1.5 nM rapamycin and incubated for 2 hrs at room temperature. Following incubation, 100 μL of PBI-3939 (50X stock diluted to 1X in assay buffer) and incubated for 3

min at room temperature. Luminescence was measured on a GLOMAX® luminometer. FIG. 77 demonstrates that the PCA constructs disclosed herein can be used to identify inhibitors of protein-protein interactions.

**[00536]** 5. To demonstrate the use of the PCA constructs in a lytic format, the complementation pairs, 103 "2/3", 157 "2/3", and 103 "1/4" were transfected into HEK293 cells and assayed with PBI-3939. 0.5 ng plasmid from each PCA pair was mixed with 5 µL OPTI-MEM® and 49 ng pGEM-3zf (Promega Corp.). The sample mixture was incubated at room temperature for 5 min. 0.15 µL FUGENE® HD was then added to the sample mixture and incubated at room temperature for 15 min. 100 µL of HEK293 cells in DMEM with 10% FBS (no antibiotics) at a concentration of $1.5x10^5$ cells/mL was added to each sample mixture. The cell sample was then transferred to a well of a 96-well plate and incubated at 37°C, 5% $CO_2$ overnight.

**[00537]** The next day, 11.1 µL of 10 µM Rapamycin (Final concentration 1 µM) was added to half of the wells and 11.1 µL water was added to other half of the wells. The 96-well plates were incubated at 37°C for 1 hr. 100 µL of assay reagent + PBI-3939 (2 µL 50X PBI-3939 mixed with 98 µL assay reagent, previously described) was added to each well and the plates were incubated at 37°C for 4 min. Luminescence was measured on a GLOMAX® luminometer at 37°C with 0.5s integration time and 1 read. (FIG. 76H).

**Example 50 - OgLuc cAMP Biosensor**

**[00538]** The OgLuc variants of the present invention can be linked to light output not only through concentration, but also through modulation of enzymatic activity. For example, a cAMP biosensor can be developed by incorporating a cAMP-binding domain from Protein Kinase A into a circularly permuted OgLuc variant. An OgLuc variant of the present invention can be circularly permuted at a site(s) tolerable to such permutation by methods known in the art (e.g., U.S. Published Application No. 2005/0153310). The resulting circularly permuted OgLuc variant chimeric protein can function as an intracellular biosensor for cAMP when expressed in mammalian cells. Upon binding of cAMP to the biosensor, the biosensor undergoes a conformational change that creates an active luciferase enzyme. Treating the cells with forskolin, an activator for adenylate cyclase, should result in an increase in luminescence with increasing concentrations of forskolin. Similar biosensors for targets including but not limited to calcium (Ca+2), cGMP, and proteases such as caspases and tobacco etch virus (TEV) can be developed by incorporating the appropriate binding domain or cleavage site for each into a circularly permuted OgLuc variant.

**[00539]** The utility of OgLuc as a biosensor was demonstrated by analysis of variant 9B8 opt in the context of a cAMP sensor. Circularly permuted constructs containing the RIIβB subunit of Protein Kinase-A flanked by OgLuc variant sequences were made and expressed in a cell free system as described in described in PCT application PCT/US2007/008176, except the sites for circular permutation were chosen as described below. The nascent protein was assayed in the presence and absence of cAMP. Response to cAMP is defined as the ratio of activity (+) cAMP/ (-) cAMP.

**[00540]** A structural model for OgLuc has been created, based on similarities to certain fatty acid binding proteins of known structure, previously described in PCT/US2010/33449. The model predicts an ordered sequence of the standard protein structural motifs; α-helix and β-sheet. The regions that transition between these structural elements as circular permutation sites were chosen (see Table 43).

**[00541]** 1. The template for expression of the biosensor constructs consisted of: C-terminal OgLuc sequence-RIIβB sequence-N-terminal OgLuc sequence in plasmid pF5 (Promega Corp.). The TNT® T7 Coupled Wheat Germ Extract System (Promega Part #L4140) was used to translate the construct. The TNT® Wheat Germ Extract Reaction included 25 µL TNT® Wheat Germ Extract (L411A), 2 µL TNT® Reaction Buffer (L462A), 1 µL Amino Acid Mixture, Complete (L446A), 1 µL RNasin® (40 U/µL) (N2615), 1 µL TNT® T7 RNA Polymerase (L516A), 1.0 µg DNA template and Nuclease-Free Water to bring the total volume to 50 µL. The reaction mixture was incubated at 30°C for 120 min.

**[00542]** An OgLuc activity assay was performed by adding to the 50 µL OgLuc translation mixture, 50 µL OgLuc Glo Reagent (100 mM MES (pH 6.0), 1 mM CDTA, 150 mM KCl, 35 mM thiourea, 2 mM DTT, 0.25% TERGITOL® NP-9 (v/v), 0.025% MAZU® DF 204, and 20 µM PBI-3939) with or without 100 µM cAMP, and performing a kinetic read for 30 min (TECAN® INFINITE® F500 Plate Reader). Response is determined by dividing the luminescence generated by the biosensor with cAMP by the luminescence generated by the biosensor without cAMP (Table 43).

**Table 43: Response of Circularly-Permuted OgLuc Biosensors to cAMP**

| CP-SITE | RESPONSE |
|---|---|
| 27 | 2.6X |
| 51 | 2.2X |
| 84 | 1.5X |

| | |
|---|---|
| 122 | 4.3X |
| 147 | 1.9X |
| 157 | 5.6X |

**[00543]** 2. A cAMP biosensor of 9B8opt circularly permuted at the CP-site 51 was created as described in 1. The biosensor was then transfected into HEK293 cells (15,000 cells/well) using FUGENE® HD according to the manufacturer's instructions into a 96-well plate, and incubated overnight at 37°C, 5% $CO_2$. After transfection, the media was removed and replaced with $CO_2$-independent media with 10% FBS. The cells were then incubated for 2 hrs at 37°C, 5% $CO_2$ after which varying amounts of FSK were added. The cells were then again incubated for 3 hrs at 37°C, 5% $CO_2$. 6 μM PBI-3939 was then added, and luminescence measured after 13 min (FIG. 78).

**[00544]** 3. Circularly permuted ("CP"; e.g., CP6 refers to the old residue 6 being new residue 1 after Met) and Straight Split ("SS"; e.g., SS6 refers to a sensor orientated as follows: OgLuc (1-6)-RIIβb binding site (SEQ ID NOs: 441 and 442) -OgLuc (7-169)) versions of L27V were used as cAMP biosensors (SEQ ID NOs: 467-574). CP (SEQ ID NOs: 467-498 and 555-574) and SS (SEQ ID NOs: 499-554) versions of the L27V variant were derived as previously described and expressed in expressed in rabbit reticulocyte lysate (RRL; Promega Corp.) following the manufacture's instructions. The linker sequence between the C-terminus of the RIIβb binding site and OgLuc luciferase sequence was GGGTCAGGTGGATCTGGAGGTAGCTCTTCT (SEQ ID NO: 575). The linker sequence between the N-terminus of the RIIβb binding site and OgLuc luciferase sequence was AGCTCAAGCGGAGGTTCAGGCGGTTCCGGA (SEQ ID NO: 576) 3.75 μL of the expression reactions were mixed with 1.25 μL 4X cAMP (final concentration 1 nM-0.1 mM), and incubated at room temperature for 15 min. Following incubation, 100 μL of PBI-3939 (50X stock diluted to 1X in assay buffer) and incubated for 3 min at room temperature. Luminescence was measured on a GLOMAX® luminometer (FIGS. 79A-B). Luminescence was also measured for CP and SS versions of the L27V variant expressed in HEK293 cells and treated with forskolin as previously described (FIGS. 79C-D). FIGS. 79A-D demonstrates that circularly permuted and straight split versions of the OgLuc variants disclosed herein can be used as biosensors.

**Example 51 - Subcellular Distribution and Localization**

**[00545]** To analysis subcellular distribution, U2OS cells were plated at $2x10^4$ cells/$cm^2$ into glass-bottom culture dishes in McCoy's 5A media (Invitrogen) containing 10% FBS. The cells

were then incubated for 24 hrs at 37°C, 5% $CO_2$. Cells were then transfected with 1/20 volume transfection mixture (FUGENE® HD and pF5A-CMV-L27V (the L27V variant (SEQ ID NO: 88) cloned into the pF5A vector with CMV promoter (Promega Corp.)) or pGEM3ZF (Promega Corp.; negative control)) and incubated for 24 hrs at 37°C, 5% $CO_2$. Following incubation, the cell media was replaced with $CO_2$-independent media with 0.5% FBS and 100 µM PBI-4378. After a 30 min incubation at 37°C, unfiltered images were captured on an Olympus LV200 bioluminescence microscope using a 60X objective (FIGS. 80A-B) for 25, 100, 1000, and 5000 ms.

**[00546]** To analyze subcellular localization, N-terminal L27V fusions with the GPCR AT1R (Angiotensin type 1 receptor (SEQ ID NOs: 459 and 460)) with IL-6 secretion sequence (SEQ ID NOs: 461 and 462) or the transcription factor, Nrf2 (SEQ ID NO: 317), were made using a GSSG linker (SEQ ID NOs: 457 and 458) and transfected into U2OS cells as described above (FIGS. 81A-C). FIG. 81C ("GPRC") shows expression of a construct where the IL6 signal sequence is upstream of the L27V variant sequence and the AT1R is downstream of the L27V variant sequence. The L27V variant alone was also transfected ("Unfused"). After a 24 hr incubation at 37°C, 5% $CO_2$, cell media was replaced with $CO_2$-independent media with 0.5% FBS and equilibrated for 1 hr at 37°C in a non-$CO_2$-regulated atmosphere. An equal volume of media + 200 µM PBI-3939 was then added, and unfiltered images were captured immediately on an Olympus LV200 bioluminescence microscope using a 60X or 150X objective (FIGS. 81A-C). For cells expressing L27V alone, PBI-3939 was washed off the cells immediately before image capture.

**Example 52 - Monitoring Intracellular Signal Pathways**

**[00547]** This example provides two examples of the novel luciferase being used to monitor intracellular signal pathways at the protein level (as opposed to the response element examples which represent transcriptional activation). The variant 9B8opt (SEQ ID NO: 24) was fused to either IkB (Gross *et al., Nature Methods* **2(8)**:607-614 (2005)) (at the C-terminus, i.e., N-IkB-(9B8opt)-C)) or ODD(oxygen-dependent degradation domain of Hif-1-α (Moroz *et al., PLoS One* **4(4)**:e5077 (2009)) (at the N-terminus, i.e., N-(9B8opt)-ODD-C)). IKB is known to be degraded in cells upon stimulation with TNFα; therefore, the IKB-(9B8opt) construct could be used as a live cell TNFα sensor. ODD (Hif-1-α) is known to accumulate inside cells upon stimulation with compounds that induce hypoxia; therefore, the ODD-(9B8opt) construct could be used as a live cell hypoxia sensor.

**[00548]** Constructs containing fusions with IkB or ODD with 9B8opt (pF5A) were expressed in HEK293 cells via reverse transfection (5 ng (IkB) or 0.05 ng (ODD) DNA (mixed with carrier DNA to give a total of 50 ng)) as previously described and incubated for 24 hrs at 37°C, 5% $CO_2$. After transfection, the media was replaced with fresh $CO_2$-independent media containing 0.5% FBS and 20 μM PBI-4377 and allowed to equilibrate for 4 hrs at 37°C, atmospheric $CO_2$. Cells were then exposed to a stimulus: TNFα for IkB fusion expressing cells and phenanthroline for ODD fusion expressing cells. DMSO (vehicle) was added to control cells. For the TNFα/IKB samples, 100 μg/mL cycloheximide was added approximately 15 min prior to adding the stimulus to prevent synthesis of new protein. At the indicated time points following treatment, cells were assayed for luminescence. For data normalization, the RLU of each sample at a given time point were divided by the RLU from the same sample immediately after stimulation. Fold response for each sensor was then determined (FIGS. 82A-C).

**[00549]** B. L27V was used to monitor the oxidative stress signal pathways at the protein level. L27V or *Renilla* luciferase (Rluc) was fused to Nrf2/NFE2L2 in a pF5K expression vector (at the C-terminus; i.e., N-Nrf2-(L27V)-C or N-Nrf2-(Rluc)-C). Keap1 is a negative regulator of Nrf2 (SEQ ID NO: 217). In order to faithfully represent regulation of Nrf2-L27V02 protein levels, Keap1, was co-expressed to keep Nrf2 levels low (via ubiquitination).

**[00550]** Nrf2-L27V or Nrf2-Rluc (5 ng, pF5K) and a HALOTAG®- Keap1 fusion protein (pFN21-HT7-Keap1 (SEQ ID NO: 316); 50 ng) were expressed in HEK293 cells by transfection of the cells at the time of seeding into the 96-well plates as previously described and incubated for 24 hrs at 37°C, 5% $CO_2$. After transfection, the media was replaced with fresh $CO_2$-independent media with 0.5% FBS and 20 μM PBI-4377 for L27V or 20 μM ENDUREN™ (Promega Corp.) for *Renilla* luciferase, and the cells equilibrated for 4 hrs at 37°C under atmospheric $CO_2$. For kinetic analysis, 20 μM D,L sulforaphane or vehicle (DMSO) were used. In FIG. 83A, luminescence was measured as previously described at the indicated time points following treatment. For data normalization, the luminescence of each sample at a given time point was divided by the luminescence from the same sample immediately after stimulation (FIGS. 83B-C).

**[00551]** C. A comparison of the response of the Nrf2 sensor described in B and Nrf2(ARE)-Luc2P reporter (Promega Corp.) was performed. Both the Nrf2 sensor and reporter were screened as described in section B above. For the firefly (Luc2P) reporter gene assay, the ONE-GLO™ assay reagent was used. FIGS. 84A-B provides the normalized response of Nrf2-L27V at 2 hrs and Nrf2(ARE)-Luc2P at 16 hrs

**Example 53 – Evaluation of OgLuc Variant as Bioluminescent Reporter with BRET**

**[00552]** Bioluminescence resonance energy transfer (BRET) allows monitoring of protein-protein interactions. The intramolecular energy transfer was examined between IV and a HT7 fusion partner where HT7 was previously labeled with a fluorophore, i.e., TMR (excitation/emission (ex/em) wavelength = 555/585 nm) or Rhodamine 110 (excitation/emission wavelength = 502/527 nm). 50 µL of a bacterial cell lysate containing the IV-HT7 fusion protein of Example 34 was incubated with or without 0.001-10 µM fluorophore ligand for 1 hr at room temperature. After the incubation, 50 µL of RENILLA-GLO™, which contains 22 µM coelenterazine-h, was added to 50 µL of the enzyme-ligand mixture, and the emission spectrum was recorded at 5 min. Example spectra of IV-HT7 with TMR (FIG. 83A) or Rhodamine 110 ("Rhod110") (FIG. 85B) are shown indicating BRET was greater when the ex/em of the ligand was closer to the 460 nm luminescent peak of OgLuc, i.e., greater with Rhodamine 110. This data shows that intramolecular energy transfer can occur between OgLuc variants and a fluorophore on a fusion protein. Three different controls were used for comparison (data not shown): 1) a non-HT fusion, 2) a HT-fusion that was not labeled with a HT ligand, and 3) a labeled HT-fusion that was proteolytically cleaved at a TEV site between OgLuc and HT (which indicated the involvement of proximity/distance). BRET was not observed in the three different controls suggesting that HT was involved to achieve BRET. BRET was greater for C1+A4E and IV with a C-terminal HT7 compared to N-terminal HT7.

**Example 54 – Protein Proximity Assays for live cells or lytic formats**

**[00553]** In one example, circularly permuted (CP) or straight split (SS) OgLuc fusion proteins is applied to measurements of protein proximity. OgLuc is permuted or split via insertion of a protease substrate amino acid sequence (e.g., TEV) to generate low bioluminescence. The inactive luciferase is tethered (e.g., via genetic fusion) to a monitor protein. A potential interacting protein is tethered (e.g., via genetic fusion) to a protease (e.g., TEV). When the two monitor proteins interact or are in sufficient proximity (e.g., via a constitutive interaction, a drug stimulus or a pathway response), the luciferase is cleaved to generate increased bioluminescence activity. The example may be applied to measurements of protein proximity in cells or in biochemical assays. Furthermore, the high thermal stability of an OgLuc variant luciferase could enable measurements of antibody-antigen interactions in lysed cells or biochemical assays.

**Example 55 - Bioluminescent Assays**

**[00554]** 1. To demonstrate the use of an OgLuc variant in a bioluminescent assay to detect caspase-3 enzyme, the 9B8 opt variant was used in a bioluminescent assay using a pro-coelenterazine substrate comprising the DEVD caspase-3 cleavage sequence. Purified caspase-3 enzyme was mixed with an *E. coli* lysate sample expressing the variant 9B8 opt, which was prepared as described in Example 27, and diluted 10-fold in a buffer containing 100 mM MES pH 6.0, 1 mM CDTA, 150 mM KCl, 35 mM thiourea, 2 mM DTT, 0.25% TERGITOL® NP-9 (v/v), 0.025% MAZU® DF 204, with or without 23.5 μM z-DEVD-coelenterazine-h in 100 mM HEPES pH 7.5. The caspase-3 enzyme was incubated with the lysate sample for 3 hrs at room temperature, and luminescence detected on a Turner MODULUS™ luminometer at various time points. A sample containing only bacterial lysate and a sample containing only caspase-3 were used as controls. Three replicates were used. FIG. 86 and Table 44 demonstrate that 9B8 opt, and thus other OgLuc variants of the present invention, can be used in a bioluminescent assay with a pro-coelenterazine substrate to detect an enzyme of interest.

**Table 44: Average luminescence in RLU generated from bacterial lysates expressing the 9B8 opt variant incubated with or without purified caspase-3 using z-DEVD-coelenterazine-h as a substrate.**

| time (min) | no caspase (RLU) | + caspase (RLU) |
|---|---|---|
| 5 | 26,023 | 25,411 |
| 15.3 | 7,707 | 36,906 |
| 29.9 | 4,013 | 41,854 |
| 60.9 | 2,305 | 43,370 |
| 190.3 | 1,155 | 42,448 |

**[00555]** 2. The L27V variant was used in a bioluminescent assay using a pro-coelenterazine substrate comprising the DEVD caspase-3 cleavage sequence. Purified caspase-3 enzyme (1 mg/mL) in 100 mM MES pH 6 (50 μL) was mixed with 227 nM L27V02 variant and 47 μM PBI-3741 (z-DEVD-coelenterazine-h) in assay buffer (50 μL). Reactions were incubated for 3 hrs at room temperature, and luminescence detected as previously described. The assay with the L27V variant was compared to a firefly luciferase version of the assay, CASPASE-GLO® 3/7-Assay system (Caspase-Glo; Promega Corp.). Table 45 demonstrate that L27V variant, and thus other OgLuc variants of the present invention, can be used in a bioluminescent assay with a pro-coelenterazine substrate to detect an enzyme of interest.

**Table 45**

| | (+) caspase | +/- | (-) caspase | +/- |
|---|---|---|---|---|
| **L27V** | 11,532 | 93 | 803 | 25 |
| **Caspase-Glo** | 15,156,567 | 793,981 | 302 | 5 |

**Example 56 - Immunoassays**

**[00556]** The OgLuc variants of the present invention are integrated into a variety of different immunoassay concepts. For example, an OgLuc variant is genetically-fused or chemically conjugated to a primary or secondary antibody to provide a method of detection for a particular analyte. As another example, an OgLuc variant is genetically-fused or chemically conjugated to protein A, protein G, protein L, or any other peptide or protein known to bind to Ig fragments, and this could then be used to detect a specific antibody bound to a particular analyte. As another example, an OgLuc variant is genetically-fused or chemically conjugated to streptavidin and used to detect a specific biotinylated antibody bound to a particular analyte. As another example, complementary fragments of an OgLuc variant are genetically-fused or chemically conjugated to primary and secondary antibodies, where the primary antibody recognizes a particular immobilized analyte, and the secondary antibody recognizes the primary antibody, all in an ELISA-like format. The OgLuc variant activity, i.e., luminescence, is reconstituted in the presence of immobilized analyte and used as a means to quantify the analyte.

**[00557]** As another example, complementary fragments of an OgLuc variant can be fused to two antibodies, where one antibody recognizes a particular analyte at one epitope, and the second antibody recognizes the analyte at a separate epitope. The OgLuc variant activity would be reconstituted in the presence of analyte. The method would be amenable to measurements of analyte quantification in a complex milieu such as a cell lysate or cell medium. As another example, complementary fragments of an OgLuc variant can be fused to two antibodies, where one antibody recognizes a particular analyte regardless of modification, and the second antibody recognizes only the modified analyte (for example, following post-translational modification). The OgLuc variant activity would be reconstituted in the presence of analyte only when it is modified. The method would be amenable to measurements of modified analyte in a complex milieu such as a cell lysate. As another example, an OgLuc variant can be conjugated to an analyte (e.g., prostaglandins) and used in a competitive sandwich ELISA format.

**Example 57 – Dimerization Assay**

**[00558]** This example demonstrates that full-length circularly permuted OgLuc variants can be fused to respective binding partners, e.g., FRB and FKBP, and used in a protein complementation-type assay. The key difference between the method disclosed herein and traditional protein complementation is that there was no complementation, but rather there was dimerization of two full length enzymes, e.g., circularly permuted OgLuc variants.

**[00559]** Briefly, the circularly permuted reporter proteins similarly configured for low activity were fused to both of the fusion protein partners (*See* FIG. 87A). For example, each fusion partner may be linked to identically structured, permuted reporters. Interaction of the fusion partners brought the permuted reporters into close proximity, thereby allowing reconstitution of a hybrid reporter having higher activity. The new hybrid reporter included portions of each of the circularly permuted reporters in a manner to reduce the structural constraint.

**[00560]** Circularly permuted, straight split L27V variants CP84 and CP103 (N-(SS-169)-(1-$SS_1$)-FRB-C and C-(1-$SS_1$)-(SS-169)-FKBP) were cloned as previously described and expressed (25 µL) in rabbit reticulocyte lysate (RRL; Promega Corp.) following the manufacture's instructions. 1.25 µL of the expression reactions for each dimerization pair were mixed with 10 µL of 2X Binding Buffer (100 mM HEPES, 200 mM NaCl, 0.2% CHAPS, 2 mM EDTA, 20% glycerol, 20 mM DTT, pH 7.5) and 7.5 µL water, and 18 µL transferred to wells of a 96-well plate. To the reactions, 2 µL rapamycin (final concentration 0 and 0.1-1000 nM) was added, and the reactions incubated at room temperature for 10 min. Following incubation, 100 µL of PBI-3939 (50X stock diluted to 1X in assay buffer) and incubated for 3 min at room temperature. Luminescence was measured on a GLOMAX® luminometer (FIG. 87B) and the response was determined (FIG. 87C). FIGS. 87B-C demonstrates that the OgLuc variants of the present invention can be used to detect protein-protein interactions via a PCA-type dimerization assay.

**Example 58 - Intercellular Half-Life**

**[00561]** The intracellular half-life of the OgLuc variants 9B8, 9B8+K33N, V2, L27V, and V2+L27M were determined. CHO cells (500,000) in 15-100 mm plates in F12 media with 10% FBS and 1X sodium pyruvate were transfected with 30 µL 100 ng/µL plasmid DNA containing 9B8, 9B8+K33N, V2, L27V ("V2+L27V") or V2+L27M (all in pF4A vector background) using TRANSIT®-LT1 (Mirus) according to the manufacture's instructions. The cells were then incubated for 6 hrs.

**[00562]** After incubation, the media was removed and 1 mL Trypsin added to dissociate the cells from the plate. 3 mL of F12 media was then added, and the cells counted. Cells were then

plated at 10,000 cells/well into 6 wells of a 96-well plate (6 wells/variant) and incubated overnight at 37°C. Samples were distributed over 3 plates. Each plate had 6 replicates for different time point measurements.

**[00563]** After overnight incubation, the media was removed from the cells for t=0 samples, and 100 µL assay buffer (previously described; no substrate) was added. The sample was frozen on dry ice and stored at -20°C. Cycloheximide (100 mg/mL) was diluted 1:100 to a final concentration of 1 mg/mL in OPTI-MEM®. DMSO (100%) was also diluted 1:100 (final concentration 1%) in OPTI-MEM®. The diluted cycloheximide (1 mg/mL) was added (11 µL) to 3 replicates of each transfected variant sample and 11 µL of the diluted DMSO (1%) was added to the other 3 replicates. The cells were then incubated at 37°C, 5% $CO_2$ and removed at various timepoints (i.e., 0, 0.5, 0.9, 2.5, 4.3, and 6.2 hrs) and processed as the t=0 samples.

**[00564]** For analysis, the samples were thawed to room temperature, and 10 µL assayed in 50 µL assay reagent. Luminescence was measured on a GLOMAX® luminometer. At each time-point, luminescence was measured for untreated and cycloheximide-treated samples. The RLU for the cells treated with cycloheximide was normalized by the RLU for the untreated cells.

**[00565]** The intracellular half-life of each variant was calculated by measuring the ratio of the luminescence from the cycloheximide (CHX)-treated to the untreated at each time-point. The ratio was then plotted ln (% treated to untreated) over time, and the half-life calculated (Table 46). The OgLuc variants had intracellular half-lives of approximately 6-9 hrs with a full strength CMV promoter, but the half lives were reduced with a CMV deletion variant (d2). The presence of a PEST degradation signal combined with the full strength CMV promoter reduces half-life significantly.

**Table 46**

| Sample | CMV no deg. | CMV d2 no deg. | CMV Pest |
|---|---|---|---|
| 9B8 | 6.32 | 3.87 | 1.43 |
| K33N | 9.24 | 3.70 | 1.18 |
| V2 | 9.63 | 4.28 | 1.61 |
| V2+L27V | 6.66 | 4.78 | 1.63 |
| V2+L27M | 8.89 | 6.98 | 1.63 |

**[00566]** Another experiment was completed using the reverse transfection protocol described in Example 52 with HEK293 cells (data not shown). The results from this experiment indicate that the intracellular half-life for the L27V variant with PEST is 10 min. The L27V variant with

no degradation signal used in this experiment did not show a decay over the course of this experiment. In this case the decay was normalized to untreated cells at t=0.

**Example 59 – Exposure of OgLuc Variants to Urea**

**[00567]** Since Firefly luciferase is known to be relatively unstable, it is much more sensitive to urea exposure. To determine whether this was also the case with the OgLuc variants, the sensitivity of the OgLuc to urea was determined. 5 µl of 45.3 µM L27V enzyme was mixed with 100 µL of a urea solution (100 mM MOPS, pH 7.2, 100 mM NaCl, 1 mM CDTA, 5% glycerol and various concentrations of urea) and incubated for 30 min at room temperature. 5 µL of the urea+L27V enzyme solution was diluted 10,000-fold into DMEM without phenol red + 0.1% PRIONEX®, 50 µL was mixed with 50 µL of assay reagent containing 100 µM PBI-3939 (previously described) and the luminescence was read at 10 min. (FIG. 88). FIG. 88 indicates that L27V is either resistant to urea or refolds to a functional enzyme very quickly upon removal of urea. This suggests that L27V could be used as a reporter enzyme when chemical denaturing conditions are involved, e.g., multiplexing in conditions where a denaturant is used to stop an enzymatic reaction prior to the OgLuc variant-based reaction.

**[00568]** A 0.31 mg/mL stock of purified L27V variant was diluted 100,000-fold into buffer (PBS + 1 mM DTT + 0.005% IGEPAL) and incubated with 3 M urea for 30 min at 25°C and then mixed 1:1 (50 µL + 50 µL) with an assay reagent containing 100 µM PBI-3939 (previously described). The reactions were read on a TECAN® INFINITE® F500 luminometer as described previously (for 100 min; 1 min read intervals) (FIG. 89). The results indicate that 3M urea reduces the activity of L27V variant by approximately 50%, but, upon diluting out the urea by 2-fold (to a 1.5 M final concentration) the activity increases, presumably due to refolding.

**Example 60 – Imaging of OgLuc Fusion Proteins**

**[00569]** This example demonstrates the use of OgLuc and OgLuc variants to monitor protein translocation in living cells without the need for fluorescence excitation. OgLuc variants were fused to human glucocorticoid receptor (GR; SEQ ID NOs: 451 and 452), human protein kinase C alpha (PKCa; SEQ ID NOs: 449 and 450) or LC3 (SEQ ID NOs: 577 and 578). To analyze subcellular protein translocation using bioluminescence imaging, HeLa cells were plated at $2x10^4$ cells/$cm^2$ into glass-bottom culture dishes (MatTek) in DMEM medium (Invitrogen) containing 10% FBS. The cells were then incubated for 24 hrs at 37°C, 5% CO2. Cells were then transfected with 1/20 volume transfection mixture (FUGENE® HD and DNA encoding L27V02-GR (SEQ ID NOs: 453 and 454) or L27V02-PKC alpha (SEQ ID NOs: 455 and 456) cloned into the pF5A vector (Promega Corp.)). The plasmid DNA for L27V02-GR was diluted 1:20 into

pGEM-3ZF (Promega Corp.) to achieve appropriate expression levels of L27V02-GR. The plasmid DNA for L27V02-LC3 and L27V02-PKC alpha was used undiluted. Cells were then incubated for 24 hrs at 37°C, 5% $CO_2$. Cells transfected with GR fusion proteins were starved of GR agonist for 20 hrs using MEM medium supplemented with 1% charcoal/dextran-treated FBS (Invitrogen). Twenty-four hrs post-transfection (for PKC alpha measurements) or 48 hrs post-transfection (for GR measurements), the cell media was replaced with $CO_2$-independent media containing 100 μM PBI-3939 immediately before imaging. Unfiltered images were immediately captured on an Olympus LV200 bioluminescence microscope using a 150X objective.

**[00570]** Cytosol-to-nucleus translocation of L27V02-GR fusion protein was achieved via stimulation with 0.5 mM dexamethasone for 15 min. Cytosol-to-plasma membrane translocation of L27V02-PKC alpha fusion protein was achieved via stimulation with 100 nM PMA for 20 min. L27V02-LC3 fusion protein transfected cells were left untreated or treated with 50 mM Chloroquine in DMEM medium (Invitrogen) containing 10% FBS.

**[00571]** ***L27V02-Glucocorticoid receptor***

**[00572]** In the absence of glucocorticoids, glucocorticoid receptor (GR) is complexed to Hsp90 proteins and resides in the cytosol. Upon interaction of GR with glucocorticoids, such as dexamethasone, GR proteins dissociate from these protein complexes and translocate to the nucleus to regulate gene transcription. FIGS. 90A-B show the bioluminescence imaging of dexamethasone-induced cytosol to nuclear receptor (NR) translocation of L27V02-glucocorticoid receptor (GR) fusion proteins using PBI-3939 substrate in HeLa cells.

**[00573]** ***L27V02-PKCa***

**[00574]** Upon treatment with phorbol esters, PKC alpha proteins are recruited to the plasma membrane and regulate cellular responses including membrane dynamics and signal transduction. FIGS. 91A-B show the bioluminescence imaging of phorbol ester-induced Protein Kinase C alpha (PKC alpha) cytosol to plasma membrane translocation of OgLuc L27V02-PKC alpha fusions using PBI3939 substrate in U-2 OS cells.

**[00575]** ***L27V-LC3***

**[00576]** Association of processed LC-3 proteins with autophagosomes represents a hallmark step in autophagy. Chloroquine treatment arrests autophagic flux at this stage, resulting in accumulation of LC-3 proteins on autophagosomes (producing a punctate subcellular distribution). FIGS. 92A-B show the bioluminescence imaging of chloroquine-induced

autophagosomal protein translocation of OgLuc L27V-LC3 fusions proteins (SEQ ID NOs: 592 and 593) using PBI-3939 substrate in two representative HeLa cell samples.

**Table 47 – Proviso List**

| C1+A4E | Additional Substitutions | | | | | |
|---|---|---|---|---|---|---|
| C1+A4E | L92G | | | | | |
| C1+A4E | L92Q | | | | | |
| C1+A4E | L92S | | | | | |
| C1+A4E | L92A | | | | | |
| C1+A4E | L72Q | | | | | |
| C1+A4E | I90T | | | | | |
| C1+A4E | Q20R | | | | | |
| C1+A4E | C164S | | | | | |
| C1+A4E | M75K | | | | | |
| C1+A4E | V79I | | | | | |
| C1+A4E | F54I | | | | | |
| C1+A4E | K89E | | | | | |
| C1+A4E | I90V | | | | | |
| C1+A4E | F77W | F68S | I90V | | | |
| C1+A4E | F54I | M75K | | | | |
| C1+A4E | F54I | M75K | I90V | | | |
| C1+A4E | F54I | F68S | M75K | | | |
| C1+A4E | F54I | I90V | | | | |
| C1+A4E | F54I | | | | | |
| C1+A4E | F54T | N135K | I167V | P104L | D139E | |
| C1+A4E | V45E | L34M | G51V | I99V | I143L | |
| C1+A4E | S28P | L34M | G51V | I99V | I143L | F54T |
| C1+A4E | S28P | L34M | G51V | I99V | I143L | F54T |
| C1+A4E | S28P | | | | | |

SEQUENCE LISTING

**SEQ ID NO:1 (Native mature OgLuc protein)** *Oplophorus gracilirostris*
FTLADFVGDWQQTAGYNQDQVLEQGGLSSLFQALGVSVTPIQKVVLSGENGLKADIHVIIPYEGL
SGFQMGLIEMIFKVVYPVDDHHFKIILHYGTLVIDGVTPNMIDYFGRPYPGIAVFDGKQITVTGT
LWNGNKIYDERLINPDGSLLFRVTINGVTGWRLCENILA

**SEQ ID NO:2 (C1A4E nucleotide)**
ATGGTGTTTACATTGGAGGATTTCGTTGGAGACTGGCGGCAGACAGCTGGATACAACCAAGATCA
AGTGTTAGAACAAGGAGGATTGTCTAGTCTGTTCCAAAAGCTGGGAGTGTCAGTCACCCCAATCC
AGAAAATTGTGCTGTCTGGGGAGAATGGGTTAAAATTTGATATTCATGTCATCATCCCTTACGAG
GGACTCAGTGGTTTTCAAATGGGTCTGATTGAAATGATCTTCAAAGTTGTTTACCCAGTGGATGA
TCATCATTTCAAGATTATTCTCCATTATGGTACACTCGTTATTGACGGTGTGACACCAAACATGA
TTGACTACTTTGGACGCCCTTACGAGGGAATTGCTGTGTTTGACGGCAAGAAGATCACAGTTACT
GGAACTCTGTGGAACGGCAACAAGATCATTGATGAGCGCCTGATCAACCCAGATGGTTCACTCCT
CTTCCGCGTTACTATCAATGGAGTCACCGGATGGCGCCTTTGCGAGCGTATTCTTGCC

**SEQ ID NO:3 (C1A4E protein)**
MVFTLEDFVGDWRQTAGYNQDQVLEQGGLSSLFQKLGVSVTPIQKIVLSGENGLKFDIHVIIPYE
GLSGFQMGLIEMIFKVVYPVDDHHFKIILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVT
GTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILA

**SEQ ID NO:4 (QC27 nucleotide)**
ATGGTGTTTACATTGGAGGATTTCGTTGGAGACTGGCGGCAGACAGCTGGATACAACCTAGATCA
AGTGTTAGAACAAGGAGGATTGTCTAGTCTGTTCCAAAAGCTGGGAGTGTCAGTCACCCCAATCC
AGAAAATTGTGCTGTCTGGGGAGAATGGGTTAAAAATTGATATTCATGTCATCATCCCTTACGAG
GGACTCAGTGGTTTTCAAATGGGTCTGATTGAAATGATCTTCAAAGTTGTTTACCCAGTGGATGA
TCATCATTTCAAGATTATTCACCATTATGGTACACTCGTTATTGACGGTGTGACACCAAACATGA
TTGACTTCTTTGGACGCCCTTACGAGGGAATTGCTGTGTTTGACGGCAAGAAGATCACAGTTACT
GGAACTCTGTGGAACGGCAACAAGATCATTGATGAGCGCCTGATCAACCCAGATGGTTCACTCCT
CTTCCGCGTTACTATCAATGGAGTCACCGGATGGCGCCTTTGCGAGCGTATTCTTGCC

**SEQ ID NO:5 (QC27 protein)**
MVFTLEDFVGDWRQTAGYNLDQVLEQGGLSSLFQKLGVSVTPIQKIVLSGENGLKIDIHVIIPYE
GLSGFQMGLIEMIFKVVYPVDDHHFKIIHHYGTLVIDGVTPNMIDFFGRPYEGIAVFDGKKITVT
GTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILA

**SEQ ID NO:6 (QC27 9a nucleotide)**
ATGGTGTTTACATTGGAGGATTTCGTTGGAGACTGGCGGCAGACAGCTGGATACAACCTAGATCA
ACTGTTAGAACAAGGAGGATTGTCTAGTCTGTTCCAAAAGCTGGGAGTGTCAGTCACCCCAATCC
AGAAAATTGTGCTGTCTGGGGAGAATGGGTTAAAAATTGATATTCATGTCATCATCCCTTACGAG
GGACTCAGTGGTTATCAAATGGGTCAGATTGAAAAGATCTTCAAAGTTGTTTACCCAGTGGATGA
TCATCATTTCAAGATTATTCGCCATTATGGTACACTCGTTATTGACGGTGTGACACCAAACATGA
TTGACTTCTTTGGACGCCCTTACGAGGGAATTGCTGTGTTTGACGGCAAGAAGATCACAGTTACT
GGAACTCTGTGGAACGGCAACAAGATCATTGATGAGCGCCTGATCAACCCAGATGGTTCACTCCT
CTTCCGCGTTACTATCAATGGAATCACCGGATGGCGCCTTTGCGAGCGTATTCTTGCC

**SEQ ID NO:7 (QC27 9a protein)**
MVFTLEDFVGDWRQTAGYNLDQLLEQGGLSSLFQKLGVSVTPIQKIVLSGENGLKIDIHVIIPYE
GLSGYQMGQIEKIFKVVYPVDDHHFKIIRHYGTLVIDGVTPNMIDFFGRPYEGIAVFDGKKITVT
GTLWNGNKIIDERLINPDGSLLFRVTINGITGWRLCERILA

**SEQ ID NO:8 (IVY nucleotide)**

ATGGTGTTTACATTGGAGGATTTCGTTGGAGACTGGCGGCAGACAGCTGGATACAACCAAGATCA
AGTGTTAGAACAAGGAGGATTGTCTAGTCTGTTCCAAAAGCTGGGAGTGTCAGTCACCCCAATCC
AGAAAATTGTGCTGTCTGGGGAGAATGGGTTAAAAATTGATATTCATGTCATCATCCCTTACGAG
GGACTCAGTGGTTTTCAAATGGGTCTGATTGAAATGATCTACAAAGTTGTTTACCCAGTGGATGA
TCATCATTTCAAGGTTATTCTCCATTATGGTACACTCGTTATTGACGGTGTGACACCAAACATGA
TTGACTACTTTGGACGCCCTTACGAGGGAATTGCTGTGTTTGACGGCAAGAAGATCACAGTTACT
GGAACTCTGTGGAACGGCAACAAGATCATTGATGAGCGCCTGATCAACCCAGATGGTTCACTCCT
CTTCCGCGTTACTATCAATGGAGTCACCGGATGGCGCCTTTGCGAGCGTATTCTTGCC

**SEQ ID NO:9 (IVY protein)**
MVFTLEDFVGDWRQTAGYNQDQVLEQGGLSSLFQKLGVSVTPIQKIVLSGENGLKIDIHVIIPYE
GLSGFQMGLIEMIYKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVT
GTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILA

**SEQ ID NO:10 (IVY+C1.3 nucleotide)**
ATGGTGTTTACATTGGAGGATTACGTTGGAGACTGGCGGCAGACAGCTGGATACAACCAAGATCA
AGTGTTAGAACAAGGAGGATTGTCTAGTCTGTTCCAAAATCTGGGAGTGTCTGTCACCCCAATCC
AGAAAATTGTGCTGTCTGGGGAGAATGGGTTAAAAATTGATATTCATGTCATCATCCCTTACGAG
GGACTCAGTGGTTTTCAAATGGGTCTGATTGAAATGATCTACAAAGTTGTTTACCCAGTGGATGA
TCATCATTTCAAGGTTATTCTCCATTATGGTACACTCGTTATTGACGGTGTGACACCAAACATGA
TTGACTACTTTGGACGCCCTTACGAGGGAATTGCTGTGTTTGACGGCAAGAAGATCACAGTTACT
GGAACTCTGTGGAACGGCGACAAGATCATTGATGAGCGCCTGATCAACCCAGATGGTTCACTCCT
CTTCCGCGTTACTACCAATGGAGTCACCGGATGGCGCCTTTGCGAGCGTATTCTTGCC

**SEQ ID NO:11 (IVY+C1.3 protein)**
MVFTLEDYVGDWRQTAGYNQDQVLEQGGLSSLFQNLGVSVTPIQKIVLSGENGLKIDIHVIIPYE
GLSGFQMGLIEMIYKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVT
GTLWNGDKIIDERLINPDGSLLFRVTTNGVTGWRLCERILA

**SEQ ID NO:12 (IVY C5.19 nucleotide)**
ATGGTGTTTACATTGGAGGATTTCGTTGGAGACTGGCGGCAGACAGCTGGATACAACCAAGATCA
AGTGTTAGAACAAGGAGGAGTGTCTAGTCTGTTCCAAAAGCTGGGAGTGTCAATCACCCCAATCC
AGAAAATTGTGCTGTCTGGGGAGAATGGGTTAAAAATTGATATTCATGTCATCATCCCTTACGAG
GGACTCAGTGGTTTTCAAATGGGTCTGATTGAAATGATCTACAAAGTTGTTTACCCAGTGGATGA
TCATCATTTCAAGGTTATTCTCCATTATGGTACACTCGTTATTGACGGTGTGACACCAAACATGA
TTGACTACTTTGGACGCCCTTACGAGGGAATTGCTGTGTTTGACGGCAAGAAGATCACAGTTACT
GGAACTCTGTGGAACGGCAACAAGATCATTGATGAGCGCCTGATCAACCCAGATGGTTCAATCCT
CTTCCGCGTTACTATCAATGGAGTCACCGGATGGCGCCTTTGCGAGCGTATTCTTGCC

**SEQ ID NO:13 (IVY C5.19 protein)**
MVFTLEDFVGDWRQTAGYNQDQVLEQGGVSSLFQKLGVSITPIQKIVLSGENGLKIDIHVIIPYE
GLSGFQMGLIEMIYKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVT
GTLWNGNKIIDERLINPDGSILFRVTINGVTGWRLCERILA

**SEQ ID NO:14 (IV nucleotide)**
ATGGTGTTTACATTGGAGGATTTCGTTGGAGACTGGCGGCAGACAGCTGGATACAACCAAGATCA
AGTGTTAGAACAAGGAGGATTGTCTAGTCTGTTCCAAAAGCTGGGAGTGTCAGTCACCCCAATCC
AGAAAATTGTGCTGTCTGGGGAGAATGGGTTAAAAATTGATATTCATGTCATCATCCCTTACGAG
GGACTCAGTGGTTTTCAAATGGGTCTGATTGAAATGATCTTCAAAGTTGTTTACCCAGTGGATGA
TCATCATTTCAAGGTTATTCTCCATTATGGTACACTCGTTATTGACGGTGTGACACCAAACATGA
TTGACTACTTTGGACGCCCTTACGAGGGAATTGCTGTGTTTGACGGCAAGAAGATCACAGTTACT
GGAACTCTGTGGAACGGCAACAAGATCATTGATGAGCGCCTGATCAACCCAGATGGTTCACTCCT
CTTCCGCGTTACTATCAATGGAGTCACCGGATGGCGCCTTTGCGAGCGTATTCTTGCC

**SEQ ID NO:15 (IV protein)**

MVFTLEDFVGDWRQTAGYNQDQVLEQGGLSSLFQKLGVSVTPIQKIVLSGENGLKIDIHVIIPYE
GLSGFQMGLIEMIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVT
GTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILA

**SEQ ID NO:16 (15C1 nucleotide)**

ATGGTGTTTACATTGAAGGATTTCGTTGGAGACTGGCGGCAGACAGCTGGATACAACCAAGATCA
AGTGTTAGAACAAGGAGGATTGTCTAGTCTGTTCCAAAATCTGGGAGTGTCAGTCACCCCAATCC
AGAAAATTGTGCTGTCTGGGGAGAATGGGTTAAAAATTGATATTCATGTCATCATCCCTTACGAG
GGACTCAGTGGTTATCAAATGGGTCAGATTGAAAAGATCTTCAAAGTTGTTTACCCAGTGGATGA
TCATCATTTCAAGGTTATTCTCCATTATGGTACACTCGTTATTGACGGTGTGACACCAAACATGA
TTGACTACTTTGGACGCCCTTACGAGGGAATTGCTGTGTTTGACGGCAAGAAGATCACAGTTACT
GGAACTCTGTGGAACGGCAACAAGATCATTGATGAGCGCCTGATCAACCCAGATGGTTCACTCCT
CTTCCGCGTTACTATCAATGGAGTCACCGGATGGCGCCTTTGCGAGCGTATTCTTGCC

**SEQ ID NO:17 (15C1 protein)**
MVFTLKDFVGDWRQTAGYNQDQVLEQGGLSSLFQNLGVSVTPIQKIVLSGENGLKIDIHVIIPYE
GLSGYQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVT
GTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILA

**SEQ ID NO:18 (9B8 nucleotide)**
ATGGTGTTTACATTGGAGGATTTCGTTGGAGACTGGCGGCAGACAGCTGGATACAACCTAGATCA
AGTGTTAGAACAAGGAGGATTGTCTAGTCTGTTCCAAAAGCTGGGAGTGTCAGTCACCCCAATCC
AGAAAATTGTGCTGTCTGGGGAGAATGGGTTAAAAATTGATATTCATGTCATCATCCCTTACGAG
GGACTCAGTGGTTATCAAATGGGTCAGATTGAAAAGATCTTCAAAGTTGTTTACCCAGTGGATGA
TCATCATTTCAAGGTTATTCTCCATTATGGTACACTCGTTATTGACGGTGTGACACCAAACATGA
TTGACTACTTTGGACGCCCTTACGAGGGAATTGCTGTGTTTGACGGCAAGAAGATCACAGTTACT
GGAACTCTGTGGAACGGCAACAAGATCATTGATGAGCGCCTGATCAACCCAGATGGTTCACTCCT
CTTCCGCGTTACTATCAATGGAGTCACCGGATGGCGCCTTTGCGAGCGTATTCTTGCC

**SEQ ID NO:19 (9B8 protein)**
MVFTLEDFVGDWRQTAGYNLDQVLEQGGLSSLFQKLGVSVTPIQKIVLSGENGLKIDIHVIIPYE
GLSGYQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVT
GTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILA

**SEQ ID NO:20 (9F6 nucleotide)**
ATGGTGTTTACATTGGAGGATTTCGTTGGAGACTGGCGGCAGACAGCTGGATACAACCTAGATCA
AGTGTTAGAACAAGGAGGAGTGTCTAGTCTGTTCCAAAAGCTGGGAGTGTCAATCACCCCAATCC
AGAAAATTGTGCTGTCTGGGGAGAATGGGTTAAAAATTGATATTCATGTCATCATCCCTTACGAG
GGACTCAGTGGTTATCAAATGGGTCAGATTGAAAAGATCTTCAAAGTTGTTTACCCAGTGGATGA
TCATCATTTCAAGGTTATTCTCCATTATGGTACACTCGTTATTGACGGTGTGACACCAAACATGA
TTGACTACTTTGGACGCCCTTACGAGGGAATTGCTGTGTTTGACGGCAAGAAGATCACAGTTACT
GGAACTCTGTGGAACGGCAACAAGATCATTGATGAGCGCCTGATCAACCCAGATGGTTCACTCCT
CTTCCGCGTTACTATCAATGGAGTCACCGGATGGCGCCTTTGCGAGCGTATTCTTGCC

**SEQ ID NO:21 (9F6 protein)**
MVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQKLGVSITPIQKIVLSGENGLKIDIHVIIPYE
GLSGYQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVT
GTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILA

**SEQ ID NO:22 (IV opt nucleotide)**
atggtgtttacactcgaagatttcgtaggggactggcggcagacagccggctacaaccaagacca
agtccttgagcagggcggtctgtccagtttgtttcagaaactcggggtgtccgtaacaccgatcc
aaaagattgtcctgagcggtgaaaacggcctgaagatcgacatccatgtcatcatcccgtatgaa
ggtctgagcggcttccagatgggcctcattgagatgatctttaaggtggtgtaccctgtggatga
tcatcactttaaggtgattctgcactatggcacactggtaatcgacggggttacgccgaacatga
tcgactatttcggacggccgtatgaaggcatcgccgtgttcgacggcaaaaagatcactgtaacc
gggaccctgtggaacggcaacaaaattatcgacgagcgcctgatcaaccccgacggctccctgct
gttccgcgtaaccatcaacggagtgaccggctggcggctgtgcgagcgcattttggcg

**SEQ ID NO:23 (IV optB nucleotide)**
atggtattcacactggaggattttgtcggtgattggcggcaaaccgctgggtacaaccaggacca
ggttctcgaacaaggggcctcagctccctgtttcaaaaactgggtgttagcgttacacctattc
aaaaaatcgtgctctccggggaaaacgggctcaaaatcgatattcatgtgattatcccttacgaa
gggctctccgggtttcagatggggctgatcgaaatgatctttaaggtcgtctatcccgtagatga
tcaccacttcaaggtgatcctccactacgggaccctcgtaattgatggcgtgacccccaacatga
tcgactattttgggcgcccttacgaggggattgctgtcttcgatggcaaaaaaattacagtgaca

ggcacactctggaacgggaataagatcattgatgagcgcctgattaatcccgatgggagcctgct
ctttcgggtgacaattaacggcgtaacaggctggcgcctctgtgaacggattctggcg

**SEQ ID NO:24 (9B8 opt nucleotide)**

atggtgtttacactcgaagatttcgtaggggactggcggcagacagccggctacaacctggacca
agtccttgagcagggcggtctgtccagtttgtttcagaaactcggggtgtccgtaacaccgatcc
aaaagattgtcctgagcggtgaaaacggcctgaagatcgacatccatgtcatcatcccgtatgaa
ggtctgagcggctatcagatgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatga
tcatcactttaaggtgattctgcactatggcacactggtaatcgacggggttacgccgaacatga
tcgactatttcggacggccgtatgaaggcatcgccgtgttcgacggcaaaaagatcactgtaacc
gggaccctgtggaacggcaacaaaattatcgacgagcgcctgatcaaccccgacggctccctgct
gttccgcgtaaccatcaacggagtgaccggctggcggctgtgcgagcgcattttggcg

**SEQ ID NO:25 (9B8 optB nucleotide)**

atggtattcacactggaggattttgtcggtgattggcggcaaaccgctgggtacaacctcgacca
ggttctcgaacaaggggggcctcagctccctgtttcaaaaactgggtgttagcgttacacctattc
aaaaaatcgtgctctccgggggaaaacgggctcaaaatcgatattcatgtgattatcccttacgaa
gggctctccgggtatcagatggggcagatcgaaaaaatctttaaggtcgtctatcccgtagatga
tcaccacttcaaggtgatcctccactacgggaccctcgtaattgatggcgtgacccccaacatga
tcgactattttgggcgcccttacgaggggattgctgtcttcgatggcaaaaaaattacagtgaca
ggcacactctggaacgggaataagatcattgatgagcgcctgattaatcccgatgggagcctgct
ctttcgggtgacaattaacggcgtaacaggctggcgcctctgtgaacggattctggcg

**SEQ ID NO:26 (8A3 nucleotide)**

Atggtgattacattggaggatttcgttggagactggcggcagacagctggatacaaccaagatca
agtgttagaacaaggaggagtgtctagtctgttccaaaagctgggagtgtcaatcaccccaatcc
agaaaattgtgctgtctggggagaatgggttaaaaattgatattcatgtcatcatcccttacgag
ggactcagtggttttcaaatgggtctgattgaaatgatcttcaaagttgtttacccagtggatga
tcatcatttcaaggttattctccattatggtacactcgttattgacggtgtgacaccaaacatga
ttgactactttggacgcccttacgagggaattgctgtgtttgacggcaagaagatcacagttact
ggaactctgtggaacggcaacaagatcattgatgagcgcctgatcaacccagatggttcactcct
cttccgcgttactatcaatggagtcaccggatggcgcctttgcgagcgtattcttgcc

**SEQ ID NO:27 (8A3 protein)**

MVITLEDFVGDWRQTAGYNQDQVLEQGGVSSLFQKLGVSITPIQKIVLSGENGLKIDIHVIIPYE
GLSGFQMGLIEMIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVT
GTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILA

**SEQ ID NO:28 (Luc2 nucleotide)**

atggaagatgccaaaaacattaagaagggcccagcgccattctacccactcgaagacgggaccgc
cggcgagcagctgcacaaagccatgaagcgctacgccctggtgcccggcaccatcgcctttaccg
acgcacatatcgaggtggacattacctacgccgagtacttcgagatgagcgttcggctggcagaa
gctatgaagcgctatgggctgaatacaaaccatcggatcgtggtgtgcagcgagaatagcttgca
gttcttcatgcccgtgttgggtgccctgttcatcggtgtggctgtggccccagctaacgacatct
acaacgagcgcgagctgctgaacagcatgggcatcagccagcccaccgtcgtattcgtgagcaag
aaagggctgcaaaagatcctcaacgtgcaaaagaagctaccgatcatacaaaagatcatcatcat
ggatagcaagaccgactaccagggcttccaaagcatgtacaccttcgtgacttcccatttgccac
ccggcttcaacgagtacgacttcgtgcccgagagcttcgaccgggacaaaaccatcgccctgatc
atgaacagtagtggcagtaccggattgcccaagggcgtagccctaccgcaccgcaccgcttgtgt
ccgattcagtcatgcccgcgaccccatcttcggcaaccagatcatccccgacaccgctatcctca
gcgtggtgccatttcaccacggcttcggcatgttcaccacgctgggctacttgatctgcggcttt
cgggtcgtgctcatgtaccgcttcgaggaggagctattcttgcgcagcttgcaagactataagat
tcaatctgccctgctggtgcccacactatttagcttcttcgctaagagcactctcatcgacaagt

acgacctaagcaacttgcacgagatcgccagcggcggggcgccgctcagcaaggaggtaggtgag
gccgtggccaaacgcttccacctaccaggcatccgccagggctacggcctgacagaaacaaccag
cgccattctgatcacccccgaaggggacgacaagcctggcgcagtaggcaaggtggtgcccttct
tcgaggctaaggtggtggacttggacaccggtaagacactgggtgtgaaccagcgcggcgagctg
tgcgtccgtggccccatgatcatgagcggctacgttaacaaccccgaggctacaaacgctctcat
cgacaaggacggctggctgcacagcggcgacatcgcctactgggacgaggacgagcacttcttca
tcgtggaccggctgaagagcctgatcaaatacaagggctaccaggtagccccagccgaactggag
agcatcctgctgcaacaccccaacatcttcgacgccggggtcgccggcctgcccgacgacgatgc
cggcgagctgcccgccgcagtcgtcgtgctggaacacggtaaaaccatgaccgagaaggagatcg
tggactatgtggccagccaggttacaaccgccaagaagctgcgcggtggtgttgtgttcgtggac
gaggtgcctaaaggactgaccggcaagttggacgcccgcaagatccgcgagattctcattaaggc
caagaagggcggcaagatcgccgtt

**SEQ ID NO:29 (Luc2 protein)**
medaknikkgpapfypledgtageqlhkamkryalvpgtiaftdahievdityaeyfemsvrlae
amkryglntnhrivvcsenslqffmpvlgalfigvavapandiynerellnsmgisqptvvfvsk
kglqkilnvqkklpiiqkiiimdsktdyqgfqsmytfvtshlppgfneydfvpesfdrdktiali
mnssgstglpkgvalphrtacvrfshardpifgnqiipdtailsvvpfhhgfgmfttlgylicgf
rvvlmyrfeeelflrslqdykiqsallvptlfsffakstlidkydlsnlheiasggaplskevge
avakrfhlpgirqgygltettsailitpegddkpgavgkvvpffeakvvdldtgktlgvnqrgel
cvrgpmimsgyvnnpeatnalidkdgwlhsgdiaywdedehffivdrlkslikykgyqvapaele
sillqhpnifdagvaglpdddagelpaavvvlehgktmtekeivdyvasqvttakklrggvvfvd
evpkgltgkldarkireilikakkggkiav

**SEQ ID NO:30 (HRL (Humanized Renilla) nucleotide)**
Atggcttccaaggtgtacgaccccgagcaacgcaaacgcatgatcactgggcctcagtggtgggc
tcgctgcaagcaaatgaacgtgctggactccttcatcaactactatgattccgagaagcacgccg
agaacgccgtgatttttctgcatggtaacgctgcctccagctacctgtggaggcacgtcgtgcct
cacatcgagcccgtggctagatgcatcatccctgatctgatcggaatgggtaagtccggcaagag
cgggaatggctcatatcgcctcctggatcactacaagtacctcaccgcttggttcgagctgctga
accttccaaagaaaatcatctttgtgggccacgactgggggcttgtctggcctttcactactcc
tacgagcaccaagacaagatcaaggccatcgtccatgctgagagtgtcgtggacgtgatcgagtc
ctgggacgagtggcctgacatcgaggaggatatcgccctgatcaagagcgaagagggcgagaaaa
tggtgcttgagaataacttcttcgtcgagaccatgctcccaagcaagatcatgcggaaactggag
cctgaggagttcgctgcctacctggagccattcaaggagaagggcgaggttagacggcctaccct
ctcctggcctcgcgagatccctctcgttaagggaggcaagcccgacgtcgtccagattgtccgca
actacaacgcctaccttcgggccagcgacgatctgcctaagatgttcatcgagtccgaccctggg
ttcttttccaacgctattgtcgagggagctaagaagttccctaacaccgagttcgtgaaggtgaa
gggcctccacttcagccaggaggacgctccagatgaaatgggtaagtacatcaagagcttcgtgg
agcgcgtgctgaagaacgagcag

**SEQ ID NO:31 (HRL (Humanized Renilla) protein)**
MASKVYDPEQRKRMITGPQWWARCKQMNVLDSFINYYDSEKHAENAVIFLHGNAASSYLWRHVVP
HIEPVARCIIPDLIGMGKSGKSGNGSYRLLDHYKYLTAWFELLNLPKKIIFVGHDWGACLAFHYS
YEHQDKIKAIVHAESVVDVIESWDEWPDIEEDIALIKSEEGEKMVLENNFFVETMLPSKIMRKLE
PEEFAAYLEPFKEKGEVRRPTLSWPREIPLVKGGKPDVVQIVRNYNAYLRASDDLPKMFIESDPG
FFSNAIVEGAKKFPNTEFVKVKGLHFSQEDAPDEMGKYIKSFVERVLKNEQ

**SEQ ID NO:32 (Id-HRL-HT7 sandwich fusion nucleotide)**
atgcttggtctgtcggagcaaagcgtgtccatctcgcgctgcgctgggacgcgcctgcccgcctt
gctggacgagcagcaggtgaacgtcctgctctacgacatgaacggctgctactcacgcctcaagg
agctggtgcccaccctgccccagaaccgcaaagtgagcaaggtggagatcctgcagcatgtaatc
gactacatcagggacctgcagctggagctgaactcggagtctgaagtcgggaccaccggaggccg

gggactgcctgtccgcgccccgctcagcaccctgaacggcgagatcagtgccttggcggccgagg
cggcatgtgttccagccgacgatcgcatcttgtgtcgcgtttctcttgagaatctttatttttcag
gcgtctggaggtggtggcggagcgatcgccatggcttccaaggtgtacgaccccgagcaacgcaa
acgcatgatcactgggcctcagtggtgggctcgctgcaagcaaatgaacgtgctggactccttca
tcaactactatgattccgagaagcacgccgagaacgccgtgatttttctgcatggtaacgctgcc
tccagctacctgtggaggcacgtcgtgcctcacatcgagcccgtggctagatgcatcatccctga
tctgatcggaatgggtaagtccggcaagagcgggaatggctcatatcgcctcctggatcactaca
agtacctcaccgcttggttcgagctgctgaaccttccaaagaaaatcatctttgtgggccacgac
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tgctgagagtgtcgtggacgtgatcgagtcctgggacgagtggcctgacatcgaggaggatatcg
ccctgatcaagagcgaagagggcgagaaaatggtgcttgagaataacttcttcgtcgagaccatg
ctcccaagcaagatcatgcggaaactggagcctgaggagttcgctgcctacctggagccattcaa
ggagaagggcgaggttagacggcctaccctctcctggcctcgcgagatccctctcgttaagggag
gcaagcccgacgtcgtccagattgtccgcaactacaacgcctaccttcgggccagcgacgatctg
cctaagatgttcatcgagtccgaccctgggttcttttccaacgctattgtcgagggagctaagaa
gttccctaacaccgagttcgtgaaggtgaagggcctccacttcagccaggaggacgctccagatg
aaatgggtaagtacatcaagagcttcgtggagcgcgtgctgaagaacgagcaggtttctctcgag
ccaaccactgaggatctgtactttcagagcgataacgatggatccgaaatcggtactggctttcc
attcgacccccattatgtggaagtcctgggcgagcgcatgcactacgtcgatgttggtccgcgcg
atggcacccctgtgctgttcctgcacggtaacccgacctcctcctacgtgtggcgcaacatcatc
ccgcatgttgcaccgacccatcgctgcattgctccagacctgatcggtatgggcaaatccgacaa
accagacctgggttatttcttcgacgaccacgtccgcttcatggatgccttcatcgaagccctgg
gtctggaagaggtcgtcctggtcattcacgactggggctccgctctgggtttccactgggccaag
cgcaatccagagcgcgtcaaaggtattgcatttatggagttcatccgccctatcccgacctggga
cgaatggccagaatttgcccgcgagaccttccaggccttccgcaccaccgacgtcggccgcaagc
tgatcatcgatcagaacgtttttatcgagggtacgctgccgatgggtgtcgtccgcccgctgact
gaagtcgagatggaccattaccgcgagccgttcctgaatcctgttgaccgcgagccactgtggcg
cttcccaaacgagctgccaatcgccggtgagccagcgaacatcgtcgcgctggtcgaagaataca
tggactggctgcaccagtcccctgtcccgaagctgctgttctggggcaccccaggcgttctgatc
ccaccggccgaagccgctcgcctggccaaaagcctgcctaactgcaaggctgtggacatcggccc
gggtctgaatctgctgcaagaagacaacccggacctgatcggcagcgagatcgcgcgctggctgt
ctactctggagatttccggt

**SEQ ID NO:33 (Id-HRL-HT7 sandwich fusion protein)**

MLGLSEQSVSISRCAGTRLPALLDEQQVNVLLYDMNGCYSRLKELVPTLPQNRKVSKVEILQHVI
DYIRDLQLELNSESEVGTTGGRGLPVRAPLSTLNGEISALAAEAACVPADDRILCRVSLENLYFQ
ASGGGGGAIAMASKVYDPEQRKRMITGPQWWARCKQMNVLDSFINYYDSEKHAENAVIFLHGNAA
SSYLWRHVVPHIEPVARCIIPDLIGMGKSGKSGNGSYRLLDHYKYLTAWFELLNLPKKIIFVGHD
WGACLAFHYSYEHQDKIKAIVHAESVVDVIESWDEWPDIEEDIALIKSEEGEKMVLENNFFVETM
LPSKIMRKLEPEEFAAYLEPFKEKGEVRRPTLSWPREIPLVKGGKPDVVQIVRNYNAYLRASDDL
PKMFIESDPGFFSNAIVEGAKKFPNTEFVKVKGLHFSQEDAPDEMGKYIKSFVERVLKNEQVSLE
PTTEDLYFQSDNDGSEIGTGFPFDPHYVEVLGERMHYVDVGPRDGTPVLFLHGNPTSSYVWRNII
PHVAPTHRCIAPDLIGMGKSDKPDLGYFFDDHVRFMDAFIEALGLEEVVLVIHDWGSALGFHWAK
RNPERVKGIAFMEFIRPIPTWDEWPEFARETFQAFRTTDVGRKLIIDQNVFIEGTLPMGVVRPLT
EVEMDHYREPFLNPVDREPLWRFPNELPIAGEPANIVALVEEYMDWLHQSPVPKLLFWGTPGVLI
PPAEAARLAKSLPNCKAVDIGPGLNLLQEDNPDLIGSEIARWLSTLEISG

**SEQ ID NO:34 (8A3-HT7 fusion nucleotide)**

atggtgattacattggaggatttcgttggagactggcggcagacagctggatacaaccaagatca
agtgttagaacaaggaggagtgtctagtctgttccaaaagctgggagtgtcaatcaccccaatcc
agaaaattgtgctgtctggggagaatgggttaaaaattgatattcatgtcatcatcccttacgag
ggactcagtggttttcaaatgggtctgattgaaatgatcttcaaagttgtttacccagtggatga
tcatcatttcaaggttattctccattatggtacactcgttattgacggtgtgacaccaaacatga

ttgactactttggacgcccttacgagggaattgctgtgtttgacggcaagaagatcacagttact
ggaactctgtggaacggcaacaagatcattgatgagcgcctgatcaacccagatggttcactcct
cttccgcgttactatcaatggagtcaccggatggcgcctttgcgagcgtattcttgccggatatc
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gcgcgatggcacccctgtgctgttcctgcacggtaacccgacctcctcctacgtgtggcgcaaca
tcatcccgcatgttgcaccgacccatcgctgcattgctccagacctgatcggtatgggcaaatcc
gacaaaccagacctgggttatttcttcgacgaccacgtccgcttcatggatgccttcatcgaagc
cctgggtctggaagaggtcgtcctggtcattcacgactggggctccgctctgggtttccactggg
ccaagcgcaatccagagcgcgtcaaaggtattgcatttatggagttcatccgccctatcccgacc
tgggacgaatggccagaatttgcccgcgagaccttccaggccttccgcaccaccgacgtcggccg
caagctgatcatcgatcagaacgtttttatcgagggtacgctgccgatgggtgtcgtccgcccgc
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tggcgcttcccaaacgagctgccaatcgccggtgagccagcgaacatcgtcgcgctggtcgaaga
atacatggactggctgcaccagtcccctgtcccgaagctgctgttctggggcaccccaggcgttc
tgatcccaccggccgaagccgctcgcctggccaaaagcctgcctaactgcaaggctgtggacatc
ggcccgggtctgaatctgctgcaagaagacaacccggacctgatcggcagcgagatcgcgcgctg
gctgtctactctggagatttccggt

**SEQ ID NO:35 (8A3-HT7 fusion protein)**

MVITLEDFVGDWRQTAGYNQDQVLEQGGVSSLFQKLGVSITPIQKIVLSGENGLKIDIHVIIPYE
GLSGFQMGLIEMIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVT
GTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILAGYLEPTTEDLYFQSDNDGSEIGTG
FPFDPHYVEVLGERMHYVDVGPRDGTPVLFLHGNPTSSYVWRNIIPHVAPTHRCIAPDLIGMGKS
DKPDLGYFFDDHVRFMDAFIEALGLEEVVLVIHDWGSALGFHWAKRNPERVKGIAFMEFIRPIPT
WDEWPEFARETFQAFRTTDVGRKLIIDQNVFIEGTLPMGVVRPLTEVEMDHYREPFLNPVDREPL
WRFPNELPIAGEPANIVALVEEYMDWLHQSPVPKLLFWGTPGVLIPPAEAARLAKSLPNCKAVDI
GPGLNLLQEDNPDLIGSEIARWLSTLEISG

**SEQ ID NO:36 (9B8-HT7 fusion nucleotide)**

atggtgtttacattggaggatttcgttggagactggcggcagacagctggatacaacctagatca
agtgttagaacaaggaggattgtctagtctgttccaaaagctgggagtgtcagtcaccccaatcc
agaaaattgtgctgtctggggagaatgggttaaaaattgatattcatgtcatcatcccttacgag
ggactcagtggttatcaaatgggtcagattgaaaagatcttcaaagttgtttacccagtggatga
tcatcatttcaaggttattctccattatggtacactcgttattgacggtgtgacaccaaacatga
ttgactactttggacgcccttacgagggaattgctgtgtttgacggcaagaagatcacagttact
ggaactctgtggaacggcaacaagatcattgatgagcgcctgatcaacccagatggttcactcct
cttccgcgttactatcaatggagtcaccggatggcgcctttgcgagcgtattcttgccggatatc
tcgagccaaccactgaggatctgtactttcagagcgataacgatggatccgaaatcggtactggc
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gcgcgatggcacccctgtgctgttcctgcacggtaacccgacctcctcctacgtgtggcgcaaca
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gacaaaccagacctgggttatttcttcgacgaccacgtccgcttcatggatgccttcatcgaagc
cctgggtctggaagaggtcgtcctggtcattcacgactggggctccgctctgggtttccactggg
ccaagcgcaatccagagcgcgtcaaaggtattgcatttatggagttcatccgccctatcccgacc
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tgatcccaccggccgaagccgctcgcctggccaaaagcctgcctaactgcaaggctgtggacatc
ggcccgggtctgaatctgctgcaagaagacaacccggacctgatcggcagcgagatcgcgcgctg
gctgtctactctggagatttccggt

**SEQ ID NO:37 (9B8-HT7 fusion protein)**

MVFTLEDFVGDWRQTAGYNLDQVLEQGGLSSLFQKLGVSVTPIQKIVLSGENGLKIDIHVIIPYE
GLSGYQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVT
GTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILAGYLEPTTEDLYFQSDNDGSEIGTG
FPFDPHYVEVLGERMHYVDVGPRDGTPVLFLHGNPTSSYVWRNIIPHVAPTHRCIAPDLIGMGKS
DKPDLGYFFDDHVRFMDAFIEALGLEEVVLVIHDWGSALGFHWAKRNPERVKGIAFMEFIRPIPT
WDEWPEFARETFQAFRTTDVGRKLIIDQNVFIEGTLPMGVVRPLTEVEMDHYREPFLNPVDREPL
WRFPNELPIAGEPANIVALVEEYMDWLHQSPVPKLLFWGTPGVLIPPAEAARLAKSLPNCKAVDI
GPGLNLLQEDNPDLIGSEIARWLSTLEISG

**SEQ ID NO:38 (9F6-HT7 fusion nucleotide)**

atggtgtttacattggaggatttcgttggagactggcggcagacagctggatacaacctagatca
agtgttagaacaaggaggagtgtctagtctgttccaaaagctgggagtgtcaatcaccccaatcc
agaaaattgtgctgtctggggagaatgggttaaaaattgatattcatgtcatcatcccttacgag
ggactcagtggttatcaaatgggtcagattgaaaagatcttcaaagttgtttacccagtggatga
tcatcatttcaaggttattctccattatggtacactcgttattgacggtgtgacaccaaacatga
ttgactactttggacgcccttacgagggaattgctgtgtttgacggcaagaagatcacagttact
ggaactctgtggaacggcaacaagatcattgatgagcgcctgatcaacccagatggttcactcct
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tcgagccaaccactgaggatctgtactttcagagcgataacgatggatccgaaatcggtactggc
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gcgcgatggcacccctgtgctgttcctgcacggtaacccgacctcctcctacgtgtggcgcaaca
tcatcccgcatgttgcaccgacccatcgctgcattgctccagacctgatcggtatgggcaaatcc
gacaaaccagacctgggttatttcttcgacgaccacgtccgcttcatggatgccttcatcgaagc
cctgggtctggaagaggtcgtcctggtcattcacgactggggctccgctctgggtttccactggg
ccaagcgcaatccagagcgcgtcaaaggtattgcatttatggagttcatccgccctatcccgacc
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tggcgcttcccaaacgagctgccaatcgccggtgagccagcgaacatcgtcgcgctggtcgaaga
atacatggactggctgcaccagtcccctgtcccgaagctgctgttctggggcaccccaggcgttc
tgatcccaccggccgaagccgctcgcctggccaaaagcctgcctaactgcaaggctgtggacatc
ggcccgggtctgaatctgctgcaagaagacaacccggacctgatcggcagcgagatcgcgcgctg
gctgtctactctggagatttccggt

**SEQ ID NO:39 (9F6-HT7 fusion protein)**

MVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQKLGVSITPIQKIVLSGENGLKIDIHVIIPYE
GLSGYQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVT
GTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILAGYLEPTTEDLYFQSDNDGSEIGTG
FPFDPHYVEVLGERMHYVDVGPRDGTPVLFLHGNPTSSYVWRNIIPHVAPTHRCIAPDLIGMGKS
DKPDLGYFFDDHVRFMDAFIEALGLEEVVLVIHDWGSALGFHWAKRNPERVKGIAFMEFIRPIPT
WDEWPEFARETFQAFRTTDVGRKLIIDQNVFIEGTLPMGVVRPLTEVEMDHYREPFLNPVDREPL
WRFPNELPIAGEPANIVALVEEYMDWLHQSPVPKLLFWGTPGVLIPPAEAARLAKSLPNCKAVDI
GPGLNLLQEDNPDLIGSEIARWLSTLEISG

**SEQ ID NO:40 (Id-9B8 opt-HT7 sandwich fusion nucleotide)**

atgcttggtctgtcggagcaaagcgtgtccatctcgcgctgcgctgggacgcgcctgcccgcctt
gctggacgagcagcaggtgaacgtcctgctctacgacatgaacggctgctactcacgcctcaagg
agctggtgcccaccctgccccagaaccgcaaagtgagcaaggtggagatcctgcagcatgtaatc
gactacatcagggacctgcagctggagctgaactcggagtctgaagtcgggaccaccggaggccg
gggactgcctgtccgcgccccgctcagcaccctgaacggcgagatcagtgccttggcggccgagg
cggcatgtgttccagccgacgatcgcatcttgtgtcgcgtttctcttgagaatctttatttcag

gcgtctggaggtggtggcggagcgatcgccatggtgtttacactcgaagatttcgtaggggactg
gcggcagacagccggctacaacctggaccaagtccttgagcagggcggtctgtccagtttgtttc
agaaactcggggtgtccgtaacaccgatccaaaagattgtcctgagcggtgaaaacggcctgaag
atcgacatccatgtcatcatcccgtatgaaggtctgagcggctatcagatgggccagatcgaaaa
aatttttaaggtggtgtaccctgtggatgatcatcactttaaggtgattctgcactatggcacac
tggtaatcgacggggttacgccgaacatgatcgactatttcggacggccgtatgaaggcatcgcc
gtgttcgacggcaaaaagatcactgtaaccgggaccctgtggaacggcaacaaaattatcgacga
gcgcctgatcaaccccgacggctccctgctgttccgcgtaaccatcaacggagtgaccggctggc
ggctgtgcgagcgtattcttgccggatatctcgagccaaccactgaggatctgtactttcagagc
gataacgatggatccgaaatcggtactggctttccattcgacccccattatgtggaagtcctggg
cgagcgcatgcactacgtcgatgttggtccgcgcgatggcacccctgtgctgttcctgcacggta
acccgacctcctcctacgtgtggcgcaacatcatcccgcatgttgcaccgacccatcgctgcatt
gctccagacctgatcggtatgggcaaatccgacaaaccagacctgggttatttcttcgacgacca
cgtccgcttcatggatgccttcatcgaagccctgggtctggaagaggtcgtcctggtcattcacg
actggggctccgctctgggtttccactgggccaagcgcaatccagagcgcgtcaaaggtattgca
tttatggagttcatccgccctatcccgacctgggacgaatggccagaatttgcccgcgagacctt
ccaggccttccgcaccaccgacgtcggccgcaagctgatcatcgatcagaacgtttttatcgagg
gtacgctgccgatgggtgtcgtccgcccgctgactgaagtcgagatggaccattaccgcgagccg
ttcctgaatcctgttgaccgcgagccactgtggcgcttcccaaacgagctgccaatcgccggtga
gccagcgaacatcgtcgcgctggtcgaagaatacatggactggctgcaccagtcccctgtcccga
agctgctgttctggggcaccccaggcgttctgatcccaccggccgaagccgctcgcctggccaaa
agcctgcctaactgcaaggctgtggacatcggcccgggtctgaatctgctgcaagaagacaaccc
ggacctgatcggcagcgagatcgcgcgctggctgtctactctggagatttccggtt

**SEQ ID NO:41 (Id-9B8 opt-HT7 sandwich fusion protein)**

MLGLSEQSVSISRCAGTRLPALLDEQQVNVLLYDMNGCYSRLKELVPTLPQNRKVSKVEILQHVI
DYIRDLQLELNSESEVGTTGGRGLPVRAPLSTLNGEISALAAEAACVPADDRILCRVSLENLYFQ
ASGGGGGAIAMVFTLEDFVGDWRQTAGYNLDQVLEQGGLSSLFQKLGVSVTPIQKIVLSGENGLK
IDIHVIIPYEGLSGYQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIA
VFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILAGYLEPTTEDLYFQS
DNDGSEIGTGFPFDPHYVEVLGERMHYVDVGPRDGTPVLFLHGNPTSSYVWRNIIPHVAPTHRCI
APDLIGMGKSDKPDLGYFFDDHVRFMDAFIEALGLEEVVLVIHDWGSALGFHWAKRNPERVKGIA
FMEFIRPIPTWDEWPEFARETFQAFRTTDVGRKLIIDQNVFIEGTLPMGVVRPLTEVEMDHYREP
FLNPVDREPLWRFPNELPIAGEPANIVALVEEYMDWLHQSPVPKLLFWGTPGVLIPPAEAARLAK
SLPNCKAVDIGPGLNLLQEDNPDLIGSEIARWLSTLEISG

**SEQ ID NO:42 (9B8 opt+K33N nucleotide)**

Atggtgtttacactcgaagatttcgtaggggactggcggcagacagccggctacaacctggacca
agtccttgagcagggcggtctgtccagtttgtttcagaatctcggggtgtccgtaacaccgatcc
aaaagattgtcctgagcggtgaaaacggcctgaagatcgacatccatgtcatcatcccgtatgaa
ggtctgagcggctatcagatgggccagatcgaaaaaattttaaggtggtgtaccctgtggatga
tcatcactttaaggtgattctgcactatggcacactggtaatcgacggggttacgccgaacatga
tcgactatttcggacggccgtatgaaggcatcgccgtgttcgacggcaaaaagatcactgtaacc
gggaccctgtggaacggcaacaaaattatcgacgagcgcctgatcaaccccgacggctccctgct
gttccgcgtaaccatcaacggagtgaccggctggcggctgtgcgagcgcattttggcg

**SEQ ID NO:43 (9B8 opt+K33N protein)**

MVFTLEDFVGDWRQTAGYNLDQVLEQGGLSSLFQNLGVSVTPIQKIVLSGENGLKIDIHVIIPYE
GLSGYQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVT
GTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILA

**SEQ ID NO:44 (QC27-HT7 nucleotide)**

atggtgtttacattggaggatttcgttggagactggcggcagacagctggatacaacctagatca
agtgttagaacaaggaggattgtctagtctgttccaaaagctgggagtgtcagtcaccccaatcc
agaaaattgtgctgtctggggagaatgggttaaaaattgatattcatgtcatcatcccttacgag
ggactcagtggttttcaaatgggtctgattgaaatgatcttcaaagttgtttacccagtggatga
tcatcatttcaagattattcaccattatggtacactcgttattgacggtgtgacaccaaacatga
ttgacttctttggacgcccttacgagggaattgctgtgtttgacggcaagaagatcacagttact
ggaactctgtggaacggcaacaagatcattgatgagcgcctgatcaacccagatggttcactcct
cttccgcgttactatcaatggagtcaccggatggcgcctttgcgagcgtattcttgccggatatc
tcgagccaaccactgaggatctgtactttcagagcgataacgatggatccgaaatcggtactggc
tttccattcgacccccattatgtggaagtcctgggcgagcgcatgcactacgtcgatgttggtcc
gcgcgatggcacccctgtgctgttcctgcacggtaacccgacctcctcctacgtgtggcgcaaca
tcatcccgcatgttgcaccgacccatcgctgcattgctccagacctgatcggtatgggcaaatcc
gacaaaccagacctgggttatttcttcgacgaccacgtccgcttcatggatgccttcatcgaagc
cctgggtctggaagaggtcgtcctggtcattcacgactggggctccgctctgggtttccactggg
ccaagcgcaatccagagcgcgtcaaaggtattgcatttatggagttcatccgccctatcccgacc
tgggacgaatggccagaatttgcccgcgagaccttccaggccttccgcaccaccgacgtcggccg
caagctgatcatcgatcagaacgtttttatcgagggtacgctgccgatgggtgtcgtccgcccgc
tgactgaagtcgagatggaccattaccgcgagccgttcctgaatcctgttgaccgcgagccactg
tggcgcttcccaaacgagctgccaatcgccggtgagccagcgaacatcgtcgcgctggtcgaaga
atacatggactggctgcaccagtcccctgtcccgaagctgctgttctggggcaccccaggcgttc
tgatcccaccggccgaagccgctcgcctggccaaaagcctgcctaactgcaaggctgtggacatc
ggcccgggtctgaatctgctgcaagaagacaacccggacctgatcggcagcgagatcgcgcgctg
gctgtctactctggagatttccggt

**SEQ ID NO:45 (QC27-HT7 protein)**
MVFTLEDFVGDWRQTAGYNLDQVLEQGGLSSLFQKLGVSVTPIQKIVLSGENGLKIDIHVIIPYE
GLSGFQMGLIEMIFKVVYPVDDHHFKIIHHYGTLVIDGVTPNMIDFFGRPYEGIAVFDGKKITVT
GTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILAGYLEPTTEDLYFQSDNDGSEIGTG
FPFDPHYVEVLGERMHYVDVGPRDGTPVLFLHGNPTSSYVWRNIIPHVAPTHRCIAPDLIGMGKS
DKPDLGYFFDDHVRFMDAFIEALGLEEVVLVIHDWGSALGFHWAKRNPERVKGIAFMEFIRPIPT
WDEWPEFARETFQAFRTTDVGRKLIIDQNVFIEGTLPMGVVRPLTEVEMDHYREPFLNPVDREPL
WRFPNELPIAGEPANIVALVEEYMDWLHQSPVPKLLFWGTPGVLIPPAEAARLAKSLPNCKAVDI
GPGLNLLQEDNPDLIGSEIARWLSTLEISG

**SEQ ID NO:46 (8F2)**
atggtgtttacattggaggatttcgttggagactggcggcagacagctggatacaaccaagatca
agtgttagaacaaggaggagtgtctagtctgttccaaaagctgggagtgtcagtcaccccaatcc
agaaaattgtgctgtctggggagaatgggttaaaaattgatattcatgtcatcatcccttacgag
ggactcagtggttttcaaatgggtctgattgaaatgatcttcaaagttgtttacccagtggatga
tcatcatttcaaggttattctccattatggtacactcgttattgacggtgtgacaccaaacatga
ttgactactttggacgcccttacgagggaattgctgtgtttgacggcaagaagatcacagttact
ggaactctgtggaacggcaacaagatcattgatgagcgcctgatcaacccagatggttcactcct
cttccgcgttactatcaatggagtcaccggatggcgcctttgcgagcgtattcttgcc

**SEQ ID NO:47 (8F2 protein)**
MVFTLEDFVGDWRQTAGYNQDQVLEQGGVSSLFQKLGVSVTPIQKIVLSGENGLKIDIHVIIPYE
GLSGFQMGLIEMIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVT
GTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILA

**SEQ ID NO:48 (IV-HT7 nucleotide)**
atggtgtttacattggaggatttcgttggagactggcggcagacagctggatacaaccaagatca
agtgttagaacaaggaggattgtctagtctgttccaaaagctgggagtgtcagtcaccccaatcc
agaaaattgtgctgtctggggagaatgggttaaaaattgatattcatgtcatcatcccttacgag

ggactcagtggttttcaaatgggtctgattgaaatgatcttcaaagttgtttacccagtggatga
tcatcatttcaaggttattctccattatggtacactcgttattgacggtgtgacaccaaacatga
ttgactactttggacgcccttacgagggaattgctgtgtttgacggcaagaagatcacagttact
ggaactctgtggaacggcaacaagatcattgatgagcgcctgatcaacccagatggttcactcct
cttccgcgttactatcaatggagtcaccggatggcgcctttgcgagcgtattcttgccggatatc
tcgagccaaccactgaggatctgtactttcagagcgataacgatggatccgaaatcggtactggc
tttccattcgacccccattatgtggaagtcctgggcgagcgcatgcactacgtcgatgttggtcc
gcgcgatggcacccctgtgctgttcctgcacggtaacccgacctcctcctacgtgtggcgcaaca
tcatcccgcatgttgcaccgacccatcgctgcattgctccagacctgatcggtatgggcaaatcc
gacaaaccagacctgggttatttcttcgacgaccacgtccgcttcatggatgccttcatcgaagc
cctgggtctggaagaggtcgtcctggtcattcacgactggggctccgctctgggtttccactggg
ccaagcgcaatccagagcgcgtcaaaggtattgcatttatggagttcatccgccctatcccgacc
tgggacgaatggccagaatttgcccgcgagaccttccaggccttccgcaccaccgacgtcggccg
caagctgatcatcgatcagaacgtttttatcgagggtacgctgccgatgggtgtcgtccgcccgc
tgactgaagtcgagatggaccattaccgcgagccgttcctgaatcctgttgaccgcgagccactg
tggcgcttcccaaacgagctgccaatcgccggtgagccagcgaacatcgtcgcgctggtcgaaga
atacatggactggctgcaccagtcccctgtcccgaagctgctgttctggggcaccccaggcgttc
tgatcccaccggccgaagccgctcgcctggccaaaagcctgcctaactgcaaggctgtggacatc
ggcccgggtctgaatctgctgcaagaagacaacccggacctgatcggcagcgagatcgcgcgctg
gctgtctactctggagatttccggt

**SEQ ID NO:49 (IV-HT7 protein)**

MVFTLEDFVGDWRQTAGYNQDQVLEQGGLSSLFQKLGVSVTPIQKIVLSGENGLKIDIHVIIPYE
GLSGFQMGLIEMIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVT
GTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILAGYLEPTTEDLYFQSDNDGSEIGTG
FPFDPHYVEVLGERMHYVDVGPRDGTPVLFLHGNPTSSYVWRNIIPHVAPTHRCIAPDLIGMGKS
DKPDLGYFFDDHVRFMDAFIEALGLEEVVLVIHDWGSALGFHWAKRNPERVKGIAFMEFIRPIPT
WDEWPEFARETFQAFRTTDVGRKLIIDQNVFIEGTLPMGVVRPLTEVEMDHYREPFLNPVDREPL
WRFPNELPIAGEPANIVALVEEYMDWLHQSPVPKLLFWGTPGVLIPPAEAARLAKSLPNCKAVDI
GPGLNLLQEDNPDLIGSEIARWLSTLEISG

**SEQ ID NO:50 (8F2-HT7 nucleotide)**

atggtgtttacattggaggatttcgttggagactggcggcagacagctggatacaaccaagatca
agtgttagaacaaggaggagtgtctagtctgttccaaaagctgggagtgtcagtcaccccaatcc
agaaaattgtgctgtctggggagaatgggttaaaaattgatattcatgtcatcatcccttacgag
ggactcagtggttttcaaatgggtctgattgaaatgatcttcaaagttgtttacccagtggatga
tcatcatttcaaggttattctccattatggtacactcgttattgacggtgtgacaccaaacatga
ttgactactttggacgcccttacgagggaattgctgtgtttgacggcaagaagatcacagttact
ggaactctgtggaacggcaacaagatcattgatgagcgcctgatcaacccagatggttcactcct
cttccgcgttactatcaatggagtcaccggatggcgcctttgcgagcgtattcttgccggatatc
tcgagccaaccactgaggatctgtactttcagagcgataacgatggatccgaaatcggtactggc
tttccattcgacccccattatgtggaagtcctgggcgagcgcatgcactacgtcgatgttggtcc
gcgcgatggcacccctgtgctgttcctgcacggtaacccgacctcctcctacgtgtggcgcaaca
tcatcccgcatgttgcaccgacccatcgctgcattgctccagacctgatcggtatgggcaaatcc
gacaaaccagacctgggttatttcttcgacgaccacgtccgcttcatggatgccttcatcgaagc
cctgggtctggaagaggtcgtcctggtcattcacgactggggctccgctctgggtttccactggg
ccaagcgcaatccagagcgcgtcaaaggtattgcatttatggagttcatccgccctatcccgacc
tgggacgaatggccagaatttgcccgcgagaccttccaggccttccgcaccaccgacgtcggccg
caagctgatcatcgatcagaacgtttttatcgagggtacgctgccgatgggtgtcgtccgcccgc
tgactgaagtcgagatggaccattaccgcgagccgttcctgaatcctgttgaccgcgagccactg
tggcgcttcccaaacgagctgccaatcgccggtgagccagcgaacatcgtcgcgctggtcgaaga
atacatggactggctgcaccagtcccctgtcccgaagctgctgttctggggcaccccaggcgttc
tgatcccaccggccgaagccgctcgcctggccaaaagcctgcctaactgcaaggctgtggacatc

ggcccgggtctgaatctgctgcaagaagacaacccggacctgatcggcagcgagatcgcgcgctg
gctgtctactctggagatttccggt

**SEQ ID NO:51 (8F2-HT7 protein)**

MVFTLEDFVGDWRQTAGYNQDQVLEQGGVSSLFQKLGVSVTPIQKIVLSGENGLKIDIHVIIPYE
GLSGFQMGLIEMIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVT
GTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILAGYLEPTTEDLYFQSDNDGSEIGTG
FPFDPHYVEVLGERMHYVDVGPRDGTPVLFLHGNPTSSYVWRNIIPHVAPTHRCIAPDLIGMGKS
DKPDLGYFFDDHVRFMDAFIEALGLEEVVLVIHDWGSALGFHWAKRNPERVKGIAFMEFIRPIPT
WDEWPEFARETFQAFRTTDVGRKLIIDQNVFIEGTLPMGVVRPLTEVEMDHYREPFLNPVDREPL
WRFPNELPIAGEPANIVALVEEYMDWLHQSPVPKLLFWGTPGVLIPPAEAARLAKSLPNCKAVDI
GPGLNLLQEDNPDLIGSEIARWLSTLEISG

**SEQ ID NO:52 (15C1-HT7 nucleotide)**

atggtgtttacattgaaggatttcgttggagactggcggcagacagctggatacaaccaagatca
agtgttagaacaaggaggattgtctagtctgttccaaaatctgggagtgtcagtcaccccaatcc
agaaaattgtgctgtctggggagaatgggttaaaaattgatattcatgtcatcatcccttacgag
ggactcagtggttatcaaatgggtcagattgaaaagatcttcaaagttgtttacccagtggatga
tcatcatttcaaggttattctccattatggtacactcgttattgacggtgtgacaccaaacatga
ttgactactttggacgcccttacgagggaattgctgtgtttgacggcaagaagatcacagttact
ggaactctgtggaacggcaacaagatcattgatgagcgcctgatcaacccagatggttcactcct
cttccgcgttactatcaatggagtcaccggatggcgcctttgcgagcgtattcttgccggatatc
tcgagccaaccactgaggatctgtactttcagagcgataacgatggatccgaaatcggtactggc
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gcgcgatggcacccctgtgctgttcctgcacggtaacccgacctcctcctacgtgtggcgcaaca
tcatcccgcatgttgcaccgacccatcgctgcattgctccagacctgatcggtatgggcaaatcc
gacaaaccagacctgggttatttcttcgacgaccacgtccgcttcatggatgccttcatcgaagc
cctgggtctggaagaggtcgtcctggtcattcacgactggggctccgctctgggtttccactggg
ccaagcgcaatccagagcgcgtcaaaggtattgcatttatggagttcatccgccctatcccgacc
tgggacgaatggccagaatttgcccgcgagaccttccaggccttccgcaccaccgacgtcggccg
caagctgatcatcgatcagaacgtttttatcgagggtacgctgccgatgggtgtcgtccgcccgc
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tggcgcttcccaaacgagctgccaatcgccggtgagccagcgaacatcgtcgcgctggtcgaaga
atacatggactggctgcaccagtcccctgtcccgaagctgctgttctggggcaccccaggcgttc
tgatcccaccggccgaagccgctcgcctggccaaaagcctgcctaactgcaaggctgtggacatc
ggcccgggtctgaatctgctgcaagaagacaacccggacctgatcggcagcgagatcgcgcgctg
gctgtctactctggagatttccggt

**SEQ ID NO:53 (15C1-HT7 protein)**

MVFTLKDFVGDWRQTAGYNQDQVLEQGGLSSLFQNLGVSVTPIQKIVLSGENGLKIDIHVIIPYE
GLSGYQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVT
GTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILAGYLEPTTEDLYFQSDNDGSEIGTG
FPFDPHYVEVLGERMHYVDVGPRDGTPVLFLHGNPTSSYVWRNIIPHVAPTHRCIAPDLIGMGKS
DKPDLGYFFDDHVRFMDAFIEALGLEEVVLVIHDWGSALGFHWAKRNPERVKGIAFMEFIRPIPT
WDEWPEFARETFQAFRTTDVGRKLIIDQNVFIEGTLPMGVVRPLTEVEMDHYREPFLNPVDREPL
WRFPNELPIAGEPANIVALVEEYMDWLHQSPVPKLLFWGTPGVLIPPAEAARLAKSLPNCKAVDI
GPGLNLLQEDNPDLIGSEIARWLSTLEISG

**SEQ ID NO:54 (OgLuc Secretion Signal Peptide)** *Oplophorus gracilirostris*

atggcttactccacactgttcatcattgctctcacagccgtcgtaacacaagcctcctccacaca
gaaaagcaacctgaca

**SEQ ID NO:55 (Id-C1A4E-HT7 sandwich fusion nucleotide)**

atgcttggtctgtcggagcaaagcgtgtccatctcgcgctgcgctgggacgcgcctgcccgcctt
gctggacgagcagcaggtgaacgtcctgctctacgacatgaacggctgctactcacgcctcaagg
agctggtgcccaccctgccccagaaccgcaaagtgagcaaggtggagatcctgcagcatgtaatc
gactacatcagggacctgcagctggagctgaactcggagtctgaagtcgggaccaccggaggccg
gggactgcctgtccgcgccccgctcagcaccctgaacggcgagatcagtgccttggcggccgagg
cggcatgtgttccagccgacgatcgcatcttgtgtcgcgtttctcttgagaatctttattttcag
gcgtctggaggtggtggcggagcgatcgccatggtgtttacattggaggatttcgttggagactg
gcggcagacagctggatacaaccaagatcaagtgttagaacaaggaggattgtctagtctgttcc
aaaagctgggagtgtcagtcaccccaatccagaaaattgtgctgtctggggagaatgggttaaaa
tttgatattcatgtcatcatcccttacgagggactcagtggttttcaaatgggtctgattgaaat
gatcttcaaagttgtttacccagtggatgatcatcatttcaagattattctccattatggtacac
tcgttattgacggtgtgacaccaaacatgattgactactttggacgcccttacgagggaattgct
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gcgcctgatcaacccagatggttcactcctcttccgcgttactatcaatggagtcaccggatggc
gcctttgcgagcgtattcttgccggatctctcgagccaaccactgaggatctgtactttcagagc
gataacgatggatccgaaatcggtactggctttccattcgacccccattatgtggaagtcctggg
cgagcgcatgcactacgtcgatgttggtccgcgcgatggcacccctgtgctgttcctgcacggta
acccgacctcctcctacgtgtggcgcaacatcatcccgcatgttgcaccgacccatcgctgcatt
gctccagacctgatcggtatgggcaaatccgacaaaccagacctgggttatttcttcgacgacca
cgtccgcttcatggatgccttcatcgaagccctgggtctggaagaggtcgtcctggtcattcacg
actggggctccgctctgggtttccactgggccaagcgcaatccagagcgcgtcaaaggtattgca
tttatggagttcatccgccctatcccgacctgggacgaatggccagaatttgcccgcgagacctt
ccaggccttccgcaccaccgacgtcggccgcaagctgatcatcgatcagaacgtttttatcgagg
gtacgctgccgatgggtgtcgtccgcccgctgactgaagtcgagatggaccattaccgcgagccg
ttcctgaatcctgttgaccgcgagccactgtggcgcttcccaaacgagctgccaatcgccggtga
gccagcgaacatcgtcgcgctggtcgaagaatacatggactggctgcaccagtcccctgtcccga
agctgctgttctggggcaccccaggcgttctgatcccaccggccgaagccgctcgcctggccaaa
agcctgcctaactgcaaggctgtggacatcggcccgggtctgaatctgctgcaagaagacaaccc
ggacctgatcggcagcgagatcgcgcgctggctgtctactctggagatttccggt

**SEQ ID NO:56 (Id-C1A4E-HT7 sandwich fusion protein)**

MLGLSEQSVSISRCAGTRLPALLDEQQVNVLLYDMNGCYSRLKELVPTLPQNRKVSKVEILQHVI
DYIRDLQLELNSESEVGTTGGRGLPVRAPLSTLNGEISALAAEAACVPADDRILCRVSLENLYFQ
ASGGGGGAIAMVFTLEDFVGDWRQTAGYNQDQVLEQGGLSSLFQKLGVSVTPIQKIVLSGENGLK
FDIHVIIPYEGLSGFQMGLIEMIFKVVYPVDDHHFKIILHYGTLVIDGVTPNMIDYFGRPYEGIA
VFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILAGSLEPTTEDLYFQS
DNDGSEIGTGFPFDPHYVEVLGERMHYVDVGPRDGTPVLFLHGNPTSSYVWRNIIPHVAPTHRCI
APDLIGMGKSDKPDLGYFFDDHVRFMDAFIEALGLEEVVLVIHDWGSALGFHWAKRNPERVKGIA
FMEFIRPIPTWDEWPEFARETFQAFRTTDVGRKLIIDQNVFIEGTLPMGVVRPLTEVEMDHYREP
FLNPVDREPLWRFPNELPIAGEPANIVALVEEYMDWLHQSPVPKLLFWGTPGVLIPPAEAARLAK
SLPNCKAVDIGPGLNLLQEDNPDLIGSEIARWLSTLEISG

**SEQ ID NO:57 (Id-IV-HT7 sandwich fusion nucleotide)**

atgcttggtctgtcggagcaaagcgtgtccatctcgcgctgcgctgggacgcgcctgcccgcctt
gctggacgagcagcaggtgaacgtcctgctctacgacatgaacggctgctactcacgcctcaagg
agctggtgcccaccctgccccagaaccgcaaagtgagcaaggtggagatcctgcagcatgtaatc
gactacatcagggacctgcagctggagctgaactcggagtctgaagtcgggaccaccggaggccg
gggactgcctgtccgcgccccgctcagcaccctgaacggcgagatcagtgccttggcggccgagg
cggcatgtgttccagccgacgatcgcatcttgtgtcgcgtttctcttgagaatctttattttcag
gcgtctggaggtggtggcggagcgatcgccatggtgtttacattggaggatttcgttggagactg
gcggcagacagctggatacaaccaagatcaagtgttagaacaaggaggattgtctagtctgttcc
aaaagctgggagtgtcagtcaccccaatccagaaaattgtgctgtctggggagaatgggttaaaa
attgatattcatgtcatcatcccttacgagggactcagtggttttcaaatgggtctgattgaaat

gatcttcaaagttgtttacccagtggatgatcatcatttcaaggttattctccattatggtacac
tcgttattgacggtgtgacaccaaacatgattgactactttggacgcccttacgagggaattgct
gtgtttgacggcaagaagatcacagttactggaactctgtggaacggcaacaagatcattgatga
gcgcctgatcaacccagatggttcactcctcttccgcgttactatcaatggagtcaccggatggc
gcctttgcgagcgtattcttgccgtttctctcgagccaaccactgaggatctgtactttcagagc
gataacgatggatccgaaatcggtactggctttccattcgacccccattatgtggaagtcctggg
cgagcgcatgcactacgtcgatgttggtccgcgcgatggcacccctgtgctgttcctgcacggta
acccgacctcctcctacgtgtggcgcaacatcatcccgcatgttgcaccgacccatcgctgcatt
gctccagacctgatcggtatgggcaaatccgacaaaccagacctgggttatttcttcgacgacca
cgtccgcttcatggatgccttcatcgaagccctgggtctggaagaggtcgtcctggtcattcacg
actggggctccgctctgggtttccactgggccaagcgcaatccagagcgcgtcaaaggtattgca
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ccaggccttccgcaccaccgacgtcggccgcaagctgatcatcgatcagaacgtttttatcgagg
gtacgctgccgatgggtgtcgtccgcccgctgactgaagtcgagatggaccattaccgcgagccg
ttcctgaatcctgttgaccgcgagccactgtggcgcttcccaaacgagctgccaatcgccggtga
gccagcgaacatcgtcgcgctggtcgaagaatacatggactggctgcaccagtcccctgtcccga
agctgctgttctggggcaccccaggcgttctgatcccaccggccgaagccgctcgcctggccaaa
agcctgcctaactgcaaggctgtggacatcggcccgggtctgaatctgctgcaagaagacaaccc
ggacctgatcggcagcgagatcgcgcgctggctgtctactctggagatttccggt

**SEQ ID NO:58 (Id-IV-HT7 sandwich fusion protein)**

MLGLSEQSVSISRCAGTRLPALLDEQQVNVLLYDMNGCYSRLKELVPTLPQNRKVSKVEILQHVI
DYIRDLQLELNSESEVGTTGGRGLPVRAPLSTLNGEISALAAEAACVPADDRILCRVSLENLYFQ
ASGGGGGAIAMVFTLEDFVGDWRQTAGYNQDQVLEQGGLSSLFQKLGVSVTPIQKIVLSGENGLK
IDIHVIIPYEGLSGFQMGLIEMIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIA
VFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILAVSLEPTTEDLYFQS
DNDGSEIGTGFPFDPHYVEVLGERMHYVDVGPRDGTPVLFLHGNPTSSYVWRNIIPHVAPTHRCI
APDLIGMGKSDKPDLGYFFDDHVRFMDAFIEALGLEEVVLVIHDWGSALGFHWAKRNPERVKGIA
FMEFIRPIPTWDEWPEFARETFQAFRTTDVGRKLIIDQNVFIEGTLPMGVVRPLTEVEMDHYREP
FLNPVDREPLWRFPNELPIAGEPANIVALVEEYMDWLHQSPVPKLLFWGTPGVLIPPAEAARLAK
SLPNCKAVDIGPGLNLLQEDNPDLIGSEIARWLSTLEISG

**SEQ ID NO:59 (Id-9B8 opt+K33N-HT7 sandwich fusion nucleotide)**

atgcttggtctgtcggagcaaagcgtgtccatctcgcgctgcgctgggacgcgcctgcccgcctt
gctggacgagcagcaggtgaacgtcctgctctacgacatgaacggctgctactcacgcctcaagg
agctggtgcccaccctgccccagaaccgcaaagtgagcaaggtggagatcctgcagcatgtaatc
gactacatcagggacctgcagctggagctgaactcggagtctgaagtcgggaccaccggaggccg
gggactgcctgtccgcgccccgctcagcaccctgaacggcgagatcagtgccttggcggccgagg
cggcatgtgttccagccgacgatcgcatcttgtgtcgcgtttctcttgagaatctttatttttcag
gcgtctggaggtggtggcggagcgatcgccatggtgtttacactcgaagatttcgtaggggactg
gcggcagacagccggctacaacctggaccaagtccttgagcagggcggtctgtccagtttgtttc
agaatctcggggtgtccgtaacaccgatccaaaagattgtcctgagcggtgaaaacggcctgaag
atcgacatccatgtcatcatcccgtatgaaggtctgagcggctatcagatgggccagatcgaaaa
aatttttaaggtggtgtaccctgtggatgatcatcactttaaggtgattctgcactatggcacac
tggtaatcgacggggttacgccgaacatgatcgactatttcggacggccgtatgaaggcatcgcc
gtgttcgacggcaaaaagatcactgtaaccgggaccctgtggaacggcaacaaaattatcgacga
gcgcctgatcaaccccgacggctccctgctgttccgcgtaaccatcaacggagtgaccggctggc
ggctgtgcgagcgcattttggcgggatatctcgagccaaccactgaggatctgtactttcagagc
gataacgatggatccgaaatcggtactggctttccattcgacccccattatgtggaagtcctggg
cgagcgcatgcactacgtcgatgttggtccgcgcgatggcacccctgtgctgttcctgcacggta
acccgacctcctcctacgtgtggcgcaacatcatcccgcatgttgcaccgacccatcgctgcatt
gctccagacctgatcggtatgggcaaatccgacaaaccagacctgggttatttcttcgacgacca
cgtccgcttcatggatgccttcatcgaagccctgggtctggaagaggtcgtcctggtcattcacg

actggggctccgctctgggtttccactgggccaagcgcaatccagagcgcgtcaaaggtattgca
tttatggagttcatccgccctatcccgacctgggacgaatggccagaatttgcccgcgagacctt
ccaggccttccgcaccaccgacgtcggccgcaagctgatcatcgatcagaacgtttttatcgagg
gtacgctgccgatgggtgtcgtccgcccgctgactgaagtcgagatggaccattaccgcgagccg
ttcctgaatcctgttgaccgcgagccactgtggcgcttcccaaacgagctgccaatcgccggtga
gccagcgaacatcgtcgcgctggtcgaagaatacatggactggctgcaccagtcccctgtcccga
agctgctgttctggggcaccccaggcgttctgatcccaccggccgaagccgctcgcctggccaaa
agcctgcctaactgcaaggctgtggacatcggcccgggtctgaatctgctgcaagaagacaaccc
ggacctgatcggcagcgagatcgcgcgctggctgtctactctggagatttccggt

**SEQ ID NO:60 (Id-9B8 opt+K33N-HT7 sandwich fusion protein)**

MLGLSEQSVSISRCAGTRLPALLDEQQVNVLLYDMNGCYSRLKELVPTLPQNRKVSKVEILQHVI
DYIRDLQLELNSESEVGTTGGRGLPVRAPLSTLNGEISALAAEAACVPADDRILCRVSLENLYFQ
ASGGGGGAIAMVFTLEDFVGDWRQTAGYNLDQVLEQGGLSSLFQNLGVSVTPIQKIVLSGENGLK
IDIHVIIPYEGLSGYQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIA
VFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILAGYLEPTTEDLYFQS
DNDGSEIGTGFPFDPHYVEVLGERMHYVDVGPRDGTPVLFLHGNPTSSYVWRNIIPHVAPTHRCI
APDLIGMGKSDKPDLGYFFDDHVRFMDAFIEALGLEEVVLVIHDWGSALGFHWAKRNPERVKGIA
FMEFIRPIPTWDEWPEFARETFQAFRTTDVGRKLIIDQNVFIEGTLPMGVVRPLTEVEMDHYREP
FLNPVDREPLWRFPNELPIAGEPANIVALVEEYMDWLHQSPVPKLLFWGTPGVLIPPAEAARLAK
SLPNCKAVDIGPGLNLLQEDNPDLIGSEIARWLSTLEISG

**SEQ ID NO:61 (Id-9B8-HT7 sandwich fusion nucleotide)**

atgcttggtctgtcggagcaaagcgtgtccatctcgcgctgcgctgggacgcgcctgcccgcctt
gctggacgagcagcaggtgaacgtcctgctctacgacatgaacggctgctactcacgcctcaagg
agctggtgcccaccctgccccagaaccgcaaagtgagcaaggtggagatcctgcagcatgtaatc
gactacatcagggacctgcagctggagctgaactcggagtctgaagtcgggaccaccggaggccg
gggactgcctgtccgcgccccgctcagcaccctgaacggcgagatcagtgccttggcggccgagg
cggcatgtgttccagccgacgatcgcatcttgtgtcgcgtttctcttgagaatctttatttttcag
gcgtctggaggtggtggcggagcgatcgccatggtgtttacattggaggatttcgttggagactg
gcggcagacagctggatacaacctagatcaagtgttagaacaaggaggattgtctagtctgttcc
aaaagctgggagtgtcagtcaccccaatccagaaaattgtgctgtctggggagaatgggttaaaa
attgatattcatgtcatcatcccttacgagggactcagtggttatcaaatgggtcagattgaaaa
gatcttcaaagttgtttacccagtggatgatcatcatttcaaggttattctccattatggtacac
tcgttattgacggtgtgacaccaaacatgattgactactttggacgcccttacgagggaattgct
gtgtttgacggcaagaagatcacagttactggaactctgtggaacggcaacaagatcattgatga
gcgcctgatcaacccagatggttcactcctcttccgcgttactatcaatggagtcaccggatggc
gcctttgcgagcgtattcttgccgtttctctcgagccaaccactgaggatctgtactttcagagc
gataacgatggatccgaaatcggtactggctttccattcgacccccattatgtggaagtcctggg
cgagcgcatgcactacgtcgatgttggtccgcgcgatggcacccctgtgctgttcctgcacggta
acccgacctcctcctacgtgtggcgcaacatcatcccgcatgttgcaccgacccatcgctgcatt
gctccagacctgatcggtatgggcaaatccgacaaaccagacctgggttatttcttcgacgacca
cgtccgcttcatggatgccttcatcgaagccctgggtctggaagaggtcgtcctggtcattcacg
actggggctccgctctgggtttccactgggccaagcgcaatccagagcgcgtcaaaggtattgca
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gtacgctgccgatgggtgtcgtccgcccgctgactgaagtcgagatggaccattaccgcgagccg
ttcctgaatcctgttgaccgcgagccactgtggcgcttcccaaacgagctgccaatcgccggtga
gccagcgaacatcgtcgcgctggtcgaagaatacatggactggctgcaccagtcccctgtcccga
agctgctgttctggggcaccccaggcgttctgatcccaccggccgaagccgctcgcctggccaaa
agcctgcctaactgcaaggctgtggacatcggcccgggtctgaatctgctgcaagaagacaaccc
ggacctgatcggcagcgagatcgcgcgctggctgtctactctggagatttccggt

**SEQ ID NO:62 (Id-9B8-HT7 sandwich fusion protein)**

MLGLSEQSVSISRCAGTRLPALLDEQQVNVLLYDMNGCYSRLKELVPTLPQNRKVSKVEILQHVI
DYIRDLQLELNSESEVGTTGGRGLPVRAPLSTLNGEISALAAEAACVPADDRILCRVSLENLYFQ
ASGGGGGAIAMVFTLEDFVGDWRQTAGYNLDQVLEQGGLSSLFQKLGVSVTPIQKIVLSGENGLK
IDIHVIIPYEGLSGYQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIA
VFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILAVSLEPTTEDLYFQS
DNDGSEIGTGFPFDPHYVEVLGERMHYVDVGPRDGTPVLFLHGNPTSSYVWRNIIPHVAPTHRCI
APDLIGMGKSDKPDLGYFFDDHVRFMDAFIEALGLEEVVLVIHDWGSALGFHWAKRNPERVKGIA
FMEFIRPIPTWDEWPEFARETFQAFRTTDVGRKLIIDQNVFIEGTLPMGVVRPLTEVEMDHYREP
FLNPVDREPLWRFPNELPIAGEPANIVALVEEYMDWLHQSPVPKLLFWGTPGVLIPPAEAARLAK
SLPNCKAVDIGPGLNLLQEDNPDLIGSEIARWLSTLEISG

**SEQ ID NO:63 (Id-9F6-HT7 sandwich fusion nucleotide)**

atgcttggtctgtcggagcaaagcgtgtccatctcgcgctgcgctgggacgcgcctgcccgcctt
gctggacgagcagcaggtgaacgtcctgctctacgacatgaacggctgctactcacgcctcaagg
agctggtgcccaccctgccccagaaccgcaaagtgagcaaggtggagatcctgcagcatgtaatc
gactacatcagggacctgcagctggagctgaactcggagtctgaagtcgggaccaccggaggccg
gggactgcctgtccgcgccccgctcagcaccctgaacggcgagatcagtgccttggcggccgagg
cggcatgtgttccagccgacgatcgcatcttgtgtcgcgtttctcttgagaatctttatttttcag
gcgtctggaggtggtggcggagcgatcgccatggtgtttacattggaggatttcgttggagactg
gcggcagacagctggatacaacctagatcaagtgttagaacaaggaggagtgtctagtctgttcc
aaaagctgggagtgtcaatcaccccaatccagaaaattgtgctgtctggggagaatgggttaaaa
attgatattcatgtcatcatcccttacgagggactcagtggttatcaaatgggtcagattgaaaa
gatcttcaaagttgtttacccagtggatgatcatcatttcaaggttattctccattatggtacac
tcgttattgacggtgtgacaccaaacatgattgactactttggacgcccttacgagggaattgct
gtgtttgacggcaagaagatcacagttactggaactctgtggaacggcaacaagatcattgatga
gcgcctgatcaacccagatggttcactcctcttccgcgttactatcaatggagtcaccggatggc
gcctttgcgagcgtattcttgccgtttctctcgagccaaccactgaggatctgtactttcagagc
gataacgatggatccgaaatcggtactggctttccattcgacccccattatgtggaagtcctggg
cgagcgcatgcactacgtcgatgttggtccgcgcgatggcacccctgtgctgttcctgcacggta
acccgacctcctcctacgtgtggcgcaacatcatcccgcatgttgcaccgacccatcgctgcatt
gctccagacctgatcggtatgggcaaatccgacaaaccagacctgggttatttcttcgacgacca
cgtccgcttcatggatgccttcatcgaagccctgggtctggaagaggtcgtcctggtcattcacg
actggggctccgctctgggtttccactgggccaagcgcaatccagagcgcgtcaaaggtattgca
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ccaggccttccgcaccaccgacgtcggccgcaagctgatcatcgatcagaacgttttatcgagg
gtacgctgccgatgggtgtcgtccgcccgctgactgaagtcgagatggaccattaccgcgagccg
ttcctgaatcctgttgaccgcgagccactgtggcgcttcccaaacgagctgccaatcgccggtga
gccagcgaacatcgtcgcgctggtcgaagaatacatggactggctgcaccagtcccctgtcccga
agctgctgttctggggcaccccaggcgttctgatcccaccggccgaagccgctcgcctggccaaa
agcctgcctaactgcaaggctgtggacatcggcccgggtctgaatctgctgcaagaagacaaccc
ggacctgatcggcagcgagatcgcgcgctggctgtctactctggagatttccggt

**SEQ ID NO:64 (Id-9F6-HT7 sandwich fusion protein)**

MLGLSEQSVSISRCAGTRLPALLDEQQVNVLLYDMNGCYSRLKELVPTLPQNRKVSKVEILQHVI
DYIRDLQLELNSESEVGTTGGRGLPVRAPLSTLNGEISALAAEAACVPADDRILCRVSLENLYFQ
ASGGGGGAIAMVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQKLGVSITPIQKIVLSGENGLK
IDIHVIIPYEGLSGYQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIA
VFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILAVSLEPTTEDLYFQS
DNDGSEIGTGFPFDPHYVEVLGERMHYVDVGPRDGTPVLFLHGNPTSSYVWRNIIPHVAPTHRCI
APDLIGMGKSDKPDLGYFFDDHVRFMDAFIEALGLEEVVLVIHDWGSALGFHWAKRNPERVKGIA
FMEFIRPIPTWDEWPEFARETFQAFRTTDVGRKLIIDQNVFIEGTLPMGVVRPLTEVEMDHYREP

FLNPVDREPLWRFPNELPIAGEPANIVALVEEYMDWLHQSPVPKLLFWGTPGVLIPPAEAARLAK
SLPNCKAVDIGPGLNLLQEDNPDLIGSEIARWLSTLEISG

**SEQ ID NO:65 (9B8 opt-P nucleotide)**
atggtgtttacactcgaagatttcgtaggggactggcggcagacagccggctacaacctggacca
agtccttgagcagggcggtctgtccagtttgtttcagaaactcggggtgtccgtaacaccgatcc
aaaagattgtcctgagcggtgaaaacggcctgaagatcgacatccatgtcatcatcccgtatgaa
ggtctgagcggctatcagatgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatga
tcatcactttaaggtgattctgcactatggcacactggtaatcgacggggttacgccgaacatga
tcgactatttcggacggccgtatgaaggcatcgccgtgttcgacggcaaaaagatcactgtaacc
gggaccctgtggaacggcaacaaaattatcgacgagcgcctgatcaaccccgacggctccctgct
gttccgcgtaaccatcaacggagtgaccggctggcggctgtgcgagcgcattttggcgaattctc
acggcttccctcccgaggtggaggagcaggccgccggcaccctgcccatgagctgcgcccaggag
agcggcatggatagacaccctgctgcttgcgccagcgccaggatcaacgtc

**SEQ ID NO:66 (2X ARE)**
TAGCTTGGAAATGACATTGCTAATGGTGACAAAGCAACTTTTAGCTTGGAAATGACATTGCTAAT
GGTGACAAAGCAACTTT

**SEQ ID NO:67 (HRE)**
CTGGAATTTTCTAGACTGGAATTTTCTAGACTGGAATTTTCTAGA

**SEQ ID NO:68 (K33N+170G nucleotide)**
atggtgtttacactcgaagatttcgtaggggactggcggcagacagccggctacaacctggacca
agtccttgagcagggcggtctgtccagtttgtttcagaatctcggggtgtccgtaacaccgatcc
aaaagattgtcctgagcggtgaaaacggcctgaagatcgacatccatgtcatcatcccgtatgaa
ggtctgagcggctatcagatgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatga
tcatcactttaaggtgattctgcactatggcacactggtaatcgacggggttacgccgaacatga
tcgactatttcggacggccgtatgaaggcatcgccgtgttcgacggcaaaaagatcactgtaacc
gggaccctgtggaacggcaacaaaattatcgacgagcgcctgatcaaccccgacggctccctgct
gttccgcgtaaccatcaacggagtgaccggctggcggctgtgcgagcgcattttggcggga

**SEQ ID NO:69 (K33N+170G protein)**
MVFTLEDFVGDWRQTAGYNLDQVLEQGGLSSLFQNLGVSVTPIQKIVLSGENGLKIDIHVIIPYE
GLSGYQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVT
GTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILAG

**SEQ ID NO:70 (27A5 (NF) nucleotide)**
ATGGTGTTTACACTCGAAGATTTCGTAGGGGACTGGCGGCAGACAGCCGGCTACAACCTGGACCA
AGTCCTTGAGCAGGGCGGTCTGTCCAGTTTGTTTCAGAATCTCGGGGTGTCCGTAACTCCGATCC
AAAAGATTGTCCTGAGCGGTGAAAACGGCCTGAAGATCGACATCCATGTCATCATCCCGTATGAA
GGTCTGAGCGGCTATCAGATGGGCCAGATCGAAAAAATTTTTAAGGTGGTGTACCCTGTGGATGA
TCATCACTTTAAGGTGATTCTGCACTATGGCACACTGGTAATCGACGGGGTTACGCCGAACATGA
TCGACTATTTCGGACGGCCGTATGAAGGCATCGCCGTGTTCGACGGCAAAAAGATCACTGTAACC
GGGACCCTGTGGAACGGCAACAAAATTATCGACGAGCGCCTGATCAACCCCGACGGCTCCCTGCT
GTTCCGCGTAACCATCAACGGAGTGACCGGCTGGCGGCTGTGCGAGCGCATTTTGGCGGGA

**SEQ ID NO:71 (27A5 (NF) protein)**
MVFTLEDFVGDWRQTAGYNLDQVLEQGGLSSLFQNLGVSVTPIQKIVLSGENGLKIDIHVIIPYE
GLSGYQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVT
GTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILAG

**SEQ ID NO:72 (23D4 (NF) nucleotide)**

ATGGTGTTTACACTCGAAGATTTCGTAGGGGACTGGCGGCAGACAGCCGGCTACAACCTGGACCA
AGTCCTTGAGCAGGGCGGCCTGTCCAGTTTGTTTCAGAATCTCGGGGTGTCCGTAACACCGATCC
AAAAGATTGTCCTGAGCGGTGAAAACGGCCTGAAGATCGACATCCATGTCATCATCCCGTATGAA
GGTCTGAGCGGCTATCAGATGGGCCAGATCGAAAAAATTTTTAAGGTGGTGTACCCTGTGGATGA
TCATCACTTTAAGGTGATTCTGCACTATGGCACACTGGTAATCGACGGGGTTACGCCGAACTTGA
TCGACTATTTCGGACGTCCGTATGAAGGCATCGCCGTGTTCGACGGCAAAAAGATCACTGTAACC
GGGACCCTGTGGAACGGCAACAAAATTATCGACGAGCGCCTGATCAACCCCGACGGCTCCCTGCT
GTTCCGCGTAACCATCAACGGAGTGACCGGCTGGCGGCTGTGCGAGCGCATTTTGGCGGGA

**SEQ ID NO:73 (23D4 (NF) protein)**

MVFTLEDFVGDWRQTAGYNLDQVLEQGGLSSLFQNLGVSVTPIQKIVLSGENGLKIDIHVIIPYE
GLSGYQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNLIDYFGRPYEGIAVFDGKKITVT
GTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILAG

**SEQ ID NO:74 (24C2 (NF) nucleotide)**

ATGGTGTTTACACTCGAAGATTTCGTAGGGGACTGGCAGCAGACAGCCGGCTACAACCTGGACCA
AGTCCTTGAGCAGGGCGGTCTGTCCAGTTTGTTTCAGAATCTCGGGGTGTCCGTAACTCCGATCC
AAAAGATTGTCCTGAGCGGTGAAAACGGCCTGAAGATCGACATCCATGTCATCATCCCGTATGAA
GGTCTGAGCGGCTATCAGATGGGCCAGATCGAAAAAATTTTTAAGGTGGTGTACCCTGTGGATGA
TCATCACTTTAAGGTGATTCTGCACTATGGCACACTGGTAATCGACGGGGTTACGCCGAACATGA
TCGACTATTTCGGACGGCCGTATGAAGGCATCGCCGTGTTCGACGGCAAAAAGATCACTGTAACC
GGGACCCTGTGGAACGGCAACAAAATTATCGACGAGCGCCTGATCAACCCCGACGGCTCCCTGCT
GTTCCGCGTAACCATCAACGGAGTGACCGGCTGGCGGCTGTGCGAGCGCATTTTGGCGGGA

**SEQ ID NO:75 (24C2 (NF) protein)**

MVFTLEDFVGDWQQTAGYNLDQVLEQGGLSSLFQNLGVSVTPIQKIVLSGENGLKIDIHVIIPYE
GLSGYQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVT
GTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILAG

**SEQ ID NO:76 (Id-23D4-HT7 sandwich fusion nucleotide)**

atgcttggtctgtcggagcaaagcgtgtccatctcgcgctgcgctgggacgcgcctgcccgcctt
gctggacgagcagcaggtgaacgtcctgctctacgacatgaacggctgctactcacgcctcaagg
agctggtgcccaccctgccccagaaccgcaaagtgagcaaggtggagatcctgcagcatgtaatc
gactacatcagggacctgcagctggagctgaactcggagtctgaagtcgggaccaccggaggccg
gggactgcctgtccgcgccccgctcagcaccctgaacggcgagatcagtgccttggcggccgagg
cggcatgtgttccagccgacgatcgcatcttgtgtcgcgtttctcttgagaatctttatttttcag
gcgtctggaggtggtggcggagcgatcgccatggtgtttacactcgaagatttcgtaggggactg
gcggcagacagccggctacaacctggaccaagtccttgagcagggcggcctgtccagtttgtttc
agaatctcggggtgtccgtaacaccgatccaaaagattgtcctgagcggtgaaaacggcctgaag
atcgacatccatgtcatcatcccgtatgaaggtctgagcggctatcagatgggccagatcgaaaa
aatttttaaggtggtgtaccctgtggatgatcatcactttaaggtgattctgcactatggcacac
tggtaatcgacggggttacgccgaacttgatcgactatttcggacgtccgtatgaaggcatcgcc
gtgttcgacggcaaaaagatcactgtaaccgggaccctgtggaacggcaacaaaattatcgacga
gcgcctgatcaaccccgacggctccctgctgttccgcgtaaccatcaacggagtgaccggctggc
ggctgtgcgagcgcattttggcgggatatctcgagccaaccactgaggatctgtactttcagagc
gataacgatggatccgaaatcggtactggctttccattcgacccccattatgtggaagtcctggg
cgagcgcatgcactacgtcgatgttggtccgcgcgatggcacccctgtgctgttcctgcacggta
acccgacctcctcctacgtgtggcgcaacatcatcccgcatgttgcaccgacccatcgctgcatt
gctccagacctgatcggtatgggcaaatccgacaaaccagacctgggttatttcttcgacgacca
cgtccgcttcatggatgccttcatcgaagccctgggtctggaagaggtcgtcctggtcattcacg
actggggctccgctctgggtttccactgggccaagcgcaatccagagcgcgtcaaaggtattgca
tttatggagttcatccgccctatcccgacctgggacgaatggccagaatttgcccgcgagacctt

ccaggccttccgcaccaccgacgtcggccgcaagctgatcatcgatcagaacgttttatcgagg
gtacgctgccgatgggtgtcgtccgcccgctgactgaagtcgagatggaccattaccgcgagccg
ttcctgaatcctgttgaccgcgagccactgtggcgcttcccaaacgagctgccaatcgccggtga
gccagcgaacatcgtcgcgctggtcgaagaatacatggactggctgcaccagtcccctgtcccga
agctgctgttctggggcaccccaggcgttctgatcccaccggccgaagccgctcgcctggccaaa
agcctgcctaactgcaaggctgtggacatcggcccgggtctg

**SEQ ID NO:77 (Id-23D4-HT7 sandwich fusion protein)**
MLGLSEQSVSISRCAGTRLPALLDEQQVNVLLLYDMNGCYSRLKELVPTLPQNRKVSKVEILQHVI
DYIRDLQLELNSESEVGTTGGRGLPVRAPLSTLNGEISALAAEAACVPADDRILCRVSLENLYFQ
ASGGGGGAIAMVFTLEDFVGDWRQTAGYNLDQVLEQGGLSSLFQNLGVSVTPIQKIVLSGENGLK
IDIHVIIPYEGLSGYQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNLIDYFGRPYEGIA
VFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILAGYLEPTTEDLYFQS
DNDGSEIGTGFPFDPHYVEVLGERMHYVDVGPRDGTPVLFLHGNPTSSYVWRNIIPHVAPTHRCI
APDLIGMGKSDKPDLGYFFDDHVRFMDAFIEALGLEEVVLVIHDWGSALGFHWAKRNPERVKGIA
FMEFIRPIPTWDEWPEFARETFQAFRTTDVGRKLIIDQNVFIEGTLPMGVVRPLTEVEMDHYREP
FLNPVDREPLWRFPNELPIAGEPANIVALVEEYMDWLHQSPVPKLLFWGTPGVLIPPAEAARLAK
SLPNCKAVDIGPGL

**SEQ ID NO:78 (Id-24C2-HT7 sandwich fusion nucleotide)**
atgcttggtctgtcggagcaaagcgtgtccatctcgcgctgcgctgggacgcgcctgcccgcctt
gctggacgagcagcaggtgaacgtcctgctctacgacatgaacggctgctactcacgcctcaagg
agctggtgcccaccctgccccagaaccgcaaagtgagcaaggtggagatcctgcagcatgtaatc
gactacatcagggacctgcagctggagctgaactcggagtctgaagtcgggaccaccggaggccg
gggactgcctgtccgcgccccgctcagcaccctgaacggcgagatcagtgccttggcggccgagg
cggcatgtgttccagccgacgatcgcatcttgtgtcgcgtttctcttgagaatctttatttcag
gcgtctggaggtggtggcggagcgatcgccatggtgtttacactcgaagatttcgtaggggactg
gcagcagacagccggctacaacctggaccaagtccttgagcagggcggtctgtccagtttgtttc
agaatctcggggtgtccgtaactccgatccaaaagattgtcctgagcggtgaaaacggcctgaag
atcgacatccatgtcatcatcccgtatgaaggtctgagcggctatcagatgggccagatcgaaaa
aatttttaaggtggtgtaccctgtggatgatcatcactttaaggtgattctgcactatggcacac
tggtaatcgacggggttacgccgaacatgatcgactatttcggacggccgtatgaaggcatcgcc
gtgttcgacggcaaaaagatcactgtaaccgggaccctgtggaacggcaacaaaattatcgacga
gcgcctgatcaaccccgacggctccctgctgttccgcgtaaccatcaacggagtgaccggctggc
ggctgtgcgagcgcattttggcgggatatctcgagccaaccactgaggatctgtactttcagagc
gataacgatggatccgaaatcggtactggctttccattcgacccccattatgtggaagtcctggg
cgagcgcatgcactacgtcgatgttggtccgcgcgatggcacccctgtgctgttcctgcacggta
acccgacctcctcctacgtgtggcgcaacatcatcccgcatgttgcaccgacccatcgctgcatt
gctccagacctgatcggtatgggcaaatccgacaaaccagacctgggttatttcttcgacgacca
cgtccgcttcatggatgccttcatcgaagccctgggtctggaagaggtcgtcctggtcattcacg
actggggctccgctctgggtttccactgggccaagcgcaatccagagcgcgtcaaaggtattgca
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ccaggccttccgcaccaccgacgtcggccgcaagctgatcatcgatcagaacgttttatcgagg
gtacgctgccgatgggtgtcgtccgcccgctgactgaagtcgagatggaccattaccgcgagccg
ttcctgaatcctgttgaccgcgagccactgtggcgcttcccaaacgagctgccaatcgccggtga
gccagcgaacatcgtcgcgctggtcgaagaatacatggactggctgcaccagtcccctgtcccga
agctgctgttctggggcaccccaggcgttctgatcccaccggccgaagccgctcgcctggccaaa
agcctgcctaactgcaaggctgtggacatcggcccgggtctgaatctgctgcaagaagacaaccc
ggacctgatcggcagcgagatcgcgcgctggctgtctactctggagatttccggt

**SEQ ID NO:79 (Id-24C2-HT7 sandwich fusion protein)**
MLGLSEQSVSISRCAGTRLPALLDEQQVNVLLLYDMNGCYSRLKELVPTLPQNRKVSKVEILQHVI
DYIRDLQLELNSESEVGTTGGRGLPVRAPLSTLNGEISALAAEAACVPADDRILCRVSLENLYFQ

ASGGGGGAIAMVFTLEDFVGDWQQTAGYNLDQVLEQGGLSSLFQNLGVSVTPIQKIVLSGENGLK
IDIHVIIPYEGLSGYQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIA
VFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILAGYLEPTTEDLYFQS
DNDGSEIGTGFPFDPHYVEVLGERMHYVDVGPRDGTPVLFLHGNPTSSYVWRNIIPHVAPTHRCI
APDLIGMGKSDKPDLGYFFDDHVRFMDAFIEALGLEEVVLVIHDWGSALGFHWAKRNPERVKGIA
FMEFIRPIPTWDEWPEFARETFQAFRTTDVGRKLIIDQNVFIEGTLPMGVVRPLTEVEMDHYREP
FLNPVDREPLWRFPNELPIAGEPANIVALVEEYMDWLHQSPVPKLLFWGTPGVLIPPAEAARLAK
SLPNCKAVDIGPGLNLLQEDNPDLIGSEIARWLSTLEISG

**SEQ ID NO:80 (1F7 (NF) nucleotide)**
ATGGTGTTTACACTCGAAGATTTCGTAGGGGACTGGCGGCAGACAGCCGGCTACAACCTGGACCA
AGTCCTTGAGCAGGGCGGTCTGTCCAGTTTGTTTCAGAATCTCGGGGTGTCCGTAACACCGATCC
AAAGGATTGTCCTGAGCGGTGAAAACGGCCTGAAGATCGACATCCATGTCATCATCCCGTATGAA
GGTCTGAGCGGCGATCAGATGGGCCAGATCGAAAAAATTTTTAAGGTGGTGTACCCTGTGGATGA
TCATCACTTTAAGGTGATTCTGCACTATGGCACACTGGTAATCGACGGGGTTACGCCGAACATGA
TCGACTATTTCGGACGGCCGTATGAAGGCATCGCCGTGTTCGACGGCAAAAAGATCACTGTAACC
GGGACCCTGTGGAACGGCAACAAAATTATCGACGAGCGCCTGATCAACCCCGACGGCTCCCTGCT
GTTCCGCGTAACCATCAACGGAGTGACCGGCTGGCGGCTGTGCGAGCGCATTTTGGCGGGA

**SEQ ID NO:81 (1F7 (NF) protein)**
MVFTLEDFVGDWRQTAGYNLDQVLEQGGLSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYE
GLSGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVT
GTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILAG

**SEQ ID NO:82 (15H1 (NF) nucleotide)**
ATGGTGTTTACACTCGAAGATTTCGTAGGGGACTGGCGGCAGACAGCCGGCTACAACCTGGATCA
AGTCCTTGAGCAGGGCGGTCTGTCCAGTTTGTTTCAGAATCTCGGGGTGTCCGTAACACCGATCC
AAAAGATTGTCCTGAGCGGTGAAAACGGCCTGAAGATCGACATCCATGTCATCATCCCGTATGAA
GGTCTGAACGGCTATCAGATGGGCCAGATCGAAAAAATTTTTAAGGTGGTGTACCCTGTGGATGA
TCATCACTTTAAGGTGATTCTGCACTATGGCACACTGGTAATCGACGGGGTTACGCCGAACATGA
TCGACTATTTCGGACGGCCGTATGAAGGCATCGCCGTGTTCGACGGCAAAAAGATCACTGTAACC
GGGACCCTGTGGAACGGCAACAAAATTATCGACGAGCGCCTGATCAACCCCGACGGCTCCCTGCT
GTTCCGCGTAACCATCAACGGAGTGACCGGCTGGCGGCTGTGCGAGCGCATTTTGGCGGGA

**SEQ ID NO:83 (15H1 (NF) protein)**
MVFTLEDFVGDWRQTAGYNLDQVLEQGGLSSLFQNLGVSVTPIQKIVLSGENGLKIDIHVIIPYE
GLNGYQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVT
GTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILAG

**SEQ ID NO:84 (Id-1F7-HT7 sandwich fusion nucleotide)**
atgcttggtctgtcggagcaaagcgtgtccatctcgcgctgcgctgggacgcgcctgcccgcctt
gctggacgagcagcaggtgaacgtcctgctctacgacatgaacggctgctactcacgcctcaagg
agctggtgcccaccctgccccagaaccgcaaagtgagcaaggtggagatcctgcagcatgtaatc
gactacatcagggacctgcagctggagctgaactcggagtctgaagtcgggaccaccggaggccg
gggactgcctgtccgcgccccgctcagcaccctgaacggcgagatcagtgccttggcggccgagg
cggcatgtgttccagccgacgatcgcatcttgtgtcgcgtttctcttgagaatctttatttttcag
gcgtctggaggtggtggcggagcgatcgccatggtgtttacactcgaagatttcgtaggggactg
gcggcagacagccggctacaacctggaccaagtccttgagcagggcggtctgtccagtttgtttc
agaatctcggggtgtccgtaacaccgatccaaaggattgtcctgagcggtgaaaacggcctgaag
atcgacatccatgtcatcatcccgtatgaaggtctgagcggcgatcagatgggccagatcgaaaa
aatttttaaggtggtgtaccctgtggatgatcatcactttaaggtgattctgcactatggcacac
tggtaatcgacggggttacgccgaacatgatcgactatttcggacggccgtatgaaggcatcgcc
gtgttcgacggcaaaaagatcactgtaaccgggaccctgtggaacggcaacaaaattatcgacga

gcgcctgatcaaccccgacggctccctgctgttccgcgtaaccatcaacggagtgaccggctggc
ggctgtgcgagcgcattttggcgggatatctcgagccaaccactgaggatctgtactttcagagc
gataacgatggatccgaaatcggtactggctttccattcgacccccattatgtggaagtcctggg
cgagcgcatgcactacgtcgatgttggtccgcgcgatggcacccctgtgctgttcctgcacggta
acccgacctcctcctacgtgtggcgcaacatcatcccgcatgttgcaccgacccatcgctgcatt
gctccagacctgatcggtatgggcaaatccgacaaaccagacctgggttatttcttcgacgacca
cgtccgcttcatggatgccttcatcgaagccctgggtctggaagaggtcgtcctggtcattcacg
actggggctccgctctgggtttccactgggccaagcgcaatccagagcgcgtcaaaggtattgca
tttatggagttcatccgccctatcccgacctgggacgaatggccagaatttgcccgcgagacctt
ccaggccttccgcaccaccgacgtcggccgcaagctgatcatcgatcagaacgtttttatcgagg
gtacgctgccgatgggtgtcgtccgcccgctgactgaagtcgagatggaccattaccgcgagccg
ttcctgaatcctgttgaccgcgagccactgtggcgcttcccaaacgagctgccaatcgccggtga
gccagcgaacatcgtcgcgctggtcgaagaatacatggactggctgcaccagtcccctgtcccga
agctgctgttctggggcaccccaggcgttctgatcccaccggccgaagccgctcgcctggccaaa
agcctgcctaactgcaaggctgtggacatcggcccgggtctgaatctgctgcaagaagacaaccc
ggacctgatcggcagcgagatcgcgcgctggctgtctactctggag

**SEQ ID NO:85 (Id-1F7-HT7 sandwich fusion protein)**

MLGLSEQSVSISRCAGTRLPALLDEQQVNVLLYDMNGCYSRLKELVPTLPQNRKVSKVEILQHVI
DYIRDLQLELNSESEVGTTGGRGLPVRAPLSTLNGEISALAAEAACVPADDRILCRVSLENLYFQ
ASGGGGGAIAMVFTLEDFVGDWRQTAGYNLDQVLEQGGLSSLFQNLGVSVTPIQRIVLSGENGLK
IDIHVIIPYEGLSGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIA
VFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILAGYLEPTTEDLYFQS
DNDGSEIGTGFPFDPHYVEVLGERMHYVDVGPRDGTPVLFLHGNPTSSYVWRNIIPHVAPTHRCI
APDLIGMGKSDKPDLGYFFDDHVRFMDAFIEALGLEEVVLVIHDWGSALGFHWAKRNPERVKGIA
FMEFIRPIPTWDEWPEFARETFQAFRTTDVGRKLIIDQNVFIEGTLPMGVVRPLTEVEMDHYREP
FLNPVDREPLWRFPNELPIAGEPANIVALVEEYMDWLHQSPVPKLLFWGTPGVLIPPAEAARLAK
SLPNCKAVDIGPGLNLLQEDNPDLIGSEIARWLSTLEISG

**SEQ ID NO:86 (Id-15H1-HT7 sandwich fusion nucleotide)**

atgcttggtctgtcggagcaaagcgtgtccatctcgcgctgcgctgggacgcgcctgcccgcctt
gctggacgagcagcaggtgaacgtcctgctctacgacatgaacggctgctactcacgcctcaagg
agctggtgcccaccctgccccagaaccgcaaagtgagcaaggtggagatcctgcagcatgtaatc
gactacatcagggacctgcagctggagctgaactcggagtctgaagtcgggaccaccggaggccg
gggactgcctgtccgcgccccgctcagcaccctgaacggcgagatcagtgccttggcggccgagg
cggcatgtgttccagccgacgatcgcatcttgtgtcgcgtttctcttgagaatctttatttttcag
gcgtctggaggtggtggcggagcgatcgccatggtgtttacactcgaagatttcgtaggggactg
gcggcagacagccggctacaacctggatcaagtccttgagcagggcggtctgtccagtttgtttc
agaatctcggggtgtccgtaacaccgatccaaaagattgtcctgagcggtgaaaacggcctgaag
atcgacatccatgtcatcatcccgtatgaaggtctgaacggctatcagatgggccagatcgaaaa
aatttttaaggtggtgtaccctgtggatgatcatcactttaaggtgattctgcactatggcacac
tggtaatcgacggggttacgccgaacatgatcgactatttcggacggccgtatgaaggcatcgcc
gtgttcgacggcaaaaagatcactgtaaccgggaccctgtggaacggcaacaaaattatcgacga
gcgcctgatcaaccccgacggctccctgctgttccgcgtaaccatcaacggagtgaccggctggc
ggctgtgcgagcgcattttggcgggatatctcgagccaaccactgaggatctgtactttcagagc
gataacgatggatccgaaatcggtactggctttccattcgacccccattatgtggaagtcctggg
cgagcgcatgcactacgtcgatgttggtccgcgcgatggcacccctgtgctgttcctgcacggta
acccgacctcctcctacgtgtggcgcaacatcatcccgcatgttgcaccgacccatcgctgcatt
gctccagacctgatcggtatgggcaaatccgacaaaccagacctgggttatttcttcgacgacca
cgtccgcttcatggatgccttcatcgaagccctgggtctggaagaggtcgtcctggtcattcacg
actggggctccgctctgggtttccactgggccaagcgcaatccagagcgcgtcaaaggtattgca
tttatggagttcatccgccctatcccgacctgggacgaatggccagaatttgcccgcgagacctt
ccaggccttccgcaccaccgacgtcggccgcaagctgatcatcgatcagaacgtttttatcgagg

gtacgctgccgatgggtgtcgtccgcccgctgactgaagtcgagatggaccattaccgcgagccg
ttcctgaatcctgttgaccgcgagccactgtggcgcttcccaaacgagctgccaatcgccggtga
gccagcgaacatcgtcgcgctggtcgaagaatacatggactggctgcaccagtcccctgtcccga
agctgctgttctggggcaccccaggcgttctgatcccaccggccgaagccgctcgcctggccaaa
agcctgcctaactgcaaggctgtggacatcggcccgggtctgaatctgctgcaagaagacaaccc
ggacctgatcggcagcgagatcgcgcgctggctgtctactctggagatttccggt

**SEQ ID NO:87 (Id-15H1-HT7 sandwich fusion protein)**
MLGLSEQSVSISRCAGTRLPALLDEQQVNVLLYDMNGCYSRLKELVPTLPQNRKVSKVEILQHVI
DYIRDLQLELNSESEVGTTGGRGLPVRAPLSTLNGEISALAAEAACVPADDRILCRVSLENLYFQ
ASGGGGGAIAMVFTLEDFVGDWRQTAGYNLDQVLEQGGLSSLFQNLGVSVTPIQKIVLSGENGLK
IDIHVIIPYEGLNGYQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIA
VFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILAGYLEPTTEDLYFQS
DNDGSEIGTGFPFDPHYVEVLGERMHYVDVGPRDGTPVLFLHGNPTSSYVWRNIIPHVAPTHRCI
APDLIGMGKSDKPDLGYFFDDHVRFMDAFIEALGLEEVVLVIHDWGSALGFHWAKRNPERVKGIA
FMEFIRPIPTWDEWPEFARETFQAFRTTDVGRKLIIDQNVFIEGTLPMGVVRPLTEVEMDHYREP
FLNPVDREPLWRFPNELPIAGEPANIVALVEEYMDWLHQSPVPKLLFWGTPGVLIPPAEAARLAK
SLPNCKAVDIGPGLNLLQEDNPDLIGSEIARWLSTLEISG

**SEQ ID NO:88 (9B8 opt+K33N+L27V+T39T+K43R+Y68D nucleotide)**
Atggtgtttacactcgaagatttcgtaggggactggcggcagacagccggctacaacctggacca
agtccttgagcagggcggtgtgtccagtttgtttcagaatctcggggtgtccgtaactccgatcc
aaaggattgtcctgagcggtgaaaacggcctgaagatcgacatccatgtcatcatcccgtatgaa
ggtctgagcggcgatcagatgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatga
tcatcactttaaggtgattctgcactatggcacactggtaatcgacggggttacgccgaacatga
tcgactatttcggacggccgtatgaaggcatcgccgtgttcgacggcaaaaagatcactgtaacc
gggaccctgtggaacggcaacaaaattatcgacgagcgcctgatcaaccccgacggctccctgct
gttccgcgtaaccatcaacggagtgaccggctggcggctgtgcgagcgcattttggcg

**SEQ ID NO:89 (9B8 opt+K33N+L27V+T39T+K43R+Y68D protein)**
MVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYE
GLSGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVT
GTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILA

**SEQ ID NO:90 (9B8 opt+K33N+L27V+T39T+K43R+Y68D sandwich fusion nucleotide)**

atgcttggtctgtcggagcaaagcgtgtccatctcgcgctgcgctgggacgcgcctgcccgcctt
gctggacgagcagcaggtgaacgtcctgctctacgacatgaacggctgctactcacgcctcaagg
agctggtgcccaccctgccccagaaccgcaaagtgagcaaggtggagatcctgcagcatgtaatc
gactacatcagggacctgcagctggagctgaactcggagtctgaagtcgggaccaccggaggccg
gggactgcctgtccgcgccccgctcagcaccctgaacggcgagatcagtgccttggcggccgagg
cggcatgtgttccagccgacgatcgcatcttgtgtcgcgtttctcttgagaatctttatttcag
gcgtctggaggtggtggcggagcgatcgccatggtgtttacactcgaagatttcgtaggggactg
gcggcagacagccggctacaacctggaccaagtccttgagcagggcggtgtgtccagtttgtttc
agaatctcggggtgtccgtaactccgatccaaaggattgtcctgagcggtgaaaacggcctgaag
atcgacatccatgtcatcatcccgtatgaaggtctgagcggcgatcagatgggccagatcgaaaa
aatttttaaggtggtgtaccctgtggatgatcatcactttaaggtgattctgcactatggcacac
tggtaatcgacggggttacgccgaacatgatcgactatttcggacggccgtatgaaggcatcgcc
gtgttcgacggcaaaaagatcactgtaaccgggaccctgtggaacggcaacaaaattatcgacga
gcgcctgatcaaccccgacggctccctgctgttccgcgtaaccatcaacggagtgaccggctggc
ggctgtgcgagcgcattttggcgggatatctcgagccaaccactgaggatctgtactttcagagc
gataacgatggatccgaaatcggtactggctttccattcgacccccattatgtggaagtcctggg
cgagcgcatgcactacgtcgatgttggtccgcgcgatggcacccctgtgctgttcctgcacggta
acccgacctcctcctacgtgtggcgcaacatcatcccgcatgttgcaccgacccatcgctgcatt
gctccagacctgatcggtatgggcaaatccgacaaaccagacctgggttatttcttcgacgacca
cgtccgcttcatggatgccttcatcgaagccctgggtctggaagaggtcgtcctggtcattcacg
actggggctccgctctgggtttccactgggccaagcgcaatccagagcgcgtcaaaggtattgca
tttatggagttcatccgccctatcccgacctgggacgaatggccagaatttgcccgcgagacctt
ccaggccttccgcaccaccgacgtcggccgcaagctgatcatcgatcagaacgtttttatcgagg
gtacgctgccgatgggtgtcgtccgcccgctgactgaagtcgagatggaccattaccgcgagccg
ttcctgaatcctgttgaccgcgagccactgtggcgcttcccaaacgagctgccaatcgccggtga
gccagcgaacatcgtcgcgctggtcgaagaatacatggactggctgcaccagtcccctgtcccga
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agcctgcctaactgcaaggctgtggacatcggcccgggtctgaatctgctgcaagaagacaaccc
ggacctgatcggcagcgagatcgcgcgctggctgtctactctggagatttccggt

**SEQ ID NO:91 (9B8 opt+K33N+L27V+T39T+K43R+Y68D sandwich fusion protein)**

MLGLSEQSVSISRCAGTRLPALLDEQQVNVLLYDMNGCYSRLKELVPTLPQNRKVSKVEILQHVI
DYIRDLQLELNSESEVGTTGGRGLPVRAPLSTLNGEISALAAEAACVPADDRILCRVSLENLYFQ
ASGGGGGAIAMVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLK
IDIHVIIPYEGLSGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIA
VFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILAGYLEPTTEDLYFQS
DNDGSEIGTGFPFDPHYVEVLGERMHYVDVGPRDGTPVLFLHGNPTSSYVWRNIIPHVAPTHRCI
APDLIGMGKSDKPDLGYFFDDHVRFMDAFIEALGLEEVVLVIHDWGSALGFHWAKRNPERVKGIA
FMEFIRPIPTWDEWPEFARETFQAFRTTDVGRKLIIDQNVFIEGTLPMGVVRPLTEVEMDHYREP
FLNPVDREPLWRFPNELPIAGEPANIVALVEEYMDWLHQSPVPKLLFWGTPGVLIPPAEAARLAK
SLPNCKAVDIGPGLNLLQEDNPDLIGSEIARWLSTLEISG

**SEQ ID NO:92 (9B8 opt+K33N+T39T+K43R+Y68D nucleotide)**

Atggtgtttacactcgaagatttcgtaggggactggcggcagacagccggctacaacctggacca
agtccttgagcagggcggtctgtccagtttgtttcagaatctcggggtgtccgtaactccgatcc
aaaggattgtcctgagcggtgaaaacggcctgaagatcgacatccatgtcatcatcccgtatgaa
ggtctgagcggcgatcagatgggccagatcgaaaaaattttaaggtggtgtaccctgtggatga
tcatcactttaaggtgattctgcactatggcacactggtaatcgacggggttacgccgaacatga
tcgactatttcggacggccgtatgaaggcatcgccgtgttcgacggcaaaaagatcactgtaacc

gggaccctgtggaacggcaacaaaattatcgacgagcgcctgatcaaccccgacggctccctgct
gttccgcgtaaccatcaacggagtgaccggctggcggctgtgcgagcgcattttggcg

**SEQ ID NO:93 (9B8 opt+K33N+T39T+K43R+Y68D protein)**

MVFTLEDFVGDWRQTAGYNLDQVLEQGGLSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYE
GLSGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVT
GTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILA

**SEQ ID NO:94 (9B8 opt+K33N+T39T+K43R+Y68D sandwich fusion nucleotide)**

atgcttggtctgtcggagcaaagcgtgtccatctcgcgctgcgctgggacgcgcctgcccgcctt
gctggacgagcagcaggtgaacgtcctgctctacgacatgaacggctgctactcacgcctcaagg
agctggtgcccaccctgccccagaaccgcaaagtgagcaaggtggagatcctgcagcatgtaatc
gactacatcagggacctgcagctggagctgaactcggagtctgaagtcgggaccaccggaggccg
gggactgcctgtccgcgccccgctcagcaccctgaacggcgagatcagtgccttggcggccgagg
cggcatgtgttccagccgacgatcgcatcttgtgtcgcgtttctcttgagaatctttatttttcag
gcgtctggaggtggtggcggagcgatcgccatggtgtttacactcgaagatttcgtaggggactg
gcggcagacagccggctacaacctggaccaagtccttgagcagggcggtctgtccagtttgtttc
agaatctcggggtgtccgtaactccgatccaaaggattgtcctgagcggtgaaaacggcctgaag
atcgacatccatgtcatcatcccgtatgaaggtctgagcggcgatcagatgggccagatcgaaaa
aatttttaaggtggtgtaccctgtggatgatcatcactttaaggtgattctgcactatggcacac
tggtaatcgacggggttacgccgaacatgatcgactatttcggacggccgtatgaaggcatcgcc
gtgttcgacggcaaaaagatcactgtaaccgggaccctgtggaacggcaacaaaattatcgacga
gcgcctgatcaaccccgacggctccctgctgttccgcgtaaccatcaacggagtgaccggctggc
ggctgtgcgagcgcattttggcgggatatctcgagccaaccactgaggatctgtactttcagagc
gataacgatggatccgaaatcggtactggctttccattcgacccccattatgtggaagtcctggg
cgagcgcatgcactacgtcgatgttggtccgcgcgatggcacccctgtgctgttcctgcacggta
acccgacctcctcctacgtgtggcgcaacatcatcccgcatgttgcaccgacccatcgctgcatt
gctccagacctgatcggtatgggcaaatccgacaaaccagacctgggttatttcttcgacgacca
cgtccgcttcatggatgccttcatcgaagccctgggtctggaagaggtcgtcctggtcattcacg
actggggctccgctctgggtttccactgggccaagcgcaatccagagcgcgtcaaaggtattgca
tttatggagttcatccgccctatcccgacctgggacgaatggccagaatttgcccgcgagacctt
ccaggccttccgcaccaccgacgtcggccgcaagctgatcatcgatcagaacgttttatcgagg
gtacgctgccgatgggtgtcgtccgcccgctgactgaagtcgagatggaccattaccgcgagccg
ttcctgaatcctgttgaccgcgagccactgtggcgcttcccaaacgagctgccaatcgccggtga
gccagcgaacatcgtcgcgctggtcgaagaatacatggactggctgcaccagtcccctgtcccga
agctgctgttctggggcaccccaggcgttctgatcccaccggccgaagccgctcgcctggccaaa
agcctgcctaactgcaaggctgtggacatcggcccgggtctgaatctgctgcaagaagacaaccc
ggacctgatcggcagcgagatcgcgcgctggctgtctactctggagatttccggt

**SEQ ID NO:95 (9B8 opt+K33N+T39T+K43R+Y68D sandwich fusion protein)**

MLGLSEQSVSISRCAGTRLPALLDEQQVNVLLYDMNGCYSRLKELVPTLPQNRKVSKVEILQHVI
DYIRDLQLELNSESEVGTTGGRGLPVRAPLSTLNGEISALAAEAACVPADDRILCRVSLENLYFQ
ASGGGGGAIAMVFTLEDFVGDWRQTAGYNLDQVLEQGGLSSLFQNLGVSVTPIQRIVLSGENGLK
IDIHVIIPYEGLSGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIA
VFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILAGYLEPTTEDLYFQS
DNDGSEIGTGFPFDPHYVEVLGERMHYVDVGPRDGTPVLFLHGNPTSSYVWRNIIPHVAPTHRCI
APDLIGMGKSDKPDLGYFFDDHVRFMDAFIEALGLEEVVLVIHDWGSALGFHWAKRNPERVKGIA
FMEFIRPIPTWDEWPEFARETFQAFRTTDVGRKLIIDQNVFIEGTLPMGVVRPLTEVEMDHYREP
FLNPVDREPLWRFPNELPIAGEPANIVALVEEYMDWLHQSPVPKLLFWGTPGVLIPPAEAARLAK
SLPNCKAVDIGPGLNLLQEDNPDLIGSEIARWLSTLEISG

**SEQ ID NO:96 (CRE)**

GCACCAGACAGTGACGTCAGCTGCCAGATCCCATGGCCGTCATACTGTGACGTCTTTCAGACACC
CCTTGACGTCAATGGGAGAACA

**SEQ ID NO:97 (Nucleotide CP 84 no linker)**

Atggatgatcatcactttaaggtgattctgcactatggcacactggtaatcgacggggttacgcc
gaacatgatcgactatttcggacggccgtatgaaggcatcgccgtgttcgacggcaaaaagatca
ctgtaaccgggaccctgtggaacggcaacaaaattatcgacgagcgcctgatcaaccccgacggc
tccctgctgttccgcgtaaccatcaacggagtgaccggctggcggctgtgcgagcgcattttggc
gatggtgtttacactcgaagatttcgtaggggactggcggcagacagccggctacaacctggacc
aagtccttgagcagggcggtgtgtccagtttgtttcagaatctcggggtgtccgtaactccgatc
caaaggattgtcctgagcggtgaaaacggcctgaagatcgacatccatgtcatcatcccgtatga
aggtctgagcggcgatcagatgggccagatcgaaaaaatttttaaggtggtgtaccctgtg

**SEQ ID NO:98 (Protein CP 84 no linker)**

MDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDG
SLLFRVTINGVTGWRLCERILAMVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPI
QRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEKIFKVVYPV

**SEQ ID NO:99 (Nucleotide CP 84 5AA linker)**

Atggatgatcatcactttaaggtgattctgcactatggcacactggtaatcgacggggttacgcc
gaacatgatcgactatttcggacggccgtatgaaggcatcgccgtgttcgacggcaaaaagatca
ctgtaaccgggaccctgtggaacggcaacaaaattatcgacgagcgcctgatcaaccccgacggc
tccctgctgttccgcgtaaccatcaacggagtgaccggctggcggctgtgcgagcgcattttggc
ggggagctccggtggaatggtgtttacactcgaagatttcgtaggggactggcggcagacagccg
gctacaacctggaccaagtccttgagcagggcggtgtgtccagtttgtttcagaatctcggggtg
tccgtaactccgatccaaaggattgtcctgagcggtgaaaacggcctgaagatcgacatccatgt
catcatcccgtatgaaggtctgagcggcgatcagatgggccagatcgaaaaaatttttaaggtgg
tgtaccctgtg

**SEQ ID NO:100 (Protein CP 84 5AA linker)**

MDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDG
SLLFRVTINGVTGWRLCERILAGSSGGMVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGV
SVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEKIFKVVYPV

**SEQ ID NO:101 (Nucleotide CP 84 10AA linker)**

Atggatgatcatcactttaaggtgattctgcactatggcacactggtaatcgacggggttacgcc
gaacatgatcgactatttcggacggccgtatgaaggcatcgccgtgttcgacggcaaaaagatca
ctgtaaccgggaccctgtggaacggcaacaaaattatcgacgagcgcctgatcaaccccgacggc
tccctgctgttccgcgtaaccatcaacggagtgaccggctggcggctgtgcgagcgcattttggc
gggaagttctggtggagggagctccggtggaatggtgtttacactcgaagatttcgtaggggact
ggcggcagacagccggctacaacctggaccaagtccttgagcagggcggtgtgtccagtttgttt
cagaatctcggggtgtccgtaactccgatccaaaggattgtcctgagcggtgaaaacggcctgaa
gatcgacatccatgtcatcatcccgtatgaaggtctgagcggcgatcagatgggccagatcgaaa
aaatttttaaggtggtgtaccctgtg

**SEQ ID NO:102 (Protein CP 84 10AA linker)**

MDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDG
SLLFRVTINGVTGWRLCERILAGSSGGGSSGGMVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLF
QNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEKIFKVVYPV

**SEQ ID NO:103 (Nucleotide CP 84 20AA linker)**

Atggatgatcatcactttaaggtgattctgcactatggcacactggtaatcgacggggttacgcc
gaacatgatcgactatttcggacggccgtatgaaggcatcgccgtgttcgacggcaaaaagatca
ctgtaaccgggaccctgtggaacggcaacaaaattatcgacgagcgcctgatcaaccccgacggc
tccctgctgttccgcgtaaccatcaacggagtgaccggctggcggctgtgcgagcgcattttggc
gggaagttctggtggagggagctccggtggaggaagttctggtggagggagctccggtggaatgg
tgtttacactcgaagatttcgtaggggactggcggcagacagccggctacaacctggaccaagtc
cttgagcagggcggtgtgtccagtttgtttcagaatctcggggtgtccgtaactccgatccaaag
gattgtcctgagcggtgaaaacggcctgaagatcgacatccatgtcatcatcccgtatgaaggtc
tgagcggcgatcagatgggccagatcgaaaaaattttaaggtggtgtaccctgtg

**SEQ ID NO:104 (Protein CP 84 20AA linker)**
MDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDG
SLLFRVTINGVTGWRLCERILAGSSGGGSSGGGSSGGGSSGGMVFTLEDFVGDWRQTAGYNLDQV
LEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEKIFKVVYPV

**SEQ ID NO:105 (Nucleotide CP 95 no linker)**
Atgggcacactggtaatcgacggggttacgccgaacatgatcgactatttcggacggccgtatga
aggcatcgccgtgttcgacggcaaaaagatcactgtaaccgggaccctgtggaacggcaacaaaa
ttatcgacgagcgcctgatcaaccccgacggctccctgctgttccgcgtaaccatcaacggagtg
accggctggcggctgtgcgagcgcattttggcgatggtgtttacactcgaagatttcgtagggga
ctggcggcagacagccggctacaacctggaccaagtccttgagcagggcggtgtgtccagtttgt
ttcagaatctcggggtgtccgtaactccgatccaaaggattgtcctgagcggtgaaaacggcctg
aagatcgacatccatgtcatcatcccgtatgaaggtctgagcggcgatcagatgggccagatcga
aaaaatttttaaggtggtgtaccctgtggatgatcatcactttaaggtgattctgcactat

**SEQ ID NO:106 (Protein CP 95 no linker)**
MGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGV
TGWRLCERILAMVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGL
KIDIHVIIPYEGLSGDQMGQIEKIFKVVYPVDDHHFKVILHY

**SEQ ID NO:107 (Nucleotide CP 95 5AA linker)**
Atgggcacactggtaatcgacggggttacgccgaacatgatcgactatttcggacggccgtatga
aggcatcgccgtgttcgacggcaaaaagatcactgtaaccgggaccctgtggaacggcaacaaaa
ttatcgacgagcgcctgatcaaccccgacggctccctgctgttccgcgtaaccatcaacggagtg
accggctggcggctgtgcgagcgcattttggcggggagctccggtggaatggtgtttacactcga
agatttcgtaggggactggcggcagacagccggctacaacctggaccaagtccttgagcagggcg
gtgtgtccagtttgtttcagaatctcggggtgtccgtaactccgatccaaaggattgtcctgagc
ggtgaaaacggcctgaagatcgacatccatgtcatcatcccgtatgaaggtctgagcggcgatca
gatgggccagatcgaaaaaattttaaggtggtgtaccctgtggatgatcatcactttaaggtga
ttctgcactat

**SEQ ID NO:108 (Protein CP 95 5AA linker)**
MGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGV
TGWRLCERILAGSSGGMVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLS
GENGLKIDIHVIIPYEGLSGDQMGQIEKIFKVVYPVDDHHFKVILHY

**SEQ ID NO:109 (Nucleotide CP 95 10AA linker)**
Atgggcacactggtaatcgacggggttacgccgaacatgatcgactatttcggacggccgtatga
aggcatcgccgtgttcgacggcaaaaagatcactgtaaccgggaccctgtggaacggcaacaaaa
ttatcgacgagcgcctgatcaaccccgacggctccctgctgttccgcgtaaccatcaacggagtg
accggctggcggctgtgcgagcgcattttggcgggaagttctggtggagggagctccggtggaat
ggtgtttacactcgaagatttcgtaggggactggcggcagacagccggctacaacctggaccaag
tccttgagcagggcggtgtgtccagtttgtttcagaatctcggggtgtccgtaactccgatccaa

aggattgtcctgagcggtgaaaacggcctgaagatcgacatccatgtcatcatcccgtatgaagg
tctgagcggcgatcagatgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatgatc
atcactttaaggtgattctgcactat

**SEQ ID NO:110 (Protein CP 95 10AA linker)**
MGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGV
TGWRLCERILAGSSGGGSSGGMVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQ
RIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEKIFKVVYPVDDHHFKVILHY

**SEQ ID NO:111 (Nucleotide CP 95 20AA linker)**
Atgggcacactggtaatcgacggggttacgccgaacatgatcgactatttcggacggccgtatga
aggcatcgccgtgttcgacggcaaaaagatcactgtaaccgggaccctgtggaacggcaacaaaa
ttatcgacgagcgcctgatcaaccccgacggctccctgctgttccgcgtaaccatcaacggagtg
accggctggcggctgtgcgagcgcattttggcgggaagttctggtggagggagctccggtggagg
aagttctggtggagggagctccggtggaatggtgtttacactcgaagatttcgtaggggactggc
ggcagacagccggctacaacctggaccaagtccttgagcagggcggtgtgtccagtttgtttcag
aatctcggggtgtccgtaactccgatccaaaggattgtcctgagcggtgaaaacggcctgaagat
cgacatccatgtcatcatcccgtatgaaggtctgagcggcgatcagatgggccagatcgaaaaaa
tttttaaggtggtgtaccctgtggatgatcatcactttaaggtgattctgcactat

**SEQ ID NO:112 (Protein CP 95 20AA linker)**
MGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGV
TGWRLCERILAGSSGGGSSGGGSSGGGSSGGMVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQ
NLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEKIFKVVYPVDDHHFKVILHY

**SEQ ID NO:113 (Linker)**
$(GSGG)_N$

**SEQ ID NO:114 (L27V CP 5 TEV)**
Atggatttcgtaggggactggcggcagacagccggctacaacctggaccaagtccttgagcaggg
cggtgtgtccagtttgtttcagaatctcggggtgtccgtaactccgatccaaaggattgtcctga
gcggtgaaaacggcctgaagatcgacatccatgtcatcatcccgtatgaaggtctgagcggcgat
cagatgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatgatcatcactttaaggt
gattctgcactatggcacactggtaatcgacggggttacgccgaacatgatcgactatttcggac
ggccgtatgaaggcatcgccgtgttcgacggcaaaaagatcactgtaaccgggaccctgtggaac
ggcaacaaaattatcgacgagcgcctgatcaaccccgacggctccctgctgttccgcgtaaccat
caacggagtgaccggctggcggctgtgcgagcgcattttggcgggaagttctggtggaggaagtt
ctggtggagagcctactactgagaacttgtacttccagagcgataacggaagttctggtggagga
agttctggtggaatggtgtttacactcgaa

**SEQ ID NO:115 (L27V CP 5 TEV)**
MDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGD
QMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWN
GNKIIDERLINPDGSLLFRVTINGVTGWRLCERILAGSSGGGSSGGEPTTENLYFQSDNGSSGGG
SSGGMVFTLE

**SEQ ID NO:116 (L27V CP 6 TEV)**
atgttcgtaggggactggcggcagacagccggctacaacctggaccaagtccttgagcagggcgg
tgtgtccagtttgtttcagaatctcggggtgtccgtaactccgatccaaaggattgtcctgagcg
gtgaaaacggcctgaagatcgacatccatgtcatcatcccgtatgaaggtctgagcggcgatcag
atgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatgatcatcactttaaggtgat
tctgcactatggcacactggtaatcgacggggttacgccgaacatgatcgactatttcggacggc
cgtatgaaggcatcgccgtgttcgacggcaaaaagatcactgtaaccgggaccctgtggaacggc

aacaaaattatcgacgagcgcctgatcaaccccgacggctccctgctgttccgcgtaaccatcaa
cggagtgaccggctggcggctgtgcgagcgcattttggcgggaagttctggtggaggaagttctg
gtggagagcctactactgagaacttgtacttccagagcgataacggaagttctggtggaggaagt
tctggtggaatggtgtttacactcgaagat

**SEQ ID NO:117 (L27V CP 6 TEV)**
MFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQ
MGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNG
NKIIDERLINPDGSLLFRVTINGVTGWRLCERILAGSSGGGSSGGEPTTENLYFQSDNGSSGGGS
SGGMVFTLED

**SEQ ID NO:118 (L27V CP 7 TEV)**
atggtaggggactggcggcagacagccggctacaacctggaccaagtccttgagcagggcggtgt
gtccagtttgtttcagaatctcggggtgtccgtaactccgatccaaaggattgtcctgagcggtg
aaaacggcctgaagatcgacatccatgtcatcatcccgtatgaaggtctgagcggcgatcagatg
ggccagatcgaaaaaatttttaaggtggtgtaccctgtggatgatcatcactttaaggtgattct
gcactatggcacactggtaatcgacggggttacgccgaacatgatcgactatttcggacggccgt
atgaaggcatcgccgtgttcgacggcaaaaagatcactgtaaccgggaccctgtggaacggcaac
aaaattatcgacgagcgcctgatcaaccccgacggctccctgctgttccgcgtaaccatcaacgg
agtgaccggctggcggctgtgcgagcgcattttggcgggaagttctggtggaggaagttctggtg
gagagcctactactgagaacttgtacttccagagcgataacggaagttctggtggaggaagttct
ggtggaatggtgtttacactcgaagatttc

**SEQ ID NO:119 (L27V CP 7 TEV)**
MVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQM
GQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGN
KIIDERLINPDGSLLFRVTINGVTGWRLCERILAGSSGGGSSGGEPTTENLYFQSDNGSSGGGSS
GGMVFTLEDF

**SEQ ID NO:120 (L27V CP 9 TEV)**
atggactggcggcagacagccggctacaacctggaccaagtccttgagcagggcggtgtgtccag
tttgtttcagaatctcggggtgtccgtaactccgatccaaaggattgtcctgagcggtgaaaacg
gcctgaagatcgacatccatgtcatcatcccgtatgaaggtctgagcggcgatcagatgggccag
atcgaaaaaatttttaaggtggtgtaccctgtggatgatcatcactttaaggtgattctgcacta
tggcacactggtaatcgacggggttacgccgaacatgatcgactatttcggacggccgtatgaag
gcatcgccgtgttcgacggcaaaaagatcactgtaaccgggaccctgtggaacggcaacaaaatt
atcgacgagcgcctgatcaaccccgacggctccctgctgttccgcgtaaccatcaacggagtgac
cggctggcggctgtgcgagcgcattttggcgggaagttctggtggaggaagttctggtggagagc
ctactactgagaacttgtacttccagagcgataacggaagttctggtggaggaagttctggtgga
atggtgtttacactcgaagatttcgtaggg

**SEQ ID NO:121 (L27V CP 9 TEV)**
MDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQ
IEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKI
IDERLINPDGSLLFRVTINGVTGWRLCERILAGSSGGGSSGGEPTTENLYFQSDNGSSGGGSSGG
MVFTLEDFVG

**SEQ ID NO:122 (L27V CP 11 TEV)**
Atgcggcagacagccggctacaacctggaccaagtccttgagcagggcggtgtgtccagtttgtt
tcagaatctcggggtgtccgtaactccgatccaaaggattgtcctgagcggtgaaaacggcctga
agatcgacatccatgtcatcatcccgtatgaaggtctgagcggcgatcagatgggccagatcgaa
aaaatttttaaggtggtgtaccctgtggatgatcatcactttaaggtgattctgcactatggcac
actggtaatcgacggggttacgccgaacatgatcgactatttcggacggccgtatgaaggcatcg

ccgtgttcgacggcaaaaagatcactgtaaccgggaccctgtggaacggcaacaaaattatcgac
gagcgcctgatcaaccccgacggctccctgctgttccgcgtaaccatcaacggagtgaccggctg
gcggctgtgcgagcgcattttggcgggaagttctggtggaggaagttctggtggagagcctacta
ctgagaacttgtacttccagagcgataacggaagttctggtggaggaagttctggtggaatggtg
tttacactcgaagatttcgtaggggactgg

**SEQ ID NO:123 (L27V CP 11 TEV)**
MRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIE
KIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIID
ERLINPDGSLLFRVTINGVTGWRLCERILAGSSGGGSSGGEPTTENLYFQSDNGSSGGGSSGGMV
FTLEDFVGDW

**SEQ ID NO:124 (L27V CP 12 TEV)**

Cagacagccggctacaacctggaccaagtccttgagcagggcggtgtgtccagtttgtttcagaa
tctcggggtgtccgtaactccgatccaaaggattgtcctgagcggtgaaaacggcctgaagatcg
acatccatgtcatcatcccgtatgaaggtctgagcggcgatcagatgggccagatcgaaaaaatt
tttaaggtggtgtaccctgtggatgatcatcactttaaggtgattctgcactatggcacactggt
aatcgacggggttacgccgaacatgatcgactatttcggacggccgtatgaaggcatcgccgtgt
tcgacggcaaaaagatcactgtaaccgggaccctgtggaacggcaacaaaattatcgacgagcgc
ctgatcaaccccgacggctccctgctgttccgcgtaaccatcaacggagtgaccggctggcggct
gtgcgagcgcattttggcgggaagttctggtggaggaagttctggtggagagcctactactgaga
acttgtacttccagagcgataacggaagttctggtggaggaagttctggtggaatggtgtttaca
ctcgaagatttcgtaggg

**SEQ ID NO:125 (L27V CP 12 TEV)**

QTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEKI
FKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDER
LINPDGSLLFRVTINGVTGWRLCERILAGSSGGGSSGGEPTTENLYFQSDNGSSGGGSSGGMVFT
LEDFVG

**SEQ ID NO:126 (L27V CP 15 TEV)**

atgggctacaacctggaccaagtccttgagcagggcggtgtgtccagtttgtttcagaatctcgg
ggtgtccgtaactccgatccaaaggattgtcctgagcggtgaaaacggcctgaagatcgacatcc
atgtcatcatcccgtatgaaggtctgagcggcgatcagatgggccagatcgaaaaaatttttaag
gtggtgtaccctgtggatgatcatcactttaaggtgattctgcactatggcacactggtaatcga
cggggttacgccgaacatgatcgactatttcggacggccgtatgaaggcatcgccgtgttcgacg
gcaaaaagatcactgtaaccgggaccctgtggaacggcaacaaaattatcgacgagcgcctgatc
aaccccgacggctccctgctgttccgcgtaaccatcaacggagtgaccggctggcggctgtgcga
gcgcattttggcgggaagttctggtggaggaagttctggtggagagcctactactgagaacttgt
acttccagagcgataacggaagttctggtggaggaagttctggtggaatggtgtttacactcgaa
gatttcgtaggggactggcggcagacagcc

**SEQ ID NO:127 (L27V CP 15 TEV)**

MGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEKIFK
VVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLI
NPDGSLLFRVTINGVTGWRLCERILAGSSGGGSSGGEPTTENLYFQSDNGSSGGGSSGGMVFTLE
DFVGDWRQTA

**SEQ ID NO:128 (L27V CP 18 TEV)**

ctggaccaagtccttgagcagggcggtgtgtccagtttgtttcagaatctcggggtgtccgtaac
tccgatccaaaggattgtcctgagcggtgaaaacggcctgaagatcgacatccatgtcatcatcc
cgtatgaaggtctgagcggcgatcagatgggccagatcgaaaaaatttttaaggtggtgtaccct
gtggatgatcatcactttaaggtgattctgcactatggcacactggtaatcgacggggttacgcc
gaacatgatcgactatttcggacggccgtatgaaggcatcgccgtgttcgacggcaaaaagatca
ctgtaaccgggaccctgtggaacggcaacaaaattatcgacgagcgcctgatcaaccccgacggc
tccctgctgttccgcgtaaccatcaacggagtgaccggctggcggctgtgcgagcgcattttggc
gggaagttctggtggaggaagttctggtggagagcctactactgagaacttgtacttccagagcg
ataacggaagttctggtggaggaagttctggtggaatggtgtttacactcgaagatttcgtaggg
gactggcggcagacagccggctacaac

**SEQ ID NO:129 (L27V CP 18 TEV)**

LDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEKIFKVVYP
VDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDG
SLLFRVTINGVTGWRLCERILAGSSGGGSSGGEPTTENLYFQSDNGSSGGGSSGGMVFTLEDFVG
DWRQTAGYN

**SEQ ID NO:130 (L27V CP 21 TEV)**

gtccttgagcagggcggtgtgtccagtttgtttcagaatctcggggtgtccgtaactccgatcca
aaggattgtcctgagcggtgaaaacggcctgaagatcgacatccatgtcatcatcccgtatgaag
gtctgagcggcgatcagatgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatgat
catcactttaaggtgattctgcactatggcacactggtaatcgacggggttacgccgaacatgat
cgactatttcggacggccgtatgaaggcatcgccgtgttcgacggcaaaaagatcactgtaaccg
ggaccctgtggaacggcaacaaaattatcgacgagcgcctgatcaaccccgacggctccctgctg
ttccgcgtaaccatcaacggagtgaccggctggcggctgtgcgagcgcattttggcgggaagttc
tggtggaggaagttctggtggagagcctactactgagaacttgtacttccagagcgataacggaa
gttctggtggaggaagttctggtggaatggtgtttacactcgaagatttcgtaggggactggcgg
cagacagccggctacaacctggaccaa

**SEQ ID NO:131 (L27V CP 21 TEV)**

VLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEKIFKVVYPVDD
HHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSLL
FRVTINGVTGWRLCERILAGSSGGGSSGGEPTTENLYFQSDNGSSGGGSSGGMVFTLEDFVGDWR
QTAGYNLDQ

**SEQ ID NO:132 (L27V CP 24 TEV)**

cagggcggtgtgtccagtttgtttcagaatctcggggtgtccgtaactccgatccaaaggattgt
cctgagcggtgaaaacggcctgaagatcgacatccatgtcatcatcccgtatgaaggtctgagcg
gcgatcagatgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatgatcatcacttt
aaggtgattctgcactatggcacactggtaatcgacggggttacgccgaacatgatcgactattt
cggacggccgtatgaaggcatcgccgtgttcgacggcaaaaagatcactgtaaccgggaccctgt
ggaacggcaacaaaattatcgacgagcgcctgatcaaccccgacggctccctgctgttccgcgta
accatcaacggagtgaccggctggcggctgtgcgagcgcattttggcgggaagttctggtggagg
aagttctggtggagagcctactactgagaacttgtacttccagagcgataacggaagttctggtg
gaggaagttctggtggaatggtgtttacactcgaagatttcgtaggggactggcggcagacagcc
ggctacaacctggaccaagtccttgag

**SEQ ID NO:133 (L27V CP 24 TEV)**

QGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEKIFKVVYPVDDHHF
KVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRV
TINGVTGWRLCERILAGSSGGGSSGGEPTTENLYFQSDNGSSGGGSSGGMVFTLEDFVGDWRQTA
GYNLDQVLE

**SEQ ID NO:134 (L27V CP 27 TEV)**

gtgtccagtttgtttcagaatctcggggtgtccgtaactccgatccaaaggattgtcctgagcgg
tgaaaacggcctgaagatcgacatccatgtcatcatcccgtatgaaggtctgagcggcgatcaga
tgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatgatcatcactttaaggtgatt
ctgcactatggcacactggtaatcgacggggttacgccgaacatgatcgactatttcggacggcc
gtatgaaggcatcgccgtgttcgacggcaaaaagatcactgtaaccgggaccctgtggaacggca
acaaaattatcgacgagcgcctgatcaaccccgacggctccctgctgttccgcgtaaccatcaac
ggagtgaccggctggcggctgtgcgagcgcattttggcgggaagttctggtggaggaagttctgg
tggagagcctactactgagaacttgtacttccagagcgataacggaagttctggtggaggaagtt
ctggtggaatggtgtttacactcgaagatttcgtaggggactggcggcagacagccggctacaac
ctggaccaagtccttgagcagggcggt

**SEQ ID NO:135 (L27V CP 27 TEV)**

VSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEKIFKVVYPVDDHHFKVI
LHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVTIN
GVTGWRLCERILAGSSGGGSSGGEPTTENLYFQSDNGSSGGGSSGGMVFTLEDFVGDWRQTAGYN
LDQVLEQGG

**SEQ ID NO:136 (L27V CP 34 TEV)**

atgctcggggtgtccgtaactccgatccaaaggattgtcctgagcggtgaaaacggcctgaagat
cgacatccatgtcatcatcccgtatgaaggtctgagcggcgatcagatgggccagatcgaaaaaa
tttttaaggtggtgtaccctgtggatgatcatcactttaaggtgattctgcactatggcacactg
gtaatcgacggggttacgccgaacatgatcgactatttcggacggccgtatgaaggcatcgccgt
gttcgacggcaaaaagatcactgtaaccgggaccctgtggaacggcaacaaaattatcgacgagc
gcctgatcaaccccgacggctccctgctgttccgcgtaaccatcaacggagtgaccggctggcgg
ctgtgcgagcgcattttggcgggaagttctggtggaggaagttctggtggagagcctactactga
gaacttgtacttccagagcgataacggaagttctggtggaggaagttctggtggaatggtgttta
cactcgaagatttcgtaggggactggcggcagacagccggctacaacctggaccaagtccttgag
cagggcggtgtgtccagtttgtttcagaat

**SEQ ID NO:137 (L27V CP 34 TEV)**

MLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEKIFKVVYPVDDHHFKVILHYGTL
VIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWR
LCERILAGSSGGGSSGGEPTTENLYFQSDNGSSGGGSSGGMVFTLEDFVGDWRQTAGYNLDQVLE
QGGVSSLFQN

**SEQ ID NO:138 (L27V CP 40 TEV)**

Atgccgatccaaaggattgtcctgagcggtgaaaacggcctgaagatcgacatccatgtcatcat
cccgtatgaaggtctgagcggcgatcagatgggccagatcgaaaaaatttttaaggtggtgtacc
ctgtggatgatcatcactttaaggtgattctgcactatggcacactggtaatcgacggggttacg
ccgaacatgatcgactatttcggacggccgtatgaaggcatcgccgtgttcgacggcaaaaagat
cactgtaaccgggaccctgtggaacggcaacaaaattatcgacgagcgcctgatcaaccccgacg
gctccctgctgttccgcgtaaccatcaacggagtgaccggctggcggctgtgcgagcgcattttg
gcgggaagttctggtggaggaagttctggtggagagcctactactgagaacttgtacttccagag
cgataacggaagttctggtggaggaagttctggtggaatggtgtttacactcgaagatttcgtag
gggactggcggcagacagccggctacaacctggaccaagtccttgagcagggcggtgtgtccagt
ttgtttcagaatctcggggtgtccgtaact

**SEQ ID NO:139 (L27V CP 40 TEV)**

MPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVT
PNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERIL
AGSSGGGSSGGEPTTENLYFQSDNGSSGGGSSGGMVFTLEDFVGDWRQTAGYNLDQVLEQGGVSS
LFQNLGVSVT

**SEQ ID NO:140 (L27V CP 43 TEV)**

Atgaggattgtcctgagcggtgaaaacggcctgaagatcgacatccatgtcatcatcccgtatga
aggtctgagcggcgatcagatgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatg
atcatcactttaaggtgattctgcactatggcacactggtaatcgacggggttacgccgaacatg
atcgactatttcggacggccgtatgaaggcatcgccgtgttcgacggcaaaaagatcactgtaac
cgggaccctgtggaacggcaacaaaattatcgacgagcgcctgatcaaccccgacggctccctgc
tgttccgcgtaaccatcaacggagtgaccggctggcggctgtgcgagcgcattttggcgggaagt
tctggtggaggaagttctggtggagagcctactactgagaacttgtacttccagagcgataacgg
aagttctggtggaggaagttctggtggaatggtgtttacactcgaagatttcgtaggggactggc
ggcagacagccggctacaacctggaccaagtccttgagcagggcggtgtgtccagtttgtttcag
aatctcggggtgtccgtaactccgatccaa

**SEQ ID NO:141 (L27V CP 43 TEV)**

MRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNM
IDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILAGS
SGGGSSGGEPTTENLYFQSDNGSSGGGSSGGMVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQ
NLGVSVTPIQ

**SEQ ID NO:142 (L27V CP 44 TEV)**

Atgattgtcctgagcggtgaaaacggcctgaagatcgacatccatgtcatcatcccgtatgaagg
tctgagcggcgatcagatgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatgatc
atcactttaaggtgattctgcactatggcacactggtaatcgacggggttacgccgaacatgatc
gactatttcggacggccgtatgaaggcatcgccgtgttcgacggcaaaaagatcactgtaaccgg
gaccctgtggaacggcaacaaaattatcgacgagcgcctgatcaaccccgacggctccctgctgt
tccgcgtaaccatcaacggagtgaccggctggcggctgtgcgagcgcattttggcgggaagttct
ggtggaggaagttctggtggagagcctactactgagaacttgtacttccagagcgataacggaag
ttctggtggaggaagttctggtggaatggtgtttacactcgaagatttcgtaggggactggcggc

agacagccggctacaacctggaccaagtccttgagcagggcggtgtgtccagtttgtttcagaat
ctcggggtgtccgtaactccgatccaaagg

**SEQ ID NO:143 (L27V CP 44 TEV)**
MIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMI
DYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILAGSS
GGGSSGGEPTTENLYFQSDNGSSGGGSSGGMVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQN
LGVSVTPIQR

**SEQ ID NO:144 (L27V CP 45 TEV)**
Atggtcctgagcggtgaaaacggcctgaagatcgacatccatgtcatcatcccgtatgaaggtct
gagcggcgatcagatgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatgatcatc
actttaaggtgattctgcactatggcacactggtaatcgacggggttacgccgaacatgatcgac
tatttcggacggccgtatgaaggcatcgccgtgttcgacggcaaaaagatcactgtaaccgggac
cctgtggaacggcaacaaaattatcgacgagcgcctgatcaaccccgacggctccctgctgttcc
gcgtaaccatcaacggagtgaccggctggcggctgtgcgagcgcattttggcgggaagttctggt
ggaggaagttctggtggagagcctactactgagaacttgtacttccagagcgataacggaagttc
tggtggaggaagttctggtggaatggtgtttacactcgaagatttcgtaggggactggcggcaga
cagccggctacaacctggaccaagtccttgagcagggcggtgtgtccagtttgtttcagaatctc
ggggtgtccgtaactccgatccaaaggatt

**SEQ ID NO:145 (L27V CP 45 TEV)**
MVLSGENGLKIDIHVIIPYEGLSGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMID
YFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILAGSSG
GGSSGGEPTTENLYFQSDNGSSGGGSSGGMVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNL
GVSVTPIQRI

**SEQ ID NO:146 (L27V CP 46 TEV)**
Atgctgagcggtgaaaacggcctgaagatcgacatccatgtcatcatcccgtatgaaggtctgag
cggcgatcagatgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatgatcatcact
ttaaggtgattctgcactatggcacactggtaatcgacggggttacgccgaacatgatcgactat
ttcggacggccgtatgaaggcatcgccgtgttcgacggcaaaaagatcactgtaaccgggaccct
gtggaacggcaacaaaattatcgacgagcgcctgatcaaccccgacggctccctgctgttccgcg
taaccatcaacggagtgaccggctggcggctgtgcgagcgcattttggcgggaagttctggtgga
ggaagttctggtggagagcctactactgagaacttgtacttccagagcgataacggaagttctgg
tggaggaagttctggtggaatggtgtttacactcgaagatttcgtaggggactggcggcagacag
ccggctacaacctggaccaagtccttgagcagggcggtgtgtccagtttgtttcagaatctcggg
gtgtccgtaactccgatccaaaggatt

**SEQ ID NO:147 (L27V CP 46 TEV)**
MLSGENGLKIDIHVIIPYEGLSGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDY
FGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILAGSSGG
GSSGGEPTTENLYFQSDNGSSGGGSSGGMVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLG
VSVTPIQRI

**SEQ ID NO:148 (L27V CP 47 TEV)**
atgagcggtgaaaacggcctgaagatcgacatccatgtcatcatcccgtatgaaggtctgagcgg
cgatcagatgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatgatcatcacttta
aggtgattctgcactatggcacactggtaatcgacggggttacgccgaacatgatcgactatttc
ggacggccgtatgaaggcatcgccgtgttcgacggcaaaaagatcactgtaaccgggaccctgtg
gaacggcaacaaaattatcgacgagcgcctgatcaaccccgacggctccctgctgttccgcgtaa
ccatcaacggagtgaccggctggcggctgtgcgagcgcattttggcgggaagttctggtggagga
agttctggtggagagcctactactgagaacttgtacttccagagcgataacggaagttctggtgg

aggaagttctggtggaatggtgtttacactcgaagatttcgtaggggactggcggcagacagccg
gctacaacctggaccaagtccttgagcagggcggtgtgtccagtttgtttcagaatctcggggtg
tccgtaactccgatccaaaggattgtcctg

**SEQ ID NO:149 (L27V CP 47 TEV)**
MSGENGLKIDIHVIIPYEGLSGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYF
GRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILAGSSGGG
SSGGEPTTENLYFQSDNGSSGGGSSGGMVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGV
SVTPIQRIVL

**SEQ ID NO:150 (L27V CP 48 TEV)**
atgggtgaaaacggcctgaagatcgacatccatgtcatcatcccgtatgaaggtctgagcggcga
tcagatgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatgatcatcactttaagg
tgattctgcactatggcacactggtaatcgacggggttacgccgaacatgatcgactatttcgga
cggccgtatgaaggcatcgccgtgttcgacggcaaaaagatcactgtaaccgggaccctgtggaa
cggcaacaaaattatcgacgagcgcctgatcaaccccgacggctccctgctgttccgcgtaacca
tcaacggagtgaccggctggcggctgtgcgagcgcatttggcgggaagttctggtggaggaagt
tctggtggagagcctactactgagaacttgtacttccagagcgataacggaagttctggtggagg
aagttctggtggaatggtgtttacactcgaagatttcgtaggggactggcggcagacagccggct
acaacctggaccaagtccttgagcagggcggtgtgtccagtttgtttcagaatctcggggtgtcc
gtaactccgatccaaaggattgtcctgagcg

**SEQ ID NO:151 (L27V CP 48 TEV)**
MGENGLKIDIHVIIPYEGLSGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFG
RPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILAGSSGGGS
SGGEPTTENLYFQSDNGSSGGGSSGGMVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVS
VTPIQRIVLS

**SEQ ID NO:152 (L27V CP 49 TEV)**
atggaaaacggcctgaagatcgacatccatgtcatcatcccgtatgaaggtctgagcggcgatca
gatgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatgatcatcactttaaggtga
ttctgcactatggcacactggtaatcgacggggttacgccgaacatgatcgactatttcggacgg
ccgtatgaaggcatcgccgtgttcgacggcaaaaagatcactgtaaccgggaccctgtggaacgg
caacaaaattatcgacgagcgcctgatcaaccccgacggctccctgctgttccgcgtaaccatca
acggagtgaccggctggcggctgtgcgagcgcattttggcgggaagttctggtggaggaagttct
ggtggagagcctactactgagaacttgtacttccagagcgataacggaagttctggtggaggaag
ttctggtggaatggtgtttacactcgaagatttcgtaggggactggcggcagacagccggctaca
acctggaccaagtccttgagcagggcggtgtgtccagtttgtttcagaatctcggggtgtccgta
actccgatccaaaggattgtcctgagcggt

**SEQ ID NO:153 (L27V CP 49 TEV)**
MENGLKIDIHVIIPYEGLSGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGR
PYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILAGSSGGGSS
GGEPTTENLYFQSDNGSSGGGSSGGMVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSV
TPIQRIVLSG

**SEQ ID NO:154 (L27V CP 50 TEV)**
atgaacggcctgaagatcgacatccatgtcatcatcccgtatgaaggtctgagcggcgatcagat
gggccagatcgaaaaaatttttaaggtggtgtaccctgtggatgatcatcactttaaggtgattc
tgcactatggcacactggtaatcgacggggttacgccgaacatgatcgactatttcggacggccg
tatgaaggcatcgccgtgttcgacggcaaaaagatcactgtaaccgggaccctgtggaacggcaa
caaaattatcgacgagcgcctgatcaaccccgacggctccctgctgttccgcgtaaccatcaacg
gagtgaccggctggcggctgtgcgagcgcattttggcgggaagttctggtggaggaagttctggt

ggagagcctactactgagaacttgtacttccagagcgataacggaagttctggtggaggaagttc
tggtggaatggtgtttacactcgaagatttcgtaggggactggcggcagacagccggctacaacc
tggaccaagtccttgagcagggcggtgtgtccagtttgtttcagaatctcggggtgtccgtaact
ccgatccaaaggattgtcctgagcggtgaa

**SEQ ID NO:155 (L27V CP 50 TEV)**
MNGLKIDIHVIIPYEGLSGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRP
YEGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILAGSSGGGSSG
GEPTTENLYFQSDNGSSGGGSSGGMVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVT
PIQRIVLSGE

**SEQ ID NO:156 (L27V CP 51 TEV)**
atgggcctgaagatcgacatccatgtcatcatcccgtatgaaggtctgagcggcgatcagatggg
ccagatcgaaaaaatttttaaggtggtgtaccctgtggatgatcatcactttaaggtgattctgc
actatggcacactggtaatcgacggggttacgccgaacatgatcgactatttcggacggccgtat
gaaggcatcgccgtgttcgacggcaaaaagatcactgtaaccgggaccctgtggaacggcaacaa
aattatcgacgagcgcctgatcaaccccgacggctccctgctgttccgcgtaaccatcaacggag
tgaccggctggcggctgtgcgagcgcattttggcgggaagttctggtggaggaagttctggtgga
gagcctactactgagaacttgtacttccagagcgataacggaagttctggtggaggaagttctgg
tggaatggtgtttacactcgaagatttcgtaggggactggcggcagacagccggctacaacctgg
accaagtccttgagcagggcggtgtgtccagtttgtttcagaatctcggggtgtccgtaactccg
atccaaaggattgtcctgagcggtgaaaac

**SEQ ID NO:157 (L27V CP 51 TEV)**
MGLKIDIHVIIPYEGLSGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPY
EGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILAGSSGGGSSGG
EPTTENLYFQSDNGSSGGGSSGGMVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTP
IQRIVLSGEN

**SEQ ID NO:158 (L27V CP 52 TEV)**
atgctgaagatcgacatccatgtcatcatcccgtatgaaggtctgagcggcgatcagatgggcca
gatcgaaaaaatttttaaggtggtgtaccctgtggatgatcatcactttaaggtgattctgcact
atggcacactggtaatcgacggggttacgccgaacatgatcgactatttcggacggccgtatgaa
ggcatcgccgtgttcgacggcaaaaagatcactgtaaccgggaccctgtggaacggcaacaaaat
tatcgacgagcgcctgatcaaccccgacggctccctgctgttccgcgtaaccatcaacggagtga
ccggctggcggctgtgcgagcgcattttggcgggaagttctggtggaggaagttctggtggagag
cctactactgagaacttgtacttccagagcgataacggaagttctggtggaggaagttctggtgg
aatggtgtttacactcgaagatttcgtaggggactggcggcagacagccggctacaacctggacc
aagtccttgagcagggcggtgtgtccagtttgtttcagaatctcggggtgtccgtaactccgatc
caaaggattgtcctgagcggtgaaaacggc

**SEQ ID NO:159 (L27V CP 52 TEV)**
MLKIDIHVIIPYEGLSGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYE
GIAVFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILAGSSGGGSSGGE
PTTENLYFQSDNGSSGGGSSGGMVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPI
QRIVLSGENG

**SEQ ID NO:160 (L27V CP 53 TEV)**
atgaagatcgacatccatgtcatcatcccgtatgaaggtctgagcggcgatcagatgggccagat
cgaaaaaatttttaaggtggtgtaccctgtggatgatcatcactttaaggtgattctgcactatg
gcacactggtaatcgacggggttacgccgaacatgatcgactatttcggacggccgtatgaaggc
atcgccgtgttcgacggcaaaaagatcactgtaaccgggaccctgtggaacggcaacaaaattat
cgacgagcgcctgatcaaccccgacggctccctgctgttccgcgtaaccatcaacggagtgaccg

gctggcggctgtgcgagcgcattttggcgggaagttctggtggaggaagttctggtggagagcct
actactgagaacttgtacttccagagcgataacggaagttctggtggaggaagttctggtggaat
ggtgtttacactcgaagatttcgtaggggactggcggcagacagccggctacaacctggaccaag
tccttgagcagggcggtgtgtccagtttgtttcagaatctcggggtgtccgtaactccgatccaa
aggattgtcctgagcggtgaaaacggcctg

**SEQ ID NO:161 (L27V CP 53 TEV)**

MKIDIHVIIPYEGLSGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEG
IAVFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILAGSSGGGSSGGEP
TTENLYFQSDNGSSGGGSSGGMVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQ
RIVLSGENGL

**SEQ ID NO:162 (L27V CP 54 TEV)**

atgatcgacatccatgtcatcatcccgtatgaaggtctgagcggcgatcagatgggccagatcga
aaaaatttttaaggtggtgtaccctgtggatgatcatcactttaaggtgattctgcactatggca
cactggtaatcgacggggttacgccgaacatgatcgactatttcggacggccgtatgaaggcatc
gccgtgttcgacggcaaaaagatcactgtaaccgggaccctgtggaacggcaacaaaattatcga
cgagcgcctgatcaaccccgacggctccctgctgttccgcgtaaccatcaacggagtgaccggct
ggcggctgtgcgagcgcattttggcgggaagttctggtggaggaagttctggtggagagcctact
actgagaacttgtacttccagagcgataacggaagttctggtggaggaagttctggtggaatggt
gtttacactcgaagatttcgtaggggactggcggcagacagccggctacaacctggaccaagtcc
ttgagcagggcggtgtgtccagtttgtttcagaatctcggggtgtccgtaactccgatccaaagg
attgtcctgagcggtgaaaacggcctgaag

**SEQ ID NO:163 (L27V CP 54 TEV)**

MIDIHVIIPYEGLSGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGI
AVFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILAGSSGGGSSGGEPT
TENLYFQSDNGSSGGGSSGGMVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQR
IVLSGENGLK

**SEQ ID NO:164 (L27V CP 55 TEV)**

atggacatccatgtcatcatcccgtatgaaggtctgagcggcgatcagatgggccagatcgaaaa
aatttttaaggtggtgtaccctgtggatgatcatcactttaaggtgattctgcactatggcacac
tggtaatcgacggggttacgccgaacatgatcgactatttcggacggccgtatgaaggcatcgcc
gtgttcgacggcaaaaagatcactgtaaccgggaccctgtggaacggcaacaaaattatcgacga
gcgcctgatcaaccccgacggctccctgctgttccgcgtaaccatcaacggagtgaccggctggc
ggctgtgcgagcgcattttggcgggaagttctggtggaggaagttctggtggagagcctactact
gagaacttgtacttccagagcgataacggaagttctggtggaggaagttctggtggaatggtgtt
tacactcgaagatttcgtaggggactggcggcagacagccggctacaacctggaccaagtccttg
agcagggcggtgtgtccagtttgtttcagaatctcggggtgtccgtaactccgatccaaaggatt
gtcctgagcggtgaaaacggcctgaagatc

**SEQ ID NO:165 (L27V CP 55 TEV)**

MDIHVIIPYEGLSGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIA
VFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILAGSSGGGSSGGEPTT
ENLYFQSDNGSSGGGSSGGMVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRI
VLSGENGLKI

**SEQ ID NO:166 (L27V CP 56 TEV)**

Atgatccatgtcatcatcccgtatgaaggtctgagcggcgatcagatgggccagatcgaaaaaat
ttttaaggtggtgtaccctgtggatgatcatcactttaaggtgattctgcactatggcacactgg
taatcgacggggttacgccgaacatgatcgactatttcggacggccgtatgaaggcatcgccgtg
ttcgacggcaaaaagatcactgtaaccgggaccctgtggaacggcaacaaaattatcgacgagcg
cctgatcaaccccgacggctccctgctgttccgcgtaaccatcaacggagtgaccggctggcggc
tgtgcgagcgcattttggcgggaagttctggtggaggaagttctggtggagagcctactactgag
aacttgtacttccagagcgataacggaagttctggtggaggaagttctggtggaatggtgtttac
actcgaagatttcgtaggggactggcggcagacagccggctacaacctggaccaagtccttgagc
agggcggtgtgtccagtttgtttcagaatctcggggtgtccgtaactccgatccaaaggattgtc
ctgagcggtgaaaacggcctgaagatcga

**SEQ ID NO:167 (L27V CP 56 TEV)**

MIHVIIPYEGLSGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAV
FDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILAGSSGGGSSGGEPTTE
NLYFQSDNGSSGGGSSGGMVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIV
LSGENGLKID

**SEQ ID NO:168 (L27V CP 58 TEV)**

atggtcatcatcccgtatgaaggtctgagcggcgatcagatgggccagatcgaaaaaatttttaa
ggtggtgtaccctgtggatgatcatcactttaaggtgattctgcactatggcacactggtaatcg
acggggttacgccgaacatgatcgactatttcggacggccgtatgaaggcatcgccgtgttcgac
ggcaaaaagatcactgtaaccgggaccctgtggaacggcaacaaaattatcgacgagcgcctgat
caaccccgacggctccctgctgttccgcgtaaccatcaacggagtgaccggctggcggctgtgcg
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tacttccagagcgataacggaagttctggtggaggaagttctggtggaatggtgtttacactcga
agatttcgtaggggactggcggcagacagccggctacaacctggaccaagtccttgagcagggcg
gtgtgtccagtttgtttcagaatctcggggtgtccgtaactccgatccaaaggattgtcctgagc
ggtgaaaacggcctgaagatcgacatccat

**SEQ ID NO:169 (L27V CP 58 TEV)**

MVIIPYEGLSGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFD
GKKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILAGSSGGGSSGGEPTTENL
YFQSDNGSSGGGSSGGMVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLS
GENGLKIDIH

**SEQ ID NO:170 (L27V CP 64 TEV)**

atgggtctgagcggcgatcagatgggccagatcgaaaaaatttttaaggtggtgtaccctgtgga
tgatcatcactttaaggtgattctgcactatggcacactggtaatcgacggggttacgccgaaca
tgatcgactatttcggacggccgtatgaaggcatcgccgtgttcgacggcaaaaagatcactgta
accgggaccctgtggaacggcaacaaaattatcgacgagcgcctgatcaaccccgacggctccct
gctgttccgcgtaaccatcaacggagtgaccggctggcggctgtgcgagcgcattttggcgggaa
gttctggtggaggaagttctggtggagagcctactactgagaacttgtacttccagagcgataac
ggaagttctggtggaggaagttctggtggaatggtgtttacactcgaagatttcgtaggggactg
gcggcagacagccggctacaacctggaccaagtccttgagcagggcggtgtgtccagtttgtttc
agaatctcggggtgtccgtaactccgatccaaaggattgtcctgagcggtgaaaacggcctgaag
atcgacatccatgtcatcatcccgtatgaa

**SEQ ID NO:171 (L27V CP 64 TEV)**

MGLSGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITV
TGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILAGSSGGGSSGGEPTTENLYFQSDN
GSSGGGSSGGMVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLK
IDIHVIIPYE

**SEQ ID NO:172 (L27V CP 67 TEV)**

atgggcgatcagatgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatgatcatca
ctttaaggtgattctgcactatggcacactggtaatcgacggggttacgccgaacatgatcgact
atttcggacggccgtatgaaggcatcgccgtgttcgacggcaaaaagatcactgtaaccgggacc
ctgtggaacggcaacaaaattatcgacgagcgcctgatcaaccccgacggctccctgctgttccg
cgtaaccatcaacggagtgaccggctggcggctgtgcgagcgcattttggcgggaagttctggtg
gaggaagttctggtggagagcctactactgagaacttgtacttccagagcgataacggaagttct
ggtggaggaagttctggtggaatggtgtttacactcgaagatttcgtaggggactggcggcagac
agccggctacaacctggaccaagtccttgagcagggcggtgtgtccagtttgtttcagaatctcg
gggtgtccgtaactccgatccaaaggattgtcctgagcggtgaaaacggcctgaagatcgacatc
catgtcatcatcccgtatgaaggtctgagc

**SEQ ID NO:173 (L27V CP 67 TEV)**

MGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGT
LWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILAGSSGGGSSGGEPTTENLYFQSDNGSS
GGGSSGGMVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDI
HVIIPYEGLS

**SEQ ID NO:174 (L27V CP 70 TEV)**

atgatgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatgatcatcactttaaggt
gattctgcactatggcacactggtaatcgacggggttacgccgaacatgatcgactatttcggac
ggccgtatgaaggcatcgccgtgttcgacggcaaaaagatcactgtaaccgggaccctgtggaac
ggcaacaaaattatcgacgagcgcctgatcaaccccgacggctccctgctgttccgcgtaaccat
caacggagtgaccggctggcggctgtgcgagcgcattttggcgggaagttctggtggaggaagtt
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agttctggtggaatggtgtttacactcgaagatttcgtaggggactggcggcagacagccggcta
caacctggaccaagtccttgagcagggcggtgtgtccagtttgtttcagaatctcggggtgtccg
taactccgatccaaaggattgtcctgagcggtgaaaacggcctgaagatcgacatccatgtcatc
atcccgtatgaaggtctgagcggcgatcag

**SEQ ID NO:175 (L27V CP 70 TEV)**
MMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWN
GNKIIDERLINPDGSLLFRVTINGVTGWRLCERILAGSSGGGSSGGEPTTENLYFQSDNGSSGGG
SSGGMVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVI
IPYEGLSGDQ

**SEQ ID NO:176 (L27V CP 73 TEV)**
atgatcgaaaaaatttttaaggtggtgtaccctgtggatgatcatcactttaaggtgattctgca
ctatggcacactggtaatcgacggggttacgccgaacatgatcgactatttcggacggccgtatg
aaggcatcgccgtgttcgacggcaaaaagatcactgtaaccgggaccctgtggaacggcaacaaa
attatcgacgagcgcctgatcaaccccgacggctccctgctgttccgcgtaaccatcaacggagt
gaccggctggcggctgtgcgagcgcattttggcgggaagttctggtggaggaagttctggtggag
agcctactactgagaacttgtacttccagagcgataacggaagttctggtggaggaagttctggt
ggaatggtgtttacactcgaagatttcgtaggggactggcggcagacagccggctacaacctgga
ccaagtccttgagcagggcggtgtgtccagtttgtttcagaatctcggggtgtccgtaactccga
tccaaaggattgtcctgagcggtgaaaacggcctgaagatcgacatccatgtcatcatcccgtat
gaaggtctgagcggcgatcagatgggccag

**SEQ ID NO:177 (L27V CP 73 TEV)**
MIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNK
IIDERLINPDGSLLFRVTINGVTGWRLCERILAGSSGGGSSGGEPTTENLYFQSDNGSSGGGSSG
GMVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPY
EGLSGDQMGQ

**SEQ ID NO:178 (L27V CP 76 TEV)**
atgatttttaaggtggtgtaccctgtggatgatcatcactttaaggtgattctgcactatggcac
actggtaatcgacggggttacgccgaacatgatcgactatttcggacggccgtatgaaggcatcg
ccgtgttcgacggcaaaaagatcactgtaaccgggaccctgtggaacggcaacaaaattatcgac
gagcgcctgatcaaccccgacggctccctgctgttccgcgtaaccatcaacggagtgaccggctg
gcggctgtgcgagcgcattttggcgggaagttctggtggaggaagttctggtggagagcctacta
ctgagaacttgtacttccagagcgataacggaagttctggtggaggaagttctggtggaatggtg
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ttgtcctgagcggtgaaaacggcctgaagatcgacatccatgtcatcatcccgtatgaaggtctg
agcggcgatcagatgggccagatcgaaaaa

**SEQ ID NO:179 (L27V CP 76 TEV)**
MIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIID
ERLINPDGSLLFRVTINGVTGWRLCERILAGSSGGGSSGGEPTTENLYFQSDNGSSGGGSSGGMV
FTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGL
SGDQMGQIEK

**SEQ ID NO:180 (L27V CP 79 TEV)**
Atggtggtgtaccctgtggatgatcatcactttaaggtgattctgcactatggcacactggtaat
cgacggggttacgccgaacatgatcgactatttcggacggccgtatgaaggcatcgccgtgttcg
acggcaaaaagatcactgtaaccgggaccctgtggaacggcaacaaaattatcgacgagcgcctg
atcaaccccgacggctccctgctgttccgcgtaaccatcaacggagtgaccggctggcggctgtg
cgagcgcattttggcgggaagttctggtggaggaagttctggtggagagcctactactgagaact
tgtacttccagagcgataacggaagttctggtggaggaagttctggtggaatggtgtttacactc
gaagatttcgtaggggactggcggcagacagccggctacaacctggaccaagtccttgagcaggg
cggtgtgtccagtttgtttcagaatctcggggtgtccgtaactccgatccaaaggattgtcctga

gcggtgaaaacggcctgaagatcgacatccatgtcatcatcccgtatgaaggtctgagcggcgat
cagatgggccagatcgaaaaaatttttaag

**SEQ ID NO:181 (L27V CP 79 TEV)**
MVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERL
INPDGSLLFRVTINGVTGWRLCERILAGSSGGGSSGGEPTTENLYFQSDNGSSGGGSSGGMVFTL
EDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGD
QMGQIEKIFK

**SEQ ID NO:182 (L27V CP 80 TEV)**
atggtgtaccctgtggatgatcatcactttaaggtgattctgcactatggcacactggtaatcga
cggggttacgccgaacatgatcgactatttcggacggccgtatgaaggcatcgccgtgttcgacg
gcaaaaagatcactgtaaccgggaccctgtggaacggcaacaaaattatcgacgagcgcctgatc
aaccccgacggctccctgctgttccgcgtaaccatcaacggagtgaccggctggcggctgtgcga
gcgcattttggcgggaagttctggtggaggaagttctggtggagagcctactactgagaacttgt
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gatttcgtaggggactggcggcagacagccggctacaacctggaccaagtccttgagcagggcgg
tgtgtccagtttgtttcagaatctcggggtgtccgtaactccgatccaaaggattgtcctgagcg
gtgaaaacggcctgaagatcgacatccatgtcatcatcccgtatgaaggtctgagcggcgatcag
atgggccagatcgaaaaaatttttaaggtg

**SEQ ID NO:183 (L27V CP 80 TEV)**
MVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLI
NPDGSLLFRVTINGVTGWRLCERILAGSSGGGSSGGEPTTENLYFQSDNGSSGGGSSGGMVFTLE
DFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQ
MGQIEKIFKV

**SEQ ID NO:184 (L27V CP 81 TEV)**
atgtaccctgtggatgatcatcactttaaggtgattctgcactatggcacactggtaatcgacgg
ggttacgccgaacatgatcgactatttcggacggccgtatgaaggcatcgccgtgttcgacggca
aaaagatcactgtaaccgggaccctgtggaacggcaacaaaattatcgacgagcgcctgatcaac
cccgacggctccctgctgttccgcgtaaccatcaacggagtgaccggctggcggctgtgcgagcg
cattttggcgggaagttctggtggaggaagttctggtggagagcctactactgagaacttgtact
tccagagcgataacggaagttctggtggaggaagttctggtggaatggtgtttacactcgaagat
ttcgtaggggactggcggcagacagccggctacaacctggaccaagtccttgagcagggcggtgt
gtccagtttgtttcagaatctcggggtgtccgtaactccgatccaaaggattgtcctgagcggtg
aaaacggcctgaagatcgacatccatgtcatcatcccgtatgaaggtctgagcggcgatcagatg
ggccagatcgaaaaaatttttaaggtggtg

**SEQ ID NO:185 (L27V CP 81 TEV)**
MYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLIN
PDGSLLFRVTINGVTGWRLCERILAGSSGGGSSGGEPTTENLYFQSDNGSSGGGSSGGMVFTLED
FVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQM
GQIEKIFKVV

**SEQ ID NO:186 (L27V CP 82 TEV)**
atgcctgtggatgatcatcactttaaggtgattctgcactatggcacactggtaatcgacggggt
tacgccgaacatgatcgactatttcggacggccgtatgaaggcatcgccgtgttcgacggcaaaa
agatcactgtaaccgggaccctgtggaacggcaacaaaattatcgacgagcgcctgatcaacccc
gacggctccctgctgttccgcgtaaccatcaacggagtgaccggctggcggctgtgcgagcgcat
tttggcgggaagttctggtggaggaagttctggtggagagcctactactgagaacttgtacttcc
agagcgataacggaagttctggtggaggaagttctggtggaatggtgtttacactcgaagatttc
gtaggggactggcggcagacagccggctacaacctggaccaagtccttgagcagggcggtgtgtc

cagtttgtttcagaatctcggggtgtccgtaactccgatccaaaggattgtcctgagcggtgaaa
acggcctgaagatcgacatccatgtcatcatcccgtatgaaggtctgagcggcgatcagatgggc
cagatcgaaaaaatttttaaggtggtgtac

**SEQ ID NO:187 (L27V CP 82 TEV)**
MPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINP
DGSLLFRVTINGVTGWRLCERILAGSSGGGSSGGEPTTENLYFQSDNGSSGGGSSGGMVFTLEDF
VGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMG
QIEKIFKVVY

**SEQ ID NO:188 (L27V CP 83 TEV)**
atggtggatgatcatcactttaaggtgattctgcactatggcacactggtaatcgacggggttac
gccgaacatgatcgactatttcggacggccgtatgaaggcatcgccgtgttcgacggcaaaaaga
tcactgtaaccgggaccctgtggaacggcaacaaaattatcgacgagcgcctgatcaaccccgac
ggctccctgctgttccgcgtaaccatcaacggagtgaccggctggcggctgtgcgagcgcatttt
ggcgggaagttctggtggaggaagttctggtggagagcctactactgagaacttgtacttccaga
gcgataacggaagttctggtggaggaagttctggtggaatggtgtttacactcgaagatttcgta
ggggactggcggcagacagccggctacaacctggaccaagtccttgagcagggcggtgtgtccag
tttgtttcagaatctcggggtgtccgtaactccgatccaaaggattgtcctgagcggtgaaaacg
gcctgaagatcgacatccatgtcatcatcccgtatgaaggtctgagcggcgatcagatgggccag
atcgaaaaaatttttaaggtggtgtaccct

**SEQ ID NO:189 (L27V CP 83 TEV)**
MVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPD
GSLLFRVTINGVTGWRLCERILAGSSGGGSSGGEPTTENLYFQSDNGSSGGGSSGGMVFTLEDFV
GDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQ
IEKIFKVVYP

**SEQ ID NO:190 (L27V CP 84 TEV)**
atggatgatcatcactttaaggtgattctgcactatggcacactggtaatcgacggggttacgcc
gaacatgatcgactatttcggacggccgtatgaaggcatcgccgtgttcgacggcaaaaagatca
ctgtaaccgggaccctgtggaacggcaacaaaattatcgacgagcgcctgatcaaccccgacggc
tccctgctgttccgcgtaaccatcaacggagtgaccggctggcggctgtgcgagcgcattttggc
gggaagttctggtggaggaagttctggtggagagcctactactgagaacttgtacttccagagcg
ataacggaagttctggtggaggaagttctggtggaatggtgtttacactcgaagatttcgtaggg
gactggcggcagacagccggctacaacctggaccaagtccttgagcagggcggtgtgtccagttt
gtttcagaatctcggggtgtccgtaactccgatccaaaggattgtcctgagcggtgaaaacggcc
tgaagatcgacatccatgtcatcatcccgtatgaaggtctgagcggcgatcagatgggccagatc
gaaaaaatttttaaggtggtgtaccctgtg

**SEQ ID NO:191 (L27V CP 84 TEV)**
MDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDG
SLLFRVTINGVTGWRLCERILAGSSGGGSSGGEPTTENLYFQSDNGSSGGGSSGGMVFTLEDFVG
DWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQI
EKIFKVVYPV

**SEQ ID NO:192 (L27V CP 85 TEV)**
atggatcatcactttaaggtgattctgcactatggcacactggtaatcgacggggttacgccgaa
catgatcgactatttcggacggccgtatgaaggcatcgccgtgttcgacggcaaaaagatcactg
taaccgggaccctgtggaacggcaacaaaattatcgacgagcgcctgatcaaccccgacggctcc
ctgctgttccgcgtaaccatcaacggagtgaccggctggcggctgtgcgagcgcattttggcggg
aagttctggtggaggaagttctggtggagagcctactactgagaacttgtacttccagagcgata
acggaagttctggtggaggaagttctggtggaatggtgtttacactcgaagatttcgtaggggac

tggcggcagacagccggctacaacctggaccaagtccttgagcagggcggtgtgtccagtttgtt
tcagaatctcggggtgtccgtaactccgatccaaaggattgtcctgagcggtgaaaacggcctga
agatcgacatccatgtcatcatcccgtatgaaggtctgagcggcgatcagatgggccagatcgaa
aaaatttttaaggtggtgtaccctgtggat

**SEQ ID NO:193 (L27V CP 85 TEV)**
MDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDGS
LLFRVTINGVTGWRLCERILAGSSGGGSSGGEPTTENLYFQSDNGSSGGGSSGGMVFTLEDFVGD
WRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIE
KIFKVVYPVD

**SEQ ID NO:194 (L27V CP 86 TEV)**
atgcatcactttaaggtgattctgcactatggcacactggtaatcgacggggttacgccgaacat
gatcgactatttcggacggccgtatgaaggcatcgccgtgttcgacggcaaaaagatcactgtaa
ccgggaccctgtggaacggcaacaaaattatcgacgagcgcctgatcaaccccgacggctccctg
ctgttccgcgtaaccatcaacggagtgaccggctggcggctgtgcgagcgcattttggcgggaag
ttctggtggaggaagttctggtggagagcctactactgagaacttgtacttccagagcgataacg
gaagttctggtggaggaagttctggtggaatggtgtttacactcgaagatttcgtaggggactgg
cggcagacagccggctacaacctggaccaagtccttgagcagggcggtgtgtccagtttgtttca
gaatctcggggtgtccgtaactccgatccaaaggattgtcctgagcggtgaaaacggcctgaaga
tcgacatccatgtcatcatcccgtatgaaggtctgagcggcgatcagatgggccagatcgaaaaa
atttttaaggtggtgtaccctgtggatgat

**SEQ ID NO:195 (L27V CP 86 TEV)**
MHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSL
LFRVTINGVTGWRLCERILAGSSGGGSSGGEPTTENLYFQSDNGSSGGGSSGGMVFTLEDFVGDW
RQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEK
IFKVVYPVDD

**SEQ ID NO:196 (L27V CP 87 TEV)**
atgcactttaaggtgattctgcactatggcacactggtaatcgacggggttacgccgaacatgat
cgactatttcggacggccgtatgaaggcatcgccgtgttcgacggcaaaaagatcactgtaaccg
ggaccctgtggaacggcaacaaaattatcgacgagcgcctgatcaaccccgacggctccctgctg
ttccgcgtaaccatcaacggagtgaccggctggcggctgtgcgagcgcattttggcgggaagttc
tggtggaggaagttctggtggagagcctactactgagaacttgtacttccagagcgataacggaa
gttctggtggaggaagttctggtggaatggtgtttacactcgaagatttcgtaggggactggcgg
cagacagccggctacaacctggaccaagtccttgagcagggcggtgtgtccagtttgtttcagaa
tctcggggtgtccgtaactccgatccaaaggattgtcctgagcggtgaaaacggcctgaagatcg
acatccatgtcatcatcccgtatgaaggtctgagcggcgatcagatgggccagatcgaaaaaatt
tttaaggtggtgtaccctgtggatgatcat

**SEQ ID NO:197 (L27V CP 87 TEV)**
MHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSLL
FRVTINGVTGWRLCERILAGSSGGGSSGGEPTTENLYFQSDNGSSGGGSSGGMVFTLEDFVGDWR
QTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEKI
FKVVYPVDDH

**SEQ ID NO:198 (L27V CP 88 TEV)**
atgtttaaggtgattctgcactatggcacactggtaatcgacggggttacgccgaacatgatcga
ctatttcggacggccgtatgaaggcatcgccgtgttcgacggcaaaaagatcactgtaaccggga
ccctgtggaacggcaacaaaattatcgacgagcgcctgatcaaccccgacggctccctgctgttc
cgcgtaaccatcaacggagtgaccggctggcggctgtgcgagcgcattttggcgggaagttctgg
tggaggaagttctggtggagagcctactactgagaacttgtacttccagagcgataacggaagtt

ctggtggaggaagttctggtggaatggtgtttacactcgaagatttcgtaggggactggcggcag
acagccggctacaacctggaccaagtccttgagcagggcggtgtgtccagtttgtttcagaatct
cggggtgtccgtaactccgatccaaaggattgtcctgagcggtgaaaacggcctgaagatcgaca
tccatgtcatcatcccgtatgaaggtctgagcggcgatcagatgggccagatcgaaaaaatttttt
aaggtggtgtaccctgtggatgatcatcac

**SEQ ID NO:199 (L27V CP 88 TEV)**

MFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSLLF
RVTINGVTGWRLCERILAGSSGGGSSGGEPTTENLYFQSDNGSSGGGSSGGMVFTLEDFVGDWRQ
TAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEKIF
KVVYPVDDHH

**SEQ ID NO:200 (L27V CP 91 TEV)**

atgattctgcactatggcacactggtaatcgacggggttacgccgaacatgatcgactatttcgg
acggccgtatgaaggcatcgccgtgttcgacggcaaaaagatcactgtaaccgggaccctgtgga
acggcaacaaaattatcgacgagcgcctgatcaaccccgacggctccctgctgttccgcgtaacc
atcaacggagtgaccggctggcggctgtgcgagcgcattttggcgggaagttctggtggaggaag
ttctggtggagagcctactactgagaacttgtacttccagagcgataacggaagttctggtggag
gaagttctggtggaatggtgtttacactcgaagatttcgtaggggactggcggcagacagccggc
tacaacctggaccaagtccttgagcagggcggtgtgtccagtttgtttcagaatctcggggtgtc
cgtaactccgatccaaaggattgtcctgagcggtgaaaacggcctgaagatcgacatccatgtca
tcatcccgtatgaaggtctgagcggcgatcagatgggccagatcgaaaaaatttttaaggtggtg
taccctgtggatgatcatcactttaaggtg

**SEQ ID NO:201 (L27V CP 91 TEV)**

MILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVT
INGVTGWRLCERILAGSSGGGSSGGEPTTENLYFQSDNGSSGGGSSGGMVFTLEDFVGDWRQTAG
YNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEKIFKVV
YPVDDHHFKV

**SEQ ID NO:202 (L27V CP 94 TEV)**

atgtatggcacactggtaatcgacggggttacgccgaacatgatcgactatttcggacggccgta
tgaaggcatcgccgtgttcgacggcaaaaagatcactgtaaccgggaccctgtggaacggcaaca
aaattatcgacgagcgcctgatcaaccccgacggctccctgctgttccgcgtaaccatcaacgga
gtgaccggctggcggctgtgcgagcgcattttggcgggaagttctggtggaggaagttctggtgg
agagcctactactgagaacttgtacttccagagcgataacggaagttctggtggaggaagttctg
gtggaatggtgtttacactcgaagatttcgtaggggactggcggcagacagccggctacaacctg
gaccaagtccttgagcagggcggtgtgtccagtttgtttcagaatctcggggtgtccgtaactcc
gatccaaaggattgtcctgagcggtgaaaacggcctgaagatcgacatccatgtcatcatcccgt
atgaaggtctgagcggcgatcagatgggccagatcgaaaaaatttttaaggtggtgtaccctgtg
gatgatcatcactttaaggtgattctgcacg

**SEQ ID NO:203 (L27V CP 94 TEV)**

MYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVTING
VTGWRLCERILAGSSGGGSSGGEPTTENLYFQSDNGSSGGGSSGGMVFTLEDFVGDWRQTAGYNL
DQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEKIFKVVYPV
DDHHFKVILH

**SEQ ID NO:204 (L27V CP 95 TEV)**

atgggcacactggtaatcgacggggttacgccgaacatgatcgactatttcggacggccgtatga
aggcatcgccgtgttcgacggcaaaaagatcactgtaaccgggaccctgtggaacggcaacaaaa
ttatcgacgagcgcctgatcaaccccgacggctccctgctgttccgcgtaaccatcaacggagtg
accggctggcggctgtgcgagcgcattttggcgggaagttctggtggaggaagttctggtggaga
gcctactactgagaacttgtacttccagagcgataacggaagttctggtggaggaagttctggtg
gaatggtgtttacactcgaagatttcgtaggggactggcggcagacagccggctacaacctggac
caagtccttgagcagggcggtgtgtccagtttgtttcagaatctcggggtgtccgtaactccgat
ccaaaggattgtcctgagcggtgaaaacggcctgaagatcgacatccatgtcatcatcccgtatg
aaggtctgagcggcgatcagatgggccagatcgaaaaaatttttaaggtggtgtaccctgtggat
gatcatcactttaaggtgattctgcactat

**SEQ ID NO:205 (L27V CP 95 TEV)**

MGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGV
TGWRLCERILAGSSGGGSSGGEPTTENLYFQSDNGSSGGGSSGGMVFTLEDFVGDWRQTAGYNLD
QVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEKIFKVVYPVD
DHHFKVILHY

**SEQ ID NO:206 (L27V CP 97 TEV)**

atgctggtaatcgacggggttacgccgaacatgatcgactatttcggacggccgtatgaaggcat
cgccgtgttcgacggcaaaaagatcactgtaaccgggaccctgtggaacggcaacaaaattatcg
acgagcgcctgatcaaccccgacggctccctgctgttccgcgtaaccatcaacggagtgaccggc
tggcggctgtgcgagcgcattttggcgggaagttctggtggaggaagttctggtggagagcctac
tactgagaacttgtacttccagagcgataacggaagttctggtggaggaagttctggtggaatgg
tgtttacactcgaagatttcgtaggggactggcggcagacagccggctacaacctggaccaagtc
cttgagcagggcggtgtgtccagtttgtttcagaatctcggggtgtccgtaactccgatccaaag
gattgtcctgagcggtgaaaacggcctgaagatcgacatccatgtcatcatcccgtatgaaggtc
tgagcggcgatcagatgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatgatcat
cactttaaggtgattctgcactatggcaca

**SEQ ID NO:207 (L27V CP 97 TEV)**

MLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTG
WRLCERILAGSSGGGSSGGEPTTENLYFQSDNGSSGGGSSGGMVFTLEDFVGDWRQTAGYNLDQV
LEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEKIFKVVYPVDDH
HFKVILHYGT

**SEQ ID NO:208 (L27V CP 100 TEV)**

Atggacggggttacgccgaacatgatcgactatttcggacggccgtatgaaggcatcgccgtgtt
cgacggcaaaaagatcactgtaaccgggaccctgtggaacggcaacaaaattatcgacgagcgcc
tgatcaaccccgacggctccctgctgttccgcgtaaccatcaacggagtgaccggctggcggctg
tgcgagcgcattttggcgggaagttctggtggaggaagttctggtggagagcctactactgagaa
cttgtacttccagagcgataacggaagttctggtggaggaagttctggtggaatggtgtttacac
tcgaagatttcgtaggggactggcggcagacagccggctacaacctggaccaagtccttgagcag
ggcggtgtgtccagtttgtttcagaatctcggggtgtccgtaactccgatccaaaggattgtcct
gagcggtgaaaacggcctgaagatcgacatccatgtcatcatcccgtatgaaggtctgagcggcg
atcagatgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatgatcatcactttaag
gtgattctgcactatggcacactggtaatc

**SEQ ID NO:209 (L27V CP 100 TEV)**

MDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRL
CERILAGSSGGGSSGGEPTTENLYFQSDNGSSGGGSSGGMVFTLEDFVGDWRQTAGYNLDQVLEQ
GGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEKIFKVVYPVDDHHFK
VILHYGTLVI

**SEQ ID NO:210 (L27V CP 101 TEV)**

atgggggttacgccgaacatgatcgactatttcggacggccgtatgaaggcatcgccgtgttcga
cggcaaaaagatcactgtaaccgggaccctgtggaacggcaacaaaattatcgacgagcgcctga
tcaaccccgacggctccctgctgttccgcgtaaccatcaacggagtgaccggctggcggctgtgc
gagcgcattttggcgggaagttctggtggaggaagttctggtggagagcctactactgagaactt
gtacttccagagcgataacggaagttctggtggaggaagttctggtggaatggtgtttacactcg
aagatttcgtaggggactggcggcagacagccggctacaacctggaccaagtccttgagcagggc
ggtgtgtccagtttgtttcagaatctcggggtgtccgtaactccgatccaaaggattgtcctgag
cggtgaaaacggcctgaagatcgacatccatgtcatcatcccgtatgaaggtctgagcggcgatc
agatgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatgatcatcactttaaggtg
attctgcactatggcacactggtaatcgac

**SEQ ID NO:211 (L27V CP 101 TEV)**

MGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLC
ERILAGSSGGGSSGGEPTTENLYFQSDNGSSGGGSSGGMVFTLEDFVGDWRQTAGYNLDQVLEQG
GVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEKIFKVVYPVDDHHFKV
ILHYGTLVID

**SEQ ID NO:212 (L27V CP 102 TEV)**

atggttacgccgaacatgatcgactatttcggacggccgtatgaaggcatcgccgtgttcgacgg
caaaaagatcactgtaaccgggaccctgtggaacggcaacaaaattatcgacgagcgcctgatca
accccgacggctccctgctgttccgcgtaaccatcaacggagtgaccggctggcggctgtgcgag
cgcattttggcgggaagttctggtggaggaagttctggtggagagcctactactgagaacttgta
cttccagagcgataacggaagttctggtggaggaagttctggtggaatggtgtttacactcgaag
atttcgtaggggactggcggcagacagccggctacaacctggaccaagtccttgagcagggcggt
gtgtccagtttgtttcagaatctcggggtgtccgtaactccgatccaaaggattgtcctgagcgg
tgaaaacggcctgaagatcgacatccatgtcatcatcccgtatgaaggtctgagcggcgatcaga
tgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatgatcatcactttaaggtgatt
ctgcactatggcacactggtaatcgacggg

**SEQ ID NO:213 (L27V CP 102 TEV)**

MVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCE
RILAGSSGGGSSGGEPTTENLYFQSDNGSSGGGSSGGMVFTLEDFVGDWRQTAGYNLDQVLEQGG
VSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEKIFKVVYPVDDHHFKVI
LHYGTLVIDG

**SEQ ID NO:214 (L27V CP 103 TEV)**

atgacgccgaacatgatcgactatttcggacggccgtatgaaggcatcgccgtgttcgacggcaa
aaagatcactgtaaccgggaccctgtggaacggcaacaaaattatcgacgagcgcctgatcaacc
ccgacggctccctgctgttccgcgtaaccatcaacggagtgaccggctggcggctgtgcgagcgc
attttggcgggaagttctggtggaggaagttctggtggagagcctactactgagaacttgtactt
ccagagcgataacggaagttctggtggaggaagttctggtggaatggtgtttacactcgaagatt
tcgtaggggactggcggcagacagccggctacaacctggaccaagtccttgagcagggcggtgtg
tccagtttgtttcagaatctcggggtgtccgtaactccgatccaaaggattgtcctgagcggtga
aaacggcctgaagatcgacatccatgtcatcatcccgtatgaaggtctgagcggcgatcagatgg
gccagatcgaaaaaatttttaaggtggtgtaccctgtggatgatcatcactttaaggtgattctg
cactatggcacactggtaatcgacggggtt

**SEQ ID NO:215 (L27V CP 103 TEV)**

MTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCER
ILAGSSGGGSSGGEPTTENLYFQSDNGSSGGGSSGGMVFTLEDFVGDWRQTAGYNLDQVLEQGGV
SSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEKIFKVVYPVDDHHFKVIL
HYGTLVIDGV

**SEQ ID NO:216 (L27V CP 104 TEV)**

atgccgaacatgatcgactatttcggacggccgtatgaaggcatcgccgtgttcgacggcaaaaa
gatcactgtaaccgggaccctgtggaacggcaacaaaattatcgacgagcgcctgatcaaccccg
acggctccctgctgttccgcgtaaccatcaacggagtgaccggctggcggctgtgcgagcgcatt
ttggcgggaagttctggtggaggaagttctggtggagagcctactactgagaacttgtacttcca
gagcgataacggaagttctggtggaggaagttctggtggaatggtgtttacactcgaagatttcg
taggggactggcggcagacagccggctacaacctggaccaagtccttgagcagggcggtgtgtcc
agtttgtttcagaatctcggggtgtccgtaactccgatccaaaggattgtcctgagcggtgaaaa
cggcctgaagatcgacatccatgtcatcatcccgtatgaaggtctgagcggcgatcagatgggcc
agatcgaaaaaatttttaaggtggtgtaccctgtggatgatcatcactttaaggtgattctgcac
tatggcacactggtaatcgacggggttacg

**SEQ ID NO:217 (L27V CP 104 TEV)**

MPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERI
LAGSSGGGSSGGEPTTENLYFQSDNGSSGGGSSGGMVFTLEDFVGDWRQTAGYNLDQVLEQGGVS
SLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEKIFKVVYPVDDHHFKVILH
YGTLVIDGVT

**SEQ ID NO:218 (L27V CP 105 TEV)**

atgaacatgatcgactatttcggacggccgtatgaaggcatcgccgtgttcgacggcaaaaagat
cactgtaaccgggaccctgtggaacggcaacaaaattatcgacgagcgcctgatcaaccccgacg
gctccctgctgttccgcgtaaccatcaacggagtgaccggctggcggctgtgcgagcgcattttg
gcgggaagttctggtggaggaagttctggtggagagcctactactgagaacttgtacttccagag
cgataacggaagttctggtggaggaagttctggtggaatggtgtttacactcgaagatttcgtag
gggactggcggcagacagccggctacaacctggaccaagtccttgagcagggcggtgtgtccagt
ttgtttcagaatctcggggtgtccgtaactccgatccaaaggattgtcctgagcggtgaaaacgg
cctgaagatcgacatccatgtcatcatcccgtatgaaggtctgagcggcgatcagatgggccaga

tcgaaaaaatttttaaggtggtgtaccctgtggatgatcatcactttaaggtgattctgcactat
ggcacactggtaatcgacggggttacg

**SEQ ID NO:219 (L27V CP 105 TEV)**
MNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERIL
AGSSGGGSSGGEPTTENLYFQSDNGSSGGGSSGGMVFTLEDFVGDWRQTAGYNLDQVLEQGGVSS
LFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEKIFKVVYPVDDHHFKVILHY
GTLVIDGVT

**SEQ ID NO:220 (L27V CP 106 TEV)**
atgatgatcgactatttcggacggccgtatgaaggcatcgccgtgttcgacggcaaaaagatcac
tgtaaccgggaccctgtggaacggcaacaaaattatcgacgagcgcctgatcaaccccgacggct
ccctgctgttccgcgtaaccatcaacggagtgaccggctggcggctgtgcgagcgcattttggcg
ggaagttctggtggaggaagttctggtggagagcctactactgagaacttgtacttccagagcga
taacggaagttctggtggaggaagttctggtggaatggtgtttacactcgaagatttcgtagggg
actggcggcagacagccggctacaacctggaccaagtccttgagcagggcggtgtgtccagtttg
tttcagaatctcggggtgtccgtaactccgatccaaaggattgtcctgagcggtgaaaacggcct
gaagatcgacatccatgtcatcatcccgtatgaaggtctgagcggcgatcagatgggccagatcg
aaaaaatttttaaggtggtgtaccctgtggatgatcatcactttaaggtgattctgcactatggc
acactggtaatcgacggggttacgccgaac

**SEQ ID NO:221 (L27V CP 106 TEV)**
MMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILA
GSSGGGSSGGEPTTENLYFQSDNGSSGGGSSGGMVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSL
FQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEKIFKVVYPVDDHHFKVILHYG
TLVIDGVTPN

**SEQ ID NO:222 (L27V CP 109 TEV)**
atgtatttcggacggccgtatgaaggcatcgccgtgttcgacggcaaaaagatcactgtaaccgg
gaccctgtggaacggcaacaaaattatcgacgagcgcctgatcaaccccgacggctccctgctgt
tccgcgtaaccatcaacggagtgaccggctggcggctgtgcgagcgcattttggcgggaagttct
ggtggaggaagttctggtggagagcctactactgagaacttgtacttccagagcgataacggaag
ttctggtggaggaagttctggtggaatggtgtttacactcgaagatttcgtaggggactggcggc
agacagccggctacaacctggaccaagtccttgagcagggcggtgtgtccagtttgtttcagaat
ctcggggtgtccgtaactccgatccaaaggattgtcctgagcggtgaaaacggcctgaagatcga
catccatgtcatcatcccgtatgaaggtctgagcggcgatcagatgggccagatcgaaaaaattt
ttaaggtggtgtaccctgtggatgatcatcactttaaggtgattctgcactatggcacactggta
atcgacggggttacgccgaacatgatcgac

**SEQ ID NO:223 (L27V CP 109 TEV)**
MYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILAGSS
GGGSSGGEPTTENLYFQSDNGSSGGGSSGGMVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQN
LGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLV
IDGVTPNMID

**SEQ ID NO:224 (L27V CP 112 TEV)**
atgcggccgtatgaaggcatcgccgtgttcgacggcaaaaagatcactgtaaccgggaccctgtg
gaacggcaacaaaattatcgacgagcgcctgatcaaccccgacggctccctgctgttccgcgtaa
ccatcaacggagtgaccggctggcggctgtgcgagcgcattttggcgggaagttctggtggagga
agttctggtggagagcctactactgagaacttgtacttccagagcgataacggaagttctggtgg
aggaagttctggtggaatggtgtttacactcgaagatttcgtaggggactggcggcagacagccg
gctacaacctggaccaagtccttgagcagggcggtgtgtccagtttgtttcagaatctcggggtg
tccgtaactccgatccaaaggattgtcctgagcggtgaaaacggcctgaagatcgacatccatgt

catcatcccgtatgaaggtctgagcggcgatcagatgggccagatcgaaaaaatttttaaggtgg
tgtaccctgtggatgatcatcactttaaggtgattctgcactatggcacactggtaatcgacggg
gttacgccgaacatgatcgactatttcgga

**SEQ ID NO:225 (L27V CP 112 TEV)**
MRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILAGSSGGG
SSGGEPTTENLYFQSDNGSSGGGSSGGMVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGV
SVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDG
VTPNMIDYFG

**SEQ ID NO:226 (L27V CP 115 TEV)**
atggaaggcatcgccgtgttcgacggcaaaaagatcactgtaaccgggaccctgtggaacggcaa
caaaattatcgacgagcgcctgatcaaccccgacggctccctgctgttccgcgtaaccatcaacg
gagtgaccggctggcggctgtgcgagcgcattttggcgggaagttctggtggaggaagttctggt
ggagagcctactactgagaacttgtacttccagagcgataacggaagttctggtggaggaagttc
tggtggaatggtgtttacactcgaagatttcgtaggggactggcggcagacagccggctacaacc
tggaccaagtccttgagcagggcggtgtgtccagtttgtttcagaatctcggggtgtccgtaact
ccgatccaaaggattgtcctgagcggtgaaaacggcctgaagatcgacatccatgtcatcatccc
gtatgaaggtctgagcggcgatcagatgggccagatcgaaaaaatttttaaggtggtgtaccctg
tggatgatcatcactttaaggtgattctgcactatggcacactggtaatcgacggggttacgccg
aacatgatcgactatttcggacggccgtat

**SEQ ID NO:227 (L27V CP 115 TEV)**
MEGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILAGSSGGGSSG
GEPTTENLYFQSDNGSSGGGSSGGMVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVT
PIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTP
NMIDYFGRPY

**SEQ ID NO:228 (L27V CP 120 TEV)**
atgttcgacggcaaaaagatcactgtaaccgggaccctgtggaacggcaacaaaattatcgacga
gcgcctgatcaaccccgacggctccctgctgttccgcgtaaccatcaacggagtgaccggctggc
ggctgtgcgagcgcattttggcgggaagttctggtggaggaagttctggtggagagcctactact
gagaacttgtacttccagagcgataacggaagttctggtggaggaagttctggtggaatggtgtt
tacactcgaagatttcgtaggggactggcggcagacagccggctacaacctggaccaagtccttg
agcagggcggtgtgtccagtttgtttcagaatctcggggtgtccgtaactccgatccaaaggatt
gtcctgagcggtgaaaacggcctgaagatcgacatccatgtcatcatcccgtatgaaggtctgag
cggcgatcagatgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatgatcatcact
ttaaggtgattctgcactatggcacactggtaatcgacggggttacgccgaacatgatcgactat
ttcggacggccgtatgaaggcatcgtggcc

**SEQ ID NO:229 (L27V CP 120 TEV)**
MFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILAGSSGGGSSGGEPTT
ENLYFQSDNGSSGGGSSGGMVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRI
VLSGENGLKIDIHVIIPYEGLSGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDY
FGRPYEGIVA

**SEQ ID NO:230 (L27V CP 121 TEV)**
atggacggcaaaaagatcactgtaaccgggaccctgtggaacggcaacaaaattatcgacgagcg
cctgatcaaccccgacggctccctgctgttccgcgtaaccatcaacggagtgaccggctggcggc
tgtgcgagcgcattttggcgggaagttctggtggaggaagttctggtggagagcctactactgag
aacttgtacttccagagcgataacggaagttctggtggaggaagttctggtggaatggtgtttac
actcgaagatttcgtaggggactggcggcagacagccggctacaacctggaccaagtccttgagc
agggcggtgtgtccagtttgtttcagaatctcggggtgtccgtaactccgatccaaaggattgtc

ctgagcggtgaaaacggcctgaagatcgacatccatgtcatcatcccgtatgaaggtctgagcgg
cgatcagatgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatgatcatcacttta
aggtgattctgcactatggcacactggtaatcgacggggttacgccgaacatgatcgactatttc
ggacggccgtatgaaggcatcgccgtgttc

**SEQ ID NO:231 (L27V CP 121 TEV)**
MDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILAGSSGGGSSGGEPTTE
NLYFQSDNGSSGGGSSGGMVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIV
LSGENGLKIDIHVIIPYEGLSGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYF
GRPYEGIAVF

**SEQ ID NO:232 (L27V CP 123 TEV)**
atgaaaaagatcactgtaaccgggaccctgtggaacggcaacaaaattatcgacgagcgcctgat
caaccccgacggctccctgctgttccgcgtaaccatcaacggagtgaccggctggcggctgtgcg
agcgcattttggcgggaagttctggtggaggaagttctggtggagagcctactactgagaacttg
tacttccagagcgataacggaagttctggtggaggaagttctggtggaatggtgtttacactcga
agatttcgtaggggactggcggcagacagccggctacaacctggaccaagtccttgagcagggcg
gtgtgtccagtttgtttcagaatctcggggtgtccgtaactccgatccaaaggattgtcctgagc
ggtgaaaacggcctgaagatcgacatccatgtcatcatcccgtatgaaggtctgagcggcgatca
gatgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatgatcatcactttaaggtga
ttctgcactatggcacactggtaatcgacggggttacgccgaacatgatcgactatttcggacgg
ccgtatgaaggcatcgccgtgttcgacggc

**SEQ ID NO:233 (L27V CP 123 TEV)**
MKKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILAGSSGGGSSGGEPTTENL
YFQSDNGSSGGGSSGGMVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLS
GENGLKIDIHVIIPYEGLSGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGR
PYEGIAVFDG

**SEQ ID NO:234 (L27V CP 124 TEV)**
Atgaagatcactgtaaccgggaccctgtggaacggcaacaaaattatcgacgagcgcctgatcaa
ccccgacggctccctgctgttccgcgtaaccatcaacggagtgaccggctggcggctgtgcgagc
gcattttggcgggaagttctggtggaggaagttctggtggagagcctactactgagaacttgtac
ttccagagcgataacggaagttctggtggaggaagttctggtggaatggtgtttacactcgaaga
tttcgtaggggactggcggcagacagccggctacaacctggaccaagtccttgagcagggcggtg
tgtccagtttgtttcagaatctcggggtgtccgtaactccgatccaaaggattgtcctgagcggt
gaaaacggcctgaagatcgacatccatgtcatcatcccgtatgaaggtctgagcggcgatcagat
gggccagatcgaaaaaatttttaaggtggtgtaccctgtggatgatcatcactttaaggtgattc
tgcactatggcacactggtaatcgacggggttacgccgaacatgatcgactatttcggacggccg
tatgaaggcatcgccgtgttcgacggcaaa

**SEQ ID NO:235 (L27V CP 124 TEV)**
MKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILAGSSGGGSSGGEPTTENLY
FQSDNGSSGGGSSGGMVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSG
ENGLKIDIHVIIPYEGLSGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRP
YEGIAVFDGK

**SEQ ID NO:236 (L27V CP 125 TEV)**
atgatcactgtaaccgggaccctgtggaacggcaacaaaattatcgacgagcgcctgatcaaccc
cgacggctccctgctgttccgcgtaaccatcaacggagtgaccggctggcggctgtgcgagcgca
ttttggcgggaagttctggtggaggaagttctggtggagagcctactactgagaacttgtacttc
cagagcgataacggaagttctggtggaggaagttctggtggaatggtgtttacactcgaagattt
cgtaggggactggcggcagacagccggctacaacctggaccaagtccttgagcagggcggtgtgt

ccagtttgtttcagaatctcggggtgtccgtaactccgatccaaaggattgtcctgagcggtgaa
aacggcctgaagatcgacatccatgtcatcatcccgtatgaaggtctgagcggcgatcagatggg
ccagatcgaaaaaatttttaaggtggtgtaccctgtggatgatcatcactttaaggtgattctgc
actatggcacactggtaatcgacggggttacgccgaacatgatcgactatttcggacggccgtat
gaaggcatcgccgtgttcgacggcaaaaag

**SEQ ID NO:237 (L27V CP 125 TEV)**

MITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILAGSSGGGSSGGEPTTENLYF
QSDNGSSGGGSSGGMVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGE
NGLKIDIHVIIPYEGLSGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPY
EGIAVFDGKK

**SEQ ID NO:238 (L27V CP 129 TEV)**

atggggaccctgtggaacggcaacaaaattatcgacgagcgcctgatcaaccccgacggctccct
gctgttccgcgtaaccatcaacggagtgaccggctggcggctgtgcgagcgcattttggcgggaa
gttctggtggaggaagttctggtggagagcctactactgagaacttgtacttccagagcgataac
ggaagttctggtggaggaagttctggtggaatggtgtttacactcgaagatttcgtaggggactg
gcggcagacagccggctacaacctggaccaagtccttgagcagggcggtgtgtccagtttgtttc
agaatctcggggtgtccgtaactccgatccaaaggattgtcctgagcggtgaaaacggcctgaag
atcgacatccatgtcatcatcccgtatgaaggtctgagcggcgatcagatgggccagatcgaaaa
aatttttaaggtggtgtaccctgtggatgatcatcactttaaggtgattctgcactatggcacac
tggtaatcgacggggttacgccgaacatgatcgactatttcggacggccgtatgaaggcatcgcc
gtgttcgacggcaaaaagatcactgtaacc

**SEQ ID NO:239 (L27V CP 129 TEV)**

MGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILAGSSGGGSSGGEPTTENLYFQSDN
GSSGGGSSGGMVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLK
IDIHVIIPYEGLSGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIA
VFDGKKITVT

**SEQ ID NO:240 (L27V CP 130 TEV)**

atgaccctgtggaacggcaacaaaattatcgacgagcgcctgatcaaccccgacggctccctgct
gttccgcgtaaccatcaacggagtgaccggctggcggctgtgcgagcgcattttggcgggaagtt
ctggtggaggaagttctggtggagagcctactactgagaacttgtacttccagagcgataacgga
agttctggtggaggaagttctggtggaatggtgtttacactcgaagatttcgtaggggactggcg
gcagacagccggctacaacctggaccaagtccttgagcagggcggtgtgtccagtttgtttcaga
atctcggggtgtccgtaactccgatccaaaggattgtcctgagcggtgaaaacggcctgaagatc
gacatccatgtcatcatcccgtatgaaggtctgagcggcgatcagatgggccagatcgaaaaaat
ttttaaggtggtgtaccctgtggatgatcatcactttaaggtgattctgcactatggcacactgg
taatcgacggggttacgccgaacatgatcgactatttcggacggccgtatgaaggcatcgccgtg
ttcgacggcaaaaagatcactgtaaccggg

**SEQ ID NO:241 (L27V CP 130 TEV)**

MTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILAGSSGGGSSGGEPTTENLYFQSDNG
SSGGGSSGGMVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKI
DIHVIIPYEGLSGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAV
FDGKKITVTG

**SEQ ID NO:242 (L27V CP 131 TEV)**

atgctgtggaacggcaacaaaattatcgacgagcgcctgatcaaccccgacggctccctgctgtt
ccgcgtaaccatcaacggagtgaccggctggcggctgtgcgagcgcattttggcgggaagttctg
gtggaggaagttctggtggagagcctactactgagaacttgtacttccagagcgataacggaagt
tctggtggaggaagttctggtggaatggtgtttacactcgaagatttcgtaggggactggcggca
gacagccggctacaacctggaccaagtccttgagcagggcggtgtgtccagtttgtttcagaatc
tcggggtgtccgtaactccgatccaaaggattgtcctgagcggtgaaaacggcctgaagatcgac
atccatgtcatcatcccgtatgaaggtctgagcggcgatcagatgggccagatcgaaaaaatttt
taaggtggtgtaccctgtggatgatcatcactttaaggtgattctgcactatggcacactggtaa
tcgacggggttacgccgaacatgatcgactatttcggacggccgtatgaaggcatcgccgtgttc
gacggcaaaaagatcactgtaaccgggacc

**SEQ ID NO:243 (L27V CP 131 TEV)**

MLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILAGSSGGGSSGGEPTTENLYFQSDNGS
SGGGSSGGMVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKID
IHVIIPYEGLSGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVF
DGKKITVTGT

**SEQ ID NO:244 (L27V CP 133 TEV)**

atgaacggcaacaaaattatcgacgagcgcctgatcaaccccgacggctccctgctgttccgcgt
aaccatcaacggagtgaccggctggcggctgtgcgagcgcattttggcgggaagttctggtggag
gaagttctggtggagagcctactactgagaacttgtacttccagagcgataacggaagttctggt
ggaggaagttctggtggaatggtgtttacactcgaagatttcgtaggggactggcggcagacagc
cggctacaacctggaccaagtccttgagcagggcggtgtgtccagtttgtttcagaatctcgggg
tgtccgtaactccgatccaaaggattgtcctgagcggtgaaaacggcctgaagatcgacatccat
gtcatcatcccgtatgaaggtctgagcggcgatcagatgggccagatcgaaaaaatttttaaggt
ggtgtaccctgtggatgatcatcactttaaggtgattctgcactatggcacactggtaatcgacg
gggttacgccgaacatgatcgactatttcggacggccgtatgaaggcatcgccgtgttcgacggc
aaaaagatcactgtaaccgggaccctgtggg

**SEQ ID NO:245 (L27V CP 133 TEV)**

MNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILAGSSGGGSSGGEPTTENLYFQSDNGSSG
GGSSGGMVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIH
VIIPYEGLSGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDG
KKITVTGTLW

**SEQ ID NO:246 (L27V CP 136 TEV)**

atgaaaattatcgacgagcgcctgatcaaccccgacggctccctgctgttccgcgtaaccatcaa
cggagtgaccggctggcggctgtgcgagcgcattttggcgggaagttctggtggaggaagttctg
gtggagagcctactactgagaacttgtacttccagagcgataacggaagttctggtggaggaagt
tctggtggaatggtgtttacactcgaagatttcgtaggggactggcggcagacagccggctacaa
cctggaccaagtccttgagcagggcggtgtgtccagtttgtttcagaatctcggggtgtccgtaa
ctccgatccaaaggattgtcctgagcggtgaaaacggcctgaagatcgacatccatgtcatcatc
ccgtatgaaggtctgagcggcgatcagatgggccagatcgaaaaaatttttaaggtggtgtaccc
tgtggatgatcatcactttaaggtgattctgcactatggcacactggtaatcgacggggttacgc
cgaacatgatcgactatttcggacggccgtatgaaggcatcgccgtgttcgacggcaaaaagatc
actgtaaccgggaccctgtggaacggcaac

**SEQ ID NO:247 (L27V CP 136 TEV)**

MKIIDERLINPDGSLLFRVTINGVTGWRLCERILAGSSGGGSSGGEPTTENLYFQSDNGSSGGGS
SGGMVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVII
PYEGLSGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKI
TVTGTLWNGN

**SEQ ID NO:248 (L27V CP 139 TEV)**

atggacgagcgcctgatcaaccccgacggctccctgctgttccgcgtaaccatcaacggagtgac
cggctggcggctgtgcgagcgcattttggcgggaagttctggtggaggaagttctggtggagagc
ctactactgagaacttgtacttccagagcgataacggaagttctggtggaggaagttctggtgga
atggtgtttacactcgaagatttcgtaggggactggcggcagacagccggctacaacctggacca
agtccttgagcagggcggtgtgtccagtttgtttcagaatctcggggtgtccgtaactccgatcc
aaaggattgtcctgagcggtgaaaacggcctgaagatcgacatccatgtcatcatcccgtatgaa
ggtctgagcggcgatcagatgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatga
tcatcactttaaggtgattctgcactatggcacactggtaatcgacggggttacgccgaacatga
tcgactatttcggacggccgtatgaaggcatcgccgtgttcgacggcaaaaagatcactgtaacc
gggaccctgtggaacggcaacaaaattatcgacgagcgc

**SEQ ID NO:249 (L27V CP 139 TEV)**

MDERLINPDGSLLFRVTINGVTGWRLCERILAGSSGGGSSGGEPTTENLYFQSDNGSSGGGSSGG
MVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYE
GLSGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVT
GTLWNGNKIIDER

**SEQ ID NO:250 (L27V CP 140 TEV)**

atggagcgcctgatcaaccccgacggctccctgctgttccgcgtaaccatcaacggagtgaccgg
ctggcggctgtgcgagcgcattttggcgggaagttctggtggaggaagttctggtggagagccta
ctactgagaacttgtacttccagagcgataacggaagttctggtggaggaagttctggtggaatg
gtgtttacactcgaagatttcgtaggggactggcggcagacagccggctacaacctggaccaagt
ccttgagcagggcggtgtgtccagtttgtttcagaatctcggggtgtccgtaactccgatccaaa
ggattgtcctgagcggtgaaaacggcctgaagatcgacatccatgtcatcatcccgtatgaaggt
ctgagcggcgatcagatgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatgatca
tcactttaaggtgattctgcactatggcacactggtaatcgacggggttacgccgaacatgatcg
actatttcggacggccgtatgaaggcatcgccgtgttcgacggcaaaaagatcactgtaaccggg
accctgtggaacggcaacaaaattatcgac

**SEQ ID NO:251 (L27V CP 140 TEV)**

MERLINPDGSLLFRVTINGVTGWRLCERILAGSSGGGSSGGEPTTENLYFQSDNGSSGGGSSGGM
VFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEG
LSGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTG
TLWNGNKIID

**SEQ ID NO:252 (L27V CP 141 TEV)**

atgcgcctgatcaaccccgacggctccctgctgttccgcgtaaccatcaacggagtgaccggctg
gcggctgtgcgagcgcattttggcgggaagttctggtggaggaagttctggtggagagcctacta
ctgagaacttgtacttccagagcgataacggaagttctggtggaggaagttctggtggaatggtg
tttacactcgaagatttcgtaggggactggcggcagacagccggctacaacctggaccaagtcct
tgagcagggcggtgtgtccagtttgtttcagaatctcggggtgtccgtaactccgatccaaagga
ttgtcctgagcggtgaaaacggcctgaagatcgacatccatgtcatcatcccgtatgaaggtctg
agcggcgatcagatgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatgatcatca
ctttaaggtgattctgcactatggcacactggtaatcgacggggttacgccgaacatgatcgact
atttcggacggccgtatgaaggcatcgccgtgttcgacggcaaaaagatcactgtaaccgggacc
ctgtggaacggcaacaaaattatcgacgag

**SEQ ID NO:253 (L27V CP 141 TEV)**

MRLINPDGSLLFRVTINGVTGWRLCERILAGSSGGGSSGGEPTTENLYFQSDNGSSGGGSSGGMV
FTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGL
SGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGT
LWNGNKIIDE

**SEQ ID NO:254 (L27V CP 142 TEV)**

atgctgatcaaccccgacggctccctgctgttccgcgtaaccatcaacggagtgaccggctggcg
gctgtgcgagcgcattttggcgggaagttctggtggaggaagttctggtggagagcctactactg
agaacttgtacttccagagcgataacggaagttctggtggaggaagttctggtggaatggtgttt
acactcgaagatttcgtaggggactggcggcagacagccggctacaacctggaccaagtccttga
gcagggcggtgtgtccagtttgtttcagaatctcggggtgtccgtaactccgatccaaaggattg
tcctgagcggtgaaaacggcctgaagatcgacatccatgtcatcatcccgtatgaaggtctgagc
ggcgatcagatgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatgatcatcactt
taaggtgattctgcactatggcacactggtaatcgacggggttacgccgaacatgatcgactatt
tcggacggccgtatgaaggcatcgccgtgttcgacggcaaaaagatcactgtaaccgggaccctg
tggaacggcaacaaaattatcgacgagcgc

**SEQ ID NO:255 (L27V CP 142 TEV)**

MLINPDGSLLFRVTINGVTGWRLCERILAGSSGGGSSGGEPTTENLYFQSDNGSSGGGSSGGMVF
TLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLS
GDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTL
WNGNKIIDER

**SEQ ID NO:256 (L27V CP 143 TEV)**

atgatcaaccccgacggctccctgctgttccgcgtaaccatcaacggagtgaccggctggcggct
gtgcgagcgcattttggcgggaagttctggtggaggaagttctggtggagagcctactactgaga
acttgtacttccagagcgataacggaagttctggtggaggaagttctggtggaatggtgtttaca
ctcgaagatttcgtaggggactggcggcagacagccggctacaacctggaccaagtccttgagca
gggcggtgtgtccagtttgtttcagaatctcggggtgtccgtaactccgatccaaaggattgtcc
tgagcggtgaaaacggcctgaagatcgacatccatgtcatcatcccgtatgaaggtctgagcggc
gatcagatgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatgatcatcactttaa
ggtgattctgcactatggcacactggtaatcgacggggttacgccgaacatgatcgactatttcg

gacggccgtatgaaggcatcgccgtgttcgacggcaaaaagatcactgtaaccgggaccctgtgg
aacggcaacaaaattatcgacgagcgcctg

**SEQ ID NO:257 (L27V CP 143 TEV)**
MINPDGSLLFRVTINGVTGWRLCERILAGSSGGGSSGGEPTTENLYFQSDNGSSGGGSSGGMVFT
LEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSG
DQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLW
NGNKIIDERL

**SEQ ID NO:258 (L27V CP 144 TEV)**
atgaaccccgacggctccctgctgttccgcgtaaccatcaacggagtgaccggctggcggctgtg
cgagcgcattttggcgggaagttctggtggaggaagttctggtggagagcctactactgagaact
tgtacttccagagcgataacggaagttctggtggaggaagttctggtggaatggtgtttacactc
gaagatttcgtaggggactggcggcagacagccggctacaacctggaccaagtccttgagcaggg
cggtgtgtccagtttgtttcagaatctcggggtgtccgtaactccgatccaaaggattgtcctga
gcggtgaaaacggcctgaagatcgacatccatgtcatcatcccgtatgaaggtctgagcggcgat
cagatgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatgatcatcactttaaggt
gattctgcactatggcacactggtaatcgacggggttacgccgaacatgatcgactatttcggac
ggccgtatgaaggcatcgccgtgttcgacggcaaaaagatcactgtaaccgggaccctgtggaac
ggcaacaaaattatcgacgagcgcctgatc

**SEQ ID NO:259 (L27V CP 144 TEV)**
MNPDGSLLFRVTINGVTGWRLCERILAGSSGGGSSGGEPTTENLYFQSDNGSSGGGSSGGMVFTL
EDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGD
QMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWN
GNKIIDERLI

**SEQ ID NO:260 (L27V CP 145 TEV)**
atgcccgacggctccctgctgttccgcgtaaccatcaacggagtgaccggctggcggctgtgcga
gcgcattttggcgggaagttctggtggaggaagttctggtggagagcctactactgagaacttgt
acttccagagcgataacggaagttctggtggaggaagttctggtggaatggtgtttacactcgaa
gatttcgtaggggactggcggcagacagccggctacaacctggaccaagtccttgagcagggcgg
tgtgtccagtttgtttcagaatctcggggtgtccgtaactccgatccaaaggattgtcctgagcg
gtgaaaacggcctgaagatcgacatccatgtcatcatcccgtatgaaggtctgagcggcgatcag
atgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatgatcatcactttaaggtgat
tctgcactatggcacactggtaatcgacggggttacgccgaacatgatcgactatttcggacggc
cgtatgaaggcatcgccgtgttcgacggcaaaaagatcactgtaaccgggaccctgtggaacggc
aacaaaattatcgacgagcgcctgatcaac

**SEQ ID NO:261 (L27V CP 145 TEV)**
MPDGSLLFRVTINGVTGWRLCERILAGSSGGGSSGGEPTTENLYFQSDNGSSGGGSSGGMVFTLE
DFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQ
MGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNG
NKIIDERLIN

**SEQ ID NO:262 (L27V CP 146 TEV)**
atggacggctccctgctgttccgcgtaaccatcaacggagtgaccggctggcggctgtgcgagcg
cattttggcgggaagttctggtggaggaagttctggtggagagcctactactgagaacttgtact
tccagagcgataacggaagttctggtggaggaagttctggtggaatggtgtttacactcgaagat
ttcgtaggggactggcggcagacagccggctacaacctggaccaagtccttgagcagggcggtgt
gtccagtttgtttcagaatctcggggtgtccgtaactccgatccaaaggattgtcctgagcggtg
aaaacggcctgaagatcgacatccatgtcatcatcccgtatgaaggtctgagcggcgatcagatg
ggccagatcgaaaaaatttttaaggtggtgtaccctgtggatgatcatcactttaaggtgattct

gcactatggcacactggtaatcgacggggttacgccgaacatgatcgactatttcggacggccgt
atgaaggcatcgccgtgttcgacggcaaaaagatcactgtaaccgggaccctgtggaacggcaac
aaaattatcgacgagcgcctgatcaacccc

**SEQ ID NO:263 (L27V CP 146 TEV)**
MDGSLLFRVTINGVTGWRLCERILAGSSGGGSSGGEPTTENLYFQSDNGSSGGGSSGGMVFTLED
FVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQM
GQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGN
KIIDERLINP

**SEQ ID NO:264 (L27V CP 147 TEV)**
atgggctccctgctgttccgcgtaaccatcaacggagtgaccggctggcggctgtgcgagcgcat
tttggcgggaagttctggtggaggaagttctggtggagagcctactactgagaacttgtacttcc
agagcgataacggaagttctggtggaggaagttctggtggaatggtgtttacactcgaagatttc
gtaggggactggcggcagacagccggctacaacctggaccaagtccttgagcagggcggtgtgtc
cagtttgtttcagaatctcggggtgtccgtaactccgatccaaaggattgtcctgagcggtgaaa
acggcctgaagatcgacatccatgtcatcatcccgtatgaaggtctgagcggcgatcagatgggc
cagatcgaaaaaatttttaaggtggtgtaccctgtggatgatcatcactttaaggtgattctgca
ctatggcacactggtaatcgacggggttacgccgaacatgatcgactatttcggacggccgtatg
aaggcatcgccgtgttcgacggcaaaaagatcactgtaaccgggaccctgtggaacggcaacaaa
attatcgacgagcgcctgatcaaccccgac

**SEQ ID NO:265 (L27V CP 147 TEV)**
MGSLLFRVTINGVTGWRLCERILAGSSGGGSSGGEPTTENLYFQSDNGSSGGGSSGGMVFTLEDF
VGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMG
QIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNK
IIDERLINPD

**SEQ ID NO:266 (L27V CP 148 TEV)**
atgtccctgctgttccgcgtaaccatcaacggagtgaccggctggcggctgtgcgagcgcatttt
ggcgggaagttctggtggaggaagttctggtggagagcctactactgagaacttgtacttccaga
gcgataacggaagttctggtggaggaagttctggtggaatggtgtttacactcgaagatttcgta
ggggactggcggcagacagccggctacaacctggaccaagtccttgagcagggcggtgtgtccag
tttgtttcagaatctcggggtgtccgtaactccgatccaaaggattgtcctgagcggtgaaaacg
gcctgaagatcgacatccatgtcatcatcccgtatgaaggtctgagcggcgatcagatgggccag
atcgaaaaaatttttaaggtggtgtaccctgtggatgatcatcactttaaggtgattctgcacta
tggcacactggtaatcgacggggttacgccgaacatgatcgactatttcggacggccgtatgaag
gcatcgccgtgttcgacggcaaaaagatcactgtaaccgggaccctgtggaacggcaacaaaatt
atcgacgagcgcctgatcaaccccgacggc

**SEQ ID NO:267 (L27V CP 148 TEV)**
MSLLFRVTINGVTGWRLCERILAGSSGGGSSGGEPTTENLYFQSDNGSSGGGSSGGMVFTLEDFV
GDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQ
IEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKI
IDERLINPDG

**SEQ ID NO:268 (L27V CP 149 TEV)**
atgctgctgttccgcgtaaccatcaacggagtgaccggctggcggctgtgcgagcgcattttggc
gggaagttctggtggaggaagttctggtggagagcctactactgagaacttgtacttccagagcg
ataacggaagttctggtggaggaagttctggtggaatggtgtttacactcgaagatttcgtaggg
gactggcggcagacagccggctacaacctggaccaagtccttgagcagggcggtgtgtccagttt
gtttcagaatctcggggtgtccgtaactccgatccaaaggattgtcctgagcggtgaaaacggcc
tgaagatcgacatccatgtcatcatcccgtatgaaggtctgagcggcgatcagatgggccagatc

gaaaaaatttttaaggtggtgtaccctgtggatgatcatcactttaaggtgattctgcactatgg
cacactggtaatcgacggggttacgccgaacatgatcgactatttcggacggccgtatgaaggca
tcgccgtgttcgacggcaaaaagatcactgtaaccgggaccctgtggaacggcaacaaaattatc
gacgagcgcctgatcaaccccgacggctcc

**SEQ ID NO:269 (L27V CP 149 TEV)**
MLLFRVTINGVTGWRLCERILAGSSGGGSSGGEPTTENLYFQSDNGSSGGGSSGGMVFTLEDFVG
DWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQI
EKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKII
DERLINPDGS

**SEQ ID NO:270 (L27V CP 150 TEV)**
atgctgttccgcgtaaccatcaacggagtgaccggctggcggctgtgcgagcgcattttggcggg
aagttctggtggaggaagttctggtggagagcctactactgagaacttgtacttccagagcgata
acggaagttctggtggaggaagttctggtggaatggtgtttacactcgaagatttcgtaggggac
tggcggcagacagccggctacaacctggaccaagtccttgagcagggcggtgtgtccagtttgtt
tcagaatctcggggtgtccgtaactccgatccaaaggattgtcctgagcggtgaaaacggcctga
agatcgacatccatgtcatcatcccgtatgaaggtctgagcggcgatcagatgggccagatcgaa
aaaatttttaaggtggtgtaccctgtggatgatcatcactttaaggtgattctgcactatggcac
actggtaatcgacggggttacgccgaacatgatcgactatttcggacggccgtatgaaggcatcg
ccgtgttcgacggcaaaaagatcactgtaaccgggaccctgtggaacggcaacaaaattatcgac
gagcgcctgatcaaccccgacggctccctg

**SEQ ID NO:271 (L27V CP 150 TEV)**
MLFRVTINGVTGWRLCERILAGSSGGGSSGGEPTTENLYFQSDNGSSGGGSSGGMVFTLEDFVGD
WRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIE
KIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIID
ERLINPDGSL

**SEQ ID NO:272 (L27V CP 151 TEV)**
atgttccgcgtaaccatcaacggagtgaccggctggcggctgtgcgagcgcattttggcgggaag
ttctggtggaggaagttctggtggagagcctactactgagaacttgtacttccagagcgataacg
gaagttctggtggaggaagttctggtggaatggtgtttacactcgaagatttcgtaggggactgg
cggcagacagccggctacaacctggaccaagtccttgagcagggcggtgtgtccagtttgtttca
gaatctcggggtgtccgtaactccgatccaaaggattgtcctgagcggtgaaaacggcctgaaga
tcgacatccatgtcatcatcccgtatgaaggtctgagcggcgatcagatgggccagatcgaaaaa
atttttaaggtggtgtaccctgtggatgatcatcactttaaggtgattctgcactatggcacact
ggtaatcgacggggttacgccgaacatgatcgactatttcggacggccgtatgaaggcatcgccg
tgttcgacggcaaaaagatcactgtaaccgggaccctgtggaacggcaacaaaattatcgacgag
cgcctgatcaaccccgacggctccctgctg

**SEQ ID NO:273 (L27V CP 151 TEV)**
MFRVTINGVTGWRLCERILAGSSGGGSSGGEPTTENLYFQSDNGSSGGGSSGGMVFTLEDFVGDW
RQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEK
IFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDE
RLINPDGSLL

**SEQ ID NO:274 (L27V CP 154 TEV)**
atgaccatcaacggagtgaccggctggcggctgtgcgagcgcattttggcgggaagttctggtgg
aggaagttctggtggagagcctactactgagaacttgtacttccagagcgataacggaagttctg
gtggaggaagttctggtggaatggtgtttacactcgaagatttcgtaggggactggcggcagaca
gccggctacaacctggaccaagtccttgagcagggcggtgtgtccagtttgtttcagaatctcgg
ggtgtccgtaactccgatccaaaggattgtcctgagcggtgaaaacggcctgaagatcgacatcc

atgtcatcatcccgtatgaaggtctgagcggcgatcagatgggccagatcgaaaaaatttttaag
gtggtgtaccctgtggatgatcatcactttaaggtgattctgcactatggcacactggtaatcga
cggggttacgccgaacatgatcgactatttcggacggccgtatgaaggcatcgccgtgttcgacg
gcaaaaagatcactgtaaccgggaccctgtggaacggcaacaaaattatcgacgagcgcctgatc
aaccccgacggctccctgctgttccgcgta

**SEQ ID NO:275 (L27V CP 154 TEV)**

MTINGVTGWRLCERILAGSSGGGSSGGEPTTENLYFQSDNGSSGGGSSGGMVFTLEDFVGDWRQT
AGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEKIFK
VVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLI
NPDGSLLFRV

**SEQ ID NO:276 (L27V CP 156 TEV)**

atgaacggagtgaccggctggcggctgtgcgagcgcattttggcgggaagttctggtggaggaag
ttctggtggagagcctactactgagaacttgtacttccagagcgataacggaagttctggtggag
gaagttctggtggaatggtgtttacactcgaagatttcgtaggggactggcggcagacagccggc
tacaacctggaccaagtccttgagcagggcggtgtgtccagtttgtttcagaatctcggggtgtc
cgtaactccgatccaaaggattgtcctgagcggtgaaaacggcctgaagatcgacatccatgtca
tcatcccgtatgaaggtctgagcggcgatcagatgggccagatcgaaaaaatttttaaggtggtg
taccctgtggatgatcatcactttaaggtgattctgcactatggcacactggtaatcgacggggt
tacgccgaacatgatcgactatttcggacggccgtatgaaggcatcgccgtgttcgacggcaaaa
agatcactgtaaccgggaccctgtggaacggcaacaaaattatcgacgagcgcctgatcaacccc
gacggctccctgctgttccgcgtaaccatc

**SEQ ID NO:277 (L27V CP 156 TEV)**

MNGVTGWRLCERILAGSSGGGSSGGEPTTENLYFQSDNGSSGGGSSGGMVFTLEDFVGDWRQTAG
YNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEKIFKVV
YPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINP
DGSLLFRVTI

**SEQ ID NO:278 (L27V CP 157 TEV)**

atgggagtgaccggctggcggctgtgcgagcgcattttggcgggaagttctggtggaggaagttc
tggtggagagcctactactgagaacttgtacttccagagcgataacggaagttctggtggaggaa
gttctggtggaatggtgtttacactcgaagatttcgtaggggactggcggcagacagccggctac
aacctggaccaagtccttgagcagggcggtgtgtccagtttgtttcagaatctcggggtgtccgt
aactccgatccaaaggattgtcctgagcggtgaaaacggcctgaagatcgacatccatgtcatca
tcccgtatgaaggtctgagcggcgatcagatgggccagatcgaaaaaatttttaaggtggtgtac
cctgtggatgatcatcactttaaggtgattctgcactatggcacactggtaatcgacggggttac
gccgaacatgatcgactatttcggacggccgtatgaaggcatcgccgtgttcgacggcaaaaaga
tcactgtaaccgggaccctgtggaacggcaacaaaattatcgacgagcgcctgatcaaccccgac
ggctccctgctgttccgcgtaaccatcaac

**SEQ ID NO:279 (L27V CP 157 TEV)**

MGVTGWRLCERILAGSSGGGSSGGEPTTENLYFQSDNGSSGGGSSGGMVFTLEDFVGDWRQTAGY
NLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEKIFKVVY
PVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPD
GSLLFRVTIN

**SEQ ID NO:280 (L27V CP 158 TEV)**

atggtgaccggctggcggctgtgcgagcgcattttggcgggaagttctggtggaggaagttctgg
tggagagcctactactgagaacttgtacttccagagcgataacggaagttctggtggaggaagtt
ctggtggaatggtgtttacactcgaagatttcgtaggggactggcggcagacagccggctacaac
ctggaccaagtccttgagcagggcggtgtgtccagtttgtttcagaatctcggggtgtccgtaac
tccgatccaaaggattgtcctgagcggtgaaaacggcctgaagatcgacatccatgtcatcatcc
cgtatgaaggtctgagcggcgatcagatgggccagatcgaaaaaatttttaaggtggtgtaccct
gtggatgatcatcactttaaggtgattctgcactatggcacactggtaatcgacggggttacgcc
gaacatgatcgactatttcggacggccgtatgaaggcatcgccgtgttcgacggcaaaaagatca
ctgtaaccgggaccctgtggaacggcaacaaaattatcgacgagcgcctgatcaaccccgacggc
tccctgctgttccgcgtaaccatcaacgga

**SEQ ID NO:281 (L27V CP 158 TEV)**

MVTGWRLCERILAGSSGGGSSGGEPTTENLYFQSDNGSSGGGSSGGMVFTLEDFVGDWRQTAGYN
LDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEKIFKVVYP
VDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDG
SLLFRVTING

**SEQ ID NO:282 (L27V CP 160 TEV)**

atgggctggcggctgtgcgagcgcattttggcgggaagttctggtggaggaagttctggtggaga
gcctactactgagaacttgtacttccagagcgataacggaagttctggtggaggaagttctggtg
gaatggtgtttacactcgaagatttcgtaggggactggcggcagacagccggctacaacctggac
caagtccttgagcagggcggtgtgtccagtttgtttcagaatctcggggtgtccgtaactccgat
ccaaaggattgtcctgagcggtgaaaacggcctgaagatcgacatccatgtcatcatcccgtatg
aaggtctgagcggcgatcagatgggccagatcgaaaaaatttttaaggtggtgtaccctgtggat
gatcatcactttaaggtgattctgcactatggcacactggtaatcgacggggttacgccgaacat
gatcgactatttcggacggccgtatgaaggcatcgccgtgttcgacggcaaaaagatcactgtaa
ccgggaccctgtggaacggcaacaaaattatcgacgagcgcctgatcaaccccgacggctccctg
ctgttccgcgtaaccatcaacggagtgacc

**SEQ ID NO:283 (L27V CP 160 TEV)**

MGWRLCERILAGSSGGGSSGGEPTTENLYFQSDNGSSGGGSSGGMVFTLEDFVGDWRQTAGYNLD
QVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEKIFKVVYPVD
DHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSL
LFRVTINGVT

**SEQ ID NO:284 (L27V CP 163 TEV)**

atgctgtgcgagcgcattttggcgggaagttctggtggaggaagttctggtggagagcctactac
tgagaacttgtacttccagagcgataacggaagttctggtggaggaagttctggtggaatggtgt
ttacactcgaagatttcgtaggggactggcggcagacagccggctacaacctggaccaagtcctt
gagcagggcggtgtgtccagtttgtttcagaatctcggggtgtccgtaactccgatccaaaggat
tgtcctgagcggtgaaaacggcctgaagatcgacatccatgtcatcatcccgtatgaaggtctga
gcggcgatcagatgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatgatcatcac
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tttcggacggccgtatgaaggcatcgccgtgttcgacggcaaaaagatcactgtaaccgggaccc
tgtggaacggcaacaaaattatcgacgagcgcctgatcaaccccgacggctccctgctgttccgc
gtaaccatcaacggagtgaccggctggcgg

**SEQ ID NO:285 (L27V CP 163 TEV)**

MLCERILAGSSGGGSSGGEPTTENLYFQSDNGSSGGGSSGGMVFTLEDFVGDWRQTAGYNLDQVL
EQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEKIFKVVYPVDDHH
FKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSLLFR
VTINGVTGWR

**SEQ ID NO:286 (L27V CP 166 TEV)**

Atgcgcattttggcgggaagttctggtggaggaagttctggtggagagcctactactgagaactt
gtacttccagagcgataacggaagttctggtggaggaagttctggtggaatggtgtttacactcg
aagatttcgtaggggactggcggcagacagccggctacaacctggaccaagtccttgagcagggc
ggtgtgtccagtttgtttcagaatctcggggtgtccgtaactccgatccaaaggattgtcctgag
cggtgaaaacggcctgaagatcgacatccatgtcatcatcccgtatgaaggtctgagcggcgatc
agatgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatgatcatcactttaaggtg
attctgcactatggcacactggtaatcgacggggttacgccgaacatgatcgactatttcggacg
gccgtatgaaggcatcgccgtgttcgacggcaaaaagatcactgtaaccgggaccctgtggaacg
gcaacaaaattatcgacgagcgcctgatcaaccccgacggctccctgctgttccgcgtaaccatc
aacggagtgaccggctggcggctgtgcgag

**SEQ ID NO:287 (L27V CP 166 TEV)**

MRILAGSSGGGSSGGEPTTENLYFQSDNGSSGGGSSGGMVFTLEDFVGDWRQTAGYNLDQVLEQG
GVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEKIFKVVYPVDDHHFKV
ILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVTI
NGVTGWRLCE

**SEQ ID NO:288 (pCA 9 FKBP-L27V02A 157-169)**

gagtgcaggtggaaaccatctccccaggagacgggcgcaccttccccaagcgcggccagacctgc
gtggtgcactacaccgggatgcttgaagatggaaagaaatttgattcctcccgggacagaaacaa
gccctttaagtttatgctaggcaagcaggaggtgatccgaggctgggaagaaggggttgcccaga
tgagtgtgggtcagagagccaaactgactatatctccagattatgcctatggtgccactgggcac
ccaggcatcatcccaccacatgccactctcgtcttcgatgtggagcttctaaaactggaaggagg
agggagctccggtggaggcagcggtggagtgaccggctggcggctgtgcgaacgcattctggcg

**SEQ ID NO:289 (pCA 9 FKBP-L27V02A 157-169)**

GVQVETISPGDGRTFPKRGQTCVVHYTGMLEDGKKFDSSRDRNKPFKFMLGKQEVIRGWEEGVAQ
MSVGQRAKLTISPDYAYGATGHPGIIPPHATLVFDVELLKLEGGGSSGGGSGGVTGWRLCERILA

**SEQ ID NO:290 (pCA 10 L27V02A 1-156-FRB)**

atggtcttcacactcgaagatttcgttggggactggcgacagacagccggctacaacctggacca
agtccttgaacagggaggtgtgtccagtttgtttcagaatctcggggtgtccgtaactccgatcc
aaaggattgtcctgagcggtgaaaatgggctgaagatcgacatccatgtcatcatcccgtatgaa
ggtctgagcggcgaccaaatgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatga
tcatcactttaaggtgatcctgcactatggcacactggtaatcgacggggttacgccgaacatga
tcgactatttcggacggccgtatgaaggcatcgccgtgttcgacggcaaaaagatcactgtaaca
gggaccctgtggaacggcaacaaaattatcgacgagcgcctgatcaaccccgacggctccctgct
gttccgagtaaccatcaacggagtgaccggaggaggtggctcaggtggagggagctccgtggcca
tcctctggcatgagatgtggcatgaaggcctggaagaggcatctcgtttgtactttggggaaagg
aacgtgaaaggcatgtttgaggtgctggagcccttgcatgctatgatggaacggggcccccagac
tctgaaggaaacatcctttaatcaggcctatggtcgagatttaatggaggcccaagagtggtgca
ggaagtacatgaaatcagggaatgtcaaggacctcacccaagcctgggacctctattatcatgtg
ttccgacgaatctca

**SEQ ID NO:291 (pCA 10 L27V02A 1-156-FRB)**

MVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYE
GLSGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVT
GTLWNGNKIIDERLINPDGSLLFRVTINGVTGGGGSGGGSSVAILWHEMWHEGLEEASRLYFGER
NVKGMFEVLEPLHAMMERGPQTLKETSFNQAYGRDLMEAQEWCRKYMKSGNVKDLTQAWDLYYHV
FRRIS

**SEQ ID NO:292 (pCA 26 FKBP-L27V02A 1-156)**

ggagtgcaggtggaaaccatctccccaggagacgggcgcaccttccccaagcgcggccagacctg
cgtggtgcactacaccgggatgcttgaagatggaaagaaatttgattcctcccgggacagaaaca
agccctttaagtttatgctaggcaagcaggaggtgatccgaggctgggaagaaggggttgcccag
atgagtgtgggtcagagagccaaactgactatatctccagattatgcctatggtgccactgggca
cccaggcatcatcccaccacatgccactctcgtcttcgatgtggagcttctaaaactggaaggag
gagggagctccggtggaggcagcggtatggtcttcacactcgaagatttcgttggggactggcga
cagacagccggctacaacctggaccaagtccttgaacagggaggtgtgtccagtttgtttcagaa
tctcggggtgtccgtaactccgatccaaaggattgtcctgagcggtgaaaatgggctgaagatcg
acatccatgtcatcatcccgtatgaaggtctgagcggcgaccaaatgggccagatcgaaaaaatt
tttaaggtggtgtaccctgtggatgatcatcactttaaggtgatcctgcactatggcacactggt
aatcgacggggttacgccgaacatgatcgactatttcggacggccgtatgaaggcatcgccgtgt
tcgacggcaaaaagatcactgtaacagggaccctgtggaacggcaacaaaattatcgacgagcgc
ctgatcaaccccgacggctccctgctgttccgagtaaccatcaac

**SEQ ID NO:293 (pCA 26 FKBP-L27V02A 1-156)**

GVQVETISPGDGRTFPKRGQTCVVHYTGMLEDGKKFDSSRDRNKPFKFMLGKQEVIRGWEEGVAQ
MSVGQRAKLTISPDYAYGATGHPGIIPPHATLVFDVELLKLEGGGSSGGGSGMVFTLEDFVGDWR
QTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEKI
FKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDER
LINPDGSLLFRVTIN

**SEQ ID NO:294 (pCA 25 L27V02A 157-169-FRB)**

atgggagtgaccggctggcggctgtgcgaacgcattctggcgggaggaggtggctcaggtggagg
gagctccgtggccatcctctggcatgagatgtggcatgaaggcctggaagaggcatctcgtttgt
actttggggaaaggaacgtgaaaggcatgtttgaggtgctggagcccttgcatgctatgatggaa
cggggcccccagactctgaaggaaacatcctttaatcaggcctatggtcgagatttaatggaggc
ccaagagtggtgcaggaagtacatgaaatcagggaatgtcaaggacctcacccaagcctgggacc
tctattatcatgtgttccgacgaatctca

**SEQ ID NO:295 (pCA 25 L27V02A 157-169-FRB)**
MGVTGWRLCERILAGGGGSGGGSSVAILWHEMWHEGLEEASRLYFGERNVKGMFEVLEPLHAMME
RGPQTLKETSFNQAYGRDLMEAQEWCRKYMKSGNVKDLTQAWDLYYHVFRRIS

**SEQ ID NO:296 (pCA 3 FKBP-L27V02A 103-169)**
atgggagtgcaggtggaaaccatctccccaggagacgggcgcaccttccccaagcgcggccagac
ctgcgtggtgcactacaccgggatgcttgaagatggaaagaaatttgattcctcccgggacagaa
acaagccctttaagtttatgctaggcaagcaggaggtgatccgaggctgggaagaaggggttgcc
cagatgagtgtgggtcagagagccaaactgactatatctccagattatgcctatggtgccactgg
gcacccaggcatcatcccaccacatgccactctcgtcttcgatgtggagcttctaaaactggaag
gaggagggagctccggtggaggcagcggtacgccgaacatgatcgactatttcggacggccgtat
gaaggcatcgccgtgttcgacggcaaaaagatcactgtaacagggaccctgtggaacggcaacaa
aattatcgacgagcgcctgatcaaccccgacggctccctgctgttccgagtaaccatcaacggag
tgaccggctggcggctgtgcgaacgcattctggc

**SEQ ID NO:297 (pCA 3 FKBP-L27V02A 103-169)**
MGVQVETISPGDGRTFPKRGQTCVVHYTGMLEDGKKFDSSRDRNKPFKFMLGKQEVIRGWEEGVA
QMSVGQRAKLTISPDYAYGATGHPGIIPPHATLVFDVELLKLEGGGSSGGGSGTPNMIDYFGRPY
EGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERIL

**SEQ ID NO:298 (pCA 4 L27V02A 1-102-FRB)**
atggtcttcacactcgaagatttcgttggggactggcgacagacagccggctacaacctggacca
agtccttgaacagggaggtgtgtccagtttgtttcagaatctcggggtgtccgtaactccgatcc
aaaggattgtcctgagcggtgaaaatgggctgaagatcgacatccatgtcatcatcccgtatgaa
ggtctgagcggcgaccaaatgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatga
tcatcactttaaggtgatcctgcactatggcacactggtaatcgacggggttggaggaggtggct
caggtggagggagctccgtggccatcctctggcatgagatgtggcatgaaggcctggaagaggca
tctcgtttgtactttggggaaaggaacgtgaaaggcatgtttgaggtgctggagcccttgcatgc
tatgatggaacggggccccagactctgaaggaaacatcctttaatcaggcctatggtcgagatt
taatggaggcccaagagtggtgcaggaagtacatgaaatcagggaatgtcaaggacctcacccaa
gcctgggacctctattatcatgtgttccgacgaatctca

**SEQ ID NO:299 (pCA 4 L27V02A 1-102-FRB)**
MGVQVETISPGDGRTFPKRGQTCVVHYTGMLEDGKKFDSSRDRNKPFKFMLGKQEVIRGWEEGVA
QMSVGQRAKLTISPDYAYGATGHPGIIPPHATLVFDVELLKLEGGGSSGGGSGTPNMIDYFGRPY
EGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERIL

**SEQ ID NO:300 (pCA 19 L27V02A 103-169-FRB)**
atgacgccgaacatgatcgactatttcggacggccgtatgaaggcatcgccgtgttcgacggcaa
aaagatcactgtaacagggaccctgtggaacggcaacaaaattatcgacgagcgcctgatcaacc
ccgacggctccctgctgttccgagtaaccatcaacggagtgaccggctggcggctgtgcgaacgc
attctggcgggaggaggtggctcaggtggagggagctccgtggccatcctctggcatgagatgtg
gcatgaaggcctggaagaggcatctcgtttgtactttggggaaaggaacgtgaaaggcatgtttg
aggtgctggagcccttgcatgctatgatggaacggggcccccagactctgaaggaaacatccttt
aatcaggcctatggtcgagatttaatggaggcccaagagtggtgcaggaagtacatgaaatcagg
gaatgtcaaggacctcacccaagcctgggacctctattatcatgtgttccgacgaatctca

**SEQ ID NO:301 (pCA 19 L27V02A 103-169-FRB)**
MTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCER
ILAGGGGSGGGSSVAILWHEMWHEGLEEASRLYFGERNVKGMFEVLEPLHAMMERGPQTLKETSF
NQAYGRDLMEAQEWCRKYMKSGNVKDLTQAWDLYYHVFRRIS

**SEQ ID NO:302 (pCA 20 FKBP-L27V02A 1-102)**

atgggagtgcaggtggaaaccatctccccaggagacgggcgcaccttccccaagcgcggccagac
ctgcgtggtgcactacaccgggatgcttgaagatggaaagaaatttgattcctcccgggacagaa
acaagccctttaagtttatgctaggcaagcaggaggtgatccgaggctgggaagaaggggttgcc
cagatgagtgtgggtcagagagccaaactgactatatctccagattatgcctatggtgccactgg
gcacccaggcatcatcccaccacatgccactctcgtcttcgatgtggagcttctaaaactggaag
gaggagggagctccggtggaggcagcggtatggtcttcacactcgaagatttcgttggggactgg
cgacagacagccggctacaacctggaccaagtccttgaacagggaggtgtgtccagtttgtttca
gaatctcggggtgtccgtaactccgatccaaaggattgtcctgagcggtgaaaatgggctgaaga
tcgacatccatgtcatcatcccgtatgaaggtctgagcggcgaccaaatgggccagatcgaaaaa
atttttaaggtggtgtaccctgtggatgatcatcactttaaggtgatcctgcactatggcacact
ggtaatcgacggggtt

**SEQ ID NO:303 (pCA 20 FKBP-L27V02A 1-102)**
MGVQVETISPGDGRTFPKRGQTCVVHYTGMLEDGKKFDSSRDRNKPFKFMLGKQEVIRGWEEGVA
QMSVGQRAKLTISPDYAYGATGHPGIIPPHATLVFDVELLKLEGGGSSGGGSGMVFTLEDFVGDW
RQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEK
IFKVVYPVDDHHFKVILHYGTLVIDGV

**SEQ ID NO:304 (pCA 11 FKBP-L27V02A 84-169)**
atgggagtgcaggtggaaaccatctccccaggagacgggcgcaccttccccaagcgcggccagac
ctgcgtggtgcactacaccgggatgcttgaagatggaaagaaatttgattcctcccgggacagaa
acaagccctttaagtttatgctaggcaagcaggaggtgatccgaggctgggaagaaggggttgcc
cagatgagtgtgggtcagagagccaaactgactatatctccagattatgcctatggtgccactgg
gcacccaggcatcatcccaccacatgccactctcgtcttcgatgtggagcttctaaaactggaag
gaggagggagctccggtggaggcagcggtgatgatcatcactttaaggtgatcctgcactatggc
acactggtaatcgacggggttacgccgaacatgatcgactatttcggacggccgtatgaaggcat
cgccgtgttcgacggcaaaaagatcactgtaacagggaccctgtggaacggcaacaaaattatcg
acgagcgcctgatcaaccccgacggctccctgctgttccgagtaaccatcaacggagtgaccggc
tggcggctgtgcgaacgcattctggcg

**SEQ ID NO:305 (pCA 11 FKBP-L27V02A 84-169)**
MGVQVETISPGDGRTFPKRGQTCVVHYTGMLEDGKKFDSSRDRNKPFKFMLGKQEVIRGWEEGVA
QMSVGQRAKLTISPDYAYGATGHPGIIPPHATLVFDVELLKLEGGGSSGGGSGDDHHFKVILHYG
TLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTG
WRLCERILA

**SEQ ID NO:306 (pCA 12 L27V02A 1-83-FRB)**

atggtcttcacactcgaagatttcgttggggactggcgacagacagccggctacaacctggacca
agtccttgaacagggaggtgtgtccagtttgtttcagaatctcggggtgtccgtaactccgatcc
aaaggattgtcctgagcggtgaaaatgggctgaagatcgacatccatgtcatcatcccgtatgaa
ggtctgagcggcgaccaaatgggccagatcgaaaaaatttttaaggtggtgtaccctgtgggagg
aggtggctcaggtggagggagctccgtggccatcctctggcatgagatgtggcatgaaggcctgg
aagaggcatctcgtttgtactttggggaaaggaacgtgaaaggcatgtttgaggtgctggagccc
ttgcatgctatgatggaacggggccccccagactctgaaggaaacatcctttaatcaggcctatgg
tcgagatttaatggaggcccaagagtggtgcaggaagtacatgaaatcagggaatgtcaaggacc
tcacccaagcctgggacctctattatcatgtgttccgacgaatctca

**SEQ ID NO:307 (pCA 12 L27V02A 1-83-FRB)**

MVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYE
GLSGDQMGQIEKIFKVVYPVGGGGSGGGSSVAILWHEMWHEGLEEASRLYFGERNVKGMFEVLEP
LHAMMERGPQTLKETSFNQAYGRDLMEAQEWCRKYMKSGNVKDLTQAWDLYYHVFRRIS

**SEQ ID NO:308 (pCA 14 L27V02A 1-83 (no fusion))**

atggtcttcacactcgaagatttcgttggggactggcgacagacagccggctacaacctggacca
agtccttgaacagggaggtgtgtccagtttgtttcagaatctcggggtgtccgtaactccgatcc
aaaggattgtcctgagcggtgaaaatgggctgaagatcgacatccatgtcatcatcccgtatgaa
ggtctgagcggcgaccaaatgggccagatcgaaaaaatttttaaggtggtgtaccctgtg

**SEQ ID NO:309 (pCA 14 L27V02A 1-83 (no fusion))**

MVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYE
GLSGDQMGQIEKIFKVVYPV

**SEQ ID NO:310 (pCA 13 L27V02A 84-169 (no fusion))**

atggatgatcatcactttaaggtgatcctgcactatggcacactggtaatcgacggggttacgcc
gaacatgatcgactatttcggacggccgtatgaaggcatcgccgtgttcgacggcaaaaagatca
ctgtaacagggaccctgtggaacggcaacaaaattatcgacgagcgcctgatcaaccccgacggc
tccctgctgttccgagtaaccatcaacggagtgaccggctggcggctgtgcgaacgcattctggc
g

**SEQ ID NO:311 (pCA 13 L27V02A 84-169 (no fusion))**

MDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDG
SLLFRVTINGVTGWRLCERILA

**SEQ ID NO:312 (pCA 28 FKBP 1-83)**

atgggagtgcaggtggaaaccatctccccaggagacgggcgcaccttccccaagcgcggccagac
ctgcgtggtgcactacaccgggatgcttgaagatggaaagaaatttgattcctcccgggacagaa
acaagccctttaagtttatgctaggcaagcaggaggtgatccgaggctgggaagaaggggttgcc
cagatgagtgtgggtcagagagccaaactgactatatctccagattatgcctatggtgccactgg
gcacccaggcatcatcccaccacatgccactctcgtcttcgatgtggagcttctaaaactggaag
gaggagggagctccggtggaggcagcggtatggtcttcacactcgaagatttcgttggggactgg
cgacagacagccggctacaacctggaccaagtccttgaacagggaggtgtgtccagtttgtttca
gaatctcggggtgtccgtaactccgatccaaaggattgtcctgagcggtgaaaatgggctgaaga
tcgacatccatgtcatcatcccgtatgaaggtctgagcggcgaccaaatgggccagatcgaaaaa
atttttaaggtggtgtaccctgtg

**SEQ ID NO:313 (pCA 28 FKBP 1-83)**

MGVQVETISPGDGRTFPKRGQTCVVHYTGMLEDGKKFDSSRDRNKPFKFMLGKQEVIRGWEEGVA
QMSVGQRAKLTISPDYAYGATGHPGIIPPHATLVFDVELLKLEGGGSSGGGSGMVFTLEDFVGDW

RQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEK
IFKVVYPV

**SEQ ID NO:314 (pCA 27 L27V02A 84-169 FRB)**

atggatgatcatcactttaaggtgatcctgcactatggcacactggtaatcgacggggttacgcc
gaacatgatcgactatttcggacggccgtatgaaggcatcgccgtgttcgacggcaaaaagatca
ctgtaacagggaccctgtggaacggcaacaaaattatcgacgagcgcctgatcaaccccgacggc
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gggaggaggtggctcaggtggagggagctccgtggccatcctctggcatgagatgtggcatgaag
gcctggaagaggcatctcgtttgtactttggggaaaggaacgtgaaaggcatgtttgaggtgctg
gagcccttgcatgctatgatggaacggggcccccagactctgaaggaaacatcctttaatcaggc
ctatggtcgagatttaatggaggcccaagagtggtgcaggaagtacatgaaatcagggaatgtca
aggacctcacccaagcctgggacctctattatcatgtgttccgacgaatctca

**SEQ ID NO:315 (pCA 27 L27V02A 84-169 FRB)**

MDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDG
SLLFRVTINGVTGWRLCERILAGGGGSGGGSSVAILWHEMWHEGLEEASRLYFGERNVKGMFEVL
EPLHAMMERGPQTLKETSFNQAYGRDLMEAQEWCRKYMKSGNVKDLTQAWDLYYHVFRRIS

**SEQ ID NO:316** (HT7-Keap1)

atggcagaaatcggtactggctttccattcgacccccattatgtggaagtcctgggcgagcgcat
gcactacgtcgatgttggtccgcgcgatggcacccctgtgctgttcctgcacggtaacccgacct
cctcctacgtgtggcgcaacatcatcccgcatgttgcaccgacccatcgctgcattgctccagac
ctgatcggtatgggcaaatccgacaaaccagacctgggttatttcttcgacgaccacgtccgctt
catggatgccttcatcgaagccctgggtctggaagaggtcgtcctggtcattcacgactggggct
ccgctctgggtttccactgggccaagcgcaatccagagcgcgtcaaaggtattgcatttatggag
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ccgcaccaccgacgtcggccgcaagctgatcatcgatcagaacgttttatcgagggtacgctgc
cgatgggtgtcgtccgcccgctgactgaagtcgagatggaccattaccgcgagccgttcctgaat
cctgttgaccgcgagccactgtggcgcttcccaaacgagctgccaatcgccggtgagccagcgaa
catcgtcgcgctggtcgaagaatacatggactggctgcaccagtcccctgtcccgaagctgctgt
tctggggcaccccaggcgttctgatcccaccggccgaagccgctcgcctggccaaaagcctgcct
aactgcaaggctgtggacatcggcccgggtctgaatctgctgcaagaagacaacccggacctgat
cggcagcgagatcgcgcgctggctgtcgacgctcgagatttccggcgagccaaccactgaggatc
tgtactttcagagcgataacgcgatcgctttcgaaggagatagaaccatgcagccagatcccagg
cctagcggggctggggcctgctgccgattcctgcccctgcagtcacagtgccctgaggggcagg
ggacgcggtgatgtacgcctccactgagtgcaaggcggaggtgacgccctcccagcatggcaacc
gcaccttcagctacaccctggaggatcataccaagcaggcctttggcatcatgaacgagctgcgg
ctcagccagcagctgtgtgacgtcacactgcaggtcaagtaccaggatgcaccggccgcccagtt
catggcccacaaggtggtgctggcctcatccagccctgttttcaaggccatgttcaccaacgggc
tgcgggagcagggcatggaggtggtgtccattgagggtatccaccccaaggtcatggagcgcctc
attgaattcgcctacacggcctccatctccatgggcgagaagtgtgtcctccacgtcatgaacgg
cgctgtcatgtaccagatcgacagcgttgtccgtgcctgcagtgacttcctggtgcagcagctgg
accccagcaatgccatcggcatcgccaacttcgctgagcagattggctgtgtggagttgcaccag
cgtgcccgggagtacatctacatgcattttggggaggtggccaagcaagaggagttcttcaacct
gtcccactgccaactggtgaccctcatcagccgggacgacctgaacgtgcgctgcgagtccgagg
tcttccacgcctgcatcaactgggtcaagtacgactgcgaacagcgacggttctacgtccaggcg
ctgctgcgggccgtgcgctgccactcgttgacgccgaacttcctgcagatgcagctgcagaagtg
cgagatcctgcagtccgactcccgctgcaaggactacctggtcaagatcttcgaggagctcaccc
tgcacaagcccacgcaggtgatgccctgccgggcgcccaaggtgggccgcctgatctacaccgcg
ggcggctacttccgacagtcgctcagctacctggaggcttacaaccccagtaacggcacctggct
ccggttggcggacctgcaggtgccgcggagcggcctggccggctgcgtggtgggcgggctgttgt
acgccgtgggcggcaggaacaactcgcccgacggcaacaccgactccagcgccctggactgttac

aaccccatgaccaatcagtggtcgccctgcgcccccatgagcgtgccccgtaaccgcatcggggt
gggggtcatcgatggccacatctatgccgtcggcggctcccacggctgcatccaccacaacagtg
tggagaggtatgagccagagcgggatgagtggcacttggtggccccaatgctgacacgaaggatc
ggggtgggcgtggctgtcctcaatcgtctgctttatgccgtgggggggctttgacgggacaaaccg
ccttaattcagctgagtgttactacccagagaggaacgagtggcgaatgatcacagcaatgaaca
ccatccgaagcggggcaggcgtctgcgtcctgcacaactgtatctatgctgctgggggctatgat
ggtcaggaccagctgaacagcgtggagcgctacgatgtggaaacagagacgtggactttcgtagc
ccccatgaagcaccggcgaagtgccctggggatcactgtccaccaggggagaatctacgtccttg
gaggctatgatggtcacacgttcctggacagtgtggagtgttacgacccagatacagacacctgg
agcgaggtgacccgaatgacatcgggccggagtggggtgggcgtggctgtcaccatggagccctg
ccggaagcagattgaccagcagaactgtacctgttacgtagtt

**SEQ ID NO:317 (Nrf2)**

TCAATATTGGCCATTAGCCATATTATTCATTGGTTATATAGCATAAATCAATATTGGCTATTGGC
CATTGCATACGTTGTATCTATATCATAATATGTACATTTATATTGGCTCATGTCCAATATGACCG
CCATGTTGGCATTGATTATTGACTAGTTATTAATAGTAATCAATTACGGGGTCATTAGTTCATAG
CCCATATATGGAGTTCCGCGTTACATAACTTACGGTAAATGGCCCGCCTGGCTGACCGCCCAACG
ACCCCCGCCCATTGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAATAGGGACTTTCCAT
TGACGTCAATGGGTGGAGTATTTACGGTAAACTGCCCACTTGGCAGTACATCAAGTGTATCATAT
GCCAAGTCCGCCCCCTATTGACGTCAATGACGGTAAATGGCCCGCCTGGCATTATGCCCAGTACA
TGACCTTACGGGACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTG
ATGCGGTTTTGGCAGTACACCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCT
CCACCCCATTGACGTCAATGGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTC
GTAATAACCCCGCCCCGTTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGC
AGAGCTGGTTTAGTGAACCGTCAGATCACTAGAAGCTTTATTGCGGTAGTTTATCACAGTTAAAT
TGCTAACGCAGTCAGTGCTTCTGACACAACAGTCTCGAACTTAAGCTGCAGAAGTTGGTCGTGAG
GCACTGGGCAGGTAAGTATCAAGGTTACAAGACAGGTTTAAGGAGACCAATAGAAACTGGGCTTG
TCGAGACAGAGAAGACTCTTGCGTTTCTGATAGGCACCTATTGGTCTTACTGACATCCACTTTGC
CTTTCTCTCCACAGGTGTCCACTCCCAGTTCAATTACAGCTCTTAAGGCTAGAGTATTAATACGA
CTCACTATAGGGCTAGCGATCGCCATGATGGACTTGGAGCTGCCGCCGCCGGGACTCCCGTCCCA
GCAGGACATGGATTTGATTGACATACTTTGGAGGCAAGATATAGATCTTGGAGTAAGTCGAGAAG
TATTTGACTTCAGTCAGCGACGGAAAGAGTATGAGCTGGAAAAACAGAAAAAACTTGAAAAGGAA
AGACAAGAACAACTCCAAAAGGAGCAAGAGAAAGCCTTTTTCGCTCAGTTACAACTAGATGAAGA
GACAGGTGAATTTCTCCCAATTCAGCCAGCCCAGCACATCCAGTCAGAAACCAGTTCTCTCGGTG
GTTCAGGTGGTGGCGGGAGCGGTGGAGGGAGCAGCGGTGGAGTGTTTACACTCGAAGATTTCGTA
GGGGACTGGCGGCAGACAGCCGGCTACAACCTGGACCAAGTCCTTGAGCAGGGCGGTGTGTCCAG
TTTGTTTCAGAATCTCGGGGTGTCCGTAACTCCGATCCAAAGGATTGTCCTGAGCGGTGAAAACG
GCCTGAAGATCGACATCCATGTCATCATCCCGTATGAAGGTCTGAGCGGCGATCAGATGGGCCAG
ATCGAAAAAATTTTTAAGGTGGTGTACCCTGTGGATGATCATCACTTTAAGGTGATTCTGCACTA
TGGCACACTGGTAATCGACGGGGTTACGCCGAACATGATCGACTATTTCGGACGGCCGTATGAAG
GCATCGCCGTGTTCGACGGCAAAAAGATCACTGTAACCGGGACCCTGTGGAACGGCAACAAAATT
ATCGACGAGCGCCTGATCAACCCCGACGGCTCCCTGCTGTTCCGCGTAACCATCAACGGAGTGAC
CGGCTGGCGGCTGTGCGAGCGCATTTTGGCGTAAGGCCGCGACTCTAGAGTCGACCTGCAGGCAT
GCAAGCTGATCCGGCTGCTAACAAAGCCCGAAAGGAAGCTGAGTTGGCTGCTGCCACCGCTGAGC
AATAACTAGCATAACCCCTTGGGGCGGCCGCTTCGAGCAGACATGATAAGATACATTGATGAGTT
TGGACAAACCACAACTAGAATGCAGTGAAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTG
CTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAACAACAATTGCATTCATTTTATG
TTTCAGGTTCAGGGGGAGATGTGGGAGGTTTTTTTAAGCAAGTAAAACCTCTACAAATGTGGTAA
AATCGAATTTTAACAAAATATTAACGCTTACAATTTCCTGATGCGGTATTTTCTCCTTACGCATC
TGTGCGGTATTTCACACCGCATACGCGGATCTGCGCAGCACCATGGCCTGAAATAACCTCTGAAA
GAGGAACTTGGTTAGGTACCTTCTGAGGCGGAAAGAACCAGCTGTGGAATGTGTGTCAGTTAGGG
TGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGC
AACCAGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATT

AGTCAGCAACCATAGTCCCGCCCCTAACTCCGCCCATCCCGCCCCTAACTCCGCCCAGTTCCGCC
CATTCTCCGCCCCATGGCTGACTAATTTTTTTTATTTATGCAGAGGCCGAGGCCGCCTCGGCCTC
TGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTTTGGAGGCCTAGGCTTTTGCAAAAAGCTTAATT
AACTGTTGACAATTAATCATCGGCATAGTATATCGGCATAGTATAATACGACAAGGTGAGGAACT
AAACCCAGGAGGCAGATCATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGT
GGAGAGGCTATTCGGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCC
GGCTGTCAGCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAA
CTGCAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTGCT
CGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAGGATCTCC
TGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCAT
ACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTAC
TCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGCCAG
CCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGACGGCGAGGATCTCGTCGTGACCCATGGC
GATGCCTGCTTGCCGAATATCATGGTGGAAAATGGCCGCTTTTCTGGATTCATCGACTGTGGCCG
GCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTG
GCGGCGAATGGGCTGACCGCTTCCTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATC
GCCTTCTATCGCCTTCTTGACGAGTTCTTCTGAGCGGGACTCTGGGGTTCGAAATGACCGACCAA
GCGACGCCCAACCTGCCATCACGATGGCCGCAATAAAATATCTTTATTTTCATTACATCTGTGTG
TTGGTTTTTTGTGTGAATCGATAGCGATAAGGATCCTCTTTGCGCTTGCGTTTTCCCTTGTCCAG
ATAGCCCAGTAGCTGACATTCATCCGGGGTCAGCACCGTTTCTGCGGACTGGCTTTCTACCCGGT
ATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACA
TGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCAT
AGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGAC
AGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCC
TGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCA
CGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCC
CGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACG
ACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCT
ACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGC
TCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCG
CTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATTTCAAGAA
GATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTT
GGTCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTATAGTCCGGAAATACAGGAACGC
ACGCTGGATGGCCCTTCGCTGGGATGGTGAAACCATGAAAAATGGCAGCTTCAGTGGATTAAGTG
GGGGTAATGTGGCCTGTACCCTCTGGTTGCATAGGTATTCATACGGTTAAAATTTATCAGGCGCG
ATTGCGGCAGTTTTTCGGGTGGTTTGTTGCCATTTTTACCTGTCTGCTGCCGTGATCGCGCTGAA
CGCGTTTTAGCGGTGCGTACAATTAAGGGATTATGGTAAATCCACTTACTGTCTGCCCTCGTAGC
CATCGAGATAAACCGCAGTACTCCGGCCACGATGCGTCCGGCGTAGAGGATCGAGATCT

**SEQ ID NO:318 (L27V02B)**

ATGGTCTTCACACTCGAAGATTTCGTAGGTGACTGGCGACAGACAGCCGGCTACAACCTGGACCA
AGTCCTTGAACAGGGTGGTGTGTCCAGTTTGTTTCAGAATCTCGGGGGTGTCCGTAACTCCGATCC
AAAGGATTGTCCTGAGCGGTGAAAATGGGCTGAAGATCGACATCCATGTCATCATCCCGTATGAA
GGTCTGAGCGGCGACCAAATGGGCCAGATCGAAAAAATTTTTAAGGTGGTGTACCCTGTGGATGA
TCATCACTTTAAGGTGATCCTGCACTATGGCACACTGGTAATCGACGGGGTTACGCCGAACATGA
TCGACTATTTCGGACGGCCGTATGAAGGCATCGCCGTGTTCGACGGCAAAAAGATCACTGTAACT
GGGACCCTGTGGAACGGCAACAAAATTATCGACGAGCGCCTGATCAACCCCGACGGCTCCCTGCT
GTTCCGAGTAACCATCAACGGAGTGACCGGCTGGCGGCTGTGCGAACGCATTCTGGCG

**SEQ ID NO:319 (L27V01)**

ATGGTGTTTACACTCGAAGATTTCGTAGGGGACTGGCGGCAGACAGCCGGCTACAACCTGGACCA
AGTCCTTGAACAGGGCGGTGTGTCCAGTTTGTTTCAGAATCTCGGGGGTGTCCGTAACTCCGATCC

AAAGGATTGTCCTGAGCGGTGAAAACGGCCTGAAGATCGACATCCATGTCATCATCCCGTATGAA
GGTCTGAGCGGCGATCAAATGGGCCAGATCGAAAAAATTTTTAAGGTGGTGTACCCTGTGGATGA
TCATCACTTTAAGGTGATCCTGCACTATGGCACACTGGTAATCGACGGGGTTACGCCGAACATGA
TCGACTATTTCGGACGGCCGTATGAAGGCATCGCCGTGTTCGACGGCAAAAAGATCACTGTAACC
GGGACCCTGTGGAACGGCAACAAAATTATCGACGAGCGCCTGATCAACCCCGACGGCTCCCTGCT
GTTCCGCGTAACCATCAACGGAGTGACCGGCTGGCGGCTGTGCGAGCGCATTTTGGCG

**SEQ ID NO:320 (L27V01-PEST00)**

ATGGTGTTTACACTCGAAGATTTCGTAGGGGACTGGCGGCAGACAGCCGGCTACAACCTGGACCA
AGTCCTTGAACAGGGCGGTGTGTCCAGTTTGTTTCAGAATCTCGGGGTGTCCGTAACTCCGATCC
AAAGGATTGTCCTGAGCGGTGAAAACGGCCTGAAGATCGACATCCATGTCATCATCCCGTATGAA
GGTCTGAGCGGCGATCAAATGGGCCAGATCGAAAAAATTTTTAAGGTGGTGTACCCTGTGGATGA
TCATCACTTTAAGGTGATCCTGCACTATGGCACACTGGTAATCGACGGGGTTACGCCGAACATGA
TCGACTATTTCGGACGGCCGTATGAAGGCATCGCCGTGTTCGACGGCAAAAAGATCACTGTAACC
GGGACCCTGTGGAACGGCAACAAAATTATCGACGAGCGCCTGATCAACCCCGACGGCTCCCTGCT
GTTCCGCGTAACCATCAACGGAGTGACCGGCTGGCGGCTGTGCGAGCGCATTTTGGCGAATTCAC
ACGGCTTTCCGCCCGAGGTTGAAGAGCAAGCCGCCGGTACATTGCCTATGTCCTGCGCACAAGAA
AGCGGTATGGACCGGCACCCAGCCGCTTGTGCTTCAGCTCGCATCAACGTC

**SEQ ID NO:321 (IL601-L27V01)**

ATGAACTCCTTCTCCACAAGCGCCTTCGGTCCAGTTGCCTTCTCCCTGGGCCTGCTCCTGGTGTT
GCCTGCTGCCTTCCCTGCCCCAGTGTTTACACTCGAAGATTTCGTAGGGGACTGGCGGCAGACAG
CCGGCTACAACCTGGACCAAGTCCTTGAACAGGGCGGTGTGTCCAGTTTGTTTCAGAATCTCGGG
GTGTCCGTAACTCCGATCCAAAGGATTGTCCTGAGCGGTGAAAACGGCCTGAAGATCGACATCCA
TGTCATCATCCCGTATGAAGGTCTGAGCGGCGATCAAATGGGCCAGATCGAAAAAATTTTTAAGG
TGGTGTACCCTGTGGATGATCATCACTTTAAGGTGATCCTGCACTATGGCACACTGGTAATCGAC
GGGGTTACGCCGAACATGATCGACTATTTCGGACGGCCGTATGAAGGCATCGCCGTGTTCGACGG
CAAAAAGATCACTGTAACCGGGACCCTGTGGAACGGCAACAAAATTATCGACGAGCGCCTGATCA
ACCCCGACGGCTCCCTGCTGTTCCGCGTAACCATCAACGGAGTGACCGGCTGGCGGCTGTGCGAG
CGCATTTTGGCG

**SEQ ID NO:322 (L27V02A)**

ATGGTCTTCACACTCGAAGATTTCGTTGGGGACTGGCGACAGACAGCCGGCTACAACCTGGACCA
AGTCCTTGAACAGGGAGGTGTGTCCAGTTTGTTTCAGAATCTCGGGGTGTCCGTAACTCCGATCC
AAAGGATTGTCCTGAGCGGTGAAAATGGGCTGAAGATCGACATCCATGTCATCATCCCGTATGAA
GGTCTGAGCGGCGACCAAATGGGCCAGATCGAAAAAATTTTTAAGGTGGTGTACCCTGTGGATGA
TCATCACTTTAAGGTGATCCTGCACTATGGCACACTGGTAATCGACGGGGTTACGCCGAACATGA
TCGACTATTTCGGACGGCCGTATGAAGGCATCGCCGTGTTCGACGGCAAAAAGATCACTGTAACA
GGGACCCTGTGGAACGGCAACAAAATTATCGACGAGCGCCTGATCAACCCCGACGGCTCCCTGCT
GTTCCGAGTAACCATCAACGGAGTGACCGGCTGGCGGCTGTGCGAACGCATTCTGGCG

**SEQ ID NO:323 (L27V02A-PEST01)**

ATGGTCTTCACACTCGAAGATTTCGTTGGGGACTGGCGACAGACAGCCGGCTACAACCTGGACCA
AGTCCTTGAACAGGGAGGTGTGTCCAGTTTGTTTCAGAATCTCGGGGTGTCCGTAACTCCGATCC
AAAGGATTGTCCTGAGCGGTGAAAATGGGCTGAAGATCGACATCCATGTCATCATCCCGTATGAA
GGTCTGAGCGGCGACCAAATGGGCCAGATCGAAAAAATTTTTAAGGTGGTGTACCCTGTGGATGA
TCATCACTTTAAGGTGATCCTGCACTATGGCACACTGGTAATCGACGGGGTTACGCCGAACATGA
TCGACTATTTCGGACGGCCGTATGAAGGCATCGCCGTGTTCGACGGCAAAAAGATCACTGTAACA
GGGACCCTGTGGAACGGCAACAAAATTATCGACGAGCGCCTGATCAACCCCGACGGCTCCCTGCT
GTTCCGAGTAACCATCAACGGAGTGACCGGCTGGCGGCTGTGCGAACGCATTCTGGCGAATTCTC
ACGGCTTTCCGCCTGAGGTTGAAGAGCAAGCCGCCGGTACATTGCCTATGTCCTGCGCACAAGAA
AGCGGTATGGACCGGCACCCAGCCGCTTGTGCTTCAGCTCGCATCAACGTC

**SEQ ID NO:324 (IL601-L27V02A)**

ATGAACTCCTTCTCCACAAGCGCCTTCGGTCCAGTTGCCTTCTCCCTGGGCCTGCTCCTGGTGTT
GCCTGCTGCCTTCCCTGCCCCAGTCTTCACACTCGAAGATTTCGTTGGGGACTGGCGACAGACAG
CCGGCTACAACCTGGACCAAGTCCTTGAACAGGGAGGTGTGTCCAGTTTGTTTCAGAATCTCGGG
GTGTCCGTAACTCCGATCCAAAGGATTGTCCTGAGCGGTGAAAATGGGCTGAAGATCGACATCCA
TGTCATCATCCCGTATGAAGGTCTGAGCGGCGACCAAATGGGCCAGATCGAAAAAATTTTTAAGG
TGGTGTACCCTGTGGATGATCATCACTTTAAGGTGATCCTGCACTATGGCACACTGGTAATCGAC
GGGGTTACGCCGAACATGATCGACTATTTCGGACGGCCGTATGAAGGCATCGCCGTGTTCGACGG
CAAAAAGATCACTGTAACAGGGACCCTGTGGAACGGCAACAAAATTATCGACGAGCGCCTGATCA
ACCCCGACGGCTCCCTGCTGTTCCGAGTAACCATCAACGGAGTGACCGGCTGGCGGCTGTGCGAA
CGCATTCTGGCG

**SEQ ID NO:325 (L27V03)**

ATGGTCTTCACACTCGAAGATTTCGTAGGTGACTGGCGACAGACAGCCGGCTACAACCTGGACCA
AGTTCTTGAACAGGGTGGTGTGTCCAGTTTGTTTCAGAATCTCGGGGTGTCCGTAACTCCAATCC

AGAGGATAGTCCTGAGTGGTGAAAATGGGCTGAAGATCGACATCCATGTCATCATCCCTTATGAA
GGTCTGAGCGGCGATCAGATGGGGCAGATCGAAAAAATTTTTAAGGTGGTGTACCCTGTGGATGA
TCATCACTTTAAGGTGATCCTGCACTATGGCACACTGGTAATCGACGGTGTTACGCCGAACATGA
TCGACTATTTCGGACGGCCGTATGAAGGCATCGCCGTGTTCGACGGCAAAAAGATTACTGTCACT
GGAACCCTGTGGAATGGGAACAAAATTATCGACGAGCGCCTGATCAACCCCGACGGCTCACTGCT
GTTCCGAGTAACCATCAATGGTGTTACCGGCTGGCGGCTCTGCGAACGCATTCTAGCA

**SEQ ID NO:326 (L27V03-PEST02)**

ATGGTCTTCACACTCGAAGATTTCGTAGGTGACTGGCGACAGACAGCCGGCTACAACCTGGACCA
AGTTCTTGAACAGGGTGGTGTGTCCAGTTTGTTTCAGAATCTCGGGGTGTCCGTAACTCCAATCC
AGAGGATAGTCCTGAGTGGTGAAAATGGGCTGAAGATCGACATCCATGTCATCATCCCTTATGAA
GGTCTGAGCGGCGATCAGATGGGGCAGATCGAAAAAATTTTTAAGGTGGTGTACCCTGTGGATGA
TCATCACTTTAAGGTGATCCTGCACTATGGCACACTGGTAATCGACGGTGTTACGCCGAACATGA
TCGACTATTTCGGACGGCCGTATGAAGGCATCGCCGTGTTCGACGGCAAAAAGATTACTGTCACT
GGAACCCTGTGGAATGGGAACAAAATTATCGACGAGCGCCTGATCAACCCCGACGGCTCACTGCT
GTTCCGAGTAACCATCAATGGTGTTACCGGCTGGCGGCTCTGCGAACGCATTCTAGCAAATAGTC
ACGGCTTTCCGCCTGAGGTTGAAGAGCAAGCCGCCGGTACATTGCCTATGTCCTGCGCACAAGAA
AGCGGTATGGACCGGCACCCAGCCGCTTGTGCTTCAGCTCGCATCAACGTC

**SEQ ID NO:327 (IL602-L27V03)**

ATGAACTCCTTCTCCACAAGCGCCTTCGGTCCAGTCGCCTTCTCCCTGGGCCTGCTCCTGGTGTT
GCCCGCTGCCTTTCCTGCCCCAGTCTTCACACTCGAAGATTTCGTAGGTGACTGGCGACAGACAG
CCGGCTACAACCTGGACCAAGTTCTTGAACAGGGTGGTGTGTCCAGTTTGTTTCAGAATCTCGGG
GTGTCCGTAACTCCAATCCAGAGGATAGTCCTGAGTGGTGAAAATGGGCTGAAGATCGACATCCA
TGTCATCATCCCTTATGAAGGTCTGAGCGGCGATCAGATGGGGCAGATCGAAAAAATTTTTAAGG
TGGTGTACCCTGTGGATGATCATCACTTTAAGGTGATCCTGCACTATGGCACACTGGTAATCGAC
GGTGTTACGCCGAACATGATCGACTATTTCGGACGGCCGTATGAAGGCATCGCCGTGTTCGACGG
CAAAAAGATTACTGTCACTGGAACCCTGTGGAATGGGAACAAAATTATCGACGAGCGCCTGATCA
ACCCCGACGGCTCACTGCTGTTCCGAGTAACCATCAATGGTGTTACCGGCTGG

**SEQ ID NO:328 (Linker)**

GSSGGGSSGGEPTTENLYFQSDNGSSGGGSSGG

**SEQ ID NO:329 (FABP Consensus Sequence)**

[GSAIVK]-{FE}-[FYW]-x-[LIVMF]-x-x-{K}-x-[NHG]-[FY]-[DE]-x-
[LIVMFY]- [LIVM]-{N}-{G}-[LIVMAKR]

**SEQ ID NO:330 (OGLUC Consensus Sequence)**

[GSAIVK]-{FE}-[FYW]-x-[LIVMFSYQ]-x-x-{K}-x-[NHGK]-x-[DE]-x-
[LIVMFY]-[LIVMWF]-x-{G}-[LIVMAKRG]

**SEQ ID NO:331 (9B8 PCA1 (pF5A/Met-[9B8 opt (51-169)]-GGGGSGGGSS-FRB)**

Atgggcctgaagatcgacatccatgtcatcatcccgtatgaaggtctgagcggctatcagatggg
ccagatcgaaaaaatttttaaggtggtgtaccctgtggatgatcatcactttaaggtgattctgc
actatggcacactggtaatcgacggggttacgccgaacatgatcgactatttcggacggccgtat
gaaggcatcgccgtgttcgacggcaaaaagatcactgtaaccgggaccctgtggaacggcaacaa
aattatcgacgagcgcctgatcaaccccgacggctccctgctgttccgcgtaaccatcaacggag
tgaccggctggcggctgtgcgagcgcattttggcgggaggaggtggctcaggtggagggagctcc
gtggccatcctctggcatgagatgtggcatgaaggcctggaagaggcatctcgtttgtactttgg
ggaaaggaacgtgaaaggcatgtttgaggtgctggagcccttgcatgctatgatggaacggggcc

cccagactctgaaggaaacatcctttaatcaggcctatggtcgagatttaatggaggcccaagag
tggtgcaggaagtacatgaaatcagggaatgtcaaggacctcacccaagcctgggacctctatta
tcatgtgttccgacgaatctca

**SEQ ID NO:332 (9B8 PCA1 (pF5A/Met-[9B8 opt (51-169)]-GGGGSGGGSS-FRB)**

MGLKIDIHVIIPYEGLSGYQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPY
EGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILAGGGGSGGGSS
VAILWHEMWHEGLEEASRLYFGERNVKGMFEVLEPLHAMMERGPQTLKETSFNQAYGRDLMEAQE
WCRKYMKSGNVKDLTQAWDLYYHVFRRIS

**SEQ ID NO:333 (9B8 PCA2 (pF5A/[9B8 opt (1-50)]-GGGGSGGGSS-FRB)**

Atggtgtttacactcgaagatttcgtaggggactggcggcagacagccggctacaacctggacca
agtccttgagcagggcggtctgtccagtttgtttcagaaactcggggtgtccgtaacaccgatcc
aaaagattgtcctgagcggtgaaaacggaggaggtggctcaggtggagggagctccgtggccatc
ctctggcatgagatgtggcatgaaggcctggaagaggcatctcgtttgtactttggggaaaggaa
cgtgaaaggcatgtttgaggtgctggagcccttgcatgctatgatggaacggggccccccagactc
tgaaggaaacatcctttaatcaggcctatggtcgagatttaatggaggcccaagagtggtgcagg
aagtacatgaaatcagggaatgtcaaggacctcacccaagcctgggacctctattatcatgtgtt
ccgacgaatctca

**SEQ ID NO:334 (9B8 PCA2 (pF5A/[9B8 opt (1-50)]-GGGGSGGGSS-FRB)**

MVFTLEDFVGDWRQTAGYNLDQVLEQGGLSSLFQKLGVSVTPIQKIVLSGENGGGGSGGGSSVAI
LWHEMWHEGLEEASRLYFGERNVKGMFEVLEPLHAMMERGPQTLKETSFNQAYGRDLMEAQEWCR
KYMKSGNVKDLTQAWDLYYHVFRRIS

**SEQ ID NO:335 (9B8 PCA 3 (& pF5A/FKBP-GGGSSGGGSG-[9B8 opt (51-169)**

atgggagtgcaggtggaaaccatctccccaggagacgggcgcaccttccccaagcgcggccagac
ctgcgtggtgcactacaccgggatgcttgaagatggaaagaaatttgattcctcccgggacagaa
acaagccctttaagtttatgctaggcaagcaggaggtgatccgaggctgggaagaaggggttgcc
cagatgagtgtgggtcagagagccaaactgactatatctccagattatgcctatggtgccactgg
gcacccaggcatcatcccaccacatgccactctcgtcttcgatgtggagcttctaaaactggaag
gaggagggagctccggtggaggcagcggtggcctgaagatcgacatccatgtcatcatcccgtat
gaaggtctgagcggctatcagatgggccagatcgaaaaaatttttaaggtggtgtaccctgtgga
tgatcatcactttaaggtgattctgcactatggcacactggtaatcgacggggttacgccgaaca
tgatcgactatttcggacggccgtatgaaggcatcgccgtgttcgacggcaaaaagatcactgta
accgggaccctgtggaacggcaacaaaattatcgacgagcgcctgatcaaccccgacggctccct
gctgttccgcgtaaccatcaacggagtgaccggctggcggctgtgcgagcgcattttggcg

**SEQ ID NO:336 (9B8 PCA 3 (& pF5A/FKBP-GGGSSGGGSG-[9B8 opt (51-169)**

MGVQVETISPGDGRTFPKRGQTCVVHYTGMLEDGKKFDSSRDRNKPFKFMLGKQEVIRGWEEGVA
QMSVGQRAKLTISPDYAYGATGHPGIIPPHATLVFDVELLKLEGGGSSGGGSGGLKIDIHVIIPY
EGLSGYQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITV
TGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILA

**SEQ ID NO:337 (9B8 PCA 4 (pF5A/FKBP-GGGSSGGGSG-[9B8 opt (1-50)**

atgggagtgcaggtggaaaccatctccccaggagacgggcgcaccttccccaagcgcggccagac
ctgcgtggtgcactacaccgggatgcttgaagatggaaagaaatttgattcctcccgggacagaa
acaagccctttaagtttatgctaggcaagcaggaggtgatccgaggctgggaagaaggggttgcc
cagatgagtgtgggtcagagagccaaactgactatatctccagattatgcctatggtgccactgg

gcacccaggcatcatcccaccacatgccactctcgtcttcgatgtggagcttctaaaactggaag
gaggagggagctccggtggaggcagcggtatggtgtttacactcgaagatttcgtaggggactgg
cggcagacagccggctacaacctggaccaagtccttgagcagggcggtctgtccagtttgtttca
gaaactcggggtgtccgtaacaccgatccaaaagattgtcctgagcggtgaaaac

**SEQ ID NO:338 (9B8 PCA 4 (pF5A/FKBP-GGGSSGGGSG-[9B8 opt (1-50)**
MGVQVETISPGDGRTFPKRGQTCVVHYTGMLEDGKKFDSSRDRNKPFKFMLGKQEVIRGWEEGVA
QMSVGQRAKLTISPDYAYGATGHPGIIPPHATLVFDVELLKLEGGGSSGGGSGMVFTLEDFVGDW
RQTAGYNLDQVLEQGGLSSLFQKLGVSVTPIQKIVLSGEN

**SEQ ID NO:339 (K33N+L27V+K43R+Y68D)**
Atggtgtttacactcgaagatttcgtaggggactggcggcagacagccggctacaacctggacca
agtccttgagcagggcggtgtgtccagtttgtttcagaatctcggggtgtccgtaacaccgatcc
aaaggattgtcctgagcggtgaaaacggcctgaagatcgacatccatgtcatcatcccgtatgaa
ggtctgagcggcgatcagatgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatga
tcatcactttaaggtgattctgcactatggcacactggtaatcgacggggttacgccgaacatga
tcgactatttcggacggccgtatgaaggcatcgccgtgttcgacggcaaaaagatcactgtaacc
gggaccctgtggaacggcaacaaaattatcgacgagcgcctgatcaaccccgacggctccctgct
gttccgcgtaaccatcaacggagtgaccggctggcggctgtgcgagcgcattttggcg

**SEQ ID NO:340 (K33N+L27V+K43R+Y68D)**
MVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYE
GLSGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVT
GTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILA

**SEQ ID NO:341 (K33N+ L27V+T39T+K43R+S66N)**
Atggtgtttacactcgaagatttcgtaggggactggcggcagacagccggctacaacctggacca
agtccttgagcagggcggtgtgtccagtttgtttcagaatctcggggtgtccgtaactccgatcc
aaaggattgtcctgagcggtgaaaacggcctgaagatcgacatccatgtcatcatcccgtatgaa
ggtctgaacggctatcagatgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatga
tcatcactttaaggtgattctgcactatggcacactggtaatcgacggggttacgccgaacatga
tcgactatttcggacggccgtatgaaggcatcgccgtgttcgacggcaaaaagatcactgtaacc
gggaccctgtggaacggcaacaaaattatcgacgagcgcctgatcaaccccgacggctccctgct
gttccgcgtaaccatcaacggagtgaccggctggcggctgtgcgagcgcattttggcg

**SEQ ID NO:342 (K33N+ L27V+T39T+K43R+S66N)**
MVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYE
GLNGYQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVT
GTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILA

**SEQ ID NO:343 (pCA 31 pCA L27V02A 45-169 FRB)**
atggtcctgagcggtgaaaatgggctgaagatcgacatccatgtcatcatcccgtatgaaggtct
gagcggcgaccaaatgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatgatcatc
actttaaggtgatcctgcactatggcacactggtaatcgacggggttacgccgaacatgatcgac
tatttcggacggccgtatgaaggcatcgccgtgttcgacggcaaaaagatcactgtaacagggac
cctgtggaacggcaacaaaattatcgacgagcgcctgatcaaccccgacggctccctgctgttcc
gagtaaccatcaacggagtgaccggctggcggctgtgcgaacgcattctggcgggaggaggtggc
tcaggtggagggagctccgtggccatcctctggcatgagatgtggcatgaaggcctggaagaggc
atctcgtttgtactttggggaaaggaacgtgaaaggcatgtttgaggtgctggagcccttgcatg
ctatgatggaacggggccccagactctgaaggaaacatcctttaatcaggcctatggtcgagat
ttaatggaggcccaagagtggtgcaggaagtacatgaaatcagggaatgtcaaggacctcaccca
agcctgggacctctattatcatgtgttccgacgaatctca

**SEQ ID NO:344 (pCA 31 pCA L27V02A 45-169 FRB)**

MVLSGENGLKIDIHVIIPYEGLSGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMID
YFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILAGGGG
SGGGSSVAILWHEMWHEGLEEASRLYFGERNVKGMFEVLEPLHAMMERGPQTLKETSFNQAYGRD
LMEAQEWCRKYMKSGNVKDLTQAWDLYYHVFRRIS

**SEQ ID NO:345 (pCA 32 FKBP L27V02A 1-44)**

atgggagtgcaggtggaaaccatctccccaggagacgggcgcaccttccccaagcgcggccagac
ctgcgtggtgcactacaccgggatgcttgaagatggaaagaaatttgattcctcccgggacagaa
acaagccctttaagtttatgctaggcaagcaggaggtgatccgaggctgggaagaaggggttgcc
cagatgagtgtgggtcagagagccaaactgactatatctccagattatgcctatggtgccactgg
gcacccaggcatcatcccaccacatgccactctcgtcttcgatgtggagcttctaaaactggaag
gaggagggagctccggtggaggcagcggtatggtcttcacactcgaagatttcgttggggactgg
cgacagacagccggctacaacctggaccaagtccttgaacagggaggtgtgtccagtttgtttca
gaatctcggggtgtccgtaactccgatccaaaggatt

**SEQ ID NO:346 (pCA 32 FKBP L27V02A 1-44)**

MGVQVETISPGDGRTFPKRGQTCVVHYTGMLEDGKKFDSSRDRNKPFKFMLGKQEVIRGWEEGVA
QMSVGQRAKLTISPDYAYGATGHPGIIPPHATLVFDVELLKLEGGGSSGGGSGMVFTLEDFVGDW
RQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRI

**SEQ ID NO:347 (pCA 33 pCA L27V02A 46-169 FRB)**

atgctgagcggtgaaaatgggctgaagatcgacatccatgtcatcatcccgtatgaaggtctgag
cggcgaccaaatgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatgatcatcact
ttaaggtgatcctgcactatggcacactggtaatcgacggggttacgccgaacatgatcgactat
ttcggacggccgtatgaaggcatcgccgtgttcgacggcaaaaagatcactgtaacagggaccct
gtggaacggcaacaaaattatcgacgagcgcctgatcaaccccgacggctccctgctgttccgag
taaccatcaacggagtgaccggctggcggctgtgcgaacgcattctggcgggaggaggtggctca
ggtggagggagctccgtggccatcctctggcatgagatgtggcatgaaggcctggaagaggcatc
tcgtttgtactttggggaaaggaacgtgaaaggcatgtttgaggtgctggagcccttgcatgcta
tgatggaacggggcccccagactctgaaggaaacatcctttaatcaggcctatggtcgagattta
atggaggcccaagagtggtgcaggaagtacatgaaatcagggaatgtcaaggacctcacccaagc
ctgggacctctattatcatgtgttccgacgaatctca

**SEQ ID NO:348 (pCA 33 pCA L27V02A 46-169 FRB)**

MLSGENGLKIDIHVIIPYEGLSGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDY
FGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILAGGGGS
GGGSSVAILWHEMWHEGLEEASRLYFGERNVKGMFEVLEPLHAMMERGPQTLKETSFNQAYGRDL
MEAQEWCRKYMKSGNVKDLTQAWDLYYHVFRRIS

**SEQ ID NO:349 (pCA 34 pCA FKBP 1-45 L27V02A)**

atgggagtgcaggtggaaaccatctccccaggagacgggcgcaccttccccaagcgcggccagac
ctgcgtggtgcactacaccgggatgcttgaagatggaaagaaatttgattcctcccgggacagaa
acaagccctttaagtttatgctaggcaagcaggaggtgatccgaggctgggaagaaggggttgcc
cagatgagtgtgggtcagagagccaaactgactatatctccagattatgcctatggtgccactgg
gcacccaggcatcatcccaccacatgccactctcgtcttcgatgtggagcttctaaaactggaag
gaggagggagctccggtggaggcagcggtatggtcttcacactcgaagatttcgttggggactgg
cgacagacagccggctacaacctggaccaagtccttgaacagggaggtgtgtccagtttgtttca
gaatctcggggtgtccgtaactccgatccaaaggattgtc

**SEQ ID NO:350 (pCA 34 pCA FKBP 1-45 L27V02A)**

MGVQVETISPGDGRTFPKRGQTCVVHYTGMLEDGKKFDSSRDRNKPFKFMLGKQEVIRGWEEGVA
QMSVGQRAKLTISPDYAYGATGHPGIIPPHATLVFDVELLKLEGGGSSGGGSGMVFTLEDFVGDW
RQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIV

**SEQ ID NO:351 (pCA 35 pCA L27V02A 100-169 FRB)**
atggacggggttacgccgaacatgatcgactatttcggacggccgtatgaaggcatcgccgtgtt
cgacggcaaaaagatcactgtaacagggaccctgtggaacggcaacaaaattatcgacgagcgcc
tgatcaaccccgacggctccctgctgttccgagtaaccatcaacggagtgaccggctggcggctg
tgcgaacgcattctggcgggaggaggtggctcaggtggagggagctccgtggccatcctctggca
tgagatgtggcatgaaggcctggaagaggcatctcgtttgtactttggggaaaggaacgtgaaag
gcatgtttgaggtgctggagcccttgcatgctatgatggaacggggcccccagactctgaaggaa
acatcctttaatcaggcctatggtcgagatttaatggaggcccaagagtggtgcaggaagtacat
gaaatcagggaatgtcaaggacctcacccaagcctgggacctctattatcatgtgttccgacgaa
tctca

**SEQ ID NO:352 (pCA 35 pCA L27V02A 100-169 FRB)**
MDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRL
CERILAGGGGSGGGSSVAILWHEMWHEGLEEASRLYFGERNVKGMFEVLEPLHAMMERGPQTLKE
TSFNQAYGRDLMEAQEWCRKYMKSGNVKDLTQAWDLYYHVFRRIS

**SEQ ID NO:353 (pCA 36 FKBP L27V02A 1-99)**
atgggagtgcaggtggaaaccatctccccaggagacgggcgcaccttccccaagcgcggccagac
ctgcgtggtgcactacaccgggatgcttgaagatggaaagaaatttgattcctcccgggacagaa
acaagccctttaagtttatgctaggcaagcaggaggtgatccgaggctgggaagaaggggttgcc
cagatgagtgtgggtcagagagccaaactgactatatctccagattatgcctatggtgccactgg
gcacccaggcatcatcccaccacatgccactctcgtcttcgatgtggagcttctaaaactggaag
gaggagggagctccggtggaggcagcggtatggtcttcacactcgaagatttcgttggggactgg
cgacagacagccggctacaacctggaccaagtccttgaacagggaggtgtgtccagtttgtttca
gaatctcggggtgtccgtaactccgatccaaaggattgtcctgagcggtgaaaatgggctgaaga
tcgacatccatgtcatcatcccgtatgaaggtctgagcggcgaccaaatgggccagatcgaaaaa
atttttaaggtggtgtaccctgtggatgatcatcactttaaggtgatcctgcactatggcacact
ggtaatc

**SEQ ID NO:354 (pCA 36 FKBP L27V02A 1-99)**
MGVQVETISPGDGRTFPKRGQTCVVHYTGMLEDGKKFDSSRDRNKPFKFMLGKQEVIRGWEEGVA
QMSVGQRAKLTISPDYAYGATGHPGIIPPHATLVFDVELLKLEGGGSSGGGSGMVFTLEDFVGDW
RQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEK
IFKVVYPVDDHHFKVILHYGTLVI

**SEQ ID NO:355 (pCA 37 L27V02A 101-169 FRB)**
atgggggttacgccgaacatgatcgactatttcggacggccgtatgaaggcatcgccgtgttcga
cggcaaaaagatcactgtaacagggaccctgtggaacggcaacaaaattatcgacgagcgcctga
tcaaccccgacggctccctgctgttccgagtaaccatcaacggagtgaccggctggcggctgtgc
gaacgcattctggcgggaggaggtggctcaggtggagggagctccgtggccatcctctggcatga
gatgtggcatgaaggcctggaagaggcatctcgtttgtactttggggaaaggaacgtgaaaggca
tgtttgaggtgctggagcccttgcatgctatgatggaacggggcccccagactctgaaggaaaca
tcctttaatcaggcctatggtcgagatttaatggaggcccaagagtggtgcaggaagtacatgaa
atcagggaatgtcaaggacctcacccaagcctgggacctctattatcatgtgttccgacgaatct
ca

**SEQ ID NO:356 (pCA 37 L27V02A 101-169 FRB)**

MGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLC
ERILAGGGGSGGGSSVAILWHEMWHEGLEEASRLYFGERNVKGMFEVLEPLHAMMERGPQTLKET
SFNQAYGRDLMEAQEWCRKYMKSGNVKDLTQAWDLYYHVFRRIS

**SEQ ID NO:357 (pCA 38 FKBP 1-100 L27V02A)**

Atgggagtgcaggtggaaaccatctccccaggagacgggcgcaccttccccaagcgcggccagac
ctgcgtggtgcactacaccgggatgcttgaagatggaaagaaatttgattcctcccgggacagaa
acaagccctttaagtttatgctaggcaagcaggaggtgatccgaggctgggaagaaggggttgcc
cagatgagtgtgggtcagagagccaaactgactatatctccagattatgcctatggtgccactgg
gcacccaggcatcatcccaccacatgccactctcgtcttcgatgtggagcttctaaaactggaag
gaggagggagctccggtggaggcagcggtatggtcttcacactcgaagatttcgttggggactgg
cgacagacagccggctacaacctggaccaagtccttgaacagggaggtgtgtccagtttgtttca
gaatctcggggtgtccgtaactccgatccaaaggattgtcctgagcggtgaaaatgggctgaaga
tcgacatccatgtcatcatcccgtatgaaggtctgagcggcgaccaaatgggccagatcgaaaaa
atttttaaggtggtgtaccctgtggatgatcatcactttaaggtgatcctgcactatggcacact
ggtaatcgac

**SEQ ID NO:358 (pCA 38 FKBP 1-100 L27V02A)**

MGVQVETISPGDGRTFPKRGQTCVVHYTGMLEDGKKFDSSRDRNKPFKFMLGKQEVIRGWEEGVA
QMSVGQRAKLTISPDYAYGATGHPGIIPPHATLVFDVELLKLEGGGSSGGGSGMVFTLEDFVGDW
RQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEK
IFKVVYPVDDHHFKVILHYGTLVID

**SEQ ID NO:359 (pCA 39 L27V02A 102-169 FRB)**

Atggttacgccgaacatgatcgactatttcggacggccgtatgaaggcatcgccgtgttcgacgg
caaaaagatcactgtaacagggaccctgtggaacggcaacaaaattatcgacgagcgcctgatca
accccgacggctccctgctgttccgagtaaccatcaacggagtgaccggctggcggctgtgcgaa
cgcattctggcgggaggaggtggctcaggtggagggagctccgtggccatcctctggcatgagat
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ttgaggtgctggagcccttgcatgctatgatggaacggggcccccagactctgaaggaaacatcc
tttaatcaggcctatggtcgagatttaatggaggcccaagagtggtgcaggaagtacatgaaatc
agggaatgtcaaggacctcacccaagcctgggacctctattatcatgtgttccgacgaatctca

**SEQ ID NO:360 (pCA 39 L27V02A 102-169 FRB)**

MVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCE
RILAGGGGSGGGSSVAILWHEMWHEGLEEASRLYFGERNVKGMFEVLEPLHAMMERGPQTLKETS
FNQAYGRDLMEAQEWCRKYMKSGNVKDLTQAWDLYYHVFRRIS

**SEQ ID NO:361 (pCA 40 FKBP L27V02A 1-101)**

atgggagtgcaggtggaaaccatctccccaggagacgggcgcaccttccccaagcgcggccagac
ctgcgtggtgcactacaccgggatgcttgaagatggaaagaaatttgattcctcccgggacagaa
acaagccctttaagtttatgctaggcaagcaggaggtgatccgaggctgggaagaaggggttgcc
cagatgagtgtgggtcagagagccaaactgactatatctccagattatgcctatggtgccactgg
gcacccaggcatcatcccaccacatgccactctcgtcttcgatgtggagcttctaaaactggaag
gaggagggagctccggtggaggcagcggtatggtcttcacactcgaagatttcgttggggactgg
cgacagacagccggctacaacctggaccaagtccttgaacagggaggtgtgtccagtttgtttca
gaatctcggggtgtccgtaactccgatccaaaggattgtcctgagcggtgaaaatgggctgaaga
tcgacatccatgtcatcatcccgtatgaaggtctgagcggcgaccaaatgggccagatcgaaaaa
atttttaaggtggtgtaccctgtggatgatcatcactttaaggtgatcctgcactatggcacact
ggtaatcgacggg

**SEQ ID NO:362 (pCA 40 FKBP L27V02A 1-101)**

MGVQVETISPGDGRTFPKRGQTCVVHYTGMLEDGKKFDSSRDRNKPFKFMLGKQEVIRGWEEGVA
QMSVGQRAKLTISPDYAYGATGHPGIIPPHATLVFDVELLKLEGGGSSGGGSGMVFTLEDFVGDW
RQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEK
IFKVVYPVDDHHFKVILHYGTLVIDG

**SEQ ID NO:363 (pCA 41 L27V02A 143-169 FRB)**
atgatcaaccccgacggctccctgctgttccgagtaaccatcaacggagtgaccggctggcggct
gtgcgaacgcattctggcgggaggaggtggctcaggtggagggagctccgtggccatcctctggc
atgagatgtggcatgaaggcctggaagaggcatctcgtttgtactttggggaaaggaacgtgaaa
ggcatgtttgaggtgctggagcccttgcatgctatgatggaacggggcccccagactctgaagga
aacatcctttaatcaggcctatggtcgagatttaatggaggcccaagagtggtgcaggaagtaca
tgaaatcagggaatgtcaaggacctcacccaagcctgggacctctattatcatgtgttccgacga
atctca

**SEQ ID NO:364 (pCA 41 L27V02A 143-169 FRB)**
MINPDGSLLFRVTINGVTGWRLCERILAGGGGSGGGSSVAILWHEMWHEGLEEASRLYFGERNVK
GMFEVLEPLHAMMERGPQTLKETSFNQAYGRDLMEAQEWCRKYMKSGNVKDLTQAWDLYYHVFRR
IS

**SEQ ID NO:365 (pCA 42 FKBP 1-142 L27V02A)**
atgggagtgcaggtggaaaccatctccccaggagacgggcgcaccttccccaagcgcggccagac
ctgcgtggtgcactacaccgggatgcttgaagatggaaagaaatttgattcctcccgggacagaa
acaagccctttaagtttatgctaggcaagcaggaggtgatccgaggctgggaagaaggggttgcc
cagatgagtgtgggtcagagagccaaactgactatatctccagattatgcctatggtgccactgg
gcacccaggcatcatcccaccacatgccactctcgtcttcgatgtggagcttctaaaactggaag
gaggagggagctccggtggaggcagcggtatggtcttcacactcgaagatttcgttggggactgg
cgacagacagccggctacaacctggaccaagtccttgaacagggaggtgtgtccagtttgtttca
gaatctcggggtgtccgtaactccgatccaaaggattgtcctgagcggtgaaaatgggctgaaga
tcgacatccatgtcatcatcccgtatgaaggtctgagcggcgaccaaatgggccagatcgaaaaa
atttttaaggtggtgtaccctgtggatgatcatcactttaaggtgatcctgcactatggcacact
ggtaatcgacggggttacgccgaacatgatcgactatttcggacggccgtatgaaggcatcgccg
tgttcgacggcaaaaagatcactgtaacagggaccctgtggaacggcaacaaaattatcgacgag
cgcctg

**SEQ ID NO:366 (pCA 42 FKBP 1-142 L27V02A)**
MGVQVETISPGDGRTFPKRGQTCVVHYTGMLEDGKKFDSSRDRNKPFKFMLGKQEVIRGWEEGVA
QMSVGQRAKLTISPDYAYGATGHPGIIPPHATLVFDVELLKLEGGGSSGGGSGMVFTLEDFVGDW
RQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEK
IFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDE
RL

**SEQ ID NO:367 (pCA 43 L27V02A 145-169 FRB)**

atgcccgacggctccctgctgttccgagtaaccatcaacggagtgaccggctggcggctgtgcga
acgcattctggcgggaggaggtggctcaggtggagggagctccgtggccatcctctggcatgaga
tgtggcatgaaggcctggaagaggcatctcgtttgtactttggggaaaggaacgtgaaaggcatg
tttgaggtgctggagcccttgcatgctatgatggaacggggcccccagactctgaaggaaacatc
ctttaatcaggcctatggtcgagatttaatggaggcccaagagtggtgcaggaagtacatgaaat
cagggaatgtcaaggacctcacccaagcctgggacctctattatcatgtgttccgacgaatctca

**SEQ ID NO:368 (pCA 43 L27V02A 145-169 FRB)**
MPDGSLLFRVTINGVTGWRLCERILAGGGGSGGGSSVAILWHEMWHEGLEEASRLYFGERNVKGM
FEVLEPLHAMMERGPQTLKETSFNQAYGRDLMEAQEWCRKYMKSGNVKDLTQAWDLYYHVFRRIS

**SEQ ID NO:369 (pCA 44 FKBP 1-144 L27V02A)**

atgggagtgcaggtggaaaccatctccccaggagacgggcgcaccttccccaagcgcggccagac
ctgcgtggtgcactacaccgggatgcttgaagatggaaagaaatttgattcctcccgggacagaa
acaagccctttaagtttatgctaggcaagcaggaggtgatccgaggctgggaagaaggggttgcc
cagatgagtgtgggtcagagagccaaactgactatatctccagattatgcctatggtgccactgg
gcacccaggcatcatcccaccacatgccactctcgtcttcgatgtggagcttctaaaactggaag
gaggagggagctccggtggaggcagcggtatggtcttcacactcgaagatttcgttggggactgg
cgacagacagccggctacaacctggaccaagtccttgaacagggaggtgtgtccagtttgtttca
gaatctcggggtgtccgtaactccgatccaaaggattgtcctgagcggtgaaaatgggctgaaga
tcgacatccatgtcatcatcccgtatgaaggtctgagcggcgaccaaatgggccagatcgaaaaa
atttttaaggtggtgtaccctgtggatgatcatcactttaaggtgatcctgcactatggcacact
ggtaatcgacggggttacgccgaacatgatcgactatttcggacggccgtatgaaggcatcgccg
tgttcgacggcaaaaagatcactgtaacagggaccctgtggaacggcaacaaaattatcgacgag
cgcctgatcaac

**SEQ ID NO:370 (pCA 44 FKBP 1-144 L27V02A)**

MGVQVETISPGDGRTFPKRGQTCVVHYTGMLEDGKKFDSSRDRNKPFKFMLGKQEVIRGWEEGVA
QMSVGQRAKLTISPDYAYGATGHPGIIPPHATLVFDVELLKLEGGGSSGGGSGMVFTLEDFVGDW
RQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEK
IFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDE
RLIN

**SEQ ID NO:371 (pCA 45 L27V02A 147-169 FRB)**

atgggctccctgctgttccgagtaaccatcaacggagtgaccggctggcggctgtgcgaacgcat
tctggcgggaggaggtggctcaggtggagggagctccgtggccatcctctggcatgagatgtggc
atgaaggcctggaagaggcatctcgtttgtactttggggaaaggaacgtgaaaggcatgtttgag
gtgctggagcccttgcatgctatgatggaacggggcccccagactctgaaggaaacatcctttaa
tcaggcctatggtcgagatttaatggaggcccaagagtggtgcaggaagtacatgaaatcaggga
atgtcaaggacctcacccaagcctgggacctctattatcatgtgttccgacgaatctca

**SEQ ID NO:372 (pCA 45 L27V02A 147-169 FRB)**

MGSLLFRVTINGVTGWRLCERILAGGGGSGGGSSVAILWHEMWHEGLEEASRLYFGERNVKGMFE
VLEPLHAMMERGPQTLKETSFNQAYGRDLMEAQEWCRKYMKSGNVKDLTQAWDLYYHVFRRIS

**SEQ ID NO:373 (pCA 46 FKBP- L27V02A 1-146)**

atgggagtgcaggtggaaaccatctccccaggagacgggcgcaccttccccaagcgcggccagac
ctgcgtggtgcactacaccgggatgcttgaagatggaaagaaatttgattcctcccgggacagaa
acaagcactttaagtttatgctaggcaagcaggaggtgatccgaggctgggaagaaggggttgcc
cagatgagtgtgggtcagagagccaaactgactatatctccagattatgcctatggtgccactgg
gcacccaggcatcatcccaccacatgccactctcgtcttcgatgtggagcttctaaaactggaag
gaggagggagctccggtggaggcagcggtatggtcttcacactcgaagatttcgttggggactgg
cgacagacagccggctacaacctggaccaagtccttgaacagggaggtgtgtccagtttgtttca
gaatctcggggtgtccgtaactccgatccaaaggattgtcctgagcggtgaaaatgggctgaaga
tcgacatccatgtcatcatcccgtatgaaggtctgagcggcgaccaaatgggccagatcgaaaaa
atttttaaggtggtgtaccctgtggatgatcatcactttaaggtgatcctgcactatggcacact
ggtaatcgacggggttacgccgaacatgatcgactatttcggacggccgtatgaaggcatcgccg
tgttcgacggcaaaaagatcactgtaacagggaccctgtggaacggcaacaaaattatcgacgag
cgcctgatcaaccccgac

**SEQ ID NO:374 (pCA 46 L27V02A-FKBP 1-146)**

MGVQVETISPGDGRTFPKRGQTCVVHYTGMLEDGKKFDSSRDRNKHFKFMLGKQEVIRGWEEGVA
QMSVGQRAKLTISPDYAYGATGHPGIIPPHATLVFDVELLKLEGGGSSGGGSGMVFTLEDFVGDW

RQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEK
IFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDE
RLINPD

**SEQ ID NO:375 (pCA 47 L27V02A 148-169 FRB)**
atgtccctgctgttccgagtaaccatcaacggagtgaccggctggcggctgtgcgaacgcattct
ggcgggaggaggtggctcaggtggagggagctccgtggccatcctctggcatgagatgtggcatg
aaggcctggaagaggcatctcgtttgtactttggggaaaggaacgtgaaaggcatgtttgaggtg
ctggagcccttgcatgctatgatggaacggggcccccagactctgaaggaaacatcctttaatca
ggcctatggtcgagatttaatggaggcccaagagtggtgcaggaagtacatgaaatcagggaatg
tcaaggacctcacccaagcctgggacctctattatcatgtgttccgacgaatctca

**SEQ ID NO:376 (pCA 47 L27V02A 148-169 FRB)**
MSLLFRVTINGVTGWRLCERILAGGGGSGGGSSVAILWHEMWHEGLEEASRLYFGERNVKGMFEV
LEPLHAMMERGPQTLKETSFNQAYGRDLMEAQEWCRKYMKSGNVKDLTQAWDLYYHVFRRIS

**SEQ ID NO:377 (pCA 48 FKBP- L27V02A 1-147)**
atgggagtgcaggtggaaaccatctccccaggagacgggcgcaccttccccaagcgcggccagac
ctgcgtggtgcactacaccgggatgcttgaagatggaaagaaatttgattcctcccgggacagaa
acaagccctttaagtttatgctaggcaagcaggaggtgatccgaggctgggaagaaggggttgcc
cagatgagtgtgggtcagagagccaaactgactatatctccagattatgcctatggtgccactgg
gcacccaggcatcatcccaccacatgccactctcgtcttcgatgtggagcttctaaaactggaag
gaggagggagctccggtggaggcagcggtatggtcttcacactcgaagatttcgttggggactgg
cgacagacagccggctacaacctggaccaagtccttgaacagggaggtgtgtccagtttgtttca
gaatctcggggtgtccgtaactccgatccaaaggattgtcctgagcggtgaaaatgggctgaaga
tcgacatccatgtcatcatcccgtatgaaggtctgagcggcgaccaaatgggccagatcgaaaaa
atttttaaggtggtgtaccctgtggatgatcatcactttaaggtgatcctgcactatggcacact
ggtaatcgacggggttacgccgaacatgatcgactatttcggacggccgtatgaaggcatcgccg
tgttcgacggcaaaaagatcactgtaacagggaccctgtggaacggcaacaaaattatcgacgag
cgcctgatcaaccccgacggc

**SEQ ID NO:378 (pCA 48 FKBP- L27V02A 1-147)**
MGVQVETISPGDGRTFPKRGQTCVVHYTGMLEDGKKFDSSRDRNKPFKFMLGKQEVIRGWEEGVA
QMSVGQRAKLTISPDYAYGATGHPGIIPPHATLVFDVELLKLEGGGSSGGGSGMVFTLEDFVGDW
RQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEK
IFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDE
RLINPDG

**SEQ ID NO:379 (pCA 49 L27V02A 156-169 FRB)**
atgaacggagtgaccggctggcggctgtgcgaacgcattctggcgggaggaggtggctcaggtgg
agggagctccgtggccatcctctggcatgagatgtggcatgaaggcctggaagaggcatctcgtt
tgtactttggggaaaggaacgtgaaaggcatgtttgaggtgctggagcccttgcatgctatgatg
gaacggggcccccagactctgaaggaaacatcctttaatcaggcctatggtcgagatttaatgga
ggcccaagagtggtgcaggaagtacatgaaatcagggaatgtcaaggacctcacccaagcctggg
acctctattatcatgtgttccgacgaatctca

**SEQ ID NO:380 (pCA 49 L27V02A 156-169 FRB)**
MNGVTGWRLCERILAGGGGSGGGSSVAILWHEMWHEGLEEASRLYFGERNVKGMFEVLEPLHAMM
ERGPQTLKETSFNQAYGRDLMEAQEWCRKYMKSGNVKDLTQAWDLYYHVFRRIS

**SEQ ID NO:381 (pCA 50 FKBP-L27V02A 1-155)**

atgggagtgcaggtggaaaccatctccccaggagacgggcgcaccttccccaagcgcggccagac
ctgcgtggtgcactacaccgggatgcttgaagatggaaagaaatttgattcctcccgggacagaa
acaagccctttaagtttatgctaggcaagcaggaggtgatccgaggctgggaagaaggggttgcc
cagatgagtgtgggtcagagagccaaactgactatatctccagattatgcctatggtgccactgg
gcacccaggcatcatcccaccacatgccactctcgtcttcgatgtggagcttctaaaactggaag
gaggagggagctccggtggaggcagcggtatggtcttcacactcgaagatttcgttggggactgg
cgacagacagccggctacaacctggaccaagtccttgaacagggaggtgtgtccagtttgtttca
gaatctcggggtgtccgtaactccgatccaaaggattgtcctgagcggtgaaaatgggctgaaga
tcgacatccatgtcatcatcccgtatgaaggtctgagcggcgaccaaatgggccagatcgaaaaa
atttttaaggtggtgtaccctgtggatgatcatcactttaaggtgatcctgcactatggcacact
ggtaatcgacggggttacgccgaacatgatcgactatttcggacggccgtatgaaggcatcgccg
tgttcgacggcaaaaagatcactgtaacagggaccctgtggaacggcaacaaaattatcgacgag
cgcctgatcaaccccgacggctccctgctgttccgagtaaccatc

**SEQ ID NO:382 (pCA 50 FKBP-L27V02A 1-155)**
MGVQVETISPGDGRTFPKRGQTCVVHYTGMLEDGKKFDSSRDRNKPFKFMLGKQEVIRGWEEGVA
QMSVGQRAKLTISPDYAYGATGHPGIIPPHATLVFDVELLKLEGGGSSGGGSGMVFTLEDFVGDW
RQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEK
IFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDE
RLINPDGSLLFRVTI

**SEQ ID NO:383 (pCA 51 L27V02A 158-169 FRB)**
atggtgaccggctggcggctgtgcgaacgcattctggcgggaggaggtggctcaggtggagggag
ctccgtggccatcctctggcatgagatgtggcatgaaggcctggaagaggcatctcgtttgtact
ttggggaaaggaacgtgaaaggcatgtttgaggtgctggagcccttgcatgctatgatggaacgg
ggcccccagactctgaaggaaacatcctttaatcaggcctatggtcgagatttaatggaggccca
agagtggtgcaggaagtacatgaaatcagggaatgtcaaggacctcacccaagcctgggacctct
attatcatgtgttccgacgaatctca

**SEQ ID NO:384 (pCA 51 L27V02A 158-169 FRB)**
MVTGWRLCERILAGGGGSGGGSSVAILWHEMWHEGLEEASRLYFGERNVKGMFEVLEPLHAMMER
GPQTLKETSFNQAYGRDLMEAQEWCRKYMKSGNVKDLTQAWDLYYHVFRRIS

**SEQ ID NO:385 (pCA 52 FKBP 1-157 L27V02A)**
atgggagtgcaggtggaaaccatctccccaggagacgggcgcaccttccccaagcgcggccagac
ctgcgtggtgcactacaccgggatgcttgaagatggaaagaaatttgattcctcccgggacagaa
acaagccctttaagtttatgctaggcaagcaggaggtgatccgaggctgggaagaaggggttgcc
cagatgagtgtgggtcagagagccaaactgactatatctccagattatgcctatggtgccactgg
gcacccaggcatcatcccaccacatgccactctcgtcttcgatgtggagcttctaaaactggaag
gaggagggagctccggtggaggcagcggtatggtcttcacactcgaagatttcgttggggactgg
cgacagacagccggctacaacctggaccaagtccttgaacagggaggtgtgtccagtttgtttca
gaatctcggggtgtccgtaactccgatccaaaggattgtcctgagcggtgaaaatgggctgaaga
tcgacatccatgtcatcatcccgtatgaaggtctgagcggcgaccaaatgggccagatcgaaaaa
atttttaaggtggtgtaccctgtggatgatcatcactttaaggtgatcctgcactatggcacact
ggtaatcgacggggttacgccgaacatgatcgactatttcggacggccgtatgaaggcatcgccg
tgttcgacggcaaaaagatcactgtaacagggaccctgtggaacggcaacaaaattatcgacgag
cgcctgatcaaccccgacggctccctgctgttccgagtaaccatcaacgga

**SEQ ID NO:386 (pCA 52 FKBP 1-157 L27V02A)**
MGVQVETISPGDGRTFPKRGQTCVVHYTGMLEDGKKFDSSRDRNKPFKFMLGKQEVIRGWEEGVA
QMSVGQRAKLTISPDYAYGATGHPGIIPPHATLVFDVELLKLEGGGSSGGGSGMVFTLEDFVGDW
RQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEK

IFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDE
RLINPDGSLLFRVTING

**SEQ ID NO:387 (pCA 53 L27V02A 166-169 FRB)**
atgcgcattctggcgggaggaggtggctcaggtggagggagctccgtggccatcctctggcatga
gatgtggcatgaaggcctggaagaggcatctcgtttgtactttggggaaaggaacgtgaaaggca
tgtttgaggtgctggagcccttgcatgctatgatggaacggggcccccagactctgaaggaaaca
tcctttaatcaggcctatggtcgagatttaatggaggcccaagagtggtgcaggaagtacatgaa
atcagggaatgtcaaggacctcacccaagcctgggacctctattatcatgtgttccgacgaatct
ca

**SEQ ID NO:388 (pCA 53 L27V02A 166-169 FRB)**
MRILAGGGGSGGGSSVAILWHEMWHEGLEEASRLYFGERNVKGMFEVLEPLHAMMERGPQTLKET
SFNQAYGRDLMEAQEWCRKYMKSGNVKDLTQAWDLYYHVFRRIS

**SEQ ID NO:389 (pCA 54 FKBP L27V02A 1-165)**
atgggagtgcaggtggaaaccatctccccaggagacgggcgcaccttccccaagcgcggccagac
ctgcgtggtgcactacaccgggatgcttgaagatggaaagaaatttgattcctcccgggacagaa
acaagccctttaagtttatgctaggcaagcaggaggtgatccgaggctgggaagaaggggttgcc
cagatgagtgtgggtcagagagccaaactgactatatctccagattatgcctatggtgccactgg
gcacccaggcatcatcccaccacatgccactctcgtcttcgatgtggagcttctaaaactggaag
gaggagggagctccggtggaggcagcggtatggtcttcacactcgaagatttcgttggggactgg
cgacagacagccggctacaacctggaccaagtccttgaacagggaggtgtgtccagtttgtttca
gaatctcggggtgtccgtaactccgatccaaaggattgtcctgagcggtgaaaatgggctgaaga
tcgacatccatgtcatcatcccgtatgaaggtctgagcggcgaccaaatgggccagatcgaaaaa
atttttaaggtggtgtaccctgtggatgatcatcactttaaggtgatcctgcactatggcacact
ggtaatcgacggggttacgccgaacatgatcgactatttcggacggccgtatgaaggcatcgccg
tgttcgacggcaaaaagatcactgtaacagggaccctgtggaacggcaacaaaattatcgacgag
cgcctgatcaaccccgacggctccctgctgttccgagtaaccatcaacggagtgaccggctggcg
gctgtgcgaa

**SEQ ID NO:390 (pCA 54 FKBP L27V02A 1-165)**
MGVQVETISPGDGRTFPKRGQTCVVHYTGMLEDGKKFDSSRDRNKPFKFMLGKQEVIRGWEEGVA
QMSVGQRAKLTISPDYAYGATGHPGIIPPHATLVFDVELLKLEGGGSSGGGSGMVFTLEDFVGDW
RQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEK
IFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDE
RLINPDGSLLFRVTINGVTGWRLCE

**SEQ ID NO:391 (pCA 55 FKBP L27V02A 1-47)**
atgggagtgcaggtggaaaccatctccccaggagacgggcgcaccttccccaagcgcggccagac
ctgcgtggtgcactacaccgggatgcttgaagatggaaagaaatttgattcctcccgggacagaa
acaagccctttaagtttatgctaggcaagcaggaggtgatccgaggctgggaagaaggggttgcc
cagatgagtgtgggtcagagagccaaactgactatatctccagattatgcctatggtgccactgg
gcacccaggcatcatcccaccacatgccactctcgtcttcgatgtggagcttctaaaactggaag
gaggagggagctccggtggaggcagcggtatggtcttcacactcgaagatttcgttggggactgg
cgacagacagccggctacaacctggaccaagtccttgaacagggaggtgtgtccagtttgtttca
gaatctcggggtgtccgtaactccgatccaaaggattgtcctgagc

**SEQ ID NO:392 (pCA 55 FKBP L27V02A 1-47)**
MGVQVETISPGDGRTFPKRGQTCVVHYTGMLEDGKKFDSSRDRNKPFKFMLGKQEVIRGWEEGVA
QMSVGQRAKLTISPDYAYGATGHPGIIPPHATLVFDVELLKLEGGGSSGGGSGMVFTLEDFVGDW
RQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLS

**SEQ ID NO:393 (pCA 56 L27V02A 48-169-FRB)**

Atgggtgaaaatgggctgaagatcgacatccatgtcatcatcccgtatgaaggtctgagcggcga
ccaaatgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatgatcatcactttaagg
tgatcctgcactatggcacactggtaatcgacggggttacgccgaacatgatcgactatttcgga
cggccgtatgaaggcatcgccgtgttcgacggcaaaaagatcactgtaacagggaccctgtggaa
cggcaacaaaattatcgacgagcgcctgatcaaccccgacggctccctgctgttccgagtaacca
tcaacggagtgaccggctggcggctgtgcgaacgcattctggcgggaggaggtggctcaggtgga
gggagctccgtggccatcctctggcatgagatgtggcatgaaggcctggaagaggcatctcgttt
gtactttggggaaaggaacgtgaaaggcatgtttgaggtgctggagcccttgcatgctatgatgg
aacggggccccccagactctgaaggaaacatcctttaatcaggcctatggtcgagatttaatggag
gcccaagagtggtgcaggaagtacatgaaatcagggaatgtcaaggacctcacccaagcctggga
cctctattatcatgtgttccgacgaatctca

**SEQ ID NO:394 (pCA 56 L27V02A 48-169-FRB)**

MGENGLKIDIHVIIPYEGLSGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFG
RPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILAGGGGSGG
GSSVAILWHEMWHEGLEEASRLYFGERNVKGMFEVLEPLHAMMERGPQTLKETSFNQAYGRDLME
AQEWCRKYMKSGNVKDLTQAWDLYYHVFRRIS

**SEQ ID NO:395 (pCA 57 FKBP L27V02A 1-49)**

atgggagtgcaggtggaaaccatctccccaggagacgggcgcaccttccccaagcgcggccagac
ctgcgtggtgcactacaccgggatgcttgaagatggaaagaaatttgattcctcccgggacagaa
acaagccctttaagtttatgctaggcaagcaggaggtgatccgaggctgggaagaaggggttgcc
cagatgagtgtgggtcagagagccaaactgactatatctccagattatgcctatggtgccactgg
gcacccaggcatcatcccaccacatgccactctcgtcttcgatgtggagcttctaaaactggaag
gaggagggagctccggtggaggcagcggtatggtcttcacactcgaagatttcgttggggactgg
cgacagacagccggctacaacctggaccaagtccttgaacagggaggtgtgtccagtttgtttca
gaatctcggggtgtccgtaactccgatccaaaggattgtcctgagcggtgaa

**SEQ ID NO:396 (pCA 57 FKBP L27V02A 1-49)**

MGVQVETISPGDGRTFPKRGQTCVVHYTGMLEDGKKFDSSRDRNKPFKFMLGKQEVIRGWEEGVA
QMSVGQRAKLTISPDYAYGATGHPGIIPPHATLVFDVELLKLEGGGSSGGGSGMVFTLEDFVGDW
RQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGE

**SEQ ID NO:397 (pCA 58 pCA L27V02A 50-169 FRB)**

atgaatgggctgaagatcgacatccatgtcatcatcccgtatgaaggtctgagcggcgaccaaat
gggccagatcgaaaaaatttttaaggtggtgtaccctgtggatgatcatcactttaaggtgatcc
tgcactatggcacactggtaatcgacggggttacgccgaacatgatcgactatttcggacggccg
tatgaaggcatcgccgtgttcgacggcaaaaagatcactgtaacagggaccctgtggaacggcaa
caaaattatcgacgagcgcctgatcaaccccgacggctccctgctgttccgagtaaccatcaacg
gagtgaccggctggcggctgtgcgaacgcattctggcgggaggaggtggctcaggtggagggagc
tccgtggccatcctctggcatgagatgtggcatgaaggcctggaagaggcatctcgtttgtactt
tggggaaaggaacgtgaaaggcatgtttgaggtgctggagcccttgcatgctatgatggaacggg
gcccccagactctgaaggaaacatcctttaatcaggcctatggtcgagatttaatggaggcccaa
gagtggtgcaggaagtacatgaaatcagggaatgtcaaggacctcacccaagcctgggacctcta
ttatcatgtgttccgacgaatctca

**SEQ ID NO:398 (pCA 58 pCA L27V02A 50-169 FRB)**

MNGLKIDIHVIIPYEGLSGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRP
YEGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILAGGGGSGGGS
SVAILWHEMWHEGLEEASRLYFGERNVKGMFEVLEPLHAMMERGPQTLKETSFNQAYGRDLMEAQ
EWCRKYMKSGNVKDLTQAWDLYYHVFRRIS

**SEQ ID NO:399 (pCA 59 FKBP L27V02A 1-82)**

atgggagtgcaggtggaaaccatctccccaggagacgggcgcaccttccccaagcgcggccagac
ctgcgtggtgcactacaccgggatgcttgaagatggaaagaaatttgattcctcccgggacagaa
acaagccctttaagtttatgctaggcaagcaggaggtgatccgaggctgggaagaaggggttgcc
cagatgagtgtgggtcagagagccaaactgactatatctccagattatgcctatggtgccactgg
gcacccaggcatcatcccaccacatgccactctcgtcttcgatgtggagcttctaaaactggaag
gaggagggagctccggtggaggcagcggtatggtcttcacactcgaagatttcgttggggactgg
cgacagacagccggctacaacctggaccaagtccttgaacagggaggtgtgtccagtttgtttca
gaatctcggggtgtccgtaactccgatccaaaggattgtcctgagcggtgaaaatgggctgaaga
tcgacatccatgtcatcatcccgtatgaaggtctgagcggcgaccaaatgggccagatcgaaaaa
atttttaaggtggtgtaccct

**SEQ ID NO:400 (pCA 59 FKBP L27V02A 1-82)**

MGVQVETISPGDGRTFPKRGQTCVVHYTGMLEDGKKFDSSRDRNKPFKFMLGKQEVIRGWEEGVA
QMSVGQRAKLTISPDYAYGATGHPGIIPPHATLVFDVELLKLEGGGSSGGGSGMVFTLEDFVGDW
RQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEK
IFKVVYP

**SEQ ID NO:401 (pCA 60 L27V02A 83-169-FRB)**

atggtggatgatcatcactttaaggtgatcctgcactatggcacactggtaatcgacggggttac
gccgaacatgatcgactatttcggacggccgtatgaaggcatcgccgtgttcgacggcaaaaaga
tcactgtaacagggaccctgtggaacggcaacaaaattatcgacgagcgcctgatcaaccccgac
ggctccctgctgttccgagtaaccatcaacggagtgaccggctggcggctgtgcgaacgcattct
ggcgggaggaggtggctcaggtggagggagctccgtggccatcctctggcatgagatgtggcatg
aaggcctggaagaggcatctcgtttgtactttggggaaaggaacgtgaaaggcatgtttgaggtg
ctggagcccttgcatgctatgatggaacggggcccccagactctgaaggaaacatcctttaatca
ggcctatggtcgagatttaatggaggcccaagagtggtgcaggaagtacatgaaatcagggaatg
tcaaggacctcacccaagcctgggacctctattatcatgtgttccgacgaatctca

**SEQ ID NO:402 (pCA 60 L27V02A 83-16-FRB)**

MVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPD
GSLLFRVTINGVTGWRLCERILAGGGGSGGGSSVAILWHEMWHEGLEEASRLYFGERNVKGMFEV
LEPLHAMMERGPQTLKETSFNQAYGRDLMEAQEWCRKYMKSGNVKDLTQAWDLYYHVFRRIS

**SEQ ID NO:403 (pCA 61 FKBP L27V02A 1-84)**

Atgggagtgcaggtggaaaccatctccccaggagacgggcgcaccttccccaagcgcggccagac
ctgcgtggtgcactacaccgggatgcttgaagatggaaagaaatttgattcctcccgggacagaa
acaagccctttaagtttatgctaggcaagcaggaggtgatccgaggctgggaagaaggggttgcc
cagatgagtgtgggtcagagagccaaactgactatatctccagattatgcctatggtgccactgg
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gaggagggagctccggtggaggcagcggtatggtcttcacactcgaagatttcgttggggactgg
cgacagacagccggctacaacctggaccaagtccttgaacagggaggtgtgtccagtttgtttca
gaatctcggggtgtccgtaactccgatccaaaggattgtcctgagcggtgaaaatgggctgaaga
tcgacatccatgtcatcatcccgtatgaaggtctgagcggcgaccaaatgggccagatcgaaaaa
atttttaaggtggtgtaccctgtggat

**SEQ ID NO:404 (pCA 61 FKBP L27V02A 1-84)**

MGVQVETISPGDGRTFPKRGQTCVVHYTGMLEDGKKFDSSRDRNKPFKFMLGKQEVIRGWEEGVA
QMSVGQRAKLTISPDYAYGATGHPGIIPPHATLVFDVELLKLEGGGSSGGGSGMVFTLEDFVGDW
RQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEK
IFKVVYPVD

**SEQ ID NO:405 (pCA 62 L27V02A 85-169-FRB)**

atggatcatcactttaaggtgatcctgcactatggcacactggtaatcgacggggttacgccgaa
catgatcgactatttcggacggccgtatgaaggcatcgccgtgttcgacggcaaaaagatcactg
taacagggaccctgtggaacggcaacaaaattatcgacgagcgcctgatcaaccccgacggctcc
ctgctgttccgagtaaccatcaacggagtgaccggctggcggctgtgcgaacgcattctggcggg
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cccttgcatgctatgatggaacggggccccccagactctgaaggaaacatcctttaatcaggccta
tggtcgagatttaatggaggcccaagagtggtgcaggaagtacatgaaatcagggaatgtcaagg
acctcacccaagcctgggacctctattatcatgtgttccgacgaatctca

**SEQ ID NO:406 (pCA 62 L27V02A 85-169-FRB)**
MDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDGS
LLFRVTINGVTGWRLCERILAGGGGSGGGSSVAILWHEMWHEGLEEASRLYFGERNVKGMFEVLE
PLHAMMERGPQTLKETSFNQAYGRDLMEAQEWCRKYMKSGNVKDLTQAWDLYYHVFRRIS

**SEQ ID NO:407 (pCA 63 FKBP L27V02A 1-122)**
atgggagtgcaggtggaaaccatctccccaggagacgggcgcaccttccccaagcgcggccagac
ctgcgtggtgcactacaccgggatgcttgaagatggaaagaaatttgattcctcccgggacagaa
acaagccctttaagtttatgctaggcaagcaggaggtgatccgaggctgggaagaaggggttgcc
cagatgagtgtgggtcagagagccaaactgactatatctccagattatgcctatggtgccactgg
gcacccaggcatcatcccaccacatgccactctcgtcttcgatgtggagcttctaaaactggaag
gaggagggagctccggtggaggcagcggtatggtcttcacactcgaagatttcgttggggactgg
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gaatctcggggtgtccgtaactccgatccaaaggattgtcctgagcggtgaaaatgggctgaaga
tcgacatccatgtcatcatcccgtatgaaggtctgagcggcgaccaaatgggccagatcgaaaaa
atttttaaggtggtgtaccctgtggatgatcatcactttaaggtgatcctgcactatggcacact
ggtaatcgacggggttacgccgaacatgatcgactatttcggacggccgtatgaaggcatcgccg
tgttcgacggc

**SEQ ID NO:408 (pCA 63 FKBP L27V02A 1-122)**
MGVQVETISPGDGRTFPKRGQTCVVHYTGMLEDGKKFDSSRDRNKPFKFMLGKQEVIRGWEEGVA
QMSVGQRAKLTISPDYAYGATGHPGIIPPHATLVFDVELLKLEGGGSSGGGSGMVFTLEDFVGDW
RQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEK
IFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDG

**SEQ ID NO:409 (pCA 64 L27V02A 123-169-FRB)**
atgaaaaagatcactgtaacagggaccctgtggaacggcaacaaaattatcgacgagcgcctgat
caaccccgacggctccctgctgttccgagtaaccatcaacggagtgaccggctggcggctgtgcg
aacgcattctggcgggaggaggtggctcaggtggagggagctccgtggccatcctctggcatgag
atgtggcatgaaggcctggaagaggcatctcgtttgtactttggggaaaggaacgtgaaaggcat
gtttgaggtgctggagcccttgcatgctatgatggaacggggcccccagactctgaaggaaacat
cctttaatcaggcctatggtcgagatttaatggaggcccaagagtggtgcaggaagtacatgaaa
tcagggaatgtcaaggacctcacccaagcctgggacctctattatcatgtgttccgacgaatctc
a

**SEQ ID NO:410 (pCA 64 L27V02A 123-169-FRB)**
MKKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILAGGGGSGGGSSVAILWHE
MWHEGLEEASRLYFGERNVKGMFEVLEPLHAMMERGPQTLKETSFNQAYGRDLMEAQEWCRKYMK
SGNVKDLTQAWDLYYHVFRRIS

**SEQ ID NO:411 (pCA 65 FKBP L27V02A 1-123)**
atgggagtgcaggtggaaaccatctccccaggagacgggcgcaccttccccaagcgcggccagac
ctgcgtggtgcactacaccgggatgcttgaagatggaaagaaatttgattcctcccgggacagaa

acaagccctttaagtttatgctaggcaagcaggaggtgatccgaggctgggaagaaggggttgcc
cagatgagtgtgggtcagagagccaaactgactatatctccagattatgcctatggtgccactgg
gcacccaggcatcatcccaccacatgccactctcgtcttcgatgtggagcttctaaaactggaag
gaggagggagctccggtggaggcagcggtatggtcttcacactcgaagatttcgttggggactgg
cgacagacagccggctacaacctggaccaagtccttgaacagggaggtgtgtccagtttgtttca
gaatctcggggtgtccgtaactccgatccaaaggattgtcctgagcggtgaaaatgggctgaaga
tcgacatccatgtcatcatcccgtatgaaggtctgagcggcgaccaaatgggccagatcgaaaaa
atttttaaggtggtgtaccctgtggatgatcatcactttaaggtgatcctgcactatggcacact
ggtaatcgacggggttacgccgaacatgatcgactatttcggacggccgtatgaaggcatcgccg
tgttcgacggcaaa

**SEQ ID NO:412 (pCA 65 FKBP L27V02A 1-123)**
MGVQVETISPGDGRTFPKRGQTCVVHYTGMLEDGKKFDSSRDRNKPFKFMLGKQEVIRGWEEGVA
QMSVGQRAKLTISPDYAYGATGHPGIIPPHATLVFDVELLKLEGGGSSGGGSGMVFTLEDFVGDW
RQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEK
IFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGK

**SEQ ID NO:413 (pCA 66 L27V02A 124-169 FRB)**
atgaagatcactgtaacagggaccctgtggaacggcaacaaaattatcgacgagcgcctgatcaa
ccccgacggctccctgctgttccgagtaaccatcaacggagtgaccggctggcggctgtgcgaac
gcattctggcgggaggaggtggctcaggtggagggagctccgtggccatcctctggcatgagatg
tggcatgaaggcctggaagaggcatctcgtttgtactttggggaaaggaacgtgaaaggcatgtt
tgaggtgctggagcccttgcatgctatgatggaacggggcccccagactctgaaggaaacatcct
ttaatcaggcctatggtcgagatttaatggaggcccaagagtggtgcaggaagtacatgaaatca
gggaatgtcaaggacctcacccaagcctgggacctctattatcatgtgttccgacgaatctca

**SEQ ID NO:414 (pCA 66 L27V02A 124-169 FRB)**
MKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILAGGGGSGGGSSVAILWHEM
WHEGLEEASRLYFGERNVKGMFEVLEPLHAMMERGPQTLKETSFNQAYGRDLMEAQEWCRKYMKS
GNVKDLTQAWDLYYHVFRRIS

**SEQ ID NO:415 (pCA 67 L27V02A 1-168)**
atgggagtgcaggtggaaaccatctccccaggagacgggcgcaccttccccaagcgcggccagac
ctgcgtggtgcactacaccgggatgcttgaagatggaaagaaatttgattcctcccgggacagaa
acaagccctttaagtttatgctaggcaagcaggaggtgatccgaggctgggaagaaggggttgcc
cagatgagtgtgggtcagagagccaaactgactatatctccagattatgcctatggtgccactgg
gcacccaggcatcatcccaccacatgccactctcgtcttcgatgtggagcttctaaaactggaag
gaggagggagctccggtggaggcagcggtatggtcttcacactcgaagatttcgttggggactgg
cgacagacagccggctacaacctggaccaagtccttgaacagggaggtgtgtccagtttgtttca
gaatctcggggtgtccgtaactccgatccaaaggattgtcctgagcggtgaaaatgggctgaaga
tcgacatccatgtcatcatcccgtatgaaggtctgagcggcgaccaaatgggccagatcgaaaaa
atttttaaggtggtgtaccctgtggatgatcatcactttaaggtgatcctgcactatggcacact
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tgttcgacggcaaaaagatcactgtaacagggaccctgtggaacggcaacaaaattatcgacgag
cgcctgatcaaccccgacggctccctgctgttccgagtaaccatcaacggagtgaccggctggcg
gctgtgcgaacgcattctg

**SEQ ID NO:416 (pCA 67 L27V02A 1-168)**
atgggagtgcaggtggaaaccatctccccaggagacgggcgcaccttccccaagcgcggccagac
ctgcgtggtgcactacaccgggatgcttgaagatggaaagaaatttgattcctcccgggacagaa
acaagccctttaagtttatgctaggcaagcaggaggtgatccgaggctgggaagaaggggttgcc
cagatgagtgtgggtcagagagccaaactgactatatctccagattatgcctatggtgccactgg
gcacccaggcatcatcccaccacatgccactctcgtcttcgatgtggagcttctaaaactggaag

gaggagggagctccggtggaggcagcggtatggtcttcacactcgaagatttcgttggggactgg
cgacagacagccggctacaacctggaccaagtccttgaacagggaggtgtgtccagtttgtttca
gaatctcggggtgtccgtaactccgatccaaaggattgtcctgagcggtgaaaatgggctgaaga
tcgacatccatgtcatcatcccgtatgaaggtctgagcggcgaccaaatgggccagatcgaaaaa
atttttaaggtggtgtaccctgtggatgatcatcactttaaggtgatcctgcactatggcacact
ggtaatcgacggggttacgccgaacatgatcgactatttcggacggccgtatgaaggcatcgccg
tgttcgacggcaaaaagatcactgtaacagggaccctgtggaacggcaacaaaattatcgacgag
cgcctgatcaaccccgacggctccctgctgttccgagtaaccatcaacggagtgaccggctggcg
gctgtgcgaacgcattctg

**SEQ ID NO:417 (pCA 67 L27V02A 1-168)**
MGVQVETISPGDGRTFPKRGQTCVVHYTGMLEDGKKFDSSRDRNKPFKFMLGKQEVIRGWEEGVA
QMSVGQRAKLTISPDYAYGATGHPGIIPPHATLVFDVELLKLEGGGSSGGGSGMVFTLEDFVGDW
RQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEK
IFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDE
RLINPDGSLLFRVTINGVTGWRLCERIL

**SEQ ID NO:418 (*pCA 68 L27V02A 169 FRB)**
Atggcgggaggaggtggctcaggtggagggagctccgtggccatcctctggcatgagatgtggca
tgaaggcctggaagaggcatctcgtttgtactttggggaaaggaacgtgaaaggcatgtttgagg
tgctggagcccttgcatgctatgatggaacggggccccccagactctgaaggaaacatcctttaat
caggcctatggtcgagatttaatggaggcccaagagtggtgcaggaagtacatgaaatcagggaa
tgtcaaggacctcacccaagcctgggacctctattatcatgtgttccgacgaatctca

**SEQ ID NO:419 (*pCA 68 L27V02A 169 FRB)**
MAGGGGSGGGSSVAILWHEMWHEGLEEASRLYFGERNVKGMFEVLEPLHAMMERGPQTLKETSFN
QAYGRDLMEAQEWCRKYMKSGNVKDLTQAWDLYYHVFRRIS

**SEQ ID NO:420 (pCA 69 FKBP L27V02A 1-166)**
atgggagtgcaggtggaaaccatctccccaggagacgggcgcaccttccccaagcgcggccagac
ctgcgtggtgcactacaccgggatgcttgaagatggaaagaaatttgattcctcccgggacagaa
acaagccctttaagtttatgctaggcaagcaggaggtgatccgaggctgggaagaaggggttgcc
cagatgagtgtgggtcagagagccaaactgactatatctccagattatgcctatggtgccactgg
gcacccaggcatcatcccaccacatgccactctcgtcttcgatgtggagcttctaaaactggaag
gaggagggagctccggtggaggcagcggtatggtcttcacactcgaagatttcgttggggactgg
cgacagacagccggctacaacctggaccaagtccttgaacagggaggtgtgtccagtttgtttca
gaatctcggggtgtccgtaactccgatccaaaggattgtcctgagcggtgaaaatgggctgaaga
tcgacatccatgtcatcatcccgtatgaaggtctgagcggcgaccaaatgggccagatcgaaaaa
atttttaaggtggtgtaccctgtggatgatcatcactttaaggtgatcctgcactatggcacact
ggtaatcgacggggttacgccgaacatgatcgactatttcggacggccgtatgaaggcatcgccg
tgttcgacggcaaaaagatcactgtaacagggaccctgtggaacggcaacaaaattatcgacgag
cgcctgatcaaccccgacggctccctgctgttccgagtaaccatcaacggagtgaccggctggcg
gctgtgcgaacgc

**SEQ ID NO:421 (pCA 69 FKBP L27V02A 1-166)**
MGVQVETISPGDGRTFPKRGQTCVVHYTGMLEDGKKFDSSRDRNKPFKFMLGKQEVIRGWEEGVA
QMSVGQRAKLTISPDYAYGATGHPGIIPPHATLVFDVELLKLEGGGSSGGGSGMVFTLEDFVGDW
RQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEK
IFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDE
RLINPDGSLLFRVTINGVTGWRLCER

**SEQ ID NO:422 (*pCA 70 L27V02A 167-169 FRB)**

Atgattctggcgggaggaggtggctcaggtggagggagctccgtggccatcctctggcatgagat
gtggcatgaaggcctggaagaggcatctcgtttgtactttggggaaaggaacgtgaaaggcatgt
ttgaggtgctggagcccttgcatgctatgatggaacggggcccccagactctgaaggaaacatcc
tttaatcaggcctatggtcgagatttaatggaggcccaagagtggtgcaggaagtacatgaaatc
agggaatgtcaaggacctcacccaagcctgggacctctattatcatgtgttccgacgaatctca

**SEQ ID NO:423 (*pCA 70 L27V02A 167-169 FRB)**
MILAGGGGSGGGSSVAILWHEMWHEGLEEASRLYFGERNVKGMFEVLEPLHAMMERGPQTLKETS
FNQAYGRDLMEAQEWCRKYMKSGNVKDLTQAWDLYYHVFRRIS

**SEQ ID NO:424 (pCA 71 FKBP L27V02A 1-164)**
atgggagtgcaggtggaaaccatctccccaggagacgggcgcaccttccccaagcgcggccagac
ctgcgtggtgcactacaccgggatgcttgaagatggaaagaaatttgattcctcccgggacagaa
acaagccctttaagtttatgctaggcaagcaggaggtgatccgaggctgggaagaaggggttgcc
cagatgagtgtgggtcagagagccaaactgactatatctccagattatgcctatggtgccactgg
gcacccaggcatcatcccaccacatgccactctcgtcttcgatgtggagcttctaaaactggaag
gaggagggagctccggtggaggcagcggtatggtcttcacactcgaagatttcgttggggactgg
cgacagacagccggctacaacctggaccaagtccttgaacagggaggtgtgtccagtttgtttca
gaatctcggggtgtccgtaactccgatccaaaggattgtcctgagcggtgaaaatgggctgaaga
tcgacatccatgtcatcatcccgtatgaaggtctgagcggcgaccaaatgggccagatcgaaaaa
atttttaaggtggtgtaccctgtggatgatcatcactttaaggtgatcctgcactatggcacact
ggtaatcgacggggttacgccgaacatgatcgactatttcggacggccgtatgaaggcatcgccg
tgttcgacggcaaaaagatcactgtaacagggaccctgtggaacggcaacaaaattatcgacgag
cgcctgatcaaccccgacggctccctgctgttccgagtaaccatcaacggagtgaccggctggcg
gctgtgc

**SEQ ID NO:425 (pCA 71 FKBP L27V02A 1-164)**
MGVQVETISPGDGRTFPKRGQTCVVHYTGMLEDGKKFDSSRDRNKPFKFMLGKQEVIRGWEEGVA
QMSVGQRAKLTISPDYAYGATGHPGIIPPHATLVFDVELLKLEGGGSSGGGSGMVFTLEDFVGDW
RQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEK
IFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDE
RLINPDGSLLFRVTINGVTGWRLC

**SEQ ID NO:426 (pCA 72 L27V02A 165-169 FRB)**
atggaacgcattctggcgggaggaggtggctcaggtggagggagctccgtggccatcctctggca
tgagatgtggcatgaaggcctggaagaggcatctcgtttgtactttggggaaaggaacgtgaaag
gcatgtttgaggtgctggagcccttgcatgctatgatggaacggggcccccagactctgaaggaa
acatcctttaatcaggcctatggtcgagatttaatggaggcccaagagtggtgcaggaagtacat
gaaatcagggaatgtcaaggacctcacccaagcctgggacctctattatcatgtgttccgacgaa
tctca

**SEQ ID NO:427 (pattern sequence)**
GSAIVK

**SEQ ID NO:428 (pCA 72 L27V02A 165-169 FRB)**
MERILAGGGGSGGGSSVAILWHEMWHEGLEEASRLYFGERNVKGMFEVLEPLHAMMERGPQTLKE
TSFNQAYGRDLMEAQEWCRKYMKSGNVKDLTQAWDLYYHVFRRIS

**SEQ ID NO:429 (pCA 73 FKBP L27V02A 1-162)**
atgggagtgcaggtggaaaccatctccccaggagacgggcgcaccttccccaagcgcggccagac
ctgcgtggtgcactacaccgggatgcttgaagatggaaagaaatttgattcctcccgggacagaa
acaagccctttaagtttatgctaggcaagcaggaggtgatccgaggctgggaagaaggggttgcc
cagatgagtgtgggtcagagagccaaactgactatatctccagattatgcctatggtgccactgg
gcacccaggcatcatcccaccacatgccactctcgtcttcgatgtggagcttctaaaactggaag

gaggagggagctccggtggaggcagcggtatggtcttcacactcgaagatttcgttggggactgg
cgacagacagccggctacaacctggaccaagtccttgaacagggaggtgtgtccagtttgtttca
gaatctcggggtgtccgtaactccgatccaaaggattgtcctgagcggtgaaaatgggctgaaga
tcgacatccatgtcatcatcccgtatgaaggtctgagcggcgaccaaatgggccagatcgaaaaa
atttttaaggtggtgtaccctgtggatgatcatcactttaaggtgatcctgcactatggcacact
ggtaatcgacggggttacgccgaacatgatcgactatttcggacggccgtatgaaggcatcgccg
tgttcgacggcaaaaagatcactgtaacagggaccctgtggaacggcaacaaaattatcgacgag
cgcctgatcaaccccgacggctccctgctgttccgagtaaccatcaacggagtgaccggctggcg
g

**SEQ ID NO:430 (pCA 73 FKBP L27V02A 1-162)**
MGVQVETISPGDGRTFPKRGQTCVVHYTGMLEDGKKFDSSRDRNKPFKFMLGKQEVIRGWEEGVA
QMSVGQRAKLTISPDYAYGATGHPGIIPPHATLVFDVELLKLEGGGSSGGGSGMVFTLEDFVGDW
RQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEK
IFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDE
RLINPDGSLLFRVTINGVTGWR

**SEQ ID NO:431 (pCA 74 L27V02A 163-169 FRB)**
atgctgtgcgaacgcattctggcgggaggaggtggctcaggtggagggagctccgtggccatcct
ctggcatgagatgtggcatgaaggcctggaagaggcatctcgtttgtactttggggaaaggaacg
tgaaaggcatgtttgaggtgctggagcccttgcatgctatgatggaacggggccccccagactctg
aaggaaacatcctttaatcaggcctatggtcgagatttaatggaggcccaagagtggtgcaggaa
gtacatgaaatcagggaatgtcaaggacctcacccaagcctgggacctctattatcatgtgttcc
gacgaatctca

**SEQ ID NO:432 (pCA 74 L27V02A 163-169 FRB)**
MLCERILAGGGGSGGGSSVAILWHEMWHEGLEEASRLYFGERNVKGMFEVLEPLHAMMERGPQTL
KETSFNQAYGRDLMEAQEWCRKYMKSGNVKDLTQAWDLYYHVFRRIS

**SEQ ID NO:433 (pCA 75 FKBP L27V02A 1-160)**
atgggagtgcaggtggaaaccatctccccaggagacgggcgcaccttccccaagcgcggccagac
ctgcgtggtgcactacaccgggatgcttgaagatggaaagaaatttgattcctcccgggacagaa
acaagccctttaagtttatgctaggcaagcaggaggtgatccgaggctgggaagaaggggttgcc
cagatgagtgtgggtcagagagccaaactgactatatctccagattatgcctatggtgccactgg
gcacccaggcatcatcccaccacatgccactctcgtcttcgatgtggagcttctaaaactggaag
gaggagggagctccggtggaggcagcggtatggtcttcacactcgaagatttcgttggggactgg
cgacagacagccggctacaacctggaccaagtccttgaacagggaggtgtgtccagtttgtttca
gaatctcggggtgtccgtaactccgatccaaaggattgtcctgagcggtgaaaatgggctgaaga
tcgacatccatgtcatcatcccgtatgaaggtctgagcggcgaccaaatgggccagatcgaaaaa
atttttaaggtggtgtaccctgtggatgatcatcactttaaggtgatcctgcactatggcacact
ggtaatcgacggggttacgccgaacatgatcgactatttcggacggccgtatgaaggcatcgccg
tgttcgacggcaaaaagatcactgtaacagggaccctgtggaacggcaacaaaattatcgacgag
cgcctgatcaaccccgacggctccctgctgttccgagtaaccatcaacggagtgaccggc

**SEQ ID NO:434 (pCA 75 FKBP L27V02A 1-160)**
MGVQVETISPGDGRTFPKRGQTCVVHYTGMLEDGKKFDSSRDRNKPFKFMLGKQEVIRGWEEGVA
QMSVGQRAKLTISPDYAYGATGHPGIIPPHATLVFDVELLKLEGGGSSGGGSGMVFTLEDFVGDW
RQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEK
IFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDE
RLINPDGSLLFRVTINGVTG

**SEQ ID NO:435 (pCA 76 L27V02A 161-169 FRB)**

atgtggcggctgtgcgaacgcattctggcgggaggaggtggctcaggtggagggagctccgtggc
catcctctggcatgagatgtggcatgaaggcctggaagaggcatctcgtttgtactttggggaaa
ggaacgtgaaaggcatgtttgaggtgctggagcccttgcatgctatgatggaacggggccccccag
actctgaaggaaacatcctttaatcaggcctatggtcgagatttaatggaggcccaagagtggtg
caggaagtacatgaaatcagggaatgtcaaggacctcacccaagcctgggacctctattatcatg
tgttccgacgaatctca

**SEQ ID NO:436 (pCA 76 L27V02A 161-169 FRB)**
MWRLCERILAGGGGSGGGSSVAILWHEMWHEGLEEASRLYFGERNVKGMFEVLEPLHAMMERGPQ
TLKETSFNQAYGRDLMEAQEWCRKYMKSGNVKDLTQAWDLYYHVFRRIS

**SEQ ID NO:437 (pCA 77 FKBP L27V02A 1-158)**
atgggagtgcaggtggaaaccatctccccaggagacgggcgcaccttccccaagcgcggccagac
ctgcgtggtgcactacaccgggatgcttgaagatggaaagaaatttgattcctcccgggacagaa
acaagccctttaagtttatgctaggcaagcaggaggtgatccgaggctgggaagaaggggttgcc
cagatgagtgtgggtcagagagccaaactgactatatctccagattatgcctatggtgccactgg
gcacccaggcatcatcccaccacatgccactctcgtcttcgatgtggagcttctaaaactggaag
gaggagggagctccggtggaggcagcggtatggtcttcacactcgaagatttcgttggggactgg
cgacagacagccggctacaacctggaccaagtccttgaacagggaggtgtgtccagtttgtttca
gaatctcggggtgtccgtaactccgatccaaaggattgtcctgagcggtgaaaatgggctgaaga
tcgacatccatgtcatcatcccgtatgaaggtctgagcggcgaccaaatgggccagatcgaaaaa
atttttaaggtggtgtaccctgtggatgatcatcactttaaggtgatcctgcactatggcacact
ggtaatcgacggggttacgccgaacatgatcgactatttcggacggccgtatgaaggcatcgccg
tgttcgacggcaaaaagatcactgtaacagggaccctgtggaacggcaacaaaattatcgacgag
cgcctgatcaaccccgacggctccctgctgttccgagtaaccatcaacggagtg

**SEQ ID NO:438 (pCA 77 FKBP L27V02A 1-158)**
MGVQVETISPGDGRTFPKRGQTCVVHYTGMLEDGKKFDSSRDRNKPFKFMLGKQEVIRGWEEGVA
QMSVGQRAKLTISPDYAYGATGHPGIIPPHATLVFDVELLKLEGGGSSGGGSGMVFTLEDFVGDW
RQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEK
IFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDE
RLINPDGSLLFRVTINGV

**SEQ ID NO:439 (pCA 78 L27V02A 159-169 FRB)**
Atgaccggctggcggctgtgcgaacgcattctggcgggaggaggtggctcaggtggagggagctc
cgtggccatcctctggcatgagatgtggcatgaaggcctggaagaggcatctcgtttgtactttg
gggaaaggaacgtgaaaggcatgtttgaggtgctggagcccttgcatgctatgatggaacggggc
ccccagactctgaaggaaacatcctttaatcaggcctatggtcgagatttaatggaggcccaaga
gtggtgcaggaagtacatgaaatcagggaatgtcaaggacctcacccaagcctgggacctctatt
atcatgtgttccgacgaatctca

**SEQ ID NO:440 (pCA 78 L27V02A 159-169 FRB)**
MTGWRLCERILAGGGGSGGGSSVAILWHEMWHEGLEEASRLYFGERNVKGMFEVLEPLHAMMERG
PQTLKETSFNQAYGRDLMEAQEWCRKYMKSGNVKDLTQAWDLYYHVFRRIS

**SEQ ID NO:441 RIIbB (nt seq)**
ATGTATGAAAGCTTTATTGAGTCACTGCCATTCCTTAAATCTTTGGAGTTTTCTGCACGCCTGAA
AGTAGTAGATGTGATAGGCACCAAAGTATACAACGATGGAGAACAAATCATTGCTCAGGGAGATT
CGGCTGATTCTTTTTTCATTATTGAATCTGGAGAAGTGAAAATTACTATGAAAAGAAAGGGTAAA
TCAGAAGTGGAAGAGAATGGTGCAGTAGAAATCGCTCGATGCTCGCGGGGACAGTACTTTGGAGA
GCTTGCCCTGGTAACTAACAAACCTCGAGCAGCTTCTGCCCACGCCATTGGGACTGTCAAATGTT

TAGCAATGGATGTGCAAGCATTTGAAAGGCTTCTGGGACCTTGCATGGAAATTATGAAAAGGAAC
ATCGCTACCTATGAAGAACAGTTAGTTGCCCTGTATGGAACGAACATGGATATTGTA

**SEQ ID NO:442 RIIbB (aa seq)**

MYESFIESLPFLKSLEFSARLKVVDVIGTKVYNDGEQIIAQGDSADSFFIIESGEVKITMKRKGK
SEVEENGAVEIARCSRGQYFGELALVTNKPRAASAHAIGTVKCLAMDVQAFERLLGPCMEIMKRN
IATYEEQLVALYGTNMDIV

**SEQ ID NO:443 (L27V CP 13 TEV)**

atgacagccggctacaacctggaccaagtccttgagcagggcggtgtgtccagtttgtttcagaa
tctcggggtgtccgtaactccgatccaaaggattgtcctgagcggtgaaaacggcctgaagatcg
acatccatgtcatcatcccgtatgaaggtctgagcggcgatcagatgggccagatcgaaaaaatt
tttaaggtggtgtaccctgtggatgatcatcactttaaggtgattctgcactatggcacactggt
aatcgacggggttacgccgaacatgatcgactatttcggacggccgtatgaaggcatcgccgtgt
tcgacggcaaaaagatcactgtaaccgggaccctgtggaacggcaacaaaattatcgacgagcgc
ctgatcaaccccgacggctccctgctgttccgcgtaaccatcaacggagtgaccggctggcggct
gtgcgagcgcattttggcgggaagttctggtggaggaagttctggtggagagcctactactgaga
acttgtacttccagagcgataacggaagttctggtggaggaagttctggtggaatggtgtttaca
ctcgaagatttcgtaggggactggcggcag

**SEQ ID NO:444 (L27V CP 13 TEV)**

MTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEKI
FKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDER
LINPDGSLLFRVTINGVTGWRLCERILAGSSGGGSSGGEPTTENLYFQSDNGSSGGGSSGGMVFT
LEDFVGDWRQ

**SEQ ID NO:445 (L27V CP 57 TEV)**

Atgcatgtcatcatcccgtatgaaggtctgagcggcgatcagatgggccagatcgaaaaaatttt
taaggtggtgtaccctgtggatgatcatcactttaaggtgattctgcactatggcacactggtaa
tcgacggggttacgccgaacatgatcgactatttcggacggccgtatgaaggcatcgccgtgttc
gacggcaaaaagatcactgtaaccgggaccctgtggaacggcaacaaaattatcgacgagcgcct
gatcaaccccgacggctccctgctgttccgcgtaaccatcaacggagtgaccggctggcggctgt
gcgagcgcattttggcgggaagttctggtggaggaagttctggtggagagcctactactgagaac
ttgtacttccagagcgataacggaagttctggtggaggaagttctggtggaatggtgtttacact
cgaagatttcgtaggggactggcggcagacagccggctacaacctggaccaagtccttgagcagg
gcggtgtgtccagtttgtttcagaatctcggggtgtccgtaactccgatccaaaggattgtcctg
agcggtgaaaacggcctgaagatcgacatc

**SEQ ID NO:446 (L27V CP 57 TEV)**

MHVIIPYEGLSGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVF
DGKKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILAGSSGGGSSGGEPTTEN
LYFQSDNGSSGGGSSGGMVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVL
SGENGLKIDI

**SEQ ID NO:447 (L27V CP 98 TEV)**

atggtaatcgacggggttacgccgaacatgatcgactatttcggacggccgtatgaaggcatcgc
cgtgttcgacggcaaaaagatcactgtaaccgggaccctgtggaacggcaacaaaattatcgacg
agcgcctgatcaaccccgacggctccctgctgttccgcgtaaccatcaacggagtgaccggctgg
cggctgtgcgagcgcattttggcgggaagttctggtggaggaagttctggtggagagcctactac
tgagaacttgtacttccagagcgataacggaagttctggtggaggaagttctggtggaatggtgt
ttacactcgaagatttcgtaggggactggcggcagacagccggctacaacctggaccaagtcctt
gagcagggcggtgtgtccagtttgtttcagaatctcggggtgtccgtaactccgatccaaaggat
tgtcctgagcggtgaaaacggcctgaagatcgacatccatgtcatcatcccgtatgaaggtctga

gcggcgatcagatgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatgatcatcac
tttaaggtgattctgcactatggcacactg

**SEQ ID NO:448 (L27V CP 98 TEV)**

MVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTGW
RLCERILAGSSGGGSSGGEPTTENLYFQSDNGSSGGGSSGGMVFTLEDFVGDWRQTAGYNLDQVL
EQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEKIFKVVYPVDDHH
FKVILHYGTL

**SEQ ID NO:449 (Human Protein Kinase C alpha (PKCa) (nt sequence)**

ATGGCTGACGTTTTCCCGGGCAACGACTCCACGGCGTCTCAGGACGTGGCCAACCGCTTCGCCCG
CAAAGGGGCGCTGAGGCAGAAGAACGTGCACGAGGTGAAGGACCACAAATTCATCGCGCGCTTCT
TCAAGCAGCCCACCTTCTGCAGCCACTGCACCGACTTCATCTGGGGGTTTGGGAAACAAGGCTTC
CAGTGCCAAGTTTGCTGTTTTGTGGTCCACAAGAGGTGCCATGAATTTGTTACTTTTTCTTGTCC
GGGTGCGGATAAGGGACCCGACACTGATGACCCCAGGAGCAAGCACAAGTTCAAAATCCACACTT
ACGGAAGCCCCACCTTCTGCGATCACTGTGGGTCACTGCTCTATGGACTTATCCATCAAGGGATG
AAATGTGACACCTGCGATATGAACGTTCACAAGCAATGCGTCATCAATGTCCCCAGCCTCTGCGG
AATGGATCACACTGAGAAGAGGGGGCGGATTTACCTAAAGGCTGAGGTTGCTGATGAAAAGCTCC
ATGTCACAGTACGAGATGCAAAAAATCTAATCCCTATGGATCCAAACGGGCTTTCAGATCCTTAT
GTGAAGCTGAAACTTATTCCTGATCCCAAGAATGAAAGCAAGCAAAAAACCAAAACCATCCGCTC
CACACTAAATCCGCAGTGGAATGAGTCCTTTACATTCAAATTGAAACCTTCAGACAAAGACCGAC
GACTGTCTGTAGAAATCTGGGACTGGGATCGAACAACAAGGAATGACTTCATGGGATCCCTTTCC
TTTGGAGTTTCGGAGCTGATGAAGATGCCGGCCAGTGGATGGTACAAGTTgCTTAACCAAGAAGA
AGGTGAGTACTACAACGTACCCATTCCGGAAGGGGACGAGGAAGGAAACATGGAACTCAGGCAGA
AATTCGAGAAAGCCAAACTTGGCCCTGCTGGCAACAAAGTCATCAGTCCCTCTGAAGACAGGAAA
CAACCTTCCAACAACCTTGACCGAGTGAAACTCACGGACTTCAATTTCCTCATGGTGTTGGGAAA
GGGGAGTTTTGGAAAGGTGATGCTTGCCGACAGGAAGGGCACAGAAGAACTGTATGCAATCAAAA
TCCTGAAGAAGGATGTGGTGATTCAGGATGATGACGTGGAGTGCACCATGGTAGAAAAGCGAGTC
TTGGCCCTGCTTGACAAACCCCCGTTCTTGACGCAGCTGCACTCCTGCTTCCAGACAGTGGATCG
GCTGTACTTCGTCATGGAATATGTCAACGGTGGGGACCTCATGTACCACATTCAGCAAGTAGGAA
AATTTAAGGAACCACAAGCAGTATTCTATGCGGCAGAGATTTCCATCGGATTGTTCTTTCTTCAT
AAAAGAGGAATCATTTATAGGGATCTGAAGTTAGATAACGTCATGTTGGATTCAGAAGGACATAT
CAAAATTGCTGACTTTGGGATGTGCAAGGAACACATGATGGATGGAGTCACGACCAGGACCTTCT
GTGGGACTCCAGATTATATCGCCCCAGAGATAATCGCTTATCAGCCGTATGGAAAATCTGTGGAC
TGGTGGGCCTATGGCGTCCTGTTGTATGAAATGCTTGCCGGGCAGCCTCCATTTGATGGTGAAGA
TGAAGACGAGCTATTTCAGTCTATCATGGAGCACAACGTTTCCTATCCAAAATCCTTGTCCAAGG
AGGCTGTTTCTATCTGCAAAGGACTGATGACCAAACACCCAGCCAAGCGGCTGGGCTGTGGGCCT
GAGGGGGAGAGGGACGTGAGAGAGCATGCCTTCTTCCGGAGGATCGACTGGGAAAAACTGGAGAA
CAGGGAGATCCAGCCACCATTCAAGCCCAAAGTGTGTGGCAAAGGAGCAGAGAACTTTGACAAGT
TCTTCACACGAGGACAGCCCGTCTTAACACCACCTGATCAGCTGGTTATTGCTAACATAGACCAG
TCTGATTTTGAAGGGTTCTCGTATGTCAACCCCCAGTTTGTGCACCCCATCTTACAGAGTGCAGT
AGTT

**SEQ ID NO:450 (Human Protein Kinase C alpha (PKCa) (aa sequence)**

MADVFPGNDSTASQDVANRFARKGALRQKNVHEVKDHKFIARFFKQPTFCSHCTDFIWGFGKQGF
QCQVCCFVVHKRCHEFVTFSCPGADKGPDTDDPRSKHKFKIHTYGSPTFCDHCGSLLYGLIHQGM
KCDTCDMNVHKQCVINVPSLCGMDHTEKRGRIYLKAEVADEKLHVTVRDAKNLIPMDPNGLSDPY
VKLKLIPDPKNESKQKTKTIRSTLNPQWNESFTFKLKPSDKDRRLSVEIWDWDRTTRNDFMGSLS
FGVSELMKMPASGWYKLLNQEEGEYYNVPIPEGDEEGNMELRQKFEKAKLGPAGNKVISPSEDRK
QPSNNLDRVKLTDFNFLMVLGKGSFGKVMLADRKGTEELYAIKILKKDVVIQDDDVECTMVEKRV
LALLDKPPFLTQLHSCFQTVDRLYFVMEYVNGGDLMYHIQQVGKFKEPQAVFYAAEISIGLFFLH
KRGIIYRDLKLDNVMLDSEGHIKIADFGMCKEHMMDGVTTRTFCGTPDYIAPEIIAYQPYGKSVD
WWAYGVLLYEMLAGQPPFDGEDEDELFQSIMEHNVSYPKSLSKEAVSICKGLMTKHPAKRLGCGP

EGERDVREHAFFRRIDWEKLENREIQPPFKPKVCGKGAENFDKFFTRGQPVLTPPDQLVIANIDQ
SDFEGFSYVNPQFVHPILQSAVV

**SEQ ID NO:451 (Human Glucocorticoid receptor (GR) (nt sequence)**

ATGGACTCCAAAGAATCATTAACTCCTGGTAGAGAAGAAAACCCCAGCAGTGTGCTTGCTCAGGA
GAGGGGAGATGTGATGGACTTCTATAAAACCCTAAGAGGAGGAGCTACTGTGAAGGTTTCTGCGT
CTTCACCCTCACTGGCTGTCGCTTCTCAATCAGACTCCAAGCAGCGAAGACTTTTGGTTGATTTT
CCAAAAGGCTCAGTAAGCAATGCGCAGCAGCCAGATCTGTCCAAAGCAGTTTCACTCTCAATGGG
ACTGTATATGGGAGAGACAGAAACAAAAGTGATGGGAAATGACCTGGGATTCCCACAGCAGGGCC
AAATCAGCCTTTCCTCGGGGGAAACAGACTTAAAGCTTTTGGAAGAAAGCATTGCAAACCTCAAT
AGGTCGACCAGTGTTCCAGAGAACCCCAAGAGTTCAGCATCCACTGCTGTGTCTGCTGCCCCCAC
AGAGAAGGAGTTTCCAAAAACTCACTCTGATGTATCTTCAGAACAGCAACATTTGAAGGGCCAGA
CTGGCACCAACGGTGGCAATGTGAAATTGTATACCACAGACCAAAGCACCTTTGACATTTTGCAG
GATTTGGAGTTTTCTTCTGGGTCCCCAGGTAAAGAGACGAATGAGAGTCCTTGGAGATCAGACCT
GTTGATAGATGAAAACTGTTTGCTTTCTCCTCTGGCGGGAGAAGACGATTCATTCCTTTTGGAAG
GAAACTCGAATGAGGACTGCAAGCCTCTCATTTTACCGGACACTAAACCCAAAATTAAGGATAAT
GGAGATCTGGTTTTGTCAAGCCCCAGTAATGTAACACTGCCCCAAGTGAAAACAGAAAAAGAAGA
TTTCATCGAACTCTGCACCCCTGGGGTAATTAAGCAAGAGAAACTGGGCACAGTTTACTGTCAGG
CAAGCTTTCCTGGAGCAAATATAATTGGTAATAAAATGTCTGCCATTTCTGTTCATGGTGTGAGT
ACCTCTGGAGGACAGATGTACCACTATGACATGAATACAGCATCCCTTTCTCAACAGCAGGATCA
GAAGCCTATTTTTAATGTCATTCCACCAATTCCCGTTGGTTCCGAAAATTGGAATAGGTGCCAAG
GATCTGGAGATGACAACTTGACTTCTCTGGGGACTCTGAACTTCCCTGGTCGAACAGTTTTTTCT
AATGGCTATTCAAGCCCCAGCATGAGACCAGATGTAAGCTCTCCTCCATCCAGCTCCTCAACAGC
AACAACAGGACCACCTCCCAAACTCTGCCTGGTGTGCTCTGATGAAGCTTCAGGATGTCATTATG
GAGTCTTAACTTGTGGAAGCTGTAAAGTTTTCTTCAAAAGAGCAGTGGAAGGACAGCACAATTAC
CTATGTGCTGGAAGGAATGATTGCATCATCGATAAAATTCGAAGAAAAAACTGCCCAGCATGCCG
CTATCGAAAATGTCTTCAGGCTGGAATGAACCTGGAAGCTCGAAAAACAAAGAAAAAAATAAAAG
GAATTCAGCAGGCCACTACAGGAGTCTCACAAGAAACCTCTGAAAATCCTGGTAACAAAACAATA
GTTCCTGCAACGTTACCACAACTCACCCCTACCCTGGTGTCACTGTTGGAGGTTATTGAACCTGA
AGTGTTATATGCAGGATATGATAGCTCTGTTCCAGACTCAACTTGGAGGATCATGACTACGCTCA
ACATGTTAGGAGGGCGGCAAGTGATTGCAGCAGTGAAATGGGCAAAGGCAATACCAGGTTTCAGG
AACTTACACCTGGATGACCAAATGACCCTACTGCAGTACTCCTGGATGTTTCTTATGGCATTTGC
TCTGGGGTGGAGATCATATAGACAATCAAGTGCAAACCTGCTGTGTTTTGCTCCTGATCTGATTA
TTAATGAGCAGAGAATGACTCTACCCTGCATGTACGACCAATGTAAACACATGCTGTATGTTTCC
TCTGAGTTACACAGGCTTCAGGTATCTTATGAAGAGTATCTCTGTATGAAAACCTTACTGCTTCT
CTCTTCAGTTCCTAAGGACGGTCTGAAGAGCCAAGAGCTATTTGATGAAATTAGAATGACCTACA
TCAAAGAGCTAGGAAAAGCCATTGTCAAGAGGGAAGGAAACTCCAGCCAGAACTGGCAGCGGTTT
TATCAACTGACAAAACTCTTGGATTCTATGCATGAAGTGGTTGAAAATCTCCTTAACTATTGCTT
CCAAACATTTTTGGATAAGACCATGAGTATTGAATTCCCCGAGATGTTAGCTGAAATCATCACCA
ATCAGATACCAAAATATTCAAATGGAAATATCAAAAAACTTCTGTTTCATCAAAAGGTT

**SEQ ID NO:452 (Human Glucocorticoid receptor (GR) (aa sequence)**

MDSKESLTPGREENPSSVLAQERGDVMDFYKTLRGGATVKVSASSPSLAVASQSDSKQRRLLVDF
PKGSVSNAQQPDLSKAVSLSMGLYMGETETKVMGNDLGFPQQGQISLSSGETDLKLLEESIANLN
RSTSVPENPKSSASTAVSAAPTEKEFPKTHSDVSSEQQHLKGQTGTNGGNVKLYTTDQSTFDILQ
DLEFSSGSPGKETNESPWRSDLLIDENCLLSPLAGEDDSFLLEGNSNEDCKPLILPDTKPKIKDN
GDLVLSSPSNVTLPQVKTEKEDFIELCTPGVIKQEKLGTVYCQASFPGANIIGNKMSAISVHGVS
TSGGQMYHYDMNTASLSQQQDQKPIFNVIPPIPVGSENWNRCQGSGDDNLTSLGTLNFPGRTVFS
NGYSSPSMRPDVSSPPSSSSTATTGPPPKLCLVCSDEASGCHYGVLTCGSCKVFFKRAVEGQHNY
LCAGRNDCIIDKIRRKNCPACRYRKCLQAGMNLEARKTKKKIKGIQQATTGVSQETSENPGNKTI
VPATLPQLTPTLVSLLEVIEPEVLYAGYDSSVPDSTWRIMTTLNMLGGRQVIAAVKWAKAIPGFR
NLHLDDQMTLLQYSWMFLMAFALGWRSYRQSSANLLCFAPDLIINEQRMTLPCMYDQCKHMLYVS

SELHRLQVSYEEYLCMKTLLLLSSVPKDGLKSQELFDEIRMTYIKELGKAIVKREGNSSQNWQRF
YQLTKLLDSMHEVVENLLNYCFQTFLDKTMSIEFPEMLAEIITNQIPKYSNGNIKKLLFHQKV

**SEQ ID NO:453 (L27V02-GR/L27V02-PKCa linker (nt sequence)**
GGTGGTTCAGGTGGTGGCGGGAGCGGTGGAGGGAGCAGCGGTGGAGCGATCGCC

**SEQ ID NO:454 (L27V02-GR/L27V02-PKCa linker (aa sequence)**
GGSGGGGSGGGSSGGAIA

**SEQ ID NO:455 (GR-L27V02/PKCa-L27V02 linker (nt sequence)**
TCTCTCGGTGGTTCAGGTGGTGGCGGGAGCGGTGGAGGGAGCAGCGGTGGA

**SEQ ID NO:456 (GR-L27V02/PKCa-L27V02 linker (aa sequence)**
SLGGSGGGGSGGGSSGG

**SEQ ID NO:457 (GSSG linker (nt sequence)**
GCTCGAGCGGA

**SEQ ID NO:458 (GSSG linker (aa sequence)**
GSSG

**SEQ ID NO:459 (AT1R (nt sequence)**
ATGATTCTCAACTCTTCTACTGAAGATGGTATTAAAAGAATCCAAGATGATTGTCCCAAAGCTGG
AAGGCATAATTACATATTTGTCATGATTCCTACTTTATACAGTATCATCTTTGTGGTGGGAATAT
TTGGAAACAGCTTGGTGGTGATAGTCATTTACTTTTATATGAAGCTGAAGACTGTGGCCAGTGTT
TTTCTTTTGAATTTAGCACTGGCTGACTTATGCTTTTTACTGACTTTGCCACTATGGGCTGTCTA
CACAGCTATGGAATACCGCTGGCCCTTTGGCAATTACCTATGTAAGATTGCTTCAGCCAGCGTCA
GTTTCAACCTGTACGCTAGTGTGTTTCTACTCACGTGTCTCAGCATTGATCGATACCTGGCTATT
GTTCACCCAATGAAGTCCCGCCTTCGACGCACAATGCTTGTAGCCAAAGTCACCTGCATCATCAT
TTGGCTGCTGGCAGGCTTGGCCAGTTTGCCAGCTATAATCCATCGAAATGTATTTTTCATTGAGA
ACACCAATATTACAGTTTGTGCTTTCCATTATGAGTCCCAAAATTCAACCCTTCCGATAGGGCTG
GGCCTGACCAAAAATATACTGGGTTTCCTGTTTCCTTTTCTGATCATTCTTACAAGTTATACTCT
TATTTGGAAGGCCCTAAAGAAGGCTTATGAAATTCAGAAGAACAAACCAAGAAATGATGATATTT
TTAAGATAATTATGGCAATTGTGCTTTTCTTTTTCTTTTCCTGGATTCCCCACCAAATATTCACT
TTTCTGGATGTATTGATTCAACTAGGCATCATACGTGACTGTAGAATTGCAGATATTGTGGACAC
GGCCATGCCTATCACCATTTGTATAGCTTATTTTAACAATTGCCTGAATCCTCTTTTTTATGGCT
TTCTGGGGAAAAAATTTAAAAGATATTTTCTCCAGCTTCTAAAATATATTCCCCCAAAAGCCAAA
TCCCACTCAAACCTTTCAACAAAAATGAGCACGCTTTCCTACCGCCCCTCAGATAATGTAAGCTC
ATCCACCAAGAAGCCTGCACCATGTTTTGAGGTTGAGTGA

**SEQ ID NO:460 (AT1R (aa sequence)**
MILNSSTEDGIKRIQDDCPKAGRHNYIFVMIPTLYSIIFVVGIFGNSLVVIVIYFYMKLKTVASV
FLLNLALADLCFLLTLPLWAVYTAMEYRWPFGNYLCKIASASVSFNLYASVFLLTCLSIDRYLAI
VHPMKSRLRRTMLVAKVTCIIIWLLAGLASLPAIIHRNVFFIENTNITVCAFHYESQNSTLPIGL
GLTKNILGFLFPFLIILTSYTLIWKALKKAYEIQKNKPRNDDIFKIIMAIVLFFFFSWIPHQIFT
FLDVLIQLGIIRDCRIADIVDTAMPITICIAYFNNCLNPLFYGFLGKKFKRYFLQLLKYIPPKAK
SHSNLSTKMSTLSYRPSDNVSSSTKKPAPCFEVE

**SEQ ID NO:461 (IL6-00 signal peptide (nt sequence)**
ATGAACTCCTTCTCCACAAGCGCCTTCGGTCCAGTTGCCTTCTCCCTGGGGCTGCTCCTGGTGTT
GCCTGCTGCCTTCCCTGCCCCA

**SEQ ID NO:462 (IL6-00 signal peptide (aa sequence)**
MNSFSTSAFGPVAFSLGLLLVLPAAFPAP

**SEQ ID NO:463 (IL6-00 L27V-00 (nt sequence)**
ATGAACTCCTTCTCCACAAGCGCCTTCGGTCCAGTTGCCTTCTCCCTGGGGCTGCTCCTGGTGTT
GCCTGCTGCCTTCCCTGCCCCAGTGTTTACACTCGAAGATTTCGTAGGGGACTGGCGGCAGACAG
CCGGCTACAACCTGGACCAAGTCCTTGAGCAGGGCGGTGTGTCCAGTTTGTTTCAGAATCTCGGG
GTGTCCGTAACTCCGATCCAAAGGATTGTCCTGAGCGGTGAAAACGGCCTGAAGATCGACATCCA
TGTCATCATCCCGTATGAAGGTCTGAGCGGCGATCAGATGGGCCAGATCGAAAAAATTTTTAAGG
TGGTGTACCCTGTGGATGATCATCACTTTAAGGTGATTCTGCACTATGGCACACTGGTAATCGAC
GGGGTTACGCCGAACATGATCGACTATTTCGGACGGCCGTATGAAGGCATCGCCGTGTTCGACGG
CAAAAAGATCACTGTAACCGGGACCCTGTGGAACGGCAACAAAATTATCGACGAGCGCCTGATCA
ACCCCGACGGCTCCCTGCTGTTCCGCGTAACCATCAACGGAGTGACCGGCTGGCGGCTGTGCGAG
CGCATTTTGGCG

**SEQ ID NO:464 (IL6-00 L27V-00 (aa sequence)**
MNSFSTSAFGPVAFSLGLLLVLPAAFPAPVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLG
VSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVID
GVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCE
RILA

**SEQ ID NO:465 (Native secretion signal + L27V (nt sequence)**
atggcttactccacactgttcatcattgctctcacagccgtcgtaacacaagcctcctccacaca
gaaaagcaacctgacaGTGTTTACACTCGAAGATTTCGTAGGGGACTGGCGGCAGACAGCCGGCT
ACAACCTGGACCAAGTCCTTGAGCAGGGCGGTGTGTCCAGTTTGTTTCAGAATCTCGGGGTGTCC
GTAACTCCGATCCAAAGGATTGTCCTGAGCGGTGAAAACGGCCTGAAGATCGACATCCATGTCAT
CATCCCGTATGAAGGTCTGAGCGGCGATCAGATGGGCCAGATCGAAAAAATTTTTAAGGTGGTGT
ACCCTGTGGATGATCATCACTTTAAGGTGATTCTGCACTATGGCACACTGGTAATCGACGGGGTT
ACGCCGAACATGATCGACTATTTCGGACGGCCGTATGAAGGCATCGCCGTGTTCGACGGCAAAAA
GATCACTGTAACCGGGACCCTGTGGAACGGCAACAAAATTATCGACGAGCGCCTGATCAACCCCG
ACGGCTCCCTGCTGTTCCGCGTAACCATCAACGGAGTGACCGGCTGGCGGCTGTGCGAGCGCATT
TTGGCG

**SEQ ID NO:466 (Native secretion signal + L27V (aa sequence)**
MAYSTLFIIALTAVVTQASSTQKSNLTVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVS
VTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGV
TPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERI
LA

**SEQ ID NO:467 (CP 6 L27V (RIIbB) (nt sequence) (nt sequence)**
Atgttcgttggggactggcgacagacagccggctacaacctggaccaagtccttgaacagggagg
tgtgtccagtttgtttcagaatctcggggtgtccgtaactccgatccaaaggattgtcctgagcg
gtgaaaatgggctgaagatcgacatccatgtcatcatcccgtatgaaggtctgagcggcgaccaa
atgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatgatcatcactttaaggtgat
cctgcactatggcacactggtaatcgacggggttacgccgaacatgatcgactatttcggacggc
cgtatgaaggcatcgccgtgttcgacggcaaaaagatcactgtaacagggaccctgtggaacggc

aacaaaattatcgacgagcgcctgatcaaccccgacggctccctgctgttccgagtaaccatcaa
cggagtgaccggctggcggctgtGCGAACGCATTCTGGCtAGCTCAAGCGGAGGTTCAGGCGGTT
CCGGAATGTATGAAAGCTTTATTGAGTCACTGCCATTCCTTAAATCTTTGGAGTTTTCTGCACGC
CTGAAAGTAGTAGATGTGATAGGCACCAAAGTATACAACGATGGAGAACAAATCATTGCTCAGGG
AGATTCGGCTGATTCTTTTTTCATTATTGAATCTGGAGAAGTGAAAATTACTATGAAAAGAAAGG
GTAAATCAGAAGTGGAAGAGAATGGTGCAGTAGAAATCGCTCGATGCTCGCGGGGACAGTACTTT
GGAGAGCTTGCCCTGGTAACTAACAAACCTCGAGCAGCTTCTGCCCACGCCATTGGGACTGTCAA
ATGTTTAGCAATGGATGTGCAAGCATTTGAAAGGCTTCTGGGACCTTGCATGGAAATTATGAAAA
GGAACATCGCTACCTATGAAGAACAGTTAGTTGCCCTGTATGGAACGAACATGGATATTGTAGGG
TCAGGTGGATCTGGAGGTAGCTCTTCTatggtcttcacactcgaagat

**SEQ ID NO:468 (CP 6 L27V (RIIbB) (aa seq)**
MFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQ
MGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNG
NKIIDERLINPDGSLLFRVTINGVTGWRLCERILASSSGGSGGSGMYESFIESLPFLKSLEFSAR
LKVVDVIGTKVYNDGEQIIAQGDSADSFFIIESGEVKITMKRKGKSEVEENGAVEIARCSRGQYF
GELALVTNKPRAASAHAIGTVKCLAMDVQAFERLLGPCMEIMKRNIATYEEQLVALYGTNMDIVG
SGGSGGSSSMVFTLED

**SEQ ID NO:469 (CP 12 L27V (RIIbB) (nt sequence) (nt sequence)**
ATGcagacagccggctacaacctggaccaagtccttgaacagggaggtgtgtccagtttgtttca
gaatctcggggtgtccgtaactccgatccaaaggattgtcctgagcggtgaaaatgggctgaaga
tcgacatccatgtcatcatcccgtatgaaggtctgagcggcgaccaaatgggccagatcgaaaaa
atttttaaggtggtgtaccctgtggatgatcatcactttaaggtgatcctgcactatggcacact
ggtaatcgacggggttacgccgaacatgatcgactatttcggacggccgtatgaaggcatcgccg
tgttcgacggcaaaaagatcactgtaacagggaccctgtggaacggcaacaaaattatcgacgag
cgcctgatcaaccccgacggctccctgctgttccgagtaaccatcaacggagtgaccggctggcg
gctgtGCGAACGCATTCTGGCtAGCTCAAGCGGAGGTTCAGGCGGTTCCGGAATGTATGAAAGCT
TTATTGAGTCACTGCCATTCCTTAAATCTTTGGAGTTTTCTGCACGCCTGAAAGTAGTAGATGTG
ATAGGCACCAAAGTATACAACGATGGAGAACAAATCATTGCTCAGGGAGATTCGGCTGATTCTTT
TTTCATTATTGAATCTGGAGAAGTGAAAATTACTATGAAAAGAAAGGGTAAATCAGAAGTGGAAG
AGAATGGTGCAGTAGAAATCGCTCGATGCTCGCGGGGACAGTACTTTGGAGAGCTTGCCCTGGTA
ACTAACAAACCTCGAGCAGCTTCTGCCCACGCCATTGGGACTGTCAAATGTTTAGCAATGGATGT
GCAAGCATTTGAAAGGCTTCTGGGACCTTGCATGGAAATTATGAAAAGGAACATCGCTACCTATG
AAGAACAGTTAGTTGCCCTGTATGGAACGAACATGGATATTGTAGGGTCAGGTGGATCTGGAGGT
AGCTCTTCTatggtcttcacactcgaagatttcgttggggactggcga

**SEQ ID NO:470 (CP 12 L27V (RIIbB) (aa seq)**
MQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEK
IFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDE
RLINPDGSLLFRVTINGVTGWRLCERILASSSGGSGGSGMYESFIESLPFLKSLEFSARLKVVDV
IGTKVYNDGEQIIAQGDSADSFFIIESGEVKITMKRKGKSEVEENGAVEIARCSRGQYFGELALV
TNKPRAASAHAIGTVKCLAMDVQAFERLLGPCMEIMKRNIATYEEQLVALYGTNMDIVGSGGSGG
SSSMVFTLEDFVGDWR

**SEQ ID NO:471 (CP 48 L27V (RIIbB) (nt sequence)**
ATGggtgaaaatgggctgaagatcgacatccatgtcatcatcccgtatgaaggtctgagcggcga
ccaaatgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatgatcatcactttaagg
tgatcctgcactatggcacactggtaatcgacggggttacgccgaacatgatcgactatttcgga
cggccgtatgaaggcatcgccgtgttcgacggcaaaaagatcactgtaacagggaccctgtggaa
cggcaacaaaattatcgacgagcgcctgatcaaccccgacggctccctgctgttccgagtaacca

tcaacggagtgaccggctggcggctgtGCGAACGCATTCTGGCtAGCTCAAGCGGAGGTTCAGGC
GGTTCCGGAATGTATGAAAGCTTTATTGAGTCACTGCCATTCCTTAAATCTTTGGAGTTTTCTGC
ACGCCTGAAAGTAGTAGATGTGATAGGCACCAAAGTATACAACGATGGAGAACAAATCATTGCTC
AGGGAGATTCGGCTGATTCTTTTTTCATTATTGAATCTGGAGAAGTGAAAATTACTATGAAAAGA
AAGGGTAAATCAGAAGTGGAAGAGAATGGTGCAGTAGAAATCGCTCGATGCTCGCGGGGACAGTA
CTTTGGAGAGCTTGCCCTGGTAACTAACAAACCTCGAGCAGCTTCTGCCCACGCCATTGGGACTG
TCAAATGTTTAGCAATGGATGTGCAAGCATTTGAAAGGCTTCTGGGACCTTGCATGGAAATTATG
AAAAGGAACATCGCTACCTATGAAGAACAGTTAGTTGCCCTGTATGGAACGAACATGGATATTGT
AGGGTCAGGTGGATCTGGAGGTAGCTCTTCTatggtcttcacactcgaagatttcgttggggact
ggcgacagacagccggctacaacctggaccaagtccttgaacagggaggtgtgtccagtttgttt
cagaatctcggggtgtccgtaactccgatccaaaggattgtcctgagc

**SEQ ID NO:472 (CP 48 L27V (RIIbB) (aa seq)**

MGENGLKIDIHVIIPYEGLSGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFG
RPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILASSSGGSG
GSGMYESFIESLPFLKSLEFSARLKVVDVIGTKVYNDGEQIIAQGDSADSFFIIESGEVKITMKR
KGKSEVEENGAVEIARCSRGQYFGELALVTNKPRAASAHAIGTVKCLAMDVQAFERLLGPCMEIM
KRNIATYEEQLVALYGTNMDIVGSGGSGGSSSMVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLF
QNLGVSVTPIQRIVLS

**SEQ ID NO:473 (CP 52 L27V (RIIbB) (nt sequence)**

ATGCTGAAGATCGACATCCATGTCATCATCCCGTATGAAGGTCTGAGCGGCGACCAAATGGGCCA
GATCGAAAAAATTTTTAAGGTGGTGTACCCTGTGGATGATCATCACTTTAAGGTGATCCTGCACT
ATGGCACACTGGTAATCGACGGGGTTACGCCGAACATGATCGACTATTTCGGACGGCCGTATGAA
GGCATCGCCGTGTTCGACGGCAAAAAGATCACTGTAACAGGGACCCTGTGGAACGGCAACAAAAT
TATCGACGAGCGCCTGATCAACCCCGACGGCTCCCTGCTGTTCCGAGTAACCATCAACGGAGTGA
CCGGCTGGCGGCTGTGCGAACGCATTCTGGCTAGCTCAAGCGGAGGTTCAGGCGGTTCCGGAATG
TATGAAAGCTTTATTGAGTCACTGCCATTCCTTAAATCTTTGGAGTTTTCTGCACGCCTGAAAGT
AGTAGATGTGATAGGCACCAAAGTATACAACGATGGAGAACAAATCATTGCTCAGGGAGATTCGG
CTGATTCTTTTTTCATTATTGAATCTGGAGAAGTGAAAATTACTATGAAAAGAAAGGGTAAATCA
GAAGTGGAAGAGAATGGTGCAGTAGAAATCGCTCGATGCTCGCGGGGACAGTACTTTGGAGAGCT
TGCCCTGGTAACTAACAAACCTCGAGCAGCTTCTGCCCACGCCATTGGGACTGTCAAATGTTTAG
CAATGGATGTGCAAGCATTTGAAAGGCTTCTGGGACCTTGCATGGAAATTATGAAAAGGAACATC
GCTACCTATGAAGAACAGTTAGTTGCCCTGTATGGAACGAACATGGATATTGTAGGGTCAGGTGG
ATCTGGAGGTAGCTCTTCTATGGTCTTCACACTCGAAGATTTCGTTGGGGACTGGCGACAGACAG
CCGGCTACAACCTGGACCAAGTCCTTGAACAGGGAGGTGTGTCCAGTTTGTTTCAGAATCTCGGG
GTGTCCGTAACTCCGATCCAAAGGATTGTCCTGAGCGGTGAAAATGGG

**SEQ ID NO:474 (CP 52 L27V (RIIbB) (aa seq)**

MLKIDIHVIIPYEGLSGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYE
GIAVFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILASSSGGSGGSGM
YESFIESLPFLKSLEFSARLKVVDVIGTKVYNDGEQIIAQGDSADSFFIIESGEVKITMKRKGKS
EVEENGAVEIARCSRGQYFGELALVTNKPRAASAHAIGTVKCLAMDVQAFERLLGPCMEIMKRNI
ATYEEQLVALYGTNMDIVGSGGSGGSSSMVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLG
VSVTPIQRIVLSGENG

**SEQ ID NO:475 (CP 55 L27V (RIIbB) (nt sequence)**

Atggacatccatgtcatcatcccgtatgaaggtctgagcggcgaccaaatgggccagatcgaaaa
aatttttaaggtggtgtaccctgtggatgatcatcactttaaggtgatcctgcactatggcacac
tggtaatcgacggggttacgccgaacatgatcgactatttcggacggccgtatgaaggcatcgcc
gtgttcgacggcaaaaagatcactgtaacagggaccctgtggaacggcaacaaaattatcgacga

gcgcctgatcaaccccgacggctccctgctgttccgagtaaccatcaacggagtgaccggctggc
ggctgtGCGAACGCATTCTGGCtAGCTCAAGCGGAGGTTCAGGCGGTTCCGGAATGTATGAAAGC
TTTATTGAGTCACTGCCATTCCTTAAATCTTTGGAGTTTTCTGCACGCCTGAAAGTAGTAGATGT
GATAGGCACCAAAGTATACAACGATGGAGAACAAATCATTGCTCAGGGAGATTCGGCTGATTCTT
TTTTCATTATTGAATCTGGAGAAGTGAAAATTACTATGAAAAGAAAGGGTAAATCAGAAGTGGAA
GAGAATGGTGCAGTAGAAATCGCTCGATGCTCGCGGGGACAGTACTTTGGAGAGCTTGCCCTGGT
AACTAACAAACCTCGAGCAGCTTCTGCCCACGCCATTGGGACTGTCAAATGTTTAGCAATGGATG
TGCAAGCATTTGAAAGGCTTCTGGGACCTTGCATGGAAATTATGAAAAGGAACATCGCTACCTAT
GAAGAACAGTTAGTTGCCCTGTATGGAACGAACATGGATATTGTAGGGTCAGGTGGATCTGGAGG
TAGCTCTTCTatggtcttcacactcgaagatttcgttggggactggcgacagacagccggctaca
acctggaccaagtccttgaacagggaggtgtgtccagtttgtttcagaatctcggggtgtccgta
actccgatccaaaggattgtcctgagcggtgaaaatgggctgaagatc

**SEQ ID NO:476 (CP 55 L27V (RIIbB) (aa seq)**
MDIHVIIPYEGLSGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIA
VFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILASSSGGSGGSGMYES
FIESLPFLKSLEFSARLKVVDVIGTKVYNDGEQIIAQGDSADSFFIIESGEVKITMKRKGKSEVE
ENGAVEIARCSRGQYFGELALVTNKPRAASAHAIGTVKCLAMDVQAFERLLGPCMEIMKRNIATY
EEQLVALYGTNMDIVGSGGSGGSSSMVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSV
TPIQRIVLSGENGLKI

**SEQ ID NO:477 (CP 83 L27V (RIIbB) (nt sequence)**
ATGgtggatgatcatcactttaaggtgatcctgcactatggcacactggtaatcgacggggttac
gccgaacatgatcgactatttcggacggccgtatgaaggcatcgccgtgttcgacggcaaaaaga
tcactgtaacagggaccctgtggaacggcaacaaaattatcgacgagcgcctgatcaaccccgac
ggctccctgctgttccgagtaaccatcaacggagtgaccggctggcggctgtGCGAACGCATTCT
GGCtAGCTCAAGCGGAGGTTCAGGCGGTTCCGGAATGTATGAAAGCTTTATTGAGTCACTGCCAT
TCCTTAAATCTTTGGAGTTTTCTGCACGCCTGAAAGTAGTAGATGTGATAGGCACCAAAGTATAC
AACGATGGAGAACAAATCATTGCTCAGGGAGATTCGGCTGATTCTTTTTTCATTATTGAATCTGG
AGAAGTGAAAATTACTATGAAAAGAAAGGGTAAATCAGAAGTGGAAGAGAATGGTGCAGTAGAAA
TCGCTCGATGCTCGCGGGGACAGTACTTTGGAGAGCTTGCCCTGGTAACTAACAAACCTCGAGCA
GCTTCTGCCCACGCCATTGGGACTGTCAAATGTTTAGCAATGGATGTGCAAGCATTTGAAAGGCT
TCTGGGACCTTGCATGGAAATTATGAAAAGGAACATCGCTACCTATGAAGAACAGTTAGTTGCCC
TGTATGGAACGAACATGGATATTGTAGGGTCAGGTGGATCTGGAGGTAGCTCTTCTatggtcttc
acactcgaagatttcgttggggactggcgacagacagccggctacaacctggaccaagtccttga
acagggaggtgtgtccagtttgtttcagaatctcggggtgtccgtaactccgatccaaaggattg
tcctgagcggtgaaaatgggctgaagatcgacatccatgtcatcatcccgtatgaaggtctgagc
ggcgaccaaatgggccagatcgaaaaaatttttaaggtggtgtaccct

**SEQ ID NO:478 (CP 83 L27V (RIIbB) (aa seq)**
MVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPD
GSLLFRVTINGVTGWRLCERILASSSGGSGGSGMYESFIESLPFLKSLEFSARLKVVDVIGTKVY
NDGEQIIAQGDSADSFFIIESGEVKITMKRKGKSEVEENGAVEIARCSRGQYFGELALVTNKPRA
ASAHAIGTVKCLAMDVQAFERLLGPCMEIMKRNIATYEEQLVALYGTNMDIVGSGGSGGSSSMVF
TLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLS
GDQMGQIEKIFKVVYP

**SEQ ID NO:479 (CP 84 L27V (RIIbB) (nt sequence)**
atggatgatcatcactttaaggtgatcctgcactatggcacactggtaatcgacggggttacgcc
gaacatgatcgactatttcggacggccgtatgaaggcatcgccgtgttcgacggcaaaaagatca
ctgtaacagggaccctgtggaacggcaacaaaattatcgacgagcgcctgatcaaccccgacggc

tccctgctgttccgagtaaccatcaacggagtgaccggctggcggctgtGCGAACGCATTCTGGC
tAGCTCAAGCGGAGGTTCAGGCGGTTCCGGAATGTATGAAAGCTTTATTGAGTCACTGCCATTCC
TTAAATCTTTGGAGTTTTCTGCACGCCTGAAAGTAGTAGATGTGATAGGCACCAAAGTATACAAC
GATGGAGAACAAATCATTGCTCAGGGAGATTCGGCTGATTCTTTTTTCATTATTGAATCTGGAGA
AGTGAAAATTACTATGAAAAGAAAGGGTAAATCAGAAGTGGAAGAGAATGGTGCAGTAGAAATCG
CTCGATGCTCGCGGGGACAGTACTTTGGAGAGCTTGCCCTGGTAACTAACAAACCTCGAGCAGCT
TCTGCCCACGCCATTGGGACTGTCAAATGTTTAGCAATGGATGTGCAAGCATTTGAAAGGCTTCT
GGGACCTTGCATGGAAATTATGAAAAGGAACATCGCTACCTATGAAGAACAGTTAGTTGCCCTGT
ATGGAACGAACATGGATATTGTAGGGTCAGGTGGATCTGGAGGTAGCTCTTCTatggtcttcaca
ctcgaagatttcgttggggactggcgacagacagccggctacaacctggaccaagtccttgaaca
gggaggtgtgtccagtttgtttcagaatctcggggtgtccgtaactccgatccaaaggattgtcc
tgagcggtgaaaatgggctgaagatcgacatccatgtcatcatcccgtatgaaggtctgagcggc
gaccaaatgggccagatcgaaaaaatttttaaggtggtgtaccctgtg

**SEQ ID NO:480 (CP 84 L27V (RIIbB) (aa seq)**
MDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDG
SLLFRVTINGVTGWRLCERILASSSGGSGGSGMYESFIESLPFLKSLEFSARLKVVDVIGTKVYN
DGEQIIAQGDSADSFFIIESGEVKITMKRKGKSEVEENGAVEIARCSRGQYFGELALVTNKPRAA
SAHAIGTVKCLAMDVQAFERLLGPCMEIMKRNIATYEEQLVALYGTNMDIVGSGGSGGSSSMVFT
LEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSG
DQMGQIEKIFKVVYPV

**SEQ ID NO:481 (CP 103 L27V (RIIbB) (nt sequence)**
ATGacgccgaacatgatcgactatttcggacggccgtatgaaggcatcgccgtgttcgacggcaa
aaagatcactgtaacagggaccctgtggaacggcaacaaaattatcgacgagcgcctgatcaacc
ccgacggctccctgctgttccgagtaaccatcaacggagtgaccggctggcggctgtGCGAACGC
ATTCTGGCtAGCTCAAGCGGAGGTTCAGGCGGTTCCGGAATGTATGAAAGCTTTATTGAGTCACT
GCCATTCCTTAAATCTTTGGAGTTTTCTGCACGCCTGAAAGTAGTAGATGTGATAGGCACCAAAG
TATACAACGATGGAGAACAAATCATTGCTCAGGGAGATTCGGCTGATTCTTTTTTCATTATTGAA
TCTGGAGAAGTGAAAATTACTATGAAAAGAAAGGGTAAATCAGAAGTGGAAGAGAATGGTGCAGT
AGAAATCGCTCGATGCTCGCGGGGACAGTACTTTGGAGAGCTTGCCCTGGTAACTAACAAACCTC
GAGCAGCTTCTGCCCACGCCATTGGGACTGTCAAATGTTTAGCAATGGATGTGCAAGCATTTGAA
AGGCTTCTGGGACCTTGCATGGAAATTATGAAAAGGAACATCGCTACCTATGAAGAACAGTTAGT
TGCCCTGTATGGAACGAACATGGATATTGTAGGGTCAGGTGGATCTGGAGGTAGCTCTTCTatgg
tcttcacactcgaagatttcgttggggactggcgacagacagccggctacaacctggaccaagtc
cttgaacagggaggtgtgtccagtttgtttcagaatctcggggtgtccgtaactccgatccaaag
gattgtcctgagcggtgaaaatgggctgaagatcgacatccatgtcatcatcccgtatgaaggtc
tgagcggcgaccaaatgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatgatcat
cactttaaggtgatcctgcactatggcacactggtaatcgacggggtt

**SEQ ID NO:482 (CP 103 L27V (RIIbB) (aa seq)**
MTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCER
ILASSSGGSGGSGMYESFIESLPFLKSLEFSARLKVVDVIGTKVYNDGEQIIAQGDSADSFFIIE
SGEVKITMKRKGKSEVEENGAVEIARCSRGQYFGELALVTNKPRAASAHAIGTVKCLAMDVQAFE
RLLGPCMEIMKRNIATYEEQLVALYGTNMDIVGSGGSGGSSSMVFTLEDFVGDWRQTAGYNLDQV
LEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEKIFKVVYPVDDH
HFKVILHYGTLVIDGV

**SEQ ID NO:483 (CP 120 L27V (RIIbB) (nt sequence)**
ATGttcgacggcaaaaagatcactgtaacagggaccctgtggaacggcaacaaaattatcgacga
gcgcctgatcaaccccgacggctccctgctgttccgagtaaccatcaacggagtgaccggctggc
ggctgtGCGAACGCATTCTGGCtAGCTCAAGCGGAGGTTCAGGCGGTTCCGGAATGTATGAAAGC

TTTATTGAGTCACTGCCATTCCTTAAATCTTTGGAGTTTTCTGCACGCCTGAAAGTAGTAGATGT
GATAGGCACCAAAGTATACAACGATGGAGAACAAATCATTGCTCAGGGAGATTCGGCTGATTCTT
TTTTCATTATTGAATCTGGAGAAGTGAAAATTACTATGAAAAGAAAGGGTAAATCAGAAGTGGAA
GAGAATGGTGCAGTAGAAATCGCTCGATGCTCGCGGGGACAGTACTTTGGAGAGCTTGCCCTGGT
AACTAACAAACCTCGAGCAGCTTCTGCCCACGCCATTGGGACTGTCAAATGTTTAGCAATGGATG
TGCAAGCATTTGAAAGGCTTCTGGGACCTTGCATGGAAATTATGAAAAGGAACATCGCTACCTAT
GAAGAACAGTTAGTTGCCCTGTATGGAACGAACATGGATATTGTAGGGTCAGGTGGATCTGGAGG
TAGCTCTTCTatggtcttcacactcgaagatttcgttggggactggcgacagacagccggctaca
acctggaccaagtccttgaacagggaggtgtgtccagtttgtttcagaatctcggggtgtccgta
actccgatccaaaggattgtcctgagcggtgaaaatgggctgaagatcgacatccatgtcatcat
cccgtatgaaggtctgagcggcgaccaaatgggccagatcgaaaaaatttttaaggtggtgtacc
ctgtggatgatcatcactttaaggtgatcctgcactatggcacactggtaatcgacggggttacg
ccgaacatgatcgactatttcggacggccgtatgaaggcatcgccgtg

**SEQ ID NO:484 (CP 120 L27V (RIIbB) (aa seq)**

MFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILASSSGGSGGSGMYES
FIESLPFLKSLEFSARLKVVDVIGTKVYNDGEQIIAQGDSADSFFIIESGEVKITMKRKGKSEVE
ENGAVEIARCSRGQYFGELALVTNKPRAASAHAIGTVKCLAMDVQAFERLLGPCMEIMKRNIATY
EEQLVALYGTNMDIVGSGGSGGSSSMVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSV
TPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVT
PNMIDYFGRPYEGIAV

**SEQ ID NO:485 (CP 123 L27V (RIIbB) (nt sequence)**

ATGaaaaagatcactgtaacagggaccctgtggaacggcaacaaaattatcgacgagcgcctgat
caaccccgacggctccctgctgttccgagtaaccatcaacggagtgaccggctggcggctgtGCG
AACGCATTCTGGCtAGCTCAAGCGGAGGTTCAGGCGGTTCCGGAATGTATGAAAGCTTTATTGAG
TCACTGCCATTCCTTAAATCTTTGGAGTTTTCTGCACGCCTGAAAGTAGTAGATGTGATAGGCAC
CAAAGTATACAACGATGGAGAACAAATCATTGCTCAGGGAGATTCGGCTGATTCTTTTTTCATTA
TTGAATCTGGAGAAGTGAAAATTACTATGAAAAGAAAGGGTAAATCAGAAGTGGAAGAGAATGGT
GCAGTAGAAATCGCTCGATGCTCGCGGGGACAGTACTTTGGAGAGCTTGCCCTGGTAACTAACAA
ACCTCGAGCAGCTTCTGCCCACGCCATTGGGACTGTCAAATGTTTAGCAATGGATGTGCAAGCAT
TTGAAAGGCTTCTGGGACCTTGCATGGAAATTATGAAAAGGAACATCGCTACCTATGAAGAACAG
TTAGTTGCCCTGTATGGAACGAACATGGATATTGTAGGGTCAGGTGGATCTGGAGGTAGCTCTTC
Tatggtcttcacactcgaagatttcgttggggactggcgacagacagccggctacaacctggacc
aagtccttgaacagggaggtgtgtccagtttgtttcagaatctcggggtgtccgtaactccgatc
caaaggattgtcctgagcggtgaaaatgggctgaagatcgacatccatgtcatcatcccgtatga
aggtctgagcggcgaccaaatgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatg
atcatcactttaaggtgatcctgcactatggcacactggtaatcgacggggttacgccgaacatg
atcgactatttcggacggccgtatgaaggcatcgccgtgttcgacggc

**SEQ ID NO:486 (CP 123 L27V (RIIbB) (aa seq)**

MKKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILASSSGGSGGSGMYESFIE
SLPFLKSLEFSARLKVVDVIGTKVYNDGEQIIAQGDSADSFFIIESGEVKITMKRKGKSEVEENG
AVEIARCSRGQYFGELALVTNKPRAASAHAIGTVKCLAMDVQAFERLLGPCMEIMKRNIATYEEQ
LVALYGTNMDIVGSGGSGGSSSMVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPI
QRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNM
IDYFGRPYEGIAVFDG

**SEQ ID NO:487 (CP 124 L27V (RIIbB) (nt sequence)**

ATGaagatcactgtaacagggaccctgtggaacggcaacaaaattatcgacgagcgcctgatcaa
ccccgacggctccctgctgttccgagtaaccatcaacggagtgaccggctggcggctgtGCGAAC

GCATTCTGGCtAGCTCAAGCGGAGGTTCAGGCGGTTCCGGAATGTATGAAAGCTTTATTGAGTCA
CTGCCATTCCTTAAATCTTTGGAGTTTTCTGCACGCCTGAAAGTAGTAGATGTGATAGGCACCAA
AGTATACAACGATGGAGAACAAATCATTGCTCAGGGAGATTCGGCTGATTCTTTTTTCATTATTG
AATCTGGAGAAGTGAAAATTACTATGAAAAGAAAGGGTAAATCAGAAGTGGAAGAGAATGGTGCA
GTAGAAATCGCTCGATGCTCGCGGGGACAGTACTTTGGAGAGCTTGCCCTGGTAACTAACAAACC
TCGAGCAGCTTCTGCCCACGCCATTGGGACTGTCAAATGTTTAGCAATGGATGTGCAAGCATTTG
AAAGGCTTCTGGGACCTTGCATGGAAATTATGAAAAGGAACATCGCTACCTATGAAGAACAGTTA
GTTGCCCTGTATGGAACGAACATGGATATTGTAGGGTCAGGTGGATCTGGAGGTAGCTCTTCTat
ggtcttcacactcgaagatttcgttggggactggcgacagacagccggctacaacctggaccaag
tccttgaacagggaggtgtgtccagtttgtttcagaatctcggggtgtccgtaactccgatccaa
aggattgtcctgagcggtgaaaatgggctgaagatcgacatccatgtcatcatcccgtatgaagg
tctgagcggcgaccaaatgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatgatc
atcactttaaggtgatcctgcactatggcacactggtaatcgacggggttacgccgaacatgatc
gactatttcggacggccgtatgaaggcatcgccgtgttcgacggcaaa

**SEQ ID NO:488 (CP 124 L27V (RIIbB) (aa seq)**
MKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILASSSGGSGGSGMYESFIES
LPFLKSLEFSARLKVVDVIGTKVYNDGEQIIAQGDSADSFFIIESGEVKITMKRKGKSEVEENGA
VEIARCSRGQYFGELALVTNKPRAASAHAIGTVKCLAMDVQAFERLLGPCMEIMKRNIATYEEQL
VALYGTNMDIVGSGGSGGSSSMVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQ
RIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMI
DYFGRPYEGIAVFDGK

**SEQ ID NO:489 (CP 125 L27V (RIIbB) (nt sequence)**
ATGatcactgtaacagggaccctgtggaacggcaacaaaattatcgacgagcgcctgatcaaccc
cgacggctccctgctgttccgagtaaccatcaacggagtgaccggctggcggctgtGCGAACGCA
TTCTGGCtAGCTCAAGCGGAGGTTCAGGCGGTTCCGGAATGTATGAAAGCTTTATTGAGTCACTG
CCATTCCTTAAATCTTTGGAGTTTTCTGCACGCCTGAAAGTAGTAGATGTGATAGGCACCAAAGT
ATACAACGATGGAGAACAAATCATTGCTCAGGGAGATTCGGCTGATTCTTTTTTCATTATTGAAT
CTGGAGAAGTGAAAATTACTATGAAAAGAAAGGGTAAATCAGAAGTGGAAGAGAATGGTGCAGTA
GAAATCGCTCGATGCTCGCGGGGACAGTACTTTGGAGAGCTTGCCCTGGTAACTAACAAACCTCG
AGCAGCTTCTGCCCACGCCATTGGGACTGTCAAATGTTTAGCAATGGATGTGCAAGCATTTGAAA
GGCTTCTGGGACCTTGCATGGAAATTATGAAAAGGAACATCGCTACCTATGAAGAACAGTTAGTT
GCCCTGTATGGAACGAACATGGATATTGTAGGGTCAGGTGGATCTGGAGGTAGCTCTTCTatggt
cttcacactcgaagatttcgttggggactggcgacagacagccggctacaacctggaccaagtcc
ttgaacagggaggtgtgtccagtttgtttcagaatctcggggtgtccgtaactccgatccaaagg
attgtcctgagcggtgaaaatgggctgaagatcgacatccatgtcatcatcccgtatgaaggtct
gagcggcgaccaaatgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatgatcatc
actttaaggtgatcctgcactatggcacactggtaatcgacggggttacgccgaacatgatcgac
tatttcggacggccgtatgaaggcatcgccgtgttcgacggcaaaaag

**SEQ ID NO:490 (CP 125 L27V (RIIbB) (aa seq)**
MITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILASSSGGSGGSGMYESFIESL
PFLKSLEFSARLKVVDVIGTKVYNDGEQIIAQGDSADSFFIIESGEVKITMKRKGKSEVEENGAV
EIARCSRGQYFGELALVTNKPRAASAHAIGTVKCLAMDVQAFERLLGPCMEIMKRNIATYEEQLV
ALYGTNMDIVGSGGSGGSSSMVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQR
IVLSGENGLKIDIHVIIPYEGLSGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMID
YFGRPYEGIAVFDGKK

**SEQ ID NO:491 (CP 130 L27V (RIIbB) (nt sequence)**

ATGaccctgtggaacggcaacaaaattatcgacgagcgcctgatcaaccccgacggctccctgct
gttccgagtaaccatcaacggagtgaccggctggcggctgtGCGAACGCATTCTGGCtAGCTCAA
GCGGAGGTTCAGGCGGTTCCGGAATGTATGAAAGCTTTATTGAGTCACTGCCATTCCTTAAATCT
TTGGAGTTTTCTGCACGCCTGAAAGTAGTAGATGTGATAGGCACCAAAGTATACAACGATGGAGA
ACAAATCATTGCTCAGGGAGATTCGGCTGATTCTTTTTTCATTATTGAATCTGGAGAAGTGAAAA
TTACTATGAAAAGAAAGGGTAAATCAGAAGTGGAAGAGAATGGTGCAGTAGAAATCGCTCGATGC
TCGCGGGGACAGTACTTTGGAGAGCTTGCCCTGGTAACTAACAAACCTCGAGCAGCTTCTGCCCA
CGCCATTGGGACTGTCAAATGTTTAGCAATGGATGTGCAAGCATTTGAAAGGCTTCTGGGACCTT
GCATGGAAATTATGAAAAGGAACATCGCTACCTATGAAGAACAGTTAGTTGCCCTGTATGGAACG
AACATGGATATTGTAGGGTCAGGTGGATCTGGAGGTAGCTCTTCTatggtcttcacactcgaaga
tttcgttggggactggcgacagacagccggctacaacctggaccaagtccttgaacagggaggtg
tgtccagtttgtttcagaatctcggggtgtccgtaactccgatccaaaggattgtcctgagcggt
gaaaatgggctgaagatcgacatccatgtcatcatcccgtatgaaggtctgagcggcgaccaaat
gggccagatcgaaaaaatttttaaggtggtgtaccctgtggatgatcatcactttaaggtgatcc
tgcactatggcacactggtaatcgacggggttacgccgaacatgatcgactatttcggacggccg
tatgaaggcatcgccgtgttcgacggcaaaaagatcactgtaacaggg

**SEQ ID NO:492 (CP 130 L27V (RIIbB) (aa seq)**
MTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILASSSGGSGGSGMYESFIESLPFLKS
LEFSARLKVVDVIGTKVYNDGEQIIAQGDSADSFFIIESGEVKITMKRKGKSEVEENGAVEIARC
SRGQYFGELALVTNKPRAASAHAIGTVKCLAMDVQAFERLLGPCMEIMKRNIATYEEQLVALYGT
NMDIVGSGGSGGSSSMVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSG
ENGLKIDIHVIIPYEGLSGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRP
YEGIAVFDGKKITVTG

**SEQ ID NO:493 (CP 145 L27V (RIIbB) (nt sequence)**
ATGcccgacggctccctgctgttccgagtaaccatcaacggagtgaccggctggcggctgtGCGA
ACGCATTCTGGCtAGCTCAAGCGGAGGTTCAGGCGGTTCCGGAATGTATGAAAGCTTTATTGAGT
CACTGCCATTCCTTAAATCTTTGGAGTTTTCTGCACGCCTGAAAGTAGTAGATGTGATAGGCACC
AAAGTATACAACGATGGAGAACAAATCATTGCTCAGGGAGATTCGGCTGATTCTTTTTTCATTAT
TGAATCTGGAGAAGTGAAAATTACTATGAAAAGAAAGGGTAAATCAGAAGTGGAAGAGAATGGTG
CAGTAGAAATCGCTCGATGCTCGCGGGGACAGTACTTTGGAGAGCTTGCCCTGGTAACTAACAAA
CCTCGAGCAGCTTCTGCCCACGCCATTGGGACTGTCAAATGTTTAGCAATGGATGTGCAAGCATT
TGAAAGGCTTCTGGGACCTTGCATGGAAATTATGAAAAGGAACATCGCTACCTATGAAGAACAGT
TAGTTGCCCTGTATGGAACGAACATGGATATTGTAGGGTCAGGTGGATCTGGAGGTAGCTCTTCT
atggtcttcacactcgaagatttcgttggggactggcgacagacagccggctacaacctggacca
agtccttgaacagggaggtgtgtccagtttgtttcagaatctcggggtgtccgtaactccgatcc
aaaggattgtcctgagcggtgaaaatgggctgaagatcgacatccatgtcatcatcccgtatgaa
ggtctgagcggcgaccaaatgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatga
tcatcactttaaggtgatcctgcactatggcacactggtaatcgacggggttacgccgaacatga
tcgactatttcggacggccgtatgaaggcatcgccgtgttcgacggcaaaaagatcactgtaaca
gggaccctgtggaacggcaacaaaattatcgacgagcgcctgatcaac

**SEQ ID NO:494 (CP 145 L27V (RIIbB) (aa seq)**
MPDGSLLFRVTINGVTGWRLCERILASSSGGSGGSGMYESFIESLPFLKSLEFSARLKVVDVIGT
KVYNDGEQIIAQGDSADSFFIIESGEVKITMKRKGKSEVEENGAVEIARCSRGQYFGELALVTNK
PRAASAHAIGTVKCLAMDVQAFERLLGPCMEIMKRNIATYEEQLVALYGTNMDIVGSGGSGGSSS
MVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYE
GLSGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVT
GTLWNGNKIIDERLIN

**SEQ ID NO:495 (CP 148 L27V (RIIbB) (nt sequence)**

ATGtccctgctgttccgagtaaccatcaacggagtgaccggctggcggctgtGCGAACGCATTCT
GGCtAGCTCAAGCGGAGGTTCAGGCGGTTCCGGAATGTATGAAAGCTTTATTGAGTCACTGCCAT
TCCTTAAATCTTTGGAGTTTTCTGCACGCCTGAAAGTAGTAGATGTGATAGGCACCAAAGTATAC
AACGATGGAGAACAAATCATTGCTCAGGGAGATTCGGCTGATTCTTTTTTCATTATTGAATCTGG
AGAAGTGAAAATTACTATGAAAAGAAAGGGTAAATCAGAAGTGGAAGAGAATGGTGCAGTAGAAA
TCGCTCGATGCTCGCGGGGACAGTACTTTGGAGAGCTTGCCCTGGTAACTAACAAACCTCGAGCA
GCTTCTGCCCACGCCATTGGGACTGTCAAATGTTTAGCAATGGATGTGCAAGCATTTGAAAGGCT
TCTGGGACCTTGCATGGAAATTATGAAAAGGAACATCGCTACCTATGAAGAACAGTTAGTTGCCC
TGTATGGAACGAACATGGATATTGTAGGGTCAGGTGGATCTGGAGGTAGCTCTTCTatggtcttc
acactcgaagatttcgttggggactggcgacagacagccggctacaacctggaccaagtccttga
acagggaggtgtgtccagtttgtttcagaatctcggggtgtccgtaactccgatccaaaggattg
tcctgagcggtgaaaatgggctgaagatcgacatccatgtcatcatcccgtatgaaggtctgagc
ggcgaccaaatgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatgatcatcactt
taaggtgatcctgcactatggcacactggtaatcgacggggttacgccgaacatgatcgactatt
tcggacggccgtatgaaggcatcgccgtgttcgacggcaaaaagatcactgtaacagggaccctg
tggaacggcaacaaaattatcgacgagcgcctgatcaaccccgacggc

**SEQ ID NO:496 (CP 148 L27V (RIIbB) (aa seq)**

MSLLFRVTINGVTGWRLCERILASSSGGSGGSGMYESFIESLPFLKSLEFSARLKVVDVIGTKVY
NDGEQIIAQGDSADSFFIIESGEVKITMKRKGKSEVEENGAVEIARCSRGQYFGELALVTNKPRA
ASAHAIGTVKCLAMDVQAFERLLGPCMEIMKRNIATYEEQLVALYGTNMDIVGSGGSGGSSSMVF
TLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLS
GDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTL
WNGNKIIDERLINPDG

**SEQ ID NO:497 (CP 157 L27V (RIIbB) (nt sequence)**

AtGGGAGTGACCGGCTGGCGGCTGTGCGAACGCATTCTGGCTAGCTCAAGCGGAGGTTCAGGCGG
TTCCGGAATGTATGAAAGCTTTATTGAGTCACTGCCATTCCTTAAATCTTTGGAGTTTTCTGCAC
GCCTGAAAGTAGTAGATGTGATAGGCACCAAAGTATACAACGATGGAGAACAAATCATTGCTCAG
GGAGATTCGGCTGATTCTTTTTTCATTATTGAATCTGGAGAAGTGAAAATTACTATGAAAAGAAA
GGGTAAATCAGAAGTGGAAGAGAATGGTGCAGTAGAAATCGCTCGATGCTCGCGGGGACAGTACT
TTGGAGAGCTTGCCCTGGTAACTAACAAACCTCGAGCAGCTTCTGCCCACGCCATTGGGACTGTC
AAATGTTTAGCAATGGATGTGCAAGCATTTGAAAGGCTTCTGGGACCTTGCATGGAAATTATGAA
AAGGAACATCGCTACCTATGAAGAACAGTTAGTTGCCCTGTATGGAACGAACATGGATATTGTAG
GGTCAGGTGGATCTGGAGGTAGCTCTTCTATGGTCTTCACACTCGAAGATTTCGTTGGGGACTGG
CGACAGACAGCCGGCTACAACCTGGACCAAGTCCTTGAACAGGGAGGTGTGTCCAGTTTGTTTCA
GAATCTCGGGGTGTCCGTAACTCCGATCCAAAGGATTGTCCTGAGCGGTGAAAATGGGCTGAAGA
TCGACATCCATGTCATCATCCCGTATGAAGGTCTGAGCGGCGACCAAATGGGCCAGATCGAAAAA
ATTTTTAAGGTGGTGTACCCTGTGGATGATCATCACTTTAAGGTGATCCTGCACTATGGCACACT
GGTAATCGACGGGGTTACGCCGAACATGATCGACTATTTCGGACGGCCGTATGAAGGCATCGCCG
TGTTCGACGGCAAAAAGATCACTGTAACAGGGACCCTGTGGAACGGCAACAAAATTATCGACGAG
CGCCTGATCAACCCCGACGGCTCCCTGCTGTTCCGAGTAACCATCAAC

**SEQ ID NO:498 (CP 157 L27V (RIIbB) (aa seq)**

MGVTGWRLCERILASSSGGSGGSGMYESFIESLPFLKSLEFSARLKVVDVIGTKVYNDGEQIIAQ
GDSADSFFIIESGEVKITMKRKGKSEVEENGAVEIARCSRGQYFGELALVTNKPRAASAHAIGTV
KCLAMDVQAFERLLGPCMEIMKRNIATYEEQLVALYGTNMDIVGSGGSGGSSSMVFTLEDFVGDW
RQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEK
IFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDE
RLINPDGSLLFRVTIN

**SEQ ID NO:499 (SS 6 L27V (RIIbB) (nt sequence)**

ATGgtcttcacactcgaagatAGCgctAGCGGAGGTTCAGGCGGTTCCGGAatgtatgaaagctt
tattgagtcactgccattccttaaatctttggagttttctgcacgcctgaaagtagtagatgtga
taggcaccaaagtatacaacgatggagaacaaatcattgctcagggagattcggctgattctttt
ttcattattgaatctggagaagtgaaaattactatgaaaagaaagggtaaatcagaagtggaaga
gaatggtgcagtagaaatcgctcgatgctcgcggggacagtactttggagagcttgccctggtaa
ctaacaaacctcgagcagcttctgcccacgccattgggactgtcaaatgtttagcaatggatgtg
caagcatttgaaaggcttctgggaccttgcatggaaattatgaaaaggaacatcgctacctatga
agaacagttagttgccctgTATggaacgaacatggatattgtaggGTCAGGTGGATCTGGAGGtA
GCTCttcTttcgttggggactggcgacagacagccggctacaacctggaccaagtccttgaacag
ggaggtgtgtccagtttgtttcagaatctcggggtgtccgtaactccgatccaaaggattgtcct
gagcggtgaaaatgggctgaagatcgacatccatgtcatcatcccgtatgaaggtctgagcggcg
accaaatgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatgatcatcactttaag
gtgatcctgcactatggcacactggtaatcgacggggttacgccgaacatgatcgactatttcgg
acggccgtatgaaggcatcgccgtgttcgacggcaaaaagatcactgtaacagggaccctgtgga
acggcaacaaaattatcgacgagcgcctgatcaaccccgacggctccctgctgttccgagtaacc
atcaacggagtgaccggctggcggctgtGCGAACGCATTCTGGCt

**SEQ ID NO:500 (SS 6 L27V (RIIbB) (aa seq)**

MVFTLEDSASGGSGGSGMYESFIESLPFLKSLEFSARLKVVDVIGTKVYNDGEQIIAQGDSADSF
FIIESGEVKITMKRKGKSEVEENGAVEIARCSRGQYFGELALVTNKPRAASAHAIGTVKCLAMDV
QAFERLLGPCMEIMKRNIATYEEQLVALYGTNMDIVGSGGSGGSSSFVGDWRQTAGYNLDQVLEQ
GGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEKIFKVVYPVDDHHFK
VILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVT
INGVTGWRLCERILA

**SEQ ID NO:501 (SS 12 L27V (RIIbB) (nt sequence)**

ATGgtcttcacactcgaagatttcgttggggactggcgaAGCgctAGCGGAGGTTCAGGCGGTTC
CGGAatgtatgaaagctttattgagtcactgccattccttaaatctttggagttttctgcacgcc
tgaaagtagtagatgtgataggcaccaaagtatacaacgatggagaacaaatcattgctcaggga
gattcggctgattctttttcattattgaatctggagaagtgaaaattactatgaaaagaaaggg
taaatcagaagtggaagagaatggtgcagtagaaatcgctcgatgctcgcggggacagtactttg
gagagcttgccctggtaactaacaaacctcgagcagcttctgcccacgccattgggactgtcaaa
tgtttagcaatggatgtgcaagcatttgaaaggcttctgggaccttgcatggaaattatgaaaag
gaacatcgctacctatgaagaacagttagttgccctgTATggaacgaacatggatattgtaggGT
CAGGTGGATCTGGAGGtAGCTCttcTcagacagccggctacaacctggaccaagtccttgaacag
ggaggtgtgtccagtttgtttcagaatctcggggtgtccgtaactccgatccaaaggattgtcct
gagcggtgaaaatgggctgaagatcgacatccatgtcatcatcccgtatgaaggtctgagcggcg
accaaatgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatgatcatcactttaag
gtgatcctgcactatggcacactggtaatcgacggggttacgccgaacatgatcgactatttcgg
acggccgtatgaaggcatcgccgtgttcgacggcaaaaagatcactgtaacagggaccctgtgga
acggcaacaaaattatcgacgagcgcctgatcaaccccgacggctccctgctgttccgagtaacc
atcaacggagtgaccggctggcggctgtGCGAACGCATTCTGGCt

**SEQ ID NO:502 (SS 12 L27V (RIIbB) (aa seq)**

MVFTLEDFVGDWRSASGGSGGSGMYESFIESLPFLKSLEFSARLKVVDVIGTKVYNDGEQIIAQG
DSADSFFIIESGEVKITMKRKGKSEVEENGAVEIARCSRGQYFGELALVTNKPRAASAHAIGTVK
CLAMDVQAFERLLGPCMEIMKRNIATYEEQLVALYGTNMDIVGSGGSGGSSSQTAGYNLDQVLEQ
GGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEKIFKVVYPVDDHHFK
VILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVT
INGVTGWRLCERILA

**SEQ ID NO:503 (SS 26 L27V (RIIbB) (nt sequence)**

ATGgtcttcacactcgaagatttcgttggggactggcgacagacagccggctacaacctggacca
agtccttgaacagggaAGCgctAGCGGAGGTTCAGGCGGTTCCGGAatgtatgaaagctttattg
agtcactgccattccttaaatctttggagttttctgcacgcctgaaagtagtagatgtgataggc
accaaagtatacaacgatggagaacaaatcattgctcagggagattcggctgattctttttcat
tattgaatctggagaagtgaaaattactatgaaaagaaagggtaaatcagaagtggaagagaatg
gtgcagtagaaatcgctcgatgctcgcggggacagtactttggagagcttgccctggtaactaac
aaacctcgagcagcttctgcccacgccattgggactgtcaaatgtttagcaatggatgtgcaagc
atttgaaaggcttctgggaccttgcatggaaattatgaaaaggaacatcgctacctatgaagaac
agttagttgccctgTATggaacgaacatggatattgtaggGTCAGGTGGATCTGGAGGtAGCTCt
tcTggtgtgtccagtttgtttcagaatctcggggtgtccgtaactccgatccaaaggattgtcct
gagcggtgaaaatgggctgaagatcgacatccatgtcatcatcccgtatgaaggtctgagcggcg
accaaatgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatgatcatcactttaag
gtgatcctgcactatggcacactggtaatcgacggggttacgccgaacatgatcgactatttcgg
acggccgtatgaaggcatcgccgtgttcgacggcaaaaagatcactgtaacagggaccctgtgga
acggcaacaaaattatcgacgagcgcctgatcaaccccgacggctccctgctgttccgagtaacc
atcaacggagtgaccggctggcggctgtGCGAACGCATTCTGGCt

**SEQ ID NO:504 (SS 26 L27V (RIIbB) (aa seq)**

MVFTLEDFVGDWRQTAGYNLDQVLEQGSASGGSGGSGMYESFIESLPFLKSLEFSARLKVVDVIG
TKVYNDGEQIIAQGDSADSFFIIESGEVKITMKRKGKSEVEENGAVEIARCSRGQYFGELALVTN
KPRAASAHAIGTVKCLAMDVQAFERLLGPCMEIMKRNIATYEEQLVALYGTNMDIVGSGGSGGSS
SGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEKIFKVVYPVDDHHFK
VILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVT
INGVTGWRLCERILA

**SEQ ID NO:505 (SS 45 L27V (RIIbB) (nt sequence)**

ATGgtcttcacactcgaagatttcgttggggactggcgacagacagccggctacaacctggacca
agtccttgaacagggaggtgtgtccagtttgtttcagaatctcggggtgtccgtaactccgatcc
aaaggattAGCgctAGCGGAGGTTCAGGCGGTTCCGGAatgtatgaaagctttattgagtcactg
ccattccttaaatctttggagttttctgcacgcctgaaagtagtagatgtgataggcaccaaagt
atacaacgatggagaacaaatcattgctcagggagattcggctgattctttttcattattgaat
ctggagaagtgaaaattactatgaaaagaaagggtaaatcagaagtggaagagaatggtgcagta
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agcagcttctgcccacgccattgggactgtcaaatgtttagcaatggatgtgcaagcatttgaaa
ggcttctgggaccttgcatggaaattatgaaaaggaacatcgctacctatgaagaacagttagtt
gccctgTATggaacgaacatggatattgtaggGTCAGGTGGATCTGGAGGtAGCTCttcTgtcct
gagcggtgaaaatgggctgaagatcgacatccatgtcatcatcccgtatgaaggtctgagcggcg
accaaatgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatgatcatcactttaag
gtgatcctgcactatggcacactggtaatcgacggggttacgccgaacatgatcgactatttcgg
acggccgtatgaaggcatcgccgtgttcgacggcaaaaagatcactgtaacagggaccctgtgga
acggcaacaaaattatcgacgagcgcctgatcaaccccgacggctccctgctgttccgagtaacc
atcaacggagtgaccggctggcggctgtGCGAACGCATTCTGGCt

**SEQ ID NO:506 (SS 45 L27V (RIIbB) (aa seq)**

MVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRISASGGSGGSGMYESFIESL
PFLKSLEFSARLKVVDVIGTKVYNDGEQIIAQGDSADSFFIIESGEVKITMKRKGKSEVEENGAV
EIARCSRGQYFGELALVTNKPRAASAHAIGTVKCLAMDVQAFERLLGPCMEIMKRNIATYEEQLV
ALYGTNMDIVGSGGSGGSSSVLSGENGLKIDIHVIIPYEGLSGDQMGQIEKIFKVVYPVDDHHFK

VILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVT
INGVTGWRLCERILA

**SEQ ID NO:507 (SS 48 L27V (RIIbB) (nt sequence)**

atggtcttcacactcgaagatttcgttggggactggcgacagacagccggctacaacctggacca
agtccttgaacagggaggtgtgtccagtttgtttcagaatctcggggtgtccgtaactccgatcc
aaaggattgtcctgagcAGCgctAGCGGAGGTTCAGGCGGTTCCGGAatgtatgaaagctttatt
gagtcactgccattccttaaatctttggagttttctgcacgcctgaaagtagtagatgtgatagg
caccaaagtatacaacgatggagaacaaatcattgctcagggagattcggctgattctttttca
ttattgaatctggagaagtgaaaattactatgaaaagaaagggtaaatcagaagtggaagagaat
ggtgcagtagaaatcgctcgatgctcgcggggacagtactttggagagcttgccctggtaactaa
caaacctcgagcagcttctgcccacgccattgggactgtcaaatgtttagcaatggatgtgcaag
catttgaaaggcttctgggaccttgcatggaaattatgaaaaggaacatcgctacctatgaagaa
cagttagttgccctgTATggaacgaacatggatattgtaggGTCAGGTGGATCTGGAGGtAGCTC
ttcTggtgaaaatgggctgaagatcgacatccatgtcatcatcccgtatgaaggtctgagcggcg
accaaatgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatgatcatcactttaag
gtgatcctgcactatggcacactggtaatcgacggggttacgccgaacatgatcgactatttcgg
acggccgtatgaaggcatcgccgtgttcgacggcaaaaagatcactgtaacagggaccctgtgga
acggcaacaaaattatcgacgagcgcctgatcaaccccgacggctccctgctgttccgagtaacc
atcaacggagtgaccggctggcggctgtGCGAACGCATTCTGGCt

**SEQ ID NO:508 (SS 48 L27V (RIIbB) (aa seq)**

MVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSSASGGSGGSGMYESFI
ESLPFLKSLEFSARLKVVDVIGTKVYNDGEQIIAQGDSADSFFIIESGEVKITMKRKGKSEVEEN
GAVEIARCSRGQYFGELALVTNKPRAASAHAIGTVKCLAMDVQAFERLLGPCMEIMKRNIATYEE
QLVALYGTNMDIVGSGGSGGSSSGENGLKIDIHVIIPYEGLSGDQMGQIEKIFKVVYPVDDHHFK
VILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVT
INGVTGWRLCERILA

**SEQ ID NO:509 (SS 52 L27V (RIIbB) (nt sequence)**

ATGgtcttcacactcgaagatttcgttggggactggcgacagacagccggctacaacctggacca
agtccttgaacagggaggtgtgtccagtttgtttcagaatctcggggtgtccgtaactccgatcc
aaaggattgtcctgagcggtgaaaatgggAGCgctAGCGGAGGTTCAGGCGGTTCCGGAatgtat
gaaagctttattgagtcactgccattccttaaatctttggagttttctgcacgcctgaaagtagt
agatgtgataggcaccaaagtatacaacgatggagaacaaatcattgctcagggagattcggctg
attctttttcattattgaatctggagaagtgaaaattactatgaaaagaaagggtaaatcagaa
gtggaagagaatggtgcagtagaaatcgctcgatgctcgcggggacagtactttggagagcttgc
cctggtaactaacaaacctcgagcagcttctgcccacgccattgggactgtcaaatgtttagcaa
tggatgtgcaagcatttgaaaggcttctgggaccttgcatggaaattatgaaaaggaacatcgct
acctatgaagaacagttagttgccctgTATggaacgaacatggatattgtaggGTCAGGTGGATC
TGGAGGtAGCTCttcTctgaagatcgacatccatgtcatcatcccgtatgaaggtctgagcggcg
accaaatgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatgatcatcactttaag
gtgatcctgcactatggcacactggtaatcgacggggttacgccgaacatgatcgactatttcgg
acggccgtatgaaggcatcgccgtgttcgacggcaaaaagatcactgtaacagggaccctgtgga
acggcaacaaaattatcgacgagcgcctgatcaaccccgacggctccctgctgttccgagtaacc
atcaacggagtgaccggctggcggctgtGCGAACGCATTCTGGCt

**SEQ ID NO:510 (SS 52 L27V (RIIbB) (aa seq)**

MVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGSASGGSGGSGMY
ESFIESLPFLKSLEFSARLKVVDVIGTKVYNDGEQIIAQGDSADSFFIIESGEVKITMKRKGKSE
VEENGAVEIARCSRGQYFGELALVTNKPRAASAHAIGTVKCLAMDVQAFERLLGPCMEIMKRNIA

TYEEQLVALYGTNMDIVGSGGSGGSSSLKIDIHVIIPYEGLSGDQMGQIEKIFKVVYPVDDHHFK
VILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVT
INGVTGWRLCERILA

**SEQ ID NO:511 (SS 55 L27V (RIIbB) (nt sequence)**

ATGgtcttcacactcgaagatttcgttggggactggcgacagacagccggctacaacctggacca
agtccttgaacagggaggtgtgtccagtttgtttcagaatctcggggtgtccgtaactccgatcc
aaaggattgtcctgagcggtgaaaatgggctgaagatcAGCgctAGCGGAGGTTCAGGCGGTTCC
GGAatgtatgaaagctttattgagtcactgccattccttaaatctttggagttttctgcacgcct
gaaagtagtagatgtgataggcaccaaagtatacaacgatggagaacaaatcattgctcagggag
attcggctgattctttttttcattattgaatctggagaagtgaaaattactatgaaaagaaagggt
aaatcagaagtggaagagaatggtgcagtagaaatcgctcgatgctcgcggggacagtactttgg
agagcttgccctggtaactaacaaacctcgagcagcttctgcccacgccattgggactgtcaaat
gtttagcaatggatgtgcaagcatttgaaaggcttctgggaccttgcatggaaattatgaaaagg
aacatcgctacctatgaagaacagttagttgccctgTATggaacgaacatggatattgtaggGTC
AGGTGGATCTGGAGGtAGCTCttcTgacatccatgtcatcatcccgtatgaaggtctgagcggcg
accaaatgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatgatcatcactttaag
gtgatcctgcactatggcacactggtaatcgacggggttacgccgaacatgatcgactatttcgg
acggccgtatgaaggcatcgccgtgttcgacggcaaaaagatcactgtaacagggaccctgtgga
acggcaacaaaattatcgacgagcgcctgatcaaccccgacggctccctgctgttccgagtaacc
atcaacggagtgaccggctggcggctgtGCGAACGCATTCTGGCt

**SEQ ID NO:512 (SS 55 L27V (RIIbB) (aa seq)**

MVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKISASGGSGGS
GMYESFIESLPFLKSLEFSARLKVVDVIGTKVYNDGEQIIAQGDSADSFFIIESGEVKITMKRKG
KSEVEENGAVEIARCSRGQYFGELALVTNKPRAASAHAIGTVKCLAMDVQAFERLLGPCMEIMKR
NIATYEEQLVALYGTNMDIVGSGGSGGSSSDIHVIIPYEGLSGDQMGQIEKIFKVVYPVDDHHFK
VILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVT
INGVTGWRLCERILA

**SEQ ID NO:513 (SS 83 L27V (RIIbB) (nt sequence)**

ATGgtcttcacactcgaagatttcgttggggactggcgacagacagccggctacaacctggacca
agtccttgaacagggaggtgtgtccagtttgtttcagaatctcggggtgtccgtaactccgatcc
aaaggattgtcctgagcggtgaaaatgggctgaagatcgacatccatgtcatcatcccgtatgaa
ggtctgagcggcgaccaaatgggccagatcgaaaaaatttttaaggtggtgtaccctAGCgctAG
CGGAGGTTCAGGCGGTTCCGGAatgtatgaaagctttattgagtcactgccattccttaaatctt
tggagttttctgcacgcctgaaagtagtagatgtgataggcaccaaagtatacaacgatggagaa
caaatcattgctcagggagattcggctgattctttttttcattattgaatctggagaagtgaaaat
tactatgaaaagaaagggtaaatcagaagtggaagagaatggtgcagtagaaatcgctcgatgct
cgcggggacagtactttggagagcttgccctggtaactaacaaacctcgagcagcttctgcccac
gccattgggactgtcaaatgtttagcaatggatgtgcaagcatttgaaaggcttctgggaccttg
catggaaattatgaaaaggaacatcgctacctatgaagaacagttagttgccctgTATggaacga
acatggatattgtaggGTCAGGTGGATCTGGAGGtAGCTCttcTgtggatgatcatcactttaag
gtgatcctgcactatggcacactggtaatcgacggggttacgccgaacatgatcgactatttcgg
acggccgtatgaaggcatcgccgtgttcgacggcaaaaagatcactgtaacagggaccctgtgga
acggcaacaaaattatcgacgagcgcctgatcaaccccgacggctccctgctgttccgagtaacc
atcaacggagtgaccggctggcggctgtGCGAACGCATTCTGGCt

**SEQ ID NO:514 (SS 83 L27V (RIIbB) (aa seq)**

MVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYE
GLSGDQMGQIEKIFKVVYPSASGGSGGSGMYESFIESLPFLKSLEFSARLKVVDVIGTKVYNDGE

QIIAQGDSADSFFIIESGEVKITMKRKGKSEVEENGAVEIARCSRGQYFGELALVTNKPRAASAH
AIGTVKCLAMDVQAFERLLGPCMEIMKRNIATYEEQLVALYGTNMDIVGSGGSGGSSSVDDHHFK
VILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVT
INGVTGWRLCERILA

**SEQ ID NO:515 (SS 84 L27V (RIIbB) (nt sequence)**

ATGgtcttcacactcgaagatttcgttggggactggcgacagacagccggctacaacctggacca
agtccttgaacagggaggtgtgtccagtttgtttcagaatctcggggtgtccgtaactccgatcc
aaaggattgtcctgagcggtgaaaatgggctgaagatcgacatccatgtcatcatcccgtatgaa
ggtctgagcggcgaccaaatgggccagatcgaaaaaatttttaaggtggtgtaccctgtgAGCgc
tAGCGGAGGTTCAGGCGGTTCCGGAatgtatgaaagctttattgagtcactgccattccttaaat
ctttggagttttctgcacgcctgaaagtagtagatgtgataggcaccaaagtatacaacgatgga
gaacaaatcattgctcagggagattcggctgattctttttcattattgaatctggagaagtgaa
aattactatgaaaagaaagggtaaatcagaagtggaagagaatggtgcagtagaaatcgctcgat
gctcgcggggacagtactttggagagcttgccctggtaactaacaaacctcgagcagcttctgcc
cacgccattgggactgtcaaatgtttagcaatggatgtgcaagcatttgaaaggcttctgggacc
ttgcatggaaattatgaaaaggaacatcgctacctatgaagaacagttagttgccctgTATggaa
cgaacatggatattgtaggGTCAGGTGGATCTGGAGGtAGCTCttcTgatgatcatcactttaag
gtgatcctgcactatggcacactggtaatcgacggggttacgccgaacatgatcgactatttcgg
acggccgtatgaaggcatcgccgtgttcgacggcaaaaagatcactgtaacagggaccctgtgga
acggcaacaaaattatcgacgagcgcctgatcaaccccgacggctccctgctgttccgagtaacc
atcaacggagtgaccggctggcggctgtGCGAACGCATTCTGGCt

**SEQ ID NO:516 (SS 84 L27V (RIIbB) (aa seq)**

MVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYE
GLSGDQMGQIEKIFKVVYPVSASGGSGGSGMYESFIESLPFLKSLEFSARLKVVDVIGTKVYNDG
EQIIAQGDSADSFFIIESGEVKITMKRKGKSEVEENGAVEIARCSRGQYFGELALVTNKPRAASA
HAIGTVKCLAMDVQAFERLLGPCMEIMKRNIATYEEQLVALYGTNMDIVGSGGSGGSSSDDHHFK
VILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVT
INGVTGWRLCERILA

**SEQ ID NO:517 (SS 85 L27V (RIIbB) (nt sequence)**

ATGgtcttcacactcgaagatttcgttggggactggcgacagacagccggctacaacctggacca
agtccttgaacagggaggtgtgtccagtttgtttcagaatctcggggtgtccgtaactccgatcc
aaaggattgtcctgagcggtgaaaatgggctgaagatcgacatccatgtcatcatcccgtatgaa
ggtctgagcggcgaccaaatgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatAG
CgctAGCGGAGGTTCAGGCGGTTCCGGAatgtatgaaagctttattgagtcactgccattcctta
aatctttggagttttctgcacgcctgaaagtagtagatgtgataggcaccaaagtatacaacgat
ggagaacaaatcattgctcagggagattcggctgattctttttcattattgaatctggagaagt
gaaaattactatgaaaagaaagggtaaatcagaagtggaagagaatggtgcagtagaaatcgctc
gatgctcgcggggacagtactttggagagcttgccctggtaactaacaaacctcgagcagcttct
gcccacgccattgggactgtcaaatgtttagcaatggatgtgcaagcatttgaaaggcttctggg
accttgcatggaaattatgaaaaggaacatcgctacctatgaagaacagttagttgccctgTATg
gaacgaacatggatattgtaggGTCAGGTGGATCTGGAGGtAGCTCttcTgatcatcactttaag
gtgatcctgcactatggcacactggtaatcgacggggttacgccgaacatgatcgactatttcgg
acggccgtatgaaggcatcgccgtgttcgacggcaaaaagatcactgtaacagggaccctgtgga
acggcaacaaaattatcgacgagcgcctgatcaaccccgacggctccctgctgttccgagtaacc
atcaacggagtgaccggctggcggctgtGCGAACGCATTCTGGCt

**SEQ ID NO:518 (SS 85 L27V (RIIbB) (aa seq)**

MVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYE
GLSGDQMGQIEKIFKVVYPVDSASGGSGGSGMYESFIESLPFLKSLEFSARLKVVDVIGTKVYND

GEQIIAQGDSADSFFIIESGEVKITMKRKGKSEVEENGAVEIARCSRGQYFGELALVTNKPRAAS
AHAIGTVKCLAMDVQAFERLLGPCMEIMKRNIATYEEQLVALYGTNMDIVGSGGSGGSSSDHHFK
VILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVT
INGVTGWRLCERILA

**SEQ ID NO:519 (SS 100 L27V (RIIbB) (nt sequence)**

ATGgtcttcacactcgaagatttcgttggggactggcgacagacagccggctacaacctggacca
agtccttgaacagggaggtgtgtccagtttgtttcagaatctcggggtgtccgtaactccgatcc
aaaggattgtcctgagcggtgaaaatgggctgaagatcgacatccatgtcatcatcccgtatgaa
ggtctgagcggcgaccaaatgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatga
tcatcactttaaggtgatcctgcactatggcacactggtaatcAGCgctAGCGGAGGTTCAGGCG
GTTCCGGAatgtatgaaagctttattgagtcactgccattccttaaatctttggagttttctgca
cgcctgaaagtagtagatgtgataggcaccaaagtatacaacgatggagaacaaatcattgctca
gggagattcggctgattctttttttcattattgaatctggagaagtgaaaattactatgaaaagaa
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caaatgtttagcaatggatgtgcaagcatttgaaaggcttctgggaccttgcatggaaattatga
aaaggaacatcgctacctatgaagaacagttagttgccctgTATggaacgaacatggatattgta
ggGTCAGGTGGATCTGGAGGtAGCTCttcTgacggggttacgccgaacatgatcgactatttcgg
acggccgtatgaaggcatcgccgtgttcgacggcaaaaagatcactgtaacagggaccctgtgga
acggcaacaaaattatcgacgagcgcctgatcaaccccgacggctccctgctgttccgagtaacc
atcaacggagtgaccggctggcggctgtGCGAACGCATTCTGGCt

**SEQ ID NO:520 (SS 100 L27V (RIIbB) (aa seq)**

MVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYE
GLSGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVISASGGSGGSGMYESFIESLPFLKSLEFSA
RLKVVDVIGTKVYNDGEQIIAQGDSADSFFIIESGEVKITMKRKGKSEVEENGAVEIARCSRGQY
FGELALVTNKPRAASAHAIGTVKCLAMDVQAFERLLGPCMEIMKRNIATYEEQLVALYGTNMDIV
GSGGSGGSSSDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVT
INGVTGWRLCERILA

**SEQ ID NO:521 (SS 101 L27V (RIIbB) (nt sequence)**

ATGgtcttcacactcgaagatttcgttggggactggcgacagacagccggctacaacctggacca
agtccttgaacagggaggtgtgtccagtttgtttcagaatctcggggtgtccgtaactccgatcc
aaaggattgtcctgagcggtgaaaatgggctgaagatcgacatccatgtcatcatcccgtatgaa
ggtctgagcggcgaccaaatgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatga
tcatcactttaaggtgatcctgcactatggcacactggtaatcgacAGCgctAGCGGAGGTTCAG
GCGGTTCCGGAatgtatgaaagctttattgagtcactgccattccttaaatctttggagttttct
gcacgcctgaaagtagtagatgtgataggcaccaaagtatacaacgatggagaacaaatcattgc
tcagggagattcggctgattctttttttcattattgaatctggagaagtgaaaattactatgaaaa
gaaagggtaaatcagaagtggaagagaatggtgcagtagaaatcgctcgatgctcgcggggacag
tactttggagagcttgccctggtaactaacaaacctcgagcagcttctgcccacgccattgggac
tgtcaaatgtttagcaatggatgtgcaagcatttgaaaggcttctgggaccttgcatggaaatta
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gtaggGTCAGGTGGATCTGGAGGtAGCTCttcTggggttacgccgaacatgatcgactatttcgg
acggccgtatgaaggcatcgccgtgttcgacggcaaaaagatcactgtaacagggaccctgtgga
acggcaacaaaattatcgacgagcgcctgatcaaccccgacggctccctgctgttccgagtaacc
atcaacggagtgaccggctggcggctgtGCGAACGCATTCTGGCt

**SEQ ID NO:522 (SS 101 L27V (RIIbB) (aa seq)**

MVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYE
GLSGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDSASGGSGGSGMYESFIESLPFLKSLEFS
ARLKVVDVIGTKVYNDGEQIIAQGDSADSFFIIESGEVKITMKRKGKSEVEENGAVEIARCSRGQ
YFGELALVTNKPRAASAHAIGTVKCLAMDVQAFERLLGPCMEIMKRNIATYEEQLVALYGTNMDI
VGSGGSGGSSSGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVT
INGVTGWRLCERILA

**SEQ ID NO:523 (SS 102 L27V (RIIbB) (nt sequence)**

ATGgtcttcacactcgaagatttcgttggggactggcgacagacagccggctacaacctggacca
agtccttgaacagggaggtgtgtccagtttgtttcagaatctcggggtgtccgtaactccgatcc
aaaggattgtcctgagcggtgaaaatgggctgaagatcgacatccatgtcatcatcccgtatgaa
ggtctgagcggcgaccaaatgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatga
tcatcactttaaggtgatcctgcactatggcacactggtaatcgacgggAGCgctAGCGGAGGTT
CAGGCGGTTCCGGAatgtatgaaagctttattgagtcactgccattccttaaatctttggagttt
tctgcacgcctgaaagtagtagatgtgataggcaccaaagtatacaacgatggagaacaaatcat
tgctcagggagattcggctgattctttttcattattgaatctggagaagtgaaaattactatga
aaagaaagggtaaatcagaagtggaagagaatggtgcagtagaaatcgctcgatgctcgcgggga
cagtactttggagagcttgccctggtaactaacaaacctcgagcagcttctgcccacgccattgg
gactgtcaaatgtttagcaatggatgtgcaagcatttgaaaggcttctgggaccttgcatggaaa
ttatgaaaaggaacatcgctacctatgaagaacagttagttgccctgTATggaacgaacatggat
attgtaggGTCAGGTGGATCTGGAGGtAGCTCttcTgttacgccgaacatgatcgactatttcgg
acggccgtatgaaggcatcgccgtgttcgacggcaaaaagatcactgtaacagggaccctgtgga
acggcaacaaaattatcgacgagcgcctgatcaaccccgacggctccctgctgttccgagtaacc
atcaacggagtgaccggctggcggctgtGCGAACGCATTCTGGCt

**SEQ ID NO:524 (SS 102 L27V (RIIbB) (aa seq)**

MVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYE
GLSGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGSASGGSGGSGMYESFIESLPFLKSLEF
SARLKVVDVIGTKVYNDGEQIIAQGDSADSFFIIESGEVKITMKRKGKSEVEENGAVEIARCSRG
QYFGELALVTNKPRAASAHAIGTVKCLAMDVQAFERLLGPCMEIMKRNIATYEEQLVALYGTNMD
IVGSGGSGGSSSVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVT
INGVTGWRLCERILA

**SEQ ID NO:525 (SS 103 L27V (RIIbB) (nt sequence)**

ATGgtcttcacactcgaagatttcgttggggactggcgacagacagccggctacaacctggacca
agtccttgaacagggaggtgtgtccagtttgtttcagaatctcggggtgtccgtaactccgatcc
aaaggattgtcctgagcggtgaaaatgggctgaagatcgacatccatgtcatcatcccgtatgaa
ggtctgagcggcgaccaaatgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatga
tcatcactttaaggtgatcctgcactatggcacactggtaatcgacggggttAGCgctAGCGGAG
GTTCAGGCGGTTCCGGAatgtatgaaagctttattgagtcactgccattccttaaatctttggag
ttttctgcacgcctgaaagtagtagatgtgataggcaccaaagtatacaacgatggagaacaaat
cattgctcagggagattcggctgattctttttcattattgaatctggagaagtgaaaattacta
tgaaaagaaagggtaaatcagaagtggaagagaatggtgcagtagaaatcgctcgatgctcgcgg
ggacagtactttggagagcttgccctggtaactaacaaacctcgagcagcttctgcccacgccat
tgggactgtcaaatgtttagcaatggatgtgcaagcatttgaaaggcttctgggaccttgcatgg
aaattatgaaaaggaacatcgctacctatgaagaacagttagttgccctgTATggaacgaacatg
gatattgtaggGTCAGGTGGATCTGGAGGtAGCTCttcTacgccgaacatgatcgactatttcgg
acggccgtatgaaggcatcgccgtgttcgacggcaaaaagatcactgtaacagggaccctgtgga
acggcaacaaaattatcgacgagcgcctgatcaaccccgacggctccctgctgttccgagtaacc
atcaacggagtgaccggctggcggctgtGCGAACGCATTCTGGCt

**SEQ ID NO:526 (SS 103 L27V (RIIbB) (aa seq)**

MVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYE
GLSGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVSASGGSGGSGMYESFIESLPFLKSLE
FSARLKVVDVIGTKVYNDGEQIIAQGDSADSFFIIESGEVKITMKRKGKSEVEENGAVEIARCSR
GQYFGELALVTNKPRAASAHAIGTVKCLAMDVQAFERLLGPCMEIMKRNIATYEEQLVALYGTNM
DIVGSGGSGGSSSTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVT
INGVTGWRLCERILA

**SEQ ID NO:527 (SS 120 L27V (RIIbB) (nt sequence)**

ATGgtcttcacactcgaagatttcgttggggactggcgacagacagccggctacaacctggacca
agtccttgaacagggaggtgtgtccagtttgtttcagaatctcggggtgtccgtaactccgatcc
aaaggattgtcctgagcggtgaaaatgggctgaagatcgacatccatgtcatcatcccgtatgaa
ggtctgagcggcgaccaaatgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatga
tcatcactttaaggtgatcctgcactatggcacactggtaatcgacggggttacgccgaacatga
tcgactatttcggacggccgtatgaaggcatcgccgtgAGCgctAGCGGAGGTTCAGGCGGTTCC
GGAatgtatgaaagctttattgagtcactgccattccttaaatctttggagttttctgcacgcct
gaaagtagtagatgtgataggcaccaaagtatacaacgatggagaacaaatcattgctcagggag
attcggctgattctttttcattattgaatctggagaagtgaaaattactatgaaaagaaagggt
aaatcagaagtggaagagaatggtgcagtagaaatcgctcgatgctcgcggggacagtactttgg
agagcttgccctggtaactaacaaacctcgagcagcttctgcccacgccattgggactgtcaaat
gtttagcaatggatgtgcaagcatttgaaaggcttctgggaccttgcatggaaattatgaaaagg
aacatcgctacctatgaagaacagttagttgccctgTATggaacgaacatggatattgtaggGTC
AGGTGGATCTGGAGGtAGCTCttcTttcgacggcaaaaagatcactgtaacagggaccctgtgga
acggcaacaaaattatcgacgagcgcctgatcaaccccgacggctccctgctgttccgagtaacc
atcaacggagtgaccggctggcggctgtGCGAACGCATTCTGGCt

**SEQ ID NO:528 (SS 120 L27V (RIIbB) (aa seq)**

MVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYE
GLSGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVSASGGSGGS
GMYESFIESLPFLKSLEFSARLKVVDVIGTKVYNDGEQIIAQGDSADSFFIIESGEVKITMKRKG
KSEVEENGAVEIARCSRGQYFGELALVTNKPRAASAHAIGTVKCLAMDVQAFERLLGPCMEIMKR
NIATYEEQLVALYGTNMDIVGSGGSGGSSSFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVT
INGVTGWRLCERILA

**SEQ ID NO:529 (SS 123 L27V (RIIbB) (nt sequence)**

ATGgtcttcacactcgaagatttcgttggggactggcgacagacagccggctacaacctggacca
agtccttgaacagggaggtgtgtccagtttgtttcagaatctcggggtgtccgtaactccgatcc
aaaggattgtcctgagcggtgaaaatgggctgaagatcgacatccatgtcatcatcccgtatgaa
ggtctgagcggcgaccaaatgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatga
tcatcactttaaggtgatcctgcactatggcacactggtaatcgacggggttacgccgaacatga
tcgactatttcggacggccgtatgaaggcatcgccgtgttcgacggcAGCgctAGCGGAGGTTCA
GGCGGTTCCGGAatgtatgaaagctttattgagtcactgccattccttaaatctttggagttttc
tgcacgcctgaaagtagtagatgtgataggcaccaaagtatacaacgatggagaacaaatcattg
ctcagggagattcggctgattctttttcattattgaatctggagaagtgaaaattactatgaaa
agaaagggtaaatcagaagtggaagagaatggtgcagtagaaatcgctcgatgctcgcggggaca
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ctgtcaaatgtttagcaatggatgtgcaagcatttgaaaggcttctgggaccttgcatggaaatt
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tgtaggGTCAGGTGGATCTGGAGGtAGCTCttcTaaaaagatcactgtaacagggaccctgtgga
acggcaacaaaattatcgacgagcgcctgatcaaccccgacggctccctgctgttccgagtaacc
atcaacggagtgaccggctggcggctgtGCGAACGCATTCTGGCt

**SEQ ID NO:530 (SS 123 L27V (RIIbB) (aa seq)**

MVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYE
GLSGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGSASGGS
GGSGMYESFIESLPFLKSLEFSARLKVVDVIGTKVYNDGEQIIAQGDSADSFFIIESGEVKITMK
RKGKSEVEENGAVEIARCSRGQYFGELALVTNKPRAASAHAIGTVKCLAMDVQAFERLLGPCMEI
MKRNIATYEEQLVALYGTNMDIVGSGGSGGSSSKKITVTGTLWNGNKIIDERLINPDGSLLFRVT
INGVTGWRLCERILA

**SEQ ID NO:531 (SS 124 L27V (RIIbB) (nt sequence)**

ATGgtcttcacactcgaagatttcgttggggactggcgacagacagccggctacaacctggacca
agtccttgaacagggaggtgtgtccagtttgtttcagaatctcggggtgtccgtaactccgatcc
aaaggattgtcctgagcggtgaaaatgggctgaagatcgacatccatgtcatcatcccgtatgaa
ggtctgagcggcgaccaaatgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatga
tcatcactttaaggtgatcctgcactatggcacactggtaatcgacggggttacgccgaacatga
tcgactatttcggacggccgtatgaaggcatcgccgtgttcgacggcaaaAGCgctAGCGGAGGT
TCAGGCGGTTCCGGAatgtatgaaagctttattgagtcactgccattccttaaatctttggagtt
ttctgcacgcctgaaagtagtagatgtgataggcaccaaagtatacaacgatggagaacaaatca
ttgctcagggagattcggctgattctttttttcattattgaatctggagaagtgaaaattactatg
aaaagaaagggtaaatcagaagtggaagagaatggtgcagtagaaatcgctcgatgctcgcgggg
acagtactttggagagcttgccctggtaactaacaaacctcgagcagcttctgcccacgccattg
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attatgaaaaggaacatcgctacctatgaagaacagttagttgccctgTATggaacgaacatgga
tattgtaggGTCAGGTGGATCTGGAGGtAGCTCttcTaagatcactgtaacagggaccctgtgga
acggcaacaaaattatcgacgagcgcctgatcaaccccgacggctccctgctgttccgagtaacc
atcaacggagtgaccggctggcggctgtGCGAACGCATTCTGGCt

**SEQ ID NO:532 (SS 124 L27V (RIIbB) (aa seq)**

MVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYE
GLSGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKSASGG
SGGSGMYESFIESLPFLKSLEFSARLKVVDVIGTKVYNDGEQIIAQGDSADSFFIIESGEVKITM
KRKGKSEVEENGAVEIARCSRGQYFGELALVTNKPRAASAHAIGTVKCLAMDVQAFERLLGPCME
IMKRNIATYEEQLVALYGTNMDIVGSGGSGGSSSKITVTGTLWNGNKIIDERLINPDGSLLFRVT
INGVTGWRLCERILA

**SEQ ID NO:533 (SS 125 L27V (RIIbB) (nt sequence)**

ATGgtcttcacactcgaagatttcgttggggactggcgacagacagccggctacaacctggacca
agtccttgaacagggaggtgtgtccagtttgtttcagaatctcggggtgtccgtaactccgatcc
aaaggattgtcctgagcggtgaaaatgggctgaagatcgacatccatgtcatcatcccgtatgaa
ggtctgagcggcgaccaaatgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatga
tcatcactttaaggtgatcctgcactatggcacactggtaatcgacggggttacgccgaacatga
tcgactatttcggacggccgtatgaaggcatcgccgtgttcgacggcaaaaagAGCgctAGCGGA
GGTTCAGGCGGTTCCGGAatgtatgaaagctttattgagtcactgccattccttaaatctttgga
gttttctgcacgcctgaaagtagtagatgtgataggcaccaaagtatacaacgatggagaacaaa
tcattgctcagggagattcggctgattctttttttcattattgaatctggagaagtgaaaattact
atgaaaagaaagggtaaatcagaagtggaagagaatggtgcagtagaaatcgctcgatgctcgcg
gggacagtactttggagagcttgccctggtaactaacaaacctcgagcagcttctgcccacgcca
ttgggactgtcaaatgtttagcaatggatgtgcaagcatttgaaaggcttctgggaccttgcatg
gaaattatgaaaaggaacatcgctacctatgaagaacagttagttgccctgTATggaacgaacat
ggatattgtaggGTCAGGTGGATCTGGAGGtAGCTCttcTatcactgtaacagggaccctgtgga

acggcaacaaaattatcgacgagcgcctgatcaaccccgacggctccctgctgttccgagtaacc
atcaacggagtgaccggctggcggctgtGCGAACGCATTCTGGCt

**SEQ ID NO:534 (SS 125 L27V (RIIbB) (aa seq)**

MVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYE
GLSGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKSASG
GSGGSGMYESFIESLPFLKSLEFSARLKVVDVIGTKVYNDGEQIIAQGDSADSFFIIESGEVKIT
MKRKGKSEVEENGAVEIARCSRGQYFGELALVTNKPRAASAHAIGTVKCLAMDVQAFERLLGPCM
EIMKRNIATYEEQLVALYGTNMDIVGSGGSGGSSSITVTGTLWNGNKIIDERLINPDGSLLFRVT
INGVTGWRLCERILA

**SEQ ID NO:535 (SS 130 L27V (RIIbB) (nt sequence)**

ATGgtcttcacactcgaagatttcgttggggactggcgacagacagccggctacaacctggacca
agtccttgaacagggaggtgtgtccagtttgtttcagaatctcggggtgtccgtaactccgatcc
aaaggattgtcctgagcggtgaaaatgggctgaagatcgacatccatgtcatcatcccgtatgaa
ggtctgagcggcgaccaaatgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatga
tcatcactttaaggtgatcctgcactatggcacactggtaatcgacggggttacgccgaacatga
tcgactatttcggacggccgtatgaaggcatcgccgtgttcgacggcaaaaagatcactgtaaca
gggAGCgctAGCGGAGGTTCAGGCGGTTCCGGAatgtatgaaagctttattgagtcactgccatt
ccttaaatctttggagttttctgcacgcctgaaagtagtagatgtgataggcaccaaagtataca
acgatggagaacaaatcattgctcagggagattcggctgattctttttcattattgaatctgga
gaagtgaaaattactatgaaaagaaagggtaaatcagaagtggaagagaatggtgcagtagaaat
cgctcgatgctcgcggggacagtactttggagagcttgccctggtaactaacaaacctcgagcag
cttctgcccacgccattgggactgtcaaatgtttagcaatggatgtgcaagcatttgaaaggctt
ctgggaccttgcatggaaattatgaaaaggaacatcgctacctatgaagaacagttagttgccct
gTATggaacgaacatggatattgtaggGTCAGGTGGATCTGGAGGtAGCTCttcTaccctgtgga
acggcaacaaaattatcgacgagcgcctgatcaaccccgacggctccctgctgttccgagtaacc
atcaacggagtgaccggctggcggctgtGCGAACGCATTCTGGCt

**SEQ ID NO:536 (SS 130 L27V (RIIbB) (aa seq)**

MVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYE
GLSGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVT
GSASGGSGGSGMYESFIESLPFLKSLEFSARLKVVDVIGTKVYNDGEQIIAQGDSADSFFIIESG
EVKITMKRKGKSEVEENGAVEIARCSRGQYFGELALVTNKPRAASAHAIGTVKCLAMDVQAFERL
LGPCMEIMKRNIATYEEQLVALYGTNMDIVGSGGSGGSSSTLWNGNKIIDERLINPDGSLLFRVT
INGVTGWRLCERILA

**SEQ ID NO:537 (SS 136 L27V (RIIbB) (nt sequence)**

ATGgtcttcacactcgaagatttcgttggggactggcgacagacagccggctacaacctggacca
agtccttgaacagggaggtgtgtccagtttgtttcagaatctcggggtgtccgtaactccgatcc
aaaggattgtcctgagcggtgaaaatgggctgaagatcgacatccatgtcatcatcccgtatgaa
ggtctgagcggcgaccaaatgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatga
tcatcactttaaggtgatcctgcactatggcacactggtaatcgacggggttacgccgaacatga
tcgactatttcggacggccgtatgaaggcatcgccgtgttcgacggcaaaaagatcactgtaaca
gggaccctgtggaacggcaacAGCgctAGCGGAGGTTCAGGCGGTTCCGGAatgtatgaaagctt
tattgagtcactgccattccttaaatctttggagttttctgcacgcctgaaagtagtagatgtga
taggcaccaaagtatacaacgatggagaacaaatcattgctcagggagattcggctgattctttt
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gaatggtgcagtagaaatcgctcgatgctcgcggggacagtactttggagagcttgccctggtaa
ctaacaaacctcgagcagcttctgcccacgccattgggactgtcaaatgtttagcaatggatgtg
caagcatttgaaaggcttctgggaccttgcatggaaattatgaaaaggaacatcgctacctatga

agaacagttagttgccctgTATggaacgaacatggatattgtaggGTCAGGTGGATCTGGAGGtA
GCTCttcTaaaattatcgacgagcgcctgatcaaccccgacggctccctgctgttccgagtaacc
atcaacggagtgaccggctggcggctgtGCGAACGCATTCTGGCt

**SEQ ID NO:538 (SS 136 L27V (RIIbB) (aa seq)**

MVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYE
GLSGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVT
GTLWNGNSASGGSGGSGMYESFIESLPFLKSLEFSARLKVVDVIGTKVYNDGEQIIAQGDSADSF
FIIESGEVKITMKRKGKSEVEENGAVEIARCSRGQYFGELALVTNKPRAASAHAIGTVKCLAMDV
QAFERLLGPCMEIMKRNIATYEEQLVALYGTNMDIVGSGGSGGSSSKIIDERLINPDGSLLFRVT
INGVTGWRLCERILA

**SEQ ID NO:539 (SS 143 L27V (RIIbB) (nt sequence)**

ATGgtcttcacactcgaagatttcgttggggactggcgacagacagccggctacaacctggacca
agtccttgaacagggaggtgtgtccagtttgtttcagaatctcggggtgtccgtaactccgatcc
aaaggattgtcctgagcggtgaaaatgggctgaagatcgacatccatgtcatcatcccgtatgaa
ggtctgagcggcgaccaaatgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatga
tcatcactttaaggtgatcctgcactatggcacactggtaatcgacggggttacgccgaacatga
tcgactatttcggacggccgtatgaaggcatcgccgtgttcgacggcaaaaagatcactgtaaca
gggaccctgtggaacggcaacaaaattatcgacgagcgcctgAGCgctAGCGGAGGTTCAGGCGG
TTCCGGAatgtatgaaagctttattgagtcactgccattccttaaatctttggagttttctgcac
gcctgaaagtagtagatgtgataggcaccaaagtatacaacgatggagaacaaatcattgctcag
ggagattcggctgattctttttttcattattgaatctggagaagtgaaaattactatgaaaagaaa
gggtaaatcagaagtggaagagaatggtgcagtagaaatcgctcgatgctcgcggggacagtact
ttggagagcttgccctggtaactaacaaacctcgagcagcttctgcccacgccattgggactgtc
aaatgtttagcaatggatgtgcaagcatttgaaaggcttctgggaccttgcatggaaattatgaa
aaggaacatcgctacctatgaagaacagttagttgccctgTATggaacgaacatggatattgtag
gGTCAGGTGGATCTGGAGGtAGCTCttcTatcaaccccgacggctccctgctgttccgagtaacc
atcaacggagtgaccggctggcggctgtGCGAACGCATTCTGGCt

**SEQ ID NO:540 (SS 143 L27V (RIIbB) (aa seq)**

MVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYE
GLSGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVT
GTLWNGNKIIDERLSASGGSGGSGMYESFIESLPFLKSLEFSARLKVVDVIGTKVYNDGEQIIAQ
GDSADSFFIIESGEVKITMKRKGKSEVEENGAVEIARCSRGQYFGELALVTNKPRAASAHAIGTV
KCLAMDVQAFERLLGPCMEIMKRNIATYEEQLVALYGTNMDIVGSGGSGGSSSINPDGSLLFRVT
INGVTGWRLCERILA

**SEQ ID NO:541 (SS 145 L27V (RIIbB) (nt sequence)**

ATGgtcttcacactcgaagatttcgttggggactggcgacagacagccggctacaacctggacca
agtccttgaacagggaggtgtgtccagtttgtttcagaatctcggggtgtccgtaactccgatcc
aaaggattgtcctgagcggtgaaaatgggctgaagatcgacatccatgtcatcatcccgtatgaa
ggtctgagcggcgaccaaatgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatga
tcatcactttaaggtgatcctgcactatggcacactggtaatcgacggggttacgccgaacatga
tcgactatttcggacggccgtatgaaggcatcgccgtgttcgacggcaaaaagatcactgtaaca
gggaccctgtggaacggcaacaaaattatcgacgagcgcctgatcaacAGCgctAGCGGAGGTTC
AGGCGGTTCCGGAatgtatgaaagctttattgagtcactgccattccttaaatctttggagtttt
ctgcacgcctgaaagtagtagatgtgataggcaccaaagtatacaacgatggagaacaaatcatt
gctcagggagattcggctgattctttttttcattattgaatctggagaagtgaaaattactatgaa
aagaaagggtaaatcagaagtggaagagaatggtgcagtagaaatcgctcgatgctcgcggggac
agtactttggagagcttgccctggtaactaacaaacctcgagcagcttctgcccacgccattggg

actgtcaaatgtttagcaatggatgtgcaagcatttgaaaggcttctgggaccttgcatggaaat
tatgaaaaggaacatcgctacctatgaagaacagttagttgccctgTATggaacgaacatggata
ttgtaggGTCAGGTGGATCTGGAGGtAGCTCttcTcccgacggctccctgctgttccgagtaacc
atcaacggagtgaccggctggcggctgtGCGAACGCATTCTGGCt

**SEQ ID NO:542 (SS 145 L27V (RIIbB) (aa seq)**

MVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYE
GLSGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVT
GTLWNGNKIIDERLINSASGGSGGSGMYESFIESLPFLKSLEFSARLKVVDVIGTKVYNDGEQII
AQGDSADSFFIIESGEVKITMKRKGKSEVEENGAVEIARCSRGQYFGELALVTNKPRAASAHAIG
TVKCLAMDVQAFERLLGPCMEIMKRNIATYEEQLVALYGTNMDIVGSGGSGGSSSPDGSLLFRVT
INGVTGWRLCERILA

**SEQ ID NO:543 (SS 147 L27V (RIIbB) (nt sequence)**

ATGgtcttcacactcgaagatttcgttggggactggcgacagacagccggctacaacctggacca
agtccttgaacagggaggtgtgtccagtttgtttcagaatctcggggtgtccgtaactccgatcc
aaaggattgtcctgagcggtgaaaatgggctgaagatcgacatccatgtcatcatcccgtatgaa
ggtctgagcggcgaccaaatgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatga
tcatcactttaaggtgatcctgcactatggcacactggtaatcgacggggttacgccgaacatga
tcgactatttcggacggccgtatgaaggcatcgccgtgttcgacggcaaaaagatcactgtaaca
gggaccctgtggaacggcaacaaaattatcgacgagcgcctgatcaaccccgacAGCgctAGCGG
AGGTTCAGGCGGTTCCGGAatgtatgaaagctttattgagtcactgccattccttaaatctttgg
agttttctgcacgcctgaaagtagtagatgtgataggcaccaaagtatacaacgatggagaacaa
atcattgctcagggagattcggctgattctttttcattattgaatctggagaagtgaaaattac
tatgaaaagaaagggtaaatcagaagtggaagagaatggtgcagtagaaatcgctcgatgctcgc
ggggacagtactttggagagcttgccctggtaactaacaaacctcgagcagcttctgcccacgcc
attgggactgtcaaatgtttagcaatggatgtgcaagcatttgaaaggcttctgggaccttgcat
ggaaattatgaaaaggaacatcgctacctatgaagaacagttagttgccctgTATggaacgaaca
tggatattgtaggGTCAGGTGGATCTGGAGGtAGCTCttcTggctccctgctgttccgagtaacc
atcaacggagtgaccggctggcggctgtGCGAACGCATTCTGGCt

**SEQ ID NO:544 (SS 147 L27V (RIIbB) (aa seq)**

MVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYE
GLSGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVT
GTLWNGNKIIDERLINPDSASGGSGGSGMYESFIESLPFLKSLEFSARLKVVDVIGTKVYNDGEQ
IIAQGDSADSFFIIESGEVKITMKRKGKSEVEENGAVEIARCSRGQYFGELALVTNKPRAASAHA
IGTVKCLAMDVQAFERLLGPCMEIMKRNIATYEEQLVALYGTNMDIVGSGGSGGSSSGSLLFRVT
INGVTGWRLCERILA

**SEQ ID NO:545 (SS 148 L27V (RIIbB) (nt sequence)**

ATGgtcttcacactcgaagatttcgttggggactggcgacagacagccggctacaacctggacca
agtccttgaacagggaggtgtgtccagtttgtttcagaatctcggggtgtccgtaactccgatcc
aaaggattgtcctgagcggtgaaaatgggctgaagatcgacatccatgtcatcatcccgtatgaa
ggtctgagcggcgaccaaatgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatga
tcatcactttaaggtgatcctgcactatggcacactggtaatcgacggggttacgccgaacatga
tcgactatttcggacggccgtatgaaggcatcgccgtgttcgacggcaaaaagatcactgtaaca
gggaccctgtggaacggcaacaaaattatcgacgagcgcctgatcaaccccgacggcAGCgctAG
CGGAGGTTCAGGCGGTTCCGGAatgtatgaaagctttattgagtcactgccattccttaaatctt
tggagttttctgcacgcctgaaagtagtagatgtgataggcaccaaagtatacaacgatggagaa
caaatcattgctcagggagattcggctgattctttttcattattgaatctggagaagtgaaaat
tactatgaaaagaaagggtaaatcagaagtggaagagaatggtgcagtagaaatcgctcgatgct

cgcggggacagtactttggagagcttgccctggtaactaacaaacctcgagcagcttctgcccac
gccattgggactgtcaaatgtttagcaatggatgtgcaagcatttgaaaggcttctgggaccttg
catggaaattatgaaaaggaacatcgctacctatgaagaacagttagttgccctgTATggaacga
acatggatattgtaggGTCAGGTGGATCTGGAGGtAGCTCttcTtccctgctgttccgagtaacc
atcaacggagtgaccggctggcggctgtGCGAACGCATTCTGGCt

**SEQ ID NO:546 (SS 148 L27V (RIIbB) (aa seq)**
MVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYE
GLSGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVT
GTLWNGNKIIDERLINPDGSASGGSGGSGMYESFIESLPFLKSLEFSARLKVVDVIGTKVYNDGE
QIIAQGDSADSFFIIESGEVKITMKRKGKSEVEENGAVEIARCSRGQYFGELALVTNKPRAASAH
AIGTVKCLAMDVQAFERLLGPCMEIMKRNIATYEEQLVALYGTNMDIVGSGGSGGSSSSLLFRVT
INGVTGWRLCERILA

**SEQ ID NO:547 (SS 156 L27V (RIIbB) (nt sequence)**
ATGgtcttcacactcgaagatttcgttggggactggcgacagacagccggctacaacctggacca
agtccttgaacagggaggtgtgtccagtttgtttcagaatctcggggtgtccgtaactccgatcc
aaaggattgtcctgagcggtgaaaatgggctgaagatcgacatccatgtcatcatcccgtatgaa
ggtctgagcggcgaccaaatgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatga
tcatcactttaaggtgatcctgcactatggcacactggtaatcgacggggttacgccgaacatga
tcgactatttcggacggccgtatgaaggcatcgccgtgttcgacggcaaaaagatcactgtaaca
gggaccctgtggaacggcaacaaaattatcgacgagcgcctgatcaaccccgacggctccctgct
gttccgagtaaccatcAGCgctAGCGGAGGTTCAGGCGGTTCCGGAatgtatgaaagctttattg
agtcactgccattccttaaatctttggagttttctgcacgcctgaaagtagtagatgtgataggc
accaaagtatacaacgatggagaacaaatcattgctcagggagattcggctgattctttttcat
tattgaatctggagaagtgaaaattactatgaaaagaaagggtaaatcagaagtggaagagaatg
gtgcagtagaaatcgctcgatgctcgcggggacagtactttggagagcttgccctggtaactaac
aaacctcgagcagcttctgcccacgccattgggactgtcaaatgtttagcaatggatgtgcaagc
atttgaaaggcttctgggaccttgcatggaaattatgaaaaggaacatcgctacctatgaagaac
agttagttgccctgTATggaacgaacatggatattgtaggGTCAGGTGGATCTGGAGGtAGCTCt
tcTaacggagtgaccggctggcggctgtGCGAACGCATTCTGGCt

**SEQ ID NO:548 (SS 156 L27V (RIIbB) (aa seq)**
MVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYE
GLSGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVT
GTLWNGNKIIDERLINPDGSLLFRVTISASGGSGGSGMYESFIESLPFLKSLEFSARLKVVDVIG
TKVYNDGEQIIAQGDSADSFFIIESGEVKITMKRKGKSEVEENGAVEIARCSRGQYFGELALVTN
KPRAASAHAIGTVKCLAMDVQAFERLLGPCMEIMKRNIATYEEQLVALYGTNMDIVGSGGSGGSS
SNGVTGWRLCERILA

**SEQ ID NO:549 (SS 157 L27V (RIIbB) (nt sequence)**
ATGgtcttcacactcgaagatttcgttggggactggcgacagacagccggctacaacctggacca
agtccttgaacagggaggtgtgtccagtttgtttcagaatctcggggtgtccgtaactccgatcc
aaaggattgtcctgagcggtgaaaatgggctgaagatcgacatccatgtcatcatcccgtatgaa
ggtctgagcggcgaccaaatgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatga
tcatcactttaaggtgatcctgcactatggcacactggtaatcgacggggttacgccgaacatga
tcgactatttcggacggccgtatgaaggcatcgccgtgttcgacggcaaaaagatcactgtaaca
gggaccctgtggaacggcaacaaaattatcgacgagcgcctgatcaaccccgacggctccctgct
gttccgagtaaccatcaacAGCgctAGCGGAGGTTCAGGCGGTTCCGGAatgtatgaaagcttta
ttgagtcactgccattccttaaatctttggagttttctgcacgcctgaaagtagtagatgtgata
ggcaccaaagtatacaacgatggagaacaaatcattgctcagggagattcggctgattctttttt

cattattgaatctggagaagtgaaaattactatgaaaagaaagggtaaatcagaagtggaagaga
atggtgcagtagaaatcgctcgatgctcgcggggacagtactttggagagcttgccctggtaact
aacaaacctcgagcagcttctgcccacgccattgggactgtcaaatgtttagcaatggatgtgca
agcatttgaaaggcttctgggaccttgcatggaaattatgaaaaggaacatcgctacctatgaag
aacagttagttgccctgTATggaacgaacatggatattgtaggGTCAGGTGGATCTGGAGGtAGC
TCttcTggagtgaccggctggcggctgtGCGAACGCATTCTGGCt

**SEQ ID NO:550 (SS 157 L27V (RIIbB) (aa seq)**
MVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYE
GLSGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVT
GTLWNGNKIIDERLINPDGSLLFRVTINSASGGSGGSGMYESFIESLPFLKSLEFSARLKVVDVI
GTKVYNDGEQIIAQGDSADSFFIIESGEVKITMKRKGKSEVEENGAVEIARCSRGQYFGELALVT
NKPRAASAHAIGTVKCLAMDVQAFERLLGPCMEIMKRNIATYEEQLVALYGTNMDIVGSGGSGGS
SSGVTGWRLCERILA

**SEQ ID NO:551 (SS 158 L27V (RIIbB) (nt sequence)**
ATGgtcttcacactcgaagatttcgttggggactggcgacagacagccggctacaacctggacca
agtccttgaacagggaggtgtgtccagtttgtttcagaatctcggggtgtccgtaactccgatcc
aaaggattgtcctgagcggtgaaaatgggctgaagatcgacatccatgtcatcatcccgtatgaa
ggtctgagcggcgaccaaatgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatga
tcatcactttaaggtgatcctgcactatggcacactggtaatcgacggggttacgccgaacatga
tcgactatttcggacggccgtatgaaggcatcgccgtgttcgacggcaaaaagatcactgtaaca
gggaccctgtggaacggcaacaaaattatcgacgagcgcctgatcaaccccgacggctccctgct
gttccgagtaaccatcaacggaAGCgctAGCGGAGGTTCAGGCGGTTCCGGAatgtatgaaagct
ttattgagtcactgccattccttaaatctttggagttttctgcacgcctgaaagtagtagatgtg
ataggcaccaaagtatacaacgatggagaacaaatcattgctcagggagattcggctgattcttt
tttcattattgaatctggagaagtgaaaattactatgaaaagaaagggtaaatcagaagtggaag
agaatggtgcagtagaaatcgctcgatgctcgcggggacagtactttggagagcttgccctggta
actaacaaacctcgagcagcttctgcccacgccattgggactgtcaaatgtttagcaatggatgt
gcaagcatttgaaaggcttctgggaccttgcatggaaattatgaaaaggaacatcgctacctatg
aagaacagttagttgccctgTATggaacgaacatggatattgtaggGTCAGGTGGATCTGGAGGt
AGCTCttcTgtgaccggctggcggctgtGCGAACGCATTCTGGCt

**SEQ ID NO:552 (SS 158 L27V (RIIbB) (aa seq)**
MVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYE
GLSGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVT
GTLWNGNKIIDERLINPDGSLLFRVTINGSASGGSGGSGMYESFIESLPFLKSLEFSARLKVVDV
IGTKVYNDGEQIIAQGDSADSFFIIESGEVKITMKRKGKSEVEENGAVEIARCSRGQYFGELALV
TNKPRAASAHAIGTVKCLAMDVQAFERLLGPCMEIMKRNIATYEEQLVALYGTNMDIVGSGGSGG
SSSVTGWRLCERILA

**SEQ ID NO:553 (SS 166 L27V (RIIbB) (nt sequence)**
ATGgtcttcacactcgaagatttcgttggggactggcgacagacagccggctacaacctggacca
agtccttgaacagggaggtgtgtccagtttgtttcagaatctcggggtgtccgtaactccgatcc
aaaggattgtcctgagcggtgaaaatgggctgaagatcgacatccatgtcatcatcccgtatgaa
ggtctgagcggcgaccaaatgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatga
tcatcactttaaggtgatcctgcactatggcacactggtaatcgacggggttacgccgaacatga
tcgactatttcggacggccgtatgaaggcatcgccgtgttcgacggcaaaaagatcactgtaaca
gggaccctgtggaacggcaacaaaattatcgacgagcgcctgatcaaccccgacggctccctgct
gttccgagtaaccatcaacggagtgaccggctggcggctgtGCGAAAGCgctAGCGGAGGTTCAG
GCGGTTCCGGAatgtatgaaagctttattgagtcactgccattccttaaatctttggagttttct

gcacgcctgaaagtagtagatgtgataggcaccaaagtatacaacgatggagaacaaatcattgc
tcagggagattcggctgattctttttcattattgaatctggagaagtgaaaattactatgaaaa
gaaagggtaaatcagaagtggaagagaatggtgcagtagaaatcgctcgatgctcgcggggacag
tactttggagagcttgccctggtaactaacaaacctcgagcagcttctgcccacgccattgggac
tgtcaaatgtttagcaatggatgtgcaagcatttgaaaggcttctgggaccttgcatggaaatta
tgaaaaggaacatcgctacctatgaagaacagttagttgccctgTATggaacgaacatggatatt
gtaggGTCAGGTGGATCTGGAGGtAGCTCttcTCGCATTCTGGCt

**SEQ ID NO:554 (SS 166 L27V (RIIbB) (aa seq)**
MVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYE
GLSGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVT
GTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCESASGGSGGSGMYESFIESLPFLKSLEFS
ARLKVVDVIGTKVYNDGEQIIAQGDSADSFFIIESGEVKITMKRKGKSEVEENGAVEIARCSRGQ
YFGELALVTNKPRAASAHAIGTVKCLAMDVQAFERLLGPCMEIMKRNIATYEEQLVALYGTNMDI
VGSGGSGGSSSRILA

**SEQ ID NO:555 (CP 26 L27V (RIIbB) (nt sequence)**
ATGggtgtgtccagtttgtttcagaatctcggggtgtccgtaactccgatccaaaggattgtcct
gagcggtgaaaatgggctgaagatcgacatccatgtcatcatcccgtatgaaggtctgagcggcg
accaaatgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatgatcatcactttaag
gtgatcctgcactatggcacactggtaatcgacggggttacgccgaacatgatcgactatttcgg
acggccgtatgaaggcatcgccgtgttcgacggcaaaaagatcactgtaacagggaccctgtgga
acggcaacaaaattatcgacgagcgcctgatcaaccccgacggctccctgctgttccgagtaacc
atcaacggagtgaccggctggcggctgtGCGAACGCATTCTGGCtAGCTCAAGCGGAGGTTCAGG
CGGTTCCGGAATGTATGAAAGCTTTATTGAGTCACTGCCATTCCTTAAATCTTTGGAGTTTTCTG
CACGCCTGAAAGTAGTAGATGTGATAGGCACCAAAGTATACAACGATGGAGAACAAATCATTGCT
CAGGGAGATTCGGCTGATTCTTTTTTCATTATTGAATCTGGAGAAGTGAAAATTACTATGAAAAG
AAAGGGTAAATCAGAAGTGGAAGAGAATGGTGCAGTAGAAATCGCTCGATGCTCGCGGGGACAGT
ACTTTGGAGAGCTTGCCCTGGTAACTAACAAACCTCGAGCAGCTTCTGCCCACGCCATTGGGACT
GTCAAATGTTTAGCAATGGATGTGCAAGCATTTGAAAGGCTTCTGGGACCTTGCATGGAAATTAT
GAAAAGGAACATCGCTACCTATGAAGAACAGTTAGTTGCCCTGTATGGAACGAACATGGATATTG
TAGGGTCAGGTGGATCTGGAGGTAGCTCTTCTatggtcttcacactcgaagatttcgttggggac
tggcgacagacagccggctacaacctggaccaagtccttgaacaggga

**SEQ ID NO:556 (CP 26 L27V (RIIbB) (aa seq)**
MGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEKIFKVVYPVDDHHFK
VILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVT
INGVTGWRLCERILASSSGGSGGSGMYESFIESLPFLKSLEFSARLKVVDVIGTKVYNDGEQIIA
QGDSADSFFIIESGEVKITMKRKGKSEVEENGAVEIARCSRGQYFGELALVTNKPRAASAHAIGT
VKCLAMDVQAFERLLGPCMEIMKRNIATYEEQLVALYGTNMDIVGSGGSGGSSSMVFTLEDFVGD
WRQTAGYNLDQVLEQG

**SEQ ID NO:557 (CP 45 L27V (RIIbB) (nt sequence)**
ATGgtcctgagcggtgaaaatgggctgaagatcgacatccatgtcatcatcccgtatgaaggtct
gagcggcgaccaaatgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatgatcatc
actttaaggtgatcctgcactatggcacactggtaatcgacggggttacgccgaacatgatcgac
tatttcggacggccgtatgaaggcatcgccgtgttcgacggcaaaaagatcactgtaacagggac
cctgtggaacggcaacaaaattatcgacgagcgcctgatcaaccccgacggctccctgctgttcc
gagtaaccatcaacggagtgaccggctggcggctgtGCGAACGCATTCTGGCtAGCTCAAGCGGA
GGTTCAGGCGGTTCCGGAATGTATGAAAGCTTTATTGAGTCACTGCCATTCCTTAAATCTTTGGA
GTTTTCTGCACGCCTGAAAGTAGTAGATGTGATAGGCACCAAAGTATACAACGATGGAGAACAAA

TCATTGCTCAGGGAGATTCGGCTGATTCTTTTTTCATTATTGAATCTGGAGAAGTGAAAATTACT
ATGAAAAGAAAGGGTAAATCAGAAGTGGAAGAGAATGGTGCAGTAGAAATCGCTCGATGCTCGCG
GGGACAGTACTTTGGAGAGCTTGCCCTGGTAACTAACAAACCTCGAGCAGCTTCTGCCCACGCCA
TTGGGACTGTCAAATGTTTAGCAATGGATGTGCAAGCATTTGAAAGGCTTCTGGGACCTTGCATG
GAAATTATGAAAAGGAACATCGCTACCTATGAAGAACAGTTAGTTGCCCTGTATGGAACGAACAT
GGATATTGTAGGGTCAGGTGGATCTGGAGGTAGCTCTTCTatggtcttcacactcgaagatttcg
ttggggactggcgacagacagccggctacaacctggaccaagtccttgaacagggaggtgtgtcc
agtttgtttcagaatctcggggtgtccgtaactccgatccaaaggatt

**SEQ ID NO:558 (CP 45 L27V (RIIbB) (aa seq)**

MVLSGENGLKIDIHVIIPYEGLSGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMID
YFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILASSSG
GSGGSGMYESFIESLPFLKSLEFSARLKVVDVIGTKVYNDGEQIIAQGDSADSFFIIESGEVKIT
MKRKGKSEVEENGAVEIARCSRGQYFGELALVTNKPRAASAHAIGTVKCLAMDVQAFERLLGPCM
EIMKRNIATYEEQLVALYGTNMDIVGSGGSGGSSSMVFTLEDFVGDWRQTAGYNLDQVLEQGGVS
SLFQNLGVSVTPIQRI

**SEQ ID NO:559 (CP 100(+1) L27V (RIIbB) (nt sequence)**

ATGgacggggttacgccgaacatgatcgactatttcggacggccgtatgaaggcatcgccgtgtt
cgacggcaaaaagatcactgtaacagggaccctgtggaacggcaacaaaattatcgacgagcgcc
tgatcaaccccgacggctccctgctgttccgagtaaccatcaacggagtgaccggctggcggctg
tGCGAACGCATTCTGGCtAGCTCAAGCGGAGGTTCAGGCGGTTCCGGAATGTATGAAAGCTTTAT
TGAGTCACTGCCATTCCTTAAATCTTTGGAGTTTTCTGCACGCCTGAAAGTAGTAGATGTGATAG
GCACCAAAGTATACAACGATGGAGAACAAATCATTGCTCAGGGAGATTCGGCTGATTCTTTTTTC
ATTATTGAATCTGGAGAAGTGAAAATTACTATGAAAAGAAAGGGTAAATCAGAAGTGGAAGAGAA
TGGTGCAGTAGAAATCGCTCGATGCTCGCGGGGACAGTACTTTGGAGAGCTTGCCCTGGTAACTA
ACAAACCTCGAGCAGCTTCTGCCCACGCCATTGGGACTGTCAAATGTTTAGCAATGGATGTGCAA
GCATTTGAAAGGCTTCTGGGACCTTGCATGGAAATTATGAAAAGGAACATCGCTACCTATGAAGA
ACAGTTAGTTGCCCTGTATGGAACGAACATGGATATTGTAGGGTCAGGTGGATCTGGAGGTAGCT
CTTCTatggtcttcacactcgaagatttcgttggggactggcgacagacagccggctacaacctg
gaccaagtccttgaacagggaggtgtgtccagtttgtttcagaatctcggggtgtccgtaactcc
gatccaaaggattgtcctgagcggtgaaaatgggctgaagatcgacatccatgtcatcatcccgt
atgaaggtctgagcggcgaccaaatgggccagatcgaaaaaatttttaaggtggtgtaccctgtg
gatgatcatcactttaaggtgatcctgcactatggcacactggtaatcGAC

**SEQ ID NO:560 (CP 100(+1) L27V (RIIbB) (aa seq)**

MDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRL
CERILASSSGGSGGSGMYESFIESLPFLKSLEFSARLKVVDVIGTKVYNDGEQIIAQGDSADSFF
IIESGEVKITMKRKGKSEVEENGAVEIARCSRGQYFGELALVTNKPRAASAHAIGTVKCLAMDVQ
AFERLLGPCMEIMKRNIATYEEQLVALYGTNMDIVGSGGSGGSSSMVFTLEDFVGDWRQTAGYNL
DQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEKIFKVVYPV
DDHHFKVILHYGTLVID

**SEQ ID NO:561 (CP 101(+1) L27V (RIIbB) (nt sequence)**

ATGggggttacgccgaacatgatcgactatttcggacggccgtatgaaggcatcgccgtgttcga
cggcaaaaagatcactgtaacagggaccctgtggaacggcaacaaaattatcgacgagcgcctga
tcaaccccgacggctccctgctgttccgagtaaccatcaacggagtgaccggctggcggctgtGC
GAACGCATTCTGGCtAGCTCAAGCGGAGGTTCAGGCGGTTCCGGAATGTATGAAAGCTTTATTGA
GTCACTGCCATTCCTTAAATCTTTGGAGTTTTCTGCACGCCTGAAAGTAGTAGATGTGATAGGCA
CCAAAGTATACAACGATGGAGAACAAATCATTGCTCAGGGAGATTCGGCTGATTCTTTTTTCATT
ATTGAATCTGGAGAAGTGAAAATTACTATGAAAAGAAAGGGTAAATCAGAAGTGGAAGAGAATGG

TGCAGTAGAAATCGCTCGATGCTCGCGGGGACAGTACTTTGGAGAGCTTGCCCTGGTAACTAACA
AACCTCGAGCAGCTTCTGCCCACGCCATTGGGACTGTCAAATGTTTAGCAATGGATGTGCAAGCA
TTTGAAAGGCTTCTGGGACCTTGCATGGAAATTATGAAAAGGAACATCGCTACCTATGAAGAACA
GTTAGTTGCCCTGTATGGAACGAACATGGATATTGTAGGGTCAGGTGGATCTGGAGGTAGCTCTT
CTatggtcttcacactcgaagatttcgttggggactggcgacagacagccggctacaacctggac
caagtccttgaacagggaggtgtgtccagtttgtttcagaatctcggggtgtccgtaactccgat
ccaaaggattgtcctgagcggtgaaaatgggctgaagatcgacatccatgtcatcatcccgtatg
aaggtctgagcggcgaccaaatgggccagatcgaaaaaatttttaaggtggtgtaccctgtggat
gatcatcactttaaggtgatcctgcactatggcacactggtaatcgacGGG

**SEQ ID NO:562 (CP 101(+1) L27V (RIIbB) (aa seq)**
MGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLC
ERILASSSGGSGGSGMYESFIESLPFLKSLEFSARLKVVDVIGTKVYNDGEQIIAQGDSADSFFI
IESGEVKITMKRKGKSEVEENGAVEIARCSRGQYFGELALVTNKPRAASAHAIGTVKCLAMDVQA
FERLLGPCMEIMKRNIATYEEQLVALYGTNMDIVGSGGSGGSSSMVFTLEDFVGDWRQTAGYNLD
QVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEKIFKVVYPVD
DHHFKVILHYGTLVIDG

**SEQ ID NO:563 (CP 102(+1) L27V (RIIbB) (nt sequence)**
ATGgttacgccgaacatgatcgactatttcggacggccgtatgaaggcatcgccgtgttcgacgg
caaaaagatcactgtaacagggaccctgtggaacggcaacaaaattatcgacgagcgcctgatca
accccgacggctccctgctgttccgagtaaccatcaacggagtgaccggctggcggctgtGCGAA
CGCATTCTGGCtAGCTCAAGCGGAGGTTCAGGCGGTTCCGGAATGTATGAAAGCTTTATTGAGTC
ACTGCCATTCCTTAAATCTTTGGAGTTTTCTGCACGCCTGAAAGTAGTAGATGTGATAGGCACCA
AAGTATACAACGATGGAGAACAAATCATTGCTCAGGGAGATTCGGCTGATTCTTTTTTCATTATT
GAATCTGGAGAAGTGAAAATTACTATGAAAAGAAAGGGTAAATCAGAAGTGGAAGAGAATGGTGC
AGTAGAAATCGCTCGATGCTCGCGGGGACAGTACTTTGGAGAGCTTGCCCTGGTAACTAACAAAC
CTCGAGCAGCTTCTGCCCACGCCATTGGGACTGTCAAATGTTTAGCAATGGATGTGCAAGCATTT
GAAAGGCTTCTGGGACCTTGCATGGAAATTATGAAAAGGAACATCGCTACCTATGAAGAACAGTT
AGTTGCCCTGTATGGAACGAACATGGATATTGTAGGGTCAGGTGGATCTGGAGGTAGCTCTTCTa
tggtcttcacactcgaagatttcgttggggactggcgacagacagccggctacaacctggaccaa
gtccttgaacagggaggtgtgtccagtttgtttcagaatctcggggtgtccgtaactccgatcca
aaggattgtcctgagcggtgaaaatgggctgaagatcgacatccatgtcatcatcccgtatgaag
gtctgagcggcgaccaaatgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatgat
catcactttaaggtgatcctgcactatggcacactggtaatcgacgggGTT

**SEQ ID NO:564 (CP 102(+1) L27V (RIIbB) (aa seq)**
MVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCE
RILASSSGGSGGSGMYESFIESLPFLKSLEFSARLKVVDVIGTKVYNDGEQIIAQGDSADSFFII
ESGEVKITMKRKGKSEVEENGAVEIARCSRGQYFGELALVTNKPRAASAHAIGTVKCLAMDVQAF
ERLLGPCMEIMKRNIATYEEQLVALYGTNMDIVGSGGSGGSSSMVFTLEDFVGDWRQTAGYNLDQ
VLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEKIFKVVYPVDD
HHFKVILHYGTLVIDGV

**SEQ ID NO:565 (CP 143(+1) L27V (RIIbB) (nt sequence)**
ATGatcaaccccgacggctccctgctgttccgagtaaccatcaacggagtgaccggctggcggct
gtGCGAACGCATTCTGGCtAGCTCAAGCGGAGGTTCAGGCGGTTCCGGAATGTATGAAAGCTTTA
TTGAGTCACTGCCATTCCTTAAATCTTTGGAGTTTTCTGCACGCCTGAAAGTAGTAGATGTGATA
GGCACCAAAGTATACAACGATGGAGAACAAATCATTGCTCAGGGAGATTCGGCTGATTCTTTTTT
CATTATTGAATCTGGAGAAGTGAAAATTACTATGAAAAGAAAGGGTAAATCAGAAGTGGAAGAGA
ATGGTGCAGTAGAAATCGCTCGATGCTCGCGGGGACAGTACTTTGGAGAGCTTGCCCTGGTAACT

AACAAACCTCGAGCAGCTTCTGCCCACGCCATTGGGACTGTCAAATGTTTAGCAATGGATGTGCA
AGCATTTGAAAGGCTTCTGGGACCTTGCATGGAAATTATGAAAAGGAACATCGCTACCTATGAAG
AACAGTTAGTTGCCCTGTATGGAACGAACATGGATATTGTAGGGTCAGGTGGATCTGGAGGTAGC
TCTTCTatggtcttcacactcgaagatttcgttggggactggcgacagacagccggctacaacct
ggaccaagtccttgaacagggaggtgtgtccagtttgtttcagaatctcggggtgtccgtaactc
cgatccaaaggattgtcctgagcggtgaaaatgggctgaagatcgacatccatgtcatcatcccg
tatgaaggtctgagcggcgaccaaatgggccagatcgaaaaaatttttaaggtggtgtaccctgt
ggatgatcatcactttaaggtgatcctgcactatggcacactggtaatcgacggggttacgccga
acatgatcgactatttcggacggccgtatgaaggcatcgccgtgttcgacggcaaaaagatcact
gtaacagggaccctgtggaacggcaacaaaattatcgacgagcgcctgATC

**SEQ ID NO:566 (CP 143(+1) L27V (RIIbB) (aa seq)**

MINPDGSLLFRVTINGVTGWRLCERILASSSGGSGGSGMYESFIESLPFLKSLEFSARLKVVDVI
GTKVYNDGEQIIAQGDSADSFFIIESGEVKITMKRKGKSEVEENGAVEIARCSRGQYFGELALVT
NKPRAASAHAIGTVKCLAMDVQAFERLLGPCMEIMKRNIATYEEQLVALYGTNMDIVGSGGSGGS
SSMVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIP
YEGLSGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKIT
VTGTLWNGNKIIDERLI

**SEQ ID NO:567 (CP 147(+1) L27V (RIIbB) (nt sequence)**

ATGggctccctgctgttccgagtaaccatcaacggagtgaccggctggcggctgtGCGAACGCAT
TCTGGCtAGCTCAAGCGGAGGTTCAGGCGGTTCCGGAATGTATGAAAGCTTTATTGAGTCACTGC
CATTCCTTAAATCTTTGGAGTTTTCTGCACGCCTGAAAGTAGTAGATGTGATAGGCACCAAAGTA
TACAACGATGGAGAACAAATCATTGCTCAGGGAGATTCGGCTGATTCTTTTTTCATTATTGAATC
TGGAGAAGTGAAAATTACTATGAAAAGAAAGGGTAAATCAGAAGTGGAAGAGAATGGTGCAGTAG
AAATCGCTCGATGCTCGCGGGGACAGTACTTTGGAGAGCTTGCCCTGGTAACTAACAAACCTCGA
GCAGCTTCTGCCCACGCCATTGGGACTGTCAAATGTTTAGCAATGGATGTGCAAGCATTTGAAAG
GCTTCTGGGACCTTGCATGGAAATTATGAAAAGGAACATCGCTACCTATGAAGAACAGTTAGTTG
CCCTGTATGGAACGAACATGGATATTGTAGGGTCAGGTGGATCTGGAGGTAGCTCTTCTatggtc
ttcacactcgaagatttcgttggggactggcgacagacagccggctacaacctggaccaagtcct
tgaacagggaggtgtgtccagtttgtttcagaatctcggggtgtccgtaactccgatccaaagga
ttgtcctgagcggtgaaaatgggctgaagatcgacatccatgtcatcatcccgtatgaaggtctg
agcggcgaccaaatgggccagatcgaaaaaatttttaaggtggtgtaccctgtggatgatcatca
ctttaaggtgatcctgcactatggcacactggtaatcgacggggttacgccgaacatgatcgact
atttcggacggccgtatgaaggcatcgccgtgttcgacggcaaaaagatcactgtaacagggacc
ctgtggaacggcaacaaaattatcgacgagcgcctgatcaaccccgacGGC

**SEQ ID NO:568 (CP 147(+1) L27V (RIIbB) (aa seq)**

MGSLLFRVTINGVTGWRLCERILASSSGGSGGSGMYESFIESLPFLKSLEFSARLKVVDVIGTKV
YNDGEQIIAQGDSADSFFIIESGEVKITMKRKGKSEVEENGAVEIARCSRGQYFGELALVTNKPR
AASAHAIGTVKCLAMDVQAFERLLGPCMEIMKRNIATYEEQLVALYGTNMDIVGSGGSGGSSSMV
FTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGL
SGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGT
LWNGNKIIDERLINPDG

**SEQ ID NO:569 (CP 156(+1) L27V (RIIbB) (nt sequence)**

ATGaacggagtgaccggctggcggctgtGCGAACGCATTCTGGCtAGCTCAAGCGGAGGTTCAGG
CGGTTCCGGAATGTATGAAAGCTTTATTGAGTCACTGCCATTCCTTAAATCTTTGGAGTTTTCTG
CACGCCTGAAAGTAGTAGATGTGATAGGCACCAAAGTATACAACGATGGAGAACAAATCATTGCT
CAGGGAGATTCGGCTGATTCTTTTTTCATTATTGAATCTGGAGAAGTGAAAATTACTATGAAAAG
AAAGGGTAAATCAGAAGTGGAAGAGAATGGTGCAGTAGAAATCGCTCGATGCTCGCGGGGACAGT

ACTTTGGAGAGCTTGCCCTGGTAACTAACAAACCTCGAGCAGCTTCTGCCCACGCCATTGGGACT
GTCAAATGTTTAGCAATGGATGTGCAAGCATTTGAAAGGCTTCTGGGACCTTGCATGGAAATTAT
GAAAAGGAACATCGCTACCTATGAAGAACAGTTAGTTGCCCTGTATGGAACGAACATGGATATTG
TAGGGTCAGGTGGATCTGGAGGTAGCTCTTCTatggtcttcacactcgaagatttcgttggggac
tggcgacagacagccggctacaacctggaccaagtccttgaacagggaggtgtgtccagtttgtt
tcagaatctcggggtgtccgtaactccgatccaaaggattgtcctgagcggtgaaaatgggctga
agatcgacatccatgtcatcatcccgtatgaaggtctgagcggcgaccaaatgggccagatcgaa
aaaatttttaaggtggtgtaccctgtggatgatcatcactttaaggtgatcctgcactatggcac
actggtaatcgacggggttacgccgaacatgatcgactatttcggacggccgtatgaaggcatcg
ccgtgttcgacggcaaaaagatcactgtaacagggaccctgtggaacggcaacaaaattatcgac
gagcgcctgatcaaccccgacggctccctgctgttccgagtaaccatcAAC

**SEQ ID NO:570 (CP 156(+1) L27V (RIIbB) (aa seq)**
MNGVTGWRLCERILASSSGGSGGSGMYESFIESLPFLKSLEFSARLKVVDVIGTKVYNDGEQIIA
QGDSADSFFIIESGEVKITMKRKGKSEVEENGAVEIARCSRGQYFGELALVTNKPRAASAHAIGT
VKCLAMDVQAFERLLGPCMEIMKRNIATYEEQLVALYGTNMDIVGSGGSGGSSSMVFTLEDFVGD
WRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIE
KIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIID
ERLINPDGSLLFRVTIN

**SEQ ID NO:571 (CP 158(+1) L27V (RIIbB) (nt sequence)**
ATGgtgaccggctggcggctgtGCGAACGCATTCTGGCtAGCTCAAGCGGAGGTTCAGGCGGTTC
CGGAATGTATGAAAGCTTTATTGAGTCACTGCCATTCCTTAAATCTTTGGAGTTTTCTGCACGCC
TGAAAGTAGTAGATGTGATAGGCACCAAAGTATACAACGATGGAGAACAAATCATTGCTCAGGGA
GATTCGGCTGATTCTTTTTTCATTATTGAATCTGGAGAAGTGAAAATTACTATGAAAAGAAAGGG
TAAATCAGAAGTGGAAGAGAATGGTGCAGTAGAAATCGCTCGATGCTCGCGGGGACAGTACTTTG
GAGAGCTTGCCCTGGTAACTAACAAACCTCGAGCAGCTTCTGCCCACGCCATTGGGACTGTCAAA
TGTTTAGCAATGGATGTGCAAGCATTTGAAAGGCTTCTGGGACCTTGCATGGAAATTATGAAAAG
GAACATCGCTACCTATGAAGAACAGTTAGTTGCCCTGTATGGAACGAACATGGATATTGTAGGGT
CAGGTGGATCTGGAGGTAGCTCTTCTatggtcttcacactcgaagatttcgttggggactggcga
cagacagccggctacaacctggaccaagtccttgaacagggaggtgtgtccagtttgtttcagaa
tctcggggtgtccgtaactccgatccaaaggattgtcctgagcggtgaaaatgggctgaagatcg
acatccatgtcatcatcccgtatgaaggtctgagcggcgaccaaatgggccagatcgaaaaaatt
tttaaggtggtgtaccctgtggatgatcatcactttaaggtgatcctgcactatggcacactggt
aatcgacggggttacgccgaacatgatcgactatttcggacggccgtatgaaggcatcgccgtgt
tcgacggcaaaaagatcactgtaacagggaccctgtggaacggcaacaaaattatcgacgagcgc
ctgatcaaccccgacggctccctgctgttccgagtaaccatcaacggaGTG

**SEQ ID NO:572 (CP 158(+1) L27V (RIIbB) (aa seq)**
MVTGWRLCERILASSSGGSGGSGMYESFIESLPFLKSLEFSARLKVVDVIGTKVYNDGEQIIAQG
DSADSFFIIESGEVKITMKRKGKSEVEENGAVEIARCSRGQYFGELALVTNKPRAASAHAIGTVK
CLAMDVQAFERLLGPCMEIMKRNIATYEEQLVALYGTNMDIVGSGGSGGSSSMVFTLEDFVGDWR
QTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEKI
FKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDER
LINPDGSLLFRVTINGV

**SEQ ID NO:573 (CP 166(+1) L27V (RIIbB) (nt sequence)**
ATGCGCATTCTGGCtAGCTCAAGCGGAGGTTCAGGCGGTTCCGGAATGTATGAAAGCTTTATTGA
GTCACTGCCATTCCTTAAATCTTTGGAGTTTTCTGCACGCCTGAAAGTAGTAGATGTGATAGGCA
CCAAAGTATACAACGATGGAGAACAAATCATTGCTCAGGGAGATTCGGCTGATTCTTTTTTCATT
ATTGAATCTGGAGAAGTGAAAATTACTATGAAAAGAAAGGGTAAATCAGAAGTGGAAGAGAATGG

TGCAGTAGAAATCGCTCGATGCTCGCGGGGACAGTACTTTGGAGAGCTTGCCCTGGTAACTAACA
AACCTCGAGCAGCTTCTGCCCACGCCATTGGGACTGTCAAATGTTTAGCAATGGATGTGCAAGCA
TTTGAAAGGCTTCTGGGACCTTGCATGGAAATTATGAAAAGGAACATCGCTACCTATGAAGAACA
GTTAGTTGCCCTGTATGGAACGAACATGGATATTGTAGGGTCAGGTGGATCTGGAGGTAGCTCTT
CTatggtcttcacactcgaagatttcgttggggactggcgacagacagccggctacaacctggac
caagtccttgaacagggaggtgtgtccagtttgtttcagaatctcggggtgtccgtaactccgat
ccaaaggattgtcctgagcggtgaaaatgggctgaagatcgacatccatgtcatcatcccgtatg
aaggtctgagcggcgaccaaatgggccagatcgaaaaaatttttaaggtggtgtaccctgtggat
gatcatcactttaaggtgatcctgcactatggcacactggtaatcgacggggttacgccgaacat
gatcgactatttcggacggccgtatgaaggcatcgccgtgttcgacggcaaaaagatcactgtaa
cagggaccctgtggaacggcaacaaaattatcgacgagcgcctgatcaaccccgacggctccctg
ctgttccgagtaaccatcaacggagtgaccggctggcggctgtGCGAACGC

**SEQ ID NO:574 (CP 166(+1) L27V (RIIbB) (aa seq)**
MRILASSSGGSGGSGMYESFIESLPFLKSLEFSARLKVVDVIGTKVYNDGEQIIAQGDSADSFFI
IESGEVKITMKRKGKSEVEENGAVEIARCSRGQYFGELALVTNKPRAASAHAIGTVKCLAMDVQA
FERLLGPCMEIMKRNIATYEEQLVALYGTNMDIVGSGGSGGSSSMVFTLEDFVGDWRQTAGYNLD
QVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEKIFKVVYPVD
DHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSL
LFRVTINGVTGWRLCER

**SEQ ID NO:575 (linker)**
GGGTCAGGTGGATCTGGAGGTAGCTCTTCT

**SEQ ID NO:576 (linker)**
AGCTCAAGCGGAGGTTCAGGCGGTTCCGGA

**SEQ ID NO:577 (LC3 (nt sequence))**

ATGCCGTCCGAGAAGACCTTCAAACAGCGCCGGAGCTTCGAACAAAGAGTGGAAGATGTCCGGCT
CATCCGGGAGCAGCACCCCACCAAGATCCCAGTGATTATAGAGCGATACAAGGGTGAGAAGCAGC
TGCCCGTCCTGGACAAGACCAGTTCCTTGTACCTGATCACGTGAATATGAGCGAACTCATCAAGA
TAATTAGAAGGCGCCTGCAGCTCAATGCTAACCAAGCCTTCTTCCTCCTGGTGAATGGGCACAGC
ATGGTGAGTGTGTCCACACCCATCTCTGAAGTGTACGAGAGCGAGAGAGATGAAGACGGCTTCCT
GTACATGGTCTATGCCTCCCAGGAGACGTTCGGGACAGCACTGGCTGTGTAA

**SEQ ID NO:578 (LC3 (aa sequence))**

MPSEKTFKQRRSFEQRVEDVRLIREQHPTKIPVIIERYKGEKQLPVLDKTKFLVPDHVNMSELIK
IIRRRLQLNANQAFFLLVNGHSMVSVSTPISEVYESERDEDGFLYMVYASQETFGTALAV

**SEQ ID NO:579 (pattern sequence)**
GSAIVK

**SEQ ID NO:580 (pattern sequence)**
NHGK

**SEQ ID NO:581 (pattern sequence)**
SILM

**SEQ ID NO:582 (pattern sequence)**
AVTK

**SEQ ID NO:583 (pattern sequence)**
LIVMFY

**SEQ ID NO:584 (pattern sequence)**
LIVMFY

**SEQ ID NO:585 (pattern sequence)**
LIVM

**SEQ ID NO:586 (pattern sequence)**
LIVMWF

**SEQ ID NO:587 (pattern sequence)**
EKTQ

**SEQ ID NO:588 (pattern sequence)**
LIVMAKR

**SEQ ID NO:589 (pattern sequence)**
LIVMAKRG

**SEQ ID NO:590 (pattern sequence)**
LIVMF

**SEQ ID NO:591 (pattern sequence)**
LIVMFSYQ

**SEQ ID NO: 592 OgLuc L27V-LC3 fusions proteins (Nt seq)**
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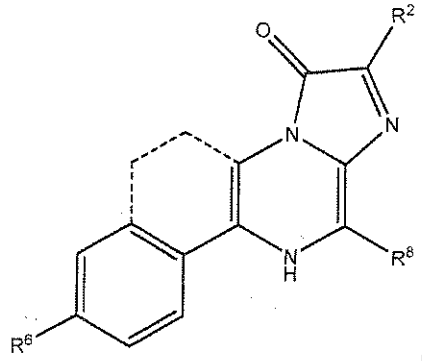
GGCGGTGTGTCCAGTTTGTTTCAGAATCTCGGGGTGTCCGTAACTCCGATCCAAAGGATTGTCCTGAGCGGTGAAAAC
GGCCTGAAGATCGACATCCATGTCATCATCCCGTATGAAGGTCTGAGCGGCGATCAGATGGGCCAGATCGAAAAAATT
TTTAAGGTGGTGTACCCTGTGGATGATCATCACTTTAAGGTGATTCTGCACTATGGCACACTGGTAATCGACGGGGTT
ACGCCGAACATGATCGACTATTTCGGACGGCCGTATGAAGGCATCGCCGTGTTCGACGGCAAAAAGATCACTGTAACC
GGGACCCTGTGGAACGGCAACAAAATTATCGACGAGCGCCTGATCAACCCCGACGGCTCCCTGCTGTTCCGCGTAACC
ATCAACGGAGTGACCGGCTGGCGGCTGTGCGAGAGAATTTTGGCGGGCTCGAGCGGAGGTGGAGGTTCAGGTGGTGGC
GGGAGCGGTGGAATGCCGTCCGAGAAGACCTTCAAACAGCGCCGGAGCTTCGAACAAAGAGTGGAAGATGTCCGGCTC
ATCCGGGAGCAGCACCCCACCAAGATCCCAGTGATTATAGAGCGATACAAGGGTGAGAAGCAGCTGCCCGTCCTGGAC
AAGACCAAGTTCCTTGTACCTGATCACGTGAATATGAGCGAACTCATCAAGATAATTAGAAGGCGCCTGCAGCTCAAT
GCTAACCAAGCCTTCTTCCTCCTGGTGAATGGGCACAGCATGGTGAGTGTGTCCACACCCATCTCTGAAGTGTACGAG
AGCGAGAGAGATGAAGACGGCTTCCTGTACATGGTCTATGCCTCCCAGGAGACGTTCGGGACAGCACTGGCTGTGTAA

**SEQ ID NO: 593 OgLuc L27V-LC3 fusions proteins (aa seq)**
MVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEKI
FKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVT
INGVTGWRLCERILAGSSGGGGSGGGGSGGMPSEKTFKQRRSFEQRVEDVRLIREQHPTKIPVIIERYKGEKQLPVLD
KTKFLVPDHVNMSELIKIIRRRLQLNANQAFFLLVNGHSMVSVSTPISEVYESERDEDGFLYMVYASQETFGTALAV

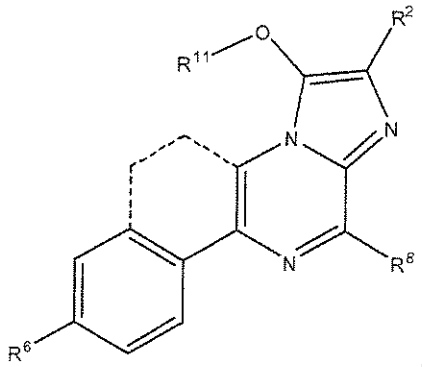
What is claimed:

1. A compound of formula (Ia) or (Ib):



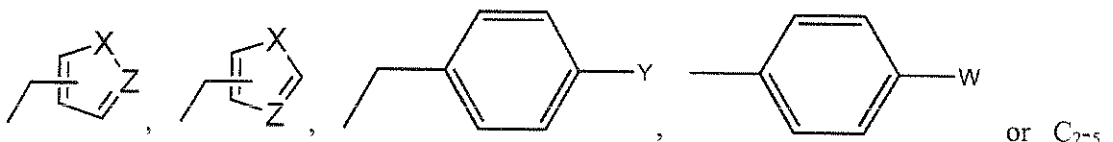
(Ia)

or



(Ib)

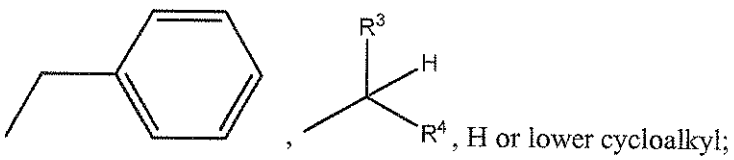
wherein $R^2$ is selected from the group consisting of



straight chain alkyl;

$R^6$ is selected from the group consisting of -H, -OH, $-NH_2$, -OC(O)R or $-OCH_2OC(O)R$;

$R^8$ is selected from the group consisting of



, H or lower cycloalkyl;

wherein $R^3$ and $R^4$ are both H or both $C_{1-2}$ alkyl;

W is $-NH_2$, halo, -OH, -NHC(O)R, $-CO_2R$;

X is –S-, –O- or –$NR^{22}$-;

Y is –H, -OH, or –$OR^{11}$;

Z is –CH- or –N-;

each $R^{11}$ is independently –C(O)R'' or –$CH_2OC(O)R''$;

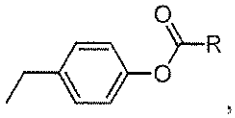
$R^{22}$ is H, $CH_3$ or $CH_2CH_3$;

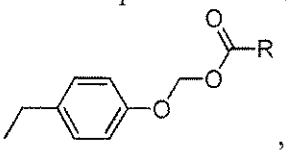
each R is independently $C_{1-7}$ straight-chain alkyl or $C_{1-7}$ branched alkyl;

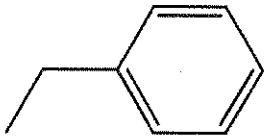
R'' is $C_{1-7}$ straight-chain alkyl or $C_{1-7}$ branched alkyl;

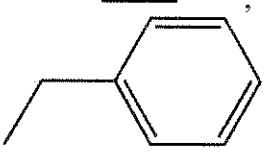
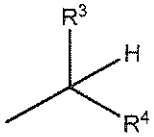
the dashed bonds indicate the presence of an optional ring, which may be saturated or unsaturated;

with the proviso that when $R^2$ is

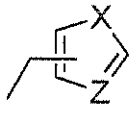
, 

, or 

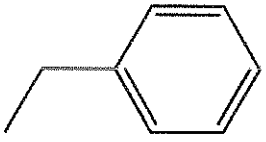
, $R^8$ is not 
;

with the proviso that when $R^2$ is 
, $R^8$ is 

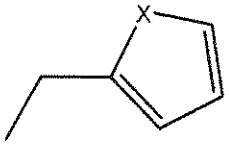
or lower cycloalkyl; and

with the proviso that when $R^6$ is $NH_2$, $R^2$ is , 

, or $C_{2-5}$ alkyl;

or $R^8$ is not 
.

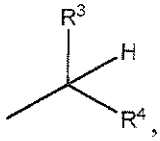
2. A compound according to claim 1,

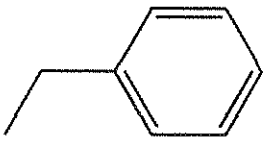
wherein $R^2$ is 

; and

X is O or S.

3. A compound according to claim 1, wherein $R^2$ is $C_{2-5}$ straight-chain alkyl.

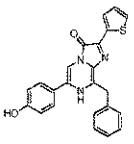
4. A compound according to any of the preceding claims, wherein $R^8$ is  , lower cycloalkyl or H.

5. A compound according to any one of claims 1-3, wherein $R^8$ is  .

6. A compound according to any one of the preceding claims, wherein $R_{11}$ is $-CH_2OC(O)C(CH_3)_3$.

7. A compound according to any one of claims 1-5, wherein R'' is $-C(CH_3)_3$, $-CH(CH_3)_2$, $-CH_2C(CH_3)_3$, or $-CH_2CH(CH_3)_2$.

8. A compound selected from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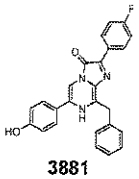
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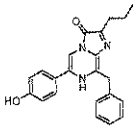
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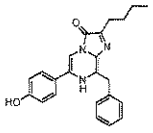
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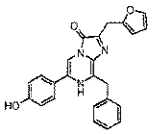
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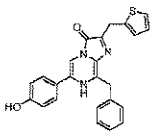
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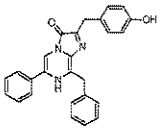
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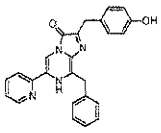
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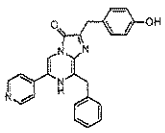
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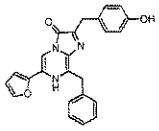
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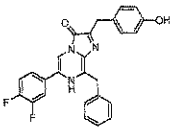
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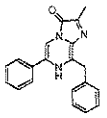
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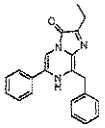
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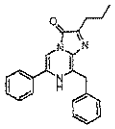
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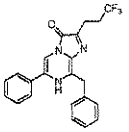
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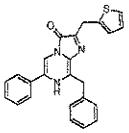
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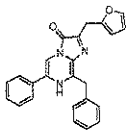
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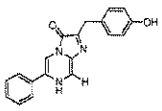
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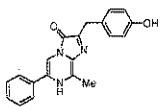
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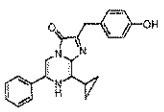
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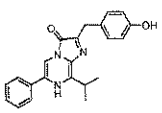
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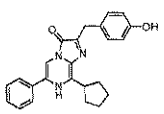
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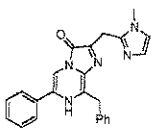
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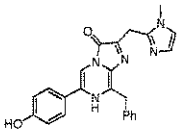
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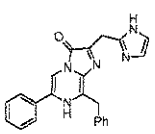
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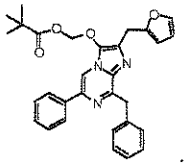
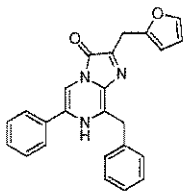


9. A compound of formula

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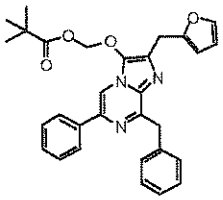


10. A kit comprising a compound according to any one of claims 1-9.

11. The kit of claim 10 further comprising a luciferase.

12. The kit of claim 11, wherein the luciferase is an *Oplophorus* or *Renilla* luciferase.

13. A kit of any one of claims 10-12, further comprising a buffer reagent.

14. A method for detecting luminescence in a sample comprising

contacting a sample with a compound according to any one of claims 1-9;

contacting the sample with a coelenterazine-utilizing luciferase, if it is not present in the sample; and

detecting luminescence.

15. The method of claim 14, wherein the sample contains live cells.

16. The method of claim 14, wherein the sample contains a coelenterazine-utilizing luciferase.

17. A method for detecting luminescence in a transgenic animal comprising

administering a compound according to any one of claims 1-9 to a transgenic animal; and

detecting luminescence;

wherein the transgenic animal expresses a coelenterazine-utilizing luciferase.

SEQUENCE LISTING

<110> Klaubert, Dieter
Meisenheimer, Poncho
Unch, James

<120> NOVEL COELENTERAZINE SUBSTRATES AND METHODS OF USE

<130> 016026-9523-US02

<140> 13/287,992
<141> 2011-11-02

<150> 61/409,422
<151> 2010-11-02

<160> 593

<170> PatentIn version 3.5

<210> 1
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| Asn | Gln | Asp | Gln | Val | Leu | Glu | Gln | Gly | Gly | Leu | Ser | Ser | Leu | Phe | Gln |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Ala | Leu | Gly | Val | Ser | Val | Thr | Pro | Ile | Gln | Lys | Val | Val | Leu | Ser | Gly |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Glu | Asn | Gly | Leu | Lys | Ala | Asp | Ile | His | Val | Ile | Ile | Pro | Tyr | Glu | Gly |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Leu | Ser | Gly | Phe | Gln | Met | Gly | Leu | Ile | Glu | Met | Ile | Phe | Lys | Val | Val |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Tyr | Pro | Val | Asp | Asp | His | His | Phe | Lys | Ile | Ile | Leu | His | Tyr | Gly | Thr |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Leu | Val | Ile | Asp | Gly | Val | Thr | Pro | Asn | Met | Ile | Asp | Tyr | Phe | Gly | Arg |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Pro | Tyr | Pro | Gly | Ile | Ala | Val | Phe | Asp | Gly | Lys | Gln | Ile | Thr | Val | Thr |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Gly | Thr | Leu | Trp | Asn | Gly | Asn | Lys | Ile | Tyr | Asp | Glu | Arg | Leu | Ile | Asn |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Pro | Asp | Gly | Ser | Leu | Leu | Phe | Arg | Val | Thr | Ile | Asn | Gly | Val | Thr | Gly |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
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<220>
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accccaatcc agaaaattgt gctgtctggg gagaatgggt taaaatttga tattcatgtc 180

atcatccctt acgagggact cagtggtttt caaatgggtc tgattgaaat gatcttcaaa 240

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attgacggtg tgacaccaaa catgattgac tactttggac gcccttacga gggaattgct 360

gtgtttgacg gcaagaagat cacagttact ggaactctgt ggaacggcaa caagatcatt 420

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Gly Tyr Asn Gln Asp Gln Val Leu Glu Gln Gly Gly Leu Ser Ser Leu
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Phe Gln Lys Leu Gly Val Ser Val Thr Pro Ile Gln Lys Ile Val Leu
35 40 45

Ser Gly Glu Asn Gly Leu Lys Phe Asp Ile His Val Ile Ile Pro Tyr
50 55 60

Glu Gly Leu Ser Gly Phe Gln Met Gly Leu Ile Glu Met Ile Phe Lys
65 70 75 80

Val Val Tyr Pro Val Asp Asp His His Phe Lys Ile Ile Leu His Tyr
85 90 95

Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe
100 105 110

Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr
115 120 125

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

Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val
145 150 155 160

Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala
165 170

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<211> 513
<212> DNA
<213> Artificial Sequence

<220>
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accccaatcc agaaaattgt gctgtctggg gagaatgggt taaaaattga tattcatgtc 180

atcatccctt acgagggact cagtggtttt caaatgggtc tgattgaaat gatcttcaaa 240

gttgtttacc cagtggatga tcatcatttc aagattattc accattatgg tacactcgtt 300

attgacggtg tgacaccaaa catgattgac ttctttggac gcccttacga gggaattgct 360

gtgtttgacg gcaagaagat cacagttact ggaactctgt ggaacggcaa caagatcatt 420

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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic polypeptide

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1 5 10 15

Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Leu Ser Ser Leu
20 25 30

Phe Gln Lys Leu Gly Val Ser Val Thr Pro Ile Gln Lys Ile Val Leu
35 40 45

Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr
50 55 60

Glu Gly Leu Ser Gly Phe Gln Met Gly Leu Ile Glu Met Ile Phe Lys
65 70 75 80

Val Val Tyr Pro Val Asp Asp His His Phe Lys Ile Ile His His Tyr
85 90 95

Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Phe Phe
100 105 110

Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr
115 120 125

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

Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val
145 150 155 160

Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala
165 170

<210> 6
<211> 513
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

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accccaatcc agaaaattgt gctgtctggg gagaatgggt taaaaattga tattcatgtc 180

atcatccctt acgagggact cagtggttat caaatgggtc agattgaaaa gatcttcaaa 240

gttgtttacc cagtggatga tcatcatttc aagattattc gccattatgg tacactcgtt 300

attgacggtg tgacaccaaa catgattgac ttctttggac gcccttacga gggaattgct 360

gtgtttgacg gcaagaagat cacagttact ggaactctgt ggaacggcaa caagatcatt 420

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accggatggc gcctttgcga gcgtattctt gcc 513

<210> 7
<211> 171
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

polypeptide

<400> 7

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Gly Tyr Asn Leu Asp Gln Leu Leu Glu Gln Gly Gly Leu Ser Ser Leu
            20                  25                  30

Phe Gln Lys Leu Gly Val Ser Val Thr Pro Ile Gln Lys Ile Val Leu
        35                  40                  45

Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr
    50                  55                  60

Glu Gly Leu Ser Gly Tyr Gln Met Gly Gln Ile Glu Lys Ile Phe Lys
65                  70                  75                  80

Val Val Tyr Pro Val Asp Asp His His Phe Lys Ile Ile Arg His Tyr
                85                  90                  95

Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Phe Phe
            100                 105                 110

Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr
        115                 120                 125

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

Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Ile
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Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala
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<210> 8
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accccaatcc agaaaattgt gctgtctggg gagaatgggt taaaaattga tattcatgtc      180

atcatccctt acgagggact cagtggtttt caaatgggtc tgattgaaat gatctacaaa      240

gttgtttacc cagtggatga tcatcatttc aaggttattc tccattatgg tacactcgtt      300

attgacggtg tgacaccaaa catgattgac tactttggac gcccttacga gggaattgct      360
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gtgtttgacg gcaagaagat cacagttact ggaactctgt ggaacggcaa caagatcatt 420

gatgagcgcc tgatcaaccc agatggttca ctcctcttcc gcgttactat caatggagtc 480

accggatggc gcctttgcga gcgtattctt gcc 513

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<211> 171
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

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Gly Tyr Asn Gln Asp Gln Val Leu Glu Gln Gly Gly Leu Ser Ser Leu
20 25 30

Phe Gln Lys Leu Gly Val Ser Val Thr Pro Ile Gln Lys Ile Val Leu
35 40 45

Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr
50 55 60

Glu Gly Leu Ser Gly Phe Gln Met Gly Leu Ile Glu Met Ile Tyr Lys
65 70 75 80

Val Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu His Tyr
85 90 95

Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe
100 105 110

Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr
115 120 125

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

Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val
145 150 155 160

Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala
165 170

<210> 10
<211> 513
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

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accccaatcc agaaaattgt gctgtctggg gagaatgggt taaaaattga tattcatgtc 180

atcatccctt acgagggact cagtggtttt caaatgggtc tgattgaaat gatctacaaa 240

gttgtttacc cagtggatga tcatcatttc aaggttattc tccattatgg tacactcgtt 300

attgacggtg tgacaccaaa catgattgac tactttggac gcccttacga gggaattgct 360

gtgtttgacg gcaagaagat cacagttact ggaactctgt ggaacggcga caagatcatt 420

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<212> PRT
<213> Artificial Sequence

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Gly Tyr Asn Gln Asp Gln Val Leu Glu Gln Gly Gly Leu Ser Ser Leu
20 25 30

Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln Lys Ile Val Leu
35 40 45

Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr
50 55 60

Glu Gly Leu Ser Gly Phe Gln Met Gly Leu Ile Glu Met Ile Tyr Lys
65 70 75 80

Val Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu His Tyr
85 90 95

Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe
100 105 110

Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr
115 120 125

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

Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Thr Asn Gly Val
145 150 155 160

Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala
165 170

<210> 12
<211> 513
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

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accccaatcc agaaaattgt gctgtctggg gagaatgggt taaaaattga tattcatgtc 180

atcatccctt acgagggact cagtggtttt caaatgggtc tgattgaaat gatctacaaa 240

gttgtttacc cagtggatga tcatcatttc aaggttattc tccattatgg tacactcgtt 300

attgacggtg tgacaccaaa catgattgac tactttggac gcccttacga gggaattgct 360

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<210> 13
<211> 171
<212> PRT
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic polypeptide

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20 25 30

Phe Gln Lys Leu Gly Val Ser Ile Thr Pro Ile Gln Lys Ile Val Leu
35 40 45

Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr
50 55 60

Glu Gly Leu Ser Gly Phe Gln Met Gly Leu Ile Glu Met Ile Tyr Lys
65 70 75 80

Val Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu His Tyr
85 90 95

Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe
100 105 110

Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr
115 120 125

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

Ile Asn Pro Asp Gly Ser Ile Leu Phe Arg Val Thr Ile Asn Gly Val
145 150 155 160

Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala
165 170

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<211> 513
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<213> Artificial Sequence

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atcatccctt acgagggact cagtggtttt caaatgggtc tgattgaaat gatcttcaaa 240

gttgtttacc cagtggatga tcatcatttc aaggttattc tccattatgg tacactcgtt 300

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Phe Gln Lys Leu Gly Val Ser Val Thr Pro Ile Gln Lys Ile Val Leu
35 40 45

Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr
50 55 60

Glu Gly Leu Ser Gly Phe Gln Met Gly Leu Ile Glu Met Ile Phe Lys
65 70 75 80

Val Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu His Tyr
85 90 95

Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe
100 105 110

Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr
115 120 125

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

Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val
145 150 155 160

Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala
165 170

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accccaatcc agaaaattgt gctgtctggg gagaatgggt taaaaattga tattcatgtc 180

atcatccctt acgagggact cagtggttat caaatgggtc agattgaaaa gatcttcaaa 240

gttgtttacc cagtggatga tcatcatttc aaggttattc tccattatgg tacactcgtt 300

attgacggtg tgacaccaaa catgattgac tactttggac gcccttacga gggaattgct 360

gtgtttgacg gcaagaagat cacagttact ggaactctgt ggaacggcaa caagatcatt 420

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20 25 30

Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln Lys Ile Val Leu
35 40 45

Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr
50 55 60

Glu Gly Leu Ser Gly Tyr Gln Met Gly Gln Ile Glu Lys Ile Phe Lys
65 70 75 80

Val Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu His Tyr
85 90 95

Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe
100 105 110

Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr
115 120 125

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

Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val
145 150 155 160

Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala
165 170

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<211> 513
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accccaatcc agaaaattgt gctgtctggg gagaatgggt taaaaattga tattcatgtc 180

atcatccctt acgagggact cagtggttat caaatgggtc agattgaaaa gatcttcaaa 240

gttgtttacc cagtggatga tcatcatttc aaggttattc tccattatgg tacactcgtt 300

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<212> PRT
<213> Artificial Sequence

<220>
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1 5 10 15

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20 25 30

Phe Gln Lys Leu Gly Val Ser Val Thr Pro Ile Gln Lys Ile Val Leu
35 40 45

Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr
50 55 60

Glu Gly Leu Ser Gly Tyr Gln Met Gly Gln Ile Glu Lys Ile Phe Lys
65 70 75 80

Val Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu His Tyr
85 90 95

Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe
100 105 110

Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr
115 120 125

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

Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val
145 150 155 160

Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala
165 170

<210> 20
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<212> DNA
<213> Artificial Sequence

<220>
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accccaatcc agaaaattgt gctgtctggg gagaatgggt taaaaattga tattcatgtc 180

atcatccctt acgagggact cagtggttat caaatgggtc agattgaaaa gatcttcaaa 240

gttgtttacc cagtggatga tcatcatttc aaggttattc tccattatgg tacactcgtt 300

attgacggtg tgacaccaaa catgattgac tactttggac gcccttacga gggaattgct 360

gtgtttgacg gcaagaagat cacagttact ggaactctgt ggaacggcaa caagatcatt 420

gatgagcgcc tgatcaaccc agatggttca ctcctcttcc gcgttactat caatggagtc 480

accggatggc gcctttgcga gcgtattctt gcc 513

<210> 21
<211> 171
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 21
Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala
1 5 10 15

Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu
20 25 30

Phe Gln Lys Leu Gly Val Ser Ile Thr Pro Ile Gln Lys Ile Val Leu
35 40 45

Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr
50 55 60

Glu Gly Leu Ser Gly Tyr Gln Met Gly Gln Ile Glu Lys Ile Phe Lys
65 70 75 80

Val Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu His Tyr
85 90 95

Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe
100 105 110

Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr
115 120 125

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

Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val
145 150 155 160

Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala
165 170

<210> 22
<211> 513
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 22
atggtgttta cactcgaaga tttcgtaggg gactggcggc agacagccgg ctacaaccaa 60

gaccaagtcc ttgagcaggg cggtctgtcc agtttgtttc agaaactcgg ggtgtccgta 120

acaccgatcc aaaagattgt cctgagcggt gaaaacggcc tgaagatcga catccatgtc 180

atcatcccgt atgaaggtct gagcggcttc cagatgggcc tcattgagat gatctttaag 240

gtggtgtacc ctgtggatga tcatcacttt aaggtgattc tgcactatgg cacactggta 300

atcgacgggg ttacgccgaa catgatcgac tatttcggac ggccgtatga aggcatcgcc 360

gtgttcgacg gcaaaaagat cactgtaacc gggaccctgt ggaacggcaa caaaattatc 420

gacgagcgcc tgatcaaccc cgacggctcc ctgctgttcc gcgtaaccat caacggagtg 480

accggctggc ggctgtgcga gcgcattttg gcg 513

<210> 23
<211> 513
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 23
atggtattca cactggagga ttttgtcggt gattggcggc aaaccgctgg gtacaaccag 60

gaccaggttc tcgaacaagg gggcctcagc tccctgtttc aaaaactggg tgttagcgtt 120

acacctattc aaaaaatcgt gctctccggg gaaaacgggc tcaaaatcga tattcatgtg 180

attatccctt acgaagggct ctccgggttt cagatggggc tgatcgaaat gatctttaag 240

gtcgtctatc ccgtagatga tcaccacttc aaggtgatcc tccactacgg gaccctcgta 300

attgatggcg tgacccccaa catgatcgac tattttgggc gcccttacga ggggattgct 360

gtcttcgatg gcaaaaaaat tacagtgaca ggcacactct ggaacgggaa taagatcatt 420

gatgagcgcc tgattaatcc cgatgggagc ctgctctttc gggtgacaat taacggcgta 480

acaggctggc gcctctgtga acggattctg gcg 513

<210> 24
<211> 513
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 24
atggtgttta cactcgaaga tttcgtaggg gactggcggc agacagccgg ctacaacctg 60

gaccaagtcc ttgagcaggg cggtctgtcc agtttgtttc agaaactcgg ggtgtccgta 120

acaccgatcc aaaagattgt cctgagcggt gaaaacggcc tgaagatcga catccatgtc 180

atcatcccgt atgaaggtct gagcggctat cagatgggcc agatcgaaaa aatttttaag 240

gtggtgtacc ctgtggatga tcatcacttt aaggtgattc tgcactatgg cacactggta 300

atcgacgggg ttacgccgaa catgatcgac tatttcggac ggccgtatga aggcatcgcc 360

gtgttcgacg gcaaaaagat cactgtaacc gggaccctgt ggaacggcaa caaaattatc 420

gacgagcgcc tgatcaaccc cgacggctcc ctgctgttcc gcgtaaccat caacggagtg 480

accggctggc ggctgtgcga gcgcattttg gcg 513

<210> 25
<211> 513
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 25
atggtattca cactggagga ttttgtcggt gattggcggc aaaccgctgg gtacaacctc 60

gaccaggttc tcgaacaagg gggcctcagc tccctgtttc aaaaactggg tgttagcgtt 120

acacctattc aaaaaatcgt gctctccggg gaaaacgggc tcaaaatcga tattcatgtg 180

attatccctt acgaagggct ctccgggtat cagatggggc agatcgaaaa aatctttaag 240

gtcgtctatc ccgtagatga tcaccacttc aaggtgatcc tccactacgg gaccctcgta 300

attgatggcg tgacccccaa catgatcgac tattttgggc gcccttacga ggggattgct 360

gtcttcgatg gcaaaaaaat tacagtgaca ggcacactct ggaacgggaa taagatcatt 420

gatgagcgcc tgattaatcc cgatgggagc ctgctctttc gggtgacaat taacggcgta 480

acaggctggc gcctctgtga acggattctg gcg 513

<210> 26
<211> 513
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 26
atggtgatta cattggagga tttcgttgga gactggcggc agacagctgg atacaaccaa 60

gatcaagtgt tagaacaagg aggagtgtct agtctgttcc aaaagctggg agtgtcaatc 120

accccaatcc agaaaattgt gctgtctggg gagaatgggt taaaaattga tattcatgtc 180

atcatccctt acgagggact cagtggtttt caaatgggtc tgattgaaat gatcttcaaa 240

gttgtttacc cagtggatga tcatcatttc aaggttattc tccattatgg tacactcgtt 300

attgacggtg tgacaccaaa catgattgac tactttggac gcccttacga gggaattgct 360

gtgtttgacg gcaagaagat cacagttact ggaactctgt ggaacggcaa caagatcatt 420

gatgagcgcc tgatcaaccc agatggttca ctcctcttcc gcgttactat caatggagtc 480

accggatggc gcctttgcga gcgtattctt gcc 513

<210> 27
<211> 171
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 27
Met Val Ile Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala
1 5 10 15

Gly Tyr Asn Gln Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu
20 25 30

Phe Gln Lys Leu Gly Val Ser Ile Thr Pro Ile Gln Lys Ile Val Leu
35 40 45

Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr
50 55 60

Glu Gly Leu Ser Gly Phe Gln Met Gly Leu Ile Glu Met Ile Phe Lys
65 70 75 80

Val Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu His Tyr
85 90 95

Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe
100 105 110

Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr
115 120 125

Val Thr Gly Thr Leu Trp Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu

130 135 140

Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val
145 150 155 160

Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala
165 170

<210> 28
<211> 1650
<212> DNA
<213> Photinus pyralis

<400> 28
atggaagatg ccaaaaacat taagaagggc ccagcgccat tctacccact cgaagacggg 60

accgccggcg agcagctgca caaagccatg aagcgctacg ccctggtgcc cggcaccatc 120

gcctttaccg acgcacatat cgaggtggac attacctacg ccgagtactt cgagatgagc 180

gttcggctgg cagaagctat gaagcgctat gggctgaata caaaccatcg gatcgtggtg 240

tgcagcgaga atagcttgca gttcttcatg cccgtgttgg gtgccctgtt catcggtgtg 300

gctgtggccc cagctaacga catctacaac gagcgcgagc tgctgaacag catgggcatc 360

agccagccca ccgtcgtatt cgtgagcaag aaagggctgc aaaagatcct caacgtgcaa 420

aagaagctac cgatcataca aaagatcatc atcatggata gcaagaccga ctaccagggc 480

ttccaaagca tgtacacctt cgtgacttcc catttgccac ccggcttcaa cgagtacgac 540

ttcgtgcccg agagcttcga ccgggacaaa accatcgccc tgatcatgaa cagtagtggc 600

agtaccggat tgcccaaggg cgtagcccta ccgcaccgca ccgcttgtgt ccgattcagt 660

catgcccgcg accccatctt cggcaaccag atcatccccg acaccgctat cctcagcgtg 720

gtgccatttc accacggctt cggcatgttc accacgctgg gctacttgat ctgcggcttt 780

cgggtcgtgc tcatgtaccg cttcgaggag gagctattct tgcgcagctt gcaagactat 840

aagattcaat ctgccctgct ggtgcccaca ctatttagct tcttcgctaa gagcactctc 900

atcgacaagt acgacctaag caacttgcac gagatcgcca gcggcggggc gccgctcagc 960

aaggaggtag gtgaggccgt ggccaaacgc ttccacctac caggcatccg ccagggctac 1020

ggcctgacag aaacaaccag cgccattctg atcacccccg aaggggacga caagcctggc 1080

gcagtaggca aggtggtgcc cttcttcgag gctaaggtgg tggacttgga caccggtaag 1140

acactgggtg tgaaccagcg cggcgagctg tgcgtccgtg gccccatgat catgagcggc 1200

tacgttaaca accccgaggc tacaaacgct ctcatcgaca aggacggctg gctgcacagc 1260

ggcgacatcg cctactggga cgaggacgag cacttcttca tcgtggaccg gctgaagagc 1320

ctgatcaaat acaagggcta ccaggtagcc ccagccgaac tggagagcat cctgctgcaa 1380

caccccaaca tcttcgacgc cggggtcgcc ggcctgcccg acgacgatgc cggcgagctg 1440

cccgccgcag tcgtcgtgct ggaacacggt aaaaccatga ccgagaagga gatcgtggac 1500

tatgtggcca gccaggttac aaccgccaag aagctgcgcg gtggtgttgt gttcgtggac 1560

gaggtgccta aaggactgac cggcaagttg gacgcccgca agatccgcga gattctcatt 1620

aaggccaaga agggcggcaa gatcgccgtt 1650

<210> 29
<211> 550
<212> PRT
<213> Photinus pyralis

<400> 29
Met Glu Asp Ala Lys Asn Ile Lys Lys Gly Pro Ala Pro Phe Tyr Pro
1 5 10 15

Leu Glu Asp Gly Thr Ala Gly Glu Gln Leu His Lys Ala Met Lys Arg
20 25 30

Tyr Ala Leu Val Pro Gly Thr Ile Ala Phe Thr Asp Ala His Ile Glu
35 40 45

Val Asp Ile Thr Tyr Ala Glu Tyr Phe Glu Met Ser Val Arg Leu Ala
50 55 60

Glu Ala Met Lys Arg Tyr Gly Leu Asn Thr Asn His Arg Ile Val Val
65 70 75 80

Cys Ser Glu Asn Ser Leu Gln Phe Phe Met Pro Val Leu Gly Ala Leu
85 90 95

Phe Ile Gly Val Ala Val Ala Pro Ala Asn Asp Ile Tyr Asn Glu Arg
100 105 110

Glu Leu Leu Asn Ser Met Gly Ile Ser Gln Pro Thr Val Val Phe Val
115 120 125

Ser Lys Lys Gly Leu Gln Lys Ile Leu Asn Val Gln Lys Lys Leu Pro
130 135 140

Ile Ile Gln Lys Ile Ile Ile Met Asp Ser Lys Thr Asp Tyr Gln Gly
145 150 155 160

Phe Gln Ser Met Tyr Thr Phe Val Thr Ser His Leu Pro Pro Gly Phe
165 170 175

Asn Glu Tyr Asp Phe Val Pro Glu Ser Phe Asp Arg Asp Lys Thr Ile
180 185 190

Ala Leu Ile Met Asn Ser Ser Gly Ser Thr Gly Leu Pro Lys Gly Val
195 200 205

Ala Leu Pro His Arg Thr Ala Cys Val Arg Phe Ser His Ala Arg Asp
210 215 220

```
Pro Ile Phe Gly Asn Gln Ile Ile Pro Asp Thr Ala Ile Leu Ser Val
225                 230                 235                 240

Val Pro Phe His His Gly Phe Gly Met Phe Thr Thr Leu Gly Tyr Leu
                245                 250                 255

Ile Cys Gly Phe Arg Val Val Leu Met Tyr Arg Phe Glu Glu Glu Leu
            260                 265                 270

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

Pro Thr Leu Phe Ser Phe Phe Ala Lys Ser Thr Leu Ile Asp Lys Tyr
    290                 295                 300

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

Lys Glu Val Gly Glu Ala Val Ala Lys Arg Phe His Leu Pro Gly Ile
                325                 330                 335

Arg Gln Gly Tyr Gly Leu Thr Glu Thr Thr Ser Ala Ile Leu Ile Thr
            340                 345                 350

Pro Glu Gly Asp Asp Lys Pro Gly Ala Val Gly Lys Val Val Pro Phe
        355                 360                 365

Phe Glu Ala Lys Val Val Asp Leu Asp Thr Gly Lys Thr Leu Gly Val
    370                 375                 380

Asn Gln Arg Gly Glu Leu Cys Val Arg Gly Pro Met Ile Met Ser Gly
385                 390                 395                 400

Tyr Val Asn Asn Pro Glu Ala Thr Asn Ala Leu Ile Asp Lys Asp Gly
                405                 410                 415

Trp Leu His Ser Gly Asp Ile Ala Tyr Trp Asp Glu Asp Glu His Phe
            420                 425                 430

Phe Ile Val Asp Arg Leu Lys Ser Leu Ile Lys Tyr Lys Gly Tyr Gln
        435                 440                 445

Val Ala Pro Ala Glu Leu Glu Ser Ile Leu Leu Gln His Pro Asn Ile
    450                 455                 460

Phe Asp Ala Gly Val Ala Gly Leu Pro Asp Asp Asp Ala Gly Glu Leu
465                 470                 475                 480

Pro Ala Ala Val Val Val Leu Glu His Gly Lys Thr Met Thr Glu Lys
                485                 490                 495
```

Glu Ile Val Asp Tyr Val Ala Ser Gln Val Thr Thr Ala Lys Lys Leu
500 505 510

Arg Gly Gly Val Val Phe Val Asp Glu Val Pro Lys Gly Leu Thr Gly
515 520 525

Lys Leu Asp Ala Arg Lys Ile Arg Glu Ile Leu Ile Lys Ala Lys Lys
530 535 540

Gly Gly Lys Ile Ala Val
545 550

<210> 30
<211> 933
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 30
atggcttcca aggtgtacga ccccgagcaa cgcaaacgca tgatcactgg gcctcagtgg 60

tgggctcgct gcaagcaaat gaacgtgctg gactccttca tcaactacta tgattccgag 120

aagcacgccg agaacgccgt gatttttctg catggtaacg ctgcctccag ctacctgtgg 180

aggcacgtcg tgcctcacat cgagcccgtg gctagatgca tcatccctga tctgatcgga 240

atgggtaagt ccggcaagag cgggaatggc tcatatcgcc tcctggatca ctacaagtac 300

ctcaccgctt ggttcgagct gctgaacctt ccaaagaaaa tcatctttgt gggccacgac 360

tgggggggctt gtctggcctt tcactactcc tacgagcacc aagacaagat caaggccatc 420

gtccatgctg agagtgtcgt ggacgtgatc gagtcctggg acgagtggcc tgacatcgag 480

gaggatatcg ccctgatcaa gagcgaagag ggcgagaaaa tggtgcttga gaataacttc 540

ttcgtcgaga ccatgctccc aagcaagatc atgcggaaac tggagcctga ggagttcgct 600

gcctacctgg agccattcaa ggagaagggc gaggttagac ggcctaccct ctcctggcct 660

cgcgagatcc ctctcgttaa gggaggcaag cccgacgtcg tccagattgt ccgcaactac 720

aacgcctacc ttcgggccag cgacgatctg cctaagatgt tcatcgagtc cgaccctggg 780

ttcttttcca acgctattgt cgagggagct aagaagttcc ctaacaccga gttcgtgaag 840

gtgaagggcc tccacttcag ccaggaggac gctccagatg aaatgggtaa gtacatcaag 900

agcttcgtgg agcgcgtgct gaagaacgag cag 933

<210> 31
<211> 311
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 31

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Met Ala Ser Lys Val Tyr Asp Pro Glu Gln Arg Lys Arg Met Ile Thr
1               5                  10                  15

Gly Pro Gln Trp Trp Ala Arg Cys Lys Gln Met Asn Val Leu Asp Ser
            20                  25                  30

Phe Ile Asn Tyr Tyr Asp Ser Glu Lys His Ala Glu Asn Ala Val Ile
        35                  40                  45

Phe Leu His Gly Asn Ala Ala Ser Ser Tyr Leu Trp Arg His Val Val
    50                  55                  60

Pro His Ile Glu Pro Val Ala Arg Cys Ile Ile Pro Asp Leu Ile Gly
65                  70                  75                  80

Met Gly Lys Ser Gly Lys Ser Gly Asn Gly Ser Tyr Arg Leu Leu Asp
                85                  90                  95

His Tyr Lys Tyr Leu Thr Ala Trp Phe Glu Leu Leu Asn Leu Pro Lys
            100                 105                 110

Lys Ile Ile Phe Val Gly His Asp Trp Gly Ala Cys Leu Ala Phe His
        115                 120                 125

Tyr Ser Tyr Glu His Gln Asp Lys Ile Lys Ala Ile Val His Ala Glu
    130                 135                 140

Ser Val Val Asp Val Ile Glu Ser Trp Asp Glu Trp Pro Asp Ile Glu
145                 150                 155                 160

Glu Asp Ile Ala Leu Ile Lys Ser Glu Glu Gly Glu Lys Met Val Leu
                165                 170                 175

Glu Asn Asn Phe Phe Val Glu Thr Met Leu Pro Ser Lys Ile Met Arg
            180                 185                 190

Lys Leu Glu Pro Glu Glu Phe Ala Ala Tyr Leu Glu Pro Phe Lys Glu
        195                 200                 205

Lys Gly Glu Val Arg Arg Pro Thr Leu Ser Trp Pro Arg Glu Ile Pro
    210                 215                 220

Leu Val Lys Gly Gly Lys Pro Asp Val Val Gln Ile Val Arg Asn Tyr
225                 230                 235                 240

Asn Ala Tyr Leu Arg Ala Ser Asp Asp Leu Pro Lys Met Phe Ile Glu
                245                 250                 255

Ser Asp Pro Gly Phe Phe Ser Asn Ala Ile Val Glu Gly Ala Lys Lys
            260                 265                 270
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Phe Pro Asn Thr Glu Phe Val Lys Val Lys Gly Leu His Phe Ser Gln
275 280 285

Glu Asp Ala Pro Asp Glu Met Gly Lys Tyr Ile Lys Ser Phe Val Glu
290 295 300

Arg Val Leu Lys Asn Glu Gln
305 310

<210> 32
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 32
atgcttggtc tgtcggagca aagcgtgtcc atctcgcgct gcgctgggac gcgcctgccc 60

gccttgctgg acgagcagca ggtgaacgtc ctgctctacg acatgaacgg ctgctactca 120

cgcctcaagg agctggtgcc caccctgccc cagaaccgca aagtgagcaa ggtggagatc 180

ctgcagcatg taatcgacta catcagggac ctgcagctgg agctgaactc ggagtctgaa 240

gtcgggacca ccggaggccg gggactgcct gtccgcgccc cgctcagcac cctgaacggc 300

gagatcagtg ccttggcggc cgaggcggca tgtgttccag ccgacgatcg catcttgtgt 360

cgcgtttctc ttgagaatct ttattttcag gcgtctggag gtggtggcgg agcgatcgcc 420

atggcttcca aggtgtacga ccccgagcaa cgcaaacgca tgatcactgg gcctcagtgg 480

tgggctcgct gcaagcaaat gaacgtgctg gactccttca tcaactacta tgattccgag 540

aagcacgccg agaacgccgt gatttttctg catggtaacg ctgcctccag ctacctgtgg 600

aggcacgtcg tgcctcacat cgagcccgtg gctagatgca tcatccctga tctgatcgga 660

atgggtaagt ccggcaagag cgggaatggc tcatatcgcc tcctggatca ctacaagtac 720

ctcaccgctt ggttcgagct gctgaacctt ccaaagaaaa tcatctttgt gggccacgac 780

tgggggggctt gtctggcctt tcactactcc tacgagcacc aagacaagat caaggccatc 840

gtccatgctg agagtgtcgt ggacgtgatc gagtcctggg acgagtggcc tgacatcgag 900

gaggatatcg ccctgatcaa gagcgaagag ggcgagaaaa tggtgcttga gaataacttc 960

ttcgtcgaga ccatgctccc aagcaagatc atgcggaaac tggagcctga ggagttcgct 1020

gcctacctgg agccattcaa ggagaagggc gaggttagac ggcctaccct ctcctggcct 1080

cgcgagatcc ctctcgttaa gggaggcaag cccgacgtcg tccagattgt ccgcaactac 1140

aacgcctacc ttcgggccag cgacgatctg cctaagatgt tcatcgagtc cgaccctggg 1200

ttcttttcca acgctattgt cgagggagct aagaagttcc ctaacaccga gttcgtgaag 1260

gtgaagggcc tccacttcag ccaggaggac gctccagatg aaatgggtaa gtacatcaag 1320

agcttcgtgg agcgcgtgct gaagaacgag caggtttctc tcgagccaac cactgaggat 1380

ctgtactttc agagcgataa cgatggatcc gaaatcggta ctggctttcc attcgacccc 1440

cattatgtgg aagtcctggg cgagcgcatg cactacgtcg atgttggtcc gcgcgatggc 1500

acccctgtgc tgttcctgca cggtaacccg acctcctcct acgtgtggcg caacatcatc 1560

ccgcatgttg caccgaccca tcgctgcatt gctccagacc tgatcggtat gggcaaatcc 1620

gacaaaccag acctgggtta tttcttcgac gaccacgtcc gcttcatgga tgccttcatc 1680

gaagccctgg gtctggaaga ggtcgtcctg gtcattcacg actggggctc cgctctgggt 1740

ttccactggg ccaagcgcaa tccagagcgc gtcaaaggta ttgcatttat ggagttcatc 1800

cgccctatcc cgacctggga cgaatggcca gaatttgccc gcgagacctt ccaggccttc 1860

cgcaccaccg acgtcggccg caagctgatc atcgatcaga acgtttttat cgagggtacg 1920

ctgccgatgg gtgtcgtccg cccgctgact gaagtcgaga tggaccatta ccgcgagccg 1980

ttcctgaatc ctgttgaccg cgagccactg tggcgcttcc caaacgagct gccaatcgcc 2040

ggtgagccag cgaacatcgt cgcgctggtc gaagaataca tggactggct gcaccagtcc 2100

cctgtcccga agctgctgtt ctggggcacc ccaggcgttc tgatcccacc ggccgaagcc 2160

gctcgcctgg ccaaaagcct gcctaactgc aaggctgtgg acatcggccc gggtctgaat 2220

ctgctgcaag aagacaaccc ggacctgatc ggcagcgaga tcgcgcgctg gctgtctact 2280

ctggagattt ccggt 2295

<210> 33
<211> 765
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 33
Met Leu Gly Leu Ser Glu Gln Ser Val Ser Ile Ser Arg Cys Ala Gly
1 5 10 15

Thr Arg Leu Pro Ala Leu Leu Asp Glu Gln Gln Val Asn Val Leu Leu
20 25 30

Tyr Asp Met Asn Gly Cys Tyr Ser Arg Leu Lys Glu Leu Val Pro Thr
35 40 45

Leu Pro Gln Asn Arg Lys Val Ser Lys Val Glu Ile Leu Gln His Val
50 55 60

Ile Asp Tyr Ile Arg Asp Leu Gln Leu Glu Leu Asn Ser Glu Ser Glu
65 70 75 80

Val Gly Thr Thr Gly Gly Arg Gly Leu Pro Val Arg Ala Pro Leu Ser
85 90 95

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Thr Leu Asn Gly Glu Ile Ser Ala Leu Ala Ala Glu Ala Ala Cys Val
            100                 105                 110

Pro Ala Asp Asp Arg Ile Leu Cys Arg Val Ser Leu Glu Asn Leu Tyr
        115                 120                 125

Phe Gln Ala Ser Gly Gly Gly Gly Gly Ala Ile Ala Met Ala Ser Lys
    130                 135                 140

Val Tyr Asp Pro Glu Gln Arg Lys Arg Met Ile Thr Gly Pro Gln Trp
145                 150                 155                 160

Trp Ala Arg Cys Lys Gln Met Asn Val Leu Asp Ser Phe Ile Asn Tyr
                165                 170                 175

Tyr Asp Ser Glu Lys His Ala Glu Asn Ala Val Ile Phe Leu His Gly
            180                 185                 190

Asn Ala Ala Ser Ser Tyr Leu Trp Arg His Val Val Pro His Ile Glu
        195                 200                 205

Pro Val Ala Arg Cys Ile Ile Pro Asp Leu Ile Gly Met Gly Lys Ser
    210                 215                 220

Gly Lys Ser Gly Asn Gly Ser Tyr Arg Leu Leu Asp His Tyr Lys Tyr
225                 230                 235                 240

Leu Thr Ala Trp Phe Glu Leu Leu Asn Leu Pro Lys Lys Ile Ile Phe
                245                 250                 255

Val Gly His Asp Trp Gly Ala Cys Leu Ala Phe His Tyr Ser Tyr Glu
            260                 265                 270

His Gln Asp Lys Ile Lys Ala Ile Val His Ala Glu Ser Val Val Asp
        275                 280                 285

Val Ile Glu Ser Trp Asp Glu Trp Pro Asp Ile Glu Glu Asp Ile Ala
    290                 295                 300

Leu Ile Lys Ser Glu Glu Gly Glu Lys Met Val Leu Glu Asn Asn Phe
305                 310                 315                 320

Phe Val Glu Thr Met Leu Pro Ser Lys Ile Met Arg Lys Leu Glu Pro
                325                 330                 335

Glu Glu Phe Ala Ala Tyr Leu Glu Pro Phe Lys Glu Lys Gly Glu Val
            340                 345                 350

Arg Arg Pro Thr Leu Ser Trp Pro Arg Glu Ile Pro Leu Val Lys Gly
        355                 360                 365
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Gly Lys Pro Asp Val Val Gln Ile Val Arg Asn Tyr Asn Ala Tyr Leu
    370                 375                 380

Arg Ala Ser Asp Asp Leu Pro Lys Met Phe Ile Glu Ser Asp Pro Gly
385                 390                 395                 400

Phe Phe Ser Asn Ala Ile Val Glu Gly Ala Lys Lys Phe Pro Asn Thr
                405                 410                 415

Glu Phe Val Lys Val Lys Gly Leu His Phe Ser Gln Glu Asp Ala Pro
            420                 425                 430

Asp Glu Met Gly Lys Tyr Ile Lys Ser Phe Val Glu Arg Val Leu Lys
        435                 440                 445

Asn Glu Gln Val Ser Leu Glu Pro Thr Thr Glu Asp Leu Tyr Phe Gln
    450                 455                 460

Ser Asp Asn Asp Gly Ser Glu Ile Gly Thr Gly Phe Pro Phe Asp Pro
465                 470                 475                 480

His Tyr Val Glu Val Leu Gly Glu Arg Met His Tyr Val Asp Val Gly
                485                 490                 495

Pro Arg Asp Gly Thr Pro Val Leu Phe Leu His Gly Asn Pro Thr Ser
            500                 505                 510

Ser Tyr Val Trp Arg Asn Ile Ile Pro His Val Ala Pro Thr His Arg
        515                 520                 525

Cys Ile Ala Pro Asp Leu Ile Gly Met Gly Lys Ser Asp Lys Pro Asp
    530                 535                 540

Leu Gly Tyr Phe Phe Asp Asp His Val Arg Phe Met Asp Ala Phe Ile
545                 550                 555                 560

Glu Ala Leu Gly Leu Glu Glu Val Val Leu Val Ile His Asp Trp Gly
                565                 570                 575

Ser Ala Leu Gly Phe His Trp Ala Lys Arg Asn Pro Glu Arg Val Lys
            580                 585                 590

Gly Ile Ala Phe Met Glu Phe Ile Arg Pro Ile Pro Thr Trp Asp Glu
        595                 600                 605

Trp Pro Glu Phe Ala Arg Glu Thr Phe Gln Ala Phe Arg Thr Thr Asp
    610                 615                 620

Val Gly Arg Lys Leu Ile Ile Asp Gln Asn Val Phe Ile Glu Gly Thr
625                 630                 635                 640
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Leu Pro Met Gly Val Val Arg Pro Leu Thr Glu Val Glu Met Asp His
645 650 655

Tyr Arg Glu Pro Phe Leu Asn Pro Val Asp Arg Glu Pro Leu Trp Arg
660 665 670

Phe Pro Asn Glu Leu Pro Ile Ala Gly Glu Pro Ala Asn Ile Val Ala
675 680 685

Leu Val Glu Glu Tyr Met Asp Trp Leu His Gln Ser Pro Val Pro Lys
690 695 700

Leu Leu Phe Trp Gly Thr Pro Gly Val Leu Ile Pro Pro Ala Glu Ala
705 710 715 720

Ala Arg Leu Ala Lys Ser Leu Pro Asn Cys Lys Ala Val Asp Ile Gly
725 730 735

Pro Gly Leu Asn Leu Leu Gln Glu Asp Asn Pro Asp Leu Ile Gly Ser
740 745 750

Glu Ile Ala Arg Trp Leu Ser Thr Leu Glu Ile Ser Gly
755 760 765

<210> 34
<211> 1455
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 34
atggtgatta cattggagga tttcgttgga gactggcggc agacagctgg atacaaccaa 60

gatcaagtgt tagaacaagg aggagtgtct agtctgttcc aaaagctggg agtgtcaatc 120

accccaatcc agaaaattgt gctgtctggg gagaatgggt taaaaattga tattcatgtc 180

atcatccctt acgagggact cagtggtttt caaatgggtc tgattgaaat gatcttcaaa 240

gttgtttacc cagtggatga tcatcatttc aaggttattc tccattatgg tacactcgtt 300

attgacggtg tgacaccaaa catgattgac tactttggac gcccttacga gggaattgct 360

gtgtttgacg gcaagaagat cacagttact ggaactctgt ggaacggcaa caagatcatt 420

gatgagcgcc tgatcaaccc agatggttca ctcctcttcc gcgttactat caatggagtc 480

accggatggc gcctttgcga gcgtattctt gccggatatc tcgagccaac cactgaggat 540

ctgtactttc agagcgataa cgatggatcc gaaatcggta ctggctttcc attcgacccc 600

cattatgtgg aagtcctggg cgagcgcatg cactacgtcg atgttggtcc gcgcgatggc 660

acccctgtgc tgttcctgca cggtaacccg acctcctcct acgtgtggcg caacatcatc 720

ccgcatgttg caccgaccca tcgctgcatt gctccagacc tgatcggtat gggcaaatcc 780

gacaaaccag acctgggtta tttcttcgac gaccacgtcc gcttcatgga tgccttcatc 840

gaagccctgg gtctggaaga ggtcgtcctg gtcattcacg actggggctc cgctctgggt 900

ttccactggg ccaagcgcaa tccagagcgc gtcaaaggta ttgcatttat ggagttcatc 960

cgccctatcc cgacctggga cgaatggcca gaatttgccc gcgagacctt ccaggccttc 1020

cgcaccaccg acgtcggccg caagctgatc atcgatcaga acgtttttat cgagggtacg 1080

ctgccgatgg gtgtcgtccg cccgctgact gaagtcgaga tggaccatta ccgcgagccg 1140

ttcctgaatc ctgttgaccg cgagccactg tggcgcttcc caaacgagct gccaatcgcc 1200

ggtgagccag cgaacatcgt cgcgctggtc gaagaataca tggactggct gcaccagtcc 1260

cctgtcccga agctgctgtt ctggggcacc ccaggcgttc tgatcccacc ggccgaagcc 1320

gctcgcctgg ccaaaagcct gcctaactgc aaggctgtgg acatcggccc gggtctgaat 1380

ctgctgcaag aagacaaccc ggacctgatc ggcagcgaga tcgcgcgctg gctgtctact 1440

ctggagattt ccggt 1455

<210> 35
<211> 485
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 35
Met Val Ile Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala
1 5 10 15

Gly Tyr Asn Gln Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu
20 25 30

Phe Gln Lys Leu Gly Val Ser Ile Thr Pro Ile Gln Lys Ile Val Leu
35 40 45

Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr
50 55 60

Glu Gly Leu Ser Gly Phe Gln Met Gly Leu Ile Glu Met Ile Phe Lys
65 70 75 80

Val Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu His Tyr
85 90 95

Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe
100 105 110

Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr
115 120 125

Val Thr Gly Thr Leu Trp Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu

130 135 140

Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val
145 150 155 160

Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala Gly Tyr Leu Glu Pro
165 170 175

Thr Thr Glu Asp Leu Tyr Phe Gln Ser Asp Asn Asp Gly Ser Glu Ile
180 185 190

Gly Thr Gly Phe Pro Phe Asp Pro His Tyr Val Glu Val Leu Gly Glu
195 200 205

Arg Met His Tyr Val Asp Val Gly Pro Arg Asp Gly Thr Pro Val Leu
210 215 220

Phe Leu His Gly Asn Pro Thr Ser Ser Tyr Val Trp Arg Asn Ile Ile
225 230 235 240

Pro His Val Ala Pro Thr His Arg Cys Ile Ala Pro Asp Leu Ile Gly
245 250 255

Met Gly Lys Ser Asp Lys Pro Asp Leu Gly Tyr Phe Phe Asp Asp His
260 265 270

Val Arg Phe Met Asp Ala Phe Ile Glu Ala Leu Gly Leu Glu Glu Val
275 280 285

Val Leu Val Ile His Asp Trp Gly Ser Ala Leu Gly Phe His Trp Ala
290 295 300

Lys Arg Asn Pro Glu Arg Val Lys Gly Ile Ala Phe Met Glu Phe Ile
305 310 315 320

Arg Pro Ile Pro Thr Trp Asp Glu Trp Pro Glu Phe Ala Arg Glu Thr
325 330 335

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

Gln Asn Val Phe Ile Glu Gly Thr Leu Pro Met Gly Val Val Arg Pro
355 360 365

Leu Thr Glu Val Glu Met Asp His Tyr Arg Glu Pro Phe Leu Asn Pro
370 375 380

Val Asp Arg Glu Pro Leu Trp Arg Phe Pro Asn Glu Leu Pro Ile Ala
385 390 395 400

Gly Glu Pro Ala Asn Ile Val Ala Leu Val Glu Glu Tyr Met Asp Trp

405 410 415

Leu His Gln Ser Pro Val Pro Lys Leu Leu Phe Trp Gly Thr Pro Gly
420 425 430

Val Leu Ile Pro Pro Ala Glu Ala Ala Arg Leu Ala Lys Ser Leu Pro
435 440 445

Asn Cys Lys Ala Val Asp Ile Gly Pro Gly Leu Asn Leu Leu Gln Glu
450 455 460

Asp Asn Pro Asp Leu Ile Gly Ser Glu Ile Ala Arg Trp Leu Ser Thr
465 470 475 480

Leu Glu Ile Ser Gly
485

<210> 36
<211> 1455
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 36
atggtgttta cattggagga tttcgttgga gactggcggc agacagctgg atacaaccta 60

gatcaagtgt tagaacaagg aggattgtct agtctgttcc aaaagctggg agtgtcagtc 120

accccaatcc agaaaattgt gctgtctggg gagaatgggt taaaaattga tattcatgtc 180

atcatccctt acgagggact cagtggttat caaatgggtc agattgaaaa gatcttcaaa 240

gttgtttacc cagtggatga tcatcatttc aaggttattc tccattatgg tacactcgtt 300

attgacggtg tgacaccaaa catgattgac tactttggac gcccttacga gggaattgct 360

gtgtttgacg gcaagaagat cacagttact ggaactctgt ggaacggcaa caagatcatt 420

gatgagcgcc tgatcaaccc agatggttca ctcctcttcc gcgttactat caatggagtc 480

accggatggc gcctttgcga gcgtattctt gccggatatc tcgagccaac cactgaggat 540

ctgtactttc agagcgataa cgatggatcc gaaatcggta ctggctttcc attcgacccc 600

cattatgtgg aagtcctggg cgagcgcatg cactacgtcg atgttggtcc gcgcgatggc 660

acccctgtgc tgttcctgca cggtaacccg acctcctcct acgtgtggcg caacatcatc 720

ccgcatgttg caccgaccca tcgctgcatt gctccagacc tgatcggtat gggcaaatcc 780

gacaaaccag acctgggtta tttcttcgac gaccacgtcc gcttcatgga tgccttcatc 840

gaagccctgg gtctggaaga ggtcgtcctg gtcattcacg actggggctc cgctctgggt 900

ttccactggg ccaagcgcaa tccagagcgc gtcaaaggta ttgcatttat ggagttcatc 960

cgccctatcc cgacctggga cgaatggcca gaatttgccc gcgagacctt ccaggccttc 1020

cgcaccaccg acgtcggccg caagctgatc atcgatcaga acgtttttat cgagggtacg 1080

ctgccgatgg gtgtcgtccg cccgctgact gaagtcgaga tggaccatta ccgcgagccg 1140

ttcctgaatc ctgttgaccg cgagccactg tggcgcttcc caaacgagct gccaatcgcc 1200

ggtgagccag cgaacatcgt cgcgctggtc gaagaataca tggactggct gcaccagtcc 1260

cctgtcccga agctgctgtt ctggggcacc ccaggcgttc tgatcccacc ggccgaagcc 1320

gctcgcctgg ccaaaagcct gcctaactgc aaggctgtgg acatcggccc gggtctgaat 1380

ctgctgcaag aagacaaccc ggacctgatc ggcagcgaga tcgcgcgctg gctgtctact 1440

ctggagattt ccggt 1455

<210> 37
<211> 485
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 37
Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala
1 5 10 15

Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Leu Ser Ser Leu
20 25 30

Phe Gln Lys Leu Gly Val Ser Val Thr Pro Ile Gln Lys Ile Val Leu
35 40 45

Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr
50 55 60

Glu Gly Leu Ser Gly Tyr Gln Met Gly Gln Ile Glu Lys Ile Phe Lys
65 70 75 80

Val Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu His Tyr
85 90 95

Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe
100 105 110

Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr
115 120 125

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

Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val
145 150 155 160

Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala Gly Tyr Leu Glu Pro
165 170 175

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Thr Thr Glu Asp Leu Tyr Phe Gln Ser Asp Asn Asp Gly Ser Glu Ile
            180                 185                 190

Gly Thr Gly Phe Pro Phe Asp Pro His Tyr Val Glu Val Leu Gly Glu
        195                 200                 205

Arg Met His Tyr Val Asp Val Gly Pro Arg Asp Gly Thr Pro Val Leu
    210                 215                 220

Phe Leu His Gly Asn Pro Thr Ser Ser Tyr Val Trp Arg Asn Ile Ile
225                 230                 235                 240

Pro His Val Ala Pro Thr His Arg Cys Ile Ala Pro Asp Leu Ile Gly
                245                 250                 255

Met Gly Lys Ser Asp Lys Pro Asp Leu Gly Tyr Phe Phe Asp Asp His
            260                 265                 270

Val Arg Phe Met Asp Ala Phe Ile Glu Ala Leu Gly Leu Glu Glu Val
        275                 280                 285

Val Leu Val Ile His Asp Trp Gly Ser Ala Leu Gly Phe His Trp Ala
    290                 295                 300

Lys Arg Asn Pro Glu Arg Val Lys Gly Ile Ala Phe Met Glu Phe Ile
305                 310                 315                 320

Arg Pro Ile Pro Thr Trp Asp Glu Trp Pro Glu Phe Ala Arg Glu Thr
                325                 330                 335

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

Gln Asn Val Phe Ile Glu Gly Thr Leu Pro Met Gly Val Val Arg Pro
        355                 360                 365

Leu Thr Glu Val Glu Met Asp His Tyr Arg Glu Pro Phe Leu Asn Pro
    370                 375                 380

Val Asp Arg Glu Pro Leu Trp Arg Phe Pro Asn Glu Leu Pro Ile Ala
385                 390                 395                 400

Gly Glu Pro Ala Asn Ile Val Ala Leu Val Glu Glu Tyr Met Asp Trp
                405                 410                 415

Leu His Gln Ser Pro Val Pro Lys Leu Leu Phe Trp Gly Thr Pro Gly
            420                 425                 430

Val Leu Ile Pro Pro Ala Glu Ala Ala Arg Leu Ala Lys Ser Leu Pro
        435                 440                 445
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Asn Cys Lys Ala Val Asp Ile Gly Pro Gly Leu Asn Leu Leu Gln Glu
450 455 460

Asp Asn Pro Asp Leu Ile Gly Ser Glu Ile Ala Arg Trp Leu Ser Thr
465 470 475 480

Leu Glu Ile Ser Gly
485

<210> 38
<211> 1455
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 38
atggtgttta cattggagga tttcgttgga gactggcggc agacagctgg atacaaccta 60

gatcaagtgt tagaacaagg aggagtgtct agtctgttcc aaaagctggg agtgtcaatc 120

accccaatcc agaaaattgt gctgtctggg gagaatgggt taaaaattga tattcatgtc 180

atcatccctt acgagggact cagtggttat caaatgggtc agattgaaaa gatcttcaaa 240

gttgtttacc cagtggatga tcatcatttc aaggttattc tccattatgg tacactcgtt 300

attgacggtg tgacaccaaa catgattgac tactttggac gcccttacga gggaattgct 360

gtgtttgacg gcaagaagat cacagttact ggaactctgt ggaacggcaa caagatcatt 420

gatgagcgcc tgatcaaccc agatggttca ctcctcttcc gcgttactat caatggagtc 480

accggatggc gcctttgcga gcgtattctt gccggatatc tcgagccaac cactgaggat 540

ctgtactttc agagcgataa cgatggatcc gaaatcggta ctggctttcc attcgacccc 600

cattatgtgg aagtcctggg cgagcgcatg cactacgtcg atgttggtcc gcgcgatggc 660

acccctgtgc tgttcctgca cggtaacccg acctcctcct acgtgtggcg caacatcatc 720

ccgcatgttg caccgaccca tcgctgcatt gctccagacc tgatcggtat gggcaaatcc 780

gacaaaccag acctgggtta tttcttcgac gaccacgtcc gcttcatgga tgccttcatc 840

gaagccctgg gtctggaaga ggtcgtcctg gtcattcacg actggggctc cgctctgggt 900

ttccactggg ccaagcgcaa tccagagcgc gtcaaaggta ttgcatttat ggagttcatc 960

cgccctatcc cgacctggga cgaatggcca gaatttgccc gcgagacctt ccaggccttc 1020

cgcaccaccg acgtcggccg caagctgatc atcgatcaga acgtttttat cgagggtacg 1080

ctgccgatgg gtgtcgtccg cccgctgact gaagtcgaga tggaccatta ccgcgagccg 1140

ttcctgaatc ctgttgaccg cgagccactg tggcgcttcc caaacgagct gccaatcgcc 1200

ggtgagccag cgaacatcgt cgcgctggtc gaagaataca tggactggct gcaccagtcc 1260

cctgtcccga agctgctgtt ctggggcacc ccaggcgttc tgatcccacc ggccgaagcc 1320

gctcgcctgg ccaaaagcct gcctaactgc aaggctgtgg acatcggccc gggtctgaat 1380

ctgctgcaag aagacaaccc ggacctgatc ggcagcgaga tcgcgcgctg gctgtctact 1440

ctggagattt ccggt 1455

<210> 39
<211> 485
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 39

Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala
1 5 10 15

Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu
20 25 30

Phe Gln Lys Leu Gly Val Ser Ile Thr Pro Ile Gln Lys Ile Val Leu
35 40 45

Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr
50 55 60

Glu Gly Leu Ser Gly Tyr Gln Met Gly Gln Ile Glu Lys Ile Phe Lys
65 70 75 80

Val Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu His Tyr
85 90 95

Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe
100 105 110

Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr
115 120 125

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

Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val
145 150 155 160

Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala Gly Tyr Leu Glu Pro
165 170 175

Thr Thr Glu Asp Leu Tyr Phe Gln Ser Asp Asn Asp Gly Ser Glu Ile
180 185 190

Gly Thr Gly Phe Pro Phe Asp Pro His Tyr Val Glu Val Leu Gly Glu
195 200 205

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Arg Met His Tyr Val Asp Val Gly Pro Arg Asp Gly Thr Pro Val Leu
    210                 215                 220

Phe Leu His Gly Asn Pro Thr Ser Ser Tyr Val Trp Arg Asn Ile Ile
225                 230                 235                 240

Pro His Val Ala Pro Thr His Arg Cys Ile Ala Pro Asp Leu Ile Gly
                245                 250                 255

Met Gly Lys Ser Asp Lys Pro Asp Leu Gly Tyr Phe Phe Asp Asp His
            260                 265                 270

Val Arg Phe Met Asp Ala Phe Ile Glu Ala Leu Gly Leu Glu Glu Val
        275                 280                 285

Val Leu Val Ile His Asp Trp Gly Ser Ala Leu Gly Phe His Trp Ala
    290                 295                 300

Lys Arg Asn Pro Glu Arg Val Lys Gly Ile Ala Phe Met Glu Phe Ile
305                 310                 315                 320

Arg Pro Ile Pro Thr Trp Asp Glu Trp Pro Glu Phe Ala Arg Glu Thr
                325                 330                 335

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

Gln Asn Val Phe Ile Glu Gly Thr Leu Pro Met Gly Val Val Arg Pro
        355                 360                 365

Leu Thr Glu Val Glu Met Asp His Tyr Arg Glu Pro Phe Leu Asn Pro
    370                 375                 380

Val Asp Arg Glu Pro Leu Trp Arg Phe Pro Asn Glu Leu Pro Ile Ala
385                 390                 395                 400

Gly Glu Pro Ala Asn Ile Val Ala Leu Val Glu Glu Tyr Met Asp Trp
                405                 410                 415

Leu His Gln Ser Pro Val Pro Lys Leu Leu Phe Trp Gly Thr Pro Gly
            420                 425                 430

Val Leu Ile Pro Pro Ala Glu Ala Ala Arg Leu Ala Lys Ser Leu Pro
        435                 440                 445

Asn Cys Lys Ala Val Asp Ile Gly Pro Gly Leu Asn Leu Leu Gln Glu
    450                 455                 460

Asp Asn Pro Asp Leu Ile Gly Ser Glu Ile Ala Arg Trp Leu Ser Thr
465                 470                 475                 480
```

Leu Glu Ile Ser Gly
485

<210> 40
<211> 1876
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 40
atgcttggtc tgtcggagca aagcgtgtcc atctcgcgct gcgctgggac gcgcctgccc 60

gccttgctgg acgagcagca ggtgaacgtc ctgctctacg acatgaacgg ctgctactca 120

cgcctcaagg agctggtgcc caccctgccc cagaaccgca aagtgagcaa ggtggagatc 180

ctgcagcatg taatcgacta catcagggac ctgcagctgg agctgaactc ggagtctgaa 240

gtcgggacca ccggaggccg gggactgcct gtccgcgccc cgctcagcac cctgaacggc 300

gagatcagtg ccttggcggc cgaggcggca tgtgttccag ccgacgatcg catcttgtgt 360

cgcgtttctc ttgagaatct ttattttcag gcgtctggag gtggtggcgg agcgatcgcc 420

atggtgttta cactcgaaga tttcgtaggg gactggcggc agacagccgg ctacaacctg 480

gaccaagtcc ttgagcaggg cggtctgtcc agtttgtttc agaaactcgg ggtgtccgta 540

acaccgatcc aaaagattgt cctgagcggt gaaaacggcc tgaagatcga catccatgtc 600

atcatcccgt atgaaggtct gagcggctat cagatgggcc agatcgaaaa aatttttaag 660

gtggtgtacc ctgtggatga tcatcacttt aaggtgattc tgcactatgg cacactggta 720

atcgacgggg ttacgccgaa catgatcgac tatttcggac ggccgtatga aggcatcgcc 780

gtgttcgacg gcaaaaagat cactgtaacc gggaccctgt ggaacggcaa caaaattatc 840

gacgagcgcc tgatcaaccc cgacggctcc ctgctgttcc gcgtaaccat caacggagtg 900

accggctggc ggctgtgcga gcgtattctt gccggatatc tcgagccaac cactgaggat 960

ctgtactttc agagcgataa cgatggatcc gaaatcggta ctggctttcc attcgacccc 1020

cattatgtgg aagtcctggg cgagcgcatg cactacgtcg atgttggtcc gcgcgatggc 1080

acccctgtgc tgttcctgca cggtaacccg acctcctcct acgtgtggcg caacatcatc 1140

ccgcatgttg caccgaccca tcgctgcatt gctccagacc tgatcggtat gggcaaatcc 1200

gacaaaccag acctgggtta tttcttcgac gaccacgtcc gcttcatgga tgccttcatc 1260

gaagccctgg gtctggaaga ggtcgtcctg gtcattcacg actggggctc cgctctgggt 1320

ttccactggg ccaagcgcaa tccagagcgc gtcaaaggta ttgcatttat ggagttcatc 1380

cgccctatcc cgacctggga cgaatggcca gaatttgccc gcgagacctt ccaggccttc 1440

cgcaccaccg acgtcggccg caagctgatc atcgatcaga acgtttttat cgagggtacg 1500

ctgccgatgg gtgtcgtccg cccgctgact gaagtcgaga tggaccatta ccgcgagccg 1560

ttcctgaatc ctgttgaccg cgagccactg tggcgcttcc caaacgagct gccaatcgcc 1620

ggtgagccag cgaacatcgt cgcgctggtc gaagaataca tggactggct gcaccagtcc 1680

cctgtcccga agctgctgtt ctggggcacc ccaggcgttc tgatcccacc ggccgaagcc 1740

gctcgcctgg ccaaaagcct gcctaactgc aaggctgtgg acatcggccc gggtctgaat 1800

ctgctgcaag aagacaaccc ggacctgatc ggcagcgaga tcgcgcgctg gctgtctact 1860

ctggagattt ccggtt 1876

<210> 41
<211> 625
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 41

Met Leu Gly Leu Ser Glu Gln Ser Val Ser Ile Ser Arg Cys Ala Gly
1 5 10 15

Thr Arg Leu Pro Ala Leu Leu Asp Glu Gln Gln Val Asn Val Leu Leu
20 25 30

Tyr Asp Met Asn Gly Cys Tyr Ser Arg Leu Lys Glu Leu Val Pro Thr
35 40 45

Leu Pro Gln Asn Arg Lys Val Ser Lys Val Glu Ile Leu Gln His Val
50 55 60

Ile Asp Tyr Ile Arg Asp Leu Gln Leu Glu Leu Asn Ser Glu Ser Glu
65 70 75 80

Val Gly Thr Thr Gly Gly Arg Gly Leu Pro Val Arg Ala Pro Leu Ser
85 90 95

Thr Leu Asn Gly Glu Ile Ser Ala Leu Ala Ala Glu Ala Ala Cys Val
100 105 110

Pro Ala Asp Asp Arg Ile Leu Cys Arg Val Ser Leu Glu Asn Leu Tyr
115 120 125

Phe Gln Ala Ser Gly Gly Gly Gly Gly Ala Ile Ala Met Val Phe Thr
130 135 140

Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu
145 150 155 160

Asp Gln Val Leu Glu Gln Gly Gly Leu Ser Ser Leu Phe Gln Lys Leu
165 170 175

Gly Val Ser Val Thr Pro Ile Gln Lys Ile Val Leu Ser Gly Glu Asn
180 185 190

```
Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr Glu Gly Leu Ser
        195                 200                 205

Gly Tyr Gln Met Gly Gln Ile Glu Lys Ile Phe Lys Val Val Tyr Pro
    210                 215                 220

Val Asp Asp His His Phe Lys Val Ile Leu His Tyr Gly Thr Leu Val
225                 230                 235                 240

Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr
                245                 250                 255

Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr
            260                 265                 270

Leu Trp Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp
        275                 280                 285

Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg
    290                 295                 300

Leu Cys Glu Arg Ile Leu Ala Gly Tyr Leu Glu Pro Thr Thr Glu Asp
305                 310                 315                 320

Leu Tyr Phe Gln Ser Asp Asn Asp Gly Ser Glu Ile Gly Thr Gly Phe
                325                 330                 335

Pro Phe Asp Pro His Tyr Val Glu Val Leu Gly Glu Arg Met His Tyr
            340                 345                 350

Val Asp Val Gly Pro Arg Asp Gly Thr Pro Val Leu Phe Leu His Gly
        355                 360                 365

Asn Pro Thr Ser Ser Tyr Val Trp Arg Asn Ile Ile Pro His Val Ala
    370                 375                 380

Pro Thr His Arg Cys Ile Ala Pro Asp Leu Ile Gly Met Gly Lys Ser
385                 390                 395                 400

Asp Lys Pro Asp Leu Gly Tyr Phe Phe Asp Asp His Val Arg Phe Met
                405                 410                 415

Asp Ala Phe Ile Glu Ala Leu Gly Leu Glu Glu Val Val Leu Val Ile
            420                 425                 430

His Asp Trp Gly Ser Ala Leu Gly Phe His Trp Ala Lys Arg Asn Pro
        435                 440                 445

Glu Arg Val Lys Gly Ile Ala Phe Met Glu Phe Ile Arg Pro Ile Pro
    450                 455                 460
```

Thr Trp Asp Glu Trp Pro Glu Phe Ala Arg Glu Thr Phe Gln Ala Phe
465 470 475 480

Arg Thr Thr Asp Val Gly Arg Lys Leu Ile Ile Asp Gln Asn Val Phe
485 490 495

Ile Glu Gly Thr Leu Pro Met Gly Val Val Arg Pro Leu Thr Glu Val
500 505 510

Glu Met Asp His Tyr Arg Glu Pro Phe Leu Asn Pro Val Asp Arg Glu
515 520 525

Pro Leu Trp Arg Phe Pro Asn Glu Leu Pro Ile Ala Gly Glu Pro Ala
530 535 540

Asn Ile Val Ala Leu Val Glu Glu Tyr Met Asp Trp Leu His Gln Ser
545 550 555 560

Pro Val Pro Lys Leu Leu Phe Trp Gly Thr Pro Gly Val Leu Ile Pro
565 570 575

Pro Ala Glu Ala Ala Arg Leu Ala Lys Ser Leu Pro Asn Cys Lys Ala
580 585 590

Val Asp Ile Gly Pro Gly Leu Asn Leu Leu Gln Glu Asp Asn Pro Asp
595 600 605

Leu Ile Gly Ser Glu Ile Ala Arg Trp Leu Ser Thr Leu Glu Ile Ser
610 615 620

Gly
625

<210> 42
<211> 513
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 42
atggtgttta cactcgaaga tttcgtaggg gactggcggc agacagccgg ctacaacctg 60

gaccaagtcc ttgagcaggg cggtctgtcc agtttgtttc agaatctcgg ggtgtccgta 120

acaccgatcc aaaagattgt cctgagcggt gaaaacggcc tgaagatcga catccatgtc 180

atcatcccgt atgaaggtct gagcggctat cagatgggcc agatcgaaaa aatttttaag 240

gtggtgtacc ctgtggatga tcatcacttt aaggtgattc tgcactatgg cacactggta 300

atcgacgggg ttacgccgaa catgatcgac tatttcggac ggccgtatga aggcatcgcc 360

gtgttcgacg gcaaaaagat cactgtaacc gggaccctgt ggaacggcaa caaaattatc 420

gacgagcgcc tgatcaaccc cgacggctcc ctgctgttcc gcgtaaccat caacggagtg 480

accggctggc ggctgtgcga gcgcattttg gcg 513

<210> 43
<211> 171
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 43
Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala
1 5 10 15

Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Leu Ser Ser Leu
20 25 30

Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln Lys Ile Val Leu
35 40 45

Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr
50 55 60

Glu Gly Leu Ser Gly Tyr Gln Met Gly Gln Ile Glu Lys Ile Phe Lys
65 70 75 80

Val Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu His Tyr
85 90 95

Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe
100 105 110

Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr
115 120 125

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

Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val
145 150 155 160

Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala
165 170

<210> 44
<211> 1455
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

polynucleotide

<400> 44
atggtgttta cattggagga tttcgttgga gactggcggc agacagctgg atacaaccta 60

gatcaagtgt tagaacaagg aggattgtct agtctgttcc aaaagctggg agtgtcagtc 120

accccaatcc agaaaattgt gctgtctggg gagaatgggt taaaaattga tattcatgtc 180

atcatccctt acgagggact cagtggtttt caaatgggtc tgattgaaat gatcttcaaa 240

gttgtttacc cagtggatga tcatcatttc aagattattc accattatgg tacactcgtt 300

attgacggtg tgacaccaaa catgattgac ttctttggac gcccttacga gggaattgct 360

gtgtttgacg gcaagaagat cacagttact ggaactctgt ggaacggcaa caagatcatt 420

gatgagcgcc tgatcaaccc agatggttca ctcctcttcc gcgttactat caatggagtc 480

accggatggc gcctttgcga gcgtattctt gccggatatc tcgagccaac cactgaggat 540

ctgtactttc agagcgataa cgatggatcc gaaatcggta ctggctttcc attcgacccc 600

cattatgtgg aagtcctggg cgagcgcatg cactacgtcg atgttggtcc gcgcgatggc 660

acccctgtgc tgttcctgca cggtaacccg acctcctcct acgtgtggcg caacatcatc 720

ccgcatgttg caccgaccca tcgctgcatt gctccagacc tgatcggtat gggcaaatcc 780

gacaaaccag acctgggtta tttcttcgac gaccacgtcc gcttcatgga tgccttcatc 840

gaagccctgg gtctggaaga ggtcgtcctg gtcattcacg actggggctc cgctctgggt 900

ttccactggg ccaagcgcaa tccagagcgc gtcaaaggta ttgcatttat ggagttcatc 960

cgccctatcc cgacctggga cgaatggcca gaatttgccc gcgagacctt ccaggccttc 1020

cgcaccaccg acgtcggccg caagctgatc atcgatcaga acgtttttat cgagggtacg 1080

ctgccgatgg gtgtcgtccg cccgctgact gaagtcgaga tggaccatta ccgcgagccg 1140

ttcctgaatc ctgttgaccg cgagccactg tggcgcttcc caaacgagct gccaatcgcc 1200

ggtgagccag cgaacatcgt cgcgctggtc gaagaataca tggactggct gcaccagtcc 1260

cctgtcccga agctgctgtt ctggggcacc ccaggcgttc tgatcccacc ggccgaagcc 1320

gctcgcctgg ccaaaagcct gcctaactgc aaggctgtgg acatcggccc gggtctgaat 1380

ctgctgcaag aagacaaccc ggacctgatc ggcagcgaga tcgcgcgctg gctgtctact 1440

ctggagattt ccggt 1455

<210> 45
<211> 485
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 45
Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala
1 5 10 15

```
Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Leu Ser Ser Leu
            20                  25                  30

Phe Gln Lys Leu Gly Val Ser Val Thr Pro Ile Gln Lys Ile Val Leu
        35                  40                  45

Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr
    50                  55                  60

Glu Gly Leu Ser Gly Phe Gln Met Gly Leu Ile Glu Met Ile Phe Lys
65                  70                  75                  80

Val Val Tyr Pro Val Asp Asp His His Phe Lys Ile Ile His His Tyr
                85                  90                  95

Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Phe Phe
            100                 105                 110

Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr
        115                 120                 125

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

Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val
145                 150                 155                 160

Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala Gly Tyr Leu Glu Pro
                165                 170                 175

Thr Thr Glu Asp Leu Tyr Phe Gln Ser Asp Asn Asp Gly Ser Glu Ile
            180                 185                 190

Gly Thr Gly Phe Pro Phe Asp Pro His Tyr Val Glu Val Leu Gly Glu
        195                 200                 205

Arg Met His Tyr Val Asp Val Gly Pro Arg Asp Gly Thr Pro Val Leu
    210                 215                 220

Phe Leu His Gly Asn Pro Thr Ser Ser Tyr Val Trp Arg Asn Ile Ile
225                 230                 235                 240

Pro His Val Ala Pro Thr His Arg Cys Ile Ala Pro Asp Leu Ile Gly
                245                 250                 255

Met Gly Lys Ser Asp Lys Pro Asp Leu Gly Tyr Phe Phe Asp Asp His
            260                 265                 270

Val Arg Phe Met Asp Ala Phe Ile Glu Ala Leu Gly Leu Glu Glu Val
        275                 280                 285
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Val Leu Val Ile His Asp Trp Gly Ser Ala Leu Gly Phe His Trp Ala
    290                 295                 300

Lys Arg Asn Pro Glu Arg Val Lys Gly Ile Ala Phe Met Glu Phe Ile
305                 310                 315                 320

Arg Pro Ile Pro Thr Trp Asp Glu Trp Pro Glu Phe Ala Arg Glu Thr
                325                 330                 335

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

Gln Asn Val Phe Ile Glu Gly Thr Leu Pro Met Gly Val Val Arg Pro
        355                 360                 365

Leu Thr Glu Val Glu Met Asp His Tyr Arg Glu Pro Phe Leu Asn Pro
    370                 375                 380

Val Asp Arg Glu Pro Leu Trp Arg Phe Pro Asn Glu Leu Pro Ile Ala
385                 390                 395                 400

Gly Glu Pro Ala Asn Ile Val Ala Leu Val Glu Glu Tyr Met Asp Trp
                405                 410                 415

Leu His Gln Ser Pro Val Pro Lys Leu Leu Phe Trp Gly Thr Pro Gly
            420                 425                 430

Val Leu Ile Pro Pro Ala Glu Ala Ala Arg Leu Ala Lys Ser Leu Pro
        435                 440                 445

Asn Cys Lys Ala Val Asp Ile Gly Pro Gly Leu Asn Leu Leu Gln Glu
    450                 455                 460

Asp Asn Pro Asp Leu Ile Gly Ser Glu Ile Ala Arg Trp Leu Ser Thr
465                 470                 475                 480

Leu Glu Ile Ser Gly
                485
```

<210> 46
<211> 513
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 46
atggtgttta cattggagga tttcgttgga gactggcggc agacagctgg atacaaccaa 60

gatcaagtgt tagaacaagg aggagtgtct agtctgttcc aaaagctggg agtgtcagtc 120

accccaatcc agaaaattgt gctgtctggg gagaatgggt taaaaattga tattcatgtc 180

atcatccctt acgagggact cagtggtttt caaatgggtc tgattgaaat gatcttcaaa 240

gttgtttacc cagtggatga tcatcatttc aaggttattc tccattatgg tacactcgtt 300

attgacggtg tgacaccaaa catgattgac tactttggac gcccttacga gggaattgct 360

gtgtttgacg gcaagaagat cacagttact ggaactctgt ggaacggcaa caagatcatt 420

gatgagcgcc tgatcaaccc agatggttca ctcctcttcc gcgttactat caatggagtc 480

accggatggc gcctttgcga gcgtattctt gcc 513

<210> 47
<211> 171
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 47

Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala
1 5 10 15

Gly Tyr Asn Gln Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu
20 25 30

Phe Gln Lys Leu Gly Val Ser Val Thr Pro Ile Gln Lys Ile Val Leu
35 40 45

Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr
50 55 60

Glu Gly Leu Ser Gly Phe Gln Met Gly Leu Ile Glu Met Ile Phe Lys
65 70 75 80

Val Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu His Tyr
85 90 95

Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe
100 105 110

Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr
115 120 125

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

Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val
145 150 155 160

Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala
165 170

<210> 48

<211> 1455
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 48
atggtgttta cattggagga tttcgttgga gactggcggc agacagctgg atacaaccaa 60

gatcaagtgt tagaacaagg aggattgtct agtctgttcc aaaagctggg agtgtcagtc 120

accccaatcc agaaaattgt gctgtctggg gagaatgggt taaaaattga tattcatgtc 180

atcatccctt acgagggact cagtggtttt caaatgggtc tgattgaaat gatcttcaaa 240

gttgtttacc cagtggatga tcatcatttc aaggttattc tccattatgg tacactcgtt 300

attgacggtg tgacaccaaa catgattgac tactttggac gcccttacga gggaattgct 360

gtgtttgacg gcaagaagat cacagttact ggaactctgt ggaacggcaa caagatcatt 420

gatgagcgcc tgatcaaccc agatggttca ctcctcttcc gcgttactat caatggagtc 480

accggatggc gcctttgcga gcgtattctt gccggatatc tcgagccaac cactgaggat 540

ctgtactttc agagcgataa cgatggatcc gaaatcggta ctggctttcc attcgacccc 600

cattatgtgg aagtcctggg cgagcgcatg cactacgtcg atgttggtcc gcgcgatggc 660

acccctgtgc tgttcctgca cggtaacccg acctcctcct acgtgtggcg caacatcatc 720

ccgcatgttg caccgaccca tcgctgcatt gctccagacc tgatcggtat gggcaaatcc 780

gacaaaccag acctgggtta tttcttcgac gaccacgtcc gcttcatgga tgccttcatc 840

gaagccctgg gtctggaaga ggtcgtcctg gtcattcacg actggggctc cgctctgggt 900

ttccactggg ccaagcgcaa tccagagcgc gtcaaaggta ttgcatttat ggagttcatc 960

cgccctatcc cgacctggga cgaatggcca gaatttgccc gcgagacctt ccaggccttc 1020

cgcaccaccg acgtcggccg caagctgatc atcgatcaga acgtttttat cgagggtacg 1080

ctgccgatgg gtgtcgtccg cccgctgact gaagtcgaga tggaccatta ccgcgagccg 1140

ttcctgaatc ctgttgaccg cgagccactg tggcgcttcc caaacgagct gccaatcgcc 1200

ggtgagccag cgaacatcgt cgcgctggtc gaagaataca tggactggct gcaccagtcc 1260

cctgtcccga agctgctgtt ctggggcacc ccaggcgttc tgatcccacc ggccgaagcc 1320

gctcgcctgg ccaaaagcct gcctaactgc aaggctgtgg acatcggccc gggtctgaat 1380

ctgctgcaag aagacaaccc ggacctgatc ggcagcgaga tcgcgcgctg gctgtctact 1440

ctggagattt ccggt 1455

<210> 49
<211> 485
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 49
Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala
1 5 10 15

Gly Tyr Asn Gln Asp Gln Val Leu Glu Gln Gly Gly Leu Ser Ser Leu
20 25 30

Phe Gln Lys Leu Gly Val Ser Val Thr Pro Ile Gln Lys Ile Val Leu
35 40 45

Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr
50 55 60

Glu Gly Leu Ser Gly Phe Gln Met Gly Leu Ile Glu Met Ile Phe Lys
65 70 75 80

Val Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu His Tyr
85 90 95

Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe
100 105 110

Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr
115 120 125

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

Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val
145 150 155 160

Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala Gly Tyr Leu Glu Pro
165 170 175

Thr Thr Glu Asp Leu Tyr Phe Gln Ser Asp Asn Asp Gly Ser Glu Ile
180 185 190

Gly Thr Gly Phe Pro Phe Asp Pro His Tyr Val Glu Val Leu Gly Glu
195 200 205

Arg Met His Tyr Val Asp Val Gly Pro Arg Asp Gly Thr Pro Val Leu
210 215 220

Phe Leu His Gly Asn Pro Thr Ser Ser Tyr Val Trp Arg Asn Ile Ile
225 230 235 240

Pro His Val Ala Pro Thr His Arg Cys Ile Ala Pro Asp Leu Ile Gly
245 250 255

Met Gly Lys Ser Asp Lys Pro Asp Leu Gly Tyr Phe Phe Asp Asp His
260 265 270

```
Val Arg Phe Met Asp Ala Phe Ile Glu Ala Leu Gly Leu Glu Glu Val
        275                 280                 285

Val Leu Val Ile His Asp Trp Gly Ser Ala Leu Gly Phe His Trp Ala
    290                 295                 300

Lys Arg Asn Pro Glu Arg Val Lys Gly Ile Ala Phe Met Glu Phe Ile
305                 310                 315                 320

Arg Pro Ile Pro Thr Trp Asp Glu Trp Pro Glu Phe Ala Arg Glu Thr
                325                 330                 335

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

Gln Asn Val Phe Ile Glu Gly Thr Leu Pro Met Gly Val Val Arg Pro
        355                 360                 365

Leu Thr Glu Val Glu Met Asp His Tyr Arg Glu Pro Phe Leu Asn Pro
    370                 375                 380

Val Asp Arg Glu Pro Leu Trp Arg Phe Pro Asn Glu Leu Pro Ile Ala
385                 390                 395                 400

Gly Glu Pro Ala Asn Ile Val Ala Leu Val Glu Glu Tyr Met Asp Trp
                405                 410                 415

Leu His Gln Ser Pro Val Pro Lys Leu Leu Phe Trp Gly Thr Pro Gly
            420                 425                 430

Val Leu Ile Pro Pro Ala Glu Ala Ala Arg Leu Ala Lys Ser Leu Pro
        435                 440                 445

Asn Cys Lys Ala Val Asp Ile Gly Pro Gly Leu Asn Leu Leu Gln Glu
    450                 455                 460

Asp Asn Pro Asp Leu Ile Gly Ser Glu Ile Ala Arg Trp Leu Ser Thr
465                 470                 475                 480

Leu Glu Ile Ser Gly
                485
```

<210> 50
<211> 1455
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 50

atggtgttta cattggagga tttcgttgga gactggcggc agacagctgg atacaaccaa 60

gatcaagtgt tagaacaagg aggagtgtct agtctgttcc aaaagctggg agtgtcagtc 120

accccaatcc agaaaattgt gctgtctggg gagaatgggt taaaaattga tattcatgtc 180

atcatccctt acgagggact cagtggtttt caaatgggtc tgattgaaat gatcttcaaa 240

gttgtttacc cagtggatga tcatcatttc aaggttattc tccattatgg tacactcgtt 300

attgacggtg tgacaccaaa catgattgac tactttggac gcccttacga gggaattgct 360

gtgtttgacg gcaagaagat cacagttact ggaactctgt ggaacggcaa caagatcatt 420

gatgagcgcc tgatcaaccc agatggttca ctcctcttcc gcgttactat caatggagtc 480

accggatggc gcctttgcga gcgtattctt gccggatatc tcgagccaac cactgaggat 540

ctgtactttc agagcgataa cgatggatcc gaaatcggta ctggctttcc attcgacccc 600

cattatgtgg aagtcctggg cgagcgcatg cactacgtcg atgttggtcc gcgcgatggc 660

acccctgtgc tgttcctgca cggtaacccg acctcctcct acgtgtggcg caacatcatc 720

ccgcatgttg caccgaccca tcgctgcatt gctccagacc tgatcggtat gggcaaatcc 780

gacaaaccag acctgggtta tttcttcgac gaccacgtcc gcttcatgga tgccttcatc 840

gaagccctgg gtctggaaga ggtcgtcctg gtcattcacg actggggctc cgctctgggt 900

ttccactggg ccaagcgcaa tccagagcgc gtcaaaggta ttgcatttat ggagttcatc 960

cgccctatcc cgacctggga cgaatggcca gaatttgccc gcgagacctt ccaggccttc 1020

cgcaccaccg acgtcggccg caagctgatc atcgatcaga acgtttttat cgagggtacg 1080

ctgccgatgg gtgtcgtccg cccgctgact gaagtcgaga tggaccatta ccgcgagccg 1140

ttcctgaatc ctgttgaccg cgagccactg tggcgcttcc caaacgagct gccaatcgcc 1200

ggtgagccag cgaacatcgt cgcgctggtc gaagaataca tggactggct gcaccagtcc 1260

cctgtcccga agctgctgtt ctggggcacc ccaggcgttc tgatcccacc ggccgaagcc 1320

gctcgcctgg ccaaaagcct gcctaactgc aaggctgtgg acatcggccc gggtctgaat 1380

ctgctgcaag aagacaaccc ggacctgatc ggcagcgaga tcgcgcgctg gctgtctact 1440

ctggagattt ccggt 1455

<210> 51
<211> 485
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 51
Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala
1 5 10 15

Gly Tyr Asn Gln Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu
20 25 30

```
Phe Gln Lys Leu Gly Val Ser Val Thr Pro Ile Gln Lys Ile Val Leu
        35                  40                  45

Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr
    50                  55                  60

Glu Gly Leu Ser Gly Phe Gln Met Gly Leu Ile Glu Met Ile Phe Lys
65                  70                  75                  80

Val Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu His Tyr
                85                  90                  95

Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe
            100                 105                 110

Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr
        115                 120                 125

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

Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val
145                 150                 155                 160

Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala Gly Tyr Leu Glu Pro
                165                 170                 175

Thr Thr Glu Asp Leu Tyr Phe Gln Ser Asp Asn Asp Gly Ser Glu Ile
            180                 185                 190

Gly Thr Gly Phe Pro Phe Asp Pro His Tyr Val Glu Val Leu Gly Glu
        195                 200                 205

Arg Met His Tyr Val Asp Val Gly Pro Arg Asp Gly Thr Pro Val Leu
    210                 215                 220

Phe Leu His Gly Asn Pro Thr Ser Ser Tyr Val Trp Arg Asn Ile Ile
225                 230                 235                 240

Pro His Val Ala Pro Thr His Arg Cys Ile Ala Pro Asp Leu Ile Gly
                245                 250                 255

Met Gly Lys Ser Asp Lys Pro Asp Leu Gly Tyr Phe Phe Asp Asp His
            260                 265                 270

Val Arg Phe Met Asp Ala Phe Ile Glu Ala Leu Gly Leu Glu Glu Val
        275                 280                 285

Val Leu Val Ile His Asp Trp Gly Ser Ala Leu Gly Phe His Trp Ala
    290                 295                 300
```

Lys Arg Asn Pro Glu Arg Val Lys Gly Ile Ala Phe Met Glu Phe Ile
305 310 315 320

Arg Pro Ile Pro Thr Trp Asp Glu Trp Pro Glu Phe Ala Arg Glu Thr
325 330 335

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

Gln Asn Val Phe Ile Glu Gly Thr Leu Pro Met Gly Val Val Arg Pro
355 360 365

Leu Thr Glu Val Glu Met Asp His Tyr Arg Glu Pro Phe Leu Asn Pro
370 375 380

Val Asp Arg Glu Pro Leu Trp Arg Phe Pro Asn Glu Leu Pro Ile Ala
385 390 395 400

Gly Glu Pro Ala Asn Ile Val Ala Leu Val Glu Glu Tyr Met Asp Trp
405 410 415

Leu His Gln Ser Pro Val Pro Lys Leu Leu Phe Trp Gly Thr Pro Gly
420 425 430

Val Leu Ile Pro Pro Ala Glu Ala Ala Arg Leu Ala Lys Ser Leu Pro
435 440 445

Asn Cys Lys Ala Val Asp Ile Gly Pro Gly Leu Asn Leu Leu Gln Glu
450 455 460

Asp Asn Pro Asp Leu Ile Gly Ser Glu Ile Ala Arg Trp Leu Ser Thr
465 470 475 480

Leu Glu Ile Ser Gly
485

<210> 52
<211> 1455
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 52
atggtgttta cattgaagga tttcgttgga gactggcggc agacagctgg atacaaccaa 60

gatcaagtgt tagaacaagg aggattgtct agtctgttcc aaaatctggg agtgtcagtc 120

accccaatcc agaaaattgt gctgtctggg gagaatgggt taaaaattga tattcatgtc 180

atcatccctt acgagggact cagtggttat caaatgggtc agattgaaaa gatcttcaaa 240

gttgtttacc cagtggatga tcatcatttc aaggttattc tccattatgg tacactcgtt 300

attgacggtg tgacaccaaa catgattgac tactttggac gcccttacga gggaattgct 360

gtgtttgacg gcaagaagat cacagttact ggaactctgt ggaacggcaa caagatcatt 420

gatgagcgcc tgatcaaccc agatggttca ctcctcttcc gcgttactat caatggagtc 480

accggatggc gcctttgcga gcgtattctt gccggatatc tcgagccaac cactgaggat 540

ctgtactttc agagcgataa cgatggatcc gaaatcggta ctggctttcc attcgacccc 600

cattatgtgg aagtcctggg cgagcgcatg cactacgtcg atgttggtcc gcgcgatggc 660

acccctgtgc tgttcctgca cggtaacccg acctcctcct acgtgtggcg caacatcatc 720

ccgcatgttg caccgaccca tcgctgcatt gctccagacc tgatcggtat gggcaaatcc 780

gacaaaccag acctgggtta tttcttcgac gaccacgtcc gcttcatgga tgccttcatc 840

gaagccctgg gtctggaaga ggtcgtcctg gtcattcacg actggggctc cgctctgggt 900

ttccactggg ccaagcgcaa tccagagcgc gtcaaaggta ttgcatttat ggagttcatc 960

cgccctatcc cgacctggga cgaatggcca gaatttgccc gcgagacctt ccaggccttc 1020

cgcaccaccg acgtcggccg caagctgatc atcgatcaga acgtttttat cgagggtacg 1080

ctgccgatgg gtgtcgtccg cccgctgact gaagtcgaga tggaccatta ccgcgagccg 1140

ttcctgaatc ctgttgaccg cgagccactg tggcgcttcc caaacgagct gccaatcgcc 1200

ggtgagccag cgaacatcgt cgcgctggtc gaagaataca tggactggct gcaccagtcc 1260

cctgtcccga agctgctgtt ctggggcacc ccaggcgttc tgatcccacc ggccgaagcc 1320

gctcgcctgg ccaaaagcct gcctaactgc aaggctgtgg acatcggccc gggtctgaat 1380

ctgctgcaag aagacaaccc ggacctgatc ggcagcgaga tcgcgcgctg gctgtctact 1440

ctggagattt ccggt 1455

<210> 53
<211> 485
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 53
Met Val Phe Thr Leu Lys Asp Phe Val Gly Asp Trp Arg Gln Thr Ala
1 5 10 15

Gly Tyr Asn Gln Asp Gln Val Leu Glu Gln Gly Gly Leu Ser Ser Leu
20 25 30

Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln Lys Ile Val Leu
35 40 45

Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr
50 55 60

```
Glu Gly Leu Ser Gly Tyr Gln Met Gly Gln Ile Glu Lys Ile Phe Lys
65                  70                  75                  80

Val Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu His Tyr
                85                  90                  95

Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe
            100                 105                 110

Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr
        115                 120                 125

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

Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val
145                 150                 155                 160

Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala Gly Tyr Leu Glu Pro
                165                 170                 175

Thr Thr Glu Asp Leu Tyr Phe Gln Ser Asp Asn Asp Gly Ser Glu Ile
            180                 185                 190

Gly Thr Gly Phe Pro Phe Asp Pro His Tyr Val Glu Val Leu Gly Glu
        195                 200                 205

Arg Met His Tyr Val Asp Val Gly Pro Arg Asp Gly Thr Pro Val Leu
    210                 215                 220

Phe Leu His Gly Asn Pro Thr Ser Ser Tyr Val Trp Arg Asn Ile Ile
225                 230                 235                 240

Pro His Val Ala Pro Thr His Arg Cys Ile Ala Pro Asp Leu Ile Gly
                245                 250                 255

Met Gly Lys Ser Asp Lys Pro Asp Leu Gly Tyr Phe Phe Asp Asp His
            260                 265                 270

Val Arg Phe Met Asp Ala Phe Ile Glu Ala Leu Gly Leu Glu Glu Val
        275                 280                 285

Val Leu Val Ile His Asp Trp Gly Ser Ala Leu Gly Phe His Trp Ala
    290                 295                 300

Lys Arg Asn Pro Glu Arg Val Lys Gly Ile Ala Phe Met Glu Phe Ile
305                 310                 315                 320

Arg Pro Ile Pro Thr Trp Asp Glu Trp Pro Glu Phe Ala Arg Glu Thr
                325                 330                 335
```

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

Gln Asn Val Phe Ile Glu Gly Thr Leu Pro Met Gly Val Val Arg Pro
355 360 365

Leu Thr Glu Val Glu Met Asp His Tyr Arg Glu Pro Phe Leu Asn Pro
370 375 380

Val Asp Arg Glu Pro Leu Trp Arg Phe Pro Asn Glu Leu Pro Ile Ala
385 390 395 400

Gly Glu Pro Ala Asn Ile Val Ala Leu Val Glu Glu Tyr Met Asp Trp
405 410 415

Leu His Gln Ser Pro Val Pro Lys Leu Leu Phe Trp Gly Thr Pro Gly
420 425 430

Val Leu Ile Pro Pro Ala Glu Ala Ala Arg Leu Ala Lys Ser Leu Pro
435 440 445

Asn Cys Lys Ala Val Asp Ile Gly Pro Gly Leu Asn Leu Leu Gln Glu
450 455 460

Asp Asn Pro Asp Leu Ile Gly Ser Glu Ile Ala Arg Trp Leu Ser Thr
465 470 475 480

Leu Glu Ile Ser Gly
485

<210> 54
<211> 81
<212> DNA
<213> Oplophorus gracilirostris

<400> 54
atggcttact ccacactgtt catcattgct ctcacagccg tcgtaacaca agcctcctcc 60

acacagaaaa gcaacctgac a 81

<210> 55
<211> 1875
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 55
atgcttggtc tgtcggagca aagcgtgtcc atctcgcgct gcgctgggac gcgcctgccc 60

gccttgctgg acgagcagca ggtgaacgtc ctgctctacg acatgaacgg ctgctactca 120

cgcctcaagg agctggtgcc caccctgccc cagaaccgca aagtgagcaa ggtggagatc 180

ctgcagcatg taatcgacta catcagggac ctgcagctgg agctgaactc ggagtctgaa 240

gtcgggacca ccggaggccg gggactgcct gtccgcgccc cgctcagcac cctgaacggc 300

gagatcagtg ccttggcggc cgaggcggca tgtgttccag ccgacgatcg catcttgtgt 360

cgcgtttctc ttgagaatct ttattttcag gcgtctggag gtggtggcgg agcgatcgcc 420

atggtgttta cattggagga tttcgttgga gactggcggc agacagctgg atacaaccaa 480

gatcaagtgt tagaacaagg aggattgtct agtctgttcc aaaagctggg agtgtcagtc 540

accccaatcc agaaaattgt gctgtctggg gagaatgggt taaaatttga tattcatgtc 600

atcatccctt acgagggact cagtggtttt caaatgggtc tgattgaaat gatcttcaaa 660

gttgtttacc cagtggatga tcatcatttc aagattattc tccattatgg tacactcgtt 720

attgacggtg tgacaccaaa catgattgac tactttggac gcccttacga gggaattgct 780

gtgtttgacg gcaagaagat cacagttact ggaactctgt ggaacggcaa caagatcatt 840

gatgagcgcc tgatcaaccc agatggttca ctcctcttcc gcgttactat caatggagtc 900

accggatggc gcctttgcga gcgtattctt gccggatctc tcgagccaac cactgaggat 960

ctgtactttc agagcgataa cgatggatcc gaaatcggta ctggctttcc attcgacccc 1020

cattatgtgg aagtcctggg cgagcgcatg cactacgtcg atgttggtcc gcgcgatggc 1080

acccctgtgc tgttcctgca cggtaacccg acctcctcct acgtgtggcg caacatcatc 1140

ccgcatgttg caccgaccca tcgctgcatt gctccagacc tgatcggtat gggcaaatcc 1200

gacaaaccag acctgggtta tttcttcgac gaccacgtcc gcttcatgga tgccttcatc 1260

gaagccctgg gtctggaaga ggtcgtcctg gtcattcacg actggggctc cgctctgggt 1320

ttccactggg ccaagcgcaa tccagagcgc gtcaaaggta ttgcatttat ggagttcatc 1380

cgccctatcc cgacctggga cgaatggcca gaatttgccc gcgagacctt ccaggccttc 1440

cgcaccaccg acgtcggccg caagctgatc atcgatcaga acgtttttat cgagggtacg 1500

ctgccgatgg gtgtcgtccg cccgctgact gaagtcgaga tggaccatta ccgcgagccg 1560

ttcctgaatc ctgttgaccg cgagccactg tggcgcttcc caaacgagct gccaatcgcc 1620

ggtgagccag cgaacatcgt cgcgctggtc gaagaataca tggactggct gcaccagtcc 1680

cctgtcccga agctgctgtt ctggggcacc ccaggcgttc tgatcccacc ggccgaagcc 1740

gctcgcctgg ccaaaagcct gcctaactgc aaggctgtgg acatcggccc gggtctgaat 1800

ctgctgcaag aagacaaccc ggacctgatc ggcagcgaga tcgcgcgctg gctgtctact 1860

ctggagattt ccggt 1875

<210> 56
<211> 625
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 56

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Met Leu Gly Leu Ser Glu Gln Ser Val Ser Ile Ser Arg Cys Ala Gly
1               5                  10                  15

Thr Arg Leu Pro Ala Leu Leu Asp Glu Gln Gln Val Asn Val Leu Leu
            20                  25                  30

Tyr Asp Met Asn Gly Cys Tyr Ser Arg Leu Lys Glu Leu Val Pro Thr
        35                  40                  45

Leu Pro Gln Asn Arg Lys Val Ser Lys Val Glu Ile Leu Gln His Val
    50                  55                  60

Ile Asp Tyr Ile Arg Asp Leu Gln Leu Glu Leu Asn Ser Glu Ser Glu
65                  70                  75                  80

Val Gly Thr Thr Gly Gly Arg Gly Leu Pro Val Arg Ala Pro Leu Ser
                85                  90                  95

Thr Leu Asn Gly Glu Ile Ser Ala Leu Ala Ala Glu Ala Ala Cys Val
            100                 105                 110

Pro Ala Asp Asp Arg Ile Leu Cys Arg Val Ser Leu Glu Asn Leu Tyr
        115                 120                 125

Phe Gln Ala Ser Gly Gly Gly Gly Gly Ala Ile Ala Met Val Phe Thr
    130                 135                 140

Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala Gly Tyr Asn Gln
145                 150                 155                 160

Asp Gln Val Leu Glu Gln Gly Gly Leu Ser Ser Leu Phe Gln Lys Leu
                165                 170                 175

Gly Val Ser Val Thr Pro Ile Gln Lys Ile Val Leu Ser Gly Glu Asn
            180                 185                 190

Gly Leu Lys Phe Asp Ile His Val Ile Ile Pro Tyr Glu Gly Leu Ser
        195                 200                 205

Gly Phe Gln Met Gly Leu Ile Glu Met Ile Phe Lys Val Val Tyr Pro
    210                 215                 220

Val Asp Asp His His Phe Lys Ile Ile Leu His Tyr Gly Thr Leu Val
225                 230                 235                 240

Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr
                245                 250                 255

Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr
            260                 265                 270
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```
Leu Trp Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp
        275                 280                 285

Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg
    290                 295                 300

Leu Cys Glu Arg Ile Leu Ala Gly Ser Leu Glu Pro Thr Thr Glu Asp
305                 310                 315                 320

Leu Tyr Phe Gln Ser Asp Asn Asp Gly Ser Glu Ile Gly Thr Gly Phe
                325                 330                 335

Pro Phe Asp Pro His Tyr Val Glu Val Leu Gly Glu Arg Met His Tyr
            340                 345                 350

Val Asp Val Gly Pro Arg Asp Gly Thr Pro Val Leu Phe Leu His Gly
        355                 360                 365

Asn Pro Thr Ser Ser Tyr Val Trp Arg Asn Ile Ile Pro His Val Ala
    370                 375                 380

Pro Thr His Arg Cys Ile Ala Pro Asp Leu Ile Gly Met Gly Lys Ser
385                 390                 395                 400

Asp Lys Pro Asp Leu Gly Tyr Phe Phe Asp Asp His Val Arg Phe Met
                405                 410                 415

Asp Ala Phe Ile Glu Ala Leu Gly Leu Glu Glu Val Val Leu Val Ile
            420                 425                 430

His Asp Trp Gly Ser Ala Leu Gly Phe His Trp Ala Lys Arg Asn Pro
        435                 440                 445

Glu Arg Val Lys Gly Ile Ala Phe Met Glu Phe Ile Arg Pro Ile Pro
    450                 455                 460

Thr Trp Asp Glu Trp Pro Glu Phe Ala Arg Glu Thr Phe Gln Ala Phe
465                 470                 475                 480

Arg Thr Thr Asp Val Gly Arg Lys Leu Ile Ile Asp Gln Asn Val Phe
                485                 490                 495

Ile Glu Gly Thr Leu Pro Met Gly Val Val Arg Pro Leu Thr Glu Val
            500                 505                 510

Glu Met Asp His Tyr Arg Glu Pro Phe Leu Asn Pro Val Asp Arg Glu
        515                 520                 525

Pro Leu Trp Arg Phe Pro Asn Glu Leu Pro Ile Ala Gly Glu Pro Ala
    530                 535                 540
```

Asn Ile Val Ala Leu Val Glu Glu Tyr Met Asp Trp Leu His Gln Ser
545 550 555 560

Pro Val Pro Lys Leu Leu Phe Trp Gly Thr Pro Gly Val Leu Ile Pro
565 570 575

Pro Ala Glu Ala Ala Arg Leu Ala Lys Ser Leu Pro Asn Cys Lys Ala
580 585 590

Val Asp Ile Gly Pro Gly Leu Asn Leu Leu Gln Glu Asp Asn Pro Asp
595 600 605

Leu Ile Gly Ser Glu Ile Ala Arg Trp Leu Ser Thr Leu Glu Ile Ser
610 615 620

Gly
625

<210> 57
<211> 1875
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 57
atgcttggtc tgtcggagca aagcgtgtcc atctcgcgct gcgctgggac gcgcctgccc 60

gccttgctgg acgagcagca ggtgaacgtc ctgctctacg acatgaacgg ctgctactca 120

cgcctcaagg agctggtgcc caccctgccc cagaaccgca aagtgagcaa ggtggagatc 180

ctgcagcatg taatcgacta catcagggac ctgcagctgg agctgaactc ggagtctgaa 240

gtcgggacca ccggaggccg gggactgcct gtccgcgccc cgctcagcac cctgaacggc 300

gagatcagtg ccttggcggc cgaggcggca tgtgttccag ccgacgatcg catcttgtgt 360

cgcgtttctc ttgagaatct ttattttcag gcgtctggag gtggtggcgg agcgatcgcc 420

atggtgttta cattggagga tttcgttgga gactggcggc agacagctgg atacaaccaa 480

gatcaagtgt tagaacaagg aggattgtct agtctgttcc aaaagctggg agtgtcagtc 540

accccaatcc agaaaattgt gctgtctggg gagaatgggt taaaaattga tattcatgtc 600

atcatccctt acgagggact cagtggtttt caaatgggtc tgattgaaat gatcttcaaa 660

gttgtttacc cagtggatga tcatcatttc aaggttattc tccattatgg tacactcgtt 720

attgacggtg tgacaccaaa catgattgac tactttggac gcccttacga gggaattgct 780

gtgtttgacg gcaagaagat cacagttact ggaactctgt ggaacggcaa caagatcatt 840

gatgagcgcc tgatcaaccc agatggttca ctcctcttcc gcgttactat caatggagtc 900

accggatggc gcctttgcga gcgtattctt gccgtttctc tcgagccaac cactgaggat 960

ctgtactttc agagcgataa cgatggatcc gaaatcggta ctggctttcc attcgacccc 1020

cattatgtgg aagtcctggg cgagcgcatg cactacgtcg atgttggtcc gcgcgatggc 1080

acccctgtgc tgttcctgca cggtaacccg acctcctcct acgtgtggcg caacatcatc 1140

ccgcatgttg caccgaccca tcgctgcatt gctccagacc tgatcggtat gggcaaatcc 1200

gacaaaccag acctgggtta tttcttcgac gaccacgtcc gcttcatgga tgccttcatc 1260

gaagccctgg gtctggaaga ggtcgtcctg gtcattcacg actggggctc cgctctgggt 1320

ttccactggg ccaagcgcaa tccagagcgc gtcaaaggta ttgcatttat ggagttcatc 1380

cgccctatcc cgacctggga cgaatggcca gaatttgccc gcgagacctt ccaggccttc 1440

cgcaccaccg acgtcggccg caagctgatc atcgatcaga acgtttttat cgagggtacg 1500

ctgccgatgg gtgtcgtccg cccgctgact gaagtcgaga tggaccatta ccgcgagccg 1560

ttcctgaatc ctgttgaccg cgagccactg tggcgcttcc caaacgagct gccaatcgcc 1620

ggtgagccag cgaacatcgt cgcgctggtc gaagaataca tggactggct gcaccagtcc 1680

cctgtcccga agctgctgtt ctggggcacc ccaggcgttc tgatcccacc ggccgaagcc 1740

gctcgcctgg ccaaaagcct gcctaactgc aaggctgtgg acatcggccc gggtctgaat 1800

ctgctgcaag aagacaaccc ggacctgatc ggcagcgaga tcgcgcgctg gctgtctact 1860

ctggagattt ccggt 1875

<210> 58
<211> 625
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 58

Met Leu Gly Leu Ser Glu Gln Ser Val Ser Ile Ser Arg Cys Ala Gly
1 5 10 15

Thr Arg Leu Pro Ala Leu Leu Asp Glu Gln Gln Val Asn Val Leu Leu
20 25 30

Tyr Asp Met Asn Gly Cys Tyr Ser Arg Leu Lys Glu Leu Val Pro Thr
35 40 45

Leu Pro Gln Asn Arg Lys Val Ser Lys Val Glu Ile Leu Gln His Val
50 55 60

Ile Asp Tyr Ile Arg Asp Leu Gln Leu Glu Leu Asn Ser Glu Ser Glu
65 70 75 80

Val Gly Thr Thr Gly Gly Arg Gly Leu Pro Val Arg Ala Pro Leu Ser
85 90 95

Thr Leu Asn Gly Glu Ile Ser Ala Leu Ala Ala Glu Ala Ala Cys Val
100 105 110

```
Pro Ala Asp Asp Arg Ile Leu Cys Arg Val Ser Leu Glu Asn Leu Tyr
        115                 120                 125

Phe Gln Ala Ser Gly Gly Gly Gly Gly Ala Ile Ala Met Val Phe Thr
    130                 135                 140

Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala Gly Tyr Asn Gln
145                 150                 155                 160

Asp Gln Val Leu Glu Gln Gly Gly Leu Ser Ser Leu Phe Gln Lys Leu
                165                 170                 175

Gly Val Ser Val Thr Pro Ile Gln Lys Ile Val Leu Ser Gly Glu Asn
            180                 185                 190

Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr Glu Gly Leu Ser
        195                 200                 205

Gly Phe Gln Met Gly Leu Ile Glu Met Ile Phe Lys Val Val Tyr Pro
    210                 215                 220

Val Asp Asp His His Phe Lys Val Ile Leu His Tyr Gly Thr Leu Val
225                 230                 235                 240

Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr
                245                 250                 255

Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr
            260                 265                 270

Leu Trp Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp
        275                 280                 285

Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg
    290                 295                 300

Leu Cys Glu Arg Ile Leu Ala Val Ser Leu Glu Pro Thr Thr Glu Asp
305                 310                 315                 320

Leu Tyr Phe Gln Ser Asp Asn Asp Gly Ser Glu Ile Gly Thr Gly Phe
                325                 330                 335

Pro Phe Asp Pro His Tyr Val Glu Val Leu Gly Glu Arg Met His Tyr
            340                 345                 350

Val Asp Val Gly Pro Arg Asp Gly Thr Pro Val Leu Phe Leu His Gly
        355                 360                 365

Asn Pro Thr Ser Ser Tyr Val Trp Arg Asn Ile Ile Pro His Val Ala
    370                 375                 380
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Pro Thr His Arg Cys Ile Ala Pro Asp Leu Ile Gly Met Gly Lys Ser
385 390 395 400

Asp Lys Pro Asp Leu Gly Tyr Phe Phe Asp Asp His Val Arg Phe Met
405 410 415

Asp Ala Phe Ile Glu Ala Leu Gly Leu Glu Glu Val Val Leu Val Ile
420 425 430

His Asp Trp Gly Ser Ala Leu Gly Phe His Trp Ala Lys Arg Asn Pro
435 440 445

Glu Arg Val Lys Gly Ile Ala Phe Met Glu Phe Ile Arg Pro Ile Pro
450 455 460

Thr Trp Asp Glu Trp Pro Glu Phe Ala Arg Glu Thr Phe Gln Ala Phe
465 470 475 480

Arg Thr Thr Asp Val Gly Arg Lys Leu Ile Ile Asp Gln Asn Val Phe
485 490 495

Ile Glu Gly Thr Leu Pro Met Gly Val Val Arg Pro Leu Thr Glu Val
500 505 510

Glu Met Asp His Tyr Arg Glu Pro Phe Leu Asn Pro Val Asp Arg Glu
515 520 525

Pro Leu Trp Arg Phe Pro Asn Glu Leu Pro Ile Ala Gly Glu Pro Ala
530 535 540

Asn Ile Val Ala Leu Val Glu Glu Tyr Met Asp Trp Leu His Gln Ser
545 550 555 560

Pro Val Pro Lys Leu Leu Phe Trp Gly Thr Pro Gly Val Leu Ile Pro
565 570 575

Pro Ala Glu Ala Ala Arg Leu Ala Lys Ser Leu Pro Asn Cys Lys Ala
580 585 590

Val Asp Ile Gly Pro Gly Leu Asn Leu Leu Gln Glu Asp Asn Pro Asp
595 600 605

Leu Ile Gly Ser Glu Ile Ala Arg Trp Leu Ser Thr Leu Glu Ile Ser
610 615 620

Gly
625

<210> 59
<211> 1875
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 59
atgcttggtc tgtcggagca aagcgtgtcc atctcgcgct gcgctgggac gcgcctgccc 60

gccttgctgg acgagcagca ggtgaacgtc ctgctctacg acatgaacgg ctgctactca 120

cgcctcaagg agctggtgcc caccctgccc cagaaccgca aagtgagcaa ggtggagatc 180

ctgcagcatg taatcgacta catcagggac ctgcagctgg agctgaactc ggagtctgaa 240

gtcgggacca ccggaggccg gggactgcct gtccgcgccc cgctcagcac cctgaacggc 300

gagatcagtg ccttggcggc cgaggcggca tgtgttccag ccgacgatcg catcttgtgt 360

cgcgtttctc ttgagaatct ttattttcag gcgtctggag gtggtggcgg agcgatcgcc 420

atggtgttta cactcgaaga tttcgtaggg gactggcggc agacagccgg ctacaacctg 480

gaccaagtcc ttgagcaggg cggtctgtcc agtttgtttc agaatctcgg ggtgtccgta 540

acaccgatcc aaaagattgt cctgagcggt gaaaacggcc tgaagatcga catccatgtc 600

atcatcccgt atgaaggtct gagcggctat cagatgggcc agatcgaaaa aatttttaag 660

gtggtgtacc ctgtggatga tcatcacttt aaggtgattc tgcactatgg cacactggta 720

atcgacgggg ttacgccgaa catgatcgac tatttcggac ggccgtatga aggcatcgcc 780

gtgttcgacg gcaaaaagat cactgtaacc gggaccctgt ggaacggcaa caaaattatc 840

gacgagcgcc tgatcaaccc cgacggctcc ctgctgttcc gcgtaaccat caacggagtg 900

accggctggc ggctgtgcga gcgcattttg gcgggatatc tcgagccaac cactgaggat 960

ctgtactttc agagcgataa cgatggatcc gaaatcggta ctggctttcc attcgacccc 1020

cattatgtgg aagtcctggg cgagcgcatg cactacgtcg atgttggtcc gcgcgatggc 1080

acccctgtgc tgttcctgca cggtaacccg acctcctcct acgtgtggcg caacatcatc 1140

ccgcatgttg caccgaccca tcgctgcatt gctccagacc tgatcggtat gggcaaatcc 1200

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gaagccctgg gtctggaaga ggtcgtcctg gtcattcacg actggggctc cgctctgggt 1320

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cgccctatcc cgacctggga cgaatggcca gaatttgccc gcgagacctt ccaggccttc 1440

cgcaccaccg acgtcggccg caagctgatc atcgatcaga acgtttttat cgagggtacg 1500

ctgccgatgg gtgtcgtccg cccgctgact gaagtcgaga tggaccatta ccgcgagccg 1560

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cctgtcccga agctgctgtt ctggggcacc ccaggcgttc tgatcccacc ggccgaagcc 1740

gctcgcctgg ccaaaagcct gcctaactgc aaggctgtgg acatcggccc gggtctgaat 1800

ctgctgcaag aagacaaccc ggacctgatc ggcagcgaga tcgcgcgctg gctgtctact 1860

ctggagattt ccggt 1875

<210> 60
<211> 625
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 60
Met Leu Gly Leu Ser Glu Gln Ser Val Ser Ile Ser Arg Cys Ala Gly
1 5 10 15

Thr Arg Leu Pro Ala Leu Leu Asp Glu Gln Gln Val Asn Val Leu Leu
20 25 30

Tyr Asp Met Asn Gly Cys Tyr Ser Arg Leu Lys Glu Leu Val Pro Thr
35 40 45

Leu Pro Gln Asn Arg Lys Val Ser Lys Val Glu Ile Leu Gln His Val
50 55 60

Ile Asp Tyr Ile Arg Asp Leu Gln Leu Glu Leu Asn Ser Glu Ser Glu
65 70 75 80

Val Gly Thr Thr Gly Gly Arg Gly Leu Pro Val Arg Ala Pro Leu Ser
85 90 95

Thr Leu Asn Gly Glu Ile Ser Ala Leu Ala Ala Glu Ala Ala Cys Val
100 105 110

Pro Ala Asp Asp Arg Ile Leu Cys Arg Val Ser Leu Glu Asn Leu Tyr
115 120 125

Phe Gln Ala Ser Gly Gly Gly Gly Gly Ala Ile Ala Met Val Phe Thr
130 135 140

Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu
145 150 155 160

Asp Gln Val Leu Glu Gln Gly Gly Leu Ser Ser Leu Phe Gln Asn Leu
165 170 175

Gly Val Ser Val Thr Pro Ile Gln Lys Ile Val Leu Ser Gly Glu Asn
180 185 190

Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr Glu Gly Leu Ser
195 200 205

Gly Tyr Gln Met Gly Gln Ile Glu Lys Ile Phe Lys Val Val Tyr Pro
210 215 220

```
Val Asp Asp His His Phe Lys Val Ile Leu His Tyr Gly Thr Leu Val
225                 230                 235                 240

Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr
                245                 250                 255

Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr
            260                 265                 270

Leu Trp Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp
        275                 280                 285

Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg
    290                 295                 300

Leu Cys Glu Arg Ile Leu Ala Gly Tyr Leu Glu Pro Thr Thr Glu Asp
305                 310                 315                 320

Leu Tyr Phe Gln Ser Asp Asn Asp Gly Ser Glu Ile Gly Thr Gly Phe
                325                 330                 335

Pro Phe Asp Pro His Tyr Val Glu Val Leu Gly Glu Arg Met His Tyr
            340                 345                 350

Val Asp Val Gly Pro Arg Asp Gly Thr Pro Val Leu Phe Leu His Gly
        355                 360                 365

Asn Pro Thr Ser Ser Tyr Val Trp Arg Asn Ile Ile Pro His Val Ala
    370                 375                 380

Pro Thr His Arg Cys Ile Ala Pro Asp Leu Ile Gly Met Gly Lys Ser
385                 390                 395                 400

Asp Lys Pro Asp Leu Gly Tyr Phe Phe Asp Asp His Val Arg Phe Met
                405                 410                 415

Asp Ala Phe Ile Glu Ala Leu Gly Leu Glu Glu Val Val Leu Val Ile
            420                 425                 430

His Asp Trp Gly Ser Ala Leu Gly Phe His Trp Ala Lys Arg Asn Pro
        435                 440                 445

Glu Arg Val Lys Gly Ile Ala Phe Met Glu Phe Ile Arg Pro Ile Pro
    450                 455                 460

Thr Trp Asp Glu Trp Pro Glu Phe Ala Arg Glu Thr Phe Gln Ala Phe
465                 470                 475                 480

Arg Thr Thr Asp Val Gly Arg Lys Leu Ile Ile Asp Gln Asn Val Phe
                485                 490                 495
```

Ile Glu Gly Thr Leu Pro Met Gly Val Val Arg Pro Leu Thr Glu Val
500 505 510

Glu Met Asp His Tyr Arg Glu Pro Phe Leu Asn Pro Val Asp Arg Glu
515 520 525

Pro Leu Trp Arg Phe Pro Asn Glu Leu Pro Ile Ala Gly Glu Pro Ala
530 535 540

Asn Ile Val Ala Leu Val Glu Glu Tyr Met Asp Trp Leu His Gln Ser
545 550 555 560

Pro Val Pro Lys Leu Leu Phe Trp Gly Thr Pro Gly Val Leu Ile Pro
565 570 575

Pro Ala Glu Ala Ala Arg Leu Ala Lys Ser Leu Pro Asn Cys Lys Ala
580 585 590

Val Asp Ile Gly Pro Gly Leu Asn Leu Leu Gln Glu Asp Asn Pro Asp
595 600 605

Leu Ile Gly Ser Glu Ile Ala Arg Trp Leu Ser Thr Leu Glu Ile Ser
610 615 620

Gly
625

<210> 61
<211> 1875
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 61
atgcttggtc tgtcggagca aagcgtgtcc atctcgcgct gcgctgggac gcgcctgccc 60

gccttgctgg acgagcagca ggtgaacgtc ctgctctacg acatgaacgg ctgctactca 120

cgcctcaagg agctggtgcc caccctgccc cagaaccgca aagtgagcaa ggtggagatc 180

ctgcagcatg taatcgacta catcagggac ctgcagctgg agctgaactc ggagtctgaa 240

gtcgggacca ccggaggccg gggactgcct gtccgcgccc cgctcagcac cctgaacggc 300

gagatcagtg ccttggcggc cgaggcggca tgtgttccag ccgacgatcg catcttgtgt 360

cgcgtttctc ttgagaatct ttattttcag gcgtctggag gtggtggcgg agcgatcgcc 420

atggtgttta cattggagga tttcgttgga gactggcggc agacagctgg atacaaccta 480

gatcaagtgt tagaacaagg aggattgtct agtctgttcc aaaagctggg agtgtcagtc 540

accccaatcc agaaaattgt gctgtctggg gagaatgggt taaaaattga tattcatgtc 600

atcatccctt acgagggact cagtggttat caaatgggtc agattgaaaa gatcttcaaa 660

gttgtttacc cagtggatga tcatcatttc aaggttattc tccattatgg tacactcgtt 720

attgacggtg tgacaccaaa catgattgac tactttggac gcccttacga gggaattgct 780

gtgtttgacg gcaagaagat cacagttact ggaactctgt ggaacggcaa caagatcatt 840

gatgagcgcc tgatcaaccc agatggttca ctcctcttcc gcgttactat caatggagtc 900

accggatggc gcctttgcga gcgtattctt gccgtttctc tcgagccaac cactgaggat 960

ctgtactttc agagcgataa cgatggatcc gaaatcggta ctggctttcc attcgacccc 1020

cattatgtgg aagtcctggg cgagcgcatg cactacgtcg atgttggtcc gcgcgatggc 1080

acccctgtgc tgttcctgca cggtaacccg acctcctcct acgtgtggcg caacatcatc 1140

ccgcatgttg caccgaccca tcgctgcatt gctccagacc tgatcggtat gggcaaatcc 1200

gacaaaccag acctgggtta tttcttcgac gaccacgtcc gcttcatgga tgccttcatc 1260

gaagccctgg gtctggaaga ggtcgtcctg gtcattcacg actggggctc cgctctgggt 1320

ttccactggg ccaagcgcaa tccagagcgc gtcaaaggta ttgcatttat ggagttcatc 1380

cgccctatcc cgacctggga cgaatggcca gaatttgccc gcgagacctt ccaggccttc 1440

cgcaccaccg acgtcggccg caagctgatc atcgatcaga acgtttttat cgagggtacg 1500

ctgccgatgg gtgtcgtccg cccgctgact gaagtcgaga tggaccatta ccgcgagccg 1560

ttcctgaatc ctgttgaccg cgagccactg tggcgcttcc caaacgagct gccaatcgcc 1620

ggtgagccag cgaacatcgt cgcgctggtc gaagaataca tggactggct gcaccagtcc 1680

cctgtcccga agctgctgtt ctggggcacc ccaggcgttc tgatcccacc ggccgaagcc 1740

gctcgcctgg ccaaaagcct gcctaactgc aaggctgtgg acatcggccc gggtctgaat 1800

ctgctgcaag aagacaaccc ggacctgatc ggcagcgaga tcgcgcgctg gctgtctact 1860

ctggagattt ccggt 1875

<210> 62
<211> 625
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 62
Met Leu Gly Leu Ser Glu Gln Ser Val Ser Ile Ser Arg Cys Ala Gly
1 5 10 15

Thr Arg Leu Pro Ala Leu Leu Asp Glu Gln Gln Val Asn Val Leu Leu
20 25 30

Tyr Asp Met Asn Gly Cys Tyr Ser Arg Leu Lys Glu Leu Val Pro Thr
35 40 45

Leu Pro Gln Asn Arg Lys Val Ser Lys Val Glu Ile Leu Gln His Val

50 55 60

Ile Asp Tyr Ile Arg Asp Leu Gln Leu Glu Leu Asn Ser Glu Ser Glu
65 70 75 80

Val Gly Thr Thr Gly Gly Arg Gly Leu Pro Val Arg Ala Pro Leu Ser
85 90 95

Thr Leu Asn Gly Glu Ile Ser Ala Leu Ala Ala Glu Ala Ala Cys Val
100 105 110

Pro Ala Asp Asp Arg Ile Leu Cys Arg Val Ser Leu Glu Asn Leu Tyr
115 120 125

Phe Gln Ala Ser Gly Gly Gly Gly Gly Ala Ile Ala Met Val Phe Thr
130 135 140

Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu
145 150 155 160

Asp Gln Val Leu Glu Gln Gly Gly Leu Ser Ser Leu Phe Gln Lys Leu
165 170 175

Gly Val Ser Val Thr Pro Ile Gln Lys Ile Val Leu Ser Gly Glu Asn
180 185 190

Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr Glu Gly Leu Ser
195 200 205

Gly Tyr Gln Met Gly Gln Ile Glu Lys Ile Phe Lys Val Val Tyr Pro
210 215 220

Val Asp Asp His His Phe Lys Val Ile Leu His Tyr Gly Thr Leu Val
225 230 235 240

Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr
245 250 255

Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr
260 265 270

Leu Trp Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp
275 280 285

Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg
290 295 300

Leu Cys Glu Arg Ile Leu Ala Val Ser Leu Glu Pro Thr Thr Glu Asp
305 310 315 320

Leu Tyr Phe Gln Ser Asp Asn Asp Gly Ser Glu Ile Gly Thr Gly Phe

325 330 335

Pro Phe Asp Pro His Tyr Val Glu Val Leu Gly Glu Arg Met His Tyr
340 345 350

Val Asp Val Gly Pro Arg Asp Gly Thr Pro Val Leu Phe Leu His Gly
355 360 365

Asn Pro Thr Ser Ser Tyr Val Trp Arg Asn Ile Ile Pro His Val Ala
370 375 380

Pro Thr His Arg Cys Ile Ala Pro Asp Leu Ile Gly Met Gly Lys Ser
385 390 395 400

Asp Lys Pro Asp Leu Gly Tyr Phe Phe Asp Asp His Val Arg Phe Met
405 410 415

Asp Ala Phe Ile Glu Ala Leu Gly Leu Glu Glu Val Val Leu Val Ile
420 425 430

His Asp Trp Gly Ser Ala Leu Gly Phe His Trp Ala Lys Arg Asn Pro
435 440 445

Glu Arg Val Lys Gly Ile Ala Phe Met Glu Phe Ile Arg Pro Ile Pro
450 455 460

Thr Trp Asp Glu Trp Pro Glu Phe Ala Arg Glu Thr Phe Gln Ala Phe
465 470 475 480

Arg Thr Thr Asp Val Gly Arg Lys Leu Ile Ile Asp Gln Asn Val Phe
485 490 495

Ile Glu Gly Thr Leu Pro Met Gly Val Val Arg Pro Leu Thr Glu Val
500 505 510

Glu Met Asp His Tyr Arg Glu Pro Phe Leu Asn Pro Val Asp Arg Glu
515 520 525

Pro Leu Trp Arg Phe Pro Asn Glu Leu Pro Ile Ala Gly Glu Pro Ala
530 535 540

Asn Ile Val Ala Leu Val Glu Glu Tyr Met Asp Trp Leu His Gln Ser
545 550 555 560

Pro Val Pro Lys Leu Leu Phe Trp Gly Thr Pro Gly Val Leu Ile Pro
565 570 575

Pro Ala Glu Ala Ala Arg Leu Ala Lys Ser Leu Pro Asn Cys Lys Ala
580 585 590

Val Asp Ile Gly Pro Gly Leu Asn Leu Leu Gln Glu Asp Asn Pro Asp

595 600 605

Leu Ile Gly Ser Glu Ile Ala Arg Trp Leu Ser Thr Leu Glu Ile Ser
610 615 620

Gly
625

<210> 63
<211> 1875
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 63
atgcttggtc tgtcggagca aagcgtgtcc atctcgcgct gcgctgggac gcgcctgccc 60

gccttgctgg acgagcagca ggtgaacgtc ctgctctacg acatgaacgg ctgctactca 120

cgcctcaagg agctggtgcc caccctgccc cagaaccgca aagtgagcaa ggtggagatc 180

ctgcagcatg taatcgacta catcagggac ctgcagctgg agctgaactc ggagtctgaa 240

gtcgggacca ccggaggccg gggactgcct gtccgcgccc cgctcagcac cctgaacggc 300

gagatcagtg ccttggcggc cgaggcggca tgtgttccag ccgacgatcg catcttgtgt 360

cgcgtttctc ttgagaatct ttattttcag gcgtctggag gtggtggcgg agcgatcgcc 420

atggtgttta cattggagga tttcgttgga gactggcggc agacagctgg atacaaccta 480

gatcaagtgt tagaacaagg aggagtgtct agtctgttcc aaaagctggg agtgtcaatc 540

accccaatcc agaaaattgt gctgtctggg gagaatgggt taaaaattga tattcatgtc 600

atcatccctt acgagggact cagtggttat caaatgggtc agattgaaaa gatcttcaaa 660

gttgtttacc cagtggatga tcatcatttc aaggttattc tccattatgg tacactcgtt 720

attgacggtg tgacaccaaa catgattgac tactttggac gcccttacga gggaattgct 780

gtgtttgacg gcaagaagat cacagttact ggaactctgt ggaacggcaa caagatcatt 840

gatgagcgcc tgatcaaccc agatggttca ctcctcttcc gcgttactat caatggagtc 900

accggatggc gcctttgcga gcgtattctt gccgtttctc tcgagccaac cactgaggat 960

ctgtactttc agagcgataa cgatggatcc gaaatcggta ctggctttcc attcgacccc 1020

cattatgtgg aagtcctggg cgagcgcatg cactacgtcg atgttggtcc gcgcgatggc 1080

acccctgtgc tgttcctgca cggtaacccg acctcctcct acgtgtggcg caacatcatc 1140

ccgcatgttg caccgaccca tcgctgcatt gctccagacc tgatcggtat gggcaaatcc 1200

gacaaaccag acctgggtta tttcttcgac gaccacgtcc gcttcatgga tgccttcatc 1260

gaagccctgg gtctggaaga ggtcgtcctg gtcattcacg actggggctc cgctctgggt 1320

ttccactggg ccaagcgcaa tccagagcgc gtcaaaggta ttgcatttat ggagttcatc 1380

cgccctatcc cgacctggga cgaatggcca gaatttgccc gcgagacctt ccaggccttc 1440

cgcaccaccg acgtcggccg caagctgatc atcgatcaga acgtttttat cgagggtacg 1500

ctgccgatgg gtgtcgtccg cccgctgact gaagtcgaga tggaccatta ccgcgagccg 1560

ttcctgaatc ctgttgaccg cgagccactg tggcgcttcc caaacgagct gccaatcgcc 1620

ggtgagccag cgaacatcgt cgcgctggtc gaagaataca tggactggct gcaccagtcc 1680

cctgtcccga agctgctgtt ctggggcacc ccaggcgttc tgatcccacc ggccgaagcc 1740

gctcgcctgg ccaaaagcct gcctaactgc aaggctgtgg acatcggccc gggtctgaat 1800

ctgctgcaag aagacaaccc ggacctgatc ggcagcgaga tcgcgcgctg gctgtctact 1860

ctggagattt ccggt 1875

<210> 64
<211> 625
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 64
Met Leu Gly Leu Ser Glu Gln Ser Val Ser Ile Ser Arg Cys Ala Gly
1 5 10 15

Thr Arg Leu Pro Ala Leu Leu Asp Glu Gln Gln Val Asn Val Leu Leu
20 25 30

Tyr Asp Met Asn Gly Cys Tyr Ser Arg Leu Lys Glu Leu Val Pro Thr
35 40 45

Leu Pro Gln Asn Arg Lys Val Ser Lys Val Glu Ile Leu Gln His Val
50 55 60

Ile Asp Tyr Ile Arg Asp Leu Gln Leu Glu Leu Asn Ser Glu Ser Glu
65 70 75 80

Val Gly Thr Thr Gly Gly Arg Gly Leu Pro Val Arg Ala Pro Leu Ser
85 90 95

Thr Leu Asn Gly Glu Ile Ser Ala Leu Ala Ala Glu Ala Ala Cys Val
100 105 110

Pro Ala Asp Asp Arg Ile Leu Cys Arg Val Ser Leu Glu Asn Leu Tyr
115 120 125

Phe Gln Ala Ser Gly Gly Gly Gly Gly Ala Ile Ala Met Val Phe Thr
130 135 140

Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu
145 150 155 160

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Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu Phe Gln Lys Leu
                165                 170                 175

Gly Val Ser Ile Thr Pro Ile Gln Lys Ile Val Leu Ser Gly Glu Asn
            180                 185                 190

Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr Glu Gly Leu Ser
        195                 200                 205

Gly Tyr Gln Met Gly Gln Ile Glu Lys Ile Phe Lys Val Val Tyr Pro
    210                 215                 220

Val Asp Asp His His Phe Lys Val Ile Leu His Tyr Gly Thr Leu Val
225                 230                 235                 240

Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr
                245                 250                 255

Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr
            260                 265                 270

Leu Trp Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp
        275                 280                 285

Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg
    290                 295                 300

Leu Cys Glu Arg Ile Leu Ala Val Ser Leu Glu Pro Thr Thr Glu Asp
305                 310                 315                 320

Leu Tyr Phe Gln Ser Asp Asn Asp Gly Ser Glu Ile Gly Thr Gly Phe
                325                 330                 335

Pro Phe Asp Pro His Tyr Val Glu Val Leu Gly Glu Arg Met His Tyr
            340                 345                 350

Val Asp Val Gly Pro Arg Asp Gly Thr Pro Val Leu Phe Leu His Gly
        355                 360                 365

Asn Pro Thr Ser Ser Tyr Val Trp Arg Asn Ile Ile Pro His Val Ala
    370                 375                 380

Pro Thr His Arg Cys Ile Ala Pro Asp Leu Ile Gly Met Gly Lys Ser
385                 390                 395                 400

Asp Lys Pro Asp Leu Gly Tyr Phe Phe Asp Asp His Val Arg Phe Met
                405                 410                 415

Asp Ala Phe Ile Glu Ala Leu Gly Leu Glu Glu Val Val Leu Val Ile
            420                 425                 430
```

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His Asp Trp Gly Ser Ala Leu Gly Phe His Trp Ala Lys Arg Asn Pro
        435                 440                 445

Glu Arg Val Lys Gly Ile Ala Phe Met Glu Phe Ile Arg Pro Ile Pro
    450                 455                 460

Thr Trp Asp Glu Trp Pro Glu Phe Ala Arg Glu Thr Phe Gln Ala Phe
465                 470                 475                 480

Arg Thr Thr Asp Val Gly Arg Lys Leu Ile Ile Asp Gln Asn Val Phe
                485                 490                 495

Ile Glu Gly Thr Leu Pro Met Gly Val Val Arg Pro Leu Thr Glu Val
            500                 505                 510

Glu Met Asp His Tyr Arg Glu Pro Phe Leu Asn Pro Val Asp Arg Glu
        515                 520                 525

Pro Leu Trp Arg Phe Pro Asn Glu Leu Pro Ile Ala Gly Glu Pro Ala
    530                 535                 540

Asn Ile Val Ala Leu Val Glu Glu Tyr Met Asp Trp Leu His Gln Ser
545                 550                 555                 560

Pro Val Pro Lys Leu Leu Phe Trp Gly Thr Pro Gly Val Leu Ile Pro
                565                 570                 575

Pro Ala Glu Ala Ala Arg Leu Ala Lys Ser Leu Pro Asn Cys Lys Ala
            580                 585                 590

Val Asp Ile Gly Pro Gly Leu Asn Leu Leu Gln Glu Asp Asn Pro Asp
        595                 600                 605

Leu Ile Gly Ser Glu Ile Ala Arg Trp Leu Ser Thr Leu Glu Ile Ser
    610                 615                 620

Gly
625
```

<210> 65
<211> 636
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 65
atggtgttta cactcgaaga tttcgtaggg gactggcggc agacagccgg ctacaacctg 60

gaccaagtcc ttgagcaggg cggtctgtcc agtttgtttc agaaactcgg ggtgtccgta 120

acaccgatcc aaaagattgt cctgagcggt gaaaacggcc tgaagatcga catccatgtc 180

atcatcccgt atgaaggtct gagcggctat cagatgggcc agatcgaaaa aatttttaag 240

gtggtgtacc ctgtggatga tcatcacttt aaggtgattc tgcactatgg cacactggta 300

atcgacgggg ttacgccgaa catgatcgac tatttcggac ggccgtatga aggcatcgcc 360

gtgttcgacg gcaaaaagat cactgtaacc gggaccctgt ggaacggcaa caaaattatc 420

gacgagcgcc tgatcaaccc cgacggctcc ctgctgttcc gcgtaaccat caacggagtg 480

accggctggc ggctgtgcga gcgcattttg gcgaattctc acggcttccc tcccgaggtg 540

gaggagcagg ccgccggcac cctgcccatg agctgcgccc aggagagcgg catggataga 600

caccctgctg cttgcgccag cgccaggatc aacgtc 636

<210> 66
<211> 82
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown: antioxidant response element (2X ARE) oligonucleotide

<400> 66
tagcttggaa atgacattgc taatggtgac aaagcaactt ttagcttgga aatgacattg 60

ctaatggtga caaagcaact tt 82

<210> 67
<211> 45
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown: heat shock response element (HRE) oligonucleotide

<400> 67
ctggaatttt ctagactgga attttctaga ctggaatttt ctaga 45

<210> 68
<211> 516
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 68
atggtgttta cactcgaaga tttcgtaggg gactggcggc agacagccgg ctacaacctg 60

gaccaagtcc ttgagcaggg cggtctgtcc agtttgtttc agaatctcgg ggtgtccgta 120

acaccgatcc aaaagattgt cctgagcggt gaaaacggcc tgaagatcga catccatgtc 180

atcatcccgt atgaaggtct gagcggctat cagatgggcc agatcgaaaa aatttttaag 240

gtggtgtacc ctgtggatga tcatcacttt aaggtgattc tgcactatgg cacactggta 300

atcgacgggg ttacgccgaa catgatcgac tatttcggac ggccgtatga aggcatcgcc 360

gtgttcgacg gcaaaaagat cactgtaacc gggaccctgt ggaacggcaa caaaattatc 420

gacgagcgcc tgatcaaccc cgacggctcc ctgctgttcc gcgtaaccat caacggagtg 480

accggctggc ggctgtgcga gcgcattttg gcggga 516

<210> 69
<211> 172
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 69
Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala
1 5 10 15

Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Leu Ser Ser Leu
20 25 30

Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln Lys Ile Val Leu
35 40 45

Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr
50 55 60

Glu Gly Leu Ser Gly Tyr Gln Met Gly Gln Ile Glu Lys Ile Phe Lys
65 70 75 80

Val Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu His Tyr
85 90 95

Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe
100 105 110

Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr
115 120 125

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

Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val
145 150 155 160

Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala Gly
165 170

<210> 70
<211> 516
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 70
atggtgttta cactcgaaga tttcgtaggg gactggcggc agacagccgg ctacaacctg 60

gaccaagtcc ttgagcaggg cggtctgtcc agtttgtttc agaatctcgg ggtgtccgta 120

actccgatcc aaaagattgt cctgagcggt gaaaacggcc tgaagatcga catccatgtc 180

atcatcccgt atgaaggtct gagcggctat cagatgggcc agatcgaaaa aatttttaag 240

gtggtgtacc ctgtggatga tcatcacttt aaggtgattc tgcactatgg cacactggta 300

atcgacgggg ttacgccgaa catgatcgac tatttcggac ggccgtatga aggcatcgcc 360

gtgttcgacg gcaaaaagat cactgtaacc gggaccctgt ggaacggcaa caaaattatc 420

gacgagcgcc tgatcaaccc cgacggctcc ctgctgttcc gcgtaaccat caacggagtg 480

accggctggc ggctgtgcga gcgcattttg gcggga 516

<210> 71
<211> 172
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 71
Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala
1 5 10 15

Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Leu Ser Ser Leu
20 25 30

Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln Lys Ile Val Leu
35 40 45

Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr
50 55 60

Glu Gly Leu Ser Gly Tyr Gln Met Gly Gln Ile Glu Lys Ile Phe Lys
65 70 75 80

Val Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu His Tyr
85 90 95

Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe
100 105 110

Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr
115 120 125

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

Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val

145 150 155 160

Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala Gly
165 170

<210> 72
<211> 516
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 72
atggtgttta cactcgaaga tttcgtaggg gactggcggc agacagccgg ctacaacctg 60

gaccaagtcc ttgagcaggg cggcctgtcc agtttgtttc agaatctcgg ggtgtccgta 120

acaccgatcc aaaagattgt cctgagcggt gaaaacggcc tgaagatcga catccatgtc 180

atcatcccgt atgaaggtct gagcggctat cagatgggcc agatcgaaaa aatttttaag 240

gtggtgtacc ctgtggatga tcatcacttt aaggtgattc tgcactatgg cacactggta 300

atcgacgggg ttacgccgaa cttgatcgac tatttcggac gtccgtatga aggcatcgcc 360

gtgttcgacg gcaaaaagat cactgtaacc gggaccctgt ggaacggcaa caaaattatc 420

gacgagcgcc tgatcaaccc cgacggctcc ctgctgttcc gcgtaaccat caacggagtg 480

accggctggc ggctgtgcga gcgcattttg gcggga 516

<210> 73
<211> 172
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 73
Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala
1 5 10 15

Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Leu Ser Ser Leu
20 25 30

Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln Lys Ile Val Leu
35 40 45

Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr
50 55 60

Glu Gly Leu Ser Gly Tyr Gln Met Gly Gln Ile Glu Lys Ile Phe Lys
65 70 75 80

Val Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu His Tyr
85 90 95

Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Leu Ile Asp Tyr Phe
100 105 110

Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr
115 120 125

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

Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val
145 150 155 160

Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala Gly
165 170

<210> 74
<211> 516
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 74
atggtgttta cactcgaaga tttcgtaggg gactggcagc agacagccgg ctacaacctg 60

gaccaagtcc ttgagcaggg cggtctgtcc agtttgtttc agaatctcgg ggtgtccgta 120

actccgatcc aaaagattgt cctgagcggt gaaaacggcc tgaagatcga catccatgtc 180

atcatcccgt atgaaggtct gagcggctat cagatgggcc agatcgaaaa aatttttaag 240

gtggtgtacc ctgtggatga tcatcacttt aaggtgattc tgcactatgg cacactggta 300

atcgacgggg ttacgccgaa catgatcgac tatttcggac ggccgtatga aggcatcgcc 360

gtgttcgacg gcaaaaagat cactgtaacc gggaccctgt ggaacggcaa caaaattatc 420

gacgagcgcc tgatcaaccc cgacggctcc ctgctgttcc gcgtaaccat caacggagtg 480

accggctggc ggctgtgcga gcgcattttg gcggga 516

<210> 75
<211> 172
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 75
Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Gln Gln Thr Ala
1 5 10 15

Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Leu Ser Ser Leu
20 25 30

Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln Lys Ile Val Leu
35 40 45

Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr
50 55 60

Glu Gly Leu Ser Gly Tyr Gln Met Gly Gln Ile Glu Lys Ile Phe Lys
65 70 75 80

Val Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu His Tyr
85 90 95

Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe
100 105 110

Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr
115 120 125

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

Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val
145 150 155 160

Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala Gly
165 170

<210> 76
<211> 1797
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 76
atgcttggtc tgtcggagca aagcgtgtcc atctcgcgct gcgctgggac gcgcctgccc 60

gccttgctgg acgagcagca ggtgaacgtc ctgctctacg acatgaacgg ctgctactca 120

cgcctcaagg agctggtgcc caccctgccc cagaaccgca aagtgagcaa ggtggagatc 180

ctgcagcatg taatcgacta catcagggac ctgcagctgg agctgaactc ggagtctgaa 240

gtcgggacca ccggaggccg gggactgcct gtccgcgccc cgctcagcac cctgaacggc 300

gagatcagtg ccttggcggc cgaggcggca tgtgttccag ccgacgatcg catcttgtgt 360

cgcgtttctc ttgagaatct ttattttcag gcgtctggag gtggtggcgg agcgatcgcc 420

atggtgttta cactcgaaga tttcgtaggg gactggcggc agacagccgg ctacaacctg 480

gaccaagtcc ttgagcaggg cggcctgtcc agtttgtttc agaatctcgg ggtgtccgta 540

acaccgatcc aaaagattgt cctgagcggt gaaaacggcc tgaagatcga catccatgtc 600

atcatcccgt atgaaggtct gagcggctat cagatgggcc agatcgaaaa aatttttaag 660

gtggtgtacc ctgtggatga tcatcacttt aaggtgattc tgcactatgg cacactggta 720

atcgacgggg ttacgccgaa cttgatcgac tatttcggac gtccgtatga aggcatcgcc 780

gtgttcgacg gcaaaaagat cactgtaacc gggaccctgt ggaacggcaa caaaattatc 840

gacgagcgcc tgatcaaccc cgacggctcc ctgctgttcc gcgtaaccat caacggagtg 900

accggctggc ggctgtgcga gcgcattttg gcgggatatc tcgagccaac cactgaggat 960

ctgtactttc agagcgataa cgatggatcc gaaatcggta ctggctttcc attcgacccc 1020

cattatgtgg aagtcctggg cgagcgcatg cactacgtcg atgttggtcc gcgcgatggc 1080

acccctgtgc tgttcctgca cggtaacccg acctcctcct acgtgtggcg caacatcatc 1140

ccgcatgttg caccgaccca tcgctgcatt gctccagacc tgatcggtat gggcaaatcc 1200

gacaaaccag acctgggtta tttcttcgac gaccacgtcc gcttcatgga tgccttcatc 1260

gaagccctgg gtctggaaga ggtcgtcctg gtcattcacg actggggctc cgctctgggt 1320

ttccactggg ccaagcgcaa tccagagcgc gtcaaaggta ttgcatttat ggagttcatc 1380

cgccctatcc cgacctggga cgaatggcca gaatttgccc gcgagacctt ccaggccttc 1440

cgcaccaccg acgtcggccg caagctgatc atcgatcaga acgtttttat cgagggtacg 1500

ctgccgatgg gtgtcgtccg cccgctgact gaagtcgaga tggaccatta ccgcgagccg 1560

ttcctgaatc ctgttgaccg cgagccactg tggcgcttcc caaacgagct gccaatcgcc 1620

ggtgagccag cgaacatcgt cgcgctggtc gaagaataca tggactggct gcaccagtcc 1680

cctgtcccga agctgctgtt ctggggcacc ccaggcgttc tgatcccacc ggccgaagcc 1740

gctcgcctgg ccaaaagcct gcctaactgc aaggctgtgg acatcggccc gggtctg 1797

<210> 77
<211> 599
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 77
Met Leu Gly Leu Ser Glu Gln Ser Val Ser Ile Ser Arg Cys Ala Gly
1 5 10 15

Thr Arg Leu Pro Ala Leu Leu Asp Glu Gln Gln Val Asn Val Leu Leu
20 25 30

Tyr Asp Met Asn Gly Cys Tyr Ser Arg Leu Lys Glu Leu Val Pro Thr
35 40 45

Leu Pro Gln Asn Arg Lys Val Ser Lys Val Glu Ile Leu Gln His Val
50 55 60

Ile Asp Tyr Ile Arg Asp Leu Gln Leu Glu Leu Asn Ser Glu Ser Glu
65 70 75 80

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Val Gly Thr Thr Gly Gly Arg Gly Leu Pro Val Arg Ala Pro Leu Ser
                85                  90                  95

Thr Leu Asn Gly Glu Ile Ser Ala Leu Ala Ala Glu Ala Ala Cys Val
            100                 105                 110

Pro Ala Asp Asp Arg Ile Leu Cys Arg Val Ser Leu Glu Asn Leu Tyr
        115                 120                 125

Phe Gln Ala Ser Gly Gly Gly Gly Gly Ala Ile Ala Met Val Phe Thr
    130                 135                 140

Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu
145                 150                 155                 160

Asp Gln Val Leu Glu Gln Gly Gly Leu Ser Ser Leu Phe Gln Asn Leu
                165                 170                 175

Gly Val Ser Val Thr Pro Ile Gln Lys Ile Val Leu Ser Gly Glu Asn
            180                 185                 190

Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr Glu Gly Leu Ser
        195                 200                 205

Gly Tyr Gln Met Gly Gln Ile Glu Lys Ile Phe Lys Val Val Tyr Pro
    210                 215                 220

Val Asp Asp His His Phe Lys Val Ile Leu His Tyr Gly Thr Leu Val
225                 230                 235                 240

Ile Asp Gly Val Thr Pro Asn Leu Ile Asp Tyr Phe Gly Arg Pro Tyr
                245                 250                 255

Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr
            260                 265                 270

Leu Trp Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp
        275                 280                 285

Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg
    290                 295                 300

Leu Cys Glu Arg Ile Leu Ala Gly Tyr Leu Glu Pro Thr Thr Glu Asp
305                 310                 315                 320

Leu Tyr Phe Gln Ser Asp Asn Asp Gly Ser Glu Ile Gly Thr Gly Phe
                325                 330                 335

Pro Phe Asp Pro His Tyr Val Glu Val Leu Gly Glu Arg Met His Tyr
            340                 345                 350
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Val Asp Val Gly Pro Arg Asp Gly Thr Pro Val Leu Phe Leu His Gly
        355                 360                 365

Asn Pro Thr Ser Ser Tyr Val Trp Arg Asn Ile Ile Pro His Val Ala
    370                 375                 380

Pro Thr His Arg Cys Ile Ala Pro Asp Leu Ile Gly Met Gly Lys Ser
385                 390                 395                 400

Asp Lys Pro Asp Leu Gly Tyr Phe Phe Asp Asp His Val Arg Phe Met
                405                 410                 415

Asp Ala Phe Ile Glu Ala Leu Gly Leu Glu Glu Val Val Leu Val Ile
            420                 425                 430

His Asp Trp Gly Ser Ala Leu Gly Phe His Trp Ala Lys Arg Asn Pro
        435                 440                 445

Glu Arg Val Lys Gly Ile Ala Phe Met Glu Phe Ile Arg Pro Ile Pro
    450                 455                 460

Thr Trp Asp Glu Trp Pro Glu Phe Ala Arg Glu Thr Phe Gln Ala Phe
465                 470                 475                 480

Arg Thr Thr Asp Val Gly Arg Lys Leu Ile Ile Asp Gln Asn Val Phe
                485                 490                 495

Ile Glu Gly Thr Leu Pro Met Gly Val Val Arg Pro Leu Thr Glu Val
            500                 505                 510

Glu Met Asp His Tyr Arg Glu Pro Phe Leu Asn Pro Val Asp Arg Glu
        515                 520                 525

Pro Leu Trp Arg Phe Pro Asn Glu Leu Pro Ile Ala Gly Glu Pro Ala
    530                 535                 540

Asn Ile Val Ala Leu Val Glu Glu Tyr Met Asp Trp Leu His Gln Ser
545                 550                 555                 560

Pro Val Pro Lys Leu Leu Phe Trp Gly Thr Pro Gly Val Leu Ile Pro
                565                 570                 575

Pro Ala Glu Ala Ala Arg Leu Ala Lys Ser Leu Pro Asn Cys Lys Ala
            580                 585                 590

Val Asp Ile Gly Pro Gly Leu
        595
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<210> 78
<211> 1875

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 78
atgcttggtc tgtcggagca aagcgtgtcc atctcgcgct gcgctgggac gcgcctgccc 60

gccttgctgg acgagcagca ggtgaacgtc ctgctctacg acatgaacgg ctgctactca 120

cgcctcaagg agctggtgcc caccctgccc cagaaccgca aagtgagcaa ggtggagatc 180

ctgcagcatg taatcgacta catcagggac ctgcagctgg agctgaactc ggagtctgaa 240

gtcgggacca ccggaggccg gggactgcct gtccgcgccc cgctcagcac cctgaacggc 300

gagatcagtg ccttggcggc cgaggcggca tgtgttccag ccgacgatcg catcttgtgt 360

cgcgtttctc ttgagaatct ttattttcag gcgtctggag gtggtggcgg agcgatcgcc 420

atggtgttta cactcgaaga tttcgtaggg gactggcagc agacagccgg ctacaacctg 480

gaccaagtcc ttgagcaggg cggtctgtcc agtttgtttc agaatctcgg ggtgtccgta 540

actccgatcc aaaagattgt cctgagcggt gaaaacggcc tgaagatcga catccatgtc 600

atcatcccgt atgaaggtct gagcggctat cagatgggcc agatcgaaaa aatttttaag 660

gtggtgtacc ctgtggatga tcatcacttt aaggtgattc tgcactatgg cacactggta 720

atcgacgggg ttacgccgaa catgatcgac tatttcggac ggccgtatga aggcatcgcc 780

gtgttcgacg gcaaaaagat cactgtaacc gggaccctgt ggaacggcaa caaaattatc 840

gacgagcgcc tgatcaaccc cgacggctcc ctgctgttcc gcgtaaccat caacggagtg 900

accggctggc ggctgtgcga gcgcattttg gcgggatatc tcgagccaac cactgaggat 960

ctgtactttc agagcgataa cgatggatcc gaaatcggta ctggctttcc attcgacccc 1020

cattatgtgg aagtcctggg cgagcgcatg cactacgtcg atgttggtcc gcgcgatggc 1080

acccctgtgc tgttcctgca cggtaacccg acctcctcct acgtgtggcg caacatcatc 1140

ccgcatgttg caccgaccca tcgctgcatt gctccagacc tgatcggtat gggcaaatcc 1200

gacaaaccag acctgggtta tttcttcgac gaccacgtcc gcttcatgga tgccttcatc 1260

gaagccctgg gtctggaaga ggtcgtcctg gtcattcacg actggggctc cgctctgggt 1320

ttccactggg ccaagcgcaa tccagagcgc gtcaaaggta ttgcatttat ggagttcatc 1380

cgccctatcc cgacctggga cgaatggcca gaatttgccc gcgagacctt ccaggccttc 1440

cgcaccaccg acgtcggccg caagctgatc atcgatcaga acgtttttat cgagggtacg 1500

ctgccgatgg gtgtcgtccg cccgctgact gaagtcgaga tggaccatta ccgcgagccg 1560

ttcctgaatc ctgttgaccg cgagccactg tggcgcttcc caaacgagct gccaatcgcc 1620

ggtgagccag cgaacatcgt cgcgctggtc gaagaataca tggactggct gcaccagtcc 1680

cctgtcccga agctgctgtt ctggggcacc ccaggcgttc tgatcccacc ggccgaagcc 1740

gctcgcctgg ccaaaagcct gcctaactgc aaggctgtgg acatcggccc gggtctgaat 1800

ctgctgcaag aagacaaccc ggacctgatc ggcagcgaga tcgcgcgctg gctgtctact 1860

ctggagattt ccggt 1875

<210> 79
<211> 625
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 79

Met Leu Gly Leu Ser Glu Gln Ser Val Ser Ile Ser Arg Cys Ala Gly
1 5 10 15

Thr Arg Leu Pro Ala Leu Leu Asp Glu Gln Gln Val Asn Val Leu Leu
20 25 30

Tyr Asp Met Asn Gly Cys Tyr Ser Arg Leu Lys Glu Leu Val Pro Thr
35 40 45

Leu Pro Gln Asn Arg Lys Val Ser Lys Val Glu Ile Leu Gln His Val
50 55 60

Ile Asp Tyr Ile Arg Asp Leu Gln Leu Glu Leu Asn Ser Glu Ser Glu
65 70 75 80

Val Gly Thr Thr Gly Gly Arg Gly Leu Pro Val Arg Ala Pro Leu Ser
85 90 95

Thr Leu Asn Gly Glu Ile Ser Ala Leu Ala Ala Glu Ala Ala Cys Val
100 105 110

Pro Ala Asp Asp Arg Ile Leu Cys Arg Val Ser Leu Glu Asn Leu Tyr
115 120 125

Phe Gln Ala Ser Gly Gly Gly Gly Gly Ala Ile Ala Met Val Phe Thr
130 135 140

Leu Glu Asp Phe Val Gly Asp Trp Gln Gln Thr Ala Gly Tyr Asn Leu
145 150 155 160

Asp Gln Val Leu Glu Gln Gly Gly Leu Ser Ser Leu Phe Gln Asn Leu
165 170 175

Gly Val Ser Val Thr Pro Ile Gln Lys Ile Val Leu Ser Gly Glu Asn
180 185 190

Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr Glu Gly Leu Ser
195 200 205

Gly Tyr Gln Met Gly Gln Ile Glu Lys Ile Phe Lys Val Val Tyr Pro

210 215 220

Val Asp Asp His His Phe Lys Val Ile Leu His Tyr Gly Thr Leu Val
225 230 235 240

Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr
245 250 255

Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr
260 265 270

Leu Trp Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp
275 280 285

Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg
290 295 300

Leu Cys Glu Arg Ile Leu Ala Gly Tyr Leu Glu Pro Thr Thr Glu Asp
305 310 315 320

Leu Tyr Phe Gln Ser Asp Asn Asp Gly Ser Glu Ile Gly Thr Gly Phe
325 330 335

Pro Phe Asp Pro His Tyr Val Glu Val Leu Gly Glu Arg Met His Tyr
340 345 350

Val Asp Val Gly Pro Arg Asp Gly Thr Pro Val Leu Phe Leu His Gly
355 360 365

Asn Pro Thr Ser Ser Tyr Val Trp Arg Asn Ile Ile Pro His Val Ala
370 375 380

Pro Thr His Arg Cys Ile Ala Pro Asp Leu Ile Gly Met Gly Lys Ser
385 390 395 400

Asp Lys Pro Asp Leu Gly Tyr Phe Phe Asp Asp His Val Arg Phe Met
405 410 415

Asp Ala Phe Ile Glu Ala Leu Gly Leu Glu Glu Val Val Leu Val Ile
420 425 430

His Asp Trp Gly Ser Ala Leu Gly Phe His Trp Ala Lys Arg Asn Pro
435 440 445

Glu Arg Val Lys Gly Ile Ala Phe Met Glu Phe Ile Arg Pro Ile Pro
450 455 460

Thr Trp Asp Glu Trp Pro Glu Phe Ala Arg Glu Thr Phe Gln Ala Phe
465 470 475 480

Arg Thr Thr Asp Val Gly Arg Lys Leu Ile Ile Asp Gln Asn Val Phe

485 490 495

Ile Glu Gly Thr Leu Pro Met Gly Val Val Arg Pro Leu Thr Glu Val
500 505 510

Glu Met Asp His Tyr Arg Glu Pro Phe Leu Asn Pro Val Asp Arg Glu
515 520 525

Pro Leu Trp Arg Phe Pro Asn Glu Leu Pro Ile Ala Gly Glu Pro Ala
530 535 540

Asn Ile Val Ala Leu Val Glu Glu Tyr Met Asp Trp Leu His Gln Ser
545 550 555 560

Pro Val Pro Lys Leu Leu Phe Trp Gly Thr Pro Gly Val Leu Ile Pro
565 570 575

Pro Ala Glu Ala Ala Arg Leu Ala Lys Ser Leu Pro Asn Cys Lys Ala
580 585 590

Val Asp Ile Gly Pro Gly Leu Asn Leu Leu Gln Glu Asp Asn Pro Asp
595 600 605

Leu Ile Gly Ser Glu Ile Ala Arg Trp Leu Ser Thr Leu Glu Ile Ser
610 615 620

Gly
625

<210> 80
<211> 516
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 80
atggtgttta cactcgaaga tttcgtaggg gactggcggc agacagccgg ctacaacctg 60

gaccaagtcc ttgagcaggg cggtctgtcc agtttgtttc agaatctcgg ggtgtccgta 120

acaccgatcc aaaggattgt cctgagcggt gaaaacggcc tgaagatcga catccatgtc 180

atcatcccgt atgaaggtct gagcggcgat cagatgggcc agatcgaaaa aatttttaag 240

gtggtgtacc ctgtggatga tcatcacttt aaggtgattc tgcactatgg cacactggta 300

atcgacgggg ttacgccgaa catgatcgac tatttcggac ggccgtatga aggcatcgcc 360

gtgttcgacg gcaaaaagat cactgtaacc gggaccctgt ggaacggcaa caaaattatc 420

gacgagcgcc tgatcaaccc cgacggctcc ctgctgttcc gcgtaaccat caacggagtg 480

accggctggc ggctgtgcga gcgcattttg gcggga 516

<210> 81
<211> 172
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 81
Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala
1 5 10 15

Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Leu Ser Ser Leu
20 25 30

Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln Arg Ile Val Leu
35 40 45

Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr
50 55 60

Glu Gly Leu Ser Gly Asp Gln Met Gly Gln Ile Glu Lys Ile Phe Lys
65 70 75 80

Val Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu His Tyr
85 90 95

Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe
100 105 110

Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr
115 120 125

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

Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val
145 150 155 160

Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala Gly
165 170

<210> 82
<211> 516
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 82
atggtgttta cactcgaaga tttcgtaggg gactggcggc agacagccgg ctacaacctg 60

gatcaagtcc ttgagcaggg cggtctgtcc agtttgtttc agaatctcgg ggtgtccgta 120

acaccgatcc aaaagattgt cctgagcggt gaaaacggcc tgaagatcga catccatgtc 180

atcatcccgt atgaaggtct gaacggctat cagatgggcc agatcgaaaa aatttttaag 240

gtggtgtacc ctgtggatga tcatcacttt aaggtgattc tgcactatgg cacactggta 300

atcgacgggg ttacgccgaa catgatcgac tatttcggac ggccgtatga aggcatcgcc 360

gtgttcgacg gcaaaaagat cactgtaacc gggaccctgt ggaacggcaa caaaattatc 420

gacgagcgcc tgatcaaccc cgacggctcc ctgctgttcc gcgtaaccat caacggagtg 480

accggctggc ggctgtgcga gcgcattttg gcggga 516

<210> 83
<211> 172
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 83
Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala
1 5 10 15

Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Leu Ser Ser Leu
20 25 30

Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln Lys Ile Val Leu
35 40 45

Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr
50 55 60

Glu Gly Leu Asn Gly Tyr Gln Met Gly Gln Ile Glu Lys Ile Phe Lys
65 70 75 80

Val Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu His Tyr
85 90 95

Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe
100 105 110

Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr
115 120 125

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

Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val
145 150 155 160

Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala Gly
165 170

<210> 84
<211> 1866
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 84
atgcttggtc tgtcggagca aagcgtgtcc atctcgcgct gcgctgggac gcgcctgccc 60

gccttgctgg acgagcagca ggtgaacgtc ctgctctacg acatgaacgg ctgctactca 120

cgcctcaagg agctggtgcc caccctgccc cagaaccgca aagtgagcaa ggtggagatc 180

ctgcagcatg taatcgacta catcagggac ctgcagctgg agctgaactc ggagtctgaa 240

gtcgggacca ccggaggccg gggactgcct gtccgcgccc cgctcagcac cctgaacggc 300

gagatcagtg ccttggcggc cgaggcggca tgtgttccag ccgacgatcg catcttgtgt 360

cgcgtttctc ttgagaatct ttattttcag gcgtctggag gtggtggcgg agcgatcgcc 420

atggtgttta cactcgaaga tttcgtaggg gactggcggc agacagccgg ctacaacctg 480

gaccaagtcc ttgagcaggg cggtctgtcc agtttgtttc agaatctcgg ggtgtccgta 540

acaccgatcc aaaggattgt cctgagcggt gaaaacggcc tgaagatcga catccatgtc 600

atcatcccgt atgaaggtct gagcggcgat cagatgggcc agatcgaaaa aatttttaag 660

gtggtgtacc ctgtggatga tcatcacttt aaggtgattc tgcactatgg cacactggta 720

atcgacgggg ttacgccgaa catgatcgac tatttcggac ggccgtatga aggcatcgcc 780

gtgttcgacg gcaaaaagat cactgtaacc gggaccctgt ggaacggcaa caaaattatc 840

gacgagcgcc tgatcaaccc cgacggctcc ctgctgttcc gcgtaaccat caacggagtg 900

accggctggc ggctgtgcga gcgcattttg gcgggatatc tcgagccaac cactgaggat 960

ctgtactttc agagcgataa cgatggatcc gaaatcggta ctggctttcc attcgacccc 1020

cattatgtgg aagtcctggg cgagcgcatg cactacgtcg atgttggtcc gcgcgatggc 1080

acccctgtgc tgttcctgca cggtaacccg acctcctcct acgtgtggcg caacatcatc 1140

ccgcatgttg caccgaccca tcgctgcatt gctccagacc tgatcggtat gggcaaatcc 1200

gacaaaccag acctgggtta tttcttcgac gaccacgtcc gcttcatgga tgccttcatc 1260

gaagccctgg gtctggaaga ggtcgtcctg gtcattcacg actggggctc cgctctgggt 1320

ttccactggg ccaagcgcaa tccagagcgc gtcaaaggta ttgcatttat ggagttcatc 1380

cgccctatcc cgacctggga cgaatggcca gaatttgccc gcgagacctt ccaggccttc 1440

cgcaccaccg acgtcggccg caagctgatc atcgatcaga acgtttttat cgagggtacg 1500

ctgccgatgg gtgtcgtccg cccgctgact gaagtcgaga tggaccatta ccgcgagccg 1560

ttcctgaatc ctgttgaccg cgagccactg tggcgcttcc caaacgagct gccaatcgcc 1620

ggtgagccag cgaacatcgt cgcgctggtc gaagaataca tggactggct gcaccagtcc 1680

cctgtcccga agctgctgtt ctggggcacc ccaggcgttc tgatcccacc ggccgaagcc 1740

gctcgcctgg ccaaaagcct gcctaactgc aaggctgtgg acatcggccc gggtctgaat 1800

ctgctgcaag aagacaaccc ggacctgatc ggcagcgaga tcgcgcgctg gctgtctact 1860

ctggag 1866

<210> 85
<211> 625
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 85
Met Leu Gly Leu Ser Glu Gln Ser Val Ser Ile Ser Arg Cys Ala Gly
1 5 10 15

Thr Arg Leu Pro Ala Leu Leu Asp Glu Gln Gln Val Asn Val Leu Leu
20 25 30

Tyr Asp Met Asn Gly Cys Tyr Ser Arg Leu Lys Glu Leu Val Pro Thr
35 40 45

Leu Pro Gln Asn Arg Lys Val Ser Lys Val Glu Ile Leu Gln His Val
50 55 60

Ile Asp Tyr Ile Arg Asp Leu Gln Leu Glu Leu Asn Ser Glu Ser Glu
65 70 75 80

Val Gly Thr Thr Gly Gly Arg Gly Leu Pro Val Arg Ala Pro Leu Ser
85 90 95

Thr Leu Asn Gly Glu Ile Ser Ala Leu Ala Ala Glu Ala Ala Cys Val
100 105 110

Pro Ala Asp Asp Arg Ile Leu Cys Arg Val Ser Leu Glu Asn Leu Tyr
115 120 125

Phe Gln Ala Ser Gly Gly Gly Gly Gly Ala Ile Ala Met Val Phe Thr
130 135 140

Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu
145 150 155 160

Asp Gln Val Leu Glu Gln Gly Gly Leu Ser Ser Leu Phe Gln Asn Leu
165 170 175

Gly Val Ser Val Thr Pro Ile Gln Arg Ile Val Leu Ser Gly Glu Asn
180 185 190

Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr Glu Gly Leu Ser
195 200 205

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Gly Asp Gln Met Gly Gln Ile Glu Lys Ile Phe Lys Val Val Tyr Pro
    210                 215                 220

Val Asp Asp His His Phe Lys Val Ile Leu His Tyr Gly Thr Leu Val
225                 230                 235                 240

Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr
                245                 250                 255

Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr
            260                 265                 270

Leu Trp Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp
        275                 280                 285

Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg
    290                 295                 300

Leu Cys Glu Arg Ile Leu Ala Gly Tyr Leu Glu Pro Thr Thr Glu Asp
305                 310                 315                 320

Leu Tyr Phe Gln Ser Asp Asn Asp Gly Ser Glu Ile Gly Thr Gly Phe
                325                 330                 335

Pro Phe Asp Pro His Tyr Val Glu Val Leu Gly Glu Arg Met His Tyr
            340                 345                 350

Val Asp Val Gly Pro Arg Asp Gly Thr Pro Val Leu Phe Leu His Gly
        355                 360                 365

Asn Pro Thr Ser Ser Tyr Val Trp Arg Asn Ile Ile Pro His Val Ala
    370                 375                 380

Pro Thr His Arg Cys Ile Ala Pro Asp Leu Ile Gly Met Gly Lys Ser
385                 390                 395                 400

Asp Lys Pro Asp Leu Gly Tyr Phe Phe Asp Asp His Val Arg Phe Met
                405                 410                 415

Asp Ala Phe Ile Glu Ala Leu Gly Leu Glu Glu Val Val Leu Val Ile
            420                 425                 430

His Asp Trp Gly Ser Ala Leu Gly Phe His Trp Ala Lys Arg Asn Pro
        435                 440                 445

Glu Arg Val Lys Gly Ile Ala Phe Met Glu Phe Ile Arg Pro Ile Pro
    450                 455                 460

Thr Trp Asp Glu Trp Pro Glu Phe Ala Arg Glu Thr Phe Gln Ala Phe
465                 470                 475                 480
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Arg Thr Thr Asp Val Gly Arg Lys Leu Ile Ile Asp Gln Asn Val Phe
485 490 495

Ile Glu Gly Thr Leu Pro Met Gly Val Val Arg Pro Leu Thr Glu Val
500 505 510

Glu Met Asp His Tyr Arg Glu Pro Phe Leu Asn Pro Val Asp Arg Glu
515 520 525

Pro Leu Trp Arg Phe Pro Asn Glu Leu Pro Ile Ala Gly Glu Pro Ala
530 535 540

Asn Ile Val Ala Leu Val Glu Glu Tyr Met Asp Trp Leu His Gln Ser
545 550 555 560

Pro Val Pro Lys Leu Leu Phe Trp Gly Thr Pro Gly Val Leu Ile Pro
565 570 575

Pro Ala Glu Ala Ala Arg Leu Ala Lys Ser Leu Pro Asn Cys Lys Ala
580 585 590

Val Asp Ile Gly Pro Gly Leu Asn Leu Leu Gln Glu Asp Asn Pro Asp
595 600 605

Leu Ile Gly Ser Glu Ile Ala Arg Trp Leu Ser Thr Leu Glu Ile Ser
610 615 620

Gly
625

<210> 86
<211> 1875
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 86
atgcttggtc tgtcggagca aagcgtgtcc atctcgcgct gcgctgggac gcgcctgccc 60

gccttgctgg acgagcagca ggtgaacgtc ctgctctacg acatgaacgg ctgctactca 120

cgcctcaagg agctggtgcc caccctgccc cagaaccgca aagtgagcaa ggtggagatc 180

ctgcagcatg taatcgacta catcagggac ctgcagctgg agctgaactc ggagtctgaa 240

gtcgggacca ccggaggccg gggactgcct gtccgcgccc cgctcagcac cctgaacggc 300

gagatcagtg ccttggcggc cgaggcggca tgtgttccag ccgacgatcg catcttgtgt 360

cgcgtttctc ttgagaatct ttattttcag gcgtctggag gtggtggcgg agcgatcgcc 420

atggtgttta cactcgaaga tttcgtaggg gactggcggc agacagccgg ctacaacctg 480

gatcaagtcc ttgagcaggg cggtctgtcc agtttgtttc agaatctcgg ggtgtccgta 540

acaccgatcc aaaagattgt cctgagcggt gaaaacggcc tgaagatcga catccatgtc 600

atcatcccgt atgaaggtct gaacggctat cagatgggcc agatcgaaaa aatttttaag 660

gtggtgtacc ctgtggatga tcatcacttt aaggtgattc tgcactatgg cacactggta 720

atcgacgggg ttacgccgaa catgatcgac tatttcggac ggccgtatga aggcatcgcc 780

gtgttcgacg gcaaaaagat cactgtaacc gggaccctgt ggaacggcaa caaaattatc 840

gacgagcgcc tgatcaaccc cgacggctcc ctgctgttcc gcgtaaccat caacggagtg 900

accggctggc ggctgtgcga gcgcattttg gcgggatatc tcgagccaac cactgaggat 960

ctgtactttc agagcgataa cgatggatcc gaaatcggta ctggctttcc attcgacccc 1020

cattatgtgg aagtcctggg cgagcgcatg cactacgtcg atgttggtcc gcgcgatggc 1080

acccctgtgc tgttcctgca cggtaacccg acctcctcct acgtgtggcg caacatcatc 1140

ccgcatgttg caccgaccca tcgctgcatt gctccagacc tgatcggtat gggcaaatcc 1200

gacaaaccag acctgggtta tttcttcgac gaccacgtcc gcttcatgga tgccttcatc 1260

gaagccctgg gtctggaaga ggtcgtcctg gtcattcacg actggggctc cgctctgggt 1320

ttccactggg ccaagcgcaa tccagagcgc gtcaaaggta ttgcatttat ggagttcatc 1380

cgccctatcc cgacctggga cgaatggcca gaatttgccc gcgagacctt ccaggccttc 1440

cgcaccaccg acgtcggccg caagctgatc atcgatcaga acgtttttat cgagggtacg 1500

ctgccgatgg gtgtcgtccg cccgctgact gaagtcgaga tggaccatta ccgcgagccg 1560

ttcctgaatc ctgttgaccg cgagccactg tggcgcttcc caaacgagct gccaatcgcc 1620

ggtgagccag cgaacatcgt cgcgctggtc gaagaataca tggactggct gcaccagtcc 1680

cctgtcccga agctgctgtt ctggggcacc ccaggcgttc tgatcccacc ggccgaagcc 1740

gctcgcctgg ccaaaagcct gcctaactgc aaggctgtgg acatcggccc gggtctgaat 1800

ctgctgcaag aagacaaccc ggacctgatc ggcagcgaga tcgcgcgctg gctgtctact 1860

ctggagattt ccggt 1875

<210> 87
<211> 625
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 87
Met Leu Gly Leu Ser Glu Gln Ser Val Ser Ile Ser Arg Cys Ala Gly
1 5 10 15

Thr Arg Leu Pro Ala Leu Leu Asp Glu Gln Gln Val Asn Val Leu Leu
20 25 30

Tyr Asp Met Asn Gly Cys Tyr Ser Arg Leu Lys Glu Leu Val Pro Thr

35 40 45

Leu Pro Gln Asn Arg Lys Val Ser Lys Val Glu Ile Leu Gln His Val
50 55 60

Ile Asp Tyr Ile Arg Asp Leu Gln Leu Glu Leu Asn Ser Glu Ser Glu
65 70 75 80

Val Gly Thr Thr Gly Gly Arg Gly Leu Pro Val Arg Ala Pro Leu Ser
85 90 95

Thr Leu Asn Gly Glu Ile Ser Ala Leu Ala Ala Glu Ala Ala Cys Val
100 105 110

Pro Ala Asp Asp Arg Ile Leu Cys Arg Val Ser Leu Glu Asn Leu Tyr
115 120 125

Phe Gln Ala Ser Gly Gly Gly Gly Gly Ala Ile Ala Met Val Phe Thr
130 135 140

Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu
145 150 155 160

Asp Gln Val Leu Glu Gln Gly Gly Leu Ser Ser Leu Phe Gln Asn Leu
165 170 175

Gly Val Ser Val Thr Pro Ile Gln Lys Ile Val Leu Ser Gly Glu Asn
180 185 190

Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr Glu Gly Leu Asn
195 200 205

Gly Tyr Gln Met Gly Gln Ile Glu Lys Ile Phe Lys Val Val Tyr Pro
210 215 220

Val Asp Asp His His Phe Lys Val Ile Leu His Tyr Gly Thr Leu Val
225 230 235 240

Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr
245 250 255

Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr
260 265 270

Leu Trp Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp
275 280 285

Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg
290 295 300

Leu Cys Glu Arg Ile Leu Ala Gly Tyr Leu Glu Pro Thr Thr Glu Asp

305 310 315 320

Leu Tyr Phe Gln Ser Asp Asn Asp Gly Ser Glu Ile Gly Thr Gly Phe
325 330 335

Pro Phe Asp Pro His Tyr Val Glu Val Leu Gly Glu Arg Met His Tyr
340 345 350

Val Asp Val Gly Pro Arg Asp Gly Thr Pro Val Leu Phe Leu His Gly
355 360 365

Asn Pro Thr Ser Ser Tyr Val Trp Arg Asn Ile Ile Pro His Val Ala
370 375 380

Pro Thr His Arg Cys Ile Ala Pro Asp Leu Ile Gly Met Gly Lys Ser
385 390 395 400

Asp Lys Pro Asp Leu Gly Tyr Phe Phe Asp Asp His Val Arg Phe Met
405 410 415

Asp Ala Phe Ile Glu Ala Leu Gly Leu Glu Glu Val Val Leu Val Ile
420 425 430

His Asp Trp Gly Ser Ala Leu Gly Phe His Trp Ala Lys Arg Asn Pro
435 440 445

Glu Arg Val Lys Gly Ile Ala Phe Met Glu Phe Ile Arg Pro Ile Pro
450 455 460

Thr Trp Asp Glu Trp Pro Glu Phe Ala Arg Glu Thr Phe Gln Ala Phe
465 470 475 480

Arg Thr Thr Asp Val Gly Arg Lys Leu Ile Ile Asp Gln Asn Val Phe
485 490 495

Ile Glu Gly Thr Leu Pro Met Gly Val Val Arg Pro Leu Thr Glu Val
500 505 510

Glu Met Asp His Tyr Arg Glu Pro Phe Leu Asn Pro Val Asp Arg Glu
515 520 525

Pro Leu Trp Arg Phe Pro Asn Glu Leu Pro Ile Ala Gly Glu Pro Ala
530 535 540

Asn Ile Val Ala Leu Val Glu Glu Tyr Met Asp Trp Leu His Gln Ser
545 550 555 560

Pro Val Pro Lys Leu Leu Phe Trp Gly Thr Pro Gly Val Leu Ile Pro
565 570 575

Pro Ala Glu Ala Ala Arg Leu Ala Lys Ser Leu Pro Asn Cys Lys Ala

580 585 590

Val Asp Ile Gly Pro Gly Leu Asn Leu Leu Gln Glu Asp Asn Pro Asp
595 600 605

Leu Ile Gly Ser Glu Ile Ala Arg Trp Leu Ser Thr Leu Glu Ile Ser
610 615 620

Gly
625

<210> 88
<211> 513
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 88
atggtgttta cactcgaaga tttcgtaggg gactggcggc agacagccgg ctacaacctg 60

gaccaagtcc ttgagcaggg cggtgtgtcc agtttgtttc agaatctcgg ggtgtccgta 120

actccgatcc aaaggattgt cctgagcggt gaaaacggcc tgaagatcga catccatgtc 180

atcatcccgt atgaaggtct gagcggcgat cagatgggcc agatcgaaaa aatttttaag 240

gtggtgtacc ctgtggatga tcatcacttt aaggtgattc tgcactatgg cacactggta 300

atcgacgggg ttacgccgaa catgatcgac tatttcggac ggccgtatga aggcatcgcc 360

gtgttcgacg gcaaaaagat cactgtaacc gggaccctgt ggaacggcaa caaaattatc 420

gacgagcgcc tgatcaaccc cgacggctcc ctgctgttcc gcgtaaccat caacggagtg 480

accggctggc ggctgtgcga gcgcattttg gcg 513

<210> 89
<211> 171
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 89
Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala
1 5 10 15

Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu
20 25 30

Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln Arg Ile Val Leu
35 40 45

Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr
50 55 60

Glu Gly Leu Ser Gly Asp Gln Met Gly Gln Ile Glu Lys Ile Phe Lys
65 70 75 80

Val Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu His Tyr
85 90 95

Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe
100 105 110

Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr
115 120 125

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

Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val
145 150 155 160

Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala
165 170

<210> 90
<211> 1875
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 90
atgcttggtc tgtcggagca aagcgtgtcc atctcgcgct gcgctgggac gcgcctgccc 60

gccttgctgg acgagcagca ggtgaacgtc ctgctctacg acatgaacgg ctgctactca 120

cgcctcaagg agctggtgcc caccctgccc cagaaccgca aagtgagcaa ggtggagatc 180

ctgcagcatg taatcgacta catcagggac ctgcagctgg agctgaactc ggagtctgaa 240

gtcgggacca ccggaggccg gggactgcct gtccgcgccc cgctcagcac cctgaacggc 300

gagatcagtg ccttggcggc cgaggcggca tgtgttccag ccgacgatcg catcttgtgt 360

cgcgtttctc ttgagaatct ttattttcag gcgtctggag gtggtggcgg agcgatcgcc 420

atggtgttta cactcgaaga tttcgtaggg gactggcggc agacagccgg ctacaacctg 480

gaccaagtcc ttgagcaggg cggtgtgtcc agtttgtttc agaatctcgg ggtgtccgta 540

actccgatcc aaaggattgt cctgagcggt gaaaacggcc tgaagatcga catccatgtc 600

atcatcccgt atgaaggtct gagcggcgat cagatgggcc agatcgaaaa aatttttaag 660

gtggtgtacc ctgtggatga tcatcacttt aaggtgattc tgcactatgg cacactggta 720

atcgacgggg ttacgccgaa catgatcgac tatttcggac ggccgtatga aggcatcgcc 780

gtgttcgacg gcaaaaagat cactgtaacc gggaccctgt ggaacggcaa caaaattatc 840

gacgagcgcc tgatcaaccc cgacggctcc ctgctgttcc gcgtaaccat caacggagtg 900

accggctggc ggctgtgcga gcgcattttg gcgggatatc tcgagccaac cactgaggat 960

ctgtactttc agagcgataa cgatggatcc gaaatcggta ctggctttcc attcgacccc 1020

cattatgtgg aagtcctggg cgagcgcatg cactacgtcg atgttggtcc gcgcgatggc 1080

acccctgtgc tgttcctgca cggtaacccg acctcctcct acgtgtggcg caacatcatc 1140

ccgcatgttg caccgaccca tcgctgcatt gctccagacc tgatcggtat gggcaaatcc 1200

gacaaaccag acctgggtta tttcttcgac gaccacgtcc gcttcatgga tgccttcatc 1260

gaagccctgg gtctggaaga ggtcgtcctg gtcattcacg actggggctc cgctctgggt 1320

ttccactggg ccaagcgcaa tccagagcgc gtcaaaggta ttgcatttat ggagttcatc 1380

cgccctatcc cgacctggga cgaatggcca gaatttgccc gcgagacctt ccaggccttc 1440

cgcaccaccg acgtcggccg caagctgatc atcgatcaga acgtttttat cgagggtacg 1500

ctgccgatgg gtgtcgtccg cccgctgact gaagtcgaga tggaccatta ccgcgagccg 1560

ttcctgaatc ctgttgaccg cgagccactg tggcgcttcc caaacgagct gccaatcgcc 1620

ggtgagccag cgaacatcgt cgcgctggtc gaagaataca tggactggct gcaccagtcc 1680

cctgtcccga agctgctgtt ctggggcacc ccaggcgttc tgatcccacc ggccgaagcc 1740

gctcgcctgg ccaaaagcct gcctaactgc aaggctgtgg acatcggccc gggtctgaat 1800

ctgctgcaag aagacaaccc ggacctgatc ggcagcgaga tcgcgcgctg gctgtctact 1860

ctggagattt ccggt 1875

<210> 91
<211> 625
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 91

Met Leu Gly Leu Ser Glu Gln Ser Val Ser Ile Ser Arg Cys Ala Gly
1 5 10 15

Thr Arg Leu Pro Ala Leu Leu Asp Glu Gln Gln Val Asn Val Leu Leu
20 25 30

Tyr Asp Met Asn Gly Cys Tyr Ser Arg Leu Lys Glu Leu Val Pro Thr
35 40 45

Leu Pro Gln Asn Arg Lys Val Ser Lys Val Glu Ile Leu Gln His Val
50 55 60

Ile Asp Tyr Ile Arg Asp Leu Gln Leu Glu Leu Asn Ser Glu Ser Glu
65 70 75 80

Val Gly Thr Thr Gly Gly Arg Gly Leu Pro Val Arg Ala Pro Leu Ser

85 90 95

Thr Leu Asn Gly Glu Ile Ser Ala Leu Ala Ala Glu Ala Ala Cys Val
100 105 110

Pro Ala Asp Asp Arg Ile Leu Cys Arg Val Ser Leu Glu Asn Leu Tyr
115 120 125

Phe Gln Ala Ser Gly Gly Gly Gly Gly Ala Ile Ala Met Val Phe Thr
130 135 140

Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu
145 150 155 160

Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu Phe Gln Asn Leu
165 170 175

Gly Val Ser Val Thr Pro Ile Gln Arg Ile Val Leu Ser Gly Glu Asn
180 185 190

Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr Glu Gly Leu Ser
195 200 205

Gly Asp Gln Met Gly Gln Ile Glu Lys Ile Phe Lys Val Val Tyr Pro
210 215 220

Val Asp Asp His His Phe Lys Val Ile Leu His Tyr Gly Thr Leu Val
225 230 235 240

Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr
245 250 255

Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr
260 265 270

Leu Trp Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp
275 280 285

Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg
290 295 300

Leu Cys Glu Arg Ile Leu Ala Gly Tyr Leu Glu Pro Thr Thr Glu Asp
305 310 315 320

Leu Tyr Phe Gln Ser Asp Asn Asp Gly Ser Glu Ile Gly Thr Gly Phe
325 330 335

Pro Phe Asp Pro His Tyr Val Glu Val Leu Gly Glu Arg Met His Tyr
340 345 350

Val Asp Val Gly Pro Arg Asp Gly Thr Pro Val Leu Phe Leu His Gly

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        355                 360                 365

Asn Pro Thr Ser Ser Tyr Val Trp Arg Asn Ile Ile Pro His Val Ala
    370                 375                 380

Pro Thr His Arg Cys Ile Ala Pro Asp Leu Ile Gly Met Gly Lys Ser
385                 390                 395                 400

Asp Lys Pro Asp Leu Gly Tyr Phe Phe Asp Asp His Val Arg Phe Met
                405                 410                 415

Asp Ala Phe Ile Glu Ala Leu Gly Leu Glu Glu Val Val Leu Val Ile
            420                 425                 430

His Asp Trp Gly Ser Ala Leu Gly Phe His Trp Ala Lys Arg Asn Pro
        435                 440                 445

Glu Arg Val Lys Gly Ile Ala Phe Met Glu Phe Ile Arg Pro Ile Pro
    450                 455                 460

Thr Trp Asp Glu Trp Pro Glu Phe Ala Arg Glu Thr Phe Gln Ala Phe
465                 470                 475                 480

Arg Thr Thr Asp Val Gly Arg Lys Leu Ile Ile Asp Gln Asn Val Phe
                485                 490                 495

Ile Glu Gly Thr Leu Pro Met Gly Val Val Arg Pro Leu Thr Glu Val
            500                 505                 510

Glu Met Asp His Tyr Arg Glu Pro Phe Leu Asn Pro Val Asp Arg Glu
        515                 520                 525

Pro Leu Trp Arg Phe Pro Asn Glu Leu Pro Ile Ala Gly Glu Pro Ala
    530                 535                 540

Asn Ile Val Ala Leu Val Glu Glu Tyr Met Asp Trp Leu His Gln Ser
545                 550                 555                 560

Pro Val Pro Lys Leu Leu Phe Trp Gly Thr Pro Gly Val Leu Ile Pro
                565                 570                 575

Pro Ala Glu Ala Ala Arg Leu Ala Lys Ser Leu Pro Asn Cys Lys Ala
            580                 585                 590

Val Asp Ile Gly Pro Gly Leu Asn Leu Leu Gln Glu Asp Asn Pro Asp
        595                 600                 605

Leu Ile Gly Ser Glu Ile Ala Arg Trp Leu Ser Thr Leu Glu Ile Ser
    610                 615                 620

Gly
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625

<210> 92
<211> 513
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 92
atggtgttta cactcgaaga tttcgtaggg gactggcggc agacagccgg ctacaacctg 60

gaccaagtcc ttgagcaggg cggtctgtcc agtttgtttc agaatctcgg ggtgtccgta 120

actccgatcc aaaggattgt cctgagcggt gaaaacggcc tgaagatcga catccatgtc 180

atcatcccgt atgaaggtct gagcggcgat cagatgggcc agatcgaaaa aatttttaag 240

gtggtgtacc ctgtggatga tcatcacttt aaggtgattc tgcactatgg cacactggta 300

atcgacgggg ttacgccgaa catgatcgac tatttcggac ggccgtatga aggcatcgcc 360

gtgttcgacg gcaaaaagat cactgtaacc gggaccctgt ggaacggcaa caaaattatc 420

gacgagcgcc tgatcaaccc cgacggctcc ctgctgttcc gcgtaaccat caacggagtg 480

accggctggc ggctgtgcga gcgcattttg gcg 513

<210> 93
<211> 171
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 93
Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala
1 5 10 15

Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Leu Ser Ser Leu
20 25 30

Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln Arg Ile Val Leu
35 40 45

Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr
50 55 60

Glu Gly Leu Ser Gly Asp Gln Met Gly Gln Ile Glu Lys Ile Phe Lys
65 70 75 80

Val Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu His Tyr
85 90 95

Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe
100 105 110

Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr
115 120 125

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

Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val
145 150 155 160

Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala
165 170

<210> 94
<211> 1875
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 94
atgcttggtc tgtcggagca aagcgtgtcc atctcgcgct gcgctgggac gcgcctgccc 60

gccttgctgg acgagcagca ggtgaacgtc ctgctctacg acatgaacgg ctgctactca 120

cgcctcaagg agctggtgcc caccctgccc cagaaccgca aagtgagcaa ggtggagatc 180

ctgcagcatg taatcgacta catcagggac ctgcagctgg agctgaactc ggagtctgaa 240

gtcgggacca ccggaggccg gggactgcct gtccgcgccc cgctcagcac cctgaacggc 300

gagatcagtg ccttggcggc cgaggcggca tgtgttccag ccgacgatcg catcttgtgt 360

cgcgtttctc ttgagaatct ttattttcag gcgtctggag gtggtggcgg agcgatcgcc 420

atggtgttta cactcgaaga tttcgtaggg gactggcggc agacagccgg ctacaacctg 480

gaccaagtcc ttgagcaggg cggtctgtcc agtttgtttc agaatctcgg ggtgtccgta 540

actccgatcc aaaggattgt cctgagcggt gaaaacggcc tgaagatcga catccatgtc 600

atcatcccgt atgaaggtct gagcggcgat cagatgggcc agatcgaaaa aatttttaag 660

gtggtgtacc ctgtggatga tcatcacttt aaggtgattc tgcactatgg cacactggta 720

atcgacgggg ttacgccgaa catgatcgac tatttcggac ggccgtatga aggcatcgcc 780

gtgttcgacg gcaaaaagat cactgtaacc gggaccctgt ggaacggcaa caaaattatc 840

gacgagcgcc tgatcaaccc cgacggctcc ctgctgttcc gcgtaaccat caacggagtg 900

accggctggc ggctgtgcga gcgcattttg gcgggatatc tcgagccaac cactgaggat 960

ctgtactttc agagcgataa cgatggatcc gaaatcggta ctggctttcc attcgacccc 1020

cattatgtgg aagtcctggg cgagcgcatg cactacgtcg atgttggtcc gcgcgatggc 1080

acccctgtgc tgttcctgca cggtaacccg acctcctcct acgtgtggcg caacatcatc 1140

ccgcatgttg caccgaccca tcgctgcatt gctccagacc tgatcggtat gggcaaatcc 1200

gacaaaccag acctgggtta tttcttcgac gaccacgtcc gcttcatgga tgccttcatc 1260

gaagccctgg gtctggaaga ggtcgtcctg gtcattcacg actggggctc cgctctgggt 1320

ttccactggg ccaagcgcaa tccagagcgc gtcaaaggta ttgcatttat ggagttcatc 1380

cgccctatcc cgacctggga cgaatggcca gaatttgccc gcgagacctt ccaggccttc 1440

cgcaccaccg acgtcggccg caagctgatc atcgatcaga acgtttttat cgagggtacg 1500

ctgccgatgg gtgtcgtccg cccgctgact gaagtcgaga tggaccatta ccgcgagccg 1560

ttcctgaatc ctgttgaccg cgagccactg tggcgcttcc caaacgagct gccaatcgcc 1620

ggtgagccag cgaacatcgt cgcgctggtc gaagaataca tggactggct gcaccagtcc 1680

cctgtcccga agctgctgtt ctggggcacc ccaggcgttc tgatcccacc ggccgaagcc 1740

gctcgcctgg ccaaaagcct gcctaactgc aaggctgtgg acatcggccc gggtctgaat 1800

ctgctgcaag aagacaaccc ggacctgatc ggcagcgaga tcgcgcgctg gctgtctact 1860

ctggagattt ccggt 1875

<210> 95
<211> 625
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 95

Met Leu Gly Leu Ser Glu Gln Ser Val Ser Ile Ser Arg Cys Ala Gly
1 5 10 15

Thr Arg Leu Pro Ala Leu Leu Asp Glu Gln Gln Val Asn Val Leu Leu
20 25 30

Tyr Asp Met Asn Gly Cys Tyr Ser Arg Leu Lys Glu Leu Val Pro Thr
35 40 45

Leu Pro Gln Asn Arg Lys Val Ser Lys Val Glu Ile Leu Gln His Val
50 55 60

Ile Asp Tyr Ile Arg Asp Leu Gln Leu Glu Leu Asn Ser Glu Ser Glu
65 70 75 80

Val Gly Thr Thr Gly Gly Arg Gly Leu Pro Val Arg Ala Pro Leu Ser
85 90 95

Thr Leu Asn Gly Glu Ile Ser Ala Leu Ala Ala Glu Ala Ala Cys Val
100 105 110

Pro Ala Asp Asp Arg Ile Leu Cys Arg Val Ser Leu Glu Asn Leu Tyr
115 120 125

Phe Gln Ala Ser Gly Gly Gly Gly Gly Ala Ile Ala Met Val Phe Thr

130 135 140

Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu
145 150 155 160

Asp Gln Val Leu Glu Gln Gly Gly Leu Ser Ser Leu Phe Gln Asn Leu
165 170 175

Gly Val Ser Val Thr Pro Ile Gln Arg Ile Val Leu Ser Gly Glu Asn
180 185 190

Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr Glu Gly Leu Ser
195 200 205

Gly Asp Gln Met Gly Gln Ile Glu Lys Ile Phe Lys Val Val Tyr Pro
210 215 220

Val Asp Asp His His Phe Lys Val Ile Leu His Tyr Gly Thr Leu Val
225 230 235 240

Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr
245 250 255

Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr
260 265 270

Leu Trp Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp
275 280 285

Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg
290 295 300

Leu Cys Glu Arg Ile Leu Ala Gly Tyr Leu Glu Pro Thr Thr Glu Asp
305 310 315 320

Leu Tyr Phe Gln Ser Asp Asn Asp Gly Ser Glu Ile Gly Thr Gly Phe
325 330 335

Pro Phe Asp Pro His Tyr Val Glu Val Leu Gly Glu Arg Met His Tyr
340 345 350

Val Asp Val Gly Pro Arg Asp Gly Thr Pro Val Leu Phe Leu His Gly
355 360 365

Asn Pro Thr Ser Ser Tyr Val Trp Arg Asn Ile Ile Pro His Val Ala
370 375 380

Pro Thr His Arg Cys Ile Ala Pro Asp Leu Ile Gly Met Gly Lys Ser
385 390 395 400

Asp Lys Pro Asp Leu Gly Tyr Phe Phe Asp Asp His Val Arg Phe Met

405 410 415

Asp Ala Phe Ile Glu Ala Leu Gly Leu Glu Glu Val Val Leu Val Ile
420 425 430

His Asp Trp Gly Ser Ala Leu Gly Phe His Trp Ala Lys Arg Asn Pro
435 440 445

Glu Arg Val Lys Gly Ile Ala Phe Met Glu Phe Ile Arg Pro Ile Pro
450 455 460

Thr Trp Asp Glu Trp Pro Glu Phe Ala Arg Glu Thr Phe Gln Ala Phe
465 470 475 480

Arg Thr Thr Asp Val Gly Arg Lys Leu Ile Ile Asp Gln Asn Val Phe
485 490 495

Ile Glu Gly Thr Leu Pro Met Gly Val Val Arg Pro Leu Thr Glu Val
500 505 510

Glu Met Asp His Tyr Arg Glu Pro Phe Leu Asn Pro Val Asp Arg Glu
515 520 525

Pro Leu Trp Arg Phe Pro Asn Glu Leu Pro Ile Ala Gly Glu Pro Ala
530 535 540

Asn Ile Val Ala Leu Val Glu Glu Tyr Met Asp Trp Leu His Gln Ser
545 550 555 560

Pro Val Pro Lys Leu Leu Phe Trp Gly Thr Pro Gly Val Leu Ile Pro
565 570 575

Pro Ala Glu Ala Ala Arg Leu Ala Lys Ser Leu Pro Asn Cys Lys Ala
580 585 590

Val Asp Ile Gly Pro Gly Leu Asn Leu Leu Gln Glu Asp Asn Pro Asp
595 600 605

Leu Ile Gly Ser Glu Ile Ala Arg Trp Leu Ser Thr Leu Glu Ile Ser
610 615 620

Gly
625

<210> 96
<211> 87
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown: cAMP-response element (CRE) oligonucleotide

<400> 96
gcaccagaca gtgacgtcag ctgccagatc ccatggccgt catactgtga cgtctttcag 60

acacccttg acgtcaatgg gagaaca 87

<210> 97
<211> 516
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 97
atggatgatc atcactttaa ggtgattctg cactatggca cactggtaat cgacggggtt 60

acgccgaaca tgatcgacta tttcggacgg ccgtatgaag gcatcgccgt gttcgacggc 120

aaaaagatca ctgtaaccgg gaccctgtgg aacggcaaca aaattatcga cgagcgcctg 180

atcaaccccg acggctccct gctgttccgc gtaaccatca acggagtgac cggctggcgg 240

ctgtgcgagc gcattttggc gatggtgttt acactcgaag atttcgtagg ggactggcgg 300

cagacagccg gctacaacct ggaccaagtc cttgagcagg gcggtgtgtc cagtttgttt 360

cagaatctcg gggtgtccgt aactccgatc caaaggattg tcctgagcgg tgaaaacggc 420

ctgaagatcg acatccatgt catcatcccg tatgaaggtc tgagcggcga tcagatgggc 480

cagatcgaaa aaatttttaa ggtggtgtac cctgtg 516

<210> 98
<211> 172
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 98
Met Asp Asp His His Phe Lys Val Ile Leu His Tyr Gly Thr Leu Val
1 5 10 15

Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr
20 25 30

Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr
35 40 45

Leu Trp Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp
50 55 60

Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg
65 70 75 80

Leu Cys Glu Arg Ile Leu Ala Met Val Phe Thr Leu Glu Asp Phe Val
85 90 95

Gly Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val Leu Glu
100 105 110

Gln Gly Gly Val Ser Ser Leu Phe Gln Asn Leu Gly Val Ser Val Thr
115 120 125

Pro Ile Gln Arg Ile Val Leu Ser Gly Glu Asn Gly Leu Lys Ile Asp
130 135 140

Ile His Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln Met Gly
145 150 155 160

Gln Ile Glu Lys Ile Phe Lys Val Val Tyr Pro Val
165 170

<210> 99
<211> 531
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 99
atggatgatc atcactttaa ggtgattctg cactatggca cactggtaat cgacggggtt 60

acgccgaaca tgatcgacta tttcggacgg ccgtatgaag gcatcgccgt gttcgacggc 120

aaaaagatca ctgtaaccgg gaccctgtgg aacggcaaca aaattatcga cgagcgcctg 180

atcaaccccg acggctccct gctgttccgc gtaaccatca acggagtgac cggctggcgg 240

ctgtgcgagc gcattttggc ggggagctcc ggtggaatgg tgtttacact cgaagatttc 300

gtaggggact ggcggcagac agccggctac aacctggacc aagtccttga gcagggcggt 360

gtgtccagtt tgtttcagaa tctcggggtg tccgtaactc cgatccaaag gattgtcctg 420

agcggtgaaa acggcctgaa gatcgacatc catgtcatca tcccgtatga aggtctgagc 480

ggcgatcaga tgggccagat cgaaaaaatt tttaaggtgg tgtaccctgt g 531

<210> 100
<211> 177
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 100
Met Asp Asp His His Phe Lys Val Ile Leu His Tyr Gly Thr Leu Val
1 5 10 15

Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr
20 25 30

Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr
35 40 45

Leu Trp Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp
50 55 60

Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg
65 70 75 80

Leu Cys Glu Arg Ile Leu Ala Gly Ser Ser Gly Gly Met Val Phe Thr
85 90 95

Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu
100 105 110

Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu Phe Gln Asn Leu
115 120 125

Gly Val Ser Val Thr Pro Ile Gln Arg Ile Val Leu Ser Gly Glu Asn
130 135 140

Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr Glu Gly Leu Ser
145 150 155 160

Gly Asp Gln Met Gly Gln Ile Glu Lys Ile Phe Lys Val Val Tyr Pro
165 170 175

Val

<210> 101
<211> 546
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 101
atggatgatc atcactttaa ggtgattctg cactatggca cactggtaat cgacggggtt 60

acgccgaaca tgatcgacta tttcggacgg ccgtatgaag gcatcgccgt gttcgacggc 120

aaaaagatca ctgtaaccgg gaccctgtgg aacggcaaca aaattatcga cgagcgcctg 180

atcaaccccg acggctccct gctgttccgc gtaaccatca acggagtgac cggctggcgg 240

ctgtgcgagc gcattttggc gggaagttct ggtggaggga gctccggtgg aatggtgttt 300

acactcgaag atttcgtagg ggactggcgg cagacagccg gctacaacct ggaccaagtc 360

cttgagcagg gcggtgtgtc cagtttgttt cagaatctcg gggtgtccgt aactccgatc 420

caaaggattg tcctgagcgg tgaaaacggc ctgaagatcg acatccatgt catcatcccg 480

tatgaaggtc tgagcggcga tcagatgggc cagatcgaaa aaatttttaa ggtggtgtac 540

cctgtg 546

<210> 102
<211> 182
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 102
Met Asp Asp His His Phe Lys Val Ile Leu His Tyr Gly Thr Leu Val
1 5 10 15

Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr
20 25 30

Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr
35 40 45

Leu Trp Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp
50 55 60

Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg
65 70 75 80

Leu Cys Glu Arg Ile Leu Ala Gly Ser Ser Gly Gly Gly Ser Ser Gly
85 90 95

Gly Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr
100 105 110

Ala Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser
115 120 125

Leu Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln Arg Ile Val
130 135 140

Leu Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro
145 150 155 160

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

Lys Val Val Tyr Pro Val
180

<210> 103
<211> 576
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

polynucleotide

<400> 103
atggatgatc atcactttaa ggtgattctg cactatggca cactggtaat cgacggggtt 60

acgccgaaca tgatcgacta tttcggacgg ccgtatgaag gcatcgccgt gttcgacggc 120

aaaaagatca ctgtaaccgg gaccctgtgg aacggcaaca aaattatcga cgagcgcctg 180

atcaaccccg acggctccct gctgttccgc gtaaccatca acggagtgac cggctggcgg 240

ctgtgcgagc gcattttggc gggaagttct ggtggaggga gctccggtgg aggaagttct 300

ggtggaggga gctccggtgg aatggtgttt acactcgaag atttcgtagg ggactggcgg 360

cagacagccg gctacaacct ggaccaagtc cttgagcagg gcggtgtgtc cagtttgttt 420

cagaatctcg gggtgtccgt aactccgatc caaaggattg tcctgagcgg tgaaaacggc 480

ctgaagatcg acatccatgt catcatcccg tatgaaggtc tgagcggcga tcagatgggc 540

cagatcgaaa aaatttttaa ggtggtgtac cctgtg 576

<210> 104
<211> 192
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 104
Met Asp Asp His His Phe Lys Val Ile Leu His Tyr Gly Thr Leu Val
1 5 10 15

Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr
20 25 30

Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr
35 40 45

Leu Trp Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp
50 55 60

Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg
65 70 75 80

Leu Cys Glu Arg Ile Leu Ala Gly Ser Ser Gly Gly Gly Ser Ser Gly
85 90 95

Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Met Val Phe Thr Leu
100 105 110

Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp
115 120 125

Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu Phe Gln Asn Leu Gly
130 135 140

Val Ser Val Thr Pro Ile Gln Arg Ile Val Leu Ser Gly Glu Asn Gly
145 150 155 160

Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly
165 170 175

Asp Gln Met Gly Gln Ile Glu Lys Ile Phe Lys Val Val Tyr Pro Val
180 185 190

<210> 105
<211> 516
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 105
atgggcacac tggtaatcga cggggttacg ccgaacatga tcgactattt cggacggccg 60

tatgaaggca tcgccgtgtt cgacggcaaa aagatcactg taaccgggac cctgtggaac 120

ggcaacaaaa ttatcgacga gcgcctgatc aaccccgacg gctccctgct gttccgcgta 180

accatcaacg gagtgaccgg ctggcggctg tgcgagcgca ttttggcgat ggtgtttaca 240

ctcgaagatt tcgtagggga ctggcggcag acagccggct acaacctgga ccaagtcctt 300

gagcagggcg gtgtgtccag tttgtttcag aatctcgggg tgtccgtaac tccgatccaa 360

aggattgtcc tgagcggtga aaacggcctg aagatcgaca tccatgtcat catcccgtat 420

gaaggtctga gcggcgatca gatgggccag atcgaaaaaa tttttaaggt ggtgtaccct 480

gtggatgatc atcactttaa ggtgattctg cactat 516

<210> 106
<211> 172
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 106
Met Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr
1 5 10 15

Phe Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile
20 25 30

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

Leu Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly
50 55 60

Val Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala Met Val Phe Thr
65 70 75 80

Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu
85 90 95

Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu Phe Gln Asn Leu
100 105 110

Gly Val Ser Val Thr Pro Ile Gln Arg Ile Val Leu Ser Gly Glu Asn
115 120 125

Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr Glu Gly Leu Ser
130 135 140

Gly Asp Gln Met Gly Gln Ile Glu Lys Ile Phe Lys Val Val Tyr Pro
145 150 155 160

Val Asp Asp His His Phe Lys Val Ile Leu His Tyr
165 170

<210> 107
<211> 531
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 107
atgggcacac tggtaatcga cggggttacg ccgaacatga tcgactattt cggacggccg 60

tatgaaggca tcgccgtgtt cgacggcaaa aagatcactg taaccgggac cctgtggaac 120

ggcaacaaaa ttatcgacga gcgcctgatc aaccccgacg gctccctgct gttccgcgta 180

accatcaacg gagtgaccgg ctggcggctg tgcgagcgca ttttggcggg gagctccggt 240

ggaatggtgt ttacactcga agatttcgta ggggactggc ggcagacagc cggctacaac 300

ctggaccaag tccttgagca gggcggtgtg tccagtttgt ttcagaatct cggggtgtcc 360

gtaactccga tccaaaggat tgtcctgagc ggtgaaaacg gcctgaagat cgacatccat 420

gtcatcatcc cgtatgaagg tctgagcggc gatcagatgg gccagatcga aaaaattttt 480

aaggtggtgt accctgtgga tgatcatcac tttaaggtga ttctgcacta t 531

<210> 108
<211> 177
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 108

Met Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr
1 5 10 15

Phe Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile
20 25 30

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

Leu Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly
50 55 60

Val Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala Gly Ser Ser Gly
65 70 75 80

Gly Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr
85 90 95

Ala Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser
100 105 110

Leu Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln Arg Ile Val
115 120 125

Leu Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro
130 135 140

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

Lys Val Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu His
165 170 175

Tyr

<210> 109
<211> 546
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 109
atgggcacac tggtaatcga cggggttacg ccgaacatga tcgactattt cggacggccg 60

tatgaaggca tcgccgtgtt cgacggcaaa aagatcactg taaccgggac cctgtggaac 120

ggcaacaaaa ttatcgacga gcgcctgatc aaccccgacg gctccctgct gttccgcgta 180

accatcaacg gagtgaccgg ctggcggctg tgcgagcgca ttttggcggg aagttctggt 240

ggagggagct ccggtggaat ggtgtttaca ctcgaagatt tcgtagggga ctggcggcag 300

acagccggct acaacctgga ccaagtcctt gagcagggcg gtgtgtccag tttgtttcag 360

aatctcgggg tgtccgtaac tccgatccaa aggattgtcc tgagcggtga aaacggcctg 420

aagatcgaca tccatgtcat catcccgtat gaaggtctga gcggcgatca gatgggccag 480

atcgaaaaaa tttttaaggt ggtgtaccct gtggatgatc atcactttaa ggtgattctg 540

cactat 546

<210> 110
<211> 182
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 110

Met Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr
1 5 10 15

Phe Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile
20 25 30

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

Leu Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly
50 55 60

Val Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala Gly Ser Ser Gly
65 70 75 80

Gly Gly Ser Ser Gly Gly Met Val Phe Thr Leu Glu Asp Phe Val Gly
85 90 95

Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln
100 105 110

Gly Gly Val Ser Ser Leu Phe Gln Asn Leu Gly Val Ser Val Thr Pro
115 120 125

Ile Gln Arg Ile Val Leu Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile
130 135 140

His Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln Met Gly Gln
145 150 155 160

Ile Glu Lys Ile Phe Lys Val Val Tyr Pro Val Asp Asp His His Phe
165 170 175

Lys Val Ile Leu His Tyr
180

<210> 111
<211> 576
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 111
atgggcacac tggtaatcga cggggttacg ccgaacatga tcgactattt cggacggccg 60

tatgaaggca tcgccgtgtt cgacggcaaa aagatcactg taaccgggac cctgtggaac 120

ggcaacaaaa ttatcgacga gcgcctgatc aaccccgacg gctccctgct gttccgcgta 180

accatcaacg gagtgaccgg ctggcggctg tgcgagcgca ttttggcggg aagttctggt 240

ggagggagct ccggtggagg aagttctggt ggagggagct ccggtggaat ggtgtttaca 300

ctcgaagatt tcgtagggga ctggcggcag acagccggct acaacctgga ccaagtcctt 360

gagcagggcg gtgtgtccag tttgtttcag aatctcgggg tgtccgtaac tccgatccaa 420

aggattgtcc tgagcggtga aaacggcctg aagatcgaca tccatgtcat catcccgtat 480

gaaggtctga gcggcgatca gatgggccag atcgaaaaaa tttttaaggt ggtgtaccct 540

gtggatgatc atcactttaa ggtgattctg cactat 576

<210> 112
<211> 192
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 112
Met Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr
1 5 10 15

Phe Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile
20 25 30

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

Leu Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly
50 55 60

Val Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala Gly Ser Ser Gly
65 70 75 80

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

Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala
100 105 110

Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu
115 120 125

Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln Arg Ile Val Leu
130 135 140

Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr
145 150 155 160

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

Val Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu His Tyr
180 185 190

<210> 113
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 113
Gly Ser Ser Gly Gly
1 5

<210> 114
<211> 615
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 114
atggatttcg taggggactg gcggcagaca gccggctaca acctggacca agtccttgag 60

cagggcggtg tgtccagttt gtttcagaat ctcggggtgt ccgtaactcc gatccaaagg 120

attgtcctga gcggtgaaaa cggcctgaag atcgacatcc atgtcatcat cccgtatgaa 180

ggtctgagcg gcgatcagat gggccagatc gaaaaaattt ttaaggtggt gtaccctgtg 240

gatgatcatc actttaaggt gattctgcac tatggcacac tggtaatcga cggggttacg 300

ccgaacatga tcgactattt cggacggccg tatgaaggca tcgccgtgtt cgacggcaaa 360

aagatcactg taaccgggac cctgtggaac ggcaacaaaa ttatcgacga gcgcctgatc 420

aaccccgacg gctccctgct gttccgcgta accatcaacg gagtgaccgg ctggcggctg 480

tgcgagcgca ttttggcggg aagttctggt ggaggaagtt ctggtggaga gcctactact 540

gagaacttgt acttccagag cgataacgga agttctggtg gaggaagttc tggtggaatg 600

gtgtttacac tcgaa 615

<210> 115
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 115
Met Asp Phe Val Gly Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp
1 5 10 15

Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu Phe Gln Asn Leu Gly
20 25 30

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

Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly
50 55 60

Asp Gln Met Gly Gln Ile Glu Lys Ile Phe Lys Val Val Tyr Pro Val
65 70 75 80

Asp Asp His His Phe Lys Val Ile Leu His Tyr Gly Thr Leu Val Ile
85 90 95

Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu
100 105 110

Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr Leu
115 120 125

Trp Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly
130 135 140

Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg Leu
145 150 155 160

Cys Glu Arg Ile Leu Ala Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly
165 170 175

Glu Pro Thr Thr Glu Asn Leu Tyr Phe Gln Ser Asp Asn Gly Ser Ser
180 185 190

Gly Gly Gly Ser Ser Gly Gly Met Val Phe Thr Leu Glu
195 200 205

<210> 116
<211> 615
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 116
atgttcgtag gggactggcg gcagacagcc ggctacaacc tggaccaagt ccttgagcag 60

ggcggtgtgt ccagtttgtt tcagaatctc ggggtgtccg taactccgat ccaaaggatt 120

gtcctgagcg gtgaaaacgg cctgaagatc gacatccatg tcatcatccc gtatgaaggt 180

ctgagcggcg atcagatggg ccagatcgaa aaaatttta aggtggtgta ccctgtggat 240

gatcatcact ttaaggtgat tctgcactat ggcacactgg taatcgacgg ggttacgccg 300

aacatgatcg actatttcgg acggccgtat gaaggcatcg ccgtgttcga cggcaaaaag 360

atcactgtaa ccgggaccct gtggaacggc aacaaaatta tcgacgagcg cctgatcaac 420

cccgacggct ccctgctgtt ccgcgtaacc atcaacggag tgaccggctg gcggctgtgc 480

gagcgcattt tggcgggaag ttctggtgga ggaagttctg gtggagagcc tactactgag 540

aacttgtact tccagagcga taacggaagt tctggtggag gaagttctgg tggaatggtg 600

tttacactcg aagat 615

<210> 117
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 117
Met Phe Val Gly Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln
1 5 10 15

Val Leu Glu Gln Gly Gly Val Ser Ser Leu Phe Gln Asn Leu Gly Val
20 25 30

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

Lys Ile Asp Ile His Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp
50 55 60

Gln Met Gly Gln Ile Glu Lys Ile Phe Lys Val Val Tyr Pro Val Asp
65 70 75 80

Asp His His Phe Lys Val Ile Leu His Tyr Gly Thr Leu Val Ile Asp
85 90 95

Gly Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly
100 105 110

Ile Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr Leu Trp
115 120 125

Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly Ser
130 135 140

Leu Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg Leu Cys
145 150 155 160

Glu Arg Ile Leu Ala Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Glu
165 170 175

Pro Thr Thr Glu Asn Leu Tyr Phe Gln Ser Asp Asn Gly Ser Ser Gly
180 185 190

Gly Gly Ser Ser Gly Gly Met Val Phe Thr Leu Glu Asp
195 200 205

<210> 118
<211> 615
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 118
atggtagggg actggcggca gacagccggc tacaacctgg accaagtcct tgagcagggc 60

ggtgtgtcca gtttgtttca gaatctcggg gtgtccgtaa ctccgatcca aaggattgtc 120

ctgagcggtg aaaacggcct gaagatcgac atccatgtca tcatcccgta tgaaggtctg 180

agcggcgatc agatgggcca gatcgaaaaa atttttaagg tggtgtaccc tgtggatgat 240

catcacttta aggtgattct gcactatggc acactggtaa tcgacggggt tacgccgaac 300

atgatcgact atttcggacg gccgtatgaa ggcatcgccg tgttcgacgg caaaaagatc 360

actgtaaccg ggaccctgtg gaacggcaac aaaattatcg acgagcgcct gatcaacccc 420

gacggctccc tgctgttccg cgtaaccatc aacggagtga ccggctggcg gctgtgcgag 480

cgcattttgg cgggaagttc tggtggagga agttctggtg gagagcctac tactgagaac 540

ttgtacttcc agagcgataa cggaagttct ggtggaggaa gttctggtgg aatggtgttt 600

acactcgaag atttc 615

<210> 119
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 119
Met Val Gly Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val
1 5 10 15

Leu Glu Gln Gly Gly Val Ser Ser Leu Phe Gln Asn Leu Gly Val Ser
20 25 30

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

Ile Asp Ile His Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln
50 55 60

Met Gly Gln Ile Glu Lys Ile Phe Lys Val Val Tyr Pro Val Asp Asp
65 70 75 80

His His Phe Lys Val Ile Leu His Tyr Gly Thr Leu Val Ile Asp Gly
85 90 95

Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly Ile
100 105 110

Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr Leu Trp Asn
115 120 125

Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly Ser Leu
130 135 140

Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg Leu Cys Glu
145 150 155 160

Arg Ile Leu Ala Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Glu Pro
165 170 175

Thr Thr Glu Asn Leu Tyr Phe Gln Ser Asp Asn Gly Ser Ser Gly Gly
180 185 190

Gly Ser Ser Gly Gly Met Val Phe Thr Leu Glu Asp Phe
195 200 205

<210> 120
<211> 615
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 120
atggactggc ggcagacagc cggctacaac ctggaccaag tccttgagca gggcggtgtg 60

tccagtttgt ttcagaatct cggggtgtcc gtaactccga tccaaaggat tgtcctgagc 120

ggtgaaaacg gcctgaagat cgacatccat gtcatcatcc cgtatgaagg tctgagcggc 180

gatcagatgg gccagatcga aaaaattttt aaggtggtgt accctgtgga tgatcatcac 240

tttaaggtga ttctgcacta tggcacactg gtaatcgacg gggttacgcc gaacatgatc 300

gactatttcg gacggccgta tgaaggcatc gccgtgttcg acggcaaaaa gatcactgta 360

accgggaccc tgtggaacgg caacaaaatt atcgacgagc gcctgatcaa ccccgacggc 420

tccctgctgt tccgcgtaac catcaacgga gtgaccggct ggcggctgtg cgagcgcatt 480

ttggcgggaa gttctggtgg aggaagttct ggtggagagc ctactactga gaacttgtac 540

ttccagagcg ataacggaag ttctggtgga ggaagttctg gtggaatggt gtttacactc 600

gaagatttcg taggg 615

<210> 121
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 121
Met Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val Leu Glu
1 5 10 15

Gln Gly Gly Val Ser Ser Leu Phe Gln Asn Leu Gly Val Ser Val Thr
20 25 30

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

Ile His Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln Met Gly
50 55 60

Gln Ile Glu Lys Ile Phe Lys Val Val Tyr Pro Val Asp Asp His His
65 70 75 80

Phe Lys Val Ile Leu His Tyr Gly Thr Leu Val Ile Asp Gly Val Thr
85 90 95

Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly Ile Ala Val
100 105 110

Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr Leu Trp Asn Gly Asn
115 120 125

Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly Ser Leu Leu Phe
130 135 140

Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg Leu Cys Glu Arg Ile
145 150 155 160

Leu Ala Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Glu Pro Thr Thr
165 170 175

Glu Asn Leu Tyr Phe Gln Ser Asp Asn Gly Ser Ser Gly Gly Gly Ser
180 185 190

Ser Gly Gly Met Val Phe Thr Leu Glu Asp Phe Val Gly
195 200 205

<210> 122
<211> 615
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 122
atgcggcaga cagccggcta caacctggac caagtccttg agcagggcgg tgtgtccagt 60

ttgtttcaga atctcggggt gtccgtaact ccgatccaaa ggattgtcct gagcggtgaa 120

aacggcctga agatcgacat ccatgtcatc atcccgtatg aaggtctgag cggcgatcag 180

atgggccaga tcgaaaaaat ttttaaggtg gtgtaccctg tggatgatca tcactttaag 240

gtgattctgc actatggcac actggtaatc gacggggtta cgccgaacat gatcgactat 300

ttcggacggc cgtatgaagg catcgccgtg ttcgacggca aaaagatcac tgtaaccggg 360

accctgtgga acggcaacaa aattatcgac gagcgcctga tcaaccccga cggctccctg 420

ctgttccgcg taaccatcaa cggagtgacc ggctggcggc tgtgcgagcg cattttggcg 480

ggaagttctg gtggaggaag ttctggtgga gagcctacta ctgagaactt gtacttccag 540

agcgataacg gaagttctgg tggaggaagt tctggtggaa tggtgtttac actcgaagat 600

ttcgtagggg actgg 615

<210> 123
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 123
Met Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly
1 5 10 15

Gly Val Ser Ser Leu Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile
20 25 30

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

Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln Met Gly Gln Ile
50 55 60

Glu Lys Ile Phe Lys Val Val Tyr Pro Val Asp Asp His His Phe Lys

65 70 75 80

Val Ile Leu His Tyr Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn
85 90 95

Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp
100 105 110

Gly Lys Lys Ile Thr Val Thr Gly Thr Leu Trp Asn Gly Asn Lys Ile
115 120 125

Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val
130 135 140

Thr Ile Asn Gly Val Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala
145 150 155 160

Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Glu Pro Thr Thr Glu Asn
165 170 175

Leu Tyr Phe Gln Ser Asp Asn Gly Ser Ser Gly Gly Gly Ser Ser Gly
180 185 190

Gly Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp
195 200 205

<210> 124
<211> 603
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 124
cagacagccg gctacaacct ggaccaagtc cttgagcagg gcggtgtgtc agtttgttt 60

cagaatctcg gggtgtccgt aactccgatc caaaggattg tcctgagcgg tgaaaacggc 120

ctgaagatcg acatccatgt catcatcccg tatgaaggtc tgagcggcga tcagatgggc 180

cagatcgaaa aaatttttaa ggtggtgtac cctgtggatg atcatcactt taaggtgatt 240

ctgcactatg gcacactggt aatcgacggg gttacgccga acatgatcga ctatttcgga 300

cggccgtatg aaggcatcgc cgtgttcgac ggcaaaaaga tcactgtaac cgggaccctg 360

tggaacggca acaaaattat cgacgagcgc ctgatcaacc ccgacggctc cctgctgttc 420

cgcgtaacca tcaacggagt gaccggctgg cggctgtgcg agcgcatttt ggcgggaagt 480

tctggtggag gaagttctgg tggagagcct actactgaga acttgtactt ccagagcgat 540

aacggaagtt ctggtggagg aagttctggt ggaatggtgt ttacactcga agatttcgta 600

ggg 603

<210> 125
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 125

```
Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Val
1               5                   10                  15

Ser Ser Leu Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln Arg
            20                  25                  30

Ile Val Leu Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile
        35                  40                  45

Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln Met Gly Gln Ile Glu Lys
    50                  55                  60

Ile Phe Lys Val Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile
65                  70                  75                  80

Leu His Tyr Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile
                85                  90                  95

Asp Tyr Phe Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys
            100                 105                 110

Lys Ile Thr Val Thr Gly Thr Leu Trp Asn Gly Asn Lys Ile Ile Asp
        115                 120                 125

Glu Arg Leu Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile
    130                 135                 140

Asn Gly Val Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala Gly Ser
145                 150                 155                 160

Ser Gly Gly Gly Ser Ser Gly Gly Glu Pro Thr Thr Glu Asn Leu Tyr
                165                 170                 175

Phe Gln Ser Asp Asn Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Met
            180                 185                 190

Val Phe Thr Leu Glu Asp Phe Val Gly
        195                 200
```

<210> 126
<211> 615
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 126
atgggctaca acctggacca agtccttgag cagggcggtg tgtccagttt gtttcagaat 60

ctcggggtgt ccgtaactcc gatccaaagg attgtcctga gcggtgaaaa cggcctgaag 120

atcgacatcc atgtcatcat cccgtatgaa ggtctgagcg gcgatcagat gggccagatc 180

gaaaaaattt ttaaggtggt gtaccctgtg gatgatcatc actttaaggt gattctgcac 240

tatggcacac tggtaatcga cggggttacg ccgaacatga tcgactattt cggacggccg 300

tatgaaggca tcgccgtgtt cgacggcaaa aagatcactg taaccgggac cctgtggaac 360

ggcaacaaaa ttatcgacga gcgcctgatc aaccccgacg gctccctgct gttccgcgta 420

accatcaacg gagtgaccgg ctggcggctg tgcgagcgca ttttggcggg aagttctggt 480

ggaggaagtt ctggtggaga gcctactact gagaacttgt acttccagag cgataacgga 540

agttctggtg gaggaagttc tggtggaatg gtgtttacac tcgaagattt cgtaggggac 600

tggcggcaga cagcc 615

<210> 127
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 127
Met Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser
1 5 10 15

Leu Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln Arg Ile Val
20 25 30

Leu Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro
35 40 45

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

Lys Val Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu His
65 70 75 80

Tyr Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr
85 90 95

Phe Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile
100 105 110

Thr Val Thr Gly Thr Leu Trp Asn Gly Asn Lys Ile Ile Asp Glu Arg
115 120 125

```
Leu Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly
    130                 135                 140

Val Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala Gly Ser Ser Gly
145                 150                 155                 160

Gly Gly Ser Ser Gly Gly Glu Pro Thr Thr Glu Asn Leu Tyr Phe Gln
                165                 170                 175

Ser Asp Asn Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Met Val Phe
            180                 185                 190

Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala
        195                 200                 205
```

<210> 128
<211> 612
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 128
ctggaccaag tccttgagca gggcggtgtg tccagtttgt ttcagaatct cggggtgtcc 60

gtaactccga tccaaaggat tgtcctgagc ggtgaaaacg gcctgaagat cgacatccat 120

gtcatcatcc cgtatgaagg tctgagcggc gatcagatgg gccagatcga aaaaattttt 180

aaggtggtgt accctgtgga tgatcatcac tttaaggtga ttctgcacta tggcacactg 240

gtaatcgacg gggttacgcc gaacatgatc gactatttcg gacggccgta tgaaggcatc 300

gccgtgttcg acggcaaaaa gatcactgta accgggaccc tgtggaacgg caacaaaatt 360

atcgacgagc gcctgatcaa ccccgacggc tccctgctgt tccgcgtaac catcaacgga 420

gtgaccggct ggcggctgtg cgagcgcatt ttggcgggaa gttctggtgg aggaagttct 480

ggtggagagc ctactactga gaacttgtac ttccagagcg ataacggaag ttctggtgga 540

ggaagttctg gtggaatggt gtttacactc gaagatttcg taggggactg gcggcagaca 600

gccggctaca ac 612

<210> 129
<211> 204
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 129
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Leu Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu Phe Gln Asn
1               5                   10                  15
```

Leu Gly Val Ser Val Thr Pro Ile Gln Arg Ile Val Leu Ser Gly Glu
20 25 30

Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr Glu Gly Leu
35 40 45

Ser Gly Asp Gln Met Gly Gln Ile Glu Lys Ile Phe Lys Val Val Tyr
50 55 60

Pro Val Asp Asp His His Phe Lys Val Ile Leu His Tyr Gly Thr Leu
65 70 75 80

Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro
85 90 95

Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly
100 105 110

Thr Leu Trp Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro
115 120 125

Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp
130 135 140

Arg Leu Cys Glu Arg Ile Leu Ala Gly Ser Ser Gly Gly Gly Ser Ser
145 150 155 160

Gly Gly Glu Pro Thr Thr Glu Asn Leu Tyr Phe Gln Ser Asp Asn Gly
165 170 175

Ser Ser Gly Gly Gly Ser Ser Gly Gly Met Val Phe Thr Leu Glu Asp
180 185 190

Phe Val Gly Asp Trp Arg Gln Thr Ala Gly Tyr Asn
195 200

<210> 130
<211> 612
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 130
gtccttgagc agggcggtgt gtccagtttg tttcagaatc tcggggtgtc cgtaactccg 60

atccaaagga ttgtcctgag cggtgaaaac ggcctgaaga tcgacatcca tgtcatcatc 120

ccgtatgaag gtctgagcgg cgatcagatg ggccagatcg aaaaaatttt taaggtggtg 180

taccctgtgg atgatcatca ctttaaggtg attctgcact atggcacact ggtaatcgac 240

ggggttacgc cgaacatgat cgactatttc ggacggccgt atgaaggcat cgccgtgttc 300

gacggcaaaa agatcactgt aaccgggacc ctgtggaacg gcaacaaaat tatcgacgag 360

cgcctgatca accccgacgg ctccctgctg ttccgcgtaa ccatcaacgg agtgaccggc 420

tggcggctgt gcgagcgcat tttggcggga agttctggtg gaggaagttc tggtggagag 480

cctactactg agaacttgta cttccagagc gataacggaa gttctggtgg aggaagttct 540

ggtggaatgg tgtttacact cgaagatttc gtaggggact ggcggcagac agccggctac 600

aacctggacc aa 612

<210> 131
<211> 204
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 131
Val Leu Glu Gln Gly Gly Val Ser Ser Leu Phe Gln Asn Leu Gly Val
1 5 10 15

Ser Val Thr Pro Ile Gln Arg Ile Val Leu Ser Gly Glu Asn Gly Leu
20 25 30

Lys Ile Asp Ile His Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp
35 40 45

Gln Met Gly Gln Ile Glu Lys Ile Phe Lys Val Val Tyr Pro Val Asp
50 55 60

Asp His His Phe Lys Val Ile Leu His Tyr Gly Thr Leu Val Ile Asp
65 70 75 80

Gly Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly
85 90 95

Ile Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr Leu Trp
100 105 110

Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly Ser
115 120 125

Leu Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg Leu Cys
130 135 140

Glu Arg Ile Leu Ala Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Glu
145 150 155 160

Pro Thr Thr Glu Asn Leu Tyr Phe Gln Ser Asp Asn Gly Ser Ser Gly
165 170 175

Gly Gly Ser Ser Gly Gly Met Val Phe Thr Leu Glu Asp Phe Val Gly

180 185 190

Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln
195 200

<210> 132
<211> 612
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 132
cagggcggtg tgtccagttt gtttcagaat ctcggggtgt ccgtaactcc gatccaaagg 60

attgtcctga gcggtgaaaa cggcctgaag atcgacatcc atgtcatcat cccgtatgaa 120

ggtctgagcg gcgatcagat gggccagatc gaaaaaattt ttaaggtggt gtaccctgtg 180

gatgatcatc actttaaggt gattctgcac tatggcacac tggtaatcga cggggttacg 240

ccgaacatga tcgactattt cggacggccg tatgaaggca tcgccgtgtt cgacggcaaa 300

aagatcactg taaccgggac cctgtggaac ggcaacaaaa ttatcgacga gcgcctgatc 360

aaccccgacg gctccctgct gttccgcgta accatcaacg gagtgaccgg ctggcggctg 420

tgcgagcgca ttttggcggg aagttctggt ggaggaagtt ctggtggaga gcctactact 480

gagaacttgt acttccagag cgataacgga agttctggtg gaggaagttc tggtggaatg 540

gtgtttacac tcgaagattt cgtaggggac tggcggcaga cagccggcta caacctggac 600

caagtccttg ag 612

<210> 133
<211> 204
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 133
Gln Gly Gly Val Ser Ser Leu Phe Gln Asn Leu Gly Val Ser Val Thr
1 5 10 15

Pro Ile Gln Arg Ile Val Leu Ser Gly Glu Asn Gly Leu Lys Ile Asp
20 25 30

Ile His Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln Met Gly
35 40 45

Gln Ile Glu Lys Ile Phe Lys Val Val Tyr Pro Val Asp Asp His His
50 55 60

Phe Lys Val Ile Leu His Tyr Gly Thr Leu Val Ile Asp Gly Val Thr
65 70 75 80

Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly Ile Ala Val
85 90 95

Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr Leu Trp Asn Gly Asn
100 105 110

Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly Ser Leu Leu Phe
115 120 125

Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg Leu Cys Glu Arg Ile
130 135 140

Leu Ala Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Glu Pro Thr Thr
145 150 155 160

Glu Asn Leu Tyr Phe Gln Ser Asp Asn Gly Ser Ser Gly Gly Gly Ser
165 170 175

Ser Gly Gly Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg
180 185 190

Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val Leu Glu
195 200

<210> 134
<211> 612
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 134
gtgtccagtt tgtttcagaa tctcggggtg tccgtaactc cgatccaaag gattgtcctg 60

agcggtgaaa acggcctgaa gatcgacatc catgtcatca tcccgtatga aggtctgagc 120

ggcgatcaga tgggccagat cgaaaaaatt tttaaggtgg tgtaccctgt ggatgatcat 180

cactttaagg tgattctgca ctatggcaca ctggtaatcg acggggttac gccgaacatg 240

atcgactatt tcggacggcc gtatgaaggc atcgccgtgt tcgacggcaa aaagatcact 300

gtaaccggga ccctgtggaa cggcaacaaa attatcgacg agcgcctgat caaccccgac 360

ggctccctgc tgttccgcgt aaccatcaac ggagtgaccg gctggcggct gtgcgagcgc 420

attttggcgg gaagttctgg tggaggaagt tctggtggag agcctactac tgagaacttg 480

tacttccaga gcgataacgg aagttctggt ggaggaagtt ctggtggaat ggtgtttaca 540

ctcgaagatt tcgtagggga ctggcggcag acagccggct acaacctgga ccaagtcctt 600

gagcagggcg gt 612

<210> 135

<211> 204
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 135
Val Ser Ser Leu Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln
1 5 10 15

Arg Ile Val Leu Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val
20 25 30

Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln Met Gly Gln Ile Glu
35 40 45

Lys Ile Phe Lys Val Val Tyr Pro Val Asp Asp His His Phe Lys Val
50 55 60

Ile Leu His Tyr Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met
65 70 75 80

Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly
85 90 95

Lys Lys Ile Thr Val Thr Gly Thr Leu Trp Asn Gly Asn Lys Ile Ile
100 105 110

Asp Glu Arg Leu Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val Thr
115 120 125

Ile Asn Gly Val Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala Gly
130 135 140

Ser Ser Gly Gly Gly Ser Ser Gly Gly Glu Pro Thr Thr Glu Asn Leu
145 150 155 160

Tyr Phe Gln Ser Asp Asn Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly
165 170 175

Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala
180 185 190

Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly
195 200

<210> 136
<211> 615
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

polynucleotide

<400> 136
atgctcgggg tgtccgtaac tccgatccaa aggattgtcc tgagcggtga aaacggcctg 60

aagatcgaca tccatgtcat catcccgtat gaaggtctga gcggcgatca gatgggccag 120

atcgaaaaaa tttttaaggt ggtgtaccct gtggatgatc atcactttaa ggtgattctg 180

cactatggca cactggtaat cgacggggtt acgccgaaca tgatcgacta tttcggacgg 240

ccgtatgaag gcatcgccgt gttcgacggc aaaaagatca ctgtaaccgg gaccctgtgg 300

aacggcaaca aaattatcga cgagcgcctg atcaaccccg acggctccct gctgttccgc 360

gtaaccatca acggagtgac cggctggcgg ctgtgcgagc gcattttggc gggaagttct 420

ggtggaggaa gttctggtgg agagcctact actgagaact tgtacttcca gagcgataac 480

ggaagttctg gtggaggaag ttctggtgga atggtgttta cactcgaaga tttcgtaggg 540

gactggcggc agacagccgg ctacaacctg gaccaagtcc ttgagcaggg cggtgtgtcc 600

agtttgtttc agaat 615

<210> 137
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 137
Met Leu Gly Val Ser Val Thr Pro Ile Gln Arg Ile Val Leu Ser Gly
1 5 10 15

Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr Glu Gly
20 25 30

Leu Ser Gly Asp Gln Met Gly Gln Ile Glu Lys Ile Phe Lys Val Val
35 40 45

Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu His Tyr Gly Thr
50 55 60

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

Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr
85 90 95

Gly Thr Leu Trp Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn
100 105 110

Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly
115 120 125

Trp Arg Leu Cys Glu Arg Ile Leu Ala Gly Ser Ser Gly Gly Gly Ser
130 135 140

Ser Gly Gly Glu Pro Thr Thr Glu Asn Leu Tyr Phe Gln Ser Asp Asn
145 150 155 160

Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Met Val Phe Thr Leu Glu
165 170 175

Asp Phe Val Gly Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln
180 185 190

Val Leu Glu Gln Gly Gly Val Ser Ser Leu Phe Gln Asn
195 200 205

<210> 138
<211> 615
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 138
atgccgatcc aaaggattgt cctgagcggt gaaaacggcc tgaagatcga catccatgtc 60

atcatcccgt atgaaggtct gagcggcgat cagatgggcc agatcgaaaa aatttttaag 120

gtggtgtacc ctgtggatga tcatcacttt aaggtgattc tgcactatgg cacactggta 180

atcgacgggg ttacgccgaa catgatcgac tatttcggac ggccgtatga aggcatcgcc 240

gtgttcgacg gcaaaaagat cactgtaacc gggaccctgt ggaacggcaa caaaattatc 300

gacgagcgcc tgatcaaccc cgacggctcc ctgctgttcc gcgtaaccat caacggagtg 360

accggctggc ggctgtgcga gcgcattttg gcgggaagtt ctggtggagg aagttctggt 420

ggagagccta ctactgagaa cttgtacttc cagagcgata acggaagttc tggtggagga 480

agttctggtg gaatggtgtt tacactcgaa gatttcgtag gggactggcg gcagacagcc 540

ggctacaacc tggaccaagt ccttgagcag ggcggtgtgt ccagtttgtt tcagaatctc 600

ggggtgtccg taact 615

<210> 139
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 139
Met Pro Ile Gln Arg Ile Val Leu Ser Gly Glu Asn Gly Leu Lys Ile
1 5 10 15

Asp Ile His Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln Met

20 25 30

Gly Gln Ile Glu Lys Ile Phe Lys Val Val Tyr Pro Val Asp Asp His
35 40 45

His Phe Lys Val Ile Leu His Tyr Gly Thr Leu Val Ile Asp Gly Val
50 55 60

Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly Ile Ala
65 70 75 80

Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr Leu Trp Asn Gly
85 90 95

Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly Ser Leu Leu
100 105 110

Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg Leu Cys Glu Arg
115 120 125

Ile Leu Ala Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Glu Pro Thr
130 135 140

Thr Glu Asn Leu Tyr Phe Gln Ser Asp Asn Gly Ser Ser Gly Gly Gly
145 150 155 160

Ser Ser Gly Gly Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp
165 170 175

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

Val Ser Ser Leu Phe Gln Asn Leu Gly Val Ser Val Thr
195 200 205

<210> 140
<211> 615
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 140
atgaggattg tcctgagcgg tgaaaacggc ctgaagatcg acatccatgt catcatcccg 60

tatgaaggtc tgagcggcga tcagatgggc cagatcgaaa aaatttttaa ggtggtgtac 120

cctgtggatg atcatcactt taaggtgatt ctgcactatg gcacactggt aatcgacggg 180

gttacgccga acatgatcga ctatttcgga cggccgtatg aaggcatcgc cgtgttcgac 240

ggcaaaaaga tcactgtaac cgggaccctg tggaacggca acaaaattat cgacgagcgc 300

ctgatcaacc ccgacggctc cctgctgttc cgcgtaacca tcaacggagt gaccggctgg 360

cggctgtgcg agcgcatttt ggcgggaagt tctggtggag gaagttctgg tggagagcct 420

actactgaga acttgtactt ccagagcgat aacggaagtt ctggtggagg aagttctggt 480

ggaatggtgt ttacactcga agatttcgta ggggactggc ggcagacagc cggctacaac 540

ctggaccaag tccttgagca gggcggtgtg tccagtttgt ttcagaatct cggggtgtcc 600

gtaactccga tccaa 615

<210> 141
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 141

Met Arg Ile Val Leu Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His
1 5 10 15

Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln Met Gly Gln Ile
20 25 30

Glu Lys Ile Phe Lys Val Val Tyr Pro Val Asp Asp His His Phe Lys
35 40 45

Val Ile Leu His Tyr Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn
50 55 60

Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp
65 70 75 80

Gly Lys Lys Ile Thr Val Thr Gly Thr Leu Trp Asn Gly Asn Lys Ile
85 90 95

Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val
100 105 110

Thr Ile Asn Gly Val Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala
115 120 125

Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Glu Pro Thr Thr Glu Asn
130 135 140

Leu Tyr Phe Gln Ser Asp Asn Gly Ser Ser Gly Gly Gly Ser Ser Gly
145 150 155 160

Gly Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr
165 170 175

Ala Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser
180 185 190

Leu Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln
195 200 205

<210> 142
<211> 615
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 142
atgattgtcc tgagcggtga aaacggcctg aagatcgaca tccatgtcat catcccgtat 60

gaaggtctga gcggcgatca gatgggccag atcgaaaaaa tttttaaggt ggtgtaccct 120

gtggatgatc atcactttaa ggtgattctg cactatggca cactggtaat cgacggggtt 180

acgccgaaca tgatcgacta tttcggacgg ccgtatgaag gcatcgccgt gttcgacggc 240

aaaaagatca ctgtaaccgg gaccctgtgg aacggcaaca aaattatcga cgagcgcctg 300

atcaaccccg acggctccct gctgttccgc gtaaccatca acggagtgac cggctggcgg 360

ctgtgcgagc gcattttggc gggaagttct ggtggaggaa gttctggtgg agagcctact 420

actgagaact tgtacttcca gagcgataac ggaagttctg gtggaggaag ttctggtgga 480

atggtgttta cactcgaaga tttcgtaggg gactggcggc agacagccgg ctacaacctg 540

gaccaagtcc ttgagcaggg cggtgtgtcc agtttgtttc agaatctcgg ggtgtccgta 600

actccgatcc aaagg 615

<210> 143
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 143
Met Ile Val Leu Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val
1 5 10 15

Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln Met Gly Gln Ile Glu
20 25 30

Lys Ile Phe Lys Val Val Tyr Pro Val Asp Asp His His Phe Lys Val
35 40 45

Ile Leu His Tyr Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met
50 55 60

Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly
65 70 75 80

Lys Lys Ile Thr Val Thr Gly Thr Leu Trp Asn Gly Asn Lys Ile Ile
85 90 95

Asp Glu Arg Leu Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val Thr
100 105 110

Ile Asn Gly Val Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala Gly
115 120 125

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

Tyr Phe Gln Ser Asp Asn Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly
145 150 155 160

Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala
165 170 175

Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu
180 185 190

Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln Arg
195 200 205

<210> 144
<211> 615
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 144
atggtcctga gcggtgaaaa cggcctgaag atcgacatcc atgtcatcat cccgtatgaa 60

ggtctgagcg gcgatcagat gggccagatc gaaaaaattt ttaaggtggt gtaccctgtg 120

gatgatcatc actttaaggt gattctgcac tatggcacac tggtaatcga cggggttacg 180

ccgaacatga tcgactattt cggacggccg tatgaaggca tcgccgtgtt cgacggcaaa 240

aagatcactg taaccgggac cctgtggaac ggcaacaaaa ttatcgacga gcgcctgatc 300

aaccccgacg gctccctgct gttccgcgta accatcaacg gagtgaccgg ctggcggctg 360

tgcgagcgca ttttggcggg aagttctggt ggaggaagtt ctggtggaga gcctactact 420

gagaacttgt acttccagag cgataacgga agttctggtg gaggaagttc tggtggaatg 480

gtgtttacac tcgaagattt cgtaggggac tggcggcaga cagccggcta caacctggac 540

caagtccttg agcagggcgg tgtgtccagt ttgtttcaga atctcggggt gtccgtaact 600

ccgatccaaa ggatt 615

<210> 145
<211> 205

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 145
Met Val Leu Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile
1 5 10 15

Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln Met Gly Gln Ile Glu Lys
20 25 30

Ile Phe Lys Val Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile
35 40 45

Leu His Tyr Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile
50 55 60

Asp Tyr Phe Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys
65 70 75 80

Lys Ile Thr Val Thr Gly Thr Leu Trp Asn Gly Asn Lys Ile Ile Asp
85 90 95

Glu Arg Leu Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile
100 105 110

Asn Gly Val Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala Gly Ser
115 120 125

Ser Gly Gly Gly Ser Ser Gly Gly Glu Pro Thr Thr Glu Asn Leu Tyr
130 135 140

Phe Gln Ser Asp Asn Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Met
145 150 155 160

Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala Gly
165 170 175

Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu Phe
180 185 190

Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln Arg Ile
195 200 205

<210> 146
<211> 612
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 146
atgctgagcg gtgaaaacgg cctgaagatc gacatccatg tcatcatccc gtatgaaggt 60

ctgagcggcg atcagatggg ccagatcgaa aaaatttta aggtggtgta ccctgtggat 120

gatcatcact ttaaggtgat tctgcactat ggcacactgg taatcgacgg ggttacgccg 180

aacatgatcg actatttcgg acggccgtat gaaggcatcg ccgtgttcga cggcaaaaag 240

atcactgtaa ccgggaccct gtggaacggc aacaaaatta tcgacgagcg cctgatcaac 300

cccgacggct ccctgctgtt ccgcgtaacc atcaacggag tgaccggctg gcggctgtgc 360

gagcgcattt tggcgggaag ttctggtgga ggaagttctg gtggagagcc tactactgag 420

aacttgtact tccagagcga taacggaagt tctggtggag gaagttctgg tggaatggtg 480

tttacactcg aagatttcgt aggggactgg cggcagacag ccggctacaa cctggaccaa 540

gtccttgagc agggcggtgt gtccagtttg tttcagaatc tcggggtgtc cgtaactccg 600

atccaaagga tt 612

<210> 147
<211> 204
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 147
Met Leu Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile
1 5 10 15

Pro Tyr Glu Gly Leu Ser Gly Asp Gln Met Gly Gln Ile Glu Lys Ile
20 25 30

Phe Lys Val Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu
35 40 45

His Tyr Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp
50 55 60

Tyr Phe Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys
65 70 75 80

Ile Thr Val Thr Gly Thr Leu Trp Asn Gly Asn Lys Ile Ile Asp Glu
85 90 95

Arg Leu Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn
100 105 110

Gly Val Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala Gly Ser Ser
115 120 125

Gly Gly Gly Ser Ser Gly Gly Glu Pro Thr Thr Glu Asn Leu Tyr Phe

130 135 140

Gln Ser Asp Asn Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Met Val
145 150 155 160

Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala Gly Tyr
165 170 175

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

Asn Leu Gly Val Ser Val Thr Pro Ile Gln Arg Ile
195 200

<210> 148
<211> 615
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 148
atgagcggtg aaaacggcct gaagatcgac atccatgtca tcatcccgta tgaaggtctg 60

agcggcgatc agatgggcca gatcgaaaaa atttttaagg tggtgtaccc tgtggatgat 120

catcacttta aggtgattct gcactatggc acactggtaa tcgacggggt tacgccgaac 180

atgatcgact atttcggacg gccgtatgaa ggcatcgccg tgttcgacgg caaaaagatc 240

actgtaaccg ggaccctgtg gaacggcaac aaaattatcg acgagcgcct gatcaacccc 300

gacggctccc tgctgttccg cgtaaccatc aacggagtga ccggctggcg gctgtgcgag 360

cgcattttgg cgggaagttc tggtggagga agttctggtg gagagcctac tactgagaac 420

ttgtacttcc agagcgataa cggaagttct ggtggaggaa gttctggtgg aatggtgttt 480

acactcgaag atttcgtagg ggactggcgg cagacagccg gctacaacct ggaccaagtc 540

cttgagcagg gcggtgtgtc cagtttgttt cagaatctcg gggtgtccgt aactccgatc 600

caaaggattg tcctg 615

<210> 149
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 149
Met Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro
1 5 10 15

Tyr Glu Gly Leu Ser Gly Asp Gln Met Gly Gln Ile Glu Lys Ile Phe
20 25 30

```
Lys Val Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu His
        35                  40                  45

Tyr Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr
    50                  55                  60

Phe Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile
65                  70                  75                  80

Thr Val Thr Gly Thr Leu Trp Asn Gly Asn Lys Ile Ile Asp Glu Arg
                85                  90                  95

Leu Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly
            100                 105                 110

Val Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala Gly Ser Ser Gly
        115                 120                 125

Gly Gly Ser Ser Gly Gly Glu Pro Thr Thr Glu Asn Leu Tyr Phe Gln
    130                 135                 140

Ser Asp Asn Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Met Val Phe
145                 150                 155                 160

Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala Gly Tyr Asn
                165                 170                 175

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

Leu Gly Val Ser Val Thr Pro Ile Gln Arg Ile Val Leu
        195                 200                 205
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<210> 150
<211> 616
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 150
atgggtgaaa acggcctgaa gatcgacatc catgtcatca tcccgtatga aggtctgagc 60

ggcgatcaga tgggccagat cgaaaaaatt tttaaggtgg tgtaccctgt ggatgatcat 120

cactttaagg tgattctgca ctatggcaca ctggtaatcg acggggttac gccgaacatg 180

atcgactatt tcggacggcc gtatgaaggc atcgccgtgt tcgacggcaa aaagatcact 240

gtaaccggga ccctgtggaa cggcaacaaa attatcgacg agcgcctgat caaccccgac 300

ggctccctgc tgttccgcgt aaccatcaac ggagtgaccg gctggcggct gtgcgagcgc 360

attttggcgg gaagttctgg tggaggaagt tctggtggag agcctactac tgagaacttg 420

tacttccaga gcgataacgg aagttctggt ggaggaagtt ctggtggaat ggtgtttaca 480

ctcgaagatt tcgtagggga ctggcggcag acagccggct acaacctgga ccaagtcctt 540

gagcagggcg gtgtgtccag tttgtttcag aatctcgggg tgtccgtaac tccgatccaa 600

aggattgtcc tgagcg 616

<210> 151
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 151
Met Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr
1 5 10 15

Glu Gly Leu Ser Gly Asp Gln Met Gly Gln Ile Glu Lys Ile Phe Lys
20 25 30

Val Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu His Tyr
35 40 45

Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe
50 55 60

Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr
65 70 75 80

Val Thr Gly Thr Leu Trp Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu
85 90 95

Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val
100 105 110

Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala Gly Ser Ser Gly Gly
115 120 125

Gly Ser Ser Gly Gly Glu Pro Thr Thr Glu Asn Leu Tyr Phe Gln Ser
130 135 140

Asp Asn Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Met Val Phe Thr
145 150 155 160

Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu
165 170 175

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

Gly Val Ser Val Thr Pro Ile Gln Arg Ile Val Leu Ser
195 200 205

<210> 152
<211> 615
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 152
atggaaaacg gcctgaagat cgacatccat gtcatcatcc cgtatgaagg tctgagcggc 60

gatcagatgg gccagatcga aaaaattttt aaggtggtgt accctgtgga tgatcatcac 120

tttaaggtga ttctgcacta tggcacactg gtaatcgacg gggttacgcc gaacatgatc 180

gactatttcg gacggccgta tgaaggcatc gccgtgttcg acggcaaaaa gatcactgta 240

accgggaccc tgtggaacgg caacaaaatt atcgacgagc gcctgatcaa ccccgacggc 300

tccctgctgt tccgcgtaac catcaacgga gtgaccggct ggcggctgtg cgagcgcatt 360

ttggcgggaa gttctggtgg aggaagttct ggtggagagc ctactactga gaacttgtac 420

ttccagagcg ataacggaag ttctggtgga ggaagttctg gtggaatggt gtttacactc 480

gaagatttcg taggggactg gcggcagaca gccggctaca acctggacca agtccttgag 540

cagggcggtg tgtccagttt gtttcagaat ctcggggtgt ccgtaactcc gatccaaagg 600

attgtcctga gcggt 615

<210> 153
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 153
Met Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr Glu
1 5 10 15

Gly Leu Ser Gly Asp Gln Met Gly Gln Ile Glu Lys Ile Phe Lys Val
20 25 30

Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu His Tyr Gly
35 40 45

Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe Gly
50 55 60

Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr Val
65 70 75 80

Thr Gly Thr Leu Trp Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile
85 90 95

Asn Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val Thr
100 105 110

Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala Gly Ser Ser Gly Gly Gly
115 120 125

Ser Ser Gly Gly Glu Pro Thr Thr Glu Asn Leu Tyr Phe Gln Ser Asp
130 135 140

Asn Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Met Val Phe Thr Leu
145 150 155 160

Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp
165 170 175

Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu Phe Gln Asn Leu Gly
180 185 190

Val Ser Val Thr Pro Ile Gln Arg Ile Val Leu Ser Gly
195 200 205

<210> 154
<211> 615
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 154
atgaacggcc tgaagatcga catccatgtc atcatcccgt atgaaggtct gagcggcgat 60

cagatgggcc agatcgaaaa aatttttaag gtggtgtacc ctgtggatga tcatcacttt 120

aaggtgattc tgcactatgg cacactggta atcgacgggg ttacgccgaa catgatcgac 180

tatttcggac ggccgtatga aggcatcgcc gtgttcgacg gcaaaaagat cactgtaacc 240

gggaccctgt ggaacggcaa caaaattatc gacgagcgcc tgatcaaccc cgacggctcc 300

ctgctgttcc gcgtaaccat caacggagtg accggctggc ggctgtgcga gcgcattttg 360

gcgggaagtt ctggtggagg aagttctggt ggagagccta ctactgagaa cttgtacttc 420

cagagcgata acggaagttc tggtggagga agttctggtg gaatggtgtt tacactcgaa 480

gatttcgtag gggactggcg gcagacagcc ggctacaacc tggaccaagt ccttgagcag 540

ggcggtgtgt ccagtttgtt tcagaatctc ggggtgtccg taactccgat ccaaaggatt 600

gtcctgagcg gtgaa 615

<210> 155
<211> 205
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 155

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Met Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr Glu Gly
1               5                  10                  15

Leu Ser Gly Asp Gln Met Gly Gln Ile Glu Lys Ile Phe Lys Val Val
            20                  25                  30

Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu His Tyr Gly Thr
        35                  40                  45

Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg
    50                  55                  60

Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr
65                  70                  75                  80

Gly Thr Leu Trp Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn
                85                  90                  95

Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly
            100                 105                 110

Trp Arg Leu Cys Glu Arg Ile Leu Ala Gly Ser Ser Gly Gly Gly Ser
        115                 120                 125

Ser Gly Gly Glu Pro Thr Thr Glu Asn Leu Tyr Phe Gln Ser Asp Asn
    130                 135                 140

Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Met Val Phe Thr Leu Glu
145                 150                 155                 160

Asp Phe Val Gly Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln
                165                 170                 175

Val Leu Glu Gln Gly Gly Val Ser Ser Leu Phe Gln Asn Leu Gly Val
            180                 185                 190

Ser Val Thr Pro Ile Gln Arg Ile Val Leu Ser Gly Glu
        195                 200                 205
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<210> 156
<211> 615
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 156
atgggcctga agatcgacat ccatgtcatc atcccgtatg aaggtctgag cggcgatcag 60

atgggccaga tcgaaaaaat ttttaaggtg gtgtaccctg tggatgatca tcactttaag 120

gtgattctgc actatggcac actggtaatc gacggggtta cgccgaacat gatcgactat 180

ttcggacggc cgtatgaagg catcgccgtg ttcgacggca aaaagatcac tgtaaccggg 240

accctgtgga acggcaacaa aattatcgac gagcgcctga tcaaccccga cggctccctg 300

ctgttccgcg taaccatcaa cggagtgacc ggctggcggc tgtgcgagcg cattttggcg 360

ggaagttctg gtggaggaag ttctggtgga gagcctacta ctgagaactt gtacttccag 420

agcgataacg gaagttctgg tggaggaagt tctggtggaa tggtgtttac actcgaagat 480

ttcgtagggg actggcggca gacagccggc tacaacctgg accaagtcct tgagcagggc 540

ggtgtgtcca gtttgtttca gaatctcggg gtgtccgtaa ctccgatcca aaggattgtc 600

ctgagcggtg aaaac 615

<210> 157
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 157
Met Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr Glu Gly Leu
1 5 10 15

Ser Gly Asp Gln Met Gly Gln Ile Glu Lys Ile Phe Lys Val Val Tyr
20 25 30

Pro Val Asp Asp His His Phe Lys Val Ile Leu His Tyr Gly Thr Leu
35 40 45

Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro
50 55 60

Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly
65 70 75 80

Thr Leu Trp Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro
85 90 95

Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp
100 105 110

Arg Leu Cys Glu Arg Ile Leu Ala Gly Ser Ser Gly Gly Gly Ser Ser
115 120 125

Gly Gly Glu Pro Thr Thr Glu Asn Leu Tyr Phe Gln Ser Asp Asn Gly
130 135 140

Ser Ser Gly Gly Gly Ser Ser Gly Gly Met Val Phe Thr Leu Glu Asp
145 150 155 160

Phe Val Gly Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val
165 170 175

Leu Glu Gln Gly Gly Val Ser Ser Leu Phe Gln Asn Leu Gly Val Ser
180 185 190

Val Thr Pro Ile Gln Arg Ile Val Leu Ser Gly Glu Asn
195 200 205

<210> 158
<211> 615
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 158
atgctgaaga tcgacatcca tgtcatcatc ccgtatgaag gtctgagcgg cgatcagatg 60

ggccagatcg aaaaaatttt taaggtggtg taccctgtgg atgatcatca ctttaaggtg 120

attctgcact atggcacact ggtaatcgac ggggttacgc cgaacatgat cgactatttc 180

ggacggccgt atgaaggcat cgccgtgttc gacggcaaaa agatcactgt aaccgggacc 240

ctgtggaacg gcaacaaaat tatcgacgag cgcctgatca accccgacgg ctccctgctg 300

ttccgcgtaa ccatcaacgg agtgaccggc tggcggctgt gcgagcgcat tttggcggga 360

agttctggtg gaggaagttc tggtggagag cctactactg agaacttgta cttccagagc 420

gataacggaa gttctggtgg aggaagttct ggtggaatgg tgtttacact cgaagatttc 480

gtaggggact ggcggcagac agccggctac aacctggacc aagtccttga gcagggcggt 540

gtgtccagtt tgtttcagaa tctcggggtg tccgtaactc cgatccaaag gattgtcctg 600

agcggtgaaa acggc 615

<210> 159
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 159
Met Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr Glu Gly Leu Ser
1 5 10 15

Gly Asp Gln Met Gly Gln Ile Glu Lys Ile Phe Lys Val Val Tyr Pro
20 25 30

Val Asp Asp His His Phe Lys Val Ile Leu His Tyr Gly Thr Leu Val
35 40 45

Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr
50 55 60

Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr
65 70 75 80

Leu Trp Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp
85 90 95

Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg
100 105 110

Leu Cys Glu Arg Ile Leu Ala Gly Ser Ser Gly Gly Gly Ser Ser Gly
115 120 125

Gly Glu Pro Thr Thr Glu Asn Leu Tyr Phe Gln Ser Asp Asn Gly Ser
130 135 140

Ser Gly Gly Gly Ser Ser Gly Gly Met Val Phe Thr Leu Glu Asp Phe
145 150 155 160

Val Gly Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val Leu
165 170 175

Glu Gln Gly Gly Val Ser Ser Leu Phe Gln Asn Leu Gly Val Ser Val
180 185 190

Thr Pro Ile Gln Arg Ile Val Leu Ser Gly Glu Asn Gly
195 200 205

<210> 160
<211> 615
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 160
atgaagatcg acatccatgt catcatcccg tatgaaggtc tgagcggcga tcagatgggc 60

cagatcgaaa aaatttttaa ggtggtgtac cctgtggatg atcatcactt taaggtgatt 120

ctgcactatg gcacactggt aatcgacggg gttacgccga acatgatcga ctatttcgga 180

cggccgtatg aaggcatcgc cgtgttcgac ggcaaaaaga tcactgtaac cgggaccctg 240

tggaacggca acaaaattat cgacgagcgc ctgatcaacc ccgacggctc cctgctgttc 300

cgcgtaacca tcaacggagt gaccggctgg cggctgtgcg agcgcatttt ggcgggaagt 360

tctggtggag gaagttctgg tggagagcct actactgaga acttgtactt ccagagcgat 420

aacggaagtt ctggtggagg aagttctggt ggaatggtgt ttacactcga agatttcgta 480

ggggactggc ggcagacagc cggctacaac ctggaccaag tccttgagca gggcggtgtg 540

tccagtttgt ttcagaatct cggggtgtcc gtaactccga tccaaaggat tgtcctgagc 600

ggtgaaaacg gcctg 615

<210> 161
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 161
Met Lys Ile Asp Ile His Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly
1 5 10 15

Asp Gln Met Gly Gln Ile Glu Lys Ile Phe Lys Val Val Tyr Pro Val
20 25 30

Asp Asp His His Phe Lys Val Ile Leu His Tyr Gly Thr Leu Val Ile
35 40 45

Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu
50 55 60

Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr Leu
65 70 75 80

Trp Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly
85 90 95

Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg Leu
100 105 110

Cys Glu Arg Ile Leu Ala Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly
115 120 125

Glu Pro Thr Thr Glu Asn Leu Tyr Phe Gln Ser Asp Asn Gly Ser Ser
130 135 140

Gly Gly Gly Ser Ser Gly Gly Met Val Phe Thr Leu Glu Asp Phe Val
145 150 155 160

Gly Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val Leu Glu
165 170 175

Gln Gly Gly Val Ser Ser Leu Phe Gln Asn Leu Gly Val Ser Val Thr
180 185 190

Pro Ile Gln Arg Ile Val Leu Ser Gly Glu Asn Gly Leu
195 200 205

<210> 162
<211> 615
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 162
atgatcgaca tccatgtcat catcccgtat gaaggtctga gcggcgatca gatgggccag 60

atcgaaaaaa tttttaaggt ggtgtaccct gtggatgatc atcactttaa ggtgattctg 120

cactatggca cactggtaat cgacggggtt acgccgaaca tgatcgacta tttcggacgg 180

ccgtatgaag gcatcgccgt gttcgacggc aaaaagatca ctgtaaccgg gaccctgtgg 240

aacggcaaca aaattatcga cgagcgcctg atcaaccccg acggctccct gctgttccgc 300

gtaaccatca acggagtgac cggctggcgg ctgtgcgagc gcattttggc gggaagttct 360

ggtggaggaa gttctggtgg agagcctact actgagaact tgtacttcca gagcgataac 420

ggaagttctg gtggaggaag ttctggtgga atggtgttta cactcgaaga tttcgtaggg 480

gactggcggc agacagccgg ctacaacctg gaccaagtcc ttgagcaggg cggtgtgtcc 540

agtttgtttc agaatctcgg ggtgtccgta actccgatcc aaaggattgt cctgagcggt 600

gaaaacggcc tgaag 615

<210> 163
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 163
Met Ile Asp Ile His Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp
1 5 10 15

Gln Met Gly Gln Ile Glu Lys Ile Phe Lys Val Val Tyr Pro Val Asp
20 25 30

Asp His His Phe Lys Val Ile Leu His Tyr Gly Thr Leu Val Ile Asp
35 40 45

Gly Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly
50 55 60

Ile Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr Leu Trp
65 70 75 80

Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly Ser

85 90 95

Leu Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg Leu Cys
100 105 110

Glu Arg Ile Leu Ala Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Glu
115 120 125

Pro Thr Thr Glu Asn Leu Tyr Phe Gln Ser Asp Asn Gly Ser Ser Gly
130 135 140

Gly Gly Ser Ser Gly Gly Met Val Phe Thr Leu Glu Asp Phe Val Gly
145 150 155 160

Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln
165 170 175

Gly Gly Val Ser Ser Leu Phe Gln Asn Leu Gly Val Ser Val Thr Pro
180 185 190

Ile Gln Arg Ile Val Leu Ser Gly Glu Asn Gly Leu Lys
195 200 205

<210> 164
<211> 615
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 164
atggacatcc atgtcatcat cccgtatgaa ggtctgagcg gcgatcagat gggccagatc 60

gaaaaaattt ttaaggtggt gtaccctgtg gatgatcatc actttaaggt gattctgcac 120

tatggcacac tggtaatcga cggggttacg ccgaacatga tcgactattt cggacggccg 180

tatgaaggca tcgccgtgtt cgacggcaaa aagatcactg taaccgggac cctgtggaac 240

ggcaacaaaa ttatcgacga gcgcctgatc aaccccgacg gctccctgct gttccgcgta 300

accatcaacg gagtgaccgg ctggcggctg tgcgagcgca ttttggcggg aagttctggt 360

ggaggaagtt ctggtggaga gcctactact gagaacttgt acttccagag cgataacgga 420

agttctggtg gaggaagttc tggtggaatg gtgtttacac tcgaagattt cgtaggggac 480

tggcggcaga cagccggcta caacctggac caagtccttg agcagggcgg tgtgtccagt 540

ttgtttcaga atctcggggt gtccgtaact ccgatccaaa ggattgtcct gagcggtgaa 600

aacggcctga agatc 615

<210> 165
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 165
Met Asp Ile His Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln
1 5 10 15

Met Gly Gln Ile Glu Lys Ile Phe Lys Val Val Tyr Pro Val Asp Asp
20 25 30

His His Phe Lys Val Ile Leu His Tyr Gly Thr Leu Val Ile Asp Gly
35 40 45

Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly Ile
50 55 60

Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr Leu Trp Asn
65 70 75 80

Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly Ser Leu
85 90 95

Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg Leu Cys Glu
100 105 110

Arg Ile Leu Ala Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Glu Pro
115 120 125

Thr Thr Glu Asn Leu Tyr Phe Gln Ser Asp Asn Gly Ser Ser Gly Gly
130 135 140

Gly Ser Ser Gly Gly Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp
145 150 155 160

Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly
165 170 175

Gly Val Ser Ser Leu Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile
180 185 190

Gln Arg Ile Val Leu Ser Gly Glu Asn Gly Leu Lys Ile
195 200 205

<210> 166
<211> 614
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 166

atgatccatg tcatcatccc gtatgaaggt ctgagcggcg atcagatggg ccagatcgaa 60

aaaattttta aggtggtgta ccctgtggat gatcatcact ttaaggtgat tctgcactat 120

ggcacactgg taatcgacgg ggttacgccg aacatgatcg actatttcgg acggccgtat 180

gaaggcatcg ccgtgttcga cggcaaaaag atcactgtaa ccgggaccct gtggaacggc 240

aacaaaatta tcgacgagcg cctgatcaac cccgacggct ccctgctgtt ccgcgtaacc 300

atcaacggag tgaccggctg gcggctgtgc gagcgcattt tggcgggaag ttctggtgga 360

ggaagttctg gtggagagcc tactactgag aacttgtact tccagagcga taacggaagt 420

tctggtggag gaagttctgg tggaatggtg tttacactcg aagatttcgt aggggactgg 480

cggcagacag ccggctacaa cctggaccaa gtccttgagc agggcggtgt gtccagtttg 540

tttcagaatc tcggggtgtc cgtaactccg atccaaagga ttgtcctgag cggtgaaaac 600

ggcctgaaga tcga 614

<210> 167
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 167
Met Ile His Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln Met
1 5 10 15

Gly Gln Ile Glu Lys Ile Phe Lys Val Val Tyr Pro Val Asp Asp His
20 25 30

His Phe Lys Val Ile Leu His Tyr Gly Thr Leu Val Ile Asp Gly Val
35 40 45

Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly Ile Ala
50 55 60

Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr Leu Trp Asn Gly
65 70 75 80

Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly Ser Leu Leu
85 90 95

Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg Leu Cys Glu Arg
100 105 110

Ile Leu Ala Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Glu Pro Thr
115 120 125

Thr Glu Asn Leu Tyr Phe Gln Ser Asp Asn Gly Ser Ser Gly Gly Gly
130 135 140

Ser Ser Gly Gly Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp
145 150 155 160

Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly
165 170 175

Val Ser Ser Leu Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln
180 185 190

Arg Ile Val Leu Ser Gly Glu Asn Gly Leu Lys Ile Asp
195 200 205

<210> 168
<211> 615
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 168
atggtcatca tcccgtatga aggtctgagc ggcgatcaga tgggccagat cgaaaaaatt 60

tttaaggtgg tgtaccctgt ggatgatcat cactttaagg tgattctgca ctatggcaca 120

ctggtaatcg acggggttac gccgaacatg atcgactatt tcggacggcc gtatgaaggc 180

atcgccgtgt tcgacggcaa aaagatcact gtaaccggga ccctgtggaa cggcaacaaa 240

attatcgacg agcgcctgat caaccccgac ggctccctgc tgttccgcgt aaccatcaac 300

ggagtgaccg gctggcggct gtgcgagcgc attttggcgg gaagttctgg tggaggaagt 360

tctggtggag agcctactac tgagaacttg tacttccaga gcgataacgg aagttctggt 420

ggaggaagtt ctggtggaat ggtgtttaca ctcgaagatt tcgtagggga ctggcggcag 480

acagccggct acaacctgga ccaagtcctt gagcagggcg gtgtgtccag tttgtttcag 540

aatctcgggg tgtccgtaac tccgatccaa aggattgtcc tgagcggtga aaacggcctg 600

aagatcgaca tccat 615

<210> 169
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 169
Met Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln Met Gly Gln
1 5 10 15

Ile Glu Lys Ile Phe Lys Val Val Tyr Pro Val Asp Asp His His Phe
20 25 30

Lys Val Ile Leu His Tyr Gly Thr Leu Val Ile Asp Gly Val Thr Pro
35 40 45

Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe
50 55 60

Asp Gly Lys Lys Ile Thr Val Thr Gly Thr Leu Trp Asn Gly Asn Lys
65 70 75 80

Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg
85 90 95

Val Thr Ile Asn Gly Val Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu
100 105 110

Ala Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Glu Pro Thr Thr Glu
115 120 125

Asn Leu Tyr Phe Gln Ser Asp Asn Gly Ser Ser Gly Gly Gly Ser Ser
130 135 140

Gly Gly Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln
145 150 155 160

Thr Ala Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Val Ser
165 170 175

Ser Leu Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln Arg Ile
180 185 190

Val Leu Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His
195 200 205

<210> 170
<211> 615
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 170
atgggtctga gcggcgatca gatgggccag atcgaaaaaa tttttaaggt ggtgtaccct 60

gtggatgatc atcactttaa ggtgattctg cactatggca cactggtaat cgacggggtt 120

acgccgaaca tgatcgacta tttcggacgg ccgtatgaag gcatcgccgt gttcgacggc 180

aaaaagatca ctgtaaccgg gaccctgtgg aacggcaaca aaattatcga cgagcgcctg 240

atcaaccccg acggctccct gctgttccgc gtaaccatca acggagtgac cggctggcgg 300

ctgtgcgagc gcattttggc gggaagttct ggtggaggaa gttctggtgg agagcctact 360

actgagaact tgtacttcca gagcgataac ggaagttctg gtggaggaag ttctggtgga 420

atggtgttta cactcgaaga tttcgtaggg gactggcggc agacagccgg ctacaacctg 480

gaccaagtcc ttgagcaggg cggtgtgtcc agtttgtttc agaatctcgg ggtgtccgta 540

actccgatcc aaaggattgt cctgagcggt gaaaacggcc tgaagatcga catccatgtc 600

atcatcccgt atgaa 615

<210> 171
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 171

Met Gly Leu Ser Gly Asp Gln Met Gly Gln Ile Glu Lys Ile Phe Lys
1 5 10 15

Val Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu His Tyr
20 25 30

Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe
35 40 45

Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr
50 55 60

Val Thr Gly Thr Leu Trp Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu
65 70 75 80

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

Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala Gly Ser Ser Gly Gly
100 105 110

Gly Ser Ser Gly Gly Glu Pro Thr Thr Glu Asn Leu Tyr Phe Gln Ser
115 120 125

Asp Asn Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Met Val Phe Thr
130 135 140

Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu
145 150 155 160

Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu Phe Gln Asn Leu
165 170 175

Gly Val Ser Val Thr Pro Ile Gln Arg Ile Val Leu Ser Gly Glu Asn
180 185 190

Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr Glu

195 200 205

<210> 172
<211> 615
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 172
atgggcgatc agatgggcca gatcgaaaaa atttttaagg tggtgtaccc tgtggatgat 60

catcacttta aggtgattct gcactatggc acactggtaa tcgacggggt tacgccgaac 120

atgatcgact atttcggacg gccgtatgaa ggcatcgccg tgttcgacgg caaaaagatc 180

actgtaaccg ggaccctgtg gaacggcaac aaaattatcg acgagcgcct gatcaacccc 240

gacggctccc tgctgttccg cgtaaccatc aacggagtga ccggctggcg gctgtgcgag 300

cgcattttgg cgggaagttc tggtggagga agttctggtg gagagcctac tactgagaac 360

ttgtacttcc agagcgataa cggaagttct ggtggaggaa gttctggtgg aatggtgttt 420

acactcgaag atttcgtagg ggactggcgg cagacagccg gctacaacct ggaccaagtc 480

cttgagcagg gcggtgtgtc cagtttgttt cagaatctcg gggtgtccgt aactccgatc 540

caaaggattg tcctgagcgg tgaaaacggc ctgaagatcg acatccatgt catcatcccg 600

tatgaaggtc tgagc 615

<210> 173
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 173
Met Gly Asp Gln Met Gly Gln Ile Glu Lys Ile Phe Lys Val Val Tyr
1 5 10 15

Pro Val Asp Asp His His Phe Lys Val Ile Leu His Tyr Gly Thr Leu
20 25 30

Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro
35 40 45

Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly
50 55 60

Thr Leu Trp Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro
65 70 75 80

Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp
85 90 95

Arg Leu Cys Glu Arg Ile Leu Ala Gly Ser Ser Gly Gly Gly Ser Ser
100 105 110

Gly Gly Glu Pro Thr Thr Glu Asn Leu Tyr Phe Gln Ser Asp Asn Gly
115 120 125

Ser Ser Gly Gly Gly Ser Ser Gly Gly Met Val Phe Thr Leu Glu Asp
130 135 140

Phe Val Gly Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val
145 150 155 160

Leu Glu Gln Gly Gly Val Ser Ser Leu Phe Gln Asn Leu Gly Val Ser
165 170 175

Val Thr Pro Ile Gln Arg Ile Val Leu Ser Gly Glu Asn Gly Leu Lys
180 185 190

Ile Asp Ile His Val Ile Ile Pro Tyr Glu Gly Leu Ser
195 200 205

<210> 174
<211> 615
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 174
atgatgggcc agatcgaaaa aatttttaag gtggtgtacc ctgtggatga tcatcacttt 60

aaggtgattc tgcactatgg cacactggta atcgacgggg ttacgccgaa catgatcgac 120

tatttcggac ggccgtatga aggcatcgcc gtgttcgacg gcaaaaagat cactgtaacc 180

gggaccctgt ggaacggcaa caaaattatc gacgagcgcc tgatcaaccc cgacggctcc 240

ctgctgttcc gcgtaaccat caacggagtg accggctggc ggctgtgcga gcgcattttg 300

gcgggaagtt ctggtggagg aagttctggt ggagagccta ctactgagaa cttgtacttc 360

cagagcgata acggaagttc tggtggagga agttctggtg gaatggtgtt tacactcgaa 420

gatttcgtag gggactggcg gcagacagcc ggctacaacc tggaccaagt ccttgagcag 480

ggcggtgtgt ccagtttgtt tcagaatctc ggggtgtccg taactccgat ccaaaggatt 540

gtcctgagcg gtgaaaacgg cctgaagatc gacatccatg tcatcatccc gtatgaaggt 600

ctgagcggcg atcag 615

<210> 175
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 175
Met Met Gly Gln Ile Glu Lys Ile Phe Lys Val Val Tyr Pro Val Asp
1 5 10 15

Asp His His Phe Lys Val Ile Leu His Tyr Gly Thr Leu Val Ile Asp
20 25 30

Gly Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly
35 40 45

Ile Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr Leu Trp
50 55 60

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

Leu Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg Leu Cys
85 90 95

Glu Arg Ile Leu Ala Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Glu
100 105 110

Pro Thr Thr Glu Asn Leu Tyr Phe Gln Ser Asp Asn Gly Ser Ser Gly
115 120 125

Gly Gly Ser Ser Gly Gly Met Val Phe Thr Leu Glu Asp Phe Val Gly
130 135 140

Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln
145 150 155 160

Gly Gly Val Ser Ser Leu Phe Gln Asn Leu Gly Val Ser Val Thr Pro
165 170 175

Ile Gln Arg Ile Val Leu Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile
180 185 190

His Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln
195 200 205

<210> 176
<211> 615
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 176
atgatcgaaa aaatttttaa ggtggtgtac cctgtggatg atcatcactt taaggtgatt 60

ctgcactatg gcacactggt aatcgacggg gttacgccga acatgatcga ctatttcgga 120

cggccgtatg aaggcatcgc cgtgttcgac ggcaaaaaga tcactgtaac cgggaccctg 180

tggaacggca acaaaattat cgacgagcgc ctgatcaacc ccgacggctc cctgctgttc 240

cgcgtaacca tcaacggagt gaccggctgg cggctgtgcg agcgcatttt ggcgggaagt 300

tctggtggag gaagttctgg tggagagcct actactgaga acttgtactt ccagagcgat 360

aacggaagtt ctggtggagg aagttctggt ggaatggtgt ttacactcga agatttcgta 420

ggggactggc ggcagacagc cggctacaac ctggaccaag tccttgagca gggcggtgtg 480

tccagtttgt ttcagaatct cggggtgtcc gtaactccga tccaaaggat tgtcctgagc 540

ggtgaaaacg gcctgaagat cgacatccat gtcatcatcc cgtatgaagg tctgagcggc 600

gatcagatgg gccag 615

<210> 177
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 177

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

Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Val
145 150 155 160

Ser Ser Leu Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln Arg
165 170 175

Ile Val Leu Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile
180 185 190

Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln Met Gly Gln
195 200 205

<210> 178
<211> 615
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 178
atgattttta aggtggtgta ccctgtggat gatcatcact ttaaggtgat tctgcactat 60

ggcacactgg taatcgacgg ggttacgccg aacatgatcg actatttcgg acggccgtat 120

gaaggcatcg ccgtgttcga cggcaaaaag atcactgtaa ccgggaccct gtggaacggc 180

aacaaaatta tcgacgagcg cctgatcaac cccgacggct ccctgctgtt ccgcgtaacc 240

atcaacggag tgaccggctg gcggctgtgc gagcgcattt tggcgggaag ttctggtgga 300

ggaagttctg gtggagagcc tactactgag aacttgtact tccagagcga taacggaagt 360

tctggtggag gaagttctgg tggaatggtg tttacactcg aagatttcgt aggggactgg 420

cggcagacag ccggctacaa cctggaccaa gtccttgagc agggcggtgt gtccagtttg 480

tttcagaatc tcggggtgtc cgtaactccg atccaaagga ttgtcctgag cggtgaaaac 540

ggcctgaaga tcgacatcca tgtcatcatc ccgtatgaag gtctgagcgg cgatcagatg 600

ggccagatcg aaaaa 615

<210> 179
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 179
Met Ile Phe Lys Val Val Tyr Pro Val Asp Asp His His Phe Lys Val
1 5 10 15

Ile Leu His Tyr Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met
20 25 30

Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly

35 40 45

Lys Lys Ile Thr Val Thr Gly Thr Leu Trp Asn Gly Asn Lys Ile Ile
50 55 60

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

Ile Asn Gly Val Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala Gly
85 90 95

Ser Ser Gly Gly Gly Ser Ser Gly Gly Glu Pro Thr Thr Glu Asn Leu
100 105 110

Tyr Phe Gln Ser Asp Asn Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly
115 120 125

Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala
130 135 140

Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu
145 150 155 160

Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln Arg Ile Val Leu
165 170 175

Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr
180 185 190

Glu Gly Leu Ser Gly Asp Gln Met Gly Gln Ile Glu Lys
195 200 205

<210> 180
<211> 615
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 180
atggtggtgt accctgtgga tgatcatcac tttaaggtga ttctgcacta tggcacactg 60

gtaatcgacg gggttacgcc gaacatgatc gactatttcg gacggccgta tgaaggcatc 120

gccgtgttcg acggcaaaaa gatcactgta accgggaccc tgtggaacgg caacaaaatt 180

atcgacgagc gcctgatcaa ccccgacggc tccctgctgt tccgcgtaac catcaacgga 240

gtgaccggct ggcggctgtg cgagcgcatt ttggcgggaa gttctggtgg aggaagttct 300

ggtggagagc ctactactga gaacttgtac ttccagagcg ataacggaag ttctggtgga 360

ggaagttctg gtggaatggt gtttacactc gaagatttcg taggggactg gcggcagaca 420

gccggctaca acctggacca agtccttgag cagggcggtg tgtccagttt gtttcagaat 480

ctcggggtgt ccgtaactcc gatccaaagg attgtcctga gcggtgaaaa cggcctgaag 540

atcgacatcc atgtcatcat cccgtatgaa ggtctgagcg gcgatcagat gggccagatc 600

gaaaaaattt ttaag 615

<210> 181
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 181
Met Val Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu His
1 5 10 15

Tyr Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr
20 25 30

Phe Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile
35 40 45

Thr Val Thr Gly Thr Leu Trp Asn Gly Asn Lys Ile Ile Asp Glu Arg
50 55 60

Leu Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly
65 70 75 80

Val Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala Gly Ser Ser Gly
85 90 95

Gly Gly Ser Ser Gly Gly Glu Pro Thr Thr Glu Asn Leu Tyr Phe Gln
100 105 110

Ser Asp Asn Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Met Val Phe
115 120 125

Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala Gly Tyr Asn
130 135 140

Leu Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu Phe Gln Asn
145 150 155 160

Leu Gly Val Ser Val Thr Pro Ile Gln Arg Ile Val Leu Ser Gly Glu
165 170 175

Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr Glu Gly Leu
180 185 190

Ser Gly Asp Gln Met Gly Gln Ile Glu Lys Ile Phe Lys
195 200 205

<210> 182
<211> 615
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 182
atggtgtacc ctgtggatga tcatcacttt aaggtgattc tgcactatgg cacactggta 60

atcgacgggg ttacgccgaa catgatcgac tatttcggac ggccgtatga aggcatcgcc 120

gtgttcgacg gcaaaaagat cactgtaacc gggaccctgt ggaacggcaa caaaattatc 180

gacgagcgcc tgatcaaccc cgacggctcc ctgctgttcc gcgtaaccat caacggagtg 240

accggctggc ggctgtgcga gcgcattttg gcgggaagtt ctggtggagg aagttctggt 300

ggagagccta ctactgagaa cttgtacttc cagagcgata acggaagttc tggtggagga 360

agttctggtg gaatggtgtt tacactcgaa gatttcgtag gggactggcg gcagacagcc 420

ggctacaacc tggaccaagt ccttgagcag ggcggtgtgt ccagtttgtt tcagaatctc 480

ggggtgtccg taactccgat ccaaaggatt gtcctgagcg gtgaaaacgg cctgaagatc 540

gacatccatg tcatcatccc gtatgaaggt ctgagcggcg atcagatggg ccagatcgaa 600

aaaatttta aggtg 615

<210> 183
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 183
Met Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu His Tyr
1 5 10 15

Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe
20 25 30

Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr
35 40 45

Val Thr Gly Thr Leu Trp Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu
50 55 60

Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val
65 70 75 80

Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala Gly Ser Ser Gly Gly
85 90 95

Gly Ser Ser Gly Gly Glu Pro Thr Thr Glu Asn Leu Tyr Phe Gln Ser
100 105 110

Asp Asn Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Met Val Phe Thr
115 120 125

Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu
130 135 140

Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu Phe Gln Asn Leu
145 150 155 160

Gly Val Ser Val Thr Pro Ile Gln Arg Ile Val Leu Ser Gly Glu Asn
165 170 175

Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr Glu Gly Leu Ser
180 185 190

Gly Asp Gln Met Gly Gln Ile Glu Lys Ile Phe Lys Val
195 200 205

<210> 184
<211> 615
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 184
atgtaccctg tggatgatca tcactttaag gtgattctgc actatggcac actggtaatc 60

gacggggtta cgccgaacat gatcgactat ttcggacggc cgtatgaagg catcgccgtg 120

ttcgacggca aaaagatcac tgtaaccggg accctgtgga acggcaacaa aattatcgac 180

gagcgcctga tcaaccccga cggctccctg ctgttccgcg taaccatcaa cggagtgacc 240

ggctggcggc tgtgcgagcg cattttggcg ggaagttctg gtggaggaag ttctggtgga 300

gagcctacta ctgagaactt gtacttccag agcgataacg gaagttctgg tggaggaagt 360

tctggtggaa tggtgtttac actcgaagat ttcgtagggg actggcggca gacagccggc 420

tacaacctgg accaagtcct tgagcagggc ggtgtgtcca gtttgtttca gaatctcggg 480

gtgtccgtaa ctccgatcca aaggattgtc ctgagcggtg aaaacggcct gaagatcgac 540

atccatgtca tcatcccgta tgaaggtctg agcggcgatc agatgggcca gatcgaaaaa 600

atttttaagg tggtg 615

<210> 185
<211> 205
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 185
Met Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu His Tyr Gly
1 5 10 15

Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe Gly
20 25 30

Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr Val
35 40 45

Thr Gly Thr Leu Trp Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile
50 55 60

Asn Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val Thr
65 70 75 80

Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala Gly Ser Ser Gly Gly Gly
85 90 95

Ser Ser Gly Gly Glu Pro Thr Thr Glu Asn Leu Tyr Phe Gln Ser Asp
100 105 110

Asn Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Met Val Phe Thr Leu
115 120 125

Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp
130 135 140

Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu Phe Gln Asn Leu Gly
145 150 155 160

Val Ser Val Thr Pro Ile Gln Arg Ile Val Leu Ser Gly Glu Asn Gly
165 170 175

Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly
180 185 190

Asp Gln Met Gly Gln Ile Glu Lys Ile Phe Lys Val Val
195 200 205

<210> 186
<211> 615
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 186
atgcctgtgg atgatcatca ctttaaggtg attctgcact atggcacact ggtaatcgac 60

ggggttacgc cgaacatgat cgactatttc ggacggccgt atgaaggcat cgccgtgttc 120

gacggcaaaa agatcactgt aaccgggacc ctgtggaacg gcaacaaaat tatcgacgag 180

cgcctgatca accccgacgg ctccctgctg ttccgcgtaa ccatcaacgg agtgaccggc 240

tggcggctgt gcgagcgcat tttggcggga agttctggtg gaggaagttc tggtggagag 300

cctactactg agaacttgta cttccagagc gataacggaa gttctggtgg aggaagttct 360

ggtggaatgg tgtttacact cgaagatttc gtaggggact ggcggcagac agccggctac 420

aacctggacc aagtccttga gcagggcggt gtgtccagtt tgtttcagaa tctcggggtg 480

tccgtaactc cgatccaaag gattgtcctg agcggtgaaa acggcctgaa gatcgacatc 540

catgtcatca tcccgtatga aggtctgagc ggcgatcaga tgggccagat cgaaaaaatt 600

tttaaggtgg tgtac 615

<210> 187
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 187

Met Pro Val Asp Asp His His Phe Lys Val Ile Leu His Tyr Gly Thr
1 5 10 15

Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg
20 25 30

Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr
35 40 45

Gly Thr Leu Trp Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn
50 55 60

Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly
65 70 75 80

Trp Arg Leu Cys Glu Arg Ile Leu Ala Gly Ser Ser Gly Gly Gly Ser
85 90 95

Ser Gly Gly Glu Pro Thr Thr Glu Asn Leu Tyr Phe Gln Ser Asp Asn
100 105 110

Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Met Val Phe Thr Leu Glu
115 120 125

Asp Phe Val Gly Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln
130 135 140

Val Leu Glu Gln Gly Gly Val Ser Ser Leu Phe Gln Asn Leu Gly Val

145 150 155 160

Ser Val Thr Pro Ile Gln Arg Ile Val Leu Ser Gly Glu Asn Gly Leu
165 170 175

Lys Ile Asp Ile His Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp
180 185 190

Gln Met Gly Gln Ile Glu Lys Ile Phe Lys Val Val Tyr
195 200 205

<210> 188
<211> 615
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 188
atggtggatg atcatcactt taaggtgatt ctgcactatg gcacactggt aatcgacggg 60

gttacgccga acatgatcga ctatttcgga cggccgtatg aaggcatcgc cgtgttcgac 120

ggcaaaaaga tcactgtaac cgggaccctg tggaacggca acaaaattat cgacgagcgc 180

ctgatcaacc ccgacggctc cctgctgttc cgcgtaacca tcaacggagt gaccggctgg 240

cggctgtgcg agcgcatttt ggcgggaagt tctggtggag gaagttctgg tggagagcct 300

actactgaga acttgtactt ccagagcgat aacggaagtt ctggtggagg aagttctggt 360

ggaatggtgt ttacactcga agatttcgta ggggactggc ggcagacagc cggctacaac 420

ctggaccaag tccttgagca gggcggtgtg tccagtttgt ttcagaatct cggggtgtcc 480

gtaactccga tccaaaggat tgtcctgagc ggtgaaaacg gcctgaagat cgacatccat 540

gtcatcatcc cgtatgaagg tctgagcggc gatcagatgg gccagatcga aaaaattttt 600

aaggtggtgt accct 615

<210> 189
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 189
Met Val Asp Asp His His Phe Lys Val Ile Leu His Tyr Gly Thr Leu
1 5 10 15

Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro
20 25 30

Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly
35 40 45

Thr Leu Trp Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro
50 55 60

Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp
65 70 75 80

Arg Leu Cys Glu Arg Ile Leu Ala Gly Ser Ser Gly Gly Gly Ser Ser
85 90 95

Gly Gly Glu Pro Thr Thr Glu Asn Leu Tyr Phe Gln Ser Asp Asn Gly
100 105 110

Ser Ser Gly Gly Gly Ser Ser Gly Gly Met Val Phe Thr Leu Glu Asp
115 120 125

Phe Val Gly Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val
130 135 140

Leu Glu Gln Gly Gly Val Ser Ser Leu Phe Gln Asn Leu Gly Val Ser
145 150 155 160

Val Thr Pro Ile Gln Arg Ile Val Leu Ser Gly Glu Asn Gly Leu Lys
165 170 175

Ile Asp Ile His Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln
180 185 190

Met Gly Gln Ile Glu Lys Ile Phe Lys Val Val Tyr Pro
195 200 205

<210> 190
<211> 615
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 190
atggatgatc atcactttaa ggtgattctg cactatggca cactggtaat cgacggggtt 60

acgccgaaca tgatcgacta tttcggacgg ccgtatgaag gcatcgccgt gttcgacggc 120

aaaaagatca ctgtaaccgg gaccctgtgg aacggcaaca aaattatcga cgagcgcctg 180

atcaaccccg acggctccct gctgttccgc gtaaccatca acggagtgac cggctggcgg 240

ctgtgcgagc gcattttggc gggaagttct ggtggaggaa gttctggtgg agagcctact 300

actgagaact tgtacttcca gagcgataac ggaagttctg gtggaggaag ttctggtgga 360

atggtgttta cactcgaaga tttcgtaggg gactggcggc agacagccgg ctacaacctg 420

gaccaagtcc ttgagcaggg cggtgtgtcc agtttgtttc agaatctcgg ggtgtccgta 480

actccgatcc aaaggattgt cctgagcggt gaaaacggcc tgaagatcga catccatgtc 540

atcatcccgt atgaaggtct gagcggcgat cagatgggcc agatcgaaaa aatttttaag 600

gtggtgtacc ctgtg 615

<210> 191
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 191

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Met Asp Asp His His Phe Lys Val Ile Leu His Tyr Gly Thr Leu Val
1               5                   10                  15

Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr
            20                  25                  30

Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr
        35                  40                  45

Leu Trp Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp
    50                  55                  60

Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg
65                  70                  75                  80

Leu Cys Glu Arg Ile Leu Ala Gly Ser Ser Gly Gly Gly Ser Ser Gly
                85                  90                  95

Gly Glu Pro Thr Thr Glu Asn Leu Tyr Phe Gln Ser Asp Asn Gly Ser
            100                 105                 110

Ser Gly Gly Gly Ser Ser Gly Gly Met Val Phe Thr Leu Glu Asp Phe
        115                 120                 125

Val Gly Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val Leu
    130                 135                 140

Glu Gln Gly Gly Val Ser Ser Leu Phe Gln Asn Leu Gly Val Ser Val
145                 150                 155                 160

Thr Pro Ile Gln Arg Ile Val Leu Ser Gly Glu Asn Gly Leu Lys Ile
                165                 170                 175

Asp Ile His Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln Met
            180                 185                 190

Gly Gln Ile Glu Lys Ile Phe Lys Val Val Tyr Pro Val
        195                 200                 205
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<210> 192
<211> 615
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 192
atggatcatc actttaaggt gattctgcac tatggcacac tggtaatcga cggggttacg 60

ccgaacatga tcgactattt cggacggccg tatgaaggca tcgccgtgtt cgacggcaaa 120

aagatcactg taaccgggac cctgtggaac ggcaacaaaa ttatcgacga gcgcctgatc 180

aaccccgacg gctccctgct gttccgcgta accatcaacg gagtgaccgg ctggcggctg 240

tgcgagcgca ttttggcggg aagttctggt ggaggaagtt ctggtggaga gcctactact 300

gagaacttgt acttccagag cgataacgga agttctggtg gaggaagttc tggtggaatg 360

gtgtttacac tcgaagattt cgtaggggac tggcggcaga cagccggcta caacctggac 420

caagtccttg agcagggcgg tgtgtccagt ttgtttcaga atctcggggt gtccgtaact 480

ccgatccaaa ggattgtcct gagcggtgaa aacggcctga agatcgacat ccatgtcatc 540

atcccgtatg aaggtctgag cggcgatcag atgggccaga tcgaaaaaat ttttaaggtg 600

gtgtaccctg tggat 615

<210> 193
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 193
Met Asp His His Phe Lys Val Ile Leu His Tyr Gly Thr Leu Val Ile
1 5 10 15

Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu
20 25 30

Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr Leu
35 40 45

Trp Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly
50 55 60

Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg Leu
65 70 75 80

Cys Glu Arg Ile Leu Ala Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly
85 90 95

Glu Pro Thr Thr Glu Asn Leu Tyr Phe Gln Ser Asp Asn Gly Ser Ser
100 105 110

Gly Gly Gly Ser Ser Gly Gly Met Val Phe Thr Leu Glu Asp Phe Val
115 120 125

Gly Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val Leu Glu
130 135 140

Gln Gly Gly Val Ser Ser Leu Phe Gln Asn Leu Gly Val Ser Val Thr
145 150 155 160

Pro Ile Gln Arg Ile Val Leu Ser Gly Glu Asn Gly Leu Lys Ile Asp
165 170 175

Ile His Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln Met Gly
180 185 190

Gln Ile Glu Lys Ile Phe Lys Val Val Tyr Pro Val Asp
195 200 205

<210> 194
<211> 615
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 194
atgcatcact ttaaggtgat tctgcactat ggcacactgg taatcgacgg ggttacgccg 60

aacatgatcg actatttcgg acggccgtat gaaggcatcg ccgtgttcga cggcaaaaag 120

atcactgtaa ccgggaccct gtggaacggc aacaaaatta tcgacgagcg cctgatcaac 180

cccgacggct ccctgctgtt ccgcgtaacc atcaacggag tgaccggctg gcggctgtgc 240

gagcgcattt tggcgggaag ttctggtgga ggaagttctg gtggagagcc tactactgag 300

aacttgtact tccagagcga taacggaagt tctggtggag gaagttctgg tggaatggtg 360

tttacactcg aagatttcgt aggggactgg cggcagacag ccggctacaa cctggaccaa 420

gtccttgagc agggcggtgt gtccagtttg tttcagaatc tcggggtgtc cgtaactccg 480

atccaaagga ttgtcctgag cggtgaaaac ggcctgaaga tcgacatcca tgtcatcatc 540

ccgtatgaag gtctgagcgg cgatcagatg ggccagatcg aaaaaatttt taaggtggtg 600

taccctgtgg atgat 615

<210> 195
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

polypeptide

<400> 195
Met His His Phe Lys Val Ile Leu His Tyr Gly Thr Leu Val Ile Asp
1 5 10 15

Gly Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly
20 25 30

Ile Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr Leu Trp
35 40 45

Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly Ser
50 55 60

Leu Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg Leu Cys
65 70 75 80

Glu Arg Ile Leu Ala Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Glu
85 90 95

Pro Thr Thr Glu Asn Leu Tyr Phe Gln Ser Asp Asn Gly Ser Ser Gly
100 105 110

Gly Gly Ser Ser Gly Gly Met Val Phe Thr Leu Glu Asp Phe Val Gly
115 120 125

Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln
130 135 140

Gly Gly Val Ser Ser Leu Phe Gln Asn Leu Gly Val Ser Val Thr Pro
145 150 155 160

Ile Gln Arg Ile Val Leu Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile
165 170 175

His Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln Met Gly Gln
180 185 190

Ile Glu Lys Ile Phe Lys Val Val Tyr Pro Val Asp Asp
195 200 205

<210> 196
<211> 615
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 196
atgcacttta aggtgattct gcactatggc acactggtaa tcgacggggt tacgccgaac 60

atgatcgact atttcggacg gccgtatgaa ggcatcgccg tgttcgacgg caaaaagatc 120

actgtaaccg ggaccctgtg gaacggcaac aaaattatcg acgagcgcct gatcaacccc 180

gacggctccc tgctgttccg cgtaaccatc aacggagtga ccggctggcg gctgtgcgag 240

cgcattttgg cgggaagttc tggtggagga agttctggtg gagagcctac tactgagaac 300

ttgtacttcc agagcgataa cggaagttct ggtggaggaa gttctggtgg aatggtgttt 360

acactcgaag atttcgtagg ggactggcgg cagacagccg gctacaacct ggaccaagtc 420

cttgagcagg gcggtgtgtc cagtttgttt cagaatctcg gggtgtccgt aactccgatc 480

caaaggattg tcctgagcgg tgaaaacggc ctgaagatcg acatccatgt catcatcccg 540

tatgaaggtc tgagcggcga tcagatgggc cagatcgaaa aaatttttaa ggtggtgtac 600

cctgtggatg atcat 615

<210> 197
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 197
Met His Phe Lys Val Ile Leu His Tyr Gly Thr Leu Val Ile Asp Gly
1 5 10 15

Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly Ile
20 25 30

Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr Leu Trp Asn
35 40 45

Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly Ser Leu
50 55 60

Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg Leu Cys Glu
65 70 75 80

Arg Ile Leu Ala Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Glu Pro
85 90 95

Thr Thr Glu Asn Leu Tyr Phe Gln Ser Asp Asn Gly Ser Ser Gly Gly
100 105 110

Gly Ser Ser Gly Gly Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp
115 120 125

Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly
130 135 140

Gly Val Ser Ser Leu Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile
145 150 155 160

Gln Arg Ile Val Leu Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His
165 170 175

Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln Met Gly Gln Ile
180 185 190

Glu Lys Ile Phe Lys Val Val Tyr Pro Val Asp Asp His
195 200 205

<210> 198
<211> 615
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 198
atgtttaagg tgattctgca ctatggcaca ctggtaatcg acggggttac gccgaacatg 60

atcgactatt tcggacggcc gtatgaaggc atcgccgtgt tcgacggcaa aaagatcact 120

gtaaccggga ccctgtggaa cggcaacaaa attatcgacg agcgcctgat caaccccgac 180

ggctccctgc tgttccgcgt aaccatcaac ggagtgaccg gctggcggct gtgcgagcgc 240

attttggcgg gaagttctgg tggaggaagt tctggtggag agcctactac tgagaacttg 300

tacttccaga gcgataacgg aagttctggt ggaggaagtt ctggtggaat ggtgtttaca 360

ctcgaagatt tcgtagggga ctggcggcag acagccggct acaacctgga ccaagtcctt 420

gagcagggcg gtgtgtccag tttgtttcag aatctcgggg tgtccgtaac tccgatccaa 480

aggattgtcc tgagcggtga aaacggcctg aagatcgaca tccatgtcat catcccgtat 540

gaaggtctga gcggcgatca gatgggccag atcgaaaaaa tttttaaggt ggtgtaccct 600

gtggatgatc atcac 615

<210> 199
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 199
Met Phe Lys Val Ile Leu His Tyr Gly Thr Leu Val Ile Asp Gly Val
1 5 10 15

Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly Ile Ala
20 25 30

Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr Leu Trp Asn Gly
35 40 45

```
Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly Ser Leu Leu
    50                  55                  60

Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg Leu Cys Glu Arg
65                  70                  75                  80

Ile Leu Ala Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Glu Pro Thr
                85                  90                  95

Thr Glu Asn Leu Tyr Phe Gln Ser Asp Asn Gly Ser Ser Gly Gly Gly
            100                 105                 110

Ser Ser Gly Gly Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp
        115                 120                 125

Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly
    130                 135                 140

Val Ser Ser Leu Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln
145                 150                 155                 160

Arg Ile Val Leu Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val
                165                 170                 175

Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln Met Gly Gln Ile Glu
            180                 185                 190

Lys Ile Phe Lys Val Val Tyr Pro Val Asp Asp His His
        195                 200                 205
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<210> 200
<211> 615
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 200

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atgattctgc actatggcac actggtaatc gacggggtta cgccgaacat gatcgactat       60

ttcggacggc cgtatgaagg catcgccgtg ttcgacggca aaaagatcac tgtaaccggg      120

accctgtgga acggcaacaa aattatcgac gagcgcctga tcaaccccga cggctccctg      180

ctgttccgcg taaccatcaa cggagtgacc ggctggcggc tgtgcgagcg cattttggcg      240

ggaagttctg gtggaggaag ttctggtgga gagcctacta ctgagaactt gtacttccag      300

agcgataacg gaagttctgg tggaggaagt tctggtggaa tggtgtttac actcgaagat      360

ttcgtagggg actggcggca gacagccggc tacaacctgg accaagtcct tgagcagggc      420

ggtgtgtcca gtttgtttca gaatctcggg gtgtccgtaa ctccgatcca aaggattgtc      480

ctgagcggtg aaaacggcct gaagatcgac atccatgtca tcatcccgta tgaaggtctg      540
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agcggcgatc agatgggcca gatcgaaaaa atttttaagg tggtgtaccc tgtggatgat 600

catcacttta aggtg 615

<210> 201
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 201
Met Ile Leu His Tyr Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn
1 5 10 15

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

Gly Lys Lys Ile Thr Val Thr Gly Thr Leu Trp Asn Gly Asn Lys Ile
35 40 45

Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val
50 55 60

Thr Ile Asn Gly Val Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala
65 70 75 80

Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Glu Pro Thr Thr Glu Asn
85 90 95

Leu Tyr Phe Gln Ser Asp Asn Gly Ser Ser Gly Gly Gly Ser Ser Gly
100 105 110

Gly Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr
115 120 125

Ala Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser
130 135 140

Leu Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln Arg Ile Val
145 150 155 160

Leu Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro
165 170 175

Tyr Glu Gly Leu Ser Gly Asp Gln Met Gly Gln Ile Glu Lys Ile Phe
180 185 190

Lys Val Val Tyr Pro Val Asp Asp His His Phe Lys Val
195 200 205

<210> 202
<211> 616
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 202
atgtatggca cactggtaat cgacggggtt acgccgaaca tgatcgacta tttcggacgg 60

ccgtatgaag gcatcgccgt gttcgacggc aaaaagatca ctgtaaccgg gaccctgtgg 120

aacggcaaca aaattatcga cgagcgcctg atcaaccccg acggctccct gctgttccgc 180

gtaaccatca acggagtgac cggctggcgg ctgtgcgagc gcattttggc gggaagttct 240

ggtggaggaa gttctggtgg agagcctact actgagaact tgtacttcca gagcgataac 300

ggaagttctg gtggaggaag ttctggtgga atggtgttta cactcgaaga tttcgtaggg 360

gactggcggc agacagccgg ctacaacctg gaccaagtcc ttgagcaggg cggtgtgtcc 420

agtttgtttc agaatctcgg ggtgtccgta actccgatcc aaaggattgt cctgagcggt 480

gaaaacggcc tgaagatcga catccatgtc atcatcccgt atgaaggtct gagcggcgat 540

cagatgggcc agatcgaaaa aatttttaag gtggtgtacc ctgtggatga tcatcacttt 600

aaggtgattc tgcacg 616

<210> 203
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 203
Met Tyr Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp
1 5 10 15

Tyr Phe Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys
20 25 30

Ile Thr Val Thr Gly Thr Leu Trp Asn Gly Asn Lys Ile Ile Asp Glu
35 40 45

Arg Leu Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn
50 55 60

Gly Val Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala Gly Ser Ser
65 70 75 80

Gly Gly Gly Ser Ser Gly Gly Glu Pro Thr Thr Glu Asn Leu Tyr Phe
85 90 95

Gln Ser Asp Asn Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Met Val

100 105 110

Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala Gly Tyr
115 120 125

Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu Phe Gln
130 135 140

Asn Leu Gly Val Ser Val Thr Pro Ile Gln Arg Ile Val Leu Ser Gly
145 150 155 160

Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr Glu Gly
165 170 175

Leu Ser Gly Asp Gln Met Gly Gln Ile Glu Lys Ile Phe Lys Val Val
180 185 190

Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu His
195 200 205

<210> 204
<211> 615
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 204
atgggcacac tggtaatcga cggggttacg ccgaacatga tcgactattt cggacggccg 60

tatgaaggca tcgccgtgtt cgacggcaaa aagatcactg taaccgggac cctgtggaac 120

ggcaacaaaa ttatcgacga gcgcctgatc aaccccgacg gctccctgct gttccgcgta 180

accatcaacg gagtgaccgg ctggcggctg tgcgagcgca ttttggcggg aagttctggt 240

ggaggaagtt ctggtggaga gcctactact gagaacttgt acttccagag cgataacgga 300

agttctggtg gaggaagttc tggtggaatg gtgtttacac tcgaagattt cgtaggggac 360

tggcggcaga cagccggcta caacctggac caagtccttg agcagggcgg tgtgtccagt 420

ttgtttcaga atctcggggt gtccgtaact ccgatccaaa ggattgtcct gagcggtgaa 480

aacggcctga agatcgacat ccatgtcatc atcccgtatg aaggtctgag cggcgatcag 540

atgggccaga tcgaaaaaat ttttaaggtg gtgtaccctg tggatgatca tcactttaag 600

gtgattctgc actat 615

<210> 205
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 205
Met Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr
1 5 10 15

Phe Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile
20 25 30

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

Leu Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly
50 55 60

Val Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala Gly Ser Ser Gly
65 70 75 80

Gly Gly Ser Ser Gly Gly Glu Pro Thr Thr Glu Asn Leu Tyr Phe Gln
85 90 95

Ser Asp Asn Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Met Val Phe
100 105 110

Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala Gly Tyr Asn
115 120 125

Leu Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu Phe Gln Asn
130 135 140

Leu Gly Val Ser Val Thr Pro Ile Gln Arg Ile Val Leu Ser Gly Glu
145 150 155 160

Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr Glu Gly Leu
165 170 175

Ser Gly Asp Gln Met Gly Gln Ile Glu Lys Ile Phe Lys Val Val Tyr
180 185 190

Pro Val Asp Asp His His Phe Lys Val Ile Leu His Tyr
195 200 205

<210> 206
<211> 615
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 206
atgctggtaa tcgacggggt tacgccgaac atgatcgact atttcggacg gccgtatgaa 60

ggcatcgccg tgttcgacgg caaaaagatc actgtaaccg ggaccctgtg gaacggcaac 120

aaaattatcg acgagcgcct gatcaacccc gacggctccc tgctgttccg cgtaaccatc 180

aacggagtga ccggctggcg gctgtgcgag cgcattttgg cgggaagttc tggtggagga 240

agttctggtg gagagcctac tactgagaac ttgtacttcc agagcgataa cggaagttct 300

ggtggaggaa gttctggtgg aatggtgttt acactcgaag atttcgtagg ggactggcgg 360

cagacagccg gctacaacct ggaccaagtc cttgagcagg gcggtgtgtc cagtttgttt 420

cagaatctcg gggtgtccgt aactccgatc caaaggattg tcctgagcgg tgaaaacggc 480

ctgaagatcg acatccatgt catcatcccg tatgaaggtc tgagcggcga tcagatgggc 540

cagatcgaaa aaatttttaa ggtggtgtac cctgtggatg atcatcactt taaggtgatt 600

ctgcactatg gcaca 615

<210> 207
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 207

| | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Met | Leu | Val | Ile | Asp | Gly | Val | Thr | Pro | Asn | Met | Ile | Asp | Tyr | Phe | Gly |
| 1 | | | | 5 | | | | 10 | | | | | 15 | | |
| Arg | Pro | Tyr | Glu | Gly | Ile | Ala | Val | Phe | Asp | Gly | Lys | Lys | Ile | Thr | Val |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Thr | Gly | Thr | Leu | Trp | Asn | Gly | Asn | Lys | Ile | Ile | Asp | Glu | Arg | Leu | Ile |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Asn | Pro | Asp | Gly | Ser | Leu | Leu | Phe | Arg | Val | Thr | Ile | Asn | Gly | Val | Thr |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Gly | Trp | Arg | Leu | Cys | Glu | Arg | Ile | Leu | Ala | Gly | Ser | Ser | Gly | Gly | Gly |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Ser | Ser | Gly | Gly | Glu | Pro | Thr | Thr | Glu | Asn | Leu | Tyr | Phe | Gln | Ser | Asp |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Asn | Gly | Ser | Ser | Gly | Gly | Gly | Ser | Ser | Gly | Gly | Met | Val | Phe | Thr | Leu |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Glu | Asp | Phe | Val | Gly | Asp | Trp | Arg | Gln | Thr | Ala | Gly | Tyr | Asn | Leu | Asp |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Gln | Val | Leu | Glu | Gln | Gly | Gly | Val | Ser | Ser | Leu | Phe | Gln | Asn | Leu | Gly |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Val | Ser | Val | Thr | Pro | Ile | Gln | Arg | Ile | Val | Leu | Ser | Gly | Glu | Asn | Gly |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |

Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly
165 170 175

Asp Gln Met Gly Gln Ile Glu Lys Ile Phe Lys Val Val Tyr Pro Val
180 185 190

Asp Asp His His Phe Lys Val Ile Leu His Tyr Gly Thr
195 200 205

<210> 208
<211> 615
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 208
atggacgggg ttacgccgaa catgatcgac tatttcggac ggccgtatga aggcatcgcc 60

gtgttcgacg gcaaaaagat cactgtaacc gggaccctgt ggaacggcaa caaaattatc 120

gacgagcgcc tgatcaaccc cgacggctcc ctgctgttcc gcgtaaccat caacggagtg 180

accggctggc ggctgtgcga gcgcattttg gcgggaagtt ctggtggagg aagttctggt 240

ggagagccta ctactgagaa cttgtacttc cagagcgata acggaagttc tggtggagga 300

agttctggtg gaatggtgtt tacactcgaa gatttcgtag gggactggcg gcagacagcc 360

ggctacaacc tggaccaagt ccttgagcag ggcggtgtgt ccagtttgtt tcagaatctc 420

ggggtgtccg taactccgat ccaaaggatt gtcctgagcg gtgaaaacgg cctgaagatc 480

gacatccatg tcatcatccc gtatgaaggt ctgagcggcg atcagatggg ccagatcgaa 540

aaaatttta aggtggtgta ccctgtggat gatcatcact ttaaggtgat tctgcactat 600

ggcacactgg taatc 615

<210> 209
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 209
Met Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr
1 5 10 15

Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr
20 25 30

Leu Trp Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp
35 40 45

Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg
50 55 60

Leu Cys Glu Arg Ile Leu Ala Gly Ser Ser Gly Gly Gly Ser Ser Gly
65 70 75 80

Gly Glu Pro Thr Thr Glu Asn Leu Tyr Phe Gln Ser Asp Asn Gly Ser
85 90 95

Ser Gly Gly Gly Ser Ser Gly Gly Met Val Phe Thr Leu Glu Asp Phe
100 105 110

Val Gly Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val Leu
115 120 125

Glu Gln Gly Gly Val Ser Ser Leu Phe Gln Asn Leu Gly Val Ser Val
130 135 140

Thr Pro Ile Gln Arg Ile Val Leu Ser Gly Glu Asn Gly Leu Lys Ile
145 150 155 160

Asp Ile His Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln Met
165 170 175

Gly Gln Ile Glu Lys Ile Phe Lys Val Val Tyr Pro Val Asp Asp His
180 185 190

His Phe Lys Val Ile Leu His Tyr Gly Thr Leu Val Ile
195 200 205

<210> 210
<211> 615
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 210
atgggggtta cgccgaacat gatcgactat ttcggacggc cgtatgaagg catcgccgtg 60

ttcgacggca aaaagatcac tgtaaccggg accctgtgga acggcaacaa aattatcgac 120

gagcgcctga tcaaccccga cggctccctg ctgttccgcg taaccatcaa cggagtgacc 180

ggctggcggc tgtgcgagcg cattttggcg ggaagttctg gtggaggaag ttctggtgga 240

gagcctacta ctgagaactt gtacttccag agcgataacg gaagttctgg tggaggaagt 300

tctggtggaa tggtgtttac actcgaagat ttcgtagggg actggcggca gacagccggc 360

tacaacctgg accaagtcct tgagcagggc ggtgtgtcca gtttgtttca gaatctcggg 420

gtgtccgtaa ctccgatcca aaggattgtc ctgagcggtg aaaacggcct gaagatcgac 480

atccatgtca tcatcccgta tgaaggtctg agcggcgatc agatgggcca gatcgaaaaa 540

attttaagg tggtgtaccc tgtggatgat catcacttta aggtgattct gcactatggc 600

acactggtaa tcgac 615

<210> 211
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 211

Met Gly Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu
1 5 10 15

Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr Leu
20 25 30

Trp Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly
35 40 45

Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg Leu
50 55 60

Cys Glu Arg Ile Leu Ala Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly
65 70 75 80

Glu Pro Thr Thr Glu Asn Leu Tyr Phe Gln Ser Asp Asn Gly Ser Ser
85 90 95

Gly Gly Gly Ser Ser Gly Gly Met Val Phe Thr Leu Glu Asp Phe Val
100 105 110

Gly Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val Leu Glu
115 120 125

Gln Gly Gly Val Ser Ser Leu Phe Gln Asn Leu Gly Val Ser Val Thr
130 135 140

Pro Ile Gln Arg Ile Val Leu Ser Gly Glu Asn Gly Leu Lys Ile Asp
145 150 155 160

Ile His Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln Met Gly
165 170 175

Gln Ile Glu Lys Ile Phe Lys Val Val Tyr Pro Val Asp Asp His His
180 185 190

Phe Lys Val Ile Leu His Tyr Gly Thr Leu Val Ile Asp
195 200 205

<210> 212

<211> 615
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 212
atggttacgc cgaacatgat cgactatttc ggacggccgt atgaaggcat cgccgtgttc 60

gacggcaaaa agatcactgt aaccgggacc ctgtggaacg gcaacaaaat tatcgacgag 120

cgcctgatca accccgacgg ctccctgctg ttccgcgtaa ccatcaacgg agtgaccggc 180

tggcggctgt gcgagcgcat tttggcggga agttctggtg gaggaagttc tggtggagag 240

cctactactg agaacttgta cttccagagc gataacggaa gttctggtgg aggaagttct 300

ggtggaatgg tgtttacact cgaagatttc gtaggggact ggcggcagac agccggctac 360

aacctggacc aagtccttga gcagggcggt gtgtccagtt tgtttcagaa tctcggggtg 420

tccgtaactc cgatccaaag gattgtcctg agcggtgaaa acggcctgaa gatcgacatc 480

catgtcatca tcccgtatga aggtctgagc ggcgatcaga tgggccagat cgaaaaaatt 540

tttaaggtgg tgtaccctgt ggatgatcat cactttaagg tgattctgca ctatggcaca 600

ctggtaatcg acggg 615

<210> 213
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 213
Met Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly
1 5 10 15

Ile Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr Leu Trp
20 25 30

Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly Ser
35 40 45

Leu Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg Leu Cys
50 55 60

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

Pro Thr Thr Glu Asn Leu Tyr Phe Gln Ser Asp Asn Gly Ser Ser Gly
85 90 95

Gly Gly Ser Ser Gly Gly Met Val Phe Thr Leu Glu Asp Phe Val Gly
100 105 110

Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln
115 120 125

Gly Gly Val Ser Ser Leu Phe Gln Asn Leu Gly Val Ser Val Thr Pro
130 135 140

Ile Gln Arg Ile Val Leu Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile
145 150 155 160

His Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln Met Gly Gln
165 170 175

Ile Glu Lys Ile Phe Lys Val Val Tyr Pro Val Asp Asp His His Phe
180 185 190

Lys Val Ile Leu His Tyr Gly Thr Leu Val Ile Asp Gly
195 200 205

<210> 214
<211> 615
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 214
atgacgccga acatgatcga ctatttcgga cggccgtatg aaggcatcgc cgtgttcgac 60

ggcaaaaaga tcactgtaac cgggaccctg tggaacggca acaaaattat cgacgagcgc 120

ctgatcaacc ccgacggctc cctgctgttc cgcgtaacca tcaacggagt gaccggctgg 180

cggctgtgcg agcgcatttt ggcgggaagt tctggtggag gaagttctgg tggagagcct 240

actactgaga acttgtactt ccagagcgat aacggaagtt ctggtggagg aagttctggt 300

ggaatggtgt ttacactcga agatttcgta ggggactggc ggcagacagc cggctacaac 360

ctggaccaag tccttgagca gggcggtgtg tccagtttgt ttcagaatct cggggtgtcc 420

gtaactccga tccaaaggat tgtcctgagc ggtgaaaacg gcctgaagat cgacatccat 480

gtcatcatcc cgtatgaagg tctgagcggc gatcagatgg gccagatcga aaaaattttt 540

aaggtggtgt accctgtgga tgatcatcac tttaaggtga ttctgcacta tggcacactg 600

gtaatcgacg gggtt 615

<210> 215
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 215
Met Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly Ile
1 5 10 15

Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr Leu Trp Asn
20 25 30

Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly Ser Leu
35 40 45

Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg Leu Cys Glu
50 55 60

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

Thr Thr Glu Asn Leu Tyr Phe Gln Ser Asp Asn Gly Ser Ser Gly Gly
85 90 95

Gly Ser Ser Gly Gly Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp
100 105 110

Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly
115 120 125

Gly Val Ser Ser Leu Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile
130 135 140

Gln Arg Ile Val Leu Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His
145 150 155 160

Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln Met Gly Gln Ile
165 170 175

Glu Lys Ile Phe Lys Val Val Tyr Pro Val Asp Asp His His Phe Lys
180 185 190

Val Ile Leu His Tyr Gly Thr Leu Val Ile Asp Gly Val
195 200 205

<210> 216
<211> 615
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 216
atgccgaaca tgatcgacta tttcggacgg ccgtatgaag gcatcgccgt gttcgacggc 60

aaaaagatca ctgtaaccgg gaccctgtgg aacggcaaca aaattatcga cgagcgcctg 120

atcaaccccg acggctccct gctgttccgc gtaaccatca acggagtgac cggctggcgg 180

ctgtgcgagc gcattttggc gggaagttct ggtggaggaa gttctggtgg agagcctact 240

actgagaact tgtacttcca gagcgataac ggaagttctg gtggaggaag ttctggtgga 300

atggtgttta cactcgaaga tttcgtaggg gactggcggc agacagccgg ctacaacctg 360

gaccaagtcc ttgagcaggg cggtgtgtcc agtttgtttc agaatctcgg ggtgtccgta 420

actccgatcc aaaggattgt cctgagcggt gaaaacggcc tgaagatcga catccatgtc 480

atcatcccgt atgaaggtct gagcggcgat cagatgggcc agatcgaaaa aatttttaag 540

gtggtgtacc ctgtggatga tcatcacttt aaggtgattc tgcactatgg cacactggta 600

atcgacgggg ttacg 615

<210> 217
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 217

Met Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly Ile Ala
1 5 10 15

Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr Leu Trp Asn Gly
20 25 30

Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly Ser Leu Leu
35 40 45

Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg Leu Cys Glu Arg
50 55 60

Ile Leu Ala Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Glu Pro Thr
65 70 75 80

Thr Glu Asn Leu Tyr Phe Gln Ser Asp Asn Gly Ser Ser Gly Gly Gly
85 90 95

Ser Ser Gly Gly Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp
100 105 110

Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly
115 120 125

Val Ser Ser Leu Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln
130 135 140

Arg Ile Val Leu Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val
145 150 155 160

Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln Met Gly Gln Ile Glu
165 170 175

Lys Ile Phe Lys Val Val Tyr Pro Val Asp Asp His His Phe Lys Val
180 185 190

Ile Leu His Tyr Gly Thr Leu Val Ile Asp Gly Val Thr
195 200 205

<210> 218
<211> 612
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 218
atgaacatga tcgactattt cggacggccg tatgaaggca tcgccgtgtt cgacggcaaa 60

aagatcactg taaccgggac cctgtggaac ggcaacaaaa ttatcgacga gcgcctgatc 120

aaccccgacg gctccctgct gttccgcgta accatcaacg gagtgaccgg ctggcggctg 180

tgcgagcgca ttttggcggg aagttctggt ggaggaagtt ctggtggaga gcctactact 240

gagaacttgt acttccagag cgataacgga agttctggtg gaggaagttc tggtggaatg 300

gtgtttacac tcgaagattt cgtaggggac tggcggcaga cagccggcta caacctggac 360

caagtccttg agcagggcgg tgtgtccagt ttgtttcaga atctcggggt gtccgtaact 420

ccgatccaaa ggattgtcct gagcggtgaa aacggcctga agatcgacat ccatgtcatc 480

atcccgtatg aaggtctgag cggcgatcag atgggccaga tcgaaaaaat ttttaaggtg 540

gtgtaccctg tggatgatca tcactttaag gtgattctgc actatggcac actggtaatc 600

gacggggtta cg 612

<210> 219
<211> 204
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 219
Met Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly Ile Ala Val
1 5 10 15

Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr Leu Trp Asn Gly Asn
20 25 30

Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly Ser Leu Leu Phe
35 40 45

Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg Leu Cys Glu Arg Ile

50 55 60

Leu Ala Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Glu Pro Thr Thr
65 70 75 80

Glu Asn Leu Tyr Phe Gln Ser Asp Asn Gly Ser Ser Gly Gly Gly Ser
85 90 95

Ser Gly Gly Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg
100 105 110

Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Val
115 120 125

Ser Ser Leu Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln Arg
130 135 140

Ile Val Leu Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile
145 150 155 160

Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln Met Gly Gln Ile Glu Lys
165 170 175

Ile Phe Lys Val Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile
180 185 190

Leu His Tyr Gly Thr Leu Val Ile Asp Gly Val Thr
195 200

<210> 220
<211> 615
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 220
atgatgatcg actatttcgg acggccgtat gaaggcatcg ccgtgttcga cggcaaaaag 60

atcactgtaa ccgggaccct gtggaacggc aacaaaatta tcgacgagcg cctgatcaac 120

cccgacggct ccctgctgtt ccgcgtaacc atcaacggag tgaccggctg gcggctgtgc 180

gagcgcattt tggcgggaag ttctggtgga ggaagttctg gtggagagcc tactactgag 240

aacttgtact tccagagcga taacggaagt tctggtggag gaagttctgg tggaatggtg 300

tttacactcg aagatttcgt aggggactgg cggcagacag ccggctacaa cctggaccaa 360

gtccttgagc agggcggtgt gtccagtttg tttcagaatc tcggggtgtc cgtaactccg 420

atccaaagga ttgtcctgag cggtgaaaac ggcctgaaga tcgacatcca tgtcatcatc 480

ccgtatgaag gtctgagcgg cgatcagatg ggccagatcg aaaaaatttt taaggtggtg 540

taccctgtgg atgatcatca ctttaaggtg attctgcact atggcacact ggtaatcgac 600

ggggttacgc cgaac 615

<210> 221
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 221
Met Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe
1 5 10 15

Asp Gly Lys Lys Ile Thr Val Thr Gly Thr Leu Trp Asn Gly Asn Lys
20 25 30

Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg
35 40 45

Val Thr Ile Asn Gly Val Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu
50 55 60

Ala Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Glu Pro Thr Thr Glu
65 70 75 80

Asn Leu Tyr Phe Gln Ser Asp Asn Gly Ser Ser Gly Gly Gly Ser Ser
85 90 95

Gly Gly Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln
100 105 110

Thr Ala Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Val Ser
115 120 125

Ser Leu Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln Arg Ile
130 135 140

Val Leu Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile
145 150 155 160

Pro Tyr Glu Gly Leu Ser Gly Asp Gln Met Gly Gln Ile Glu Lys Ile
165 170 175

Phe Lys Val Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu
180 185 190

His Tyr Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn
195 200 205

<210> 222
<211> 615

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 222
atgtatttcg gacggccgta tgaaggcatc gccgtgttcg acggcaaaaa gatcactgta 60

accgggaccc tgtggaacgg caacaaaatt atcgacgagc gcctgatcaa ccccgacggc 120

tccctgctgt tccgcgtaac catcaacgga gtgaccggct ggcggctgtg cgagcgcatt 180

ttggcgggaa gttctggtgg aggaagttct ggtggagagc ctactactga gaacttgtac 240

ttccagagcg ataacggaag ttctggtgga ggaagttctg gtggaatggt gtttacactc 300

gaagatttcg taggggactg gcggcagaca gccggctaca acctggacca agtccttgag 360

cagggcggtg tgtccagttt gtttcagaat ctcggggtgt ccgtaactcc gatccaaagg 420

attgtcctga gcggtgaaaa cggcctgaag atcgacatcc atgtcatcat cccgtatgaa 480

ggtctgagcg gcgatcagat gggccagatc gaaaaaattt ttaaggtggt gtaccctgtg 540

gatgatcatc actttaaggt gattctgcac tatggcacac tggtaatcga cggggttacg 600

ccgaacatga tcgac 615

<210> 223
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 223
Met Tyr Phe Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys
1 5 10 15

Lys Ile Thr Val Thr Gly Thr Leu Trp Asn Gly Asn Lys Ile Ile Asp
20 25 30

Glu Arg Leu Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile
35 40 45

Asn Gly Val Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala Gly Ser
50 55 60

Ser Gly Gly Gly Ser Ser Gly Gly Glu Pro Thr Thr Glu Asn Leu Tyr
65 70 75 80

Phe Gln Ser Asp Asn Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Met
85 90 95

Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala Gly
100 105 110

Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu Phe
115 120 125

Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln Arg Ile Val Leu Ser
130 135 140

Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr Glu
145 150 155 160

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

Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu His Tyr Gly
180 185 190

Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp
195 200 205

<210> 224
<211> 615
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 224
atgcggccgt atgaaggcat cgccgtgttc gacggcaaaa agatcactgt aaccgggacc 60

ctgtggaacg gcaacaaaat tatcgacgag cgcctgatca accccgacgg ctccctgctg 120

ttccgcgtaa ccatcaacgg agtgaccggc tggcggctgt gcgagcgcat tttggcggga 180

agttctggtg gaggaagttc tggtggagag cctactactg agaacttgta cttccagagc 240

gataacggaa gttctggtgg aggaagttct ggtggaatgg tgtttacact cgaagatttc 300

gtaggggact ggcggcagac agccggctac aacctggacc aagtccttga gcagggcggt 360

gtgtccagtt tgtttcagaa tctcggggtg tccgtaactc cgatccaaag gattgtcctg 420

agcggtgaaa acggcctgaa gatcgacatc catgtcatca tcccgtatga aggtctgagc 480

ggcgatcaga tgggccagat cgaaaaaatt tttaaggtgg tgtaccctgt ggatgatcat 540

cactttaagg tgattctgca ctatggcaca ctggtaatcg acggggttac gccgaacatg 600

atcgactatt tcgga 615

<210> 225
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 225

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Met Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr
1               5                  10                  15

Val Thr Gly Thr Leu Trp Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu
            20                  25                  30

Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val
        35                  40                  45

Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala Gly Ser Ser Gly Gly
    50                  55                  60

Gly Ser Ser Gly Gly Glu Pro Thr Thr Glu Asn Leu Tyr Phe Gln Ser
65                  70                  75                  80

Asp Asn Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Met Val Phe Thr
                85                  90                  95

Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu
            100                 105                 110

Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu Phe Gln Asn Leu
        115                 120                 125

Gly Val Ser Val Thr Pro Ile Gln Arg Ile Val Leu Ser Gly Glu Asn
    130                 135                 140

Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr Glu Gly Leu Ser
145                 150                 155                 160

Gly Asp Gln Met Gly Gln Ile Glu Lys Ile Phe Lys Val Val Tyr Pro
                165                 170                 175

Val Asp Asp His His Phe Lys Val Ile Leu His Tyr Gly Thr Leu Val
            180                 185                 190

Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe Gly
        195                 200                 205


<210> 226
<211> 615
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 226
atggaaggca tcgccgtgtt cgacggcaaa aagatcactg taaccgggac cctgtggaac       60

ggcaacaaaa ttatcgacga gcgcctgatc aaccccgacg gctccctgct gttccgcgta      120

accatcaacg gagtgaccgg ctggcggctg tgcgagcgca ttttggcggg aagttctggt      180
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ggaggaagtt ctggtggaga gcctactact gagaacttgt acttccagag cgataacgga 240

agttctggtg gaggaagttc tggtggaatg gtgtttacac tcgaagattt cgtaggggac 300

tggcggcaga cagccggcta caacctggac caagtccttg agcagggcgg tgtgtccagt 360

ttgtttcaga atctcggggt gtccgtaact ccgatccaaa ggattgtcct gagcggtgaa 420

aacggcctga agatcgacat ccatgtcatc atcccgtatg aaggtctgag cggcgatcag 480

atgggccaga tcgaaaaaat ttttaaggtg gtgtaccctg tggatgatca tcactttaag 540

gtgattctgc actatggcac actggtaatc gacggggtta cgccgaacat gatcgactat 600

ttcggacggc cgtat 615

<210> 227
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 227
Met Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly
1 5 10 15

Thr Leu Trp Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro
20 25 30

Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp
35 40 45

Arg Leu Cys Glu Arg Ile Leu Ala Gly Ser Ser Gly Gly Gly Ser Ser
50 55 60

Gly Gly Glu Pro Thr Thr Glu Asn Leu Tyr Phe Gln Ser Asp Asn Gly
65 70 75 80

Ser Ser Gly Gly Gly Ser Ser Gly Gly Met Val Phe Thr Leu Glu Asp
85 90 95

Phe Val Gly Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val
100 105 110

Leu Glu Gln Gly Gly Val Ser Ser Leu Phe Gln Asn Leu Gly Val Ser
115 120 125

Val Thr Pro Ile Gln Arg Ile Val Leu Ser Gly Glu Asn Gly Leu Lys
130 135 140

Ile Asp Ile His Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln
145 150 155 160

Met Gly Gln Ile Glu Lys Ile Phe Lys Val Val Tyr Pro Val Asp Asp

165 170 175

His His Phe Lys Val Ile Leu His Tyr Gly Thr Leu Val Ile Asp Gly
180 185 190

Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr
195 200 205

<210> 228
<211> 615
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 228
atgttcgacg gcaaaaagat cactgtaacc gggaccctgt ggaacggcaa caaaattatc 60

gacgagcgcc tgatcaaccc cgacggctcc ctgctgttcc gcgtaaccat caacggagtg 120

accggctggc ggctgtgcga gcgcattttg gcgggaagtt ctggtggagg aagttctggt 180

ggagagccta ctactgagaa cttgtacttc cagagcgata acggaagttc tggtggagga 240

agttctggtg gaatggtgtt tacactcgaa gatttcgtag gggactggcg gcagacagcc 300

ggctacaacc tggaccaagt ccttgagcag ggcggtgtgt ccagtttgtt tcagaatctc 360

ggggtgtccg taactccgat ccaaaggatt gtcctgagcg gtgaaaacgg cctgaagatc 420

gacatccatg tcatcatccc gtatgaaggt ctgagcggcg atcagatggg ccagatcgaa 480

aaaatttta aggtggtgta ccctgtggat gatcatcact ttaaggtgat tctgcactat 540

ggcacactgg taatcgacgg ggttacgccg aacatgatcg actatttcgg acggccgtat 600

gaaggcatcg tggcc 615

<210> 229
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 229
Met Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr Leu Trp Asn Gly
1 5 10 15

Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly Ser Leu Leu
20 25 30

Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg Leu Cys Glu Arg
35 40 45

Ile Leu Ala Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Glu Pro Thr
50 55 60

Thr Glu Asn Leu Tyr Phe Gln Ser Asp Asn Gly Ser Ser Gly Gly Gly
65 70 75 80

Ser Ser Gly Gly Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp
85 90 95

Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly
100 105 110

Val Ser Ser Leu Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln
115 120 125

Arg Ile Val Leu Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val
130 135 140

Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln Met Gly Gln Ile Glu
145 150 155 160

Lys Ile Phe Lys Val Val Tyr Pro Val Asp Asp His His Phe Lys Val
165 170 175

Ile Leu His Tyr Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met
180 185 190

Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly Ile Val Ala
195 200 205

<210> 230
<211> 615
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 230
atggacggca aaaagatcac tgtaaccggg accctgtgga acggcaacaa aattatcgac 60

gagcgcctga tcaaccccga cggctccctg ctgttccgcg taaccatcaa cggagtgacc 120

ggctggcggc tgtgcgagcg cattttggcg ggaagttctg gtggaggaag ttctggtgga 180

gagcctacta ctgagaactt gtacttccag agcgataacg gaagttctgg tggaggaagt 240

tctggtggaa tggtgtttac actcgaagat ttcgtagggg actggcggca gacagccggc 300

tacaacctgg accaagtcct tgagcagggc ggtgtgtcca gtttgtttca gaatctcggg 360

gtgtccgtaa ctccgatcca aaggattgtc ctgagcggtg aaaacggcct gaagatcgac 420

atccatgtca tcatcccgta tgaaggtctg agcggcgatc agatgggcca gatcgaaaaa 480

atttttaagg tggtgtaccc tgtggatgat catcacttta aggtgattct gcactatggc 540

acactggtaa tcgacggggt tacgccgaac atgatcgact atttcggacg gccgtatgaa 600

ggcatcgccg tgttc 615

<210> 231
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 231

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Met Asp Gly Lys Lys Ile Thr Val Thr Gly Thr Leu Trp Asn Gly Asn
1               5                  10                  15

Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly Ser Leu Leu Phe
            20                  25                  30

Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg Leu Cys Glu Arg Ile
        35                  40                  45

Leu Ala Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Glu Pro Thr Thr
    50                  55                  60

Glu Asn Leu Tyr Phe Gln Ser Asp Asn Gly Ser Ser Gly Gly Gly Ser
65                  70                  75                  80

Ser Gly Gly Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg
                85                  90                  95

Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Val
            100                 105                 110

Ser Ser Leu Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln Arg
        115                 120                 125

Ile Val Leu Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile
    130                 135                 140

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

Ile Phe Lys Val Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile
                165                 170                 175

Leu His Tyr Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile
            180                 185                 190

Asp Tyr Phe Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe
        195                 200                 205
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<210> 232
<211> 615
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 232
atgaaaaaga tcactgtaac cgggaccctg tggaacggca acaaaattat cgacgagcgc 60

ctgatcaacc ccgacggctc cctgctgttc cgcgtaacca tcaacggagt gaccggctgg 120

cggctgtgcg agcgcatttt ggcgggaagt tctggtggag gaagttctgg tggagagcct 180

actactgaga acttgtactt ccagagcgat aacggaagtt ctggtggagg aagttctggt 240

ggaatggtgt ttacactcga agatttcgta ggggactggc ggcagacagc cggctacaac 300

ctggaccaag tccttgagca gggcggtgtg tccagtttgt ttcagaatct cggggtgtcc 360

gtaactccga tccaaaggat tgtcctgagc ggtgaaaacg gcctgaagat cgacatccat 420

gtcatcatcc cgtatgaagg tctgagcggc gatcagatgg gccagatcga aaaaattttt 480

aaggtggtgt accctgtgga tgatcatcac tttaaggtga ttctgcacta tggcacactg 540

gtaatcgacg gggttacgcc gaacatgatc gactatttcg gacggccgta tgaaggcatc 600

gccgtgttcg acggc 615

<210> 233
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 233
Met Lys Lys Ile Thr Val Thr Gly Thr Leu Trp Asn Gly Asn Lys Ile
1 5 10 15

Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val
20 25 30

Thr Ile Asn Gly Val Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala
35 40 45

Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Glu Pro Thr Thr Glu Asn
50 55 60

Leu Tyr Phe Gln Ser Asp Asn Gly Ser Ser Gly Gly Gly Ser Ser Gly
65 70 75 80

Gly Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr
85 90 95

Ala Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser
100 105 110

Leu Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln Arg Ile Val
115 120 125

Leu Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro
130 135 140

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

Lys Val Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu His
165 170 175

Tyr Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr
180 185 190

Phe Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly
195 200 205

<210> 234
<211> 615
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 234
atgaagatca ctgtaaccgg gaccctgtgg aacggcaaca aaattatcga cgagcgcctg 60

atcaaccccg acggctccct gctgttccgc gtaaccatca acggagtgac cggctggcgg 120

ctgtgcgagc gcattttggc gggaagttct ggtggaggaa gttctggtgg agagcctact 180

actgagaact tgtacttcca gagcgataac ggaagttctg gtggaggaag ttctggtgga 240

atggtgttta cactcgaaga tttcgtaggg gactggcggc agacagccgg ctacaacctg 300

gaccaagtcc ttgagcaggg cggtgtgtcc agtttgtttc agaatctcgg ggtgtccgta 360

actccgatcc aaaggattgt cctgagcggt gaaaacggcc tgaagatcga catccatgtc 420

atcatcccgt atgaaggtct gagcggcgat cagatgggcc agatcgaaaa aatttttaag 480

gtggtgtacc ctgtggatga tcatcacttt aaggtgattc tgcactatgg cacactggta 540

atcgacgggg ttacgccgaa catgatcgac tatttcggac ggccgtatga aggcatcgcc 600

gtgttcgacg gcaaa 615

<210> 235
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 235
Met Lys Ile Thr Val Thr Gly Thr Leu Trp Asn Gly Asn Lys Ile Ile

1 5 10 15

Asp Glu Arg Leu Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val Thr
20 25 30

Ile Asn Gly Val Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala Gly
35 40 45

Ser Ser Gly Gly Gly Ser Ser Gly Gly Glu Pro Thr Thr Glu Asn Leu
50 55 60

Tyr Phe Gln Ser Asp Asn Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly
65 70 75 80

Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala
85 90 95

Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu
100 105 110

Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln Arg Ile Val Leu
115 120 125

Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr
130 135 140

Glu Gly Leu Ser Gly Asp Gln Met Gly Gln Ile Glu Lys Ile Phe Lys
145 150 155 160

Val Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu His Tyr
165 170 175

Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe
180 185 190

Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys
195 200 205

<210> 236
<211> 615
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 236
atgatcactg taaccgggac cctgtggaac ggcaacaaaa ttatcgacga gcgcctgatc 60

aaccccgacg gctccctgct gttccgcgta accatcaacg gagtgaccgg ctggcggctg 120

tgcgagcgca ttttggcggg aagttctggt ggaggaagtt ctggtggaga gcctactact 180

gagaacttgt acttccagag cgataacgga agttctggtg gaggaagttc tggtggaatg 240

gtgtttacac tcgaagattt cgtaggggac tggcggcaga cagccggcta caacctggac 300

caagtccttg agcagggcgg tgtgtccagt ttgtttcaga atctcggggt gtccgtaact 360

ccgatccaaa ggattgtcct gagcggtgaa aacggcctga agatcgacat ccatgtcatc 420

atcccgtatg aaggtctgag cggcgatcag atgggccaga tcgaaaaaat ttttaaggtg 480

gtgtaccctg tggatgatca tcactttaag gtgattctgc actatggcac actggtaatc 540

gacggggtta cgccgaacat gatcgactat ttcggacggc cgtatgaagg catcgccgtg 600

ttcgacggca aaaag 615

<210> 237
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 237
Met Ile Thr Val Thr Gly Thr Leu Trp Asn Gly Asn Lys Ile Ile Asp
1 5 10 15

Glu Arg Leu Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile
20 25 30

Asn Gly Val Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala Gly Ser
35 40 45

Ser Gly Gly Gly Ser Ser Gly Gly Glu Pro Thr Thr Glu Asn Leu Tyr
50 55 60

Phe Gln Ser Asp Asn Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Met
65 70 75 80

Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala Gly
85 90 95

Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu Phe
100 105 110

Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln Arg Ile Val Leu Ser
115 120 125

Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr Glu
130 135 140

Gly Leu Ser Gly Asp Gln Met Gly Gln Ile Glu Lys Ile Phe Lys Val
145 150 155 160

Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu His Tyr Gly
165 170 175

Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe Gly
180 185 190

Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys
195 200 205

<210> 238
<211> 615
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 238
atggggaccc tgtggaacgg caacaaaatt atcgacgagc gcctgatcaa ccccgacggc 60

tccctgctgt tccgcgtaac catcaacgga gtgaccggct ggcggctgtg cgagcgcatt 120

ttggcgggaa gttctggtgg aggaagttct ggtggagagc ctactactga gaacttgtac 180

ttccagagcg ataacggaag ttctggtgga ggaagttctg gtggaatggt gtttacactc 240

gaagatttcg taggggactg gcggcagaca gccggctaca acctggacca agtccttgag 300

cagggcggtg tgtccagttt gtttcagaat ctcggggtgt ccgtaactcc gatccaaagg 360

attgtcctga gcggtgaaaa cggcctgaag atcgacatcc atgtcatcat cccgtatgaa 420

ggtctgagcg gcgatcagat gggccagatc gaaaaaattt ttaaggtggt gtaccctgtg 480

gatgatcatc actttaaggt gattctgcac tatggcacac tggtaatcga cggggttacg 540

ccgaacatga tcgactattt cggacggccg tatgaaggca tcgccgtgtt cgacggcaaa 600

aagatcactg taacc 615

<210> 239
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 239
Met Gly Thr Leu Trp Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile
1 5 10 15

Asn Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val Thr
20 25 30

Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala Gly Ser Ser Gly Gly Gly
35 40 45

Ser Ser Gly Gly Glu Pro Thr Thr Glu Asn Leu Tyr Phe Gln Ser Asp
50 55 60

Asn Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Met Val Phe Thr Leu
65 70 75 80

Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp
85 90 95

Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu Phe Gln Asn Leu Gly
100 105 110

Val Ser Val Thr Pro Ile Gln Arg Ile Val Leu Ser Gly Glu Asn Gly
115 120 125

Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly
130 135 140

Asp Gln Met Gly Gln Ile Glu Lys Ile Phe Lys Val Val Tyr Pro Val
145 150 155 160

Asp Asp His His Phe Lys Val Ile Leu His Tyr Gly Thr Leu Val Ile
165 170 175

Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu
180 185 190

Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr
195 200 205

<210> 240
<211> 615
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 240
atgaccctgt ggaacggcaa caaaattatc gacgagcgcc tgatcaaccc cgacggctcc 60

ctgctgttcc gcgtaaccat caacggagtg accggctggc ggctgtgcga gcgcattttg 120

gcgggaagtt ctggtggagg aagttctggt ggagagccta ctactgagaa cttgtacttc 180

cagagcgata acggaagttc tggtggagga agttctggtg gaatggtgtt tacactcgaa 240

gatttcgtag gggactggcg gcagacagcc ggctacaacc tggaccaagt ccttgagcag 300

ggcggtgtgt ccagtttgtt tcagaatctc ggggtgtccg taactccgat ccaaaggatt 360

gtcctgagcg gtgaaaacgg cctgaagatc gacatccatg tcatcatccc gtatgaaggt 420

ctgagcggcg atcagatggg ccagatcgaa aaaatttta aggtggtgta ccctgtggat 480

gatcatcact ttaaggtgat tctgcactat ggcacactgg taatcgacgg ggttacgccg 540

aacatgatcg actatttcgg acggccgtat gaaggcatcg ccgtgttcga cggcaaaaag 600

atcactgtaa ccggg 615

<210> 241
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 241
Met Thr Leu Trp Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn
1 5 10 15

Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly
20 25 30

Trp Arg Leu Cys Glu Arg Ile Leu Ala Gly Ser Ser Gly Gly Gly Ser
35 40 45

Ser Gly Gly Glu Pro Thr Thr Glu Asn Leu Tyr Phe Gln Ser Asp Asn
50 55 60

Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Met Val Phe Thr Leu Glu
65 70 75 80

Asp Phe Val Gly Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln
85 90 95

Val Leu Glu Gln Gly Gly Val Ser Ser Leu Phe Gln Asn Leu Gly Val
100 105 110

Ser Val Thr Pro Ile Gln Arg Ile Val Leu Ser Gly Glu Asn Gly Leu
115 120 125

Lys Ile Asp Ile His Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp
130 135 140

Gln Met Gly Gln Ile Glu Lys Ile Phe Lys Val Val Tyr Pro Val Asp
145 150 155 160

Asp His His Phe Lys Val Ile Leu His Tyr Gly Thr Leu Val Ile Asp
165 170 175

Gly Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly
180 185 190

Ile Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly
195 200 205

<210> 242
<211> 615
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 242
atgctgtgga acggcaacaa aattatcgac gagcgcctga tcaaccccga cggctccctg 60

ctgttccgcg taaccatcaa cggagtgacc ggctggcggc tgtgcgagcg cattttggcg 120

ggaagttctg gtggaggaag ttctggtgga gagcctacta ctgagaactt gtacttccag 180

agcgataacg gaagttctgg tggaggaagt tctggtggaa tggtgtttac actcgaagat 240

ttcgtagggg actggcggca gacagccggc tacaacctgg accaagtcct tgagcagggc 300

ggtgtgtcca gtttgtttca gaatctcggg gtgtccgtaa ctccgatcca aaggattgtc 360

ctgagcggtg aaaacggcct gaagatcgac atccatgtca tcatcccgta tgaaggtctg 420

agcggcgatc agatgggcca gatcgaaaaa atttttaagg tggtgtaccc tgtggatgat 480

catcacttta aggtgattct gcactatggc acactggtaa tcgacggggt tacgccgaac 540

atgatcgact atttcggacg gccgtatgaa ggcatcgccg tgttcgacgg caaaaagatc 600

actgtaaccg ggacc 615

<210> 243
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 243
Met Leu Trp Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro
1 5 10 15

Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp
20 25 30

Arg Leu Cys Glu Arg Ile Leu Ala Gly Ser Ser Gly Gly Gly Ser Ser
35 40 45

Gly Gly Glu Pro Thr Thr Glu Asn Leu Tyr Phe Gln Ser Asp Asn Gly
50 55 60

Ser Ser Gly Gly Gly Ser Ser Gly Gly Met Val Phe Thr Leu Glu Asp
65 70 75 80

Phe Val Gly Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val
85 90 95

Leu Glu Gln Gly Gly Val Ser Ser Leu Phe Gln Asn Leu Gly Val Ser
100 105 110

Val Thr Pro Ile Gln Arg Ile Val Leu Ser Gly Glu Asn Gly Leu Lys

115 120 125

Ile Asp Ile His Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln
130 135 140

Met Gly Gln Ile Glu Lys Ile Phe Lys Val Val Tyr Pro Val Asp Asp
145 150 155 160

His His Phe Lys Val Ile Leu His Tyr Gly Thr Leu Val Ile Asp Gly
165 170 175

Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly Ile
180 185 190

Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr
195 200 205

<210> 244
<211> 616
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 244
atgaacggca acaaaattat cgacgagcgc ctgatcaacc ccgacggctc cctgctgttc 60

cgcgtaacca tcaacggagt gaccggctgg cggctgtgcg agcgcatttt ggcgggaagt 120

tctggtggag gaagttctgg tggagagcct actactgaga acttgtactt ccagagcgat 180

aacggaagtt ctggtggagg aagttctggt ggaatggtgt ttacactcga agatttcgta 240

ggggactggc ggcagacagc cggctacaac ctggaccaag tccttgagca gggcggtgtg 300

tccagtttgt ttcagaatct cggggtgtcc gtaactccga tccaaaggat tgtcctgagc 360

ggtgaaaacg gcctgaagat cgacatccat gtcatcatcc cgtatgaagg tctgagcggc 420

gatcagatgg gccagatcga aaaaattttt aaggtggtgt accctgtgga tgatcatcac 480

tttaaggtga ttctgcacta tggcacactg gtaatcgacg gggttacgcc gaacatgatc 540

gactatttcg gacggccgta tgaaggcatc gccgtgttcg acggcaaaaa gatcactgta 600

accgggaccc tgtggg 616

<210> 245
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 245
Met Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly
1 5 10 15

Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg Leu
20 25 30

Cys Glu Arg Ile Leu Ala Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly
35 40 45

Glu Pro Thr Thr Glu Asn Leu Tyr Phe Gln Ser Asp Asn Gly Ser Ser
50 55 60

Gly Gly Gly Ser Ser Gly Gly Met Val Phe Thr Leu Glu Asp Phe Val
65 70 75 80

Gly Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val Leu Glu
85 90 95

Gln Gly Gly Val Ser Ser Leu Phe Gln Asn Leu Gly Val Ser Val Thr
100 105 110

Pro Ile Gln Arg Ile Val Leu Ser Gly Glu Asn Gly Leu Lys Ile Asp
115 120 125

Ile His Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln Met Gly
130 135 140

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

Phe Lys Val Ile Leu His Tyr Gly Thr Leu Val Ile Asp Gly Val Thr
165 170 175

Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly Ile Ala Val
180 185 190

Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr Leu Trp
195 200 205

<210> 246
<211> 615
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 246
atgaaaatta tcgacgagcg cctgatcaac cccgacggct ccctgctgtt ccgcgtaacc 60

atcaacggag tgaccggctg gcggctgtgc gagcgcattt tggcgggaag ttctggtgga 120

ggaagttctg gtggagagcc tactactgag aacttgtact tccagagcga taacggaagt 180

tctggtggag gaagttctgg tggaatggtg tttacactcg aagatttcgt aggggactgg 240

cggcagacag ccggctacaa cctggaccaa gtccttgagc agggcggtgt gtccagtttg 300

tttcagaatc tcggggtgtc cgtaactccg atccaaagga ttgtcctgag cggtgaaaac 360

ggcctgaaga tcgacatcca tgtcatcatc ccgtatgaag gtctgagcgg cgatcagatg 420

ggccagatcg aaaaaatttt taaggtggtg taccctgtgg atgatcatca ctttaaggtg 480

attctgcact atggcacact ggtaatcgac ggggttacgc cgaacatgat cgactatttc 540

ggacggccgt atgaaggcat cgccgtgttc gacggcaaaa agatcactgt aaccgggacc 600

ctgtggaacg gcaac 615

<210> 247
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 247

Met Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly Ser Leu Leu
1 5 10 15

Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg Leu Cys Glu Arg
20 25 30

Ile Leu Ala Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Glu Pro Thr
35 40 45

Thr Glu Asn Leu Tyr Phe Gln Ser Asp Asn Gly Ser Ser Gly Gly Gly
50 55 60

Ser Ser Gly Gly Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp
65 70 75 80

Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly
85 90 95

Val Ser Ser Leu Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln
100 105 110

Arg Ile Val Leu Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val
115 120 125

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

Lys Ile Phe Lys Val Val Tyr Pro Val Asp Asp His His Phe Lys Val
145 150 155 160

Ile Leu His Tyr Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met
165 170 175

Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly
180 185 190

Lys Lys Ile Thr Val Thr Gly Thr Leu Trp Asn Gly Asn
195 200 205

<210> 248
<211> 624
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 248
atggacgagc gcctgatcaa ccccgacggc tccctgctgt tccgcgtaac catcaacgga 60

gtgaccggct ggcggctgtg cgagcgcatt ttggcgggaa gttctggtgg aggaagttct 120

ggtggagagc ctactactga gaacttgtac ttccagagcg ataacggaag ttctggtgga 180

ggaagttctg gtggaatggt gtttacactc gaagatttcg taggggactg gcggcagaca 240

gccggctaca acctggacca agtccttgag cagggcggtg tgtccagttt gtttcagaat 300

ctcggggtgt ccgtaactcc gatccaaagg attgtcctga gcggtgaaaa cggcctgaag 360

atcgacatcc atgtcatcat cccgtatgaa ggtctgagcg gcgatcagat gggccagatc 420

gaaaaaattt ttaaggtggt gtaccctgtg gatgatcatc actttaaggt gattctgcac 480

tatggcacac tggtaatcga cggggttacg ccgaacatga tcgactattt cggacggccg 540

tatgaaggca tcgccgtgtt cgacggcaaa aagatcactg taaccgggac cctgtggaac 600

ggcaacaaaa ttatcgacga gcgc 624

<210> 249
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 249
Met Asp Glu Arg Leu Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val
1 5 10 15

Thr Ile Asn Gly Val Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala
20 25 30

Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Glu Pro Thr Thr Glu Asn
35 40 45

Leu Tyr Phe Gln Ser Asp Asn Gly Ser Ser Gly Gly Gly Ser Ser Gly
50 55 60

Gly Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr
65 70 75 80

Ala Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser
85 90 95

Leu Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln Arg Ile Val
100 105 110

Leu Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro
115 120 125

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

Lys Val Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu His
145 150 155 160

Tyr Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr
165 170 175

Phe Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile
180 185 190

Thr Val Thr Gly Thr Leu Trp Asn Gly Asn Lys Ile Ile Asp Glu Arg
195 200 205

<210> 250
<211> 615
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 250
atggagcgcc tgatcaaccc cgacggctcc ctgctgttcc gcgtaaccat caacggagtg 60

accggctggc ggctgtgcga gcgcattttg gcgggaagtt ctggtggagg aagttctggt 120

ggagagccta ctactgagaa cttgtacttc cagagcgata acggaagttc tggtggagga 180

agttctggtg gaatggtgtt tacactcgaa gatttcgtag gggactggcg gcagacagcc 240

ggctacaacc tggaccaagt ccttgagcag ggcggtgtgt ccagtttgtt tcagaatctc 300

ggggtgtccg taactccgat ccaaaggatt gtcctgagcg gtgaaaacgg cctgaagatc 360

gacatccatg tcatcatccc gtatgaaggt ctgagcggcg atcagatggg ccagatcgaa 420

aaaattttta aggtggtgta ccctgtggat gatcatcact ttaaggtgat tctgcactat 480

ggcacactgg taatcgacgg ggttacgccg aacatgatcg actatttcgg acggccgtat 540

gaaggcatcg ccgtgttcga cggcaaaaag atcactgtaa ccgggaccct gtggaacggc 600

aacaaaatta tcgac 615

<210> 251
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 251
Met Glu Arg Leu Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val Thr
1 5 10 15

Ile Asn Gly Val Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala Gly
20 25 30

Ser Ser Gly Gly Gly Ser Ser Gly Gly Glu Pro Thr Thr Glu Asn Leu
35 40 45

Tyr Phe Gln Ser Asp Asn Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly
50 55 60

Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala
65 70 75 80

Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu
85 90 95

Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln Arg Ile Val Leu
100 105 110

Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr
115 120 125

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

Val Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu His Tyr
145 150 155 160

Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe
165 170 175

Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr
180 185 190

Val Thr Gly Thr Leu Trp Asn Gly Asn Lys Ile Ile Asp
195 200 205

<210> 252
<211> 615
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 252
atgcgcctga tcaaccccga cggctccctg ctgttccgcg taaccatcaa cggagtgacc 60

ggctggcggc tgtgcgagcg cattttggcg ggaagttctg gtggaggaag ttctggtgga 120

gagcctacta ctgagaactt gtacttccag agcgataacg gaagttctgg tggaggaagt 180

tctggtggaa tggtgtttac actcgaagat ttcgtagggg actggcggca gacagccggc 240

tacaacctgg accaagtcct tgagcagggc ggtgtgtcca gtttgtttca gaatctcggg 300

gtgtccgtaa ctccgatcca aaggattgtc ctgagcggtg aaaacggcct gaagatcgac 360

atccatgtca tcatcccgta tgaaggtctg agcggcgatc agatgggcca gatcgaaaaa 420

atttttaagg tggtgtaccc tgtggatgat catcacttta aggtgattct gcactatggc 480

acactggtaa tcgacggggt tacgccgaac atgatcgact atttcggacg gccgtatgaa 540

ggcatcgccg tgttcgacgg caaaaagatc actgtaaccg ggaccctgtg gaacggcaac 600

aaaattatcg acgag 615

<210> 253
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 253
Met Arg Leu Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile
1 5 10 15

Asn Gly Val Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala Gly Ser
20 25 30

Ser Gly Gly Gly Ser Ser Gly Gly Glu Pro Thr Thr Glu Asn Leu Tyr
35 40 45

Phe Gln Ser Asp Asn Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Met
50 55 60

Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala Gly
65 70 75 80

Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu Phe
85 90 95

Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln Arg Ile Val Leu Ser
100 105 110

Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr Glu
115 120 125

Gly Leu Ser Gly Asp Gln Met Gly Gln Ile Glu Lys Ile Phe Lys Val
130 135 140

Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu His Tyr Gly
145 150 155 160

Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe Gly
165 170 175

Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr Val
180 185 190

Thr Gly Thr Leu Trp Asn Gly Asn Lys Ile Ile Asp Glu
195 200 205

<210> 254
<211> 615
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 254
atgctgatca accccgacgg ctccctgctg ttccgcgtaa ccatcaacgg agtgaccggc 60

tggcggctgt gcgagcgcat tttggcggga agttctggtg gaggaagttc tggtggagag 120

cctactactg agaacttgta cttccagagc gataacggaa gttctggtgg aggaagttct 180

ggtggaatgg tgtttacact cgaagatttc gtaggggact ggcggcagac agccggctac 240

aacctggacc aagtccttga gcagggcggt gtgtccagtt tgtttcagaa tctcggggtg 300

tccgtaactc cgatccaaag gattgtcctg agcggtgaaa acggcctgaa gatcgacatc 360

catgtcatca tcccgtatga aggtctgagc ggcgatcaga tgggccagat cgaaaaaatt 420

tttaaggtgg tgtaccctgt ggatgatcat cactttaagg tgattctgca ctatggcaca 480

ctggtaatcg acggggttac gccgaacatg atcgactatt tcggacggcc gtatgaaggc 540

atcgccgtgt tcgacggcaa aaagatcact gtaaccggga ccctgtggaa cggcaacaaa 600

attatcgacg agcgc 615

<210> 255
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 255
Met Leu Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn
1 5 10 15

Gly Val Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala Gly Ser Ser
20 25 30

Gly Gly Gly Ser Ser Gly Gly Glu Pro Thr Thr Glu Asn Leu Tyr Phe
35 40 45

Gln Ser Asp Asn Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Met Val
50 55 60

Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala Gly Tyr
65 70 75 80

Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu Phe Gln
85 90 95

Asn Leu Gly Val Ser Val Thr Pro Ile Gln Arg Ile Val Leu Ser Gly
100 105 110

Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr Glu Gly
115 120 125

Leu Ser Gly Asp Gln Met Gly Gln Ile Glu Lys Ile Phe Lys Val Val
130 135 140

Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu His Tyr Gly Thr
145 150 155 160

Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg
165 170 175

Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr
180 185 190

Gly Thr Leu Trp Asn Gly Asn Lys Ile Ile Asp Glu Arg
195 200 205

<210> 256
<211> 615
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 256
atgatcaacc ccgacggctc cctgctgttc cgcgtaacca tcaacggagt gaccggctgg 60

cggctgtgcg agcgcatttt ggcgggaagt tctggtggag gaagttctgg tggagagcct 120

actactgaga acttgtactt ccagagcgat aacggaagtt ctggtggagg aagttctggt 180

ggaatggtgt ttacactcga agatttcgta ggggactggc ggcagacagc cggctacaac 240

ctggaccaag tccttgagca gggcggtgtg tccagtttgt ttcagaatct cggggtgtcc 300

gtaactccga tccaaaggat tgtcctgagc ggtgaaaacg gcctgaagat cgacatccat 360

gtcatcatcc cgtatgaagg tctgagcggc gatcagatgg gccagatcga aaaaattttt 420

aaggtggtgt accctgtgga tgatcatcac tttaaggtga ttctgcacta tggcacactg 480

gtaatcgacg gggttacgcc gaacatgatc gactatttcg gacggccgta tgaaggcatc 540

gccgtgttcg acggcaaaaa gatcactgta accgggaccc tgtggaacgg caacaaaatt 600

atcgacgagc gcctg 615

<210> 257
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 257

Met Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly
1 5 10 15

Val Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala Gly Ser Ser Gly
20 25 30

Gly Gly Ser Ser Gly Gly Glu Pro Thr Thr Glu Asn Leu Tyr Phe Gln
35 40 45

Ser Asp Asn Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Met Val Phe
50 55 60

Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala Gly Tyr Asn
65 70 75 80

Leu Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu Phe Gln Asn
85 90 95

Leu Gly Val Ser Val Thr Pro Ile Gln Arg Ile Val Leu Ser Gly Glu
100 105 110

Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr Glu Gly Leu
115 120 125

Ser Gly Asp Gln Met Gly Gln Ile Glu Lys Ile Phe Lys Val Val Tyr
130 135 140

Pro Val Asp Asp His His Phe Lys Val Ile Leu His Tyr Gly Thr Leu
145 150 155 160

Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro
165 170 175

Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly
180 185 190

Thr Leu Trp Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu
195 200 205

<210> 258
<211> 615
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 258
atgaaccccg acggctccct gctgttccgc gtaaccatca acggagtgac cggctggcgg 60

ctgtgcgagc gcattttggc gggaagttct ggtggaggaa gttctggtgg agagcctact 120

actgagaact tgtacttcca gagcgataac ggaagttctg gtggaggaag ttctggtgga 180

atggtgttta cactcgaaga tttcgtaggg gactggcggc agacagccgg ctacaacctg 240

gaccaagtcc ttgagcaggg cggtgtgtcc agtttgtttc agaatctcgg ggtgtccgta 300

actccgatcc aaaggattgt cctgagcggt gaaaacggcc tgaagatcga catccatgtc 360

atcatcccgt atgaaggtct gagcggcgat cagatgggcc agatcgaaaa aatttttaag 420

gtggtgtacc ctgtggatga tcatcacttt aaggtgattc tgcactatgg cacactggta 480

atcgacgggg ttacgccgaa catgatcgac tatttcggac ggccgtatga aggcatcgcc 540

gtgttcgacg gcaaaaagat cactgtaacc gggaccctgt ggaacggcaa caaaattatc 600

gacgagcgcc tgatc 615

<210> 259
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 259
Met Asn Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val
1 5 10 15

Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala Gly Ser Ser Gly Gly
20 25 30

Gly Ser Ser Gly Gly Glu Pro Thr Thr Glu Asn Leu Tyr Phe Gln Ser
35 40 45

Asp Asn Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Met Val Phe Thr
50 55 60

Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu

65 70 75 80

Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu Phe Gln Asn Leu
85 90 95

Gly Val Ser Val Thr Pro Ile Gln Arg Ile Val Leu Ser Gly Glu Asn
100 105 110

Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr Glu Gly Leu Ser
115 120 125

Gly Asp Gln Met Gly Gln Ile Glu Lys Ile Phe Lys Val Val Tyr Pro
130 135 140

Val Asp Asp His His Phe Lys Val Ile Leu His Tyr Gly Thr Leu Val
145 150 155 160

Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr
165 170 175

Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr
180 185 190

Leu Trp Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile
195 200 205

<210> 260
<211> 615
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 260
atgcccgacg gctccctgct gttccgcgta accatcaacg gagtgaccgg ctggcggctg 60

tgcgagcgca ttttggcggg aagttctggt ggaggaagtt ctggtggaga gcctactact 120

gagaacttgt acttccagag cgataacgga agttctggtg gaggaagttc tggtggaatg 180

gtgtttacac tcgaagattt cgtaggggac tggcggcaga cagccggcta caacctggac 240

caagtccttg agcagggcgg tgtgtccagt ttgtttcaga atctcggggt gtccgtaact 300

ccgatccaaa ggattgtcct gagcggtgaa aacggcctga agatcgacat ccatgtcatc 360

atcccgtatg aaggtctgag cggcgatcag atgggccaga tcgaaaaaat ttttaaggtg 420

gtgtaccctg tggatgatca tcactttaag gtgattctgc actatggcac actggtaatc 480

gacggggtta cgccgaacat gatcgactat ttcggacggc cgtatgaagg catcgccgtg 540

ttcgacggca aaaagatcac tgtaaccggg accctgtgga acggcaacaa aattatcgac 600

gagcgcctga tcaac 615

<210> 261
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 261

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Met Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val Thr
1               5                   10                  15

Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala Gly Ser Ser Gly Gly Gly
            20                  25                  30

Ser Ser Gly Gly Glu Pro Thr Thr Glu Asn Leu Tyr Phe Gln Ser Asp
        35                  40                  45

Asn Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Met Val Phe Thr Leu
    50                  55                  60

Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp
65                  70                  75                  80

Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu Phe Gln Asn Leu Gly
                85                  90                  95

Val Ser Val Thr Pro Ile Gln Arg Ile Val Leu Ser Gly Glu Asn Gly
            100                 105                 110

Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly
        115                 120                 125

Asp Gln Met Gly Gln Ile Glu Lys Ile Phe Lys Val Val Tyr Pro Val
    130                 135                 140

Asp Asp His His Phe Lys Val Ile Leu His Tyr Gly Thr Leu Val Ile
145                 150                 155                 160

Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu
                165                 170                 175

Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr Leu
            180                 185                 190

Trp Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn
        195                 200                 205
```

<210> 262
<211> 615
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 262
atggacggct ccctgctgtt ccgcgtaacc atcaacggag tgaccggctg gcggctgtgc 60

gagcgcattt tggcgggaag ttctggtgga ggaagttctg gtggagagcc tactactgag 120

aacttgtact tccagagcga taacggaagt tctggtggag gaagttctgg tggaatggtg 180

tttacactcg aagatttcgt aggggactgg cggcagacag ccggctacaa cctggaccaa 240

gtccttgagc agggcggtgt gtccagtttg tttcagaatc tcggggtgtc cgtaactccg 300

atccaaagga ttgtcctgag cggtgaaaac ggcctgaaga tcgacatcca tgtcatcatc 360

ccgtatgaag gtctgagcgg cgatcagatg ggccagatcg aaaaaatttt taaggtggtg 420

taccctgtgg atgatcatca ctttaaggtg attctgcact atggcacact ggtaatcgac 480

ggggttacgc cgaacatgat cgactatttc ggacggccgt atgaaggcat cgccgtgttc 540

gacggcaaaa agatcactgt aaccgggacc ctgtggaacg gcaacaaaat tatcgacgag 600

cgcctgatca acccc 615

<210> 263
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 263
Met Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly
1 5 10 15

Trp Arg Leu Cys Glu Arg Ile Leu Ala Gly Ser Ser Gly Gly Gly Ser
20 25 30

Ser Gly Gly Glu Pro Thr Thr Glu Asn Leu Tyr Phe Gln Ser Asp Asn
35 40 45

Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Met Val Phe Thr Leu Glu
50 55 60

Asp Phe Val Gly Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln
65 70 75 80

Val Leu Glu Gln Gly Gly Val Ser Ser Leu Phe Gln Asn Leu Gly Val
85 90 95

Ser Val Thr Pro Ile Gln Arg Ile Val Leu Ser Gly Glu Asn Gly Leu
100 105 110

Lys Ile Asp Ile His Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp
115 120 125

```
Gln Met Gly Gln Ile Glu Lys Ile Phe Lys Val Val Tyr Pro Val Asp
    130                 135                 140

Asp His His Phe Lys Val Ile Leu His Tyr Gly Thr Leu Val Ile Asp
145                 150                 155                 160

Gly Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly
                165                 170                 175

Ile Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr Leu Trp
            180                 185                 190

Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro
        195                 200                 205
```

<210> 264
<211> 615
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 264
atgggctccc tgctgttccg cgtaaccatc aacggagtga ccggctggcg gctgtgcgag 60

cgcattttgg cgggaagttc tggtggagga agttctggtg gagagcctac tactgagaac 120

ttgtacttcc agagcgataa cggaagttct ggtggaggaa gttctggtgg aatggtgttt 180

acactcgaag atttcgtagg ggactggcgg cagacagccg gctacaacct ggaccaagtc 240

cttgagcagg gcggtgtgtc cagtttgttt cagaatctcg gggtgtccgt aactccgatc 300

caaaggattg tcctgagcgg tgaaaacggc ctgaagatcg acatccatgt catcatcccg 360

tatgaaggtc tgagcggcga tcagatgggc cagatcgaaa aaatttttaa ggtggtgtac 420

cctgtggatg atcatcactt taaggtgatt ctgcactatg gcacactggt aatcgacggg 480

gttacgccga acatgatcga ctatttcgga cggccgtatg aaggcatcgc cgtgttcgac 540

ggcaaaaaga tcactgtaac cgggaccctg tggaacggca acaaaattat cgacgagcgc 600

ctgatcaacc ccgac 615

<210> 265
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 265
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Met Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp
1               5                   10                  15
```

Arg Leu Cys Glu Arg Ile Leu Ala Gly Ser Ser Gly Gly Gly Ser Ser
20 25 30

Gly Gly Glu Pro Thr Thr Glu Asn Leu Tyr Phe Gln Ser Asp Asn Gly
35 40 45

Ser Ser Gly Gly Gly Ser Ser Gly Gly Met Val Phe Thr Leu Glu Asp
50 55 60

Phe Val Gly Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val
65 70 75 80

Leu Glu Gln Gly Gly Val Ser Ser Leu Phe Gln Asn Leu Gly Val Ser
85 90 95

Val Thr Pro Ile Gln Arg Ile Val Leu Ser Gly Glu Asn Gly Leu Lys
100 105 110

Ile Asp Ile His Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln
115 120 125

Met Gly Gln Ile Glu Lys Ile Phe Lys Val Val Tyr Pro Val Asp Asp
130 135 140

His His Phe Lys Val Ile Leu His Tyr Gly Thr Leu Val Ile Asp Gly
145 150 155 160

Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly Ile
165 170 175

Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr Leu Trp Asn
180 185 190

Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp
195 200 205

<210> 266
<211> 615
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 266
atgtccctgc tgttccgcgt aaccatcaac ggagtgaccg gctggcggct gtgcgagcgc 60

attttggcgg gaagttctgg tggaggaagt tctggtggag agcctactac tgagaacttg 120

tacttccaga gcgataacgg aagttctggt ggaggaagtt ctggtggaat ggtgtttaca 180

ctcgaagatt tcgtagggga ctggcggcag acagccggct acaacctgga ccaagtcctt 240

gagcagggcg gtgtgtccag tttgtttcag aatctcgggg tgtccgtaac tccgatccaa 300

aggattgtcc tgagcggtga aaacggcctg aagatcgaca tccatgtcat catcccgtat 360

gaaggtctga gcggcgatca gatgggccag atcgaaaaaa tttttaaggt ggtgtaccct 420

gtggatgatc atcactttaa ggtgattctg cactatggca cactggtaat cgacggggtt 480

acgccgaaca tgatcgacta tttcggacgg ccgtatgaag gcatcgccgt gttcgacggc 540

aaaaagatca ctgtaaccgg gaccctgtgg aacggcaaca aaattatcga cgagcgcctg 600

atcaaccccg acggc 615

<210> 267
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 267

Met Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg
1 5 10 15

Leu Cys Glu Arg Ile Leu Ala Gly Ser Ser Gly Gly Gly Ser Ser Gly
20 25 30

Gly Glu Pro Thr Thr Glu Asn Leu Tyr Phe Gln Ser Asp Asn Gly Ser
35 40 45

Ser Gly Gly Gly Ser Ser Gly Gly Met Val Phe Thr Leu Glu Asp Phe
50 55 60

Val Gly Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val Leu
65 70 75 80

Glu Gln Gly Gly Val Ser Ser Leu Phe Gln Asn Leu Gly Val Ser Val
85 90 95

Thr Pro Ile Gln Arg Ile Val Leu Ser Gly Glu Asn Gly Leu Lys Ile
100 105 110

Asp Ile His Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln Met
115 120 125

Gly Gln Ile Glu Lys Ile Phe Lys Val Val Tyr Pro Val Asp Asp His
130 135 140

His Phe Lys Val Ile Leu His Tyr Gly Thr Leu Val Ile Asp Gly Val
145 150 155 160

Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly Ile Ala
165 170 175

Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr Leu Trp Asn Gly

180 185 190

Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly
195 200 205

<210> 268
<211> 615
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 268
atgctgctgt tccgcgtaac catcaacgga gtgaccggct ggcggctgtg cgagcgcatt 60

ttggcgggaa gttctggtgg aggaagttct ggtggagagc ctactactga gaacttgtac 120

ttccagagcg ataacggaag ttctggtgga ggaagttctg gtggaatggt gtttacactc 180

gaagatttcg taggggactg gcggcagaca gccggctaca acctggacca agtccttgag 240

cagggcggtg tgtccagttt gtttcagaat ctcggggtgt ccgtaactcc gatccaaagg 300

attgtcctga gcggtgaaaa cggcctgaag atcgacatcc atgtcatcat cccgtatgaa 360

ggtctgagcg gcgatcagat gggccagatc gaaaaaattt ttaaggtggt gtaccctgtg 420

gatgatcatc actttaaggt gattctgcac tatggcacac tggtaatcga cggggttacg 480

ccgaacatga tcgactattt cggacggccg tatgaaggca tcgccgtgtt cgacggcaaa 540

aagatcactg taaccgggac cctgtggaac ggcaacaaaa ttatcgacga gcgcctgatc 600

aaccccgacg gctcc 615

<210> 269
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 269
Met Leu Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg Leu
1 5 10 15

Cys Glu Arg Ile Leu Ala Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly
20 25 30

Glu Pro Thr Thr Glu Asn Leu Tyr Phe Gln Ser Asp Asn Gly Ser Ser
35 40 45

Gly Gly Gly Ser Ser Gly Gly Met Val Phe Thr Leu Glu Asp Phe Val
50 55 60

Gly Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val Leu Glu
65 70 75 80

Gln Gly Gly Val Ser Ser Leu Phe Gln Asn Leu Gly Val Ser Val Thr
85 90 95

Pro Ile Gln Arg Ile Val Leu Ser Gly Glu Asn Gly Leu Lys Ile Asp
100 105 110

Ile His Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln Met Gly
115 120 125

Gln Ile Glu Lys Ile Phe Lys Val Val Tyr Pro Val Asp Asp His His
130 135 140

Phe Lys Val Ile Leu His Tyr Gly Thr Leu Val Ile Asp Gly Val Thr
145 150 155 160

Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly Ile Ala Val
165 170 175

Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr Leu Trp Asn Gly Asn
180 185 190

Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly Ser
195 200 205

<210> 270
<211> 615
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 270
atgctgttcc gcgtaaccat caacggagtg accggctggc ggctgtgcga gcgcattttg 60

gcgggaagtt ctggtggagg aagttctggt ggagagccta ctactgagaa cttgtacttc 120

cagagcgata acggaagttc tggtggagga agttctggtg gaatggtgtt tacactcgaa 180

gatttcgtag gggactggcg gcagacagcc ggctacaacc tggaccaagt ccttgagcag 240

ggcggtgtgt ccagtttgtt tcagaatctc ggggtgtccg taactccgat ccaaaggatt 300

gtcctgagcg gtgaaaacgg cctgaagatc gacatccatg tcatcatccc gtatgaaggt 360

ctgagcggcg atcagatggg ccagatcgaa aaaatttta aggtggtgta ccctgtggat 420

gatcatcact ttaaggtgat tctgcactat ggcacactgg taatcgacgg ggttacgccg 480

aacatgatcg actatttcgg acggccgtat gaaggcatcg ccgtgttcga cggcaaaaag 540

atcactgtaa ccgggaccct gtggaacggc aacaaaatta tcgacgagcg cctgatcaac 600

cccgacggct ccctg 615

<210> 271

<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 271
Met Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg Leu Cys
1 5 10 15

Glu Arg Ile Leu Ala Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Glu
20 25 30

Pro Thr Thr Glu Asn Leu Tyr Phe Gln Ser Asp Asn Gly Ser Ser Gly
35 40 45

Gly Gly Ser Ser Gly Gly Met Val Phe Thr Leu Glu Asp Phe Val Gly
50 55 60

Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln
65 70 75 80

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

Ile Gln Arg Ile Val Leu Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile
100 105 110

His Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln Met Gly Gln
115 120 125

Ile Glu Lys Ile Phe Lys Val Val Tyr Pro Val Asp Asp His His Phe
130 135 140

Lys Val Ile Leu His Tyr Gly Thr Leu Val Ile Asp Gly Val Thr Pro
145 150 155 160

Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe
165 170 175

Asp Gly Lys Lys Ile Thr Val Thr Gly Thr Leu Trp Asn Gly Asn Lys
180 185 190

Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly Ser Leu
195 200 205

<210> 272
<211> 615
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

polynucleotide

<400> 272
atgttccgcg taaccatcaa cggagtgacc ggctggcggc tgtgcgagcg cattttggcg 60

ggaagttctg gtggaggaag ttctggtgga gagcctacta ctgagaactt gtacttccag 120

agcgataacg gaagttctgg tggaggaagt tctggtggaa tggtgtttac actcgaagat 180

ttcgtagggg actggcggca gacagccggc tacaacctgg accaagtcct tgagcagggc 240

ggtgtgtcca gtttgtttca gaatctcggg gtgtccgtaa ctccgatcca aaggattgtc 300

ctgagcggtg aaaacggcct gaagatcgac atccatgtca tcatcccgta tgaaggtctg 360

agcggcgatc agatgggcca gatcgaaaaa atttttaagg tggtgtaccc tgtggatgat 420

catcacttta aggtgattct gcactatggc acactggtaa tcgacggggt tacgccgaac 480

atgatcgact atttcggacg gccgtatgaa ggcatcgccg tgttcgacgg caaaaagatc 540

actgtaaccg ggaccctgtg gaacggcaac aaaattatcg acgagcgcct gatcaacccc 600

gacggctccc tgctg 615

<210> 273
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 273
Met Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg Leu Cys Glu
1 5 10 15

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

Thr Thr Glu Asn Leu Tyr Phe Gln Ser Asp Asn Gly Ser Ser Gly Gly
35 40 45

Gly Ser Ser Gly Gly Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp
50 55 60

Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly
65 70 75 80

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

Gln Arg Ile Val Leu Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His
100 105 110

Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln Met Gly Gln Ile
115 120 125

Glu Lys Ile Phe Lys Val Val Tyr Pro Val Asp Asp His His Phe Lys
130 135 140

Val Ile Leu His Tyr Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn
145 150 155 160

Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp
165 170 175

Gly Lys Lys Ile Thr Val Thr Gly Thr Leu Trp Asn Gly Asn Lys Ile
180 185 190

Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly Ser Leu Leu
195 200 205

<210> 274
<211> 615
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 274
atgaccatca acggagtgac cggctggcgg ctgtgcgagc gcattttggc gggaagttct 60

ggtggaggaa gttctggtgg agagcctact actgagaact tgtacttcca gagcgataac 120

ggaagttctg gtggaggaag ttctggtgga atggtgttta cactcgaaga tttcgtaggg 180

gactggcggc agacagccgg ctacaacctg gaccaagtcc ttgagcaggg cggtgtgtcc 240

agtttgtttc agaatctcgg ggtgtccgta actccgatcc aaaggattgt cctgagcggt 300

gaaaacggcc tgaagatcga catccatgtc atcatcccgt atgaaggtct gagcggcgat 360

cagatgggcc agatcgaaaa aatttttaag gtggtgtacc ctgtggatga tcatcacttt 420

aaggtgattc tgcactatgg cacactggta atcgacgggg ttacgccgaa catgatcgac 480

tatttcggac ggccgtatga aggcatcgcc gtgttcgacg gcaaaaagat cactgtaacc 540

gggaccctgt ggaacggcaa caaaattatc gacgagcgcc tgatcaaccc cgacggctcc 600

ctgctgttcc gcgta 615

<210> 275
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 275
Met Thr Ile Asn Gly Val Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu
1 5 10 15

Ala Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Glu Pro Thr Thr Glu

20 25 30

Asn Leu Tyr Phe Gln Ser Asp Asn Gly Ser Ser Gly Gly Gly Ser Ser
35 40 45

Gly Gly Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln
50 55 60

Thr Ala Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Val Ser
65 70 75 80

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

Val Leu Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile
100 105 110

Pro Tyr Glu Gly Leu Ser Gly Asp Gln Met Gly Gln Ile Glu Lys Ile
115 120 125

Phe Lys Val Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu
130 135 140

His Tyr Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp
145 150 155 160

Tyr Phe Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys
165 170 175

Ile Thr Val Thr Gly Thr Leu Trp Asn Gly Asn Lys Ile Ile Asp Glu
180 185 190

Arg Leu Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val
195 200 205

<210> 276
<211> 615
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 276
atgaacggag tgaccggctg gcggctgtgc gagcgcattt tggcgggaag ttctggtgga 60

ggaagttctg gtggagagcc tactactgag aacttgtact tccagagcga taacggaagt 120

tctggtggag gaagttctgg tggaatggtg tttacactcg aagatttcgt aggggactgg 180

cggcagacag ccggctacaa cctggaccaa gtccttgagc agggcggtgt gtccagtttg 240

tttcagaatc tcggggtgtc cgtaactccg atccaaagga ttgtcctgag cggtgaaaac 300

ggcctgaaga tcgacatcca tgtcatcatc ccgtatgaag gtctgagcgg cgatcagatg 360

ggccagatcg aaaaaatttt taaggtggtg taccctgtgg atgatcatca ctttaaggtg 420

attctgcact atggcacact ggtaatcgac ggggttacgc cgaacatgat cgactatttc 480

ggacggccgt atgaaggcat cgccgtgttc gacggcaaaa agatcactgt aaccgggacc 540

ctgtggaacg gcaacaaaat tatcgacgag cgcctgatca accccgacgg ctccctgctg 600

ttccgcgtaa ccatc 615

<210> 277
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 277

| | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Met | Asn | Gly | Val | Thr | Gly | Trp | Arg | Leu | Cys | Glu | Arg | Ile | Leu | Ala | Gly |
| 1 | | | | 5 | | | | 10 | | | | 15 | | | |
| Ser | Ser | Gly | Gly | Gly | Ser | Ser | Gly | Gly | Glu | Pro | Thr | Thr | Glu | Asn | Leu |
| | | 20 | | | | | 25 | | | | | 30 | | | |
| Tyr | Phe | Gln | Ser | Asp | Asn | Gly | Ser | Ser | Gly | Gly | Gly | Ser | Ser | Gly | Gly |
| | 35 | | | | | 40 | | | | | 45 | | | | |
| Met | Val | Phe | Thr | Leu | Glu | Asp | Phe | Val | Gly | Asp | Trp | Arg | Gln | Thr | Ala |
| 50 | | | | | 55 | | | | | 60 | | | | | |
| Gly | Tyr | Asn | Leu | Asp | Gln | Val | Leu | Glu | Gln | Gly | Gly | Val | Ser | Ser | Leu |
| 65 | | | | 70 | | | | | 75 | | | | | 80 | |
| Phe | Gln | Asn | Leu | Gly | Val | Ser | Val | Thr | Pro | Ile | Gln | Arg | Ile | Val | Leu |
| | | | 85 | | | | | 90 | | | | | 95 | | |
| Ser | Gly | Glu | Asn | Gly | Leu | Lys | Ile | Asp | Ile | His | Val | Ile | Ile | Pro | Tyr |
| | | 100 | | | | | 105 | | | | | 110 | | | |
| Glu | Gly | Leu | Ser | Gly | Asp | Gln | Met | Gly | Gln | Ile | Glu | Lys | Ile | Phe | Lys |
| | 115 | | | | | 120 | | | | | 125 | | | | |
| Val | Val | Tyr | Pro | Val | Asp | Asp | His | His | Phe | Lys | Val | Ile | Leu | His | Tyr |
| 130 | | | | | 135 | | | | | 140 | | | | | |
| Gly | Thr | Leu | Val | Ile | Asp | Gly | Val | Thr | Pro | Asn | Met | Ile | Asp | Tyr | Phe |
| 145 | | | | 150 | | | | | 155 | | | | | 160 | |
| Gly | Arg | Pro | Tyr | Glu | Gly | Ile | Ala | Val | Phe | Asp | Gly | Lys | Lys | Ile | Thr |
| | | | 165 | | | | | 170 | | | | | 175 | | |
| Val | Thr | Gly | Thr | Leu | Trp | Asn | Gly | Asn | Lys | Ile | Ile | Asp | Glu | Arg | Leu |
| | | 180 | | | | | 185 | | | | | 190 | | | |

Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile
195 200 205

<210> 278
<211> 615
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 278
atgggagtga ccggctggcg gctgtgcgag cgcattttgg cgggaagttc tggtggagga 60

agttctggtg gagagcctac tactgagaac ttgtacttcc agagcgataa cggaagttct 120

ggtggaggaa gttctggtgg aatggtgttt acactcgaag atttcgtagg ggactggcgg 180

cagacagccg gctacaacct ggaccaagtc cttgagcagg gcggtgtgtc cagtttgttt 240

cagaatctcg gggtgtccgt aactccgatc caaaggattg tcctgagcgg tgaaaacggc 300

ctgaagatcg acatccatgt catcatcccg tatgaaggtc tgagcggcga tcagatgggc 360

cagatcgaaa aaatttttaa ggtggtgtac cctgtggatg atcatcactt taaggtgatt 420

ctgcactatg gcacactggt aatcgacggg gttacgccga acatgatcga ctatttcgga 480

cggccgtatg aaggcatcgc cgtgttcgac ggcaaaaaga tcactgtaac cgggaccctg 540

tggaacggca acaaaattat cgacgagcgc ctgatcaacc ccgacggctc cctgctgttc 600

cgcgtaacca tcaac 615

<210> 279
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 279
Met Gly Val Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala Gly Ser
1 5 10 15

Ser Gly Gly Gly Ser Ser Gly Gly Glu Pro Thr Thr Glu Asn Leu Tyr
20 25 30

Phe Gln Ser Asp Asn Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Met
35 40 45

Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala Gly
50 55 60

Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu Phe
65 70 75 80

Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln Arg Ile Val Leu Ser
85 90 95

Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr Glu
100 105 110

Gly Leu Ser Gly Asp Gln Met Gly Gln Ile Glu Lys Ile Phe Lys Val
115 120 125

Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu His Tyr Gly
130 135 140

Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe Gly
145 150 155 160

Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr Val
165 170 175

Thr Gly Thr Leu Trp Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile
180 185 190

Asn Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn
195 200 205

<210> 280
<211> 615
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 280
atggtgaccg gctggcggct gtgcgagcgc attttggcgg gaagttctgg tggaggaagt 60

tctggtggag agcctactac tgagaacttg tacttccaga gcgataacgg aagttctggt 120

ggaggaagtt ctggtggaat ggtgtttaca ctcgaagatt tcgtagggga ctggcggcag 180

acagccggct acaacctgga ccaagtcctt gagcagggcg gtgtgtccag tttgtttcag 240

aatctcgggg tgtccgtaac tccgatccaa aggattgtcc tgagcggtga aaacggcctg 300

aagatcgaca tccatgtcat catcccgtat gaaggtctga gcggcgatca gatgggccag 360

atcgaaaaaa tttttaaggt ggtgtaccct gtggatgatc atcactttaa ggtgattctg 420

cactatggca cactggtaat cgacggggtt acgccgaaca tgatcgacta tttcggacgg 480

ccgtatgaag gcatcgccgt gttcgacggc aaaaagatca ctgtaaccgg gaccctgtgg 540

aacggcaaca aaattatcga cgagcgcctg atcaaccccg acggctccct gctgttccgc 600

gtaaccatca acgga 615

<210> 281
<211> 205

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 281
Met Val Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala Gly Ser Ser
1 5 10 15

Gly Gly Gly Ser Ser Gly Gly Glu Pro Thr Thr Glu Asn Leu Tyr Phe
20 25 30

Gln Ser Asp Asn Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Met Val
35 40 45

Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala Gly Tyr
50 55 60

Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu Phe Gln
65 70 75 80

Asn Leu Gly Val Ser Val Thr Pro Ile Gln Arg Ile Val Leu Ser Gly
85 90 95

Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr Glu Gly
100 105 110

Leu Ser Gly Asp Gln Met Gly Gln Ile Glu Lys Ile Phe Lys Val Val
115 120 125

Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu His Tyr Gly Thr
130 135 140

Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg
145 150 155 160

Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr
165 170 175

Gly Thr Leu Trp Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn
180 185 190

Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly
195 200 205

<210> 282
<211> 615
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 282
atgggctggc ggctgtgcga gcgcattttg gcgggaagtt ctggtggagg aagttctggt 60

ggagagccta ctactgagaa cttgtacttc cagagcgata acggaagttc tggtggagga 120

agttctggtg gaatggtgtt tacactcgaa gatttcgtag gggactggcg gcagacagcc 180

ggctacaacc tggaccaagt ccttgagcag ggcggtgtgt ccagtttgtt tcagaatctc 240

ggggtgtccg taactccgat ccaaaggatt gtcctgagcg gtgaaaacgg cctgaagatc 300

gacatccatg tcatcatccc gtatgaaggt ctgagcggcg atcagatggg ccagatcgaa 360

aaaatttta aggtggtgta ccctgtggat gatcatcact ttaaggtgat tctgcactat 420

ggcacactgg taatcgacgg ggttacgccg aacatgatcg actatttcgg acggccgtat 480

gaaggcatcg ccgtgttcga cggcaaaaag atcactgtaa ccgggaccct gtggaacggc 540

aacaaaatta tcgacgagcg cctgatcaac cccgacggct ccctgctgtt ccgcgtaacc 600

atcaacggag tgacc 615

<210> 283
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 283
Met Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala Gly Ser Ser Gly Gly
1 5 10 15

Gly Ser Ser Gly Gly Glu Pro Thr Thr Glu Asn Leu Tyr Phe Gln Ser
20 25 30

Asp Asn Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Met Val Phe Thr
35 40 45

Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu
50 55 60

Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu Phe Gln Asn Leu
65 70 75 80

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

Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr Glu Gly Leu Ser
100 105 110

Gly Asp Gln Met Gly Gln Ile Glu Lys Ile Phe Lys Val Val Tyr Pro
115 120 125

Val Asp Asp His His Phe Lys Val Ile Leu His Tyr Gly Thr Leu Val

130 135 140

Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr
145 150 155 160

Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr
165 170 175

Leu Trp Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp
180 185 190

Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val Thr
195 200 205

<210> 284
<211> 615
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 284
atgctgtgcg agcgcatttt ggcgggaagt tctggtggag gaagttctgg tggagagcct 60

actactgaga acttgtactt ccagagcgat aacggaagtt ctggtggagg aagttctggt 120

ggaatggtgt ttacactcga agatttcgta ggggactggc ggcagacagc cggctacaac 180

ctggaccaag tccttgagca gggcggtgtg tccagtttgt ttcagaatct cggggtgtcc 240

gtaactccga tccaaaggat tgtcctgagc ggtgaaaacg gcctgaagat cgacatccat 300

gtcatcatcc cgtatgaagg tctgagcggc gatcagatgg gccagatcga aaaaattttt 360

aaggtggtgt accctgtgga tgatcatcac tttaaggtga ttctgcacta tggcacactg 420

gtaatcgacg gggttacgcc gaacatgatc gactatttcg gacggccgta tgaaggcatc 480

gccgtgttcg acggcaaaaa gatcactgta accgggaccc tgtggaacgg caacaaaatt 540

atcgacgagc gcctgatcaa ccccgacggc tccctgctgt tccgcgtaac catcaacgga 600

gtgaccggct ggcgg 615

<210> 285
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 285
Met Leu Cys Glu Arg Ile Leu Ala Gly Ser Ser Gly Gly Gly Ser Ser
1 5 10 15

Gly Gly Glu Pro Thr Thr Glu Asn Leu Tyr Phe Gln Ser Asp Asn Gly
20 25 30

Ser Ser Gly Gly Gly Ser Ser Gly Gly Met Val Phe Thr Leu Glu Asp
35 40 45

Phe Val Gly Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val
50 55 60

Leu Glu Gln Gly Gly Val Ser Ser Leu Phe Gln Asn Leu Gly Val Ser
65 70 75 80

Val Thr Pro Ile Gln Arg Ile Val Leu Ser Gly Glu Asn Gly Leu Lys
85 90 95

Ile Asp Ile His Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln
100 105 110

Met Gly Gln Ile Glu Lys Ile Phe Lys Val Val Tyr Pro Val Asp Asp
115 120 125

His His Phe Lys Val Ile Leu His Tyr Gly Thr Leu Val Ile Asp Gly
130 135 140

Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly Ile
145 150 155 160

Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr Leu Trp Asn
165 170 175

Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly Ser Leu
180 185 190

Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg
195 200 205

<210> 286
<211> 615
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 286
atgcgcattt tggcgggaag ttctggtgga ggaagttctg gtggagagcc tactactgag 60

aacttgtact tccagagcga taacggaagt tctggtggag gaagttctgg tggaatggtg 120

tttacactcg aagatttcgt aggggactgg cggcagacag ccggctacaa cctggaccaa 180

gtccttgagc agggcggtgt gtccagtttg tttcagaatc tcggggtgtc cgtaactccg 240

atccaaagga ttgtcctgag cggtgaaaac ggcctgaaga tcgacatcca tgtcatcatc 300

ccgtatgaag gtctgagcgg cgatcagatg ggccagatcg aaaaaatttt taaggtggtg 360

taccctgtgg atgatcatca ctttaaggtg attctgcact atggcacact ggtaatcgac 420

ggggttacgc cgaacatgat cgactatttc ggacggccgt atgaaggcat cgccgtgttc 480

gacggcaaaa agatcactgt aaccgggacc ctgtggaacg gcaacaaaat tatcgacgag 540

cgcctgatca accccgacgg ctccctgctg ttccgcgtaa ccatcaacgg agtgaccggc 600

tggcggctgt gcgag 615

<210> 287
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 287

Met Arg Ile Leu Ala Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Glu
1 5 10 15

Pro Thr Thr Glu Asn Leu Tyr Phe Gln Ser Asp Asn Gly Ser Ser Gly
20 25 30

Gly Gly Ser Ser Gly Gly Met Val Phe Thr Leu Glu Asp Phe Val Gly
35 40 45

Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln
50 55 60

Gly Gly Val Ser Ser Leu Phe Gln Asn Leu Gly Val Ser Val Thr Pro
65 70 75 80

Ile Gln Arg Ile Val Leu Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile
85 90 95

His Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln Met Gly Gln
100 105 110

Ile Glu Lys Ile Phe Lys Val Val Tyr Pro Val Asp Asp His His Phe
115 120 125

Lys Val Ile Leu His Tyr Gly Thr Leu Val Ile Asp Gly Val Thr Pro
130 135 140

Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe
145 150 155 160

Asp Gly Lys Lys Ile Thr Val Thr Gly Thr Leu Trp Asn Gly Asn Lys
165 170 175

Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg
180 185 190

Val Thr Ile Asn Gly Val Thr Gly Trp Arg Leu Cys Glu
195 200 205

<210> 288
<211> 389
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 288
gagtgcaggt ggaaaccatc tccccaggag acgggcgcac cttccccaag cgcggccaga 60

cctgcgtggt gcactacacc gggatgcttg aagatggaaa gaaatttgat tcctcccggg 120

acagaaacaa gcccctttaag tttatgctag gcaagcagga ggtgatccga ggctgggaag 180

aaggggttgc ccagatgagt gtgggtcaga gagccaaact gactatatct ccagattatg 240

cctatggtgc cactgggcac ccaggcatca tcccaccaca tgccactctc gtcttcgatg 300

tggagcttct aaaactggaa ggaggaggga gctccggtgg aggcagcggt ggagtgaccg 360

gctggcggct gtgcgaacgc attctggcg 389

<210> 289
<211> 130
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 289
Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe Pro
1 5 10 15

Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu Asp
20 25 30

Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys Phe
35 40 45

Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val Ala
50 55 60

Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp Tyr
65 70 75 80

Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala Thr
85 90 95

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

Gly Gly Gly Ser Gly Gly Val Thr Gly Trp Arg Leu Cys Glu Arg Ile
115 120 125

Leu Ala
130

<210> 290
<211> 795
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 290
atggtcttca cactcgaaga tttcgttggg gactggcgac agacagccgg ctacaacctg 60

gaccaagtcc ttgaacaggg aggtgtgtcc agtttgtttc agaatctcgg ggtgtccgta 120

actccgatcc aaaggattgt cctgagcggt gaaaatgggc tgaagatcga catccatgtc 180

atcatcccgt atgaaggtct gagcggcgac caaatgggcc agatcgaaaa aatttttaag 240

gtggtgtacc ctgtggatga tcatcacttt aaggtgatcc tgcactatgg cacactggta 300

atcgacgggg ttacgccgaa catgatcgac tatttcggac ggccgtatga aggcatcgcc 360

gtgttcgacg gcaaaaagat cactgtaaca gggaccctgt ggaacggcaa caaaattatc 420

gacgagcgcc tgatcaaccc cgacggctcc ctgctgttcc gagtaaccat caacggagtg 480

accggaggag gtggctcagg tggagggagc tccgtggcca tcctctggca tgagatgtgg 540

catgaaggcc tggaagaggc atctcgtttg tactttgggg aaaggaacgt gaaaggcatg 600

tttgaggtgc tggagccctt gcatgctatg atggaacggg gcccccagac tctgaaggaa 660

acatccttta atcaggccta tggtcgagat ttaatggagg cccaagagtg gtgcaggaag 720

tacatgaaat cagggaatgt caaggacctc acccaagcct gggacctcta ttatcatgtg 780

ttccgacgaa tctca 795

<210> 291
<211> 265
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 291
Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala
1 5 10 15

Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu
20 25 30

Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln Arg Ile Val Leu
35 40 45

Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr
50 55 60

Glu Gly Leu Ser Gly Asp Gln Met Gly Gln Ile Glu Lys Ile Phe Lys
65 70 75 80

Val Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu His Tyr
85 90 95

Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe
100 105 110

Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr
115 120 125

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

Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val
145 150 155 160

Thr Gly Gly Gly Gly Ser Gly Gly Gly Ser Ser Val Ala Ile Leu Trp
165 170 175

His Glu Met Trp His Glu Gly Leu Glu Glu Ala Ser Arg Leu Tyr Phe
180 185 190

Gly Glu Arg Asn Val Lys Gly Met Phe Glu Val Leu Glu Pro Leu His
195 200 205

Ala Met Met Glu Arg Gly Pro Gln Thr Leu Lys Glu Thr Ser Phe Asn
210 215 220

Gln Ala Tyr Gly Arg Asp Leu Met Glu Ala Gln Glu Trp Cys Arg Lys
225 230 235 240

Tyr Met Lys Ser Gly Asn Val Lys Asp Leu Thr Gln Ala Trp Asp Leu
245 250 255

Tyr Tyr His Val Phe Arg Arg Ile Ser
260 265

<210> 292
<211> 825
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 292
ggagtgcagg tggaaaccat ctccccagga gacgggcgca ccttccccaa gcgcggccag 60

acctgcgtgg tgcactacac cgggatgctt gaagatggaa agaaatttga ttcctcccgg 120

gacagaaaca agcccttaa gtttatgcta ggcaagcagg aggtgatccg aggctgggaa 180

gaaggggttg cccagatgag tgtgggtcag agagccaaac tgactatatc tccagattat 240

gcctatggtg ccactgggca cccaggcatc atcccaccac atgccactct cgtcttcgat 300

gtggagcttc taaaactgga aggaggaggg agctccggtg gaggcagcgg tatggtcttc 360

acactcgaag atttcgttgg ggactggcga cagacagccg gctacaacct ggaccaagtc 420

cttgaacagg gaggtgtgtc cagtttgttt cagaatctcg gggtgtccgt aactccgatc 480

caaaggattg tcctgagcgg tgaaaatggg ctgaagatcg acatccatgt catcatcccg 540

tatgaaggtc tgagcggcga ccaaatgggc cagatcgaaa aaatttttaa ggtggtgtac 600

cctgtggatg atcatcactt taaggtgatc ctgcactatg gcacactggt aatcgacggg 660

gttacgccga acatgatcga ctatttcgga cggccgtatg aaggcatcgc cgtgttcgac 720

ggcaaaaaga tcactgtaac agggaccctg tggaacggca acaaaattat cgacgagcgc 780

ctgatcaacc ccgacggctc cctgctgttc cgagtaacca tcaac 825

<210> 293
<211> 275
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 293
Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe Pro
1 5 10 15

Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu Asp
20 25 30

Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys Phe
35 40 45

Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val Ala
50 55 60

Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp Tyr
65 70 75 80

Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala Thr
85 90 95

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

Gly Gly Gly Ser Gly Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp
115 120 125

Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly
130 135 140

Gly Val Ser Ser Leu Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile
145 150 155 160

Gln Arg Ile Val Leu Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His
165 170 175

Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln Met Gly Gln Ile
180 185 190

Glu Lys Ile Phe Lys Val Val Tyr Pro Val Asp Asp His His Phe Lys
195 200 205

Val Ile Leu His Tyr Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn
210 215 220

Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp
225 230 235 240

Gly Lys Lys Ile Thr Val Thr Gly Thr Leu Trp Asn Gly Asn Lys Ile
245 250 255

Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val
260 265 270

Thr Ile Asn
275

<210> 294
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 294
atgggagtga ccggctggcg gctgtgcgaa cgcattctgg cgggaggagg tggctcaggt 60

ggagggagct ccgtggccat cctctggcat gagatgtggc atgaaggcct ggaagaggca 120

tctcgtttgt actttgggga aaggaacgtg aaaggcatgt ttgaggtgct ggagcccttg 180

catgctatga tggaacgggg cccccagact ctgaaggaaa catcctttaa tcaggcctat 240

ggtcgagatt taatggaggc ccaagagtgg tgcaggaagt acatgaaatc agggaatgtc 300

aaggacctca cccaagcctg ggacctctat tatcatgtgt tccgacgaat ctca 354

<210> 295
<211> 118
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 295
Met Gly Val Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala Gly Gly
1 5 10 15

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

Trp His Glu Gly Leu Glu Glu Ala Ser Arg Leu Tyr Phe Gly Glu Arg
35 40 45

Asn Val Lys Gly Met Phe Glu Val Leu Glu Pro Leu His Ala Met Met
50 55 60

Glu Arg Gly Pro Gln Thr Leu Lys Glu Thr Ser Phe Asn Gln Ala Tyr
65 70 75 80

Gly Arg Asp Leu Met Glu Ala Gln Glu Trp Cys Arg Lys Tyr Met Lys
85 90 95

Ser Gly Asn Val Lys Asp Leu Thr Gln Ala Trp Asp Leu Tyr Tyr His
100 105 110

Val Phe Arg Arg Ile Ser
115

<210> 296
<211> 554
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 296
atgggagtgc aggtggaaac catctcccca ggagacgggc gcaccttccc caagcgcggc 60

cagacctgcg tggtgcacta caccgggatg cttgaagatg gaaagaaatt tgattcctcc 120

cgggacagaa acaagccctt taagtttatg ctaggcaagc aggaggtgat ccgaggctgg 180

gaagaagggg ttgcccagat gagtgtgggt cagagagcca aactgactat atctccagat 240

tatgcctatg gtgccactgg gcacccaggc atcatcccac cacatgccac tctcgtcttc 300

gatgtggagc ttctaaaact ggaaggagga gggagctccg gtggaggcag cggtacgccg 360

aacatgatcg actatttcgg acggccgtat gaaggcatcg ccgtgttcga cggcaaaaag 420

atcactgtaa cagggaccct gtggaacggc aacaaaatta tcgacgagcg cctgatcaac 480

cccgacggct ccctgctgtt ccgagtaacc atcaacggag tgaccggctg gcggctgtgc 540

gaacgcattc tggc 554

<210> 297
<211> 184
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 297
Met Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe
1 5 10 15

Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu
20 25 30

Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys
35 40 45

Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val
50 55 60

Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp
65 70 75 80

Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala
85 90 95

Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu Gly Gly Gly Ser
100 105 110

Ser Gly Gly Gly Ser Gly Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg
115 120 125

Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr
130 135 140

Gly Thr Leu Trp Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn
145 150 155 160

Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly
165 170 175

Trp Arg Leu Cys Glu Arg Ile Leu
180

<210> 298
<211> 624
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 298
atggtcttca cactcgaaga tttcgttggg gactggcgac agacagccgg ctacaacctg 60

gaccaagtcc ttgaacaggg aggtgtgtcc agtttgtttc agaatctcgg ggtgtccgta 120

actccgatcc aaaggattgt cctgagcggt gaaaatgggc tgaagatcga catccatgtc 180

atcatcccgt atgaaggtct gagcggcgac caaatgggcc agatcgaaaa aatttttaag 240

gtggtgtacc ctgtggatga tcatcacttt aaggtgatcc tgcactatgg cacactggta 300

atcgacgggg ttggaggagg tggctcaggt ggagggagct ccgtggccat cctctggcat 360

gagatgtggc atgaaggcct ggaagaggca tctcgtttgt actttgggga aaggaacgtg 420

aaaggcatgt ttgaggtgct ggagcccttg catgctatga tggaacgggg cccccagact 480

ctgaaggaaa catcctttaa tcaggcctat ggtcgagatt taatggaggc ccaagagtgg 540

tgcaggaagt acatgaaatc agggaatgtc aaggacctca cccaagcctg ggacctctat 600

tatcatgtgt tccgacgaat ctca 624

<210> 299
<211> 184
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 299
Met Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe
1 5 10 15

Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu
20 25 30

Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys
35 40 45

Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val
50 55 60

Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp
65 70 75 80

Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala
85 90 95

Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu Gly Gly Gly Ser
100 105 110

Ser Gly Gly Gly Ser Gly Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg
115 120 125

Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr

130 135 140

Gly Thr Leu Trp Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn
145 150 155 160

Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly
165 170 175

Trp Arg Leu Cys Glu Arg Ile Leu
180

<210> 300
<211> 516
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 300
atgacgccga acatgatcga ctatttcgga cggccgtatg aaggcatcgc cgtgttcgac 60

ggcaaaaaga tcactgtaac agggaccctg tggaacggca acaaaattat cgacgagcgc 120

ctgatcaacc ccgacggctc cctgctgttc cgagtaacca tcaacggagt gaccggctgg 180

cggctgtgcg aacgcattct ggcgggagga ggtggctcag gtggagggag ctccgtggcc 240

atcctctggc atgagatgtg gcatgaaggc ctggaagagg catctcgttt gtactttggg 300

gaaaggaacg tgaaaggcat gtttgaggtg ctggagccct tgcatgctat gatggaacgg 360

ggcccccaga ctctgaagga aacatccttt aatcaggcct atggtcgaga tttaatggag 420

gcccaagagt ggtgcaggaa gtacatgaaa tcagggaatg tcaaggacct cacccaagcc 480

tgggacctct attatcatgt gttccgacga atctca 516

<210> 301
<211> 172
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 301
Met Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly Ile
1 5 10 15

Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr Leu Trp Asn
20 25 30

Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly Ser Leu
35 40 45

Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg Leu Cys Glu
50 55 60

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

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

Leu Tyr Phe Gly Glu Arg Asn Val Lys Gly Met Phe Glu Val Leu Glu
100 105 110

Pro Leu His Ala Met Met Glu Arg Gly Pro Gln Thr Leu Lys Glu Thr
115 120 125

Ser Phe Asn Gln Ala Tyr Gly Arg Asp Leu Met Glu Ala Gln Glu Trp
130 135 140

Cys Arg Lys Tyr Met Lys Ser Gly Asn Val Lys Asp Leu Thr Gln Ala
145 150 155 160

Trp Asp Leu Tyr Tyr His Val Phe Arg Arg Ile Ser
165 170

<210> 302
<211> 666
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 302
atgggagtgc aggtggaaac catctcccca ggagacgggc gcaccttccc caagcgcggc 60

cagacctgcg tggtgcacta caccgggatg cttgaagatg gaaagaaatt tgattcctcc 120

cgggacagaa acaagccctt taagtttatg ctaggcaagc aggaggtgat ccgaggctgg 180

gaagaagggg ttgcccagat gagtgtgggt cagagagcca aactgactat atctccagat 240

tatgcctatg gtgccactgg gcacccaggc atcatcccac cacatgccac tctcgtcttc 300

gatgtggagc ttctaaaact ggaaggagga gggagctccg gtggaggcag cggtatggtc 360

ttcacactcg aagatttcgt tggggactgg cgacagacag ccggctacaa cctggaccaa 420

gtccttgaac agggaggtgt gtccagtttg tttcagaatc tcggggtgtc cgtaactccg 480

atccaaagga ttgtcctgag cggtgaaaat gggctgaaga tcgacatcca tgtcatcatc 540

ccgtatgaag gtctgagcgg cgaccaaatg ggccagatcg aaaaaatttt taaggtggtg 600

taccctgtgg atgatcatca ctttaaggtg atcctgcact atggcacact ggtaatcgac 660

ggggtt 666

<210> 303
<211> 222
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 303
Met Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe
1 5 10 15

Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu
20 25 30

Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys
35 40 45

Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val
50 55 60

Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp
65 70 75 80

Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala
85 90 95

Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu Gly Gly Gly Ser
100 105 110

Ser Gly Gly Gly Ser Gly Met Val Phe Thr Leu Glu Asp Phe Val Gly
115 120 125

Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln
130 135 140

Gly Gly Val Ser Ser Leu Phe Gln Asn Leu Gly Val Ser Val Thr Pro
145 150 155 160

Ile Gln Arg Ile Val Leu Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile
165 170 175

His Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln Met Gly Gln
180 185 190

Ile Glu Lys Ile Phe Lys Val Val Tyr Pro Val Asp Asp His His Phe
195 200 205

Lys Val Ile Leu His Tyr Gly Thr Leu Val Ile Asp Gly Val
210 215 220

<210> 304
<211> 612
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 304
atgggagtgc aggtggaaac catctcccca ggagacgggc gcaccttccc caagcgcggc 60

cagacctgcg tggtgcacta caccgggatg cttgaagatg gaaagaaatt tgattcctcc 120

cgggacagaa acaagccctt taagtttatg ctaggcaagc aggaggtgat ccgaggctgg 180

gaagaagggg ttgcccagat gagtgtgggt cagagagcca aactgactat atctccagat 240

tatgcctatg gtgccactgg gcacccaggc atcatcccac cacatgccac tctcgtcttc 300

gatgtggagc ttctaaaact ggaaggagga gggagctccg gtggaggcag cggtgatgat 360

catcacttta aggtgatcct gcactatggc acactggtaa tcgacggggt tacgccgaac 420

atgatcgact atttcggacg gccgtatgaa ggcatcgccg tgttcgacgg caaaaagatc 480

actgtaacag ggaccctgtg gaacggcaac aaaattatcg acgagcgcct gatcaacccc 540

gacggctccc tgctgttccg agtaaccatc aacggagtga ccggctggcg gctgtgcgaa 600

cgcattctgg cg 612

<210> 305
<211> 204
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 305
Met Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe
1 5 10 15

Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu
20 25 30

Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys
35 40 45

Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val
50 55 60

Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp
65 70 75 80

Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala
85 90 95

Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu Gly Gly Gly Ser
100 105 110

Ser Gly Gly Gly Ser Gly Asp Asp His His Phe Lys Val Ile Leu His
115 120 125

Tyr Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr
130 135 140

Phe Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile
145 150 155 160

Thr Val Thr Gly Thr Leu Trp Asn Gly Asn Lys Ile Ile Asp Glu Arg
165 170 175

Leu Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly
180 185 190

Val Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala
195 200

<210> 306
<211> 567
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 306
atggtcttca cactcgaaga tttcgttggg gactggcgac agacagccgg ctacaacctg 60

gaccaagtcc ttgaacaggg aggtgtgtcc agtttgtttc agaatctcgg ggtgtccgta 120

actccgatcc aaaggattgt cctgagcggt gaaaatgggc tgaagatcga catccatgtc 180

atcatcccgt atgaaggtct gagcggcgac caaatgggcc agatcgaaaa aatttttaag 240

gtggtgtacc ctgtgggagg aggtggctca ggtggaggga gctccgtggc catcctctgg 300

catgagatgt ggcatgaagg cctggaagag gcatctcgtt tgtactttgg ggaaaggaac 360

gtgaaaggca tgtttgaggt gctggagccc ttgcatgcta tgatggaacg gggcccccag 420

actctgaagg aaacatcctt taatcaggcc tatggtcgag atttaatgga ggcccaagag 480

tggtgcagga agtacatgaa atcagggaat gtcaaggacc tcacccaagc ctgggacctc 540

tattatcatg tgttccgacg aatctca 567

<210> 307
<211> 189
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 307
Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala
1 5 10 15

Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu

20 25 30

Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln Arg Ile Val Leu
35 40 45

Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr
50 55 60

Glu Gly Leu Ser Gly Asp Gln Met Gly Gln Ile Glu Lys Ile Phe Lys
65 70 75 80

Val Val Tyr Pro Val Gly Gly Gly Gly Ser Gly Gly Gly Ser Ser Val
85 90 95

Ala Ile Leu Trp His Glu Met Trp His Glu Gly Leu Glu Glu Ala Ser
100 105 110

Arg Leu Tyr Phe Gly Glu Arg Asn Val Lys Gly Met Phe Glu Val Leu
115 120 125

Glu Pro Leu His Ala Met Met Glu Arg Gly Pro Gln Thr Leu Lys Glu
130 135 140

Thr Ser Phe Asn Gln Ala Tyr Gly Arg Asp Leu Met Glu Ala Gln Glu
145 150 155 160

Trp Cys Arg Lys Tyr Met Lys Ser Gly Asn Val Lys Asp Leu Thr Gln
165 170 175

Ala Trp Asp Leu Tyr Tyr His Val Phe Arg Arg Ile Ser
180 185

<210> 308
<211> 255
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 308
atggtcttca cactcgaaga tttcgttggg gactggcgac agacagccgg ctacaacctg 60

gaccaagtcc ttgaacaggg aggtgtgtcc agtttgtttc agaatctcgg ggtgtccgta 120

actccgatcc aaaggattgt cctgagcggt gaaaatgggc tgaagatcga catccatgtc 180

atcatcccgt atgaaggtct gagcggcgac caaatgggcc agatcgaaaa aatttttaag 240

gtggtgtacc ctgtg 255

<210> 309
<211> 85
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 309
Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala
1 5 10 15

Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu
20 25 30

Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln Arg Ile Val Leu
35 40 45

Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr
50 55 60

Glu Gly Leu Ser Gly Asp Gln Met Gly Gln Ile Glu Lys Ile Phe Lys
65 70 75 80

Val Val Tyr Pro Val
85

<210> 310
<211> 261
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 310
atggatgatc atcactttaa ggtgatcctg cactatggca cactggtaat cgacggggtt 60

acgccgaaca tgatcgacta tttcggacgg ccgtatgaag gcatcgccgt gttcgacggc 120

aaaaagatca ctgtaacagg gaccctgtgg aacggcaaca aaattatcga cgagcgcctg 180

atcaaccccg acggctccct gctgttccga gtaaccatca acggagtgac cggctggcgg 240

ctgtgcgaac gcattctggc g 261

<210> 311
<211> 87
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 311
Met Asp Asp His His Phe Lys Val Ile Leu His Tyr Gly Thr Leu Val
1 5 10 15

Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr
20 25 30

Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr
35 40 45

Leu Trp Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp
50 55 60

Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg
65 70 75 80

Leu Cys Glu Arg Ile Leu Ala
85

<210> 312
<211> 609
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 312
atgggagtgc aggtggaaac catctcccca ggagacgggc gcaccttccc caagcgcggc 60

cagacctgcg tggtgcacta caccgggatg cttgaagatg gaaagaaatt tgattcctcc 120

cgggacagaa acaagccctt taagtttatg ctaggcaagc aggaggtgat ccgaggctgg 180

gaagaagggg ttgcccagat gagtgtgggt cagagagcca aactgactat atctccagat 240

tatgcctatg gtgccactgg gcacccaggc atcatcccac cacatgccac tctcgtcttc 300

gatgtggagc ttctaaaact ggaaggagga gggagctccg gtggaggcag cggtatggtc 360

ttcacactcg aagatttcgt tggggactgg cgacagacag ccggctacaa cctggaccaa 420

gtccttgaac agggaggtgt gtccagtttg tttcagaatc tcggggtgtc cgtaactccg 480

atccaaagga ttgtcctgag cggtgaaaat gggctgaaga tcgacatcca tgtcatcatc 540

ccgtatgaag gtctgagcgg cgaccaaatg ggccagatcg aaaaaatttt taaggtggtg 600

taccctgtg 609

<210> 313
<211> 203
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 313
Met Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe
1 5 10 15

Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu
20 25 30

Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys
35 40 45

Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val
50 55 60

Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp
65 70 75 80

Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala
85 90 95

Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu Gly Gly Gly Ser
100 105 110

Ser Gly Gly Gly Ser Gly Met Val Phe Thr Leu Glu Asp Phe Val Gly
115 120 125

Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln
130 135 140

Gly Gly Val Ser Ser Leu Phe Gln Asn Leu Gly Val Ser Val Thr Pro
145 150 155 160

Ile Gln Arg Ile Val Leu Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile
165 170 175

His Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln Met Gly Gln
180 185 190

Ile Glu Lys Ile Phe Lys Val Val Tyr Pro Val
195 200

<210> 314
<211> 573
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 314
atggatgatc atcactttaa ggtgatcctg cactatggca cactggtaat cgacggggtt 60

acgccgaaca tgatcgacta tttcggacgg ccgtatgaag gcatcgccgt gttcgacggc 120

aaaaagatca ctgtaacagg gaccctgtgg aacggcaaca aaattatcga cgagcgcctg 180

atcaaccccg acggctccct gctgttccga gtaaccatca acggagtgac cggctggcgg 240

ctgtgcgaac gcattctggc gggaggaggt ggctcaggtg gagggagctc cgtggccatc 300

ctctggcatg agatgtggca tgaaggcctg gaagaggcat ctcgtttgta ctttggggaa 360

aggaacgtga aaggcatgtt tgaggtgctg gagcccttgc atgctatgat ggaacggggc 420

ccccagactc tgaaggaaac atcctttaat caggcctatg gtcgagattt aatggaggcc 480

caagagtggt gcaggaagta catgaaatca gggaatgtca aggacctcac ccaagcctgg 540

gacctctatt atcatgtgtt ccgacgaatc tca 573

<210> 315
<211> 191
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 315

| | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Met | Asp | Asp | His | His | Phe | Lys | Val | Ile | Leu | His | Tyr | Gly | Thr | Leu | Val |
| 1 | | | | 5 | | | | 10 | | | | | | 15 | |
| Ile | Asp | Gly | Val | Thr | Pro | Asn | Met | Ile | Asp | Tyr | Phe | Gly | Arg | Pro | Tyr |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Glu | Gly | Ile | Ala | Val | Phe | Asp | Gly | Lys | Lys | Ile | Thr | Val | Thr | Gly | Thr |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Leu | Trp | Asn | Gly | Asn | Lys | Ile | Ile | Asp | Glu | Arg | Leu | Ile | Asn | Pro | Asp |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Gly | Ser | Leu | Leu | Phe | Arg | Val | Thr | Ile | Asn | Gly | Val | Thr | Gly | Trp | Arg |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Leu | Cys | Glu | Arg | Ile | Leu | Ala | Gly | Gly | Gly | Gly | Ser | Gly | Gly | Gly | Ser |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Ser | Val | Ala | Ile | Leu | Trp | His | Glu | Met | Trp | His | Glu | Gly | Leu | Glu | Glu |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Ala | Ser | Arg | Leu | Tyr | Phe | Gly | Glu | Arg | Asn | Val | Lys | Gly | Met | Phe | Glu |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Val | Leu | Glu | Pro | Leu | His | Ala | Met | Met | Glu | Arg | Gly | Pro | Gln | Thr | Leu |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Lys | Glu | Thr | Ser | Phe | Asn | Gln | Ala | Tyr | Gly | Arg | Asp | Leu | Met | Glu | Ala |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| Gln | Glu | Trp | Cys | Arg | Lys | Tyr | Met | Lys | Ser | Gly | Asn | Val | Lys | Asp | Leu |
| | | | | 165 | | | | | 170 | | | | | 175 | |
| Thr | Gln | Ala | Trp | Asp | Leu | Tyr | Tyr | His | Val | Phe | Arg | Arg | Ile | Ser | |
| | | | 180 | | | | | 185 | | | | | 190 | | |

<210> 316
<211> 2838
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 316
atggcagaaa tcggtactgg ctttccattc gacccccatt atgtggaagt cctgggcgag 60

cgcatgcact acgtcgatgt tggtccgcgc gatggcaccc ctgtgctgtt cctgcacggt 120

aacccgacct cctcctacgt gtggcgcaac atcatcccgc atgttgcacc gacccatcgc 180

tgcattgctc cagacctgat cggtatgggc aaatccgaca aaccagacct gggttatttc 240

ttcgacgacc acgtccgctt catggatgcc ttcatcgaag ccctgggtct ggaagaggtc 300

gtcctggtca ttcacgactg gggctccgct ctgggtttcc actgggccaa gcgcaatcca 360

gagcgcgtca aaggtattgc atttatggag ttcatccgcc ctatcccgac ctgggacgaa 420

tggccagaat ttgcccgcga gaccttccag gccttccgca ccaccgacgt cggccgcaag 480

ctgatcatcg atcagaacgt ttttatcgag ggtacgctgc cgatgggtgt cgtccgcccg 540

ctgactgaag tcgagatgga ccattaccgc gagccgttcc tgaatcctgt tgaccgcgag 600

ccactgtggc gcttcccaaa cgagctgcca atcgccggtg agccagcgaa catcgtcgcg 660

ctggtcgaag aatacatgga ctggctgcac cagtcccctg tcccgaagct gctgttctgg 720

ggcaccccag gcgttctgat cccaccggcc gaagccgctc gcctggccaa aagcctgcct 780

aactgcaagg ctgtggacat cggcccgggt ctgaatctgc tgcaagaaga caacccggac 840

ctgatcggca gcgagatcgc gcgctggctg tcgacgctcg agatttccgg cgagccaacc 900

actgaggatc tgtactttca gagcgataac gcgatcgctt tcgaaggaga tagaaccatg 960

cagccagatc ccaggcctag cggggctggg gcctgctgcc gattcctgcc cctgcagtca 1020

cagtgccctg agggggcagg ggacgcggtg atgtacgcct ccactgagtg caaggcggag 1080

gtgacgccct cccagcatgg caaccgcacc ttcagctaca ccctggagga tcataccaag 1140

caggcctttg gcatcatgaa cgagctgcgg ctcagccagc agctgtgtga cgtcacactg 1200

caggtcaagt accaggatgc accggccgcc cagttcatgg cccacaaggt ggtgctggcc 1260

tcatccagcc ctgttttcaa ggccatgttc accaacgggc tgcgggagca gggcatggag 1320

gtggtgtcca ttgagggtat ccaccccaag gtcatggagc gcctcattga attcgcctac 1380

acggcctcca tctccatggg cgagaagtgt gtcctccacg tcatgaacgg cgctgtcatg 1440

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cagatgcagc tgcagaagtg cgagatcctg cagtccgact cccgctgcaa ggactacctg 1860

gtcaagatct tcgaggagct caccctgcac aagcccacgc aggtgatgcc ctgccgggcg 1920

cccaaggtgg gccgcctgat ctacaccgcg ggcggctact tccgacagtc gctcagctac 1980

ctggaggctt acaaccccag taacggcacc tggctccggt tggcggacct gcaggtgccg 2040

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cagtggtcgc cctgcgcccc catgagcgtg ccccgtaacc gcatcggggt gggggtcatc 2220

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aggtatgagc cagagcggga tgagtggcac ttggtggccc caatgctgac acgaaggatc 2340

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aaccgcctta attcagctga gtgttactac ccagagagga acgagtggcg aatgatcaca 2460

gcaatgaaca ccatccgaag cggggcaggc gtctgcgtcc tgcacaactg tatctatgct 2520

gctgggggct atgatggtca ggaccagctg aacagcgtgg agcgctacga tgtggaaaca 2580

gagacgtgga ctttcgtagc ccccatgaag caccggcgaa gtgccctggg gatcactgtc 2640

caccagggga gaatctacgt ccttggaggc tatgatggtc acacgttcct ggacagtgtg 2700

gagtgttacg acccagatac agacacctgg agcgaggtga cccgaatgac atcgggccgg 2760

agtggggtgg gcgtggctgt caccatggag ccctgccgga agcagattga ccagcagaac 2820

tgtacctgtt acgtagtt 2838

<210> 317
<211> 5064
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 317
tcaatattgg ccattagcca tattattcat tggttatata gcataaatca atattggcta 60

ttggccattg catacgttgt atctatatca taatatgtac atttatattg gctcatgtcc 120

aatatgaccg ccatgttggc attgattatt gactagttat taatagtaat caattacggg 180

gtcattagtt catagcccat atatggagtt ccgcgttaca taacttacgg taaatggccc 240

gcctggctga ccgcccaacg acccccgccc attgacgtca ataatgacgt atgttcccat 300

agtaacgcca atagggactt tccattgacg tcaatgggtg gagtatttac ggtaaactgc 360

ccacttggca gtacatcaag tgtatcatat gccaagtccg ccccctattg acgtcaatga 420

cggtaaatgg cccgcctggc attatgccca gtacatgacc ttacgggact ttcctacttg 480

gcagtacatc tacgtattag tcatcgctat taccatggtg atgcggtttt ggcagtacac 540

caatgggcgt ggatagcggt ttgactcacg gggatttcca agtctccacc ccattgacgt 600

caatgggagt ttgttttggc accaaaatca acgggacttt ccaaaatgtc gtaataaccc 660

cgccccgttg acgcaaatgg gcggtaggcg tgtacggtgg gaggtctata taagcagagc 720

tggtttagtg aaccgtcaga tcactagaag ctttattgcg gtagtttatc acagttaaat 780

tgctaacgca gtcagtgctt ctgacacaac agtctcgaac ttaagctgca gaagttggtc 840

gtgaggcact gggcaggtaa gtatcaaggt tacaagacag gtttaaggag accaatagaa 900

actgggcttg tcgagacaga gaagactctt gcgtttctga taggcaccta ttggtcttac 960

tgacatccac tttgcctttc tctccacagg tgtccactcc cagttcaatt acagctctta 1020

aggctagagt attaatacga ctcactatag ggctagcgat cgccatgatg gacttggagc 1080

tgccgccgcc gggactcccg tcccagcagg acatggattt gattgacata ctttggaggc 1140

aagatataga tcttggagta agtcgagaag tatttgactt cagtcagcga cggaaagagt 1200

atgagctgga aaaacagaaa aaacttgaaa aggaaagaca agaacaactc caaaaggagc 1260

aagagaaagc ctttttcgct cagttacaac tagatgaaga gacaggtgaa tttctcccaa 1320

ttcagccagc ccagcacatc cagtcagaaa ccagttctct cggtggttca ggtggtggcg 1380

ggagcggtgg agggagcagc ggtggagtgt ttacactcga agatttcgta ggggactggc 1440

ggcagacagc cggctacaac ctggaccaag tccttgagca gggcggtgtg tccagtttgt 1500

ttcagaatct cggggtgtcc gtaactccga tccaaaggat tgtcctgagc ggtgaaaacg 1560

gcctgaagat cgacatccat gtcatcatcc cgtatgaagg tctgagcggc gatcagatgg 1620

gccagatcga aaaaattttt aaggtggtgt accctgtgga tgatcatcac tttaaggtga 1680

ttctgcacta tggcacactg gtaatcgacg gggttacgcc gaacatgatc gactatttcg 1740

gacggccgta tgaaggcatc gccgtgttcg acggcaaaaa gatcactgta accgggaccc 1800

tgtggaacgg caacaaaatt atcgacgagc gcctgatcaa ccccgacggc tccctgctgt 1860

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gccgcgactc tagagtcgac ctgcaggcat gcaagctgat ccggctgcta acaaagcccg 1980

aaaggaagct gagttggctg ctgccaccgc tgagcaataa ctagcataac cccttggggc 2040

ggccgcttcg agcagacatg ataagataca ttgatgagtt tggacaaacc acaactagaa 2100

tgcagtgaaa aaaatgcttt atttgtgaaa tttgtgatgc tattgcttta tttgtaacca 2160

ttataagctg caataaacaa gttaacaaca acaattgcat tcattttatg tttcaggttc 2220

agggggagat gtgggaggtt tttttaagca agtaaaacct ctacaaatgt ggtaaaatcg 2280

aattttaaca aaatattaac gcttacaatt tcctgatgcg gtattttctc cttacgcatc 2340

tgtgcggtat ttcacaccgc atacgcggat ctgcgcagca ccatggcctg aaataacctc 2400

tgaaagagga acttggttag gtaccttctg aggcggaaag aaccagctgt ggaatgtgtg 2460

tcagttaggg tgtggaaagt ccccaggctc cccagcaggc agaagtatgc aaagcatgca 2520

tctcaattag tcagcaacca ggtgtggaaa gtccccaggc tccccagcag gcagaagtat 2580

gcaaagcatg catctcaatt agtcagcaac catagtcccg cccctaactc cgcccatccc 2640

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ctatgactgg gcacaacaga caatcggctg ctctgatgcc gccgtgttcc ggctgtcagc 3000

gcaggggcgc ccggttcttt ttgtcaagac cgacctgtcc ggtgccctga atgaactgca 3060

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tctcctgtca tctcaccttg ctcctgccga gaaagtatcc atcatggctg atgcaatgcg 3240

gcggctgcat acgcttgatc cggctacctg cccattcgac caccaagcga aacatcgcat 3300

cgagcgagca cgtactcgga tggaagccgg tcttgtcgat caggatgatc tggacgaaga 3360

gcatcagggg ctcgcgccag ccgaactgtt cgccaggctc aaggcgcgca tgcccgacgg 3420

cgaggatctc gtcgtgaccc atggcgatgc ctgcttgccg aatatcatgg tggaaaatgg 3480

ccgcttttct ggattcatcg actgtggccg gctgggtgtg gcggaccgct atcaggacat 3540

agcgttggct acccgtgata ttgctgaaga gcttggcggc gaatgggctg accgcttcct 3600

cgtgctttac ggtatcgccg ctcccgattc gcagcgcatc gccttctatc gccttcttga 3660

cgagttcttc tgagcgggac tctggggttc gaaatgaccg accaagcgac gcccaacctg 3720

ccatcacgat ggccgcaata aaatatcttt attttcatta catctgtgtg ttggtttttt 3780

gtgtgaatcg atagcgataa ggatcctctt tgcgcttgcg ttttcccttg tccagatagc 3840

ccagtagctg acattcatcc ggggtcagca ccgtttctgc ggactggctt tctacccggt 3900

atcagctcac tcaaaggcgg taatacggtt atccacagaa tcaggggata acgcaggaaa 3960

gaacatgtga gcaaaaggcc agcaaaaggc caggaaccgt aaaaaggccg cgttgctggc 4020

gtttttccat aggctccgcc cccctgacga gcatcacaaa aatcgacgct caagtcagag 4080

gtggcgaaac ccgacaggac tataaagata ccaggcgttt ccccctggaa gctccctcgt 4140

gcgctctcct gttccgaccc tgccgcttac cggatacctg tccgcctttc tcccttcggg 4200

aagcgtggcg ctttctcata gctcacgctg taggtatctc agttcggtgt aggtcgttcg 4260

ctccaagctg ggctgtgtgc acgaaccccc cgttcagccc gaccgctgcg ccttatccgg 4320

taactatcgt cttgagtcca acccggtaag acacgactta tcgccactgg cagcagccac 4380

tggtaacagg attagcagag cgaggtatgt aggcggtgct acagagttct tgaagtggtg 4440

gcctaactac ggctacacta gaaggacagt atttggtatc tgcgctctgc tgaagccagt 4500

taccttcgga aaaagagttg gtagctcttg atccggcaaa caaaccaccg ctggtagcgg 4560

tggtttttt gtttgcaagc agcagattac gcgcagaaaa aaaggatttc aagaagatcc 4620

tttgatcttt tctacggggt ctgacgctca gtggaacgaa aactcacgtt aagggatttt 4680

ggtcatgaga ttatcaaaaa ggatcttcac ctagatcctt ttatagtccg gaaatacagg 4740

aacgcacgct ggatggccct tcgctgggat ggtgaaacca tgaaaaatgg cagcttcagt 4800

ggattaagtg ggggtaatgt ggcctgtacc ctctggttgc ataggtattc atacggttaa 4860

aatttatcag gcgcgattgc ggcagttttt cgggtggttt gttgccattt ttacctgtct 4920

gctgccgtga tcgcgctgaa cgcgttttag cggtgcgtac aattaaggga ttatggtaaa 4980

tccacttact gtctgccctc gtagccatcg agataaaccg cagtactccg gccacgatgc 5040

gtccggcgta gaggatcgag atct 5064

<210> 318
<211> 513
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 318
atggtcttca cactcgaaga tttcgtaggt gactggcgac agacagccgg ctacaacctg 60

gaccaagtcc ttgaacaggg tggtgtgtcc agtttgtttc agaatctcgg ggtgtccgta 120

actccgatcc aaaggattgt cctgagcggt gaaaatgggc tgaagatcga catccatgtc 180

atcatcccgt atgaaggtct gagcggcgac caaatgggcc agatcgaaaa aatttttaag 240

gtggtgtacc ctgtggatga tcatcacttt aaggtgatcc tgcactatgg cacactggta 300

atcgacgggg ttacgccgaa catgatcgac tatttcggac ggccgtatga aggcatcgcc 360

gtgttcgacg gcaaaaagat cactgtaact gggaccctgt ggaacggcaa caaaattatc 420

gacgagcgcc tgatcaaccc cgacggctcc ctgctgttcc gagtaaccat caacggagtg 480

accggctggc ggctgtgcga acgcattctg gcg 513

<210> 319
<211> 513
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 319
atggtgttta cactcgaaga tttcgtaggg gactggcggc agacagccgg ctacaacctg 60

gaccaagtcc ttgaacaggg cggtgtgtcc agtttgtttc agaatctcgg ggtgtccgta 120

actccgatcc aaaggattgt cctgagcggt gaaaacggcc tgaagatcga catccatgtc 180

atcatcccgt atgaaggtct gagcggcgat caaatgggcc agatcgaaaa aatttttaag 240

gtggtgtacc ctgtggatga tcatcacttt aaggtgatcc tgcactatgg cacactggta 300

atcgacgggg ttacgccgaa catgatcgac tatttcggac ggccgtatga aggcatcgcc 360

gtgttcgacg gcaaaaagat cactgtaacc gggaccctgt ggaacggcaa caaaattatc 420

gacgagcgcc tgatcaaccc cgacggctcc ctgctgttcc gcgtaaccat caacggagtg 480

accggctggc ggctgtgcga gcgcattttg gcg 513

<210> 320
<211> 636
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 320
atggtgttta cactcgaaga tttcgtaggg gactggcggc agacagccgg ctacaacctg 60

gaccaagtcc ttgaacaggg cggtgtgtcc agtttgtttc agaatctcgg ggtgtccgta 120

actccgatcc aaaggattgt cctgagcggt gaaaacggcc tgaagatcga catccatgtc 180

atcatcccgt atgaaggtct gagcggcgat caaatgggcc agatcgaaaa aatttttaag 240

gtggtgtacc ctgtggatga tcatcacttt aaggtgatcc tgcactatgg cacactggta 300

atcgacgggg ttacgccgaa catgatcgac tatttcggac ggccgtatga aggcatcgcc 360

gtgttcgacg gcaaaaagat cactgtaacc gggaccctgt ggaacggcaa caaaattatc 420

gacgagcgcc tgatcaaccc cgacggctcc ctgctgttcc gcgtaaccat caacggagtg 480

accggctggc ggctgtgcga gcgcattttg gcgaattcac acggctttcc gcccgaggtt 540

gaagagcaag ccgccggtac attgcctatg tcctgcgcac aagaaagcgg tatggaccgg 600

cacccagccg cttgtgcttc agctcgcatc aacgtc 636

<210> 321
<211> 597
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 321
atgaactcct tctccacaag cgccttcggt ccagttgcct tctccctggg cctgctcctg 60

gtgttgcctg ctgccttccc tgccccagtg tttacactcg aagatttcgt aggggactgg 120

cggcagacag ccggctacaa cctggaccaa gtccttgaac agggcggtgt gtccagtttg 180

tttcagaatc tcggggtgtc cgtaactccg atccaaagga ttgtcctgag cggtgaaaac 240

ggcctgaaga tcgacatcca tgtcatcatc ccgtatgaag gtctgagcgg cgatcaaatg 300

ggccagatcg aaaaaatttt taaggtggtg taccctgtgg atgatcatca ctttaaggtg 360

atcctgcact atggcacact ggtaatcgac ggggttacgc cgaacatgat cgactatttc 420

ggacggccgt atgaaggcat cgccgtgttc gacggcaaaa agatcactgt aaccgggacc 480

ctgtggaacg gcaacaaaat tatcgacgag cgcctgatca accccgacgg ctccctgctg 540

ttccgcgtaa ccatcaacgg agtgaccggc tggcggctgt gcgagcgcat tttggcg 597

<210> 322

<211> 513
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 322
atggtcttca cactcgaaga tttcgttggg gactggcgac agacagccgg ctacaacctg 60

gaccaagtcc ttgaacaggg aggtgtgtcc agtttgtttc agaatctcgg ggtgtccgta 120

actccgatcc aaaggattgt cctgagcggt gaaaatgggc tgaagatcga catccatgtc 180

atcatcccgt atgaaggtct gagcggcgac caaatgggcc agatcgaaaa aatttttaag 240

gtggtgtacc ctgtggatga tcatcacttt aaggtgatcc tgcactatgg cacactggta 300

atcgacgggg ttacgccgaa catgatcgac tatttcggac ggccgtatga aggcatcgcc 360

gtgttcgacg gcaaaaagat cactgtaaca gggaccctgt ggaacggcaa caaaattatc 420

gacgagcgcc tgatcaaccc cgacggctcc ctgctgttcc gagtaaccat caacggagtg 480

accggctggc ggctgtgcga acgcattctg gcg 513

<210> 323
<211> 636
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 323
atggtcttca cactcgaaga tttcgttggg gactggcgac agacagccgg ctacaacctg 60

gaccaagtcc ttgaacaggg aggtgtgtcc agtttgtttc agaatctcgg ggtgtccgta 120

actccgatcc aaaggattgt cctgagcggt gaaaatgggc tgaagatcga catccatgtc 180

atcatcccgt atgaaggtct gagcggcgac caaatgggcc agatcgaaaa aatttttaag 240

gtggtgtacc ctgtggatga tcatcacttt aaggtgatcc tgcactatgg cacactggta 300

atcgacgggg ttacgccgaa catgatcgac tatttcggac ggccgtatga aggcatcgcc 360

gtgttcgacg gcaaaaagat cactgtaaca gggaccctgt ggaacggcaa caaaattatc 420

gacgagcgcc tgatcaaccc cgacggctcc ctgctgttcc gagtaaccat caacggagtg 480

accggctggc ggctgtgcga acgcattctg gcgaattctc acggctttcc gcctgaggtt 540

gaagagcaag ccgccggtac attgcctatg tcctgcgcac aagaaagcgg tatggaccgg 600

cacccagccg cttgtgcttc agctcgcatc aacgtc 636

<210> 324
<211> 597
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

polynucleotide

<400> 324
atgaactcct tctccacaag cgccttcggt ccagttgcct tctccctggg cctgctcctg 60

gtgttgcctg ctgccttccc tgccccagtc ttcacactcg aagatttcgt tggggactgg 120

cgacagacag ccggctacaa cctggaccaa gtccttgaac agggaggtgt gtccagtttg 180

tttcagaatc tcggggtgtc cgtaactccg atccaaagga ttgtcctgag cggtgaaaat 240

gggctgaaga tcgacatcca tgtcatcatc ccgtatgaag gtctgagcgg cgaccaaatg 300

ggccagatcg aaaaaatttt taaggtggtg taccctgtgg atgatcatca ctttaaggtg 360

atcctgcact atggcacact ggtaatcgac ggggttacgc cgaacatgat cgactatttc 420

ggacggccgt atgaaggcat cgccgtgttc gacggcaaaa agatcactgt aacagggacc 480

ctgtggaacg gcaacaaaat tatcgacgag cgcctgatca accccgacgg ctccctgctg 540

ttccgagtaa ccatcaacgg agtgaccggc tggcggctgt gcgaacgcat tctggcg 597

<210> 325
<211> 513
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 325
atggtcttca cactcgaaga tttcgtaggt gactggcgac agacagccgg ctacaacctg 60

gaccaagttc ttgaacaggg tggtgtgtcc agtttgtttc agaatctcgg ggtgtccgta 120

actccaatcc agaggatagt cctgagtggt gaaaatgggc tgaagatcga catccatgtc 180

atcatccctt atgaaggtct gagcggcgat cagatggggc agatcgaaaa aatttttaag 240

gtggtgtacc ctgtggatga tcatcacttt aaggtgatcc tgcactatgg cacactggta 300

atcgacggtg ttacgccgaa catgatcgac tatttcggac ggccgtatga aggcatcgcc 360

gtgttcgacg gcaaaaagat tactgtcact ggaaccctgt ggaatgggaa caaaattatc 420

gacgagcgcc tgatcaaccc cgacggctca ctgctgttcc gagtaaccat caatggtgtt 480

accggctggc ggctctgcga acgcattcta gca 513

<210> 326
<211> 636
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 326
atggtcttca cactcgaaga tttcgtaggt gactggcgac agacagccgg ctacaacctg 60

gaccaagttc ttgaacaggg tggtgtgtcc agtttgtttc agaatctcgg ggtgtccgta 120

actccaatcc agaggatagt cctgagtggt gaaaatgggc tgaagatcga catccatgtc 180

atcatccctt atgaaggtct gagcggcgat cagatggggc agatcgaaaa aatttttaag 240

gtggtgtacc ctgtggatga tcatcacttt aaggtgatcc tgcactatgg cacactggta 300

atcgacggtg ttacgccgaa catgatcgac tatttcggac ggccgtatga aggcatcgcc 360

gtgttcgacg gcaaaaagat tactgtcact ggaaccctgt ggaatgggaa caaaattatc 420

gacgagcgcc tgatcaaccc cgacggctca ctgctgttcc gagtaaccat caatggtgtt 480

accggctggc ggctctgcga acgcattcta gcaaatagtc acggctttcc gcctgaggtt 540

gaagagcaag ccgccggtac attgcctatg tcctgcgcac aagaaagcgg tatggaccgg 600

cacccagccg cttgtgcttc agctcgcatc aacgtc 636

<210> 327
<211> 573
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 327
atgaactcct tctccacaag cgccttcggt ccagtcgcct tctccctggg cctgctcctg 60

gtgttgcccg ctgcctttcc tgccccagtc ttcacactcg aagatttcgt aggtgactgg 120

cgacagacag ccggctacaa cctggaccaa gttcttgaac agggtggtgt gtccagtttg 180

tttcagaatc tcggggtgtc cgtaactcca atccagagga tagtcctgag tggtgaaaat 240

gggctgaaga tcgacatcca tgtcatcatc ccttatgaag gtctgagcgg cgatcagatg 300

gggcagatcg aaaaaatttt taaggtggtg taccctgtgg atgatcatca ctttaaggtg 360

atcctgcact atggcacact ggtaatcgac ggtgttacgc cgaacatgat cgactatttc 420

ggacggccgt atgaaggcat cgccgtgttc gacggcaaaa agattactgt cactggaacc 480

ctgtggaatg ggaacaaaat tatcgacgag cgcctgatca accccgacgg ctcactgctg 540

ttccgagtaa ccatcaatgg tgttaccggc tgg 573

<210> 328
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 328
Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Glu Pro Thr Thr Glu Asn
1 5 10 15

Leu Tyr Phe Gln Ser Asp Asn Gly Ser Ser Gly Gly Gly Ser Ser Gly
20 25 30

Gly

<210> 329
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
FABP consensus peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Gly, Ser, Ala, Ile, Val, or Lys

<220>
<221> MOD_RES
<222> (2)..(2)
<223> Any amino acid except Phe or Glu

<220>
<221> MOD_RES
<222> (3)..(3)
<223> Phe, Tyr, or Trp

<220>
<221> MOD_RES
<222> (4)..(4)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (5)..(5)
<223> Leu, Ile, Val, Met, or Phe

<220>
<221> MOD_RES
<222> (6)..(7)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (8)..(8)
<223> Any amino acid except Lys

<220>
<221> MOD_RES
<222> (9)..(9)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (10)..(10)
<223> Asn, His, or Gly

<220>
<221> MOD_RES
<222> (11)..(11)
<223> Phe or Tyr

<220>
<221> MOD_RES
<222> (12)..(12)
<223> Asp or Glu

<220>
<221> MOD_RES
<222> (13)..(13)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (14)..(14)
<223> Leu, Ile, Val, Met, Phe, or Tyr

<220>
<221> MOD_RES
<222> (15)..(15)
<223> Leu, Ile, Val, or Met

<220>
<221> MOD_RES
<222> (16)..(16)
<223> Any amino acid except Asn

<220>
<221> MOD_RES
<222> (17)..(17)
<223> Any amino acid except Gly

<220>
<221> MOD_RES
<222> (18)..(18)
<223> Leu, Ile, Val, Met, Ala, Lys, or Arg

<400> 329
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15

Xaa Xaa

<210> 330
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
OGLUC consensus peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Gly, Ser, Ala, Ile, Val, or Lys

<220>
<221> MOD_RES
<222> (2)..(2)
<223> Any amino acid except Phe or Glu

<220>
<221> MOD_RES
<222> (3)..(3)
<223> Phe, Tyr, or Trp

<220>
<221> MOD_RES
<222> (4)..(4)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (5)..(5)
<223> Leu, Ile, Val, Met, Phe, Ser, Tyr, or Gln

<220>
<221> MOD_RES
<222> (6)..(7)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (8)..(8)
<223> Any amino acid except Lys

<220>
<221> MOD_RES
<222> (9)..(9)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (10)..(10)
<223> Asn, His, Gly, or Lys

<220>
<221> MOD_RES
<222> (11)..(11)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (12)..(12)
<223> Asp or Glu

<220>
<221> MOD_RES
<222> (13)..(13)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (14)..(14)
<223> Leu, Ile, Val, Met, Phe, or Tyr

<220>
<221> MOD_RES
<222> (15)..(15)
<223> Leu, Ile, Val, Met, Trp, or Phe

<220>
<221> MOD_RES
<222> (16)..(16)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (17)..(17)
<223> Any amino acid except Gly

<220>
<221> MOD_RES
<222> (18)..(18)
<223> Leu, Ile, Val, Met, Ala, Lys, Arg, or Gly

<400> 330
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

1 5 10 15

Xaa Xaa

<210> 331
<211> 672
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 331
atgggcctga agatcgacat ccatgtcatc atcccgtatg aaggtctgag cggctatcag 60

atgggccaga tcgaaaaaat ttttaaggtg gtgtaccctg tggatgatca tcactttaag 120

gtgattctgc actatggcac actggtaatc gacggggtta cgccgaacat gatcgactat 180

ttcggacggc cgtatgaagg catcgccgtg ttcgacggca aaaagatcac tgtaaccggg 240

accctgtgga acggcaacaa aattatcgac gagcgcctga tcaaccccga cggctccctg 300

ctgttccgcg taaccatcaa cggagtgacc ggctggcggc tgtgcgagcg cattttggcg 360

ggaggaggtg gctcaggtgg agggagctcc gtggccatcc tctggcatga gatgtggcat 420

gaaggcctgg aagaggcatc tcgtttgtac tttggggaaa ggaacgtgaa aggcatgttt 480

gaggtgctgg agcccttgca tgctatgatg gaacggggcc cccagactct gaaggaaaca 540

tcctttaatc aggcctatgg tcgagattta atggaggccc aagagtggtg caggaagtac 600

atgaaatcag ggaatgtcaa ggacctcacc caagcctggg acctctatta tcatgtgttc 660

cgacgaatct ca 672

<210> 332
<211> 224
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 332
Met Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr Glu Gly Leu
1 5 10 15

Ser Gly Tyr Gln Met Gly Gln Ile Glu Lys Ile Phe Lys Val Val Tyr
20 25 30

Pro Val Asp Asp His His Phe Lys Val Ile Leu His Tyr Gly Thr Leu
35 40 45

Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro
50 55 60

Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly
65 70 75 80

Thr Leu Trp Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro
85 90 95

Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp
100 105 110

Arg Leu Cys Glu Arg Ile Leu Ala Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Ser Ser Val Ala Ile Leu Trp His Glu Met Trp His Glu Gly Leu Glu
130 135 140

Glu Ala Ser Arg Leu Tyr Phe Gly Glu Arg Asn Val Lys Gly Met Phe
145 150 155 160

Glu Val Leu Glu Pro Leu His Ala Met Met Glu Arg Gly Pro Gln Thr
165 170 175

Leu Lys Glu Thr Ser Phe Asn Gln Ala Tyr Gly Arg Asp Leu Met Glu
180 185 190

Ala Gln Glu Trp Cys Arg Lys Tyr Met Lys Ser Gly Asn Val Lys Asp
195 200 205

Leu Thr Gln Ala Trp Asp Leu Tyr Tyr His Val Phe Arg Arg Ile Ser
210 215 220

<210> 333
<211> 468
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 333
atggtgttta cactcgaaga tttcgtaggg gactggcggc agacagccgg ctacaacctg 60

gaccaagtcc ttgagcaggg cggtctgtcc agtttgtttc agaaactcgg ggtgtccgta 120

acaccgatcc aaaagattgt cctgagcggt gaaaacggag gaggtggctc aggtggaggg 180

agctccgtgg ccatcctctg gcatgagatg tggcatgaag gcctggaaga ggcatctcgt 240

ttgtactttg gggaaaggaa cgtgaaaggc atgtttgagg tgctggagcc cttgcatgct 300

atgatggaac ggggccccca gactctgaag gaaacatcct ttaatcaggc ctatggtcga 360

gatttaatgg aggcccaaga gtggtgcagg aagtacatga aatcagggaa tgtcaaggac 420

ctcacccaag cctgggacct ctattatcat gtgttccgac gaatctca 468

<210> 334

<211> 156
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 334
Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala
1 5 10 15

Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Leu Ser Ser Leu
20 25 30

Phe Gln Lys Leu Gly Val Ser Val Thr Pro Ile Gln Lys Ile Val Leu
35 40 45

Ser Gly Glu Asn Gly Gly Gly Gly Ser Gly Gly Gly Ser Ser Val Ala
50 55 60

Ile Leu Trp His Glu Met Trp His Glu Gly Leu Glu Glu Ala Ser Arg
65 70 75 80

Leu Tyr Phe Gly Glu Arg Asn Val Lys Gly Met Phe Glu Val Leu Glu
85 90 95

Pro Leu His Ala Met Met Glu Arg Gly Pro Gln Thr Leu Lys Glu Thr
100 105 110

Ser Phe Asn Gln Ala Tyr Gly Arg Asp Leu Met Glu Ala Gln Glu Trp
115 120 125

Cys Arg Lys Tyr Met Lys Ser Gly Asn Val Lys Asp Leu Thr Gln Ala
130 135 140

Trp Asp Leu Tyr Tyr His Val Phe Arg Arg Ile Ser
145 150 155

<210> 335
<211> 711
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 335
atgggagtgc aggtggaaac catctcccca ggagacgggc gcaccttccc caagcgcggc 60

cagacctgcg tggtgcacta caccgggatg cttgaagatg gaaagaaatt tgattcctcc 120

cgggacagaa acaagccctt taagtttatg ctaggcaagc aggaggtgat ccgaggctgg 180

gaagaagggg ttgcccagat gagtgtgggt cagagagcca aactgactat atctccagat 240

tatgcctatg gtgccactgg gcacccaggc atcatcccac cacatgccac tctcgtcttc 300

gatgtggagc ttctaaaact ggaaggagga gggagctccg gtggaggcag cggtggcctg 360

aagatcgaca tccatgtcat catcccgtat gaaggtctga gcggctatca gatgggccag 420

atcgaaaaaa tttttaaggt ggtgtaccct gtggatgatc atcactttaa ggtgattctg 480

cactatggca cactggtaat cgacggggtt acgccgaaca tgatcgacta tttcggacgg 540

ccgtatgaag gcatcgccgt gttcgacggc aaaaagatca ctgtaaccgg gaccctgtgg 600

aacggcaaca aaattatcga cgagcgcctg atcaaccccg acggctccct gctgttccgc 660

gtaaccatca acggagtgac cggctggcgg ctgtgcgagc gcattttggc g 711

<210> 336
<211> 237
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 336
Met Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe
1 5 10 15

Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu
20 25 30

Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys
35 40 45

Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val
50 55 60

Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp
65 70 75 80

Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala
85 90 95

Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu Gly Gly Gly Ser
100 105 110

Ser Gly Gly Gly Ser Gly Gly Leu Lys Ile Asp Ile His Val Ile Ile
115 120 125

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

Phe Lys Val Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu
145 150 155 160

His Tyr Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp
165 170 175

Tyr Phe Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys
180 185 190

Ile Thr Val Thr Gly Thr Leu Trp Asn Gly Asn Lys Ile Ile Asp Glu
195 200 205

Arg Leu Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn
210 215 220

Gly Val Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala
225 230 235

<210> 337
<211> 510
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 337
atgggagtgc aggtggaaac catctcccca ggagacgggc gcaccttccc caagcgcggc 60

cagacctgcg tggtgcacta caccgggatg cttgaagatg gaaagaaatt tgattcctcc 120

cgggacagaa acaagccctt taagtttatg ctaggcaagc aggaggtgat ccgaggctgg 180

gaagaagggg ttgcccagat gagtgtgggt cagagagcca aactgactat atctccagat 240

tatgcctatg gtgccactgg gcacccaggc atcatcccac cacatgccac tctcgtcttc 300

gatgtggagc ttctaaaact ggaaggagga gggagctccg gtggaggcag cggtatggtg 360

tttacactcg aagatttcgt aggggactgg cggcagacag ccggctacaa cctggaccaa 420

gtccttgagc agggcggtct gtccagtttg tttcagaaac tcggggtgtc cgtaacaccg 480

atccaaaaga ttgtcctgag cggtgaaaac 510

<210> 338
<211> 170
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 338
Met Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe
1 5 10 15

Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu
20 25 30

Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys
35 40 45

Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val
50 55 60

Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp
65 70 75 80

Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala
85 90 95

Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu Gly Gly Gly Ser
100 105 110

Ser Gly Gly Gly Ser Gly Met Val Phe Thr Leu Glu Asp Phe Val Gly
115 120 125

Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln
130 135 140

Gly Gly Leu Ser Ser Leu Phe Gln Lys Leu Gly Val Ser Val Thr Pro
145 150 155 160

Ile Gln Lys Ile Val Leu Ser Gly Glu Asn
165 170

<210> 339
<211> 513
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 339
atggtgttta cactcgaaga tttcgtaggg gactggcggc agacagccgg ctacaacctg 60

gaccaagtcc ttgagcaggg cggtgtgtcc agtttgtttc agaatctcgg ggtgtccgta 120

acaccgatcc aaaggattgt cctgagcggt gaaaacggcc tgaagatcga catccatgtc 180

atcatcccgt atgaaggtct gagcggcgat cagatgggcc agatcgaaaa aatttttaag 240

gtggtgtacc ctgtggatga tcatcacttt aaggtgattc tgcactatgg cacactggta 300

atcgacgggg ttacgccgaa catgatcgac tatttcggac ggccgtatga aggcatcgcc 360

gtgttcgacg gcaaaaagat cactgtaacc gggaccctgt ggaacggcaa caaaattatc 420

gacgagcgcc tgatcaaccc cgacggctcc ctgctgttcc gcgtaaccat caacggagtg 480

accggctggc ggctgtgcga gcgcattttg gcg 513

<210> 340
<211> 171
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 340
Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala
1 5 10 15

Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu
20 25 30

Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln Arg Ile Val Leu
35 40 45

Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr
50 55 60

Glu Gly Leu Ser Gly Asp Gln Met Gly Gln Ile Glu Lys Ile Phe Lys
65 70 75 80

Val Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu His Tyr
85 90 95

Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe
100 105 110

Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr
115 120 125

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

Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val
145 150 155 160

Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala
165 170

<210> 341
<211> 513
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 341
atggtgttta cactcgaaga tttcgtaggg gactggcggc agacagccgg ctacaacctg 60

gaccaagtcc ttgagcaggg cggtgtgtcc agtttgtttc agaatctcgg ggtgtccgta 120

actccgatcc aaaggattgt cctgagcggt gaaaacggcc tgaagatcga catccatgtc 180

atcatcccgt atgaaggtct gaacggctat cagatgggcc agatcgaaaa aatttttaag 240

gtggtgtacc ctgtggatga tcatcacttt aaggtgattc tgcactatgg cacactggta 300

atcgacgggg ttacgccgaa catgatcgac tatttcggac ggccgtatga aggcatcgcc 360

gtgttcgacg gcaaaaagat cactgtaacc gggaccctgt ggaacggcaa caaaattatc 420

gacgagcgcc tgatcaaccc cgacggctcc ctgctgttcc gcgtaaccat caacggagtg 480

accggctggc ggctgtgcga gcgcattttg gcg 513

<210> 342
<211> 171
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 342
Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala
1 5 10 15

Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu
20 25 30

Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln Arg Ile Val Leu
35 40 45

Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr
50 55 60

Glu Gly Leu Asn Gly Tyr Gln Met Gly Gln Ile Glu Lys Ile Phe Lys
65 70 75 80

Val Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu His Tyr
85 90 95

Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe
100 105 110

Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr
115 120 125

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

Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val
145 150 155 160

Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala
165 170

<210> 343
<211> 690
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 343
atggtcctga gcggtgaaaa tgggctgaag atcgacatcc atgtcatcat cccgtatgaa 60

ggtctgagcg gcgaccaaat gggccagatc gaaaaaattt ttaaggtggt gtaccctgtg 120

gatgatcatc actttaaggt gatcctgcac tatggcacac tggtaatcga cggggttacg 180

ccgaacatga tcgactattt cggacggccg tatgaaggca tcgccgtgtt cgacggcaaa 240

aagatcactg taacagggac cctgtggaac ggcaacaaaa ttatcgacga gcgcctgatc 300

aaccccgacg gctccctgct gttccgagta accatcaacg gagtgaccgg ctggcggctg 360

tgcgaacgca ttctggcggg aggaggtggc tcaggtggag ggagctccgt ggccatcctc 420

tggcatgaga tgtggcatga aggcctggaa gaggcatctc gtttgtactt tggggaaagg 480

aacgtgaaag gcatgtttga ggtgctggag cccttgcatg ctatgatgga acggggcccc 540

cagactctga aggaaacatc ctttaatcag gcctatggtc gagatttaat ggaggcccaa 600

gagtggtgca ggaagtacat gaaatcaggg aatgtcaagg acctcaccca agcctgggac 660

ctctattatc atgtgttccg acgaatctca 690

<210> 344
<211> 230
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 344
Met Val Leu Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile
1 5 10 15

Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln Met Gly Gln Ile Glu Lys
20 25 30

Ile Phe Lys Val Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile
35 40 45

Leu His Tyr Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile
50 55 60

Asp Tyr Phe Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys
65 70 75 80

Lys Ile Thr Val Thr Gly Thr Leu Trp Asn Gly Asn Lys Ile Ile Asp
85 90 95

Glu Arg Leu Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile
100 105 110

Asn Gly Val Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala Gly Gly
115 120 125

Gly Gly Ser Gly Gly Gly Ser Ser Val Ala Ile Leu Trp His Glu Met
130 135 140

Trp His Glu Gly Leu Glu Glu Ala Ser Arg Leu Tyr Phe Gly Glu Arg
145 150 155 160

Asn Val Lys Gly Met Phe Glu Val Leu Glu Pro Leu His Ala Met Met
165 170 175

Glu Arg Gly Pro Gln Thr Leu Lys Glu Thr Ser Phe Asn Gln Ala Tyr
180 185 190

Gly Arg Asp Leu Met Glu Ala Gln Glu Trp Cys Arg Lys Tyr Met Lys
195 200 205

Ser Gly Asn Val Lys Asp Leu Thr Gln Ala Trp Asp Leu Tyr Tyr His
210 215 220

Val Phe Arg Arg Ile Ser
225 230

<210> 345
<211> 492
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 345
atgggagtgc aggtggaaac catctcccca ggagacgggc gcaccttccc caagcgcggc 60

cagacctgcg tggtgcacta caccgggatg cttgaagatg gaaagaaatt tgattcctcc 120

cgggacagaa acaagccctt taagtttatg ctaggcaagc aggaggtgat ccgaggctgg 180

gaagaagggg ttgcccagat gagtgtgggt cagagagcca aactgactat atctccagat 240

tatgcctatg gtgccactgg gcacccaggc atcatcccac cacatgccac tctcgtcttc 300

gatgtggagc ttctaaaact ggaaggagga gggagctccg gtggaggcag cggtatggtc 360

ttcacactcg aagatttcgt tggggactgg cgacagacag ccggctacaa cctggaccaa 420

gtccttgaac agggaggtgt gtccagtttg tttcagaatc tcggggtgtc cgtaactccg 480

atccaaagga tt 492

<210> 346
<211> 164
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

polypeptide

<400> 346
Met Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe
1 5 10 15

Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu
20 25 30

Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys
35 40 45

Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val
50 55 60

Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp
65 70 75 80

Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala
85 90 95

Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu Gly Gly Gly Ser
100 105 110

Ser Gly Gly Gly Ser Gly Met Val Phe Thr Leu Glu Asp Phe Val Gly
115 120 125

Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln
130 135 140

Gly Gly Val Ser Ser Leu Phe Gln Asn Leu Gly Val Ser Val Thr Pro
145 150 155 160

Ile Gln Arg Ile

<210> 347
<211> 687
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 347
atgctgagcg gtgaaaatgg gctgaagatc gacatccatg tcatcatccc gtatgaaggt 60

ctgagcggcg accaaatggg ccagatcgaa aaaatttta aggtggtgta ccctgtggat 120

gatcatcact ttaaggtgat cctgcactat ggcacactgg taatcgacgg ggttacgccg 180

aacatgatcg actatttcgg acggccgtat gaaggcatcg ccgtgttcga cggcaaaaag 240

atcactgtaa cagggaccct gtggaacggc aacaaaatta tcgacgagcg cctgatcaac 300

cccgacggct ccctgctgtt ccgagtaacc atcaacggag tgaccggctg gcggctgtgc 360

gaacgcattc tggcgggagg aggtggctca ggtggaggga gctccgtggc catcctctgg 420

catgagatgt ggcatgaagg cctggaagag gcatctcgtt tgtactttgg ggaaaggaac 480

gtgaaaggca tgtttgaggt gctggagccc ttgcatgcta tgatggaacg gggcccccag 540

actctgaagg aaacatcctt taatcaggcc tatggtcgag atttaatgga ggcccaagag 600

tggtgcagga agtacatgaa atcagggaat gtcaaggacc tcacccaagc ctgggacctc 660

tattatcatg tgttccgacg aatctca 687

<210> 348
<211> 229
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 348
Met Leu Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile
1 5 10 15

Pro Tyr Glu Gly Leu Ser Gly Asp Gln Met Gly Gln Ile Glu Lys Ile
20 25 30

Phe Lys Val Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu
35 40 45

His Tyr Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp
50 55 60

Tyr Phe Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys
65 70 75 80

Ile Thr Val Thr Gly Thr Leu Trp Asn Gly Asn Lys Ile Ile Asp Glu
85 90 95

Arg Leu Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn
100 105 110

Gly Val Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Ser Ser Val Ala Ile Leu Trp His Glu Met Trp
130 135 140

His Glu Gly Leu Glu Glu Ala Ser Arg Leu Tyr Phe Gly Glu Arg Asn
145 150 155 160

Val Lys Gly Met Phe Glu Val Leu Glu Pro Leu His Ala Met Met Glu
165 170 175

Arg Gly Pro Gln Thr Leu Lys Glu Thr Ser Phe Asn Gln Ala Tyr Gly
180 185 190

Arg Asp Leu Met Glu Ala Gln Glu Trp Cys Arg Lys Tyr Met Lys Ser
195 200 205

Gly Asn Val Lys Asp Leu Thr Gln Ala Trp Asp Leu Tyr Tyr His Val
210 215 220

Phe Arg Arg Ile Ser
225

<210> 349
<211> 495
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 349
atgggagtgc aggtggaaac catctcccca ggagacgggc gcaccttccc caagcgcggc 60

cagacctgcg tggtgcacta caccgggatg cttgaagatg gaaagaaatt tgattcctcc 120

cgggacagaa acaagccctt taagtttatg ctaggcaagc aggaggtgat ccgaggctgg 180

gaagaagggg ttgcccagat gagtgtgggt cagagagcca aactgactat atctccagat 240

tatgcctatg gtgccactgg gcacccaggc atcatcccac cacatgccac tctcgtcttc 300

gatgtggagc ttctaaaact ggaaggagga gggagctccg gtggaggcag cggtatggtc 360

ttcacactcg aagatttcgt tggggactgg cgacagacag ccggctacaa cctggaccaa 420

gtccttgaac agggaggtgt gtccagtttg tttcagaatc tcggggtgtc cgtaactccg 480

atccaaagga ttgtc 495

<210> 350
<211> 165
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 350
Met Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe
1 5 10 15

Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu
20 25 30

Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys
35 40 45

Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val

50 55 60

Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp
65 70 75 80

Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala
85 90 95

Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu Gly Gly Gly Ser
100 105 110

Ser Gly Gly Gly Ser Gly Met Val Phe Thr Leu Glu Asp Phe Val Gly
115 120 125

Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln
130 135 140

Gly Gly Val Ser Ser Leu Phe Gln Asn Leu Gly Val Ser Val Thr Pro
145 150 155 160

Ile Gln Arg Ile Val
165

<210> 351
<211> 525
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 351
atggacgggg ttacgccgaa catgatcgac tatttcggac ggccgtatga aggcatcgcc 60

gtgttcgacg gcaaaaagat cactgtaaca gggaccctgt ggaacggcaa caaaattatc 120

gacgagcgcc tgatcaaccc cgacggctcc ctgctgttcc gagtaaccat caacggagtg 180

accggctggc ggctgtgcga acgcattctg gcgggaggag gtggctcagg tggagggagc 240

tccgtggcca tcctctggca tgagatgtgg catgaaggcc tggaagaggc atctcgtttg 300

tactttgggg aaaggaacgt gaaaggcatg tttgaggtgc tggagccctt gcatgctatg 360

atggaacggg gcccccagac tctgaaggaa acatccttta atcaggccta tggtcgagat 420

ttaatggagg cccaagagtg gtgcaggaag tacatgaaat cagggaatgt caaggacctc 480

acccaagcct gggacctcta ttatcatgtg ttccgacgaa tctca 525

<210> 352
<211> 175
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 352
Met Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr
1 5 10 15

Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr
20 25 30

Leu Trp Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp
35 40 45

Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg
50 55 60

Leu Cys Glu Arg Ile Leu Ala Gly Gly Gly Gly Ser Gly Gly Gly Ser
65 70 75 80

Ser Val Ala Ile Leu Trp His Glu Met Trp His Glu Gly Leu Glu Glu
85 90 95

Ala Ser Arg Leu Tyr Phe Gly Glu Arg Asn Val Lys Gly Met Phe Glu
100 105 110

Val Leu Glu Pro Leu His Ala Met Met Glu Arg Gly Pro Gln Thr Leu
115 120 125

Lys Glu Thr Ser Phe Asn Gln Ala Tyr Gly Arg Asp Leu Met Glu Ala
130 135 140

Gln Glu Trp Cys Arg Lys Tyr Met Lys Ser Gly Asn Val Lys Asp Leu
145 150 155 160

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

<210> 353
<211> 657
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 353
atgggagtgc aggtggaaac catctcccca ggagacgggc gcaccttccc caagcgcggc 60

cagacctgcg tggtgcacta caccgggatg cttgaagatg gaaagaaatt tgattcctcc 120

cgggacagaa acaagccctt taagtttatg ctaggcaagc aggaggtgat ccgaggctgg 180

gaagaagggg ttgcccagat gagtgtgggt cagagagcca aactgactat atctccagat 240

tatgcctatg gtgccactgg gcacccaggc atcatcccac cacatgccac tctcgtcttc 300

gatgtggagc ttctaaaact ggaaggagga gggagctccg gtggaggcag cggtatggtc 360

ttcacactcg aagatttcgt tggggactgg cgacagacag ccggctacaa cctggaccaa 420

gtccttgaac agggaggtgt gtccagtttg tttcagaatc tcggggtgtc cgtaactccg 480

atccaaagga ttgtcctgag cggtgaaaat gggctgaaga tcgacatcca tgtcatcatc 540

ccgtatgaag gtctgagcgg cgaccaaatg ggccagatcg aaaaaatttt taaggtggtg 600

taccctgtgg atgatcatca ctttaaggtg atcctgcact atggcacact ggtaatc 657

<210> 354
<211> 219
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 354

Met Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe
1 5 10 15

Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu
20 25 30

Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys
35 40 45

Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val
50 55 60

Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp
65 70 75 80

Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala
85 90 95

Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu Gly Gly Gly Ser
100 105 110

Ser Gly Gly Gly Ser Gly Met Val Phe Thr Leu Glu Asp Phe Val Gly
115 120 125

Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln
130 135 140

Gly Gly Val Ser Ser Leu Phe Gln Asn Leu Gly Val Ser Val Thr Pro
145 150 155 160

Ile Gln Arg Ile Val Leu Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile
165 170 175

His Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln Met Gly Gln
180 185 190

Ile Glu Lys Ile Phe Lys Val Val Tyr Pro Val Asp Asp His His Phe
195 200 205

Lys Val Ile Leu His Tyr Gly Thr Leu Val Ile
210 215

<210> 355
<211> 522
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 355
atgggggtta cgccgaacat gatcgactat ttcggacggc cgtatgaagg catcgccgtg 60

ttcgacggca aaaagatcac tgtaacaggg accctgtgga acggcaacaa aattatcgac 120

gagcgcctga tcaaccccga cggctccctg ctgttccgag taaccatcaa cggagtgacc 180

ggctggcggc tgtgcgaacg cattctggcg ggaggaggtg gctcaggtgg agggagctcc 240

gtggccatcc tctggcatga gatgtggcat gaaggcctgg aagaggcatc tcgtttgtac 300

tttggggaaa ggaacgtgaa aggcatgttt gaggtgctgg agcccttgca tgctatgatg 360

gaacggggcc cccagactct gaaggaaaca tcctttaatc aggcctatgg tcgagattta 420

atggaggccc aagagtggtg caggaagtac atgaaatcag ggaatgtcaa ggacctcacc 480

caagcctggg acctctatta tcatgtgttc cgacgaatct ca 522

<210> 356
<211> 174
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 356
Met Gly Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu
1 5 10 15

Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr Leu
20 25 30

Trp Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly
35 40 45

Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg Leu
50 55 60

Cys Glu Arg Ile Leu Ala Gly Gly Gly Gly Ser Gly Gly Gly Ser Ser
65 70 75 80

Val Ala Ile Leu Trp His Glu Met Trp His Glu Gly Leu Glu Glu Ala
85 90 95

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

Leu Glu Pro Leu His Ala Met Met Glu Arg Gly Pro Gln Thr Leu Lys
115 120 125

Glu Thr Ser Phe Asn Gln Ala Tyr Gly Arg Asp Leu Met Glu Ala Gln
130 135 140

Glu Trp Cys Arg Lys Tyr Met Lys Ser Gly Asn Val Lys Asp Leu Thr
145 150 155 160

Gln Ala Trp Asp Leu Tyr Tyr His Val Phe Arg Arg Ile Ser
165 170

<210> 357
<211> 660
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 357
atgggagtgc aggtggaaac catctcccca ggagacgggc gcaccttccc caagcgcggc 60

cagacctgcg tggtgcacta caccgggatg cttgaagatg gaaagaaatt tgattcctcc 120

cgggacagaa acaagccctt taagtttatg ctaggcaagc aggaggtgat ccgaggctgg 180

gaagaagggg ttgcccagat gagtgtgggt cagagagcca aactgactat atctccagat 240

tatgcctatg gtgccactgg gcacccaggc atcatcccac cacatgccac tctcgtcttc 300

gatgtggagc ttctaaaact ggaaggagga gggagctccg gtggaggcag cggtatggtc 360

ttcacactcg aagatttcgt tggggactgg cgacagacag ccggctacaa cctggaccaa 420

gtccttgaac agggaggtgt gtccagtttg tttcagaatc tcggggtgtc cgtaactccg 480

atccaaagga ttgtcctgag cggtgaaaat gggctgaaga tcgacatcca tgtcatcatc 540

ccgtatgaag gtctgagcgg cgaccaaatg ggccagatcg aaaaaatttt taaggtggtg 600

taccctgtgg atgatcatca ctttaaggtg atcctgcact atggcacact ggtaatcgac 660

<210> 358
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 358
Met Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe

1 5 10 15

Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu
20 25 30

Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys
35 40 45

Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val
50 55 60

Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp
65 70 75 80

Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala
85 90 95

Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu Gly Gly Gly Ser
100 105 110

Ser Gly Gly Gly Ser Gly Met Val Phe Thr Leu Glu Asp Phe Val Gly
115 120 125

Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln
130 135 140

Gly Gly Val Ser Ser Leu Phe Gln Asn Leu Gly Val Ser Val Thr Pro
145 150 155 160

Ile Gln Arg Ile Val Leu Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile
165 170 175

His Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln Met Gly Gln
180 185 190

Ile Glu Lys Ile Phe Lys Val Val Tyr Pro Val Asp Asp His His Phe
195 200 205

Lys Val Ile Leu His Tyr Gly Thr Leu Val Ile Asp
210 215 220

<210> 359
<211> 519
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 359
atggttacgc cgaacatgat cgactatttc ggacggccgt atgaaggcat cgccgtgttc 60

gacggcaaaa agatcactgt aacagggacc ctgtggaacg gcaacaaaat tatcgacgag 120

cgcctgatca accccgacgg ctccctgctg ttccgagtaa ccatcaacgg agtgaccggc 180

tggcggctgt gcgaacgcat tctggcggga ggaggtggct caggtggagg gagctccgtg 240

gccatcctct ggcatgagat gtggcatgaa ggcctggaag aggcatctcg tttgtacttt 300

ggggaaagga acgtgaaagg catgtttgag gtgctggagc ccttgcatgc tatgatggaa 360

cggggccccc agactctgaa ggaaacatcc tttaatcagg cctatggtcg agatttaatg 420

gaggcccaag agtggtgcag gaagtacatg aaatcaggga atgtcaagga cctcacccaa 480

gcctgggacc tctattatca tgtgttccga cgaatctca 519

<210> 360
<211> 173
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 360
Met Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly
1 5 10 15

Ile Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr Leu Trp
20 25 30

Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly Ser
35 40 45

Leu Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg Leu Cys
50 55 60

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

Ala Ile Leu Trp His Glu Met Trp His Glu Gly Leu Glu Glu Ala Ser
85 90 95

Arg Leu Tyr Phe Gly Glu Arg Asn Val Lys Gly Met Phe Glu Val Leu
100 105 110

Glu Pro Leu His Ala Met Met Glu Arg Gly Pro Gln Thr Leu Lys Glu
115 120 125

Thr Ser Phe Asn Gln Ala Tyr Gly Arg Asp Leu Met Glu Ala Gln Glu
130 135 140

Trp Cys Arg Lys Tyr Met Lys Ser Gly Asn Val Lys Asp Leu Thr Gln
145 150 155 160

Ala Trp Asp Leu Tyr Tyr His Val Phe Arg Arg Ile Ser
165 170

<210> 361
<211> 663
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 361
atgggagtgc aggtggaaac catctcccca ggagacgggc gcaccttccc caagcgcggc 60

cagacctgcg tggtgcacta caccgggatg cttgaagatg gaaagaaatt tgattcctcc 120

cgggacagaa acaagccctt taagtttatg ctaggcaagc aggaggtgat ccgaggctgg 180

gaagaagggg ttgcccagat gagtgtgggt cagagagcca aactgactat atctccagat 240

tatgcctatg gtgccactgg gcacccaggc atcatcccac cacatgccac tctcgtcttc 300

gatgtggagc ttctaaaact ggaaggagga gggagctccg gtggaggcag cggtatggtc 360

ttcacactcg aagatttcgt tggggactgg cgacagacag ccggctacaa cctggaccaa 420

gtccttgaac agggaggtgt gtccagtttg tttcagaatc tcggggtgtc cgtaactccg 480

atccaaagga ttgtcctgag cggtgaaaat gggctgaaga tcgacatcca tgtcatcatc 540

ccgtatgaag gtctgagcgg cgaccaaatg ggccagatcg aaaaaatttt taaggtggtg 600

taccctgtgg atgatcatca ctttaaggtg atcctgcact atggcacact ggtaatcgac 660

ggg 663

<210> 362
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 362
Met Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe
1 5 10 15

Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu
20 25 30

Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys
35 40 45

Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val
50 55 60

Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp
65 70 75 80

Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala

85 90 95

Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu Gly Gly Gly Ser
100 105 110

Ser Gly Gly Gly Ser Gly Met Val Phe Thr Leu Glu Asp Phe Val Gly
115 120 125

Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln
130 135 140

Gly Gly Val Ser Ser Leu Phe Gln Asn Leu Gly Val Ser Val Thr Pro
145 150 155 160

Ile Gln Arg Ile Val Leu Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile
165 170 175

His Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln Met Gly Gln
180 185 190

Ile Glu Lys Ile Phe Lys Val Val Tyr Pro Val Asp Asp His His Phe
195 200 205

Lys Val Ile Leu His Tyr Gly Thr Leu Val Ile Asp Gly
210 215 220

<210> 363
<211> 396
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 363
atgatcaacc ccgacggctc cctgctgttc cgagtaacca tcaacggagt gaccggctgg 60

cggctgtgcg aacgcattct ggcgggagga ggtggctcag gtggagggag ctccgtggcc 120

atcctctggc atgagatgtg gcatgaaggc ctggaagagg catctcgttt gtactttggg 180

gaaaggaacg tgaaaggcat gtttgaggtg ctggagccct tgcatgctat gatggaacgg 240

ggcccccaga ctctgaagga aacatccttt aatcaggcct atggtcgaga tttaatggag 300

gcccaagagt ggtgcaggaa gtacatgaaa tcagggaatg tcaaggacct cacccaagcc 360

tgggacctct attatcatgt gttccgacga atctca 396

<210> 364
<211> 132
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 364
Met Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly
1 5 10 15

Val Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala Gly Gly Gly Gly
20 25 30

Ser Gly Gly Gly Ser Ser Val Ala Ile Leu Trp His Glu Met Trp His
35 40 45

Glu Gly Leu Glu Glu Ala Ser Arg Leu Tyr Phe Gly Glu Arg Asn Val
50 55 60

Lys Gly Met Phe Glu Val Leu Glu Pro Leu His Ala Met Met Glu Arg
65 70 75 80

Gly Pro Gln Thr Leu Lys Glu Thr Ser Phe Asn Gln Ala Tyr Gly Arg
85 90 95

Asp Leu Met Glu Ala Gln Glu Trp Cys Arg Lys Tyr Met Lys Ser Gly
100 105 110

Asn Val Lys Asp Leu Thr Gln Ala Trp Asp Leu Tyr Tyr His Val Phe
115 120 125

Arg Arg Ile Ser
130

<210> 365
<211> 786
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 365
atgggagtgc aggtggaaac catctcccca ggagacgggc gcaccttccc caagcgcggc 60

cagacctgcg tggtgcacta caccgggatg cttgaagatg gaaagaaatt tgattcctcc 120

cgggacagaa acaagccctt taagtttatg ctaggcaagc aggaggtgat ccgaggctgg 180

gaagaagggg ttgcccagat gagtgtgggt cagagagcca aactgactat atctccagat 240

tatgcctatg gtgccactgg gcacccaggc atcatcccac cacatgccac tctcgtcttc 300

gatgtggagc ttctaaaact ggaaggagga gggagctccg gtggaggcag cggtatggtc 360

ttcacactcg aagatttcgt tggggactgg cgacagacag ccggctacaa cctggaccaa 420

gtccttgaac agggaggtgt gtccagtttg tttcagaatc tcggggtgtc cgtaactccg 480

atccaaagga ttgtcctgag cggtgaaaat gggctgaaga tcgacatcca tgtcatcatc 540

ccgtatgaag gtctgagcgg cgaccaaatg ggccagatcg aaaaaatttt taaggtggtg 600

taccctgtgg atgatcatca ctttaaggtg atcctgcact atggcacact ggtaatcgac 660

ggggttacgc cgaacatgat cgactatttc ggacggccgt atgaaggcat cgccgtgttc 720

gacggcaaaa agatcactgt aacagggacc ctgtggaacg gcaacaaaat tatcgacgag 780

cgcctg 786

<210> 366
<211> 262
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 366
Met Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe
1 5 10 15

Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu
20 25 30

Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys
35 40 45

Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val
50 55 60

Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp
65 70 75 80

Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala
85 90 95

Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu Gly Gly Gly Ser
100 105 110

Ser Gly Gly Gly Ser Gly Met Val Phe Thr Leu Glu Asp Phe Val Gly
115 120 125

Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln
130 135 140

Gly Gly Val Ser Ser Leu Phe Gln Asn Leu Gly Val Ser Val Thr Pro
145 150 155 160

Ile Gln Arg Ile Val Leu Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile
165 170 175

His Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln Met Gly Gln
180 185 190

Ile Glu Lys Ile Phe Lys Val Val Tyr Pro Val Asp Asp His His Phe

195 200 205

Lys Val Ile Leu His Tyr Gly Thr Leu Val Ile Asp Gly Val Thr Pro
210 215 220

Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe
225 230 235 240

Asp Gly Lys Lys Ile Thr Val Thr Gly Thr Leu Trp Asn Gly Asn Lys
245 250 255

Ile Ile Asp Glu Arg Leu
260

<210> 367
<211> 390
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 367
atgcccgacg gctccctgct gttccgagta accatcaacg gagtgaccgg ctggcggctg 60

tgcgaacgca ttctggcggg aggaggtggc tcaggtggag ggagctccgt ggccatcctc 120

tggcatgaga tgtggcatga aggcctggaa gaggcatctc gtttgtactt tggggaaagg 180

aacgtgaaag gcatgtttga ggtgctggag cccttgcatg ctatgatgga acggggcccc 240

cagactctga aggaaacatc ctttaatcag gcctatggtc gagatttaat ggaggcccaa 300

gagtggtgca ggaagtacat gaaatcaggg aatgtcaagg acctcaccca agcctgggac 360

ctctattatc atgtgttccg acgaatctca 390

<210> 368
<211> 130
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 368
Met Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val Thr
1 5 10 15

Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala Gly Gly Gly Gly Ser Gly
20 25 30

Gly Gly Ser Ser Val Ala Ile Leu Trp His Glu Met Trp His Glu Gly
35 40 45

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

Met Phe Glu Val Leu Glu Pro Leu His Ala Met Met Glu Arg Gly Pro
65 70 75 80

Gln Thr Leu Lys Glu Thr Ser Phe Asn Gln Ala Tyr Gly Arg Asp Leu
85 90 95

Met Glu Ala Gln Glu Trp Cys Arg Lys Tyr Met Lys Ser Gly Asn Val
100 105 110

Lys Asp Leu Thr Gln Ala Trp Asp Leu Tyr Tyr His Val Phe Arg Arg
115 120 125

Ile Ser
130

<210> 369
<211> 792
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 369
atgggagtgc aggtggaaac catctcccca ggagacgggc gcaccttccc caagcgcggc 60

cagacctgcg tggtgcacta caccgggatg cttgaagatg gaaagaaatt tgattcctcc 120

cgggacagaa acaagccctt taagtttatg ctaggcaagc aggaggtgat ccgaggctgg 180

gaagaagggg ttgcccagat gagtgtgggt cagagagcca aactgactat atctccagat 240

tatgcctatg gtgccactgg gcacccaggc atcatcccac cacatgccac tctcgtcttc 300

gatgtggagc ttctaaaact ggaaggagga gggagctccg gtggaggcag cggtatggtc 360

ttcacactcg aagatttcgt tggggactgg cgacagacag ccggctacaa cctggaccaa 420

gtccttgaac agggaggtgt gtccagtttg tttcagaatc tcggggtgtc cgtaactccg 480

atccaaagga ttgtcctgag cggtgaaaat gggctgaaga tcgacatcca tgtcatcatc 540

ccgtatgaag gtctgagcgg cgaccaaatg ggccagatcg aaaaaatttt taaggtggtg 600

taccctgtgg atgatcatca ctttaaggtg atcctgcact atggcacact ggtaatcgac 660

ggggttacgc cgaacatgat cgactatttc ggacggccgt atgaaggcat cgccgtgttc 720

gacggcaaaa agatcactgt aacagggacc ctgtggaacg gcaacaaaat tatcgacgag 780

cgcctgatca ac 792

<210> 370
<211> 264
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

polypeptide

<400> 370

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Met Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe
1               5                  10                  15

Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu
            20                  25                  30

Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys
        35                  40                  45

Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val
    50                  55                  60

Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp
65                  70                  75                  80

Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala
                85                  90                  95

Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu Gly Gly Gly Ser
            100                 105                 110

Ser Gly Gly Gly Ser Gly Met Val Phe Thr Leu Glu Asp Phe Val Gly
        115                 120                 125

Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln
    130                 135                 140

Gly Gly Val Ser Ser Leu Phe Gln Asn Leu Gly Val Ser Val Thr Pro
145                 150                 155                 160

Ile Gln Arg Ile Val Leu Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile
                165                 170                 175

His Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln Met Gly Gln
            180                 185                 190

Ile Glu Lys Ile Phe Lys Val Val Tyr Pro Val Asp Asp His His Phe
        195                 200                 205

Lys Val Ile Leu His Tyr Gly Thr Leu Val Ile Asp Gly Val Thr Pro
    210                 215                 220

Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe
225                 230                 235                 240

Asp Gly Lys Lys Ile Thr Val Thr Gly Thr Leu Trp Asn Gly Asn Lys
                245                 250                 255

Ile Ile Asp Glu Arg Leu Ile Asn
```

260

<210> 371
<211> 384
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 371
atgggctccc tgctgttccg agtaaccatc aacggagtga ccggctggcg gctgtgcgaa 60

cgcattctgg cgggaggagg tggctcaggt ggagggagct ccgtggccat cctctggcat 120

gagatgtggc atgaaggcct ggaagaggca tctcgtttgt actttgggga aaggaacgtg 180

aaaggcatgt ttgaggtgct ggagcccttg catgctatga tggaacgggg cccccagact 240

ctgaaggaaa catcctttaa tcaggcctat ggtcgagatt taatggaggc ccaagagtgg 300

tgcaggaagt acatgaaatc agggaatgtc aaggacctca cccaagcctg ggacctctat 360

tatcatgtgt tccgacgaat ctca 384

<210> 372
<211> 128
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 372
Met Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp
1 5 10 15

Arg Leu Cys Glu Arg Ile Leu Ala Gly Gly Gly Gly Ser Gly Gly Gly
20 25 30

Ser Ser Val Ala Ile Leu Trp His Glu Met Trp His Glu Gly Leu Glu
35 40 45

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

Glu Val Leu Glu Pro Leu His Ala Met Met Glu Arg Gly Pro Gln Thr
65 70 75 80

Leu Lys Glu Thr Ser Phe Asn Gln Ala Tyr Gly Arg Asp Leu Met Glu
85 90 95

Ala Gln Glu Trp Cys Arg Lys Tyr Met Lys Ser Gly Asn Val Lys Asp
100 105 110

Leu Thr Gln Ala Trp Asp Leu Tyr Tyr His Val Phe Arg Arg Ile Ser
115 120 125

<210> 373
<211> 798
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 373
atgggagtgc aggtggaaac catctcccca ggagacgggc gcaccttccc caagcgcggc 60

cagacctgcg tggtgcacta caccgggatg cttgaagatg gaaagaaatt tgattcctcc 120

cgggacagaa acaagcactt taagtttatg ctaggcaagc aggaggtgat ccgaggctgg 180

gaagaagggg ttgcccagat gagtgtgggt cagagagcca aactgactat atctccagat 240

tatgcctatg gtgccactgg gcacccaggc atcatcccac cacatgccac tctcgtcttc 300

gatgtggagc ttctaaaact ggaaggagga gggagctccg gtggaggcag cggtatggtc 360

ttcacactcg aagatttcgt tggggactgg cgacagacag ccggctacaa cctggaccaa 420

gtccttgaac agggaggtgt gtccagtttg tttcagaatc tcggggtgtc cgtaactccg 480

atccaaagga ttgtcctgag cggtgaaaat gggctgaaga tcgacatcca tgtcatcatc 540

ccgtatgaag gtctgagcgg cgaccaaatg ggccagatcg aaaaaatttt taaggtggtg 600

taccctgtgg atgatcatca ctttaaggtg atcctgcact atggcacact ggtaatcgac 660

ggggttacgc cgaacatgat cgactatttc ggacggccgt atgaaggcat cgccgtgttc 720

gacggcaaaa agatcactgt aacagggacc ctgtggaacg gcaacaaaat tatcgacgag 780

cgcctgatca accccgac 798

<210> 374
<211> 266
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 374
Met Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe
1 5 10 15

Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu
20 25 30

Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn Lys His Phe Lys
35 40 45

Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val
50 55 60

Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp

65 70 75 80

Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala
85 90 95

Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu Gly Gly Gly Ser
100 105 110

Ser Gly Gly Gly Ser Gly Met Val Phe Thr Leu Glu Asp Phe Val Gly
115 120 125

Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln
130 135 140

Gly Gly Val Ser Ser Leu Phe Gln Asn Leu Gly Val Ser Val Thr Pro
145 150 155 160

Ile Gln Arg Ile Val Leu Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile
165 170 175

His Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln Met Gly Gln
180 185 190

Ile Glu Lys Ile Phe Lys Val Val Tyr Pro Val Asp Asp His His Phe
195 200 205

Lys Val Ile Leu His Tyr Gly Thr Leu Val Ile Asp Gly Val Thr Pro
210 215 220

Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe
225 230 235 240

Asp Gly Lys Lys Ile Thr Val Thr Gly Thr Leu Trp Asn Gly Asn Lys
245 250 255

Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp
260 265

<210> 375
<211> 381
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 375
atgtccctgc tgttccgagt aaccatcaac ggagtgaccg gctggcggct gtgcgaacgc 60

attctggcgg gaggaggtgg ctcaggtgga gggagctccg tggccatcct ctggcatgag 120

atgtggcatg aaggcctgga agaggcatct cgtttgtact ttggggaaag gaacgtgaaa 180

ggcatgtttg aggtgctgga gcccttgcat gctatgatgg aacggggccc ccagactctg 240

aaggaaacat cctttaatca ggcctatggt cgagatttaa tggaggccca agagtggtgc 300

aggaagtaca tgaaatcagg gaatgtcaag gacctcaccc aagcctggga cctctattat 360

catgtgttcc gacgaatctc a 381

<210> 376
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 376
Met Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg
1 5 10 15

Leu Cys Glu Arg Ile Leu Ala Gly Gly Gly Gly Ser Gly Gly Gly Ser
20 25 30

Ser Val Ala Ile Leu Trp His Glu Met Trp His Glu Gly Leu Glu Glu
35 40 45

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

Val Leu Glu Pro Leu His Ala Met Met Glu Arg Gly Pro Gln Thr Leu
65 70 75 80

Lys Glu Thr Ser Phe Asn Gln Ala Tyr Gly Arg Asp Leu Met Glu Ala
85 90 95

Gln Glu Trp Cys Arg Lys Tyr Met Lys Ser Gly Asn Val Lys Asp Leu
100 105 110

Thr Gln Ala Trp Asp Leu Tyr Tyr His Val Phe Arg Arg Ile Ser
115 120 125

<210> 377
<211> 801
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 377
atgggagtgc aggtggaaac catctcccca ggagacgggc gcaccttccc caagcgcggc 60

cagacctgcg tggtgcacta caccgggatg cttgaagatg gaaagaaatt tgattcctcc 120

cgggacagaa acaagccctt taagtttatg ctaggcaagc aggaggtgat ccgaggctgg 180

gaagaagggg ttgcccagat gagtgtgggt cagagagcca aactgactat atctccagat 240

tatgcctatg gtgccactgg gcacccaggc atcatcccac cacatgccac tctcgtcttc 300

gatgtggagc ttctaaaact ggaaggagga gggagctccg gtggaggcag cggtatggtc 360

ttcacactcg aagatttcgt tggggactgg cgacagacag ccggctacaa cctggaccaa 420

gtccttgaac agggaggtgt gtccagtttg tttcagaatc tcggggtgtc cgtaactccg 480

atccaaagga ttgtcctgag cggtgaaaat gggctgaaga tcgacatcca tgtcatcatc 540

ccgtatgaag gtctgagcgg cgaccaaatg ggccagatcg aaaaaatttt taaggtggtg 600

taccctgtgg atgatcatca ctttaaggtg atcctgcact atggcacact ggtaatcgac 660

ggggttacgc cgaacatgat cgactatttc ggacggccgt atgaaggcat cgccgtgttc 720

gacggcaaaa agatcactgt aacagggacc ctgtggaacg gcaacaaaat tatcgacgag 780

cgcctgatca accccgacgg c 801

<210> 378
<211> 267
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 378

Met Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe
1 5 10 15

Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu
20 25 30

Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys
35 40 45

Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val
50 55 60

Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp
65 70 75 80

Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala
85 90 95

Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu Gly Gly Gly Ser
100 105 110

Ser Gly Gly Gly Ser Gly Met Val Phe Thr Leu Glu Asp Phe Val Gly
115 120 125

Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln
130 135 140

Gly Gly Val Ser Ser Leu Phe Gln Asn Leu Gly Val Ser Val Thr Pro

145 150 155 160

Ile Gln Arg Ile Val Leu Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile
165 170 175

His Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln Met Gly Gln
180 185 190

Ile Glu Lys Ile Phe Lys Val Val Tyr Pro Val Asp Asp His His Phe
195 200 205

Lys Val Ile Leu His Tyr Gly Thr Leu Val Ile Asp Gly Val Thr Pro
210 215 220

Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe
225 230 235 240

Asp Gly Lys Lys Ile Thr Val Thr Gly Thr Leu Trp Asn Gly Asn Lys
245 250 255

Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly
260 265

<210> 379
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 379
atgaacggag tgaccggctg gcggctgtgc gaacgcattc tggcgggagg aggtggctca 60

ggtggaggga gctccgtggc catcctctgg catgagatgt ggcatgaagg cctggaagag 120

gcatctcgtt tgtactttgg ggaaaggaac gtgaaaggca tgtttgaggt gctggagccc 180

ttgcatgcta tgatggaacg gggcccccag actctgaagg aaacatcctt taatcaggcc 240

tatggtcgag atttaatgga ggcccaagag tggtgcagga agtacatgaa atcagggaat 300

gtcaaggacc tcacccaagc ctgggacctc tattatcatg tgttccgacg aatctca 357

<210> 380
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 380
Met Asn Gly Val Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala Gly
1 5 10 15

Gly Gly Gly Ser Gly Gly Gly Ser Ser Val Ala Ile Leu Trp His Glu
20 25 30

Met Trp His Glu Gly Leu Glu Glu Ala Ser Arg Leu Tyr Phe Gly Glu
35 40 45

Arg Asn Val Lys Gly Met Phe Glu Val Leu Glu Pro Leu His Ala Met
50 55 60

Met Glu Arg Gly Pro Gln Thr Leu Lys Glu Thr Ser Phe Asn Gln Ala
65 70 75 80

Tyr Gly Arg Asp Leu Met Glu Ala Gln Glu Trp Cys Arg Lys Tyr Met
85 90 95

Lys Ser Gly Asn Val Lys Asp Leu Thr Gln Ala Trp Asp Leu Tyr Tyr
100 105 110

His Val Phe Arg Arg Ile Ser
115

<210> 381
<211> 825
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 381
atgggagtgc aggtggaaac catctcccca ggagacgggc gcaccttccc caagcgcggc 60

cagacctgcg tggtgcacta caccgggatg cttgaagatg gaaagaaatt tgattcctcc 120

cgggacagaa acaagccctt taagtttatg ctaggcaagc aggaggtgat ccgaggctgg 180

gaagaagggg ttgcccagat gagtgtgggt cagagagcca aactgactat atctccagat 240

tatgcctatg gtgccactgg gcacccaggc atcatcccac cacatgccac tctcgtcttc 300

gatgtggagc ttctaaaact ggaaggagga gggagctccg gtggaggcag cggtatggtc 360

ttcacactcg aagatttcgt tggggactgg cgacagacag ccggctacaa cctggaccaa 420

gtccttgaac agggaggtgt gtccagtttg tttcagaatc tcggggtgtc cgtaactccg 480

atccaaagga ttgtcctgag cggtgaaaat gggctgaaga tcgacatcca tgtcatcatc 540

ccgtatgaag gtctgagcgg cgaccaaatg ggccagatcg aaaaaatttt taaggtggtg 600

taccctgtgg atgatcatca ctttaaggtg atcctgcact atggcacact ggtaatcgac 660

ggggttacgc cgaacatgat cgactatttc ggacggccgt atgaaggcat cgccgtgttc 720

gacggcaaaa agatcactgt aacagggacc ctgtggaacg gcaacaaaat tatcgacgag 780

cgcctgatca accccgacgg ctccctgctg ttccgagtaa ccatc 825

<210> 382

<211> 275
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 382

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Met Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe
1               5                  10                  15

Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu
            20                  25                  30

Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys
        35                  40                  45

Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val
    50                  55                  60

Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp
65                  70                  75                  80

Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala
                85                  90                  95

Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu Gly Gly Gly Ser
            100                 105                 110

Ser Gly Gly Gly Ser Gly Met Val Phe Thr Leu Glu Asp Phe Val Gly
        115                 120                 125

Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln
    130                 135                 140

Gly Gly Val Ser Ser Leu Phe Gln Asn Leu Gly Val Ser Val Thr Pro
145                 150                 155                 160

Ile Gln Arg Ile Val Leu Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile
                165                 170                 175

His Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln Met Gly Gln
            180                 185                 190

Ile Glu Lys Ile Phe Lys Val Val Tyr Pro Val Asp Asp His His Phe
        195                 200                 205

Lys Val Ile Leu His Tyr Gly Thr Leu Val Ile Asp Gly Val Thr Pro
    210                 215                 220

Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe
225                 230                 235                 240
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Asp Gly Lys Lys Ile Thr Val Thr Gly Thr Leu Trp Asn Gly Asn Lys
245 250 255

Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg
260 265 270

Val Thr Ile
275

<210> 383
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 383
atggtgaccg gctggcggct gtgcgaacgc attctggcgg gaggaggtgg ctcaggtgga 60

gggagctccg tggccatcct ctggcatgag atgtggcatg aaggcctgga agaggcatct 120

cgtttgtact ttggggaaag gaacgtgaaa ggcatgtttg aggtgctgga gcccttgcat 180

gctatgatgg aacggggccc ccagactctg aaggaaacat cctttaatca ggcctatggt 240

cgagatttaa tggaggccca agagtggtgc aggaagtaca tgaaatcagg gaatgtcaag 300

gacctcaccc aagcctggga cctctattat catgtgttcc gacgaatctc a 351

<210> 384
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 384
Met Val Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala Gly Gly Gly
1 5 10 15

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

His Glu Gly Leu Glu Glu Ala Ser Arg Leu Tyr Phe Gly Glu Arg Asn
35 40 45

Val Lys Gly Met Phe Glu Val Leu Glu Pro Leu His Ala Met Met Glu
50 55 60

Arg Gly Pro Gln Thr Leu Lys Glu Thr Ser Phe Asn Gln Ala Tyr Gly
65 70 75 80

Arg Asp Leu Met Glu Ala Gln Glu Trp Cys Arg Lys Tyr Met Lys Ser
85 90 95

Gly Asn Val Lys Asp Leu Thr Gln Ala Trp Asp Leu Tyr Tyr His Val
100 105 110

Phe Arg Arg Ile Ser
115

<210> 385
<211> 831
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 385
atgggagtgc aggtggaaac catctcccca ggagacgggc gcaccttccc caagcgcggc 60

cagacctgcg tggtgcacta caccgggatg cttgaagatg gaaagaaatt tgattcctcc 120

cgggacagaa acaagccctt taagtttatg ctaggcaagc aggaggtgat ccgaggctgg 180

gaagaagggg ttgcccagat gagtgtgggt cagagagcca aactgactat atctccagat 240

tatgcctatg gtgccactgg gcacccaggc atcatcccac cacatgccac tctcgtcttc 300

gatgtggagc ttctaaaact ggaaggagga gggagctccg gtggaggcag cggtatggtc 360

ttcacactcg aagatttcgt tggggactgg cgacagacag ccggctacaa cctggaccaa 420

gtccttgaac agggaggtgt gtccagtttg tttcagaatc tcggggtgtc cgtaactccg 480

atccaaagga ttgtcctgag cggtgaaaat gggctgaaga tcgacatcca tgtcatcatc 540

ccgtatgaag gtctgagcgg cgaccaaatg ggccagatcg aaaaaatttt taaggtggtg 600

taccctgtgg atgatcatca ctttaaggtg atcctgcact atggcacact ggtaatcgac 660

ggggttacgc cgaacatgat cgactatttc ggacggccgt atgaaggcat cgccgtgttc 720

gacggcaaaa agatcactgt aacagggacc ctgtggaacg gcaacaaaat tatcgacgag 780

cgcctgatca accccgacgg ctccctgctg ttccgagtaa ccatcaacgg a 831

<210> 386
<211> 277
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 386
Met Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe
1 5 10 15

Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu
20 25 30

Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys

35 40 45

Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val
50 55 60

Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp
65 70 75 80

Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala
85 90 95

Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu Gly Gly Gly Ser
100 105 110

Ser Gly Gly Gly Ser Gly Met Val Phe Thr Leu Glu Asp Phe Val Gly
115 120 125

Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln
130 135 140

Gly Gly Val Ser Ser Leu Phe Gln Asn Leu Gly Val Ser Val Thr Pro
145 150 155 160

Ile Gln Arg Ile Val Leu Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile
165 170 175

His Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln Met Gly Gln
180 185 190

Ile Glu Lys Ile Phe Lys Val Val Tyr Pro Val Asp Asp His His Phe
195 200 205

Lys Val Ile Leu His Tyr Gly Thr Leu Val Ile Asp Gly Val Thr Pro
210 215 220

Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe
225 230 235 240

Asp Gly Lys Lys Ile Thr Val Thr Gly Thr Leu Trp Asn Gly Asn Lys
245 250 255

Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg
260 265 270

Val Thr Ile Asn Gly
275

<210> 387
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 387
atgcgcattc tggcgggagg aggtggctca ggtggaggga gctccgtggc catcctctgg 60

catgagatgt ggcatgaagg cctggaagag gcatctcgtt tgtactttgg ggaaaggaac 120

gtgaaaggca tgtttgaggt gctggagccc ttgcatgcta tgatggaacg gggcccccag 180

actctgaagg aaacatcctt taatcaggcc tatggtcgag atttaatgga ggcccaagag 240

tggtgcagga agtacatgaa atcagggaat gtcaaggacc tcacccaagc ctgggacctc 300

tattatcatg tgttccgacg aatctca 327

<210> 388
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 388
Met Arg Ile Leu Ala Gly Gly Gly Gly Ser Gly Gly Gly Ser Ser Val
1 5 10 15

Ala Ile Leu Trp His Glu Met Trp His Glu Gly Leu Glu Glu Ala Ser
20 25 30

Arg Leu Tyr Phe Gly Glu Arg Asn Val Lys Gly Met Phe Glu Val Leu
35 40 45

Glu Pro Leu His Ala Met Met Glu Arg Gly Pro Gln Thr Leu Lys Glu
50 55 60

Thr Ser Phe Asn Gln Ala Tyr Gly Arg Asp Leu Met Glu Ala Gln Glu
65 70 75 80

Trp Cys Arg Lys Tyr Met Lys Ser Gly Asn Val Lys Asp Leu Thr Gln
85 90 95

Ala Trp Asp Leu Tyr Tyr His Val Phe Arg Arg Ile Ser
100 105

<210> 389
<211> 855
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 389
atgggagtgc aggtggaaac catctcccca ggagacgggc gcaccttccc caagcgcggc 60

cagacctgcg tggtgcacta caccgggatg cttgaagatg gaaagaaatt tgattcctcc 120

cgggacagaa acaagccctt taagtttatg ctaggcaagc aggaggtgat ccgaggctgg 180

gaagaagggg ttgcccagat gagtgtgggt cagagagcca aactgactat atctccagat 240

tatgcctatg gtgccactgg gcacccaggc atcatcccac cacatgccac tctcgtcttc 300

gatgtggagc ttctaaaact ggaaggagga gggagctccg gtggaggcag cggtatggtc 360

ttcacactcg aagatttcgt tggggactgg cgacagacag ccggctacaa cctggaccaa 420

gtccttgaac agggaggtgt gtccagtttg tttcagaatc tcggggtgtc cgtaactccg 480

atccaaagga ttgtcctgag cggtgaaaat gggctgaaga tcgacatcca tgtcatcatc 540

ccgtatgaag gtctgagcgg cgaccaaatg ggccagatcg aaaaaatttt taaggtggtg 600

taccctgtgg atgatcatca ctttaaggtg atcctgcact atggcacact ggtaatcgac 660

ggggttacgc cgaacatgat cgactatttc ggacggccgt atgaaggcat cgccgtgttc 720

gacggcaaaa agatcactgt aacagggacc ctgtggaacg gcaacaaaat tatcgacgag 780

cgcctgatca accccgacgg ctccctgctg ttccgagtaa ccatcaacgg agtgaccggc 840

tggcggctgt gcgaa 855

<210> 390
<211> 285
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 390
Met Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe
1 5 10 15

Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu
20 25 30

Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys
35 40 45

Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val
50 55 60

Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp
65 70 75 80

Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala
85 90 95

Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu Gly Gly Gly Ser
100 105 110

Ser Gly Gly Gly Ser Gly Met Val Phe Thr Leu Glu Asp Phe Val Gly

115 120 125

Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln
130 135 140

Gly Gly Val Ser Ser Leu Phe Gln Asn Leu Gly Val Ser Val Thr Pro
145 150 155 160

Ile Gln Arg Ile Val Leu Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile
165 170 175

His Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln Met Gly Gln
180 185 190

Ile Glu Lys Ile Phe Lys Val Val Tyr Pro Val Asp Asp His His Phe
195 200 205

Lys Val Ile Leu His Tyr Gly Thr Leu Val Ile Asp Gly Val Thr Pro
210 215 220

Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe
225 230 235 240

Asp Gly Lys Lys Ile Thr Val Thr Gly Thr Leu Trp Asn Gly Asn Lys
245 250 255

Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg
260 265 270

Val Thr Ile Asn Gly Val Thr Gly Trp Arg Leu Cys Glu
275 280 285

<210> 391
<211> 501
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 391
atgggagtgc aggtggaaac catctcccca ggagacgggc gcaccttccc caagcgcggc 60

cagacctgcg tggtgcacta caccgggatg cttgaagatg gaaagaaatt tgattcctcc 120

cgggacagaa acaagccctt taagtttatg ctaggcaagc aggaggtgat ccgaggctgg 180

gaagaagggg ttgcccagat gagtgtgggt cagagagcca aactgactat atctccagat 240

tatgcctatg gtgccactgg gcacccaggc atcatcccac cacatgccac tctcgtcttc 300

gatgtggagc ttctaaaact ggaaggagga gggagctccg gtggaggcag cggtatggtc 360

ttcacactcg aagatttcgt tggggactgg cgacagacag ccggctacaa cctggaccaa 420

gtccttgaac agggaggtgt gtccagtttg tttcagaatc tcggggtgtc cgtaactccg 480

atccaaagga ttgtcctgag c 501

<210> 392
<211> 167
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 392
Met Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe
1 5 10 15

Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu
20 25 30

Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys
35 40 45

Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val
50 55 60

Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp
65 70 75 80

Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala
85 90 95

Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu Gly Gly Gly Ser
100 105 110

Ser Gly Gly Gly Ser Gly Met Val Phe Thr Leu Glu Asp Phe Val Gly
115 120 125

Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln
130 135 140

Gly Gly Val Ser Ser Leu Phe Gln Asn Leu Gly Val Ser Val Thr Pro
145 150 155 160

Ile Gln Arg Ile Val Leu Ser
165

<210> 393
<211> 681
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 393

atgggtgaaa atgggctgaa gatcgacatc catgtcatca tcccgtatga aggtctgagc 60

ggcgaccaaa tgggccagat cgaaaaaatt tttaaggtgg tgtaccctgt ggatgatcat 120

cactttaagg tgatcctgca ctatggcaca ctggtaatcg acggggttac gccgaacatg 180

atcgactatt tcggacggcc gtatgaaggc atcgccgtgt tcgacggcaa aaagatcact 240

gtaacaggga ccctgtggaa cggcaacaaa attatcgacg agcgcctgat caaccccgac 300

ggctccctgc tgttccgagt aaccatcaac ggagtgaccg gctggcggct gtgcgaacgc 360

attctggcgg gaggaggtgg ctcaggtgga gggagctccg tggccatcct ctggcatgag 420

atgtggcatg aaggcctgga agaggcatct cgtttgtact ttggggaaag gaacgtgaaa 480

ggcatgtttg aggtgctgga gcccttgcat gctatgatgg aacggggccc ccagactctg 540

aaggaaacat cctttaatca ggcctatggt cgagatttaa tggaggccca agagtggtgc 600

aggaagtaca tgaaatcagg gaatgtcaag gacctcaccc aagcctggga cctctattat 660

catgtgttcc gacgaatctc a 681

<210> 394
<211> 227
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 394
Met Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr
1 5 10 15

Glu Gly Leu Ser Gly Asp Gln Met Gly Gln Ile Glu Lys Ile Phe Lys
20 25 30

Val Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu His Tyr
35 40 45

Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe
50 55 60

Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr
65 70 75 80

Val Thr Gly Thr Leu Trp Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu
85 90 95

Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val
100 105 110

Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Ser Ser Val Ala Ile Leu Trp His Glu Met Trp His Glu

130 135 140

Gly Leu Glu Glu Ala Ser Arg Leu Tyr Phe Gly Glu Arg Asn Val Lys
145 150 155 160

Gly Met Phe Glu Val Leu Glu Pro Leu His Ala Met Met Glu Arg Gly
165 170 175

Pro Gln Thr Leu Lys Glu Thr Ser Phe Asn Gln Ala Tyr Gly Arg Asp
180 185 190

Leu Met Glu Ala Gln Glu Trp Cys Arg Lys Tyr Met Lys Ser Gly Asn
195 200 205

Val Lys Asp Leu Thr Gln Ala Trp Asp Leu Tyr Tyr His Val Phe Arg
210 215 220

Arg Ile Ser
225

<210> 395
<211> 507
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 395
atgggagtgc aggtggaaac catctcccca ggagacgggc gcaccttccc caagcgcggc 60

cagacctgcg tggtgcacta caccgggatg cttgaagatg gaaagaaatt tgattcctcc 120

cgggacagaa acaagccctt taagtttatg ctaggcaagc aggaggtgat ccgaggctgg 180

gaagaagggg ttgcccagat gagtgtgggt cagagagcca aactgactat atctccagat 240

tatgcctatg gtgccactgg gcacccaggc atcatcccac cacatgccac tctcgtcttc 300

gatgtggagc ttctaaaact ggaaggagga gggagctccg gtggaggcag cggtatggtc 360

ttcacactcg aagatttcgt tggggactgg cgacagacag ccggctacaa cctggaccaa 420

gtccttgaac agggaggtgt gtccagtttg tttcagaatc tcggggtgtc cgtaactccg 480

atccaaagga ttgtcctgag cggtgaa 507

<210> 396
<211> 169
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 396
Met Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe
1 5 10 15

Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu
20 25 30

Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys
35 40 45

Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val
50 55 60

Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp
65 70 75 80

Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala
85 90 95

Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu Gly Gly Gly Ser
100 105 110

Ser Gly Gly Gly Ser Gly Met Val Phe Thr Leu Glu Asp Phe Val Gly
115 120 125

Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln
130 135 140

Gly Gly Val Ser Ser Leu Phe Gln Asn Leu Gly Val Ser Val Thr Pro
145 150 155 160

Ile Gln Arg Ile Val Leu Ser Gly Glu
165

<210> 397
<211> 675
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 397
atgaatgggc tgaagatcga catccatgtc atcatcccgt atgaaggtct gagcggcgac 60

caaatgggcc agatcgaaaa aatttttaag gtggtgtacc ctgtggatga tcatcacttt 120

aaggtgatcc tgcactatgg cacactggta atcgacgggg ttacgccgaa catgatcgac 180

tatttcggac ggccgtatga aggcatcgcc gtgttcgacg gcaaaaagat cactgtaaca 240

gggaccctgt ggaacggcaa caaaattatc gacgagcgcc tgatcaaccc cgacggctcc 300

ctgctgttcc gagtaaccat caacggagtg accggctggc ggctgtgcga acgcattctg 360

gcgggaggag gtggctcagg tggagggagc tccgtggcca tcctctggca tgagatgtgg 420

catgaaggcc tggaagaggc atctcgtttg tactttgggg aaaggaacgt gaaaggcatg 480

tttgaggtgc tggagccctt gcatgctatg atggaacggg gcccccagac tctgaaggaa 540

acatccttta atcaggccta tggtcgagat ttaatggagg cccaagagtg gtgcaggaag 600

tacatgaaat cagggaatgt caaggacctc acccaagcct gggacctcta ttatcatgtg 660

ttccgacgaa tctca 675

<210> 398
<211> 225
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 398

Met Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr Glu Gly
1 5 10 15

Leu Ser Gly Asp Gln Met Gly Gln Ile Glu Lys Ile Phe Lys Val Val
20 25 30

Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu His Tyr Gly Thr
35 40 45

Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg
50 55 60

Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr
65 70 75 80

Gly Thr Leu Trp Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn
85 90 95

Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly
100 105 110

Trp Arg Leu Cys Glu Arg Ile Leu Ala Gly Gly Gly Gly Ser Gly Gly
115 120 125

Gly Ser Ser Val Ala Ile Leu Trp His Glu Met Trp His Glu Gly Leu
130 135 140

Glu Glu Ala Ser Arg Leu Tyr Phe Gly Glu Arg Asn Val Lys Gly Met
145 150 155 160

Phe Glu Val Leu Glu Pro Leu His Ala Met Met Glu Arg Gly Pro Gln
165 170 175

Thr Leu Lys Glu Thr Ser Phe Asn Gln Ala Tyr Gly Arg Asp Leu Met
180 185 190

Glu Ala Gln Glu Trp Cys Arg Lys Tyr Met Lys Ser Gly Asn Val Lys

195 200 205

Asp Leu Thr Gln Ala Trp Asp Leu Tyr Tyr His Val Phe Arg Arg Ile
210 215 220

Ser
225

<210> 399
<211> 606
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 399
atgggagtgc aggtggaaac catctcccca ggagacgggc gcaccttccc caagcgcggc 60

cagacctgcg tggtgcacta caccgggatg cttgaagatg gaaagaaatt tgattcctcc 120

cgggacagaa acaagccctt taagtttatg ctaggcaagc aggaggtgat ccgaggctgg 180

gaagaagggg ttgcccagat gagtgtgggt cagagagcca aactgactat atctccagat 240

tatgcctatg gtgccactgg gcacccaggc atcatcccac cacatgccac tctcgtcttc 300

gatgtggagc ttctaaaact ggaaggagga gggagctccg gtggaggcag cggtatggtc 360

ttcacactcg aagatttcgt tggggactgg cgacagacag ccggctacaa cctggaccaa 420

gtccttgaac agggaggtgt gtccagtttg tttcagaatc tcggggtgtc cgtaactccg 480

atccaaagga ttgtcctgag cggtgaaaat gggctgaaga tcgacatcca tgtcatcatc 540

ccgtatgaag gtctgagcgg cgaccaaatg ggccagatcg aaaaaatttt taaggtggtg 600

taccct 606

<210> 400
<211> 202
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 400
Met Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe
1 5 10 15

Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu
20 25 30

Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys
35 40 45

Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val
50 55 60

Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp
65 70 75 80

Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala
85 90 95

Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu Gly Gly Gly Ser
100 105 110

Ser Gly Gly Gly Ser Gly Met Val Phe Thr Leu Glu Asp Phe Val Gly
115 120 125

Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln
130 135 140

Gly Gly Val Ser Ser Leu Phe Gln Asn Leu Gly Val Ser Val Thr Pro
145 150 155 160

Ile Gln Arg Ile Val Leu Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile
165 170 175

His Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln Met Gly Gln
180 185 190

Ile Glu Lys Ile Phe Lys Val Val Tyr Pro
195 200

<210> 401
<211> 576
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 401
atggtggatg atcatcactt taaggtgatc ctgcactatg gcacactggt aatcgacggg 60

gttacgccga acatgatcga ctatttcgga cggccgtatg aaggcatcgc cgtgttcgac 120

ggcaaaaaga tcactgtaac agggaccctg tggaacggca acaaaattat cgacgagcgc 180

ctgatcaacc ccgacggctc cctgctgttc cgagtaacca tcaacggagt gaccggctgg 240

cggctgtgcg aacgcattct ggcgggagga ggtggctcag gtggagggag ctccgtggcc 300

atcctctggc atgagatgtg gcatgaaggc ctggaagagg catctcgttt gtactttggg 360

gaaaggaacg tgaaaggcat gtttgaggtg ctggagccct tgcatgctat gatggaacgg 420

ggcccccaga ctctgaagga aacatccttt aatcaggcct atggtcgaga tttaatggag 480

gcccaagagt ggtgcaggaa gtacatgaaa tcagggaatg tcaaggacct cacccaagcc 540

tgggacctct attatcatgt gttccgacga atctca 576

<210> 402
<211> 192
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 402
Met Val Asp Asp His His Phe Lys Val Ile Leu His Tyr Gly Thr Leu
1 5 10 15

Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro
20 25 30

Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly
35 40 45

Thr Leu Trp Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro
50 55 60

Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp
65 70 75 80

Arg Leu Cys Glu Arg Ile Leu Ala Gly Gly Gly Gly Ser Gly Gly Gly
85 90 95

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

Glu Ala Ser Arg Leu Tyr Phe Gly Glu Arg Asn Val Lys Gly Met Phe
115 120 125

Glu Val Leu Glu Pro Leu His Ala Met Met Glu Arg Gly Pro Gln Thr
130 135 140

Leu Lys Glu Thr Ser Phe Asn Gln Ala Tyr Gly Arg Asp Leu Met Glu
145 150 155 160

Ala Gln Glu Trp Cys Arg Lys Tyr Met Lys Ser Gly Asn Val Lys Asp
165 170 175

Leu Thr Gln Ala Trp Asp Leu Tyr Tyr His Val Phe Arg Arg Ile Ser
180 185 190

<210> 403
<211> 612
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 403
atgggagtgc aggtggaaac catctcccca ggagacgggc gcaccttccc caagcgcggc 60

cagacctgcg tggtgcacta caccgggatg cttgaagatg gaaagaaatt tgattcctcc 120

cgggacagaa acaagccctt taagtttatg ctaggcaagc aggaggtgat ccgaggctgg 180

gaagaagggg ttgcccagat gagtgtgggt cagagagcca aactgactat atctccagat 240

tatgcctatg gtgccactgg gcacccaggc atcatcccac cacatgccac tctcgtcttc 300

gatgtggagc ttctaaaact ggaaggagga gggagctccg gtggaggcag cggtatggtc 360

ttcacactcg aagatttcgt tggggactgg cgacagacag ccggctacaa cctggaccaa 420

gtccttgaac agggaggtgt gtccagtttg tttcagaatc tcggggtgtc cgtaactccg 480

atccaaagga ttgtcctgag cggtgaaaat gggctgaaga tcgacatcca tgtcatcatc 540

ccgtatgaag gtctgagcgg cgaccaaatg ggccagatcg aaaaaatttt taaggtggtg 600

taccctgtgg at 612

<210> 404
<211> 204
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 404
Met Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe
1 5 10 15

Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu
20 25 30

Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys
35 40 45

Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val
50 55 60

Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp
65 70 75 80

Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala
85 90 95

Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu Gly Gly Gly Ser
100 105 110

Ser Gly Gly Gly Ser Gly Met Val Phe Thr Leu Glu Asp Phe Val Gly
115 120 125

Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln
130 135 140

Gly Gly Val Ser Ser Leu Phe Gln Asn Leu Gly Val Ser Val Thr Pro
145 150 155 160

Ile Gln Arg Ile Val Leu Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile
165 170 175

His Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln Met Gly Gln
180 185 190

Ile Glu Lys Ile Phe Lys Val Val Tyr Pro Val Asp
195 200

<210> 405
<211> 570
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 405
atggatcatc actttaaggt gatcctgcac tatggcacac tggtaatcga cggggttacg 60

ccgaacatga tcgactattt cggacggccg tatgaaggca tcgccgtgtt cgacggcaaa 120

aagatcactg taacagggac cctgtggaac ggcaacaaaa ttatcgacga gcgcctgatc 180

aaccccgacg gctccctgct gttccgagta accatcaacg gagtgaccgg ctggcggctg 240

tgcgaacgca ttctggcggg aggaggtggc tcaggtggag ggagctccgt ggccatcctc 300

tggcatgaga tgtggcatga aggcctggaa gaggcatctc gtttgtactt tggggaaagg 360

aacgtgaaag gcatgtttga ggtgctggag cccttgcatg ctatgatgga acggggcccc 420

cagactctga aggaaacatc ctttaatcag gcctatggtc gagatttaat ggaggcccaa 480

gagtggtgca ggaagtacat gaaatcaggg aatgtcaagg acctcaccca agcctgggac 540

ctctattatc atgtgttccg acgaatctca 570

<210> 406
<211> 190
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 406
Met Asp His His Phe Lys Val Ile Leu His Tyr Gly Thr Leu Val Ile
1 5 10 15

Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu
20 25 30

Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr Leu

35 40 45

Trp Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly
50 55 60

Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg Leu
65 70 75 80

Cys Glu Arg Ile Leu Ala Gly Gly Gly Gly Ser Gly Gly Gly Ser Ser
85 90 95

Val Ala Ile Leu Trp His Glu Met Trp His Glu Gly Leu Glu Glu Ala
100 105 110

Ser Arg Leu Tyr Phe Gly Glu Arg Asn Val Lys Gly Met Phe Glu Val
115 120 125

Leu Glu Pro Leu His Ala Met Met Glu Arg Gly Pro Gln Thr Leu Lys
130 135 140

Glu Thr Ser Phe Asn Gln Ala Tyr Gly Arg Asp Leu Met Glu Ala Gln
145 150 155 160

Glu Trp Cys Arg Lys Tyr Met Lys Ser Gly Asn Val Lys Asp Leu Thr
165 170 175

Gln Ala Trp Asp Leu Tyr Tyr His Val Phe Arg Arg Ile Ser
180 185 190

<210> 407
<211> 726
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 407
atgggagtgc aggtggaaac catctcccca ggagacgggc gcaccttccc caagcgcggc 60

cagacctgcg tggtgcacta caccgggatg cttgaagatg gaaagaaatt tgattcctcc 120

cgggacagaa acaagccctt taagtttatg ctaggcaagc aggaggtgat ccgaggctgg 180

gaagaagggg ttgcccagat gagtgtgggt cagagagcca aactgactat atctccagat 240

tatgcctatg gtgccactgg gcacccaggc atcatcccac cacatgccac tctcgtcttc 300

gatgtggagc ttctaaaact ggaaggagga gggagctccg gtggaggcag cggtatggtc 360

ttcacactcg aagatttcgt tggggactgg cgacagacag ccggctacaa cctggaccaa 420

gtccttgaac agggaggtgt gtccagtttg tttcagaatc tcggggtgtc cgtaactccg 480

atccaaagga ttgtcctgag cggtgaaaat gggctgaaga tcgacatcca tgtcatcatc 540

ccgtatgaag gtctgagcgg cgaccaaatg ggccagatcg aaaaaatttt taaggtggtg 600

taccctgtgg atgatcatca ctttaaggtg atcctgcact atggcacact ggtaatcgac 660

ggggttacgc cgaacatgat cgactatttc ggacggccgt atgaaggcat cgccgtgttc 720

gacggc 726

<210> 408
<211> 242
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 408
Met Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe
1 5 10 15

Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu
20 25 30

Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys
35 40 45

Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val
50 55 60

Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp
65 70 75 80

Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala
85 90 95

Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu Gly Gly Gly Ser
100 105 110

Ser Gly Gly Gly Ser Gly Met Val Phe Thr Leu Glu Asp Phe Val Gly
115 120 125

Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln
130 135 140

Gly Gly Val Ser Ser Leu Phe Gln Asn Leu Gly Val Ser Val Thr Pro
145 150 155 160

Ile Gln Arg Ile Val Leu Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile
165 170 175

His Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln Met Gly Gln
180 185 190

Ile Glu Lys Ile Phe Lys Val Val Tyr Pro Val Asp Asp His His Phe
195 200 205

Lys Val Ile Leu His Tyr Gly Thr Leu Val Ile Asp Gly Val Thr Pro
210 215 220

Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe
225 230 235 240

Asp Gly

<210> 409
<211> 456
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 409
atgaaaaaga tcactgtaac agggaccctg tggaacggca acaaaattat cgacgagcgc 60

ctgatcaacc ccgacggctc cctgctgttc cgagtaacca tcaacggagt gaccggctgg 120

cggctgtgcg aacgcattct ggcgggagga ggtggctcag gtggagggag ctccgtggcc 180

atcctctggc atgagatgtg gcatgaaggc ctggaagagg catctcgttt gtactttggg 240

gaaaggaacg tgaaaggcat gtttgaggtg ctggagccct tgcatgctat gatggaacgg 300

ggcccccaga ctctgaagga aacatccttt aatcaggcct atggtcgaga tttaatggag 360

gcccaagagt ggtgcaggaa gtacatgaaa tcagggaatg tcaaggacct cacccaagcc 420

tgggacctct attatcatgt gttccgacga atctca 456

<210> 410
<211> 152
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 410
Met Lys Lys Ile Thr Val Thr Gly Thr Leu Trp Asn Gly Asn Lys Ile
1 5 10 15

Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val
20 25 30

Thr Ile Asn Gly Val Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala
35 40 45

Gly Gly Gly Gly Ser Gly Gly Gly Ser Ser Val Ala Ile Leu Trp His
50 55 60

Glu Met Trp His Glu Gly Leu Glu Glu Ala Ser Arg Leu Tyr Phe Gly

65 70 75 80

Glu Arg Asn Val Lys Gly Met Phe Glu Val Leu Glu Pro Leu His Ala
85 90 95

Met Met Glu Arg Gly Pro Gln Thr Leu Lys Glu Thr Ser Phe Asn Gln
100 105 110

Ala Tyr Gly Arg Asp Leu Met Glu Ala Gln Glu Trp Cys Arg Lys Tyr
115 120 125

Met Lys Ser Gly Asn Val Lys Asp Leu Thr Gln Ala Trp Asp Leu Tyr
130 135 140

Tyr His Val Phe Arg Arg Ile Ser
145 150

<210> 411
<211> 729
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 411
atgggagtgc aggtggaaac catctcccca ggagacgggc gcaccttccc caagcgcggc 60

cagacctgcg tggtgcacta caccgggatg cttgaagatg gaaagaaatt tgattcctcc 120

cgggacagaa acaagccctt taagtttatg ctaggcaagc aggaggtgat ccgaggctgg 180

gaagaagggg ttgcccagat gagtgtgggt cagagagcca aactgactat atctccagat 240

tatgcctatg gtgccactgg gcacccaggc atcatcccac cacatgccac tctcgtcttc 300

gatgtggagc ttctaaaact ggaaggagga gggagctccg gtggaggcag cggtatggtc 360

ttcacactcg aagatttcgt tggggactgg cgacagacag ccggctacaa cctggaccaa 420

gtccttgaac agggaggtgt gtccagtttg tttcagaatc tcggggtgtc cgtaactccg 480

atccaaagga ttgtcctgag cggtgaaaat gggctgaaga tcgacatcca tgtcatcatc 540

ccgtatgaag gtctgagcgg cgaccaaatg ggccagatcg aaaaaatttt taaggtggtg 600

taccctgtgg atgatcatca ctttaaggtg atcctgcact atggcacact ggtaatcgac 660

ggggttacgc cgaacatgat cgactatttc ggacggccgt atgaaggcat cgccgtgttc 720

gacggcaaa 729

<210> 412
<211> 243
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 412
Met Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe
1 5 10 15

Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu
20 25 30

Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys
35 40 45

Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val
50 55 60

Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp
65 70 75 80

Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala
85 90 95

Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu Gly Gly Gly Ser
100 105 110

Ser Gly Gly Gly Ser Gly Met Val Phe Thr Leu Glu Asp Phe Val Gly
115 120 125

Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln
130 135 140

Gly Gly Val Ser Ser Leu Phe Gln Asn Leu Gly Val Ser Val Thr Pro
145 150 155 160

Ile Gln Arg Ile Val Leu Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile
165 170 175

His Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln Met Gly Gln
180 185 190

Ile Glu Lys Ile Phe Lys Val Val Tyr Pro Val Asp Asp His His Phe
195 200 205

Lys Val Ile Leu His Tyr Gly Thr Leu Val Ile Asp Gly Val Thr Pro
210 215 220

Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe
225 230 235 240

Asp Gly Lys

<210> 413
<211> 453

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 413
atgaagatca ctgtaacagg gaccctgtgg aacggcaaca aaattatcga cgagcgcctg 60

atcaaccccg acggctccct gctgttccga gtaaccatca acggagtgac cggctggcgg 120

ctgtgcgaac gcattctggc gggaggaggt ggctcaggtg gagggagctc cgtggccatc 180

ctctggcatg agatgtggca tgaaggcctg gaagaggcat ctcgtttgta ctttggggaa 240

aggaacgtga aaggcatgtt tgaggtgctg gagcccttgc atgctatgat ggaacggggc 300

ccccagactc tgaaggaaac atcctttaat caggcctatg gtcgagattt aatggaggcc 360

caagagtggt gcaggaagta catgaaatca gggaatgtca aggacctcac ccaagcctgg 420

gacctctatt atcatgtgtt ccgacgaatc tca 453

<210> 414
<211> 151
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 414
Met Lys Ile Thr Val Thr Gly Thr Leu Trp Asn Gly Asn Lys Ile Ile
1 5 10 15

Asp Glu Arg Leu Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val Thr
20 25 30

Ile Asn Gly Val Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala Gly
35 40 45

Gly Gly Gly Ser Gly Gly Gly Ser Ser Val Ala Ile Leu Trp His Glu
50 55 60

Met Trp His Glu Gly Leu Glu Glu Ala Ser Arg Leu Tyr Phe Gly Glu
65 70 75 80

Arg Asn Val Lys Gly Met Phe Glu Val Leu Glu Pro Leu His Ala Met
85 90 95

Met Glu Arg Gly Pro Gln Thr Leu Lys Glu Thr Ser Phe Asn Gln Ala
100 105 110

Tyr Gly Arg Asp Leu Met Glu Ala Gln Glu Trp Cys Arg Lys Tyr Met
115 120 125

Lys Ser Gly Asn Val Lys Asp Leu Thr Gln Ala Trp Asp Leu Tyr Tyr

130 135 140

His Val Phe Arg Arg Ile Ser
145 150

<210> 415
<211> 864
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 415
atgggagtgc aggtggaaac catctcccca ggagacgggc gcaccttccc caagcgcggc 60

cagacctgcg tggtgcacta caccgggatg cttgaagatg gaaagaaatt tgattcctcc 120

cgggacagaa acaagccctt taagtttatg ctaggcaagc aggaggtgat ccgaggctgg 180

gaagaagggg ttgcccagat gagtgtgggt cagagagcca aactgactat atctccagat 240

tatgcctatg gtgccactgg gcacccaggc atcatcccac cacatgccac tctcgtcttc 300

gatgtggagc ttctaaaact ggaaggagga gggagctccg gtggaggcag cggtatggtc 360

ttcacactcg aagatttcgt tggggactgg cgacagacag ccggctacaa cctggaccaa 420

gtccttgaac agggaggtgt gtccagtttg tttcagaatc tcggggtgtc cgtaactccg 480

atccaaagga ttgtcctgag cggtgaaaat gggctgaaga tcgacatcca tgtcatcatc 540

ccgtatgaag gtctgagcgg cgaccaaatg ggccagatcg aaaaaatttt taaggtggtg 600

taccctgtgg atgatcatca ctttaaggtg atcctgcact atggcacact ggtaatcgac 660

ggggttacgc cgaacatgat cgactatttc ggacggccgt atgaaggcat cgccgtgttc 720

gacggcaaaa agatcactgt aacagggacc ctgtggaacg gcaacaaaat tatcgacgag 780

cgcctgatca accccgacgg ctccctgctg ttccgagtaa ccatcaacgg agtgaccggc 840

tggcggctgt gcgaacgcat tctg 864

<210> 416
<211> 864
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 416
atgggagtgc aggtggaaac catctcccca ggagacgggc gcaccttccc caagcgcggc 60

cagacctgcg tggtgcacta caccgggatg cttgaagatg gaaagaaatt tgattcctcc 120

cgggacagaa acaagccctt taagtttatg ctaggcaagc aggaggtgat ccgaggctgg 180

gaagaagggg ttgcccagat gagtgtgggt cagagagcca aactgactat atctccagat 240

tatgcctatg gtgccactgg gcacccaggc atcatcccac cacatgccac tctcgtcttc 300

gatgtggagc ttctaaaact ggaaggagga gggagctccg gtggaggcag cggtatggtc 360

ttcacactcg aagatttcgt tggggactgg cgacagacag ccggctacaa cctggaccaa 420

gtccttgaac agggaggtgt gtccagtttg tttcagaatc tcggggtgtc cgtaactccg 480

atccaaagga ttgtcctgag cggtgaaaat gggctgaaga tcgacatcca tgtcatcatc 540

ccgtatgaag gtctgagcgg cgaccaaatg ggccagatcg aaaaaatttt taaggtggtg 600

taccctgtgg atgatcatca ctttaaggtg atcctgcact atggcacact ggtaatcgac 660

ggggttacgc cgaacatgat cgactatttc ggacggccgt atgaaggcat cgccgtgttc 720

gacggcaaaa agatcactgt aacagggacc ctgtggaacg gcaacaaaat tatcgacgag 780

cgcctgatca accccgacgg ctccctgctg ttccgagtaa ccatcaacgg agtgaccggc 840

tggcggctgt gcgaacgcat tctg 864

<210> 417
<211> 288
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 417
Met Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe
1 5 10 15

Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu
20 25 30

Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys
35 40 45

Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val
50 55 60

Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp
65 70 75 80

Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala
85 90 95

Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu Gly Gly Gly Ser
100 105 110

Ser Gly Gly Gly Ser Gly Met Val Phe Thr Leu Glu Asp Phe Val Gly
115 120 125

Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln
130 135 140

Gly Gly Val Ser Ser Leu Phe Gln Asn Leu Gly Val Ser Val Thr Pro

145 150 155 160

Ile Gln Arg Ile Val Leu Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile
165 170 175

His Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln Met Gly Gln
180 185 190

Ile Glu Lys Ile Phe Lys Val Val Tyr Pro Val Asp Asp His His Phe
195 200 205

Lys Val Ile Leu His Tyr Gly Thr Leu Val Ile Asp Gly Val Thr Pro
210 215 220

Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe
225 230 235 240

Asp Gly Lys Lys Ile Thr Val Thr Gly Thr Leu Trp Asn Gly Asn Lys
245 250 255

Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg
260 265 270

Val Thr Ile Asn Gly Val Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu
275 280 285

<210> 418
<211> 318
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 418
atggcgggag gaggtggctc aggtggaggg agctccgtgg ccatcctctg gcatgagatg 60

tggcatgaag gcctggaaga ggcatctcgt ttgtactttg gggaaaggaa cgtgaaaggc 120

atgtttgagg tgctggagcc cttgcatgct atgatggaac ggggccccca gactctgaag 180

gaaacatcct ttaatcaggc ctatggtcga gatttaatgg aggcccaaga gtggtgcagg 240

aagtacatga aatcagggaa tgtcaaggac ctcacccaag cctgggacct ctattatcat 300

gtgttccgac gaatctca 318

<210> 419
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 419

155193_1

Met Ala Gly Gly Gly Gly Ser Gly Gly Gly Ser Ser Val Ala Ile Leu
1 5 10 15

Trp His Glu Met Trp His Glu Gly Leu Glu Glu Ala Ser Arg Leu Tyr
20 25 30

Phe Gly Glu Arg Asn Val Lys Gly Met Phe Glu Val Leu Glu Pro Leu
35 40 45

His Ala Met Met Glu Arg Gly Pro Gln Thr Leu Lys Glu Thr Ser Phe
50 55 60

Asn Gln Ala Tyr Gly Arg Asp Leu Met Glu Ala Gln Glu Trp Cys Arg
65 70 75 80

Lys Tyr Met Lys Ser Gly Asn Val Lys Asp Leu Thr Gln Ala Trp Asp
85 90 95

Leu Tyr Tyr His Val Phe Arg Arg Ile Ser
100 105

<210> 420
<211> 858
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 420
atgggagtgc aggtggaaac catctcccca ggagacgggc gcaccttccc caagcgcggc 60

cagacctgcg tggtgcacta caccgggatg cttgaagatg gaaagaaatt tgattcctcc 120

cgggacagaa acaagccctt taagtttatg ctaggcaagc aggaggtgat ccgaggctgg 180

gaagaagggg ttgcccagat gagtgtgggt cagagagcca aactgactat atctccagat 240

tatgcctatg gtgccactgg gcacccaggc atcatcccac cacatgccac tctcgtcttc 300

gatgtggagc ttctaaaact ggaaggagga gggagctccg gtggaggcag cggtatggtc 360

ttcacactcg aagatttcgt tggggactgg cgacagacag ccggctacaa cctggaccaa 420

gtccttgaac agggaggtgt gtccagtttg tttcagaatc tcggggtgtc cgtaactccg 480

atccaaagga ttgtcctgag cggtgaaaat gggctgaaga tcgacatcca tgtcatcatc 540

ccgtatgaag gtctgagcgg cgaccaaatg ggccagatcg aaaaaatttt taaggtggtg 600

taccctgtgg atgatcatca ctttaaggtg atcctgcact atggcacact ggtaatcgac 660

ggggttacgc cgaacatgat cgactatttc ggacggccgt atgaaggcat cgccgtgttc 720

gacggcaaaa agatcactgt aacagggacc ctgtggaacg gcaacaaaat tatcgacgag 780

cgcctgatca accccgacgg ctccctgctg ttccgagtaa ccatcaacgg agtgaccggc 840

tggcggctgt gcgaacgc 858

<210> 421
<211> 286
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 421
Met Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe
1 5 10 15

Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu
20 25 30

Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys
35 40 45

Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val
50 55 60

Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp
65 70 75 80

Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala
85 90 95

Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu Gly Gly Gly Ser
100 105 110

Ser Gly Gly Gly Ser Gly Met Val Phe Thr Leu Glu Asp Phe Val Gly
115 120 125

Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln
130 135 140

Gly Gly Val Ser Ser Leu Phe Gln Asn Leu Gly Val Ser Val Thr Pro
145 150 155 160

Ile Gln Arg Ile Val Leu Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile
165 170 175

His Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln Met Gly Gln
180 185 190

Ile Glu Lys Ile Phe Lys Val Val Tyr Pro Val Asp Asp His His Phe
195 200 205

Lys Val Ile Leu His Tyr Gly Thr Leu Val Ile Asp Gly Val Thr Pro
210 215 220

Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe

225 230 235 240

Asp Gly Lys Lys Ile Thr Val Thr Gly Thr Leu Trp Asn Gly Asn Lys
245 250 255

Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg
260 265 270

Val Thr Ile Asn Gly Val Thr Gly Trp Arg Leu Cys Glu Arg
275 280 285

<210> 422
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 422
atgattctgg cgggaggagg tggctcaggt ggagggagct ccgtggccat cctctggcat 60

gagatgtggc atgaaggcct ggaagaggca tctcgtttgt actttgggga aaggaacgtg 120

aaaggcatgt ttgaggtgct ggagcccttg catgctatga tggaacgggg cccccagact 180

ctgaaggaaa catcctttaa tcaggcctat ggtcgagatt taatggaggc ccaagagtgg 240

tgcaggaagt acatgaaatc agggaatgtc aaggacctca cccaagcctg ggacctctat 300

tatcatgtgt tccgacgaat ctca 324

<210> 423
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 423
Met Ile Leu Ala Gly Gly Gly Gly Ser Gly Gly Gly Ser Ser Val Ala
1 5 10 15

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

Leu Tyr Phe Gly Glu Arg Asn Val Lys Gly Met Phe Glu Val Leu Glu
35 40 45

Pro Leu His Ala Met Met Glu Arg Gly Pro Gln Thr Leu Lys Glu Thr
50 55 60

Ser Phe Asn Gln Ala Tyr Gly Arg Asp Leu Met Glu Ala Gln Glu Trp
65 70 75 80

Cys Arg Lys Tyr Met Lys Ser Gly Asn Val Lys Asp Leu Thr Gln Ala
85 90 95

Trp Asp Leu Tyr Tyr His Val Phe Arg Arg Ile Ser
100 105

<210> 424
<211> 852
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 424
atgggagtgc aggtggaaac catctcccca ggagacgggc gcaccttccc caagcgcggc 60

cagacctgcg tggtgcacta caccgggatg cttgaagatg gaaagaaatt tgattcctcc 120

cgggacagaa acaagccctt taagtttatg ctaggcaagc aggaggtgat ccgaggctgg 180

gaagaagggg ttgcccagat gagtgtgggt cagagagcca aactgactat atctccagat 240

tatgcctatg gtgccactgg gcacccaggc atcatcccac cacatgccac tctcgtcttc 300

gatgtggagc ttctaaaact ggaaggagga gggagctccg gtggaggcag cggtatggtc 360

ttcacactcg aagatttcgt tggggactgg cgacagacag ccggctacaa cctggaccaa 420

gtccttgaac agggaggtgt gtccagtttg tttcagaatc tcggggtgtc cgtaactccg 480

atccaaagga ttgtcctgag cggtgaaaat gggctgaaga tcgacatcca tgtcatcatc 540

ccgtatgaag gtctgagcgg cgaccaaatg ggccagatcg aaaaaatttt taaggtggtg 600

taccctgtgg atgatcatca ctttaaggtg atcctgcact atggcacact ggtaatcgac 660

ggggttacgc cgaacatgat cgactatttc ggacggccgt atgaaggcat cgccgtgttc 720

gacggcaaaa agatcactgt aacagggacc ctgtggaacg gcaacaaaat tatcgacgag 780

cgcctgatca accccgacgg ctccctgctg ttccgagtaa ccatcaacgg agtgaccggc 840

tggcggctgt gc 852

<210> 425
<211> 284
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 425
Met Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe
1 5 10 15

Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu
20 25 30

Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys

35 40 45

Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val
50 55 60

Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp
65 70 75 80

Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala
85 90 95

Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu Gly Gly Gly Ser
100 105 110

Ser Gly Gly Gly Ser Gly Met Val Phe Thr Leu Glu Asp Phe Val Gly
115 120 125

Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln
130 135 140

Gly Gly Val Ser Ser Leu Phe Gln Asn Leu Gly Val Ser Val Thr Pro
145 150 155 160

Ile Gln Arg Ile Val Leu Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile
165 170 175

His Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln Met Gly Gln
180 185 190

Ile Glu Lys Ile Phe Lys Val Val Tyr Pro Val Asp Asp His His Phe
195 200 205

Lys Val Ile Leu His Tyr Gly Thr Leu Val Ile Asp Gly Val Thr Pro
210 215 220

Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe
225 230 235 240

Asp Gly Lys Lys Ile Thr Val Thr Gly Thr Leu Trp Asn Gly Asn Lys
245 250 255

Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg
260 265 270

Val Thr Ile Asn Gly Val Thr Gly Trp Arg Leu Cys
275 280

<210> 426
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 426
atggaacgca ttctggcggg aggaggtggc tcaggtggag ggagctccgt ggccatcctc 60

tggcatgaga tgtggcatga aggcctggaa gaggcatctc gtttgtactt tggggaaagg 120

aacgtgaaag gcatgtttga ggtgctggag cccttgcatg ctatgatgga acggggcccc 180

cagactctga aggaaacatc ctttaatcag gcctatggtc gagatttaat ggaggcccaa 240

gagtggtgca ggaagtacat gaaatcaggg aatgtcaagg acctcaccca agcctgggac 300

ctctattatc atgtgttccg acgaatctca 330

<210> 427
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Dinoflagellate
luciferase consensus sequence

<220>
<221> MOD_RES
<222> (6)..(6)
<223> Val or Ile

<220>
<221> MOD_RES
<222> (11)..(11)
<223> Ala, Val, Thr, or Lys

<220>
<221> MOD_RES
<222> (12)..(12)
<223> Ala or Glu

<220>
<221> MOD_RES
<222> (16)..(16)
<223> Glu, Lys, Thr, or Gln

<220>
<221> MOD_RES
<222> (17)..(17)
<223> Ala or Val

<220>
<221> MOD_RES
<222> (18)..(18)
<223> Val or Ile

<400> 427
Gly Arg Trp Ile Thr Xaa Ser Gly Gly Gln Xaa Xaa Phe Ile Lys Xaa
1 5 10 15

Xaa Xaa

<210> 428

<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 428
Met Glu Arg Ile Leu Ala Gly Gly Gly Gly Ser Gly Gly Gly Ser Ser
1 5 10 15

Val Ala Ile Leu Trp His Glu Met Trp His Glu Gly Leu Glu Glu Ala
20 25 30

Ser Arg Leu Tyr Phe Gly Glu Arg Asn Val Lys Gly Met Phe Glu Val
35 40 45

Leu Glu Pro Leu His Ala Met Met Glu Arg Gly Pro Gln Thr Leu Lys
50 55 60

Glu Thr Ser Phe Asn Gln Ala Tyr Gly Arg Asp Leu Met Glu Ala Gln
65 70 75 80

Glu Trp Cys Arg Lys Tyr Met Lys Ser Gly Asn Val Lys Asp Leu Thr
85 90 95

Gln Ala Trp Asp Leu Tyr Tyr His Val Phe Arg Arg Ile Ser
100 105 110

<210> 429
<211> 846
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 429
atgggagtgc aggtggaaac catctcccca ggagacgggc gcaccttccc caagcgcggc 60

cagacctgcg tggtgcacta caccgggatg cttgaagatg gaaagaaatt tgattcctcc 120

cgggacagaa acaagccctt taagtttatg ctaggcaagc aggaggtgat ccgaggctgg 180

gaagaagggg ttgcccagat gagtgtgggt cagagagcca aactgactat atctccagat 240

tatgcctatg gtgccactgg gcacccaggc atcatcccac cacatgccac tctcgtcttc 300

gatgtggagc ttctaaaact ggaaggagga gggagctccg gtggaggcag cggtatggtc 360

ttcacactcg aagatttcgt tggggactgg cgacagacag ccggctacaa cctggaccaa 420

gtccttgaac agggaggtgt gtccagtttg tttcagaatc tcggggtgtc cgtaactccg 480

atccaaagga ttgtcctgag cggtgaaaat gggctgaaga tcgacatcca tgtcatcatc 540

ccgtatgaag gtctgagcgg cgaccaaatg ggccagatcg aaaaaatttt taaggtggtg 600

taccctgtgg atgatcatca ctttaaggtg atcctgcact atggcacact ggtaatcgac 660

ggggttacgc cgaacatgat cgactatttc ggacggccgt atgaaggcat cgccgtgttc 720

gacggcaaaa agatcactgt aacagggacc ctgtggaacg gcaacaaaat tatcgacgag 780

cgcctgatca accccgacgg ctccctgctg ttccgagtaa ccatcaacgg agtgaccggc 840

tggcgg 846

<210> 430
<211> 282
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 430
Met Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe
1 5 10 15

Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu
20 25 30

Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys
35 40 45

Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val
50 55 60

Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp
65 70 75 80

Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala
85 90 95

Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu Gly Gly Gly Ser
100 105 110

Ser Gly Gly Gly Ser Gly Met Val Phe Thr Leu Glu Asp Phe Val Gly
115 120 125

Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln
130 135 140

Gly Gly Val Ser Ser Leu Phe Gln Asn Leu Gly Val Ser Val Thr Pro
145 150 155 160

Ile Gln Arg Ile Val Leu Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile
165 170 175

His Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln Met Gly Gln
180 185 190

Ile Glu Lys Ile Phe Lys Val Val Tyr Pro Val Asp Asp His His Phe
195 200 205

Lys Val Ile Leu His Tyr Gly Thr Leu Val Ile Asp Gly Val Thr Pro
210 215 220

Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe
225 230 235 240

Asp Gly Lys Lys Ile Thr Val Thr Gly Thr Leu Trp Asn Gly Asn Lys
245 250 255

Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg
260 265 270

Val Thr Ile Asn Gly Val Thr Gly Trp Arg
275 280

<210> 431
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 431
atgctgtgcg aacgcattct ggcgggagga ggtggctcag gtggagggag ctccgtggcc 60

atcctctggc atgagatgtg gcatgaaggc ctggaagagg catctcgttt gtactttggg 120

gaaaggaacg tgaaaggcat gtttgaggtg ctggagccct tgcatgctat gatggaacgg 180

ggcccccaga ctctgaagga aacatccttt aatcaggcct atggtcgaga tttaatggag 240

gcccaagagt ggtgcaggaa gtacatgaaa tcagggaatg tcaaggacct cacccaagcc 300

tgggacctct attatcatgt gttccgacga atctca 336

<210> 432
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 432
Met Leu Cys Glu Arg Ile Leu Ala Gly Gly Gly Gly Ser Gly Gly Gly
1 5 10 15

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

Glu Ala Ser Arg Leu Tyr Phe Gly Glu Arg Asn Val Lys Gly Met Phe
35 40 45

Glu Val Leu Glu Pro Leu His Ala Met Met Glu Arg Gly Pro Gln Thr
50 55 60

Leu Lys Glu Thr Ser Phe Asn Gln Ala Tyr Gly Arg Asp Leu Met Glu
65 70 75 80

Ala Gln Glu Trp Cys Arg Lys Tyr Met Lys Ser Gly Asn Val Lys Asp
85 90 95

Leu Thr Gln Ala Trp Asp Leu Tyr Tyr His Val Phe Arg Arg Ile Ser
100 105 110

<210> 433
<211> 840
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 433
atgggagtgc aggtggaaac catctcccca ggagacgggc gcaccttccc caagcgcggc 60

cagacctgcg tggtgcacta caccgggatg cttgaagatg gaaagaaatt tgattcctcc 120

cgggacagaa acaagccctt taagtttatg ctaggcaagc aggaggtgat ccgaggctgg 180

gaagaagggg ttgcccagat gagtgtgggt cagagagcca aactgactat atctccagat 240

tatgcctatg gtgccactgg gcacccaggc atcatcccac cacatgccac tctcgtcttc 300

gatgtggagc ttctaaaact ggaaggagga gggagctccg gtggaggcag cggtatggtc 360

ttcacactcg aagatttcgt tggggactgg cgacagacag ccggctacaa cctggaccaa 420

gtccttgaac agggaggtgt gtccagtttg tttcagaatc tcggggtgtc cgtaactccg 480

atccaaagga ttgtcctgag cggtgaaaat gggctgaaga tcgacatcca tgtcatcatc 540

ccgtatgaag gtctgagcgg cgaccaaatg ggccagatcg aaaaaatttt taaggtggtg 600

taccctgtgg atgatcatca ctttaaggtg atcctgcact atggcacact ggtaatcgac 660

ggggttacgc cgaacatgat cgactatttc ggacggccgt atgaaggcat cgccgtgttc 720

gacggcaaaa agatcactgt aacagggacc ctgtggaacg gcaacaaaat tatcgacgag 780

cgcctgatca accccgacgg ctccctgctg ttccgagtaa ccatcaacgg agtgaccggc 840

<210> 434
<211> 280
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 434
Met Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe
1 5 10 15

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Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu
            20                  25                  30

Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys
        35                  40                  45

Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val
    50                  55                  60

Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp
65                  70                  75                  80

Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala
                85                  90                  95

Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu Gly Gly Gly Ser
            100                 105                 110

Ser Gly Gly Gly Ser Gly Met Val Phe Thr Leu Glu Asp Phe Val Gly
        115                 120                 125

Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln
    130                 135                 140

Gly Gly Val Ser Ser Leu Phe Gln Asn Leu Gly Val Ser Val Thr Pro
145                 150                 155                 160

Ile Gln Arg Ile Val Leu Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile
                165                 170                 175

His Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln Met Gly Gln
            180                 185                 190

Ile Glu Lys Ile Phe Lys Val Val Tyr Pro Val Asp Asp His His Phe
        195                 200                 205

Lys Val Ile Leu His Tyr Gly Thr Leu Val Ile Asp Gly Val Thr Pro
    210                 215                 220

Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe
225                 230                 235                 240

Asp Gly Lys Lys Ile Thr Val Thr Gly Thr Leu Trp Asn Gly Asn Lys
                245                 250                 255

Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg
            260                 265                 270

Val Thr Ile Asn Gly Val Thr Gly
        275                 280
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<210> 435
<211> 342
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 435
atgtggcggc tgtgcgaacg cattctggcg ggaggaggtg gctcaggtgg agggagctcc 60

gtggccatcc tctggcatga gatgtggcat gaaggcctgg aagaggcatc tcgtttgtac 120

tttggggaaa ggaacgtgaa aggcatgttt gaggtgctgg agcccttgca tgctatgatg 180

gaacggggcc cccagactct gaaggaaaca tcctttaatc aggcctatgg tcgagattta 240

atggaggccc aagagtggtg caggaagtac atgaaatcag ggaatgtcaa ggacctcacc 300

caagcctggg acctctatta tcatgtgttc cgacgaatct ca 342

<210> 436
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 436
Met Trp Arg Leu Cys Glu Arg Ile Leu Ala Gly Gly Gly Gly Ser Gly
1 5 10 15

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

Leu Glu Glu Ala Ser Arg Leu Tyr Phe Gly Glu Arg Asn Val Lys Gly
35 40 45

Met Phe Glu Val Leu Glu Pro Leu His Ala Met Met Glu Arg Gly Pro
50 55 60

Gln Thr Leu Lys Glu Thr Ser Phe Asn Gln Ala Tyr Gly Arg Asp Leu
65 70 75 80

Met Glu Ala Gln Glu Trp Cys Arg Lys Tyr Met Lys Ser Gly Asn Val
85 90 95

Lys Asp Leu Thr Gln Ala Trp Asp Leu Tyr Tyr His Val Phe Arg Arg
100 105 110

Ile Ser

<210> 437

<211> 834
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 437
atgggagtgc aggtggaaac catctcccca ggagacgggc gcaccttccc caagcgcggc 60

cagacctgcg tggtgcacta caccgggatg cttgaagatg gaaagaaatt tgattcctcc 120

cgggacagaa acaagccctt taagtttatg ctaggcaagc aggaggtgat ccgaggctgg 180

gaagaagggg ttgcccagat gagtgtgggt cagagagcca aactgactat atctccagat 240

tatgcctatg gtgccactgg gcacccaggc atcatcccac cacatgccac tctcgtcttc 300

gatgtggagc ttctaaaact ggaaggagga gggagctccg gtggaggcag cggtatggtc 360

ttcacactcg aagatttcgt tggggactgg cgacagacag ccggctacaa cctggaccaa 420

gtccttgaac agggaggtgt gtccagtttg tttcagaatc tcggggtgtc cgtaactccg 480

atccaaagga ttgtcctgag cggtgaaaat gggctgaaga tcgacatcca tgtcatcatc 540

ccgtatgaag gtctgagcgg cgaccaaatg ggccagatcg aaaaaatttt taaggtggtg 600

taccctgtgg atgatcatca ctttaaggtg atcctgcact atggcacact ggtaatcgac 660

ggggttacgc cgaacatgat cgactatttc ggacggccgt atgaaggcat cgccgtgttc 720

gacggcaaaa agatcactgt aacagggacc ctgtggaacg gcaacaaaat tatcgacgag 780

cgcctgatca accccgacgg ctccctgctg ttccgagtaa ccatcaacgg agtg 834

<210> 438
<211> 278
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 438
Met Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe
1 5 10 15

Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu
20 25 30

Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys
35 40 45

Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val
50 55 60

Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp
65 70 75 80

Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala
85 90 95

Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu Gly Gly Gly Ser
100 105 110

Ser Gly Gly Gly Ser Gly Met Val Phe Thr Leu Glu Asp Phe Val Gly
115 120 125

Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln
130 135 140

Gly Gly Val Ser Ser Leu Phe Gln Asn Leu Gly Val Ser Val Thr Pro
145 150 155 160

Ile Gln Arg Ile Val Leu Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile
165 170 175

His Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln Met Gly Gln
180 185 190

Ile Glu Lys Ile Phe Lys Val Val Tyr Pro Val Asp Asp His His Phe
195 200 205

Lys Val Ile Leu His Tyr Gly Thr Leu Val Ile Asp Gly Val Thr Pro
210 215 220

Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe
225 230 235 240

Asp Gly Lys Lys Ile Thr Val Thr Gly Thr Leu Trp Asn Gly Asn Lys
245 250 255

Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg
260 265 270

Val Thr Ile Asn Gly Val
275

<210> 439
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 439
atgaccggct ggcggctgtg cgaacgcatt ctggcgggag gaggtggctc aggtggaggg 60

agctccgtgg ccatcctctg gcatgagatg tggcatgaag gcctggaaga ggcatctcgt 120

ttgtactttg gggaaaggaa cgtgaaaggc atgtttgagg tgctggagcc cttgcatgct 180

atgatggaac ggggccccca gactctgaag gaaacatcct ttaatcaggc ctatggtcga 240

gatttaatgg aggcccaaga gtggtgcagg aagtacatga aatcagggaa tgtcaaggac 300

ctcacccaag cctgggacct ctattatcat gtgttccgac gaatctca 348

<210> 440
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 440
Met Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala Gly Gly Gly Gly
1 5 10 15

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

Glu Gly Leu Glu Glu Ala Ser Arg Leu Tyr Phe Gly Glu Arg Asn Val
35 40 45

Lys Gly Met Phe Glu Val Leu Glu Pro Leu His Ala Met Met Glu Arg
50 55 60

Gly Pro Gln Thr Leu Lys Glu Thr Ser Phe Asn Gln Ala Tyr Gly Arg
65 70 75 80

Asp Leu Met Glu Ala Gln Glu Trp Cys Arg Lys Tyr Met Lys Ser Gly
85 90 95

Asn Val Lys Asp Leu Thr Gln Ala Trp Asp Leu Tyr Tyr His Val Phe
100 105 110

Arg Arg Ile Ser
115

<210> 441
<211> 447
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 441
atgtatgaaa gctttattga gtcactgcca ttccttaaat ctttggagtt ttctgcacgc 60

ctgaaagtag tagatgtgat aggcaccaaa gtatacaacg atggagaaca aatcattgct 120

cagggagatt cggctgattc ttttttcatt attgaatctg gagaagtgaa aattactatg 180

aaaagaaagg gtaaatcaga agtggaagag aatggtgcag tagaaatcgc tcgatgctcg 240

cggggacagt actttggaga gcttgccctg gtaactaaca aacctcgagc agcttctgcc 300

cacgccattg ggactgtcaa atgtttagca atggatgtgc aagcatttga aaggcttctg 360

ggaccttgca tggaaattat gaaaaggaac atcgctacct atgaagaaca gttagttgcc 420

ctgtatggaa cgaacatgga tattgta 447

<210> 442
<211> 149
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 442
Met Tyr Glu Ser Phe Ile Glu Ser Leu Pro Phe Leu Lys Ser Leu Glu
1 5 10 15

Phe Ser Ala Arg Leu Lys Val Val Asp Val Ile Gly Thr Lys Val Tyr
20 25 30

Asn Asp Gly Glu Gln Ile Ile Ala Gln Gly Asp Ser Ala Asp Ser Phe
35 40 45

Phe Ile Ile Glu Ser Gly Glu Val Lys Ile Thr Met Lys Arg Lys Gly
50 55 60

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

Arg Gly Gln Tyr Phe Gly Glu Leu Ala Leu Val Thr Asn Lys Pro Arg
85 90 95

Ala Ala Ser Ala His Ala Ile Gly Thr Val Lys Cys Leu Ala Met Asp
100 105 110

Val Gln Ala Phe Glu Arg Leu Leu Gly Pro Cys Met Glu Ile Met Lys
115 120 125

Arg Asn Ile Ala Thr Tyr Glu Glu Gln Leu Val Ala Leu Tyr Gly Thr
130 135 140

Asn Met Asp Ile Val
145

<210> 443
<211> 615
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 443

atgacagccg gctacaacct ggaccaagtc cttgagcagg gcggtgtgtc cagtttgttt 60

cagaatctcg gggtgtccgt aactccgatc caaaggattg tcctgagcgg tgaaaacggc 120

ctgaagatcg acatccatgt catcatcccg tatgaaggtc tgagcggcga tcagatgggc 180

cagatcgaaa aaatttttaa ggtggtgtac cctgtggatg atcatcactt taaggtgatt 240

ctgcactatg gcacactggt aatcgacggg gttacgccga acatgatcga ctatttcgga 300

cggccgtatg aaggcatcgc cgtgttcgac ggcaaaaaga tcactgtaac cgggaccctg 360

tggaacggca acaaaattat cgacgagcgc ctgatcaacc ccgacggctc cctgctgttc 420

cgcgtaacca tcaacggagt gaccggctgg cggctgtgcg agcgcatttt ggcgggaagt 480

tctggtggag gaagttctgg tggagagcct actactgaga acttgtactt ccagagcgat 540

aacggaagtt ctggtggagg aagttctggt ggaatggtgt ttacactcga agatttcgta 600

ggggactggc ggcag 615

<210> 444
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 444

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

Asn Gly Val Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala Gly Ser
145 150 155 160

Ser Gly Gly Gly Ser Ser Gly Gly Glu Pro Thr Thr Glu Asn Leu Tyr
165 170 175

Phe Gln Ser Asp Asn Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Met
180 185 190

Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln
195 200 205

<210> 445
<211> 615
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 445
atgcatgtca tcatcccgta tgaaggtctg agcggcgatc agatgggcca gatcgaaaaa 60

atttttaagg tggtgtaccc tgtggatgat catcacttta aggtgattct gcactatggc 120

acactggtaa tcgacggggt tacgccgaac atgatcgact atttcggacg gccgtatgaa 180

ggcatcgccg tgttcgacgg caaaaagatc actgtaaccg ggaccctgtg gaacggcaac 240

aaaattatcg acgagcgcct gatcaacccc gacggctccc tgctgttccg cgtaaccatc 300

aacggagtga ccggctggcg gctgtgcgag cgcattttgg cgggaagttc tggtggagga 360

agttctggtg gagagcctac tactgagaac ttgtacttcc agagcgataa cggaagttct 420

ggtggaggaa gttctggtgg aatggtgttt acactcgaag atttcgtagg ggactggcgg 480

cagacagccg gctacaacct ggaccaagtc cttgagcagg gcggtgtgtc cagtttgttt 540

cagaatctcg gggtgtccgt aactccgatc caaaggattg tcctgagcgg tgaaaacggc 600

ctgaagatcg acatc 615

<210> 446
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 446
Met His Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln Met Gly
1 5 10 15

Gln Ile Glu Lys Ile Phe Lys Val Val Tyr Pro Val Asp Asp His His
20 25 30

Phe Lys Val Ile Leu His Tyr Gly Thr Leu Val Ile Asp Gly Val Thr
35 40 45

Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly Ile Ala Val
50 55 60

Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr Leu Trp Asn Gly Asn
65 70 75 80

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

Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg Leu Cys Glu Arg Ile
100 105 110

Leu Ala Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Glu Pro Thr Thr
115 120 125

Glu Asn Leu Tyr Phe Gln Ser Asp Asn Gly Ser Ser Gly Gly Gly Ser
130 135 140

Ser Gly Gly Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg
145 150 155 160

Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Val
165 170 175

Ser Ser Leu Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln Arg
180 185 190

Ile Val Leu Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile
195 200 205

<210> 447
<211> 615
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 447
atggtaatcg acggggttac gccgaacatg atcgactatt tcggacggcc gtatgaaggc 60

atcgccgtgt tcgacggcaa aaagatcact gtaaccggga ccctgtggaa cggcaacaaa 120

attatcgacg agcgcctgat caaccccgac ggctccctgc tgttccgcgt aaccatcaac 180

ggagtgaccg gctggcggct gtgcgagcgc attttggcgg gaagttctgg tggaggaagt 240

tctggtggag agcctactac tgagaacttg tacttccaga gcgataacgg aagttctggt 300

ggaggaagtt ctggtggaat ggtgtttaca ctcgaagatt tcgtagggga ctggcggcag 360

acagccggct acaacctgga ccaagtcctt gagcagggcg gtgtgtccag tttgtttcag 420

aatctcgggg tgtccgtaac tccgatccaa aggattgtcc tgagcggtga aaacggcctg 480

aagatcgaca tccatgtcat catcccgtat gaaggtctga gcggcgatca gatgggccag 540

atcgaaaaaa tttttaaggt ggtgtaccct gtggatgatc atcactttaa ggtgattctg 600

cactatggca cactg 615

<210> 448
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 448
Met Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg
1 5 10 15

Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr
20 25 30

Gly Thr Leu Trp Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn
35 40 45

Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly
50 55 60

Trp Arg Leu Cys Glu Arg Ile Leu Ala Gly Ser Ser Gly Gly Gly Ser
65 70 75 80

Ser Gly Gly Glu Pro Thr Thr Glu Asn Leu Tyr Phe Gln Ser Asp Asn
85 90 95

Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Met Val Phe Thr Leu Glu
100 105 110

Asp Phe Val Gly Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln
115 120 125

Val Leu Glu Gln Gly Gly Val Ser Ser Leu Phe Gln Asn Leu Gly Val
130 135 140

Ser Val Thr Pro Ile Gln Arg Ile Val Leu Ser Gly Glu Asn Gly Leu
145 150 155 160

Lys Ile Asp Ile His Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp
165 170 175

Gln Met Gly Gln Ile Glu Lys Ile Phe Lys Val Val Tyr Pro Val Asp
180 185 190

Asp His His Phe Lys Val Ile Leu His Tyr Gly Thr Leu

195 200 205

<210> 449
<211> 2019
<212> DNA
<213> Homo sapiens

<400> 449
atggctgacg ttttcccggg caacgactcc acggcgtctc aggacgtggc caaccgcttc 60

gcccgcaaag gggcgctgag gcagaagaac gtgcacgagg tgaaggacca caaattcatc 120

gcgcgcttct tcaagcagcc caccttctgc agccactgca ccgacttcat ctgggggttt 180

gggaaacaag gcttccagtg ccaagtttgc tgttttgtgg tccacaagag gtgccatgaa 240

tttgttactt tttcttgtcc gggtgcggat aagggacccg acactgatga ccccaggagc 300

aagcacaagt tcaaaatcca cacttacgga agccccacct tctgcgatca ctgtgggtca 360

ctgctctatg gacttatcca tcaagggatg aaatgtgaca cctgcgatat gaacgttcac 420

aagcaatgcg tcatcaatgt ccccagcctc tgcggaatgg atcacactga gaagaggggg 480

cggatttacc taaaggctga ggttgctgat gaaaagctcc atgtcacagt acgagatgca 540

aaaaatctaa tccctatgga tccaaacggg ctttcagatc cttatgtgaa gctgaaactt 600

attcctgatc ccaagaatga aagcaagcaa aaaaccaaaa ccatccgctc cacactaaat 660

ccgcagtgga atgagtcctt tacattcaaa ttgaaacctt cagacaaaga ccgacgactg 720

tctgtagaaa tctgggactg ggatcgaaca acaaggaatg acttcatggg atccctttcc 780

tttggagttt cggagctgat gaagatgccg gccagtggat ggtacaagtt gcttaaccaa 840

gaagaaggtg agtactacaa cgtacccatt ccggaagggg acgaggaagg aaacatggaa 900

ctcaggcaga aattcgagaa agccaaactt ggccctgctg gcaacaaagt catcagtccc 960

tctgaagaca ggaaacaacc ttccaacaac cttgaccgag tgaaactcac ggacttcaat 1020

ttcctcatgg tgttgggaaa ggggagtttt ggaaaggtga tgcttgccga caggaagggc 1080

acagaagaac tgtatgcaat caaaatcctg aagaaggatg tggtgattca ggatgatgac 1140

gtggagtgca ccatggtaga aaagcgagtc ttggccctgc ttgacaaacc cccgttcttg 1200

acgcagctgc actcctgctt ccagacagtg gatcggctgt acttcgtcat ggaatatgtc 1260

aacggtgggg acctcatgta ccacattcag caagtaggaa aatttaagga accacaagca 1320

gtattctatg cggcagagat ttccatcgga ttgttctttc ttcataaaag aggaatcatt 1380

tatagggatc tgaagttaga taacgtcatg ttggattcag aaggacatat caaaattgct 1440

gactttggga tgtgcaagga acacatgatg gatggagtca cgaccaggac cttctgtggg 1500

actccagatt atatcgcccc agagataatc gcttatcagc cgtatggaaa atctgtggac 1560

tggtgggcct atggcgtcct gttgtatgaa atgcttgccg ggcagcctcc atttgatggt 1620

gaagatgaag acgagctatt tcagtctatc atggagcaca acgtttccta tccaaaatcc 1680

ttgtccaagg aggctgtttc tatctgcaaa ggactgatga ccaaacaccc agccaagcgg 1740

ctgggctgtg ggcctgaggg ggagagggac gtgagagagc atgccttctt ccggaggatc 1800

gactgggaaa aactggagaa cagggagatc cagccaccat tcaagcccaa agtgtgtggc 1860

aaaggagcag agaactttga caagttcttc acacgaggac agcccgtctt aacaccacct 1920

gatcagctgg ttattgctaa catagaccag tctgattttg aagggttctc gtatgtcaac 1980

ccccagtttg tgcaccccat cttacagagt gcagtagtt 2019

<210> 450
<211> 673
<212> PRT
<213> Homo sapiens

<400> 450
Met Ala Asp Val Phe Pro Gly Asn Asp Ser Thr Ala Ser Gln Asp Val
1 5 10 15

Ala Asn Arg Phe Ala Arg Lys Gly Ala Leu Arg Gln Lys Asn Val His
20 25 30

Glu Val Lys Asp His Lys Phe Ile Ala Arg Phe Phe Lys Gln Pro Thr
35 40 45

Phe Cys Ser His Cys Thr Asp Phe Ile Trp Gly Phe Gly Lys Gln Gly
50 55 60

Phe Gln Cys Gln Val Cys Cys Phe Val Val His Lys Arg Cys His Glu
65 70 75 80

Phe Val Thr Phe Ser Cys Pro Gly Ala Asp Lys Gly Pro Asp Thr Asp
85 90 95

Asp Pro Arg Ser Lys His Lys Phe Lys Ile His Thr Tyr Gly Ser Pro
100 105 110

Thr Phe Cys Asp His Cys Gly Ser Leu Leu Tyr Gly Leu Ile His Gln
115 120 125

Gly Met Lys Cys Asp Thr Cys Asp Met Asn Val His Lys Gln Cys Val
130 135 140

Ile Asn Val Pro Ser Leu Cys Gly Met Asp His Thr Glu Lys Arg Gly
145 150 155 160

Arg Ile Tyr Leu Lys Ala Glu Val Ala Asp Glu Lys Leu His Val Thr
165 170 175

Val Arg Asp Ala Lys Asn Leu Ile Pro Met Asp Pro Asn Gly Leu Ser
180 185 190

Asp Pro Tyr Val Lys Leu Lys Leu Ile Pro Asp Pro Lys Asn Glu Ser
195 200 205

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Lys Gln Lys Thr Lys Thr Ile Arg Ser Thr Leu Asn Pro Gln Trp Asn
    210                 215                 220

Glu Ser Phe Thr Phe Lys Leu Lys Pro Ser Asp Lys Asp Arg Arg Leu
225                 230                 235                 240

Ser Val Glu Ile Trp Asp Trp Asp Arg Thr Thr Arg Asn Asp Phe Met
                245                 250                 255

Gly Ser Leu Ser Phe Gly Val Ser Glu Leu Met Lys Met Pro Ala Ser
            260                 265                 270

Gly Trp Tyr Lys Leu Leu Asn Gln Glu Glu Gly Glu Tyr Tyr Asn Val
        275                 280                 285

Pro Ile Pro Glu Gly Asp Glu Glu Gly Asn Met Glu Leu Arg Gln Lys
    290                 295                 300

Phe Glu Lys Ala Lys Leu Gly Pro Ala Gly Asn Lys Val Ile Ser Pro
305                 310                 315                 320

Ser Glu Asp Arg Lys Gln Pro Ser Asn Asn Leu Asp Arg Val Lys Leu
                325                 330                 335

Thr Asp Phe Asn Phe Leu Met Val Leu Gly Lys Gly Ser Phe Gly Lys
            340                 345                 350

Val Met Leu Ala Asp Arg Lys Gly Thr Glu Glu Leu Tyr Ala Ile Lys
        355                 360                 365

Ile Leu Lys Lys Asp Val Val Ile Gln Asp Asp Asp Val Glu Cys Thr
    370                 375                 380

Met Val Glu Lys Arg Val Leu Ala Leu Leu Asp Lys Pro Pro Phe Leu
385                 390                 395                 400

Thr Gln Leu His Ser Cys Phe Gln Thr Val Asp Arg Leu Tyr Phe Val
                405                 410                 415

Met Glu Tyr Val Asn Gly Gly Asp Leu Met Tyr His Ile Gln Gln Val
            420                 425                 430

Gly Lys Phe Lys Glu Pro Gln Ala Val Phe Tyr Ala Ala Glu Ile Ser
        435                 440                 445

Ile Gly Leu Phe Phe Leu His Lys Arg Gly Ile Ile Tyr Arg Asp Leu
    450                 455                 460

Lys Leu Asp Asn Val Met Leu Asp Ser Glu Gly His Ile Lys Ile Ala
465                 470                 475                 480
```

Asp Phe Gly Met Cys Lys Glu His Met Met Asp Gly Val Thr Thr Arg
485 490 495

Thr Phe Cys Gly Thr Pro Asp Tyr Ile Ala Pro Glu Ile Ile Ala Tyr
500 505 510

Gln Pro Tyr Gly Lys Ser Val Asp Trp Trp Ala Tyr Gly Val Leu Leu
515 520 525

Tyr Glu Met Leu Ala Gly Gln Pro Pro Phe Asp Gly Glu Asp Glu Asp
530 535 540

Glu Leu Phe Gln Ser Ile Met Glu His Asn Val Ser Tyr Pro Lys Ser
545 550 555 560

Leu Ser Lys Glu Ala Val Ser Ile Cys Lys Gly Leu Met Thr Lys His
565 570 575

Pro Ala Lys Arg Leu Gly Cys Gly Pro Glu Gly Glu Arg Asp Val Arg
580 585 590

Glu His Ala Phe Phe Arg Arg Ile Asp Trp Glu Lys Leu Glu Asn Arg
595 600 605

Glu Ile Gln Pro Pro Phe Lys Pro Lys Val Cys Gly Lys Gly Ala Glu
610 615 620

Asn Phe Asp Lys Phe Phe Thr Arg Gly Gln Pro Val Leu Thr Pro Pro
625 630 635 640

Asp Gln Leu Val Ile Ala Asn Ile Asp Gln Ser Asp Phe Glu Gly Phe
645 650 655

Ser Tyr Val Asn Pro Gln Phe Val His Pro Ile Leu Gln Ser Ala Val
660 665 670

Val

<210> 451
<211> 2334
<212> DNA
<213> Homo sapiens

<400> 451
atggactcca aagaatcatt aactcctggt agagaagaaa accccagcag tgtgcttgct 60

caggagaggg gagatgtgat ggacttctat aaaaccctaa gaggaggagc tactgtgaag 120

gtttctgcgt cttcaccctc actggctgtc gcttctcaat cagactccaa gcagcgaaga 180

cttttggttg attttccaaa aggctcagta agcaatgcgc agcagccaga tctgtccaaa 240

gcagtttcac tctcaatggg actgtatatg ggagagacag aaacaaaagt gatgggaaat 300

gacctgggat tcccacagca gggccaaatc agcctttcct cgggggaaac agacttaaag 360

cttttggaag aaagcattgc aaacctcaat aggtcgacca gtgttccaga gaaccccaag 420

agttcagcat ccactgctgt gtctgctgcc cccacagaga aggagtttcc aaaaactcac 480

tctgatgtat cttcagaaca gcaacatttg aagggccaga ctggcaccaa cggtggcaat 540

gtgaaattgt ataccacaga ccaaagcacc tttgacattt tgcaggattt ggagttttct 600

tctgggtccc caggtaaaga gacgaatgag agtccttgga gatcagacct gttgatagat 660

gaaaactgtt tgctttctcc tctggcggga gaagacgatt cattcctttt ggaaggaaac 720

tcgaatgagg actgcaagcc tctcatttta ccggacacta aacccaaaat taaggataat 780

ggagatctgg ttttgtcaag ccccagtaat gtaacactgc cccaagtgaa aacagaaaaa 840

gaagatttca tcgaactctg caccctgggg gtaattaagc aagagaaact gggcacagtt 900

tactgtcagg caagctttcc tggagcaaat ataattggta ataaaatgtc tgccatttct 960

gttcatggtg tgagtacctc tggaggacag atgtaccact atgacatgaa tacagcatcc 1020

ctttctcaac agcaggatca gaagcctatt tttaatgtca ttccaccaat tcccgttggt 1080

tccgaaaatt ggaataggtg ccaaggatct ggagatgaca acttgacttc tctggggact 1140

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gatgtaagct ctcctccatc cagctcctca acagcaacaa caggaccacc tcccaaactc 1260

tgcctggtgt gctctgatga agcttcagga tgtcattatg gagtcttaac ttgtggaagc 1320

tgtaaagttt tcttcaaaag agcagtggaa ggacagcaca attacctatg tgctggaagg 1380

aatgattgca tcatcgataa aattcgaaga aaaaactgcc cagcatgccg ctatcgaaaa 1440

tgtcttcagg ctggaatgaa cctggaagct cgaaaaacaa agaaaaaaat aaaaggaatt 1500

cagcaggcca ctacaggagt ctcacaagaa acctctgaaa atcctggtaa caaaacaata 1560

gttcctgcaa cgttaccaca actcacccct accctggtgt cactgttgga ggttattgaa 1620

cctgaagtgt tatatgcagg atatgatagc tctgttccag actcaacttg gaggatcatg 1680

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atgtttctta tggcatttgc tctggggtgg agatcatata gacaatcaag tgcaaacctg 1860

ctgtgttttg ctcctgatct gattattaat gagcagagaa tgactctacc ctgcatgtac 1920

gaccaatgta aacacatgct gtatgtttcc tctgagttac acaggcttca ggtatcttat 1980

gaagagtatc tctgtatgaa aaccttactg cttctctctt cagttcctaa ggacggtctg 2040

aagagccaag agctatttga tgaaattaga atgacctaca tcaaagagct aggaaaagcc 2100

attgtcaaga gggaaggaaa ctccagccag aactggcagc ggttttatca actgacaaaa 2160

ctcttggatt ctatgcatga agtggttgaa aatctcctta actattgctt ccaaacattt 2220

ttggataaga ccatgagtat tgaattcccc gagatgttag ctgaaatcat caccaatcag 2280

ataccaaaat attcaaatgg aaatatcaaa aaacttctgt ttcatcaaaa ggtt 2334

<210> 452
<211> 778
<212> PRT
<213> Homo sapiens

<400> 452
Met Asp Ser Lys Glu Ser Leu Thr Pro Gly Arg Glu Glu Asn Pro Ser
1 5 10 15

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

Leu Arg Gly Gly Ala Thr Val Lys Val Ser Ala Ser Ser Pro Ser Leu
35 40 45

Ala Val Ala Ser Gln Ser Asp Ser Lys Gln Arg Arg Leu Leu Val Asp
50 55 60

Phe Pro Lys Gly Ser Val Ser Asn Ala Gln Gln Pro Asp Leu Ser Lys
65 70 75 80

Ala Val Ser Leu Ser Met Gly Leu Tyr Met Gly Glu Thr Glu Thr Lys
85 90 95

Val Met Gly Asn Asp Leu Gly Phe Pro Gln Gln Gly Gln Ile Ser Leu
100 105 110

Ser Ser Gly Glu Thr Asp Leu Lys Leu Leu Glu Glu Ser Ile Ala Asn
115 120 125

Leu Asn Arg Ser Thr Ser Val Pro Glu Asn Pro Lys Ser Ser Ala Ser
130 135 140

Thr Ala Val Ser Ala Ala Pro Thr Glu Lys Glu Phe Pro Lys Thr His
145 150 155 160

Ser Asp Val Ser Ser Glu Gln Gln His Leu Lys Gly Gln Thr Gly Thr
165 170 175

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

Ile Leu Gln Asp Leu Glu Phe Ser Ser Gly Ser Pro Gly Lys Glu Thr
195 200 205

Asn Glu Ser Pro Trp Arg Ser Asp Leu Leu Ile Asp Glu Asn Cys Leu
210 215 220

Leu Ser Pro Leu Ala Gly Glu Asp Asp Ser Phe Leu Leu Glu Gly Asn
225 230 235 240

Ser Asn Glu Asp Cys Lys Pro Leu Ile Leu Pro Asp Thr Lys Pro Lys

245 250 255

Ile Lys Asp Asn Gly Asp Leu Val Leu Ser Ser Pro Ser Asn Val Thr
260 265 270

Leu Pro Gln Val Lys Thr Glu Lys Glu Asp Phe Ile Glu Leu Cys Thr
275 280 285

Pro Gly Val Ile Lys Gln Glu Lys Leu Gly Thr Val Tyr Cys Gln Ala
290 295 300

Ser Phe Pro Gly Ala Asn Ile Ile Gly Asn Lys Met Ser Ala Ile Ser
305 310 315 320

Val His Gly Val Ser Thr Ser Gly Gly Gln Met Tyr His Tyr Asp Met
325 330 335

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

Val Ile Pro Pro Ile Pro Val Gly Ser Glu Asn Trp Asn Arg Cys Gln
355 360 365

Gly Ser Gly Asp Asp Asn Leu Thr Ser Leu Gly Thr Leu Asn Phe Pro
370 375 380

Gly Arg Thr Val Phe Ser Asn Gly Tyr Ser Ser Pro Ser Met Arg Pro
385 390 395 400

Asp Val Ser Ser Pro Pro Ser Ser Ser Ser Thr Ala Thr Thr Gly Pro
405 410 415

Pro Pro Lys Leu Cys Leu Val Cys Ser Asp Glu Ala Ser Gly Cys His
420 425 430

Tyr Gly Val Leu Thr Cys Gly Ser Cys Lys Val Phe Phe Lys Arg Ala
435 440 445

Val Glu Gly Gln His Asn Tyr Leu Cys Ala Gly Arg Asn Asp Cys Ile
450 455 460

Ile Asp Lys Ile Arg Arg Lys Asn Cys Pro Ala Cys Arg Tyr Arg Lys
465 470 475 480

Cys Leu Gln Ala Gly Met Asn Leu Glu Ala Arg Lys Thr Lys Lys Lys
485 490 495

Ile Lys Gly Ile Gln Gln Ala Thr Thr Gly Val Ser Gln Glu Thr Ser
500 505 510

Glu Asn Pro Gly Asn Lys Thr Ile Val Pro Ala Thr Leu Pro Gln Leu

515 520 525

Thr Pro Thr Leu Val Ser Leu Leu Glu Val Ile Glu Pro Glu Val Leu
530 535 540

Tyr Ala Gly Tyr Asp Ser Ser Val Pro Asp Ser Thr Trp Arg Ile Met
545 550 555 560

Thr Thr Leu Asn Met Leu Gly Gly Arg Gln Val Ile Ala Ala Val Lys
565 570 575

Trp Ala Lys Ala Ile Pro Gly Phe Arg Asn Leu His Leu Asp Asp Gln
580 585 590

Met Thr Leu Leu Gln Tyr Ser Trp Met Phe Leu Met Ala Phe Ala Leu
595 600 605

Gly Trp Arg Ser Tyr Arg Gln Ser Ser Ala Asn Leu Leu Cys Phe Ala
610 615 620

Pro Asp Leu Ile Ile Asn Glu Gln Arg Met Thr Leu Pro Cys Met Tyr
625 630 635 640

Asp Gln Cys Lys His Met Leu Tyr Val Ser Ser Glu Leu His Arg Leu
645 650 655

Gln Val Ser Tyr Glu Glu Tyr Leu Cys Met Lys Thr Leu Leu Leu Leu
660 665 670

Ser Ser Val Pro Lys Asp Gly Leu Lys Ser Gln Glu Leu Phe Asp Glu
675 680 685

Ile Arg Met Thr Tyr Ile Lys Glu Leu Gly Lys Ala Ile Val Lys Arg
690 695 700

Glu Gly Asn Ser Ser Gln Asn Trp Gln Arg Phe Tyr Gln Leu Thr Lys
705 710 715 720

Leu Leu Asp Ser Met His Glu Val Val Glu Asn Leu Leu Asn Tyr Cys
725 730 735

Phe Gln Thr Phe Leu Asp Lys Thr Met Ser Ile Glu Phe Pro Glu Met
740 745 750

Leu Ala Glu Ile Ile Thr Asn Gln Ile Pro Lys Tyr Ser Asn Gly Asn
755 760 765

Ile Lys Lys Leu Leu Phe His Gln Lys Val
770 775

<210> 453

<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 453
ggtggttcag gtggtggcgg gagcggtgga gggagcagcg gtggagcgat cgcc 54

<210> 454
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 454
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Ser Gly Gly Ala
1 5 10 15

Ile Ala

<210> 455
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 455
tctctcggtg gttcaggtgg tggcgggagc ggtggaggga gcagcggtgg a 51

<210> 456
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 456
Ser Leu Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Ser Gly
1 5 10 15

Gly

<210> 457
<211> 11
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

oligonucleotide

<400> 457
gctcgagcgg a 11

<210> 458
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 458
Gly Ser Ser Gly
1

<210> 459
<211> 1080
<212> DNA
<213> Homo sapiens

<400> 459
atgattctca actcttctac tgaagatggt attaaaagaa tccaagatga ttgtcccaaa 60

gctggaaggc ataattacat atttgtcatg attcctactt tatacagtat catctttgtg 120

gtgggaatat ttggaaacag cttggtggtg atagtcattt acttttatat gaagctgaag 180

actgtggcca gtgtttttct tttgaattta gcactggctg acttatgctt tttactgact 240

ttgccactat gggctgtcta cacagctatg gaataccgct ggccctttgg caattaccta 300

tgtaagattg cttcagccag cgtcagtttc aacctgtacg ctagtgtgtt tctactcacg 360

tgtctcagca ttgatcgata cctggctatt gttcacccaa tgaagtcccg ccttcgacgc 420

acaatgcttg tagccaaagt cacctgcatc atcatttggc tgctggcagg cttggccagt 480

ttgccagcta taatccatcg aaatgtattt ttcattgaga acaccaatat tacagtttgt 540

gctttccatt atgagtccca aaattcaacc cttccgatag ggctgggcct gaccaaaaat 600

atactgggtt tcctgtttcc ttttctgatc attcttacaa gttatactct tatttggaag 660

gccctaaaga aggcttatga aattcagaag aacaaaccaa gaaatgatga tatttttaag 720

ataattatgg caattgtgct tttctttttc ttttcctgga ttccccacca aatattcact 780

tttctggatg tattgattca actaggcatc atacgtgact gtagaattgc agatattgtg 840

gacacggcca tgcctatcac catttgtata gcttatttta acaattgcct gaatcctctt 900

ttttatggct ttctggggaa aaaatttaaa agatattttc tccagcttct aaaatatatt 960

cccccaaaag ccaaatccca ctcaaacctt tcaacaaaaa tgagcacgct ttcctaccgc 1020

ccctcagata atgtaagctc atccaccaag aagcctgcac catgttttga ggttgagtga 1080

<210> 460
<211> 359
<212> PRT
<213> Homo sapiens

<400> 460

Met Ile Leu Asn Ser Ser Thr Glu Asp Gly Ile Lys Arg Ile Gln Asp
1 5 10 15

Asp Cys Pro Lys Ala Gly Arg His Asn Tyr Ile Phe Val Met Ile Pro
20 25 30

Thr Leu Tyr Ser Ile Ile Phe Val Val Gly Ile Phe Gly Asn Ser Leu
35 40 45

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

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

Leu Pro Leu Trp Ala Val Tyr Thr Ala Met Glu Tyr Arg Trp Pro Phe
85 90 95

Gly Asn Tyr Leu Cys Lys Ile Ala Ser Ala Ser Val Ser Phe Asn Leu
100 105 110

Tyr Ala Ser Val Phe Leu Leu Thr Cys Leu Ser Ile Asp Arg Tyr Leu
115 120 125

Ala Ile Val His Pro Met Lys Ser Arg Leu Arg Arg Thr Met Leu Val
130 135 140

Ala Lys Val Thr Cys Ile Ile Ile Trp Leu Leu Ala Gly Leu Ala Ser
145 150 155 160

Leu Pro Ala Ile Ile His Arg Asn Val Phe Phe Ile Glu Asn Thr Asn
165 170 175

Ile Thr Val Cys Ala Phe His Tyr Glu Ser Gln Asn Ser Thr Leu Pro
180 185 190

Ile Gly Leu Gly Leu Thr Lys Asn Ile Leu Gly Phe Leu Phe Pro Phe
195 200 205

Leu Ile Ile Leu Thr Ser Tyr Thr Leu Ile Trp Lys Ala Leu Lys Lys
210 215 220

Ala Tyr Glu Ile Gln Lys Asn Lys Pro Arg Asn Asp Asp Ile Phe Lys
225 230 235 240

Ile Ile Met Ala Ile Val Leu Phe Phe Phe Phe Ser Trp Ile Pro His
245 250 255

Gln Ile Phe Thr Phe Leu Asp Val Leu Ile Gln Leu Gly Ile Ile Arg
260 265 270

Asp Cys Arg Ile Ala Asp Ile Val Asp Thr Ala Met Pro Ile Thr Ile
275 280 285

Cys Ile Ala Tyr Phe Asn Asn Cys Leu Asn Pro Leu Phe Tyr Gly Phe
290 295 300

Leu Gly Lys Lys Phe Lys Arg Tyr Phe Leu Gln Leu Leu Lys Tyr Ile
305 310 315 320

Pro Pro Lys Ala Lys Ser His Ser Asn Leu Ser Thr Lys Met Ser Thr
325 330 335

Leu Ser Tyr Arg Pro Ser Asp Asn Val Ser Ser Ser Thr Lys Lys Pro
340 345 350

Ala Pro Cys Phe Glu Val Glu
355

<210> 461
<211> 87
<212> DNA
<213> Homo sapiens

<400> 461
atgaactcct tctccacaag cgccttcggt ccagttgcct tctccctggg gctgctcctg 60

gtgttgcctg ctgccttccc tgcccca 87

<210> 462
<211> 29
<212> PRT
<213> Homo sapiens

<400> 462
Met Asn Ser Phe Ser Thr Ser Ala Phe Gly Pro Val Ala Phe Ser Leu
1 5 10 15

Gly Leu Leu Leu Val Leu Pro Ala Ala Phe Pro Ala Pro
20 25

<210> 463
<211> 597
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 463
atgaactcct tctccacaag cgccttcggt ccagttgcct tctccctggg gctgctcctg 60

gtgttgcctg ctgccttccc tgccccagtg tttacactcg aagatttcgt aggggactgg 120

cggcagacag ccggctacaa cctggaccaa gtccttgagc agggcggtgt gtccagtttg 180

tttcagaatc tcggggtgtc cgtaactccg atccaaagga ttgtcctgag cggtgaaaac 240

ggcctgaaga tcgacatcca tgtcatcatc ccgtatgaag gtctgagcgg cgatcagatg 300

ggccagatcg aaaaaatttt taaggtggtg taccctgtgg atgatcatca ctttaaggtg 360

attctgcact atggcacact ggtaatcgac ggggttacgc cgaacatgat cgactatttc 420

ggacggccgt atgaaggcat cgccgtgttc gacggcaaaa agatcactgt aaccgggacc 480

ctgtggaacg gcaacaaaat tatcgacgag cgcctgatca accccgacgg ctccctgctg 540

ttccgcgtaa ccatcaacgg agtgaccggc tggcggctgt gcgagcgcat tttggcg 597

<210> 464
<211> 199
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 464

Met Asn Ser Phe Ser Thr Ser Ala Phe Gly Pro Val Ala Phe Ser Leu
1 5 10 15

Gly Leu Leu Leu Val Leu Pro Ala Ala Phe Pro Ala Pro Val Phe Thr
20 25 30

Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu
35 40 45

Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu Phe Gln Asn Leu
50 55 60

Gly Val Ser Val Thr Pro Ile Gln Arg Ile Val Leu Ser Gly Glu Asn
65 70 75 80

Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr Glu Gly Leu Ser
85 90 95

Gly Asp Gln Met Gly Gln Ile Glu Lys Ile Phe Lys Val Val Tyr Pro
100 105 110

Val Asp Asp His His Phe Lys Val Ile Leu His Tyr Gly Thr Leu Val
115 120 125

Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr
130 135 140

Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr
145 150 155 160

Leu Trp Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp
165 170 175

Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg

180 185 190

Leu Cys Glu Arg Ile Leu Ala
195

<210> 465
<211> 591
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 465
atggcttact ccacactgtt catcattgct ctcacagccg tcgtaacaca agcctcctcc 60

acacagaaaa gcaacctgac agtgtttaca ctcgaagatt tcgtagggga ctggcggcag 120

acagccggct acaacctgga ccaagtcctt gagcagggcg gtgtgtccag tttgtttcag 180

aatctcgggg tgtccgtaac tccgatccaa aggattgtcc tgagcggtga aaacggcctg 240

aagatcgaca tccatgtcat catcccgtat gaaggtctga gcggcgatca gatgggccag 300

atcgaaaaaa tttttaaggt ggtgtaccct gtggatgatc atcactttaa ggtgattctg 360

cactatggca cactggtaat cgacggggtt acgccgaaca tgatcgacta tttcggacgg 420

ccgtatgaag gcatcgccgt gttcgacggc aaaaagatca ctgtaaccgg gaccctgtgg 480

aacggcaaca aaattatcga cgagcgcctg atcaaccccg acggctccct gctgttccgc 540

gtaaccatca acggagtgac cggctggcgg ctgtgcgagc gcattttggc g 591

<210> 466
<211> 197
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 466
Met Ala Tyr Ser Thr Leu Phe Ile Ile Ala Leu Thr Ala Val Val Thr
1 5 10 15

Gln Ala Ser Ser Thr Gln Lys Ser Asn Leu Thr Val Phe Thr Leu Glu
20 25 30

Asp Phe Val Gly Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln
35 40 45

Val Leu Glu Gln Gly Gly Val Ser Ser Leu Phe Gln Asn Leu Gly Val
50 55 60

Ser Val Thr Pro Ile Gln Arg Ile Val Leu Ser Gly Glu Asn Gly Leu
65 70 75 80

Lys Ile Asp Ile His Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp
85 90 95

Gln Met Gly Gln Ile Glu Lys Ile Phe Lys Val Val Tyr Pro Val Asp
100 105 110

Asp His His Phe Lys Val Ile Leu His Tyr Gly Thr Leu Val Ile Asp
115 120 125

Gly Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly
130 135 140

Ile Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr Leu Trp
145 150 155 160

Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly Ser
165 170 175

Leu Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg Leu Cys
180 185 190

Glu Arg Ile Leu Ala
195

<210> 467
<211> 1023
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 467
atgttcgttg gggactggcg acagacagcc ggctacaacc tggaccaagt ccttgaacag 60

ggaggtgtgt ccagtttgtt tcagaatctc ggggtgtccg taactccgat ccaaaggatt 120

gtcctgagcg gtgaaaatgg gctgaagatc gacatccatg tcatcatccc gtatgaaggt 180

ctgagcggcg accaaatggg ccagatcgaa aaaatttta aggtggtgta ccctgtggat 240

gatcatcact ttaaggtgat cctgcactat ggcacactgg taatcgacgg ggttacgccg 300

aacatgatcg actatttcgg acggccgtat gaaggcatcg ccgtgttcga cggcaaaaag 360

atcactgtaa cagggaccct gtggaacggc aacaaaatta tcgacgagcg cctgatcaac 420

cccgacggct ccctgctgtt ccgagtaacc atcaacggag tgaccggctg gcggctgtgc 480

gaacgcattc tggctagctc aagcggaggt tcaggcggtt ccggaatgta tgaaagcttt 540

attgagtcac tgccattcct taaatctttg gagttttctg cacgcctgaa agtagtagat 600

gtgataggca ccaaagtata caacgatgga gaacaaatca ttgctcaggg agattcggct 660

gattcttttt tcattattga atctggagaa gtgaaaatta ctatgaaaag aaagggtaaa 720

tcagaagtgg aagagaatgg tgcagtagaa atcgctcgat gctcgcgggg acagtacttt 780

ggagagcttg ccctggtaac taacaaacct cgagcagctt ctgcccacgc cattgggact 840

gtcaaatgtt tagcaatgga tgtgcaagca tttgaaaggc ttctgggacc ttgcatggaa 900

attatgaaaa ggaacatcgc tacctatgaa gaacagttag ttgccctgta tggaacgaac 960

atggatattg tagggtcagg tggatctgga ggtagctctt ctatggtctt cacactcgaa 1020

gat 1023

<210> 468
<211> 341
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 468

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Met Phe Val Gly Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln
1               5                  10                  15

Val Leu Glu Gln Gly Gly Val Ser Ser Leu Phe Gln Asn Leu Gly Val
            20                  25                  30

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

Lys Ile Asp Ile His Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp
    50                  55                  60

Gln Met Gly Gln Ile Glu Lys Ile Phe Lys Val Val Tyr Pro Val Asp
65                  70                  75                  80

Asp His His Phe Lys Val Ile Leu His Tyr Gly Thr Leu Val Ile Asp
                85                  90                  95

Gly Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly
            100                 105                 110

Ile Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr Leu Trp
        115                 120                 125

Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly Ser
    130                 135                 140

Leu Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg Leu Cys
145                 150                 155                 160

Glu Arg Ile Leu Ala Ser Ser Ser Gly Gly Ser Gly Gly Ser Gly Met
                165                 170                 175

Tyr Glu Ser Phe Ile Glu Ser Leu Pro Phe Leu Lys Ser Leu Glu Phe
            180                 185                 190
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Ser Ala Arg Leu Lys Val Val Asp Val Ile Gly Thr Lys Val Tyr Asn
195 200 205

Asp Gly Glu Gln Ile Ile Ala Gln Gly Asp Ser Ala Asp Ser Phe Phe
210 215 220

Ile Ile Glu Ser Gly Glu Val Lys Ile Thr Met Lys Arg Lys Gly Lys
225 230 235 240

Ser Glu Val Glu Glu Asn Gly Ala Val Glu Ile Ala Arg Cys Ser Arg
245 250 255

Gly Gln Tyr Phe Gly Glu Leu Ala Leu Val Thr Asn Lys Pro Arg Ala
260 265 270

Ala Ser Ala His Ala Ile Gly Thr Val Lys Cys Leu Ala Met Asp Val
275 280 285

Gln Ala Phe Glu Arg Leu Leu Gly Pro Cys Met Glu Ile Met Lys Arg
290 295 300

Asn Ile Ala Thr Tyr Glu Glu Gln Leu Val Ala Leu Tyr Gly Thr Asn
305 310 315 320

Met Asp Ile Val Gly Ser Gly Gly Ser Gly Gly Ser Ser Ser Met Val
325 330 335

Phe Thr Leu Glu Asp
340

<210> 469
<211> 1023
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 469
atgcagacag ccggctacaa cctggaccaa gtccttgaac agggaggtgt gtccagtttg 60

tttcagaatc tcggggtgtc cgtaactccg atccaaagga ttgtcctgag cggtgaaaat 120

gggctgaaga tcgacatcca tgtcatcatc ccgtatgaag gtctgagcgg cgaccaaatg 180

ggccagatcg aaaaaatttt taaggtggtg taccctgtgg atgatcatca ctttaaggtg 240

atcctgcact atggcacact ggtaatcgac ggggttacgc cgaacatgat cgactatttc 300

ggacggccgt atgaaggcat cgccgtgttc gacggcaaaa agatcactgt aacagggacc 360

ctgtggaacg gcaacaaaat tatcgacgag cgcctgatca accccgacgg ctccctgctg 420

ttccgagtaa ccatcaacgg agtgaccggc tggcggctgt gcgaacgcat tctggctagc 480

tcaagcggag gttcaggcgg ttccggaatg tatgaaagct ttattgagtc actgccattc 540

cttaaatctt tggagttttc tgcacgcctg aaagtagtag atgtgatagg caccaaagta 600

tacaacgatg gagaacaaat cattgctcag ggagattcgg ctgattcttt tttcattatt 660

gaatctggag aagtgaaaat tactatgaaa agaaagggta aatcagaagt ggaagagaat 720

ggtgcagtag aaatcgctcg atgctcgcgg ggacagtact ttggagagct tgccctggta 780

actaacaaac ctcgagcagc ttctgcccac gccattggga ctgtcaaatg tttagcaatg 840

gatgtgcaag catttgaaag gcttctggga ccttgcatgg aaattatgaa aaggaacatc 900

gctacctatg aagaacagtt agttgccctg tatggaacga acatggatat tgtagggtca 960

ggtggatctg gaggtagctc ttctatggtc ttcacactcg aagatttcgt tggggactgg 1020

cga 1023

<210> 470
<211> 341
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 470
Met Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly
1 5 10 15

Val Ser Ser Leu Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln
20 25 30

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

Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln Met Gly Gln Ile Glu
50 55 60

Lys Ile Phe Lys Val Val Tyr Pro Val Asp Asp His His Phe Lys Val
65 70 75 80

Ile Leu His Tyr Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met
85 90 95

Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly
100 105 110

Lys Lys Ile Thr Val Thr Gly Thr Leu Trp Asn Gly Asn Lys Ile Ile
115 120 125

Asp Glu Arg Leu Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val Thr
130 135 140

Ile Asn Gly Val Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala Ser
145 150 155 160

Ser Ser Gly Gly Ser Gly Gly Ser Gly Met Tyr Glu Ser Phe Ile Glu
165 170 175

Ser Leu Pro Phe Leu Lys Ser Leu Glu Phe Ser Ala Arg Leu Lys Val
180 185 190

Val Asp Val Ile Gly Thr Lys Val Tyr Asn Asp Gly Glu Gln Ile Ile
195 200 205

Ala Gln Gly Asp Ser Ala Asp Ser Phe Phe Ile Ile Glu Ser Gly Glu
210 215 220

Val Lys Ile Thr Met Lys Arg Lys Gly Lys Ser Glu Val Glu Glu Asn
225 230 235 240

Gly Ala Val Glu Ile Ala Arg Cys Ser Arg Gly Gln Tyr Phe Gly Glu
245 250 255

Leu Ala Leu Val Thr Asn Lys Pro Arg Ala Ala Ser Ala His Ala Ile
260 265 270

Gly Thr Val Lys Cys Leu Ala Met Asp Val Gln Ala Phe Glu Arg Leu
275 280 285

Leu Gly Pro Cys Met Glu Ile Met Lys Arg Asn Ile Ala Thr Tyr Glu
290 295 300

Glu Gln Leu Val Ala Leu Tyr Gly Thr Asn Met Asp Ile Val Gly Ser
305 310 315 320

Gly Gly Ser Gly Gly Ser Ser Ser Met Val Phe Thr Leu Glu Asp Phe
325 330 335

Val Gly Asp Trp Arg
340

<210> 471
<211> 1023
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 471
atgggtgaaa atgggctgaa gatcgacatc catgtcatca tcccgtatga aggtctgagc 60

ggcgaccaaa tgggccagat cgaaaaaatt tttaaggtgg tgtaccctgt ggatgatcat 120

cactttaagg tgatcctgca ctatggcaca ctggtaatcg acggggttac gccgaacatg 180

atcgactatt tcggacggcc gtatgaaggc atcgccgtgt tcgacggcaa aaagatcact 240

gtaacaggga ccctgtggaa cggcaacaaa attatcgacg agcgcctgat caaccccgac 300

ggctccctgc tgttccgagt aaccatcaac ggagtgaccg gctggcggct gtgcgaacgc 360

attctggcta gctcaagcgg aggttcaggc ggttccggaa tgtatgaaag ctttattgag 420

tcactgccat tccttaaatc tttggagttt tctgcacgcc tgaaagtagt agatgtgata 480

ggcaccaaag tatacaacga tggagaacaa atcattgctc agggagattc ggctgattct 540

tttttcatta ttgaatctgg agaagtgaaa attactatga aaagaaaggg taaatcagaa 600

gtggaagaga atggtgcagt agaaatcgct cgatgctcgc ggggacagta ctttggagag 660

cttgccctgg taactaacaa acctcgagca gcttctgccc acgccattgg gactgtcaaa 720

tgtttagcaa tggatgtgca agcatttgaa aggcttctgg gaccttgcat ggaaattatg 780

aaaaggaaca tcgctaccta tgaagaacag ttagttgccc tgtatggaac gaacatggat 840

attgtagggt caggtggatc tggaggtagc tcttctatgg tcttcacact cgaagatttc 900

gttggggact ggcgacagac agccggctac aacctggacc aagtccttga acagggaggt 960

gtgtccagtt tgtttcagaa tctcggggtg tccgtaactc cgatccaaag gattgtcctg 1020

agc 1023

<210> 472
<211> 341
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 472
Met Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr
1 5 10 15

Glu Gly Leu Ser Gly Asp Gln Met Gly Gln Ile Glu Lys Ile Phe Lys
20 25 30

Val Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu His Tyr
35 40 45

Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe
50 55 60

Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr
65 70 75 80

Val Thr Gly Thr Leu Trp Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu
85 90 95

Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val
100 105 110

Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala Ser Ser Ser Gly Gly

115 120 125

Ser Gly Gly Ser Gly Met Tyr Glu Ser Phe Ile Glu Ser Leu Pro Phe
130 135 140

Leu Lys Ser Leu Glu Phe Ser Ala Arg Leu Lys Val Val Asp Val Ile
145 150 155 160

Gly Thr Lys Val Tyr Asn Asp Gly Glu Gln Ile Ile Ala Gln Gly Asp
165 170 175

Ser Ala Asp Ser Phe Phe Ile Ile Glu Ser Gly Glu Val Lys Ile Thr
180 185 190

Met Lys Arg Lys Gly Lys Ser Glu Val Glu Glu Asn Gly Ala Val Glu
195 200 205

Ile Ala Arg Cys Ser Arg Gly Gln Tyr Phe Gly Glu Leu Ala Leu Val
210 215 220

Thr Asn Lys Pro Arg Ala Ala Ser Ala His Ala Ile Gly Thr Val Lys
225 230 235 240

Cys Leu Ala Met Asp Val Gln Ala Phe Glu Arg Leu Leu Gly Pro Cys
245 250 255

Met Glu Ile Met Lys Arg Asn Ile Ala Thr Tyr Glu Glu Gln Leu Val
260 265 270

Ala Leu Tyr Gly Thr Asn Met Asp Ile Val Gly Ser Gly Gly Ser Gly
275 280 285

Gly Ser Ser Ser Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp
290 295 300

Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly
305 310 315 320

Val Ser Ser Leu Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln
325 330 335

Arg Ile Val Leu Ser
340

<210> 473
<211> 1023
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 473
atgctgaaga tcgacatcca tgtcatcatc ccgtatgaag gtctgagcgg cgaccaaatg 60

ggccagatcg aaaaaatttt taaggtggtg taccctgtgg atgatcatca ctttaaggtg 120

atcctgcact atggcacact ggtaatcgac ggggttacgc cgaacatgat cgactatttc 180

ggacggccgt atgaaggcat cgccgtgttc gacggcaaaa agatcactgt aacagggacc 240

ctgtggaacg gcaacaaaat tatcgacgag cgcctgatca accccgacgg ctccctgctg 300

ttccgagtaa ccatcaacgg agtgaccggc tggcggctgt gcgaacgcat tctggctagc 360

tcaagcggag gttcaggcgg ttccggaatg tatgaaagct ttattgagtc actgccattc 420

cttaaatctt tggagttttc tgcacgcctg aaagtagtag atgtgatagg caccaaagta 480

tacaacgatg gagaacaaat cattgctcag ggagattcgg ctgattcttt tttcattatt 540

gaatctggag aagtgaaaat tactatgaaa agaaagggta aatcagaagt ggaagagaat 600

ggtgcagtag aaatcgctcg atgctcgcgg ggacagtact ttggagagct tgccctggta 660

actaacaaac ctcgagcagc ttctgcccac gccattggga ctgtcaaatg tttagcaatg 720

gatgtgcaag catttgaaag gcttctggga ccttgcatgg aaattatgaa aaggaacatc 780

gctacctatg aagaacagtt agttgccctg tatggaacga acatggatat tgtagggtca 840

ggtggatctg gaggtagctc ttctatggtc ttcacactcg aagatttcgt tggggactgg 900

cgacagacag ccggctacaa cctggaccaa gtccttgaac agggaggtgt gtccagtttg 960

tttcagaatc tcggggtgtc cgtaactccg atccaaagga ttgtcctgag cggtgaaaat 1020

ggg 1023

<210> 474
<211> 341
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 474
Met Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr Glu Gly Leu Ser
1 5 10 15

Gly Asp Gln Met Gly Gln Ile Glu Lys Ile Phe Lys Val Val Tyr Pro
20 25 30

Val Asp Asp His His Phe Lys Val Ile Leu His Tyr Gly Thr Leu Val
35 40 45

Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr
50 55 60

Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr
65 70 75 80

```
Leu Trp Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp
                85                  90                  95

Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg
            100                 105                 110

Leu Cys Glu Arg Ile Leu Ala Ser Ser Ser Gly Gly Ser Gly Gly Ser
        115                 120                 125

Gly Met Tyr Glu Ser Phe Ile Glu Ser Leu Pro Phe Leu Lys Ser Leu
    130                 135                 140

Glu Phe Ser Ala Arg Leu Lys Val Val Asp Val Ile Gly Thr Lys Val
145                 150                 155                 160

Tyr Asn Asp Gly Glu Gln Ile Ile Ala Gln Gly Asp Ser Ala Asp Ser
                165                 170                 175

Phe Phe Ile Ile Glu Ser Gly Glu Val Lys Ile Thr Met Lys Arg Lys
            180                 185                 190

Gly Lys Ser Glu Val Glu Glu Asn Gly Ala Val Glu Ile Ala Arg Cys
        195                 200                 205

Ser Arg Gly Gln Tyr Phe Gly Glu Leu Ala Leu Val Thr Asn Lys Pro
    210                 215                 220

Arg Ala Ala Ser Ala His Ala Ile Gly Thr Val Lys Cys Leu Ala Met
225                 230                 235                 240

Asp Val Gln Ala Phe Glu Arg Leu Leu Gly Pro Cys Met Glu Ile Met
                245                 250                 255

Lys Arg Asn Ile Ala Thr Tyr Glu Glu Gln Leu Val Ala Leu Tyr Gly
            260                 265                 270

Thr Asn Met Asp Ile Val Gly Ser Gly Gly Ser Gly Gly Ser Ser Ser
        275                 280                 285

Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala
    290                 295                 300

Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu
305                 310                 315                 320

Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln Arg Ile Val Leu
                325                 330                 335

Ser Gly Glu Asn Gly
            340
```

<210> 475
<211> 1023
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 475
atggacatcc atgtcatcat cccgtatgaa ggtctgagcg gcgaccaaat gggccagatc 60

gaaaaaattt ttaaggtggt gtaccctgtg gatgatcatc actttaaggt gatcctgcac 120

tatggcacac tggtaatcga cggggttacg ccgaacatga tcgactattt cggacggccg 180

tatgaaggca tcgccgtgtt cgacggcaaa aagatcactg taacagggac cctgtggaac 240

ggcaacaaaa ttatcgacga gcgcctgatc aaccccgacg gctccctgct gttccgagta 300

accatcaacg gagtgaccgg ctggcggctg tgcgaacgca ttctggctag ctcaagcgga 360

ggttcaggcg gttccggaat gtatgaaagc tttattgagt cactgccatt ccttaaatct 420

ttggagtttt ctgcacgcct gaaagtagta gatgtgatag gcaccaaagt atacaacgat 480

ggagaacaaa tcattgctca gggagattcg gctgattctt ttttcattat tgaatctgga 540

gaagtgaaaa ttactatgaa aagaaagggt aaatcagaag tggaagagaa tggtgcagta 600

gaaatcgctc gatgctcgcg gggacagtac tttggagagc ttgccctggt aactaacaaa 660

cctcgagcag cttctgccca cgccattggg actgtcaaat gtttagcaat ggatgtgcaa 720

gcatttgaaa ggcttctggg accttgcatg gaaattatga aaaggaacat cgctacctat 780

gaagaacagt tagttgccct gtatggaacg aacatggata ttgtagggtc aggtggatct 840

ggaggtagct cttctatggt cttcacactc gaagatttcg ttggggactg gcgacagaca 900

gccggctaca acctggacca agtccttgaa cagggaggtg tgtccagttt gtttcagaat 960

ctcggggtgt ccgtaactcc gatccaaagg attgtcctga gcggtgaaaa tgggctgaag 1020

atc 1023

<210> 476
<211> 341
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 476
Met Asp Ile His Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln
1 5 10 15

Met Gly Gln Ile Glu Lys Ile Phe Lys Val Val Tyr Pro Val Asp Asp
20 25 30

His His Phe Lys Val Ile Leu His Tyr Gly Thr Leu Val Ile Asp Gly
35 40 45

```
Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly Ile
    50                  55                  60

Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr Leu Trp Asn
65                  70                  75                  80

Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly Ser Leu
                85                  90                  95

Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg Leu Cys Glu
            100                 105                 110

Arg Ile Leu Ala Ser Ser Ser Gly Gly Ser Gly Gly Ser Gly Met Tyr
        115                 120                 125

Glu Ser Phe Ile Glu Ser Leu Pro Phe Leu Lys Ser Leu Glu Phe Ser
    130                 135                 140

Ala Arg Leu Lys Val Val Asp Val Ile Gly Thr Lys Val Tyr Asn Asp
145                 150                 155                 160

Gly Glu Gln Ile Ile Ala Gln Gly Asp Ser Ala Asp Ser Phe Phe Ile
                165                 170                 175

Ile Glu Ser Gly Glu Val Lys Ile Thr Met Lys Arg Lys Gly Lys Ser
            180                 185                 190

Glu Val Glu Glu Asn Gly Ala Val Glu Ile Ala Arg Cys Ser Arg Gly
        195                 200                 205

Gln Tyr Phe Gly Glu Leu Ala Leu Val Thr Asn Lys Pro Arg Ala Ala
    210                 215                 220

Ser Ala His Ala Ile Gly Thr Val Lys Cys Leu Ala Met Asp Val Gln
225                 230                 235                 240

Ala Phe Glu Arg Leu Leu Gly Pro Cys Met Glu Ile Met Lys Arg Asn
                245                 250                 255

Ile Ala Thr Tyr Glu Glu Gln Leu Val Ala Leu Tyr Gly Thr Asn Met
            260                 265                 270

Asp Ile Val Gly Ser Gly Gly Ser Gly Gly Ser Ser Ser Met Val Phe
        275                 280                 285

Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala Gly Tyr Asn
    290                 295                 300

Leu Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu Phe Gln Asn
305                 310                 315                 320
```

Leu Gly Val Ser Val Thr Pro Ile Gln Arg Ile Val Leu Ser Gly Glu
325 330 335

Asn Gly Leu Lys Ile
340

<210> 477
<211> 1023
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 477
atggtggatg atcatcactt taaggtgatc ctgcactatg gcacactggt aatcgacggg 60

gttacgccga acatgatcga ctatttcgga cggccgtatg aaggcatcgc cgtgttcgac 120

ggcaaaaaga tcactgtaac agggaccctg tggaacggca acaaaattat cgacgagcgc 180

ctgatcaacc ccgacggctc cctgctgttc cgagtaacca tcaacggagt gaccggctgg 240

cggctgtgcg aacgcattct ggctagctca agcggaggtt caggcggttc cggaatgtat 300

gaaagcttta ttgagtcact gccattcctt aaatctttgg agttttctgc acgcctgaaa 360

gtagtagatg tgataggcac caaagtatac aacgatggag aacaaatcat tgctcaggga 420

gattcggctg attctttttt cattattgaa tctggagaag tgaaaattac tatgaaaaga 480

aagggtaaat cagaagtgga agagaatggt gcagtagaaa tcgctcgatg ctcgcgggga 540

cagtactttg gagagcttgc cctggtaact aacaaacctc gagcagcttc tgcccacgcc 600

attgggactg tcaaatgttt agcaatggat gtgcaagcat ttgaaaggct tctgggacct 660

tgcatggaaa ttatgaaaag gaacatcgct acctatgaag aacagttagt tgccctgtat 720

ggaacgaaca tggatattgt agggtcaggt ggatctggag gtagctcttc tatggtcttc 780

acactcgaag atttcgttgg ggactggcga cagacagccg gctacaacct ggaccaagtc 840

cttgaacagg gaggtgtgtc cagtttgttt cagaatctcg gggtgtccgt aactccgatc 900

caaaggattg tcctgagcgg tgaaaatggg ctgaagatcg acatccatgt catcatcccg 960

tatgaaggtc tgagcggcga ccaaatgggc cagatcgaaa aaatttttaa ggtggtgtac 1020

cct 1023

<210> 478
<211> 341
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 478
Met Val Asp Asp His His Phe Lys Val Ile Leu His Tyr Gly Thr Leu
1 5 10 15

```
Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro
            20                  25                  30

Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly
        35                  40                  45

Thr Leu Trp Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro
    50                  55                  60

Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp
65                  70                  75                  80

Arg Leu Cys Glu Arg Ile Leu Ala Ser Ser Ser Gly Gly Ser Gly Gly
                85                  90                  95

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

Leu Glu Phe Ser Ala Arg Leu Lys Val Val Asp Val Ile Gly Thr Lys
        115                 120                 125

Val Tyr Asn Asp Gly Glu Gln Ile Ile Ala Gln Gly Asp Ser Ala Asp
    130                 135                 140

Ser Phe Phe Ile Ile Glu Ser Gly Glu Val Lys Ile Thr Met Lys Arg
145                 150                 155                 160

Lys Gly Lys Ser Glu Val Glu Glu Asn Gly Ala Val Glu Ile Ala Arg
                165                 170                 175

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

Pro Arg Ala Ala Ser Ala His Ala Ile Gly Thr Val Lys Cys Leu Ala
        195                 200                 205

Met Asp Val Gln Ala Phe Glu Arg Leu Leu Gly Pro Cys Met Glu Ile
    210                 215                 220

Met Lys Arg Asn Ile Ala Thr Tyr Glu Glu Gln Leu Val Ala Leu Tyr
225                 230                 235                 240

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

Ser Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr
            260                 265                 270

Ala Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser
        275                 280                 285
```

Leu Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln Arg Ile Val
290 295 300

Leu Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro
305 310 315 320

Tyr Glu Gly Leu Ser Gly Asp Gln Met Gly Gln Ile Glu Lys Ile Phe
325 330 335

Lys Val Val Tyr Pro
340

<210> 479
<211> 1023
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 479
atggatgatc atcactttaa ggtgatcctg cactatggca cactggtaat cgacggggtt 60

acgccgaaca tgatcgacta tttcggacgg ccgtatgaag gcatcgccgt gttcgacggc 120

aaaaagatca ctgtaacagg gaccctgtgg aacggcaaca aaattatcga cgagcgcctg 180

atcaaccccg acggctccct gctgttccga gtaaccatca acggagtgac cggctggcgg 240

ctgtgcgaac gcattctggc tagctcaagc ggaggttcag gcggttccgg aatgtatgaa 300

agctttattg agtcactgcc attccttaaa tctttggagt tttctgcacg cctgaaagta 360

gtagatgtga taggcaccaa agtatacaac gatggagaac aaatcattgc tcagggagat 420

tcggctgatt ctttttcat tattgaatct ggagaagtga aaattactat gaaaagaaag 480

ggtaaatcag aagtggaaga gaatggtgca gtagaaatcg ctcgatgctc gcggggacag 540

tactttggag agcttgccct ggtaactaac aaacctcgag cagcttctgc ccacgccatt 600

gggactgtca aatgtttagc aatggatgtg caagcatttg aaaggcttct gggaccttgc 660

atggaaatta tgaaaaggaa catcgctacc tatgaagaac agttagttgc cctgtatgga 720

acgaacatgg atattgtagg gtcaggtgga tctggaggta gctcttctat ggtcttcaca 780

ctcgaagatt tcgttgggga ctggcgacag acagccggct acaacctgga ccaagtcctt 840

gaacagggag gtgtgtccag tttgtttcag aatctcgggg tgtccgtaac tccgatccaa 900

aggattgtcc tgagcggtga aaatgggctg aagatcgaca tccatgtcat catcccgtat 960

gaaggtctga gcggcgacca aatgggccag atcgaaaaaa tttttaaggt ggtgtaccct 1020

gtg 1023

<210> 480
<211> 341
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 480
Met Asp Asp His His Phe Lys Val Ile Leu His Tyr Gly Thr Leu Val
1 5 10 15

Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr
20 25 30

Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr
35 40 45

Leu Trp Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp
50 55 60

Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg
65 70 75 80

Leu Cys Glu Arg Ile Leu Ala Ser Ser Ser Gly Gly Ser Gly Gly Ser
85 90 95

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

Glu Phe Ser Ala Arg Leu Lys Val Val Asp Val Ile Gly Thr Lys Val
115 120 125

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

Phe Phe Ile Ile Glu Ser Gly Glu Val Lys Ile Thr Met Lys Arg Lys
145 150 155 160

Gly Lys Ser Glu Val Glu Glu Asn Gly Ala Val Glu Ile Ala Arg Cys
165 170 175

Ser Arg Gly Gln Tyr Phe Gly Glu Leu Ala Leu Val Thr Asn Lys Pro
180 185 190

Arg Ala Ala Ser Ala His Ala Ile Gly Thr Val Lys Cys Leu Ala Met
195 200 205

Asp Val Gln Ala Phe Glu Arg Leu Leu Gly Pro Cys Met Glu Ile Met
210 215 220

Lys Arg Asn Ile Ala Thr Tyr Glu Glu Gln Leu Val Ala Leu Tyr Gly
225 230 235 240

Thr Asn Met Asp Ile Val Gly Ser Gly Gly Ser Gly Gly Ser Ser Ser

245 250 255

Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala
260 265 270

Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu
275 280 285

Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln Arg Ile Val Leu
290 295 300

Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr
305 310 315 320

Glu Gly Leu Ser Gly Asp Gln Met Gly Gln Ile Glu Lys Ile Phe Lys
325 330 335

Val Val Tyr Pro Val
340

<210> 481
<211> 1023
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 481
atgacgccga acatgatcga ctatttcgga cggccgtatg aaggcatcgc cgtgttcgac 60

ggcaaaaaga tcactgtaac agggaccctg tggaacggca acaaaattat cgacgagcgc 120

ctgatcaacc ccgacggctc cctgctgttc cgagtaacca tcaacggagt gaccggctgg 180

cggctgtgcg aacgcattct ggctagctca agcggaggtt caggcggttc cggaatgtat 240

gaaagcttta ttgagtcact gccattcctt aaatctttgg agttttctgc acgcctgaaa 300

gtagtagatg tgataggcac caaagtatac aacgatggag aacaaatcat tgctcaggga 360

gattcggctg attcttttt cattattgaa tctggagaag tgaaaattac tatgaaaaga 420

aagggtaaat cagaagtgga agagaatggt gcagtagaaa tcgctcgatg ctcgcgggga 480

cagtactttg gagagcttgc cctggtaact aacaaacctc gagcagcttc tgcccacgcc 540

attgggactg tcaaatgttt agcaatggat gtgcaagcat ttgaaaggct tctgggacct 600

tgcatggaaa ttatgaaaag gaacatcgct acctatgaag aacagttagt tgccctgtat 660

ggaacgaaca tggatattgt agggtcaggt ggatctggag gtagctcttc tatggtcttc 720

acactcgaag atttcgttgg ggactggcga cagacagccg gctacaacct ggaccaagtc 780

cttgaacagg gaggtgtgtc cagtttgttt cagaatctcg gggtgtccgt aactccgatc 840

caaaggattg tcctgagcgg tgaaaatggg ctgaagatcg acatccatgt catcatcccg 900

tatgaaggtc tgagcggcga ccaaatgggc cagatcgaaa aaatttttaa ggtggtgtac 960

cctgtggatg atcatcactt taaggtgatc ctgcactatg gcacactggt aatcgacggg 1020

gtt 1023

<210> 482
<211> 341
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 482
Met Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly Ile
1 5 10 15

Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr Leu Trp Asn
20 25 30

Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly Ser Leu
35 40 45

Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg Leu Cys Glu
50 55 60

Arg Ile Leu Ala Ser Ser Ser Gly Gly Ser Gly Gly Ser Gly Met Tyr
65 70 75 80

Glu Ser Phe Ile Glu Ser Leu Pro Phe Leu Lys Ser Leu Glu Phe Ser
85 90 95

Ala Arg Leu Lys Val Val Asp Val Ile Gly Thr Lys Val Tyr Asn Asp
100 105 110

Gly Glu Gln Ile Ile Ala Gln Gly Asp Ser Ala Asp Ser Phe Phe Ile
115 120 125

Ile Glu Ser Gly Glu Val Lys Ile Thr Met Lys Arg Lys Gly Lys Ser
130 135 140

Glu Val Glu Glu Asn Gly Ala Val Glu Ile Ala Arg Cys Ser Arg Gly
145 150 155 160

Gln Tyr Phe Gly Glu Leu Ala Leu Val Thr Asn Lys Pro Arg Ala Ala
165 170 175

Ser Ala His Ala Ile Gly Thr Val Lys Cys Leu Ala Met Asp Val Gln
180 185 190

Ala Phe Glu Arg Leu Leu Gly Pro Cys Met Glu Ile Met Lys Arg Asn
195 200 205

Ile Ala Thr Tyr Glu Glu Gln Leu Val Ala Leu Tyr Gly Thr Asn Met
210 215 220

Asp Ile Val Gly Ser Gly Gly Ser Gly Gly Ser Ser Ser Met Val Phe
225 230 235 240

Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala Gly Tyr Asn
245 250 255

Leu Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu Phe Gln Asn
260 265 270

Leu Gly Val Ser Val Thr Pro Ile Gln Arg Ile Val Leu Ser Gly Glu
275 280 285

Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr Glu Gly Leu
290 295 300

Ser Gly Asp Gln Met Gly Gln Ile Glu Lys Ile Phe Lys Val Val Tyr
305 310 315 320

Pro Val Asp Asp His His Phe Lys Val Ile Leu His Tyr Gly Thr Leu
325 330 335

Val Ile Asp Gly Val
340

<210> 483
<211> 1023
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 483
atgttcgacg gcaaaaagat cactgtaaca gggaccctgt ggaacggcaa caaaattatc 60

gacgagcgcc tgatcaaccc cgacggctcc ctgctgttcc gagtaaccat caacggagtg 120

accggctggc ggctgtgcga acgcattctg gctagctcaa gcggaggttc aggcggttcc 180

ggaatgtatg aaagctttat tgagtcactg ccattcctta aatctttgga gttttctgca 240

cgcctgaaag tagtagatgt gataggcacc aaagtataca acgatggaga acaaatcatt 300

gctcagggag attcggctga ttctttttc attattgaat ctggagaagt gaaaattact 360

atgaaaagaa agggtaaatc agaagtggaa gagaatggtg cagtagaaat cgctcgatgc 420

tcgcggggac agtactttgg agagcttgcc ctggtaacta acaaacctcg agcagcttct 480

gcccacgcca ttgggactgt caaatgttta gcaatggatg tgcaagcatt tgaaaggctt 540

ctgggacctt gcatggaaat tatgaaaagg aacatcgcta cctatgaaga acagttagtt 600

gccctgtatg gaacgaacat ggatattgta gggtcaggtg gatctggagg tagctcttct 660

atggtcttca cactcgaaga tttcgttggg gactggcgac agacagccgg ctacaacctg 720

gaccaagtcc ttgaacaggg aggtgtgtcc agtttgtttc agaatctcgg ggtgtccgta 780

actccgatcc aaaggattgt cctgagcggt gaaaatgggc tgaagatcga catccatgtc 840

atcatcccgt atgaaggtct gagcggcgac caaatgggcc agatcgaaaa aatttttaag 900

gtggtgtacc ctgtggatga tcatcacttt aaggtgatcc tgcactatgg cacactggta 960

atcgacgggg ttacgccgaa catgatcgac tatttcggac ggccgtatga aggcatcgcc 1020

gtg 1023

<210> 484
<211> 341
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 484

Met Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr Leu Trp Asn Gly
1 5 10 15

Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly Ser Leu Leu
20 25 30

Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg Leu Cys Glu Arg
35 40 45

Ile Leu Ala Ser Ser Ser Gly Gly Ser Gly Gly Ser Gly Met Tyr Glu
50 55 60

Ser Phe Ile Glu Ser Leu Pro Phe Leu Lys Ser Leu Glu Phe Ser Ala
65 70 75 80

Arg Leu Lys Val Val Asp Val Ile Gly Thr Lys Val Tyr Asn Asp Gly
85 90 95

Glu Gln Ile Ile Ala Gln Gly Asp Ser Ala Asp Ser Phe Phe Ile Ile
100 105 110

Glu Ser Gly Glu Val Lys Ile Thr Met Lys Arg Lys Gly Lys Ser Glu
115 120 125

Val Glu Glu Asn Gly Ala Val Glu Ile Ala Arg Cys Ser Arg Gly Gln
130 135 140

Tyr Phe Gly Glu Leu Ala Leu Val Thr Asn Lys Pro Arg Ala Ala Ser
145 150 155 160

Ala His Ala Ile Gly Thr Val Lys Cys Leu Ala Met Asp Val Gln Ala
165 170 175

Phe Glu Arg Leu Leu Gly Pro Cys Met Glu Ile Met Lys Arg Asn Ile
180 185 190

Ala Thr Tyr Glu Glu Gln Leu Val Ala Leu Tyr Gly Thr Asn Met Asp
195 200 205

Ile Val Gly Ser Gly Gly Ser Gly Gly Ser Ser Ser Met Val Phe Thr
210 215 220

Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu
225 230 235 240

Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu Phe Gln Asn Leu
245 250 255

Gly Val Ser Val Thr Pro Ile Gln Arg Ile Val Leu Ser Gly Glu Asn
260 265 270

Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr Glu Gly Leu Ser
275 280 285

Gly Asp Gln Met Gly Gln Ile Glu Lys Ile Phe Lys Val Val Tyr Pro
290 295 300

Val Asp Asp His His Phe Lys Val Ile Leu His Tyr Gly Thr Leu Val
305 310 315 320

Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr
325 330 335

Glu Gly Ile Ala Val
340

<210> 485
<211> 1023
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 485
atgaaaaaga tcactgtaac agggaccctg tggaacggca acaaaattat cgacgagcgc 60

ctgatcaacc ccgacggctc cctgctgttc cgagtaacca tcaacggagt gaccggctgg 120

cggctgtgcg aacgcattct ggctagctca agcggaggtt caggcggttc cggaatgtat 180

gaaagcttta ttgagtcact gccattcctt aaatctttgg agttttctgc acgcctgaaa 240

gtagtagatg tgataggcac caaagtatac aacgatggag aacaaatcat tgctcaggga 300

gattcggctg attcttttt cattattgaa tctggagaag tgaaaattac tatgaaaaga 360

aagggtaaat cagaagtgga agagaatggt gcagtagaaa tcgctcgatg ctcgcgggga 420

cagtactttg gagagcttgc cctggtaact aacaaacctc gagcagcttc tgcccacgcc 480

attgggactg tcaaatgttt agcaatggat gtgcaagcat ttgaaaggct tctgggacct 540

tgcatggaaa ttatgaaaag gaacatcgct acctatgaag aacagttagt tgccctgtat 600

ggaacgaaca tggatattgt agggtcaggt ggatctggag gtagctcttc tatggtcttc 660

acactcgaag atttcgttgg ggactggcga cagacagccg gctacaacct ggaccaagtc 720

cttgaacagg gaggtgtgtc cagtttgttt cagaatctcg gggtgtccgt aactccgatc 780

caaaggattg tcctgagcgg tgaaaatggg ctgaagatcg acatccatgt catcatcccg 840

tatgaaggtc tgagcggcga ccaaatgggc cagatcgaaa aaatttttaa ggtggtgtac 900

cctgtggatg atcatcactt taaggtgatc ctgcactatg gcacactggt aatcgacggg 960

gttacgccga acatgatcga ctatttcgga cggccgtatg aaggcatcgc cgtgttcgac 1020

ggc 1023

<210> 486
<211> 341
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 486
Met Lys Lys Ile Thr Val Thr Gly Thr Leu Trp Asn Gly Asn Lys Ile
1 5 10 15

Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val
20 25 30

Thr Ile Asn Gly Val Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala
35 40 45

Ser Ser Ser Gly Gly Ser Gly Gly Ser Gly Met Tyr Glu Ser Phe Ile
50 55 60

Glu Ser Leu Pro Phe Leu Lys Ser Leu Glu Phe Ser Ala Arg Leu Lys
65 70 75 80

Val Val Asp Val Ile Gly Thr Lys Val Tyr Asn Asp Gly Glu Gln Ile
85 90 95

Ile Ala Gln Gly Asp Ser Ala Asp Ser Phe Phe Ile Ile Glu Ser Gly
100 105 110

Glu Val Lys Ile Thr Met Lys Arg Lys Gly Lys Ser Glu Val Glu Glu
115 120 125

Asn Gly Ala Val Glu Ile Ala Arg Cys Ser Arg Gly Gln Tyr Phe Gly
130 135 140

Glu Leu Ala Leu Val Thr Asn Lys Pro Arg Ala Ala Ser Ala His Ala
145 150 155 160

Ile Gly Thr Val Lys Cys Leu Ala Met Asp Val Gln Ala Phe Glu Arg
165 170 175

Leu Leu Gly Pro Cys Met Glu Ile Met Lys Arg Asn Ile Ala Thr Tyr
180 185 190

Glu Glu Gln Leu Val Ala Leu Tyr Gly Thr Asn Met Asp Ile Val Gly
195 200 205

Ser Gly Gly Ser Gly Gly Ser Ser Ser Met Val Phe Thr Leu Glu Asp
210 215 220

Phe Val Gly Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val
225 230 235 240

Leu Glu Gln Gly Gly Val Ser Ser Leu Phe Gln Asn Leu Gly Val Ser
245 250 255

Val Thr Pro Ile Gln Arg Ile Val Leu Ser Gly Glu Asn Gly Leu Lys
260 265 270

Ile Asp Ile His Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln
275 280 285

Met Gly Gln Ile Glu Lys Ile Phe Lys Val Val Tyr Pro Val Asp Asp
290 295 300

His His Phe Lys Val Ile Leu His Tyr Gly Thr Leu Val Ile Asp Gly
305 310 315 320

Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly Ile
325 330 335

Ala Val Phe Asp Gly
340

<210> 487
<211> 1023
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 487
atgaagatca ctgtaacagg gaccctgtgg aacggcaaca aaattatcga cgagcgcctg 60

atcaaccccg acggctccct gctgttccga gtaaccatca acggagtgac cggctggcgg 120

ctgtgcgaac gcattctggc tagctcaagc ggaggttcag gcggttccgg aatgtatgaa 180

agctttattg agtcactgcc attccttaaa tctttggagt tttctgcacg cctgaaagta 240

gtagatgtga taggcaccaa agtatacaac gatggagaac aaatcattgc tcagggagat 300

tcggctgatt ctttttcat tattgaatct ggagaagtga aaattactat gaaaagaaag 360

ggtaaatcag aagtggaaga gaatggtgca gtagaaatcg ctcgatgctc gcggggacag 420

tactttggag agcttgccct ggtaactaac aaacctcgag cagcttctgc ccacgccatt 480

gggactgtca aatgtttagc aatggatgtg caagcatttg aaaggcttct gggaccttgc 540

atggaaatta tgaaaaggaa catcgctacc tatgaagaac agttagttgc cctgtatgga 600

acgaacatgg atattgtagg gtcaggtgga tctggaggta gctcttctat ggtcttcaca 660

ctcgaagatt tcgttgggga ctggcgacag acagccggct acaacctgga ccaagtcctt 720

gaacagggag gtgtgtccag tttgtttcag aatctcgggg tgtccgtaac tccgatccaa 780

aggattgtcc tgagcggtga aaatgggctg aagatcgaca tccatgtcat catcccgtat 840

gaaggtctga gcggcgacca aatgggccag atcgaaaaaa tttttaaggt ggtgtaccct 900

gtggatgatc atcactttaa ggtgatcctg cactatggca cactggtaat cgacggggtt 960

acgccgaaca tgatcgacta tttcggacgg ccgtatgaag gcatcgccgt gttcgacggc 1020

aaa 1023

<210> 488
<211> 341
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 488
Met Lys Ile Thr Val Thr Gly Thr Leu Trp Asn Gly Asn Lys Ile Ile
1 5 10 15

Asp Glu Arg Leu Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val Thr
20 25 30

Ile Asn Gly Val Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala Ser
35 40 45

Ser Ser Gly Gly Ser Gly Gly Ser Gly Met Tyr Glu Ser Phe Ile Glu
50 55 60

Ser Leu Pro Phe Leu Lys Ser Leu Glu Phe Ser Ala Arg Leu Lys Val
65 70 75 80

Val Asp Val Ile Gly Thr Lys Val Tyr Asn Asp Gly Glu Gln Ile Ile
85 90 95

Ala Gln Gly Asp Ser Ala Asp Ser Phe Phe Ile Ile Glu Ser Gly Glu

100 105 110

Val Lys Ile Thr Met Lys Arg Lys Gly Lys Ser Glu Val Glu Glu Asn
115 120 125

Gly Ala Val Glu Ile Ala Arg Cys Ser Arg Gly Gln Tyr Phe Gly Glu
130 135 140

Leu Ala Leu Val Thr Asn Lys Pro Arg Ala Ala Ser Ala His Ala Ile
145 150 155 160

Gly Thr Val Lys Cys Leu Ala Met Asp Val Gln Ala Phe Glu Arg Leu
165 170 175

Leu Gly Pro Cys Met Glu Ile Met Lys Arg Asn Ile Ala Thr Tyr Glu
180 185 190

Glu Gln Leu Val Ala Leu Tyr Gly Thr Asn Met Asp Ile Val Gly Ser
195 200 205

Gly Gly Ser Gly Gly Ser Ser Ser Met Val Phe Thr Leu Glu Asp Phe
210 215 220

Val Gly Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val Leu
225 230 235 240

Glu Gln Gly Gly Val Ser Ser Leu Phe Gln Asn Leu Gly Val Ser Val
245 250 255

Thr Pro Ile Gln Arg Ile Val Leu Ser Gly Glu Asn Gly Leu Lys Ile
260 265 270

Asp Ile His Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln Met
275 280 285

Gly Gln Ile Glu Lys Ile Phe Lys Val Val Tyr Pro Val Asp Asp His
290 295 300

His Phe Lys Val Ile Leu His Tyr Gly Thr Leu Val Ile Asp Gly Val
305 310 315 320

Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly Ile Ala
325 330 335

Val Phe Asp Gly Lys
340

<210> 489
<211> 1023
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 489
atgatcactg taacagggac cctgtggaac ggcaacaaaa ttatcgacga gcgcctgatc 60

aaccccgacg gctccctgct gttccgagta accatcaacg gagtgaccgg ctggcggctg 120

tgcgaacgca ttctggctag ctcaagcgga ggttcaggcg gttccggaat gtatgaaagc 180

tttattgagt cactgccatt ccttaaatct ttggagtttt ctgcacgcct gaaagtagta 240

gatgtgatag gcaccaaagt atacaacgat ggagaacaaa tcattgctca gggagattcg 300

gctgattctt ttttcattat tgaatctgga gaagtgaaaa ttactatgaa aagaaagggt 360

aaatcagaag tggaagagaa tggtgcagta gaaatcgctc gatgctcgcg gggacagtac 420

tttggagagc ttgccctggt aactaacaaa cctcgagcag cttctgccca cgccattggg 480

actgtcaaat gtttagcaat ggatgtgcaa gcatttgaaa ggcttctggg accttgcatg 540

gaaattatga aaaggaacat cgctacctat gaagaacagt tagttgccct gtatggaacg 600

aacatggata ttgtagggtc aggtggatct ggaggtagct cttctatggt cttcacactc 660

gaagatttcg ttggggactg gcgacagaca gccggctaca acctggacca agtccttgaa 720

cagggaggtg tgtccagttt gtttcagaat ctcggggtgt ccgtaactcc gatccaaagg 780

attgtcctga gcggtgaaaa tgggctgaag atcgacatcc atgtcatcat cccgtatgaa 840

ggtctgagcg gcgaccaaat gggccagatc gaaaaaattt ttaaggtggt gtaccctgtg 900

gatgatcatc actttaaggt gatcctgcac tatggcacac tggtaatcga cggggttacg 960

ccgaacatga tcgactattt cggacggccg tatgaaggca tcgccgtgtt cgacggcaaa 1020

aag 1023

<210> 490
<211> 341
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 490
Met Ile Thr Val Thr Gly Thr Leu Trp Asn Gly Asn Lys Ile Ile Asp
1 5 10 15

Glu Arg Leu Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile
20 25 30

Asn Gly Val Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala Ser Ser
35 40 45

Ser Gly Gly Ser Gly Gly Ser Gly Met Tyr Glu Ser Phe Ile Glu Ser
50 55 60

```
Leu Pro Phe Leu Lys Ser Leu Glu Phe Ser Ala Arg Leu Lys Val Val
65                  70                  75                  80

Asp Val Ile Gly Thr Lys Val Tyr Asn Asp Gly Glu Gln Ile Ile Ala
                85                  90                  95

Gln Gly Asp Ser Ala Asp Ser Phe Phe Ile Ile Glu Ser Gly Glu Val
            100                 105                 110

Lys Ile Thr Met Lys Arg Lys Gly Lys Ser Glu Val Glu Glu Asn Gly
        115                 120                 125

Ala Val Glu Ile Ala Arg Cys Ser Arg Gly Gln Tyr Phe Gly Glu Leu
    130                 135                 140

Ala Leu Val Thr Asn Lys Pro Arg Ala Ala Ser Ala His Ala Ile Gly
145                 150                 155                 160

Thr Val Lys Cys Leu Ala Met Asp Val Gln Ala Phe Glu Arg Leu Leu
                165                 170                 175

Gly Pro Cys Met Glu Ile Met Lys Arg Asn Ile Ala Thr Tyr Glu Glu
            180                 185                 190

Gln Leu Val Ala Leu Tyr Gly Thr Asn Met Asp Ile Val Gly Ser Gly
        195                 200                 205

Gly Ser Gly Gly Ser Ser Ser Met Val Phe Thr Leu Glu Asp Phe Val
    210                 215                 220

Gly Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val Leu Glu
225                 230                 235                 240

Gln Gly Gly Val Ser Ser Leu Phe Gln Asn Leu Gly Val Ser Val Thr
                245                 250                 255

Pro Ile Gln Arg Ile Val Leu Ser Gly Glu Asn Gly Leu Lys Ile Asp
            260                 265                 270

Ile His Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln Met Gly
        275                 280                 285

Gln Ile Glu Lys Ile Phe Lys Val Val Tyr Pro Val Asp Asp His His
    290                 295                 300

Phe Lys Val Ile Leu His Tyr Gly Thr Leu Val Ile Asp Gly Val Thr
305                 310                 315                 320

Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly Ile Ala Val
                325                 330                 335
```

Phe Asp Gly Lys Lys
340

<210> 491
<211> 1023
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 491
atgaccctgt ggaacggcaa caaaattatc gacgagcgcc tgatcaaccc cgacggctcc 60

ctgctgttcc gagtaaccat caacggagtg accggctggc ggctgtgcga acgcattctg 120

gctagctcaa gcggaggttc aggcggttcc ggaatgtatg aaagctttat tgagtcactg 180

ccattcctta aatctttgga gttttctgca cgcctgaaag tagtagatgt gataggcacc 240

aaagtataca acgatggaga acaaatcatt gctcagggag attcggctga ttctttttc 300

attattgaat ctggagaagt gaaaattact atgaaaagaa agggtaaatc agaagtggaa 360

gagaatggtg cagtagaaat cgctcgatgc tcgcggggac agtactttgg agagcttgcc 420

ctggtaacta acaaacctcg agcagcttct gcccacgcca ttgggactgt caaatgttta 480

gcaatggatg tgcaagcatt tgaaaggctt ctgggacctt gcatggaaat tatgaaaagg 540

aacatcgcta cctatgaaga acagttagtt gccctgtatg gaacgaacat ggatattgta 600

gggtcaggtg gatctggagg tagctcttct atggtcttca cactcgaaga tttcgttggg 660

gactggcgac agacagccgg ctacaacctg gaccaagtcc ttgaacaggg aggtgtgtcc 720

agtttgtttc agaatctcgg ggtgtccgta actccgatcc aaaggattgt cctgagcggt 780

gaaaatgggc tgaagatcga catccatgtc atcatcccgt atgaaggtct gagcggcgac 840

caaatgggcc agatcgaaaa aatttttaag gtggtgtacc ctgtggatga tcatcacttt 900

aaggtgatcc tgcactatgg cacactggta atcgacgggg ttacgccgaa catgatcgac 960

tatttcggac ggccgtatga aggcatcgcc gtgttcgacg gcaaaaagat cactgtaaca 1020

ggg 1023

<210> 492
<211> 341
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 492
Met Thr Leu Trp Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn
1 5 10 15

Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly
20 25 30

```
Trp Arg Leu Cys Glu Arg Ile Leu Ala Ser Ser Ser Gly Gly Ser Gly
        35                  40                  45

Gly Ser Gly Met Tyr Glu Ser Phe Ile Glu Ser Leu Pro Phe Leu Lys
    50                  55                  60

Ser Leu Glu Phe Ser Ala Arg Leu Lys Val Val Asp Val Ile Gly Thr
65                  70                  75                  80

Lys Val Tyr Asn Asp Gly Glu Gln Ile Ile Ala Gln Gly Asp Ser Ala
                85                  90                  95

Asp Ser Phe Phe Ile Ile Glu Ser Gly Glu Val Lys Ile Thr Met Lys
            100                 105                 110

Arg Lys Gly Lys Ser Glu Val Glu Glu Asn Gly Ala Val Glu Ile Ala
        115                 120                 125

Arg Cys Ser Arg Gly Gln Tyr Phe Gly Glu Leu Ala Leu Val Thr Asn
    130                 135                 140

Lys Pro Arg Ala Ala Ser Ala His Ala Ile Gly Thr Val Lys Cys Leu
145                 150                 155                 160

Ala Met Asp Val Gln Ala Phe Glu Arg Leu Leu Gly Pro Cys Met Glu
                165                 170                 175

Ile Met Lys Arg Asn Ile Ala Thr Tyr Glu Glu Gln Leu Val Ala Leu
            180                 185                 190

Tyr Gly Thr Asn Met Asp Ile Val Gly Ser Gly Gly Ser Gly Gly Ser
        195                 200                 205

Ser Ser Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln
    210                 215                 220

Thr Ala Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Val Ser
225                 230                 235                 240

Ser Leu Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln Arg Ile
                245                 250                 255

Val Leu Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile
            260                 265                 270

Pro Tyr Glu Gly Leu Ser Gly Asp Gln Met Gly Gln Ile Glu Lys Ile
        275                 280                 285

Phe Lys Val Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu
    290                 295                 300
```

His Tyr Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp
305 310 315 320

Tyr Phe Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys
325 330 335

Ile Thr Val Thr Gly
340

<210> 493
<211> 1023
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 493
atgcccgacg gctccctgct gttccgagta accatcaacg gagtgaccgg ctggcggctg 60

tgcgaacgca ttctggctag ctcaagcgga ggttcaggcg gttccggaat gtatgaaagc 120

tttattgagt cactgccatt ccttaaatct ttggagtttt ctgcacgcct gaaagtagta 180

gatgtgatag gcaccaaagt atacaacgat ggagaacaaa tcattgctca gggagattcg 240

gctgattctt ttttcattat tgaatctgga gaagtgaaaa ttactatgaa aagaaagggt 300

aaatcagaag tggaagagaa tggtgcagta gaaatcgctc gatgctcgcg gggacagtac 360

tttggagagc ttgccctggt aactaacaaa cctcgagcag cttctgccca cgccattggg 420

actgtcaaat gtttagcaat ggatgtgcaa gcatttgaaa ggcttctggg accttgcatg 480

gaaattatga aaaggaacat cgctacctat gaagaacagt tagttgccct gtatggaacg 540

aacatggata ttgtagggtc aggtggatct ggaggtagct cttctatggt cttcacactc 600

gaagatttcg ttggggactg gcgacagaca gccggctaca acctggacca agtccttgaa 660

cagggaggtg tgtccagttt gtttcagaat ctcggggtgt ccgtaactcc gatccaaagg 720

attgtcctga gcggtgaaaa tgggctgaag atcgacatcc atgtcatcat cccgtatgaa 780

ggtctgagcg gcgaccaaat gggccagatc gaaaaaattt ttaaggtggt gtaccctgtg 840

gatgatcatc actttaaggt gatcctgcac tatggcacac tggtaatcga cggggttacg 900

ccgaacatga tcgactattt cggacggccg tatgaaggca tcgccgtgtt cgacggcaaa 960

aagatcactg taacagggac cctgtggaac ggcaacaaaa ttatcgacga gcgcctgatc 1020

aac 1023

<210> 494
<211> 341
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 494
Met Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val Thr
1 5 10 15

Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala Ser Ser Ser Gly Gly Ser
20 25 30

Gly Gly Ser Gly Met Tyr Glu Ser Phe Ile Glu Ser Leu Pro Phe Leu
35 40 45

Lys Ser Leu Glu Phe Ser Ala Arg Leu Lys Val Val Asp Val Ile Gly
50 55 60

Thr Lys Val Tyr Asn Asp Gly Glu Gln Ile Ile Ala Gln Gly Asp Ser
65 70 75 80

Ala Asp Ser Phe Phe Ile Ile Glu Ser Gly Glu Val Lys Ile Thr Met
85 90 95

Lys Arg Lys Gly Lys Ser Glu Val Glu Glu Asn Gly Ala Val Glu Ile
100 105 110

Ala Arg Cys Ser Arg Gly Gln Tyr Phe Gly Glu Leu Ala Leu Val Thr
115 120 125

Asn Lys Pro Arg Ala Ala Ser Ala His Ala Ile Gly Thr Val Lys Cys
130 135 140

Leu Ala Met Asp Val Gln Ala Phe Glu Arg Leu Leu Gly Pro Cys Met
145 150 155 160

Glu Ile Met Lys Arg Asn Ile Ala Thr Tyr Glu Glu Gln Leu Val Ala
165 170 175

Leu Tyr Gly Thr Asn Met Asp Ile Val Gly Ser Gly Gly Ser Gly Gly
180 185 190

Ser Ser Ser Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg
195 200 205

Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Val
210 215 220

Ser Ser Leu Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln Arg
225 230 235 240

Ile Val Leu Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile
245 250 255

Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln Met Gly Gln Ile Glu Lys
260 265 270

Ile Phe Lys Val Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile
275 280 285

Leu His Tyr Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile
290 295 300

Asp Tyr Phe Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys
305 310 315 320

Lys Ile Thr Val Thr Gly Thr Leu Trp Asn Gly Asn Lys Ile Ile Asp
325 330 335

Glu Arg Leu Ile Asn
340

<210> 495
<211> 1023
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 495
atgtccctgc tgttccgagt aaccatcaac ggagtgaccg gctggcggct gtgcgaacgc 60

attctggcta gctcaagcgg aggttcaggc ggttccggaa tgtatgaaag ctttattgag 120

tcactgccat tccttaaatc tttggagttt tctgcacgcc tgaaagtagt agatgtgata 180

ggcaccaaag tatacaacga tggagaacaa atcattgctc agggagattc ggctgattct 240

tttttcatta ttgaatctgg agaagtgaaa attactatga aaagaaaggg taaatcagaa 300

gtggaagaga atggtgcagt agaaatcgct cgatgctcgc ggggacagta ctttggagag 360

cttgccctgg taactaacaa acctcgagca gcttctgccc acgccattgg gactgtcaaa 420

tgtttagcaa tggatgtgca agcatttgaa aggcttctgg gaccttgcat ggaaattatg 480

aaaaggaaca tcgctaccta tgaagaacag ttagttgccc tgtatggaac gaacatggat 540

attgtagggt caggtggatc tggaggtagc tcttctatgg tcttcacact cgaagatttc 600

gttggggact ggcgacagac agccggctac aacctggacc aagtccttga acagggaggt 660

gtgtccagtt tgtttcagaa tctcggggtg tccgtaactc cgatccaaag gattgtcctg 720

agcggtgaaa atgggctgaa gatcgacatc catgtcatca tcccgtatga aggtctgagc 780

ggcgaccaaa tgggccagat cgaaaaaatt tttaaggtgg tgtaccctgt ggatgatcat 840

cactttaagg tgatcctgca ctatggcaca ctggtaatcg acggggttac gccgaacatg 900

atcgactatt tcggacggcc gtatgaaggc atcgccgtgt tcgacggcaa aaagatcact 960

gtaacaggga ccctgtggaa cggcaacaaa attatcgacg agcgcctgat caaccccgac 1020

ggc 1023

<210> 496
<211> 341
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 496
Met Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg
1 5 10 15

Leu Cys Glu Arg Ile Leu Ala Ser Ser Ser Gly Gly Ser Gly Gly Ser
20 25 30

Gly Met Tyr Glu Ser Phe Ile Glu Ser Leu Pro Phe Leu Lys Ser Leu
35 40 45

Glu Phe Ser Ala Arg Leu Lys Val Val Asp Val Ile Gly Thr Lys Val
50 55 60

Tyr Asn Asp Gly Glu Gln Ile Ile Ala Gln Gly Asp Ser Ala Asp Ser
65 70 75 80

Phe Phe Ile Ile Glu Ser Gly Glu Val Lys Ile Thr Met Lys Arg Lys
85 90 95

Gly Lys Ser Glu Val Glu Glu Asn Gly Ala Val Glu Ile Ala Arg Cys
100 105 110

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

Arg Ala Ala Ser Ala His Ala Ile Gly Thr Val Lys Cys Leu Ala Met
130 135 140

Asp Val Gln Ala Phe Glu Arg Leu Leu Gly Pro Cys Met Glu Ile Met
145 150 155 160

Lys Arg Asn Ile Ala Thr Tyr Glu Glu Gln Leu Val Ala Leu Tyr Gly
165 170 175

Thr Asn Met Asp Ile Val Gly Ser Gly Gly Ser Gly Gly Ser Ser Ser
180 185 190

Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala
195 200 205

Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu
210 215 220

Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln Arg Ile Val Leu

225 230 235 240

Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr
245 250 255

Glu Gly Leu Ser Gly Asp Gln Met Gly Gln Ile Glu Lys Ile Phe Lys
260 265 270

Val Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu His Tyr
275 280 285

Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe
290 295 300

Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr
305 310 315 320

Val Thr Gly Thr Leu Trp Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu
325 330 335

Ile Asn Pro Asp Gly
340

<210> 497
<211> 1023
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 497
atgggagtga ccggctggcg gctgtgcgaa cgcattctgg ctagctcaag cggaggttca 60

ggcggttccg gaatgtatga aagctttatt gagtcactgc cattccttaa atctttggag 120

ttttctgcac gcctgaaagt agtagatgtg ataggcacca aagtatacaa cgatggagaa 180

caaatcattg ctcagggaga ttcggctgat tctttttca ttattgaatc tggagaagtg 240

aaaattacta tgaaaagaaa gggtaaatca gaagtggaag agaatggtgc agtagaaatc 300

gctcgatgct cgcggggaca gtactttgga gagcttgccc tggtaactaa caaacctcga 360

gcagcttctg cccacgccat tgggactgtc aaatgtttag caatggatgt gcaagcattt 420

gaaaggcttc tgggaccttg catggaaatt atgaaaagga acatcgctac ctatgaagaa 480

cagttagttg ccctgtatgg aacgaacatg gatattgtag ggtcaggtgg atctggaggt 540

agctcttcta tggtcttcac actcgaagat ttcgttgggg actggcgaca gacagccggc 600

tacaacctgg accaagtcct tgaacaggga ggtgtgtcca gtttgtttca gaatctcggg 660

gtgtccgtaa ctccgatcca aaggattgtc ctgagcggtg aaaatgggct gaagatcgac 720

atccatgtca tcatcccgta tgaaggtctg agcggcgacc aaatgggcca gatcgaaaaa 780

atttttaagg tggtgtaccc tgtggatgat catcacttta aggtgatcct gcactatggc 840

acactggtaa tcgacggggt tacgccgaac atgatcgact atttcggacg gccgtatgaa 900

ggcatcgccg tgttcgacgg caaaaagatc actgtaacag ggaccctgtg gaacggcaac 960

aaaattatcg acgagcgcct gatcaacccc gacggctccc tgctgttccg agtaaccatc 1020

aac 1023

<210> 498
<211> 341
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 498
Met Gly Val Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala Ser Ser
1 5 10 15

Ser Gly Gly Ser Gly Gly Ser Gly Met Tyr Glu Ser Phe Ile Glu Ser
20 25 30

Leu Pro Phe Leu Lys Ser Leu Glu Phe Ser Ala Arg Leu Lys Val Val
35 40 45

Asp Val Ile Gly Thr Lys Val Tyr Asn Asp Gly Glu Gln Ile Ile Ala
50 55 60

Gln Gly Asp Ser Ala Asp Ser Phe Phe Ile Ile Glu Ser Gly Glu Val
65 70 75 80

Lys Ile Thr Met Lys Arg Lys Gly Lys Ser Glu Val Glu Glu Asn Gly
85 90 95

Ala Val Glu Ile Ala Arg Cys Ser Arg Gly Gln Tyr Phe Gly Glu Leu
100 105 110

Ala Leu Val Thr Asn Lys Pro Arg Ala Ala Ser Ala His Ala Ile Gly
115 120 125

Thr Val Lys Cys Leu Ala Met Asp Val Gln Ala Phe Glu Arg Leu Leu
130 135 140

Gly Pro Cys Met Glu Ile Met Lys Arg Asn Ile Ala Thr Tyr Glu Glu
145 150 155 160

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

Gly Ser Gly Gly Ser Ser Ser Met Val Phe Thr Leu Glu Asp Phe Val
180 185 190

Gly Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val Leu Glu
195 200 205

Gln Gly Gly Val Ser Ser Leu Phe Gln Asn Leu Gly Val Ser Val Thr
210 215 220

Pro Ile Gln Arg Ile Val Leu Ser Gly Glu Asn Gly Leu Lys Ile Asp
225 230 235 240

Ile His Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln Met Gly
245 250 255

Gln Ile Glu Lys Ile Phe Lys Val Val Tyr Pro Val Asp Asp His His
260 265 270

Phe Lys Val Ile Leu His Tyr Gly Thr Leu Val Ile Asp Gly Val Thr
275 280 285

Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly Ile Ala Val
290 295 300

Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr Leu Trp Asn Gly Asn
305 310 315 320

Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly Ser Leu Leu Phe
325 330 335

Arg Val Thr Ile Asn
340

<210> 499
<211> 1020
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 499
atggtcttca cactcgaaga tagcgctagc ggaggttcag gcggttccgg aatgtatgaa 60

agctttattg agtcactgcc attccttaaa tctttggagt tttctgcacg cctgaaagta 120

gtagatgtga taggcaccaa agtatacaac gatggagaac aaatcattgc tcagggagat 180

tcggctgatt ctttttttcat tattgaatct ggagaagtga aaattactat gaaaagaaag 240

ggtaaatcag aagtggaaga gaatggtgca gtagaaatcg ctcgatgctc gcggggacag 300

tactttggag agcttgccct ggtaactaac aaacctcgag cagcttctgc ccacgccatt 360

gggactgtca aatgtttagc aatggatgtg caagcatttg aaaggcttct gggaccttgc 420

atggaaatta tgaaaaggaa catcgctacc tatgaagaac agttagttgc cctgtatgga 480

acgaacatgg atattgtagg gtcaggtgga tctggaggta gctcttcttt cgttggggac 540

tggcgacaga cagccggcta caacctggac caagtccttg aacagggagg tgtgtccagt 600

ttgtttcaga atctcggggt gtccgtaact ccgatccaaa ggattgtcct gagcggtgaa 660

aatgggctga agatcgacat ccatgtcatc atcccgtatg aaggtctgag cggcgaccaa 720

atgggccaga tcgaaaaaat ttttaaggtg gtgtaccctg tggatgatca tcactttaag 780

gtgatcctgc actatggcac actggtaatc gacggggtta cgccgaacat gatcgactat 840

ttcggacggc cgtatgaagg catcgccgtg ttcgacggca aaaagatcac tgtaacaggg 900

accctgtgga acggcaacaa aattatcgac gagcgcctga tcaaccccga cggctccctg 960

ctgttccgag taaccatcaa cggagtgacc ggctggcggc tgtgcgaacg cattctggct 1020

<210> 500
<211> 340
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 500
Met Val Phe Thr Leu Glu Asp Ser Ala Ser Gly Gly Ser Gly Gly Ser
1 5 10 15

Gly Met Tyr Glu Ser Phe Ile Glu Ser Leu Pro Phe Leu Lys Ser Leu
20 25 30

Glu Phe Ser Ala Arg Leu Lys Val Val Asp Val Ile Gly Thr Lys Val
35 40 45

Tyr Asn Asp Gly Glu Gln Ile Ile Ala Gln Gly Asp Ser Ala Asp Ser
50 55 60

Phe Phe Ile Ile Glu Ser Gly Glu Val Lys Ile Thr Met Lys Arg Lys
65 70 75 80

Gly Lys Ser Glu Val Glu Glu Asn Gly Ala Val Glu Ile Ala Arg Cys
85 90 95

Ser Arg Gly Gln Tyr Phe Gly Glu Leu Ala Leu Val Thr Asn Lys Pro
100 105 110

Arg Ala Ala Ser Ala His Ala Ile Gly Thr Val Lys Cys Leu Ala Met
115 120 125

Asp Val Gln Ala Phe Glu Arg Leu Leu Gly Pro Cys Met Glu Ile Met
130 135 140

Lys Arg Asn Ile Ala Thr Tyr Glu Glu Gln Leu Val Ala Leu Tyr Gly
145 150 155 160

Thr Asn Met Asp Ile Val Gly Ser Gly Gly Ser Gly Gly Ser Ser Ser

165 170 175

Phe Val Gly Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val
180 185 190

Leu Glu Gln Gly Gly Val Ser Ser Leu Phe Gln Asn Leu Gly Val Ser
195 200 205

Val Thr Pro Ile Gln Arg Ile Val Leu Ser Gly Glu Asn Gly Leu Lys
210 215 220

Ile Asp Ile His Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln
225 230 235 240

Met Gly Gln Ile Glu Lys Ile Phe Lys Val Val Tyr Pro Val Asp Asp
245 250 255

His His Phe Lys Val Ile Leu His Tyr Gly Thr Leu Val Ile Asp Gly
260 265 270

Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly Ile
275 280 285

Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr Leu Trp Asn
290 295 300

Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly Ser Leu
305 310 315 320

Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg Leu Cys Glu
325 330 335

Arg Ile Leu Ala
340

<210> 501
<211> 1020
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 501
atggtcttca cactcgaaga tttcgttggg gactggcgaa gcgctagcgg aggttcaggc 60

ggttccggaa tgtatgaaag ctttattgag tcactgccat tccttaaatc tttggagttt 120

tctgcacgcc tgaaagtagt agatgtgata ggcaccaaag tatacaacga tggagaacaa 180

atcattgctc agggagattc ggctgattct tttttcatta ttgaatctgg agaagtgaaa 240

attactatga aaagaaaggg taaatcagaa gtggaagaga atggtgcagt agaaatcgct 300

cgatgctcgc ggggacagta ctttggagag cttgccctgg taactaacaa acctcgagca 360

gcttctgccc acgccattgg gactgtcaaa tgtttagcaa tggatgtgca agcatttgaa 420

aggcttctgg gaccttgcat ggaaattatg aaaaggaaca tcgctaccta tgaagaacag 480

ttagttgccc tgtatggaac gaacatggat attgtagggt caggtggatc tggaggtagc 540

tcttctcaga cagccggcta caacctggac caagtccttg aacagggagg tgtgtccagt 600

ttgtttcaga atctcggggt gtccgtaact ccgatccaaa ggattgtcct gagcggtgaa 660

aatgggctga agatcgacat ccatgtcatc atcccgtatg aaggtctgag cggcgaccaa 720

atgggccaga tcgaaaaaat ttttaaggtg gtgtaccctg tggatgatca tcactttaag 780

gtgatcctgc actatggcac actggtaatc gacggggtta cgccgaacat gatcgactat 840

ttcggacggc cgtatgaagg catcgccgtg ttcgacggca aaaagatcac tgtaacaggg 900

accctgtgga acggcaacaa aattatcgac gagcgcctga tcaaccccga cggctccctg 960

ctgttccgag taaccatcaa cggagtgacc ggctggcggc tgtgcgaacg cattctggct 1020

<210> 502
<211> 340
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 502
Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Ser Ala Ser
1 5 10 15

Gly Gly Ser Gly Gly Ser Gly Met Tyr Glu Ser Phe Ile Glu Ser Leu
20 25 30

Pro Phe Leu Lys Ser Leu Glu Phe Ser Ala Arg Leu Lys Val Val Asp
35 40 45

Val Ile Gly Thr Lys Val Tyr Asn Asp Gly Glu Gln Ile Ile Ala Gln
50 55 60

Gly Asp Ser Ala Asp Ser Phe Phe Ile Ile Glu Ser Gly Glu Val Lys
65 70 75 80

Ile Thr Met Lys Arg Lys Gly Lys Ser Glu Val Glu Glu Asn Gly Ala
85 90 95

Val Glu Ile Ala Arg Cys Ser Arg Gly Gln Tyr Phe Gly Glu Leu Ala
100 105 110

Leu Val Thr Asn Lys Pro Arg Ala Ala Ser Ala His Ala Ile Gly Thr
115 120 125

Val Lys Cys Leu Ala Met Asp Val Gln Ala Phe Glu Arg Leu Leu Gly
130 135 140

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Pro Cys Met Glu Ile Met Lys Arg Asn Ile Ala Thr Tyr Glu Glu Gln
145                 150                 155                 160

Leu Val Ala Leu Tyr Gly Thr Asn Met Asp Ile Val Gly Ser Gly Gly
                165                 170                 175

Ser Gly Gly Ser Ser Ser Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val
            180                 185                 190

Leu Glu Gln Gly Gly Val Ser Ser Leu Phe Gln Asn Leu Gly Val Ser
        195                 200                 205

Val Thr Pro Ile Gln Arg Ile Val Leu Ser Gly Glu Asn Gly Leu Lys
    210                 215                 220

Ile Asp Ile His Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln
225                 230                 235                 240

Met Gly Gln Ile Glu Lys Ile Phe Lys Val Val Tyr Pro Val Asp Asp
                245                 250                 255

His His Phe Lys Val Ile Leu His Tyr Gly Thr Leu Val Ile Asp Gly
            260                 265                 270

Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly Ile
        275                 280                 285

Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr Leu Trp Asn
    290                 295                 300

Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly Ser Leu
305                 310                 315                 320

Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg Leu Cys Glu
                325                 330                 335

Arg Ile Leu Ala
            340
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<210> 503
<211> 1020
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 503
atggtcttca cactcgaaga tttcgttggg gactggcgac agacagccgg ctacaacctg 60

gaccaagtcc ttgaacaggg aagcgctagc ggaggttcag gcggttccgg aatgtatgaa 120

agctttattg agtcactgcc attccttaaa tctttggagt tttctgcacg cctgaaagta 180

gtagatgtga taggcaccaa agtatacaac gatggagaac aaatcattgc tcagggagat 240

tcggctgatt ctttttcat tattgaatct ggagaagtga aaattactat gaaaagaaag 300

ggtaaatcag aagtggaaga gaatggtgca gtagaaatcg ctcgatgctc gcggggacag 360

tactttggag agcttgccct ggtaactaac aaacctcgag cagcttctgc ccacgccatt 420

gggactgtca aatgtttagc aatggatgtg caagcatttg aaaggcttct gggaccttgc 480

atggaaatta tgaaaaggaa catcgctacc tatgaagaac agttagttgc cctgtatgga 540

acgaacatgg atattgtagg gtcaggtgga tctggaggta gctcttctgg tgtgtccagt 600

ttgtttcaga atctcggggt gtccgtaact ccgatccaaa ggattgtcct gagcggtgaa 660

aatgggctga agatcgacat ccatgtcatc atcccgtatg aaggtctgag cggcgaccaa 720

atgggccaga tcgaaaaaat ttttaaggtg gtgtaccctg tggatgatca tcactttaag 780

gtgatcctgc actatggcac actggtaatc gacggggtta cgccgaacat gatcgactat 840

ttcggacggc cgtatgaagg catcgccgtg ttcgacggca aaaagatcac tgtaacaggg 900

accctgtgga acggcaacaa aattatcgac gagcgcctga tcaaccccga cggctccctg 960

ctgttccgag taaccatcaa cggagtgacc ggctggcggc tgtgcgaacg cattctggct 1020

<210> 504
<211> 340
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 504
Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala
1 5 10 15

Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Ser Ala Ser Gly Gly
20 25 30

Ser Gly Gly Ser Gly Met Tyr Glu Ser Phe Ile Glu Ser Leu Pro Phe
35 40 45

Leu Lys Ser Leu Glu Phe Ser Ala Arg Leu Lys Val Val Asp Val Ile
50 55 60

Gly Thr Lys Val Tyr Asn Asp Gly Glu Gln Ile Ile Ala Gln Gly Asp
65 70 75 80

Ser Ala Asp Ser Phe Phe Ile Ile Glu Ser Gly Glu Val Lys Ile Thr
85 90 95

Met Lys Arg Lys Gly Lys Ser Glu Val Glu Glu Asn Gly Ala Val Glu
100 105 110

Ile Ala Arg Cys Ser Arg Gly Gln Tyr Phe Gly Glu Leu Ala Leu Val
115 120 125

Thr Asn Lys Pro Arg Ala Ala Ser Ala His Ala Ile Gly Thr Val Lys
130 135 140

Cys Leu Ala Met Asp Val Gln Ala Phe Glu Arg Leu Leu Gly Pro Cys
145 150 155 160

Met Glu Ile Met Lys Arg Asn Ile Ala Thr Tyr Glu Glu Gln Leu Val
165 170 175

Ala Leu Tyr Gly Thr Asn Met Asp Ile Val Gly Ser Gly Gly Ser Gly
180 185 190

Gly Ser Ser Ser Gly Val Ser Ser Leu Phe Gln Asn Leu Gly Val Ser
195 200 205

Val Thr Pro Ile Gln Arg Ile Val Leu Ser Gly Glu Asn Gly Leu Lys
210 215 220

Ile Asp Ile His Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln
225 230 235 240

Met Gly Gln Ile Glu Lys Ile Phe Lys Val Val Tyr Pro Val Asp Asp
245 250 255

His His Phe Lys Val Ile Leu His Tyr Gly Thr Leu Val Ile Asp Gly
260 265 270

Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly Ile
275 280 285

Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr Leu Trp Asn
290 295 300

Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly Ser Leu
305 310 315 320

Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg Leu Cys Glu
325 330 335

Arg Ile Leu Ala
340

<210> 505
<211> 1020
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

polynucleotide

<400> 505
atggtcttca cactcgaaga tttcgttggg gactggcgac agacagccgg ctacaacctg 60

gaccaagtcc ttgaacaggg aggtgtgtcc agtttgtttc agaatctcgg ggtgtccgta 120

actccgatcc aaaggattag cgctagcgga ggttcaggcg gttccggaat gtatgaaagc 180

tttattgagt cactgccatt ccttaaatct ttggagtttt ctgcacgcct gaaagtagta 240

gatgtgatag gcaccaaagt atacaacgat ggagaacaaa tcattgctca gggagattcg 300

gctgattctt ttttcattat tgaatctgga gaagtgaaaa ttactatgaa aagaaagggt 360

aaatcagaag tggaagagaa tggtgcagta gaaatcgctc gatgctcgcg gggacagtac 420

tttggagagc ttgccctggt aactaacaaa cctcgagcag cttctgccca cgccattggg 480

actgtcaaat gtttagcaat ggatgtgcaa gcatttgaaa ggcttctggg accttgcatg 540

gaaattatga aaaggaacat cgctacctat gaagaacagt tagttgccct gtatggaacg 600

aacatggata ttgtagggtc aggtggatct ggaggtagct cttctgtcct gagcggtgaa 660

aatgggctga agatcgacat ccatgtcatc atcccgtatg aaggtctgag cggcgaccaa 720

atgggccaga tcgaaaaaat ttttaaggtg gtgtaccctg tggatgatca tcactttaag 780

gtgatcctgc actatggcac actggtaatc gacggggtta cgccgaacat gatcgactat 840

ttcggacggc cgtatgaagg catcgccgtg ttcgacggca aaaagatcac tgtaacaggg 900

accctgtgga acggcaacaa aattatcgac gagcgcctga tcaaccccga cggctccctg 960

ctgttccgag taaccatcaa cggagtgacc ggctggcggc tgtgcgaacg cattctggct 1020

<210> 506
<211> 340
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 506
Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala
1 5 10 15

Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu
20 25 30

Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln Arg Ile Ser Ala
35 40 45

Ser Gly Gly Ser Gly Gly Ser Gly Met Tyr Glu Ser Phe Ile Glu Ser
50 55 60

Leu Pro Phe Leu Lys Ser Leu Glu Phe Ser Ala Arg Leu Lys Val Val
65 70 75 80

```
Asp Val Ile Gly Thr Lys Val Tyr Asn Asp Gly Glu Gln Ile Ile Ala
                85                  90                  95

Gln Gly Asp Ser Ala Asp Ser Phe Phe Ile Ile Glu Ser Gly Glu Val
            100                 105                 110

Lys Ile Thr Met Lys Arg Lys Gly Lys Ser Glu Val Glu Glu Asn Gly
        115                 120                 125

Ala Val Glu Ile Ala Arg Cys Ser Arg Gly Gln Tyr Phe Gly Glu Leu
    130                 135                 140

Ala Leu Val Thr Asn Lys Pro Arg Ala Ala Ser Ala His Ala Ile Gly
145                 150                 155                 160

Thr Val Lys Cys Leu Ala Met Asp Val Gln Ala Phe Glu Arg Leu Leu
                165                 170                 175

Gly Pro Cys Met Glu Ile Met Lys Arg Asn Ile Ala Thr Tyr Glu Glu
            180                 185                 190

Gln Leu Val Ala Leu Tyr Gly Thr Asn Met Asp Ile Val Gly Ser Gly
        195                 200                 205

Gly Ser Gly Gly Ser Ser Ser Val Leu Ser Gly Glu Asn Gly Leu Lys
    210                 215                 220

Ile Asp Ile His Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln
225                 230                 235                 240

Met Gly Gln Ile Glu Lys Ile Phe Lys Val Val Tyr Pro Val Asp Asp
                245                 250                 255

His His Phe Lys Val Ile Leu His Tyr Gly Thr Leu Val Ile Asp Gly
            260                 265                 270

Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly Ile
        275                 280                 285

Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr Leu Trp Asn
    290                 295                 300

Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly Ser Leu
305                 310                 315                 320

Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg Leu Cys Glu
                325                 330                 335

Arg Ile Leu Ala
            340
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<210> 507
<211> 1020
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 507
atggtcttca cactcgaaga tttcgttggg gactggcgac agacagccgg ctacaacctg 60

gaccaagtcc ttgaacaggg aggtgtgtcc agtttgtttc agaatctcgg ggtgtccgta 120

actccgatcc aaaggattgt cctgagcagc gctagcggag gttcaggcgg ttccggaatg 180

tatgaaagct ttattgagtc actgccattc cttaaatctt tggagttttc tgcacgcctg 240

aaagtagtag atgtgatagg caccaaagta tacaacgatg gagaacaaat cattgctcag 300

ggagattcgg ctgattcttt tttcattatt gaatctggag aagtgaaaat tactatgaaa 360

agaaagggta aatcagaagt ggaagagaat ggtgcagtag aaatcgctcg atgctcgcgg 420

ggacagtact ttggagagct tgccctggta actaacaaac ctcgagcagc ttctgcccac 480

gccattggga ctgtcaaatg tttagcaatg gatgtgcaag catttgaaag gcttctggga 540

ccttgcatgg aaattatgaa aaggaacatc gctacctatg aagaacagtt agttgccctg 600

tatggaacga acatggatat tgtagggtca ggtggatctg gaggtagctc ttctggtgaa 660

aatgggctga agatcgacat ccatgtcatc atcccgtatg aaggtctgag cggcgaccaa 720

atgggccaga tcgaaaaaat ttttaaggtg gtgtaccctg tggatgatca tcactttaag 780

gtgatcctgc actatggcac actggtaatc gacggggtta cgccgaacat gatcgactat 840

ttcggacggc cgtatgaagg catcgccgtg ttcgacggca aaaagatcac tgtaacaggg 900

accctgtgga acggcaacaa aattatcgac gagcgcctga tcaaccccga cggctccctg 960

ctgttccgag taaccatcaa cggagtgacc ggctggcggc tgtgcgaacg cattctggct 1020

<210> 508
<211> 340
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 508
Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala
1 5 10 15

Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu
20 25 30

Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln Arg Ile Val Leu
35 40 45

Ser Ser Ala Ser Gly Gly Ser Gly Gly Ser Gly Met Tyr Glu Ser Phe

50 55 60

Ile Glu Ser Leu Pro Phe Leu Lys Ser Leu Glu Phe Ser Ala Arg Leu
65 70 75 80

Lys Val Val Asp Val Ile Gly Thr Lys Val Tyr Asn Asp Gly Glu Gln
85 90 95

Ile Ile Ala Gln Gly Asp Ser Ala Asp Ser Phe Phe Ile Ile Glu Ser
100 105 110

Gly Glu Val Lys Ile Thr Met Lys Arg Lys Gly Lys Ser Glu Val Glu
115 120 125

Glu Asn Gly Ala Val Glu Ile Ala Arg Cys Ser Arg Gly Gln Tyr Phe
130 135 140

Gly Glu Leu Ala Leu Val Thr Asn Lys Pro Arg Ala Ala Ser Ala His
145 150 155 160

Ala Ile Gly Thr Val Lys Cys Leu Ala Met Asp Val Gln Ala Phe Glu
165 170 175

Arg Leu Leu Gly Pro Cys Met Glu Ile Met Lys Arg Asn Ile Ala Thr
180 185 190

Tyr Glu Glu Gln Leu Val Ala Leu Tyr Gly Thr Asn Met Asp Ile Val
195 200 205

Gly Ser Gly Gly Ser Gly Gly Ser Ser Ser Gly Glu Asn Gly Leu Lys
210 215 220

Ile Asp Ile His Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln
225 230 235 240

Met Gly Gln Ile Glu Lys Ile Phe Lys Val Val Tyr Pro Val Asp Asp
245 250 255

His His Phe Lys Val Ile Leu His Tyr Gly Thr Leu Val Ile Asp Gly
260 265 270

Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly Ile
275 280 285

Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr Leu Trp Asn
290 295 300

Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly Ser Leu
305 310 315 320

Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg Leu Cys Glu

325 330 335

Arg Ile Leu Ala
340

<210> 509
<211> 1020
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 509
atggtcttca cactcgaaga tttcgttggg gactggcgac agacagccgg ctacaacctg 60

gaccaagtcc ttgaacaggg aggtgtgtcc agtttgtttc agaatctcgg ggtgtccgta 120

actccgatcc aaaggattgt cctgagcggt gaaaatggga gcgctagcgg aggttcaggc 180

ggttccggaa tgtatgaaag ctttattgag tcactgccat tccttaaatc tttggagttt 240

tctgcacgcc tgaaagtagt agatgtgata ggcaccaaag tatacaacga tggagaacaa 300

atcattgctc agggagattc ggctgattct tttttcatta ttgaatctgg agaagtgaaa 360

attactatga aaagaaaggg taaatcagaa gtggaagaga atggtgcagt agaaatcgct 420

cgatgctcgc ggggacagta ctttggagag cttgccctgg taactaacaa acctcgagca 480

gcttctgccc acgccattgg gactgtcaaa tgtttagcaa tggatgtgca agcatttgaa 540

aggcttctgg gaccttgcat ggaaattatg aaaaggaaca tcgctaccta tgaagaacag 600

ttagttgccc tgtatggaac gaacatggat attgtagggt caggtggatc tggaggtagc 660

tcttctctga agatcgacat ccatgtcatc atcccgtatg aaggtctgag cggcgaccaa 720

atgggccaga tcgaaaaaat ttttaaggtg gtgtaccctg tggatgatca tcactttaag 780

gtgatcctgc actatggcac actggtaatc gacggggtta cgccgaacat gatcgactat 840

ttcggacggc cgtatgaagg catcgccgtg ttcgacggca aaaagatcac tgtaacaggg 900

accctgtgga acggcaacaa aattatcgac gagcgcctga tcaaccccga cggctccctg 960

ctgttccgag taaccatcaa cggagtgacc ggctggcggc tgtgcgaacg cattctggct 1020

<210> 510
<211> 340
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 510
Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala
1 5 10 15

Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu
20 25 30

```
Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln Arg Ile Val Leu
        35                  40                  45

Ser Gly Glu Asn Gly Ser Ala Ser Gly Gly Ser Gly Gly Ser Gly Met
    50                  55                  60

Tyr Glu Ser Phe Ile Glu Ser Leu Pro Phe Leu Lys Ser Leu Glu Phe
65                  70                  75                  80

Ser Ala Arg Leu Lys Val Val Asp Val Ile Gly Thr Lys Val Tyr Asn
                85                  90                  95

Asp Gly Glu Gln Ile Ile Ala Gln Gly Asp Ser Ala Asp Ser Phe Phe
            100                 105                 110

Ile Ile Glu Ser Gly Glu Val Lys Ile Thr Met Lys Arg Lys Gly Lys
        115                 120                 125

Ser Glu Val Glu Glu Asn Gly Ala Val Glu Ile Ala Arg Cys Ser Arg
    130                 135                 140

Gly Gln Tyr Phe Gly Glu Leu Ala Leu Val Thr Asn Lys Pro Arg Ala
145                 150                 155                 160

Ala Ser Ala His Ala Ile Gly Thr Val Lys Cys Leu Ala Met Asp Val
                165                 170                 175

Gln Ala Phe Glu Arg Leu Leu Gly Pro Cys Met Glu Ile Met Lys Arg
            180                 185                 190

Asn Ile Ala Thr Tyr Glu Glu Gln Leu Val Ala Leu Tyr Gly Thr Asn
        195                 200                 205

Met Asp Ile Val Gly Ser Gly Gly Ser Gly Gly Ser Ser Ser Leu Lys
    210                 215                 220

Ile Asp Ile His Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln
225                 230                 235                 240

Met Gly Gln Ile Glu Lys Ile Phe Lys Val Val Tyr Pro Val Asp Asp
                245                 250                 255

His His Phe Lys Val Ile Leu His Tyr Gly Thr Leu Val Ile Asp Gly
            260                 265                 270

Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly Ile
        275                 280                 285

Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr Leu Trp Asn
    290                 295                 300
```

Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly Ser Leu
305 310 315 320

Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg Leu Cys Glu
325 330 335

Arg Ile Leu Ala
340

<210> 511
<211> 1020
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 511
atggtcttca cactcgaaga tttcgttggg gactggcgac agacagccgg ctacaacctg 60

gaccaagtcc ttgaacaggg aggtgtgtcc agtttgtttc agaatctcgg ggtgtccgta 120

actccgatcc aaaggattgt cctgagcggt gaaaatgggc tgaagatcag cgctagcgga 180

ggttcaggcg gttccggaat gtatgaaagc tttattgagt cactgccatt ccttaaatct 240

ttggagtttt ctgcacgcct gaaagtagta gatgtgatag gcaccaaagt atacaacgat 300

ggagaacaaa tcattgctca gggagattcg gctgattctt ttttcattat tgaatctgga 360

gaagtgaaaa ttactatgaa aagaaagggt aaatcagaag tggaagagaa tggtgcagta 420

gaaatcgctc gatgctcgcg gggacagtac tttggagagc ttgccctggt aactaacaaa 480

cctcgagcag cttctgccca cgccattggg actgtcaaat gtttagcaat ggatgtgcaa 540

gcatttgaaa ggcttctggg accttgcatg gaaattatga aaaggaacat cgctacctat 600

gaagaacagt tagttgccct gtatggaacg aacatggata ttgtagggtc aggtggatct 660

ggaggtagct cttctgacat ccatgtcatc atcccgtatg aaggtctgag cggcgaccaa 720

atgggccaga tcgaaaaaat ttttaaggtg gtgtaccctg tggatgatca tcactttaag 780

gtgatcctgc actatggcac actggtaatc gacggggtta cgccgaacat gatcgactat 840

ttcggacggc cgtatgaagg catcgccgtg ttcgacggca aaaagatcac tgtaacaggg 900

accctgtgga acggcaacaa aattatcgac gagcgcctga tcaaccccga cggctccctg 960

ctgttccgag taaccatcaa cggagtgacc ggctggcggc tgtgcgaacg cattctggct 1020

<210> 512
<211> 340
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 512

Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala
1 5 10 15

Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu
20 25 30

Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln Arg Ile Val Leu
35 40 45

Ser Gly Glu Asn Gly Leu Lys Ile Ser Ala Ser Gly Gly Ser Gly Gly
50 55 60

Ser Gly Met Tyr Glu Ser Phe Ile Glu Ser Leu Pro Phe Leu Lys Ser
65 70 75 80

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

Val Tyr Asn Asp Gly Glu Gln Ile Ile Ala Gln Gly Asp Ser Ala Asp
100 105 110

Ser Phe Phe Ile Ile Glu Ser Gly Glu Val Lys Ile Thr Met Lys Arg
115 120 125

Lys Gly Lys Ser Glu Val Glu Glu Asn Gly Ala Val Glu Ile Ala Arg
130 135 140

Cys Ser Arg Gly Gln Tyr Phe Gly Glu Leu Ala Leu Val Thr Asn Lys
145 150 155 160

Pro Arg Ala Ala Ser Ala His Ala Ile Gly Thr Val Lys Cys Leu Ala
165 170 175

Met Asp Val Gln Ala Phe Glu Arg Leu Leu Gly Pro Cys Met Glu Ile
180 185 190

Met Lys Arg Asn Ile Ala Thr Tyr Glu Glu Gln Leu Val Ala Leu Tyr
195 200 205

Gly Thr Asn Met Asp Ile Val Gly Ser Gly Gly Ser Gly Gly Ser Ser
210 215 220

Ser Asp Ile His Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln
225 230 235 240

Met Gly Gln Ile Glu Lys Ile Phe Lys Val Val Tyr Pro Val Asp Asp
245 250 255

His His Phe Lys Val Ile Leu His Tyr Gly Thr Leu Val Ile Asp Gly
260 265 270

Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly Ile
275 280 285

Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr Leu Trp Asn
290 295 300

Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly Ser Leu
305 310 315 320

Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg Leu Cys Glu
325 330 335

Arg Ile Leu Ala
340

<210> 513
<211> 1020
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 513
atggtcttca cactcgaaga tttcgttggg gactggcgac agacagccgg ctacaacctg 60

gaccaagtcc ttgaacaggg aggtgtgtcc agtttgtttc agaatctcgg ggtgtccgta 120

actccgatcc aaaggattgt cctgagcggt gaaaatgggc tgaagatcga catccatgtc 180

atcatcccgt atgaaggtct gagcggcgac caaatgggcc agatcgaaaa aatttttaag 240

gtggtgtacc ctagcgctag cggaggttca ggcggttccg gaatgtatga aagctttatt 300

gagtcactgc cattccttaa atctttggag ttttctgcac gcctgaaagt agtagatgtg 360

ataggcacca aagtatacaa cgatggagaa caaatcattg ctcagggaga ttcggctgat 420

tctttttca ttattgaatc tggagaagtg aaaattacta tgaaaagaaa gggtaaatca 480

gaagtggaag agaatggtgc agtagaaatc gctcgatgct cgcggggaca gtactttgga 540

gagcttgccc tggtaactaa caaacctcga gcagcttctg cccacgccat tgggactgtc 600

aaatgtttag caatggatgt gcaagcattt gaaaggcttc tgggaccttg catggaaatt 660

atgaaaagga acatcgctac ctatgaagaa cagttagttg ccctgtatgg aacgaacatg 720

gatattgtag ggtcaggtgg atctggaggt agctcttctg tggatgatca tcactttaag 780

gtgatcctgc actatggcac actggtaatc gacggggtta cgccgaacat gatcgactat 840

ttcggacggc cgtatgaagg catcgccgtg ttcgacggca aaaagatcac tgtaacaggg 900

accctgtgga acggcaacaa aattatcgac gagcgcctga tcaaccccga cggctccctg 960

ctgttccgag taaccatcaa cggagtgacc ggctggcggc tgtgcgaacg cattctggct 1020

<210> 514
<211> 340

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 514

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Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala
1               5                  10                  15

Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu
            20                  25                  30

Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln Arg Ile Val Leu
        35                  40                  45

Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr
    50                  55                  60

Glu Gly Leu Ser Gly Asp Gln Met Gly Gln Ile Glu Lys Ile Phe Lys
65                  70                  75                  80

Val Val Tyr Pro Ser Ala Ser Gly Gly Ser Gly Gly Ser Gly Met Tyr
                85                  90                  95

Glu Ser Phe Ile Glu Ser Leu Pro Phe Leu Lys Ser Leu Glu Phe Ser
            100                 105                 110

Ala Arg Leu Lys Val Val Asp Val Ile Gly Thr Lys Val Tyr Asn Asp
        115                 120                 125

Gly Glu Gln Ile Ile Ala Gln Gly Asp Ser Ala Asp Ser Phe Phe Ile
    130                 135                 140

Ile Glu Ser Gly Glu Val Lys Ile Thr Met Lys Arg Lys Gly Lys Ser
145                 150                 155                 160

Glu Val Glu Glu Asn Gly Ala Val Glu Ile Ala Arg Cys Ser Arg Gly
                165                 170                 175

Gln Tyr Phe Gly Glu Leu Ala Leu Val Thr Asn Lys Pro Arg Ala Ala
            180                 185                 190

Ser Ala His Ala Ile Gly Thr Val Lys Cys Leu Ala Met Asp Val Gln
        195                 200                 205

Ala Phe Glu Arg Leu Leu Gly Pro Cys Met Glu Ile Met Lys Arg Asn
    210                 215                 220

Ile Ala Thr Tyr Glu Glu Gln Leu Val Ala Leu Tyr Gly Thr Asn Met
225                 230                 235                 240
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Asp Ile Val Gly Ser Gly Gly Ser Gly Gly Ser Ser Ser Val Asp Asp
245 250 255

His His Phe Lys Val Ile Leu His Tyr Gly Thr Leu Val Ile Asp Gly
260 265 270

Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly Ile
275 280 285

Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr Leu Trp Asn
290 295 300

Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly Ser Leu
305 310 315 320

Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg Leu Cys Glu
325 330 335

Arg Ile Leu Ala
340

<210> 515
<211> 1020
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 515
atggtcttca cactcgaaga tttcgttggg gactggcgac agacagccgg ctacaacctg 60

gaccaagtcc ttgaacaggg aggtgtgtcc agtttgtttc agaatctcgg ggtgtccgta 120

actccgatcc aaaggattgt cctgagcggt gaaaatgggc tgaagatcga catccatgtc 180

atcatcccgt atgaaggtct gagcggcgac caaatgggcc agatcgaaaa aatttttaag 240

gtggtgtacc ctgtgagcgc tagcggaggt tcaggcggtt ccggaatgta tgaaagcttt 300

attgagtcac tgccattcct taaatctttg gagttttctg cacgcctgaa agtagtagat 360

gtgataggca ccaaagtata caacgatgga gaacaaatca ttgctcaggg agattcggct 420

gattcttttt tcattattga atctggagaa gtgaaaatta ctatgaaaag aaagggtaaa 480

tcagaagtgg aagagaatgg tgcagtagaa atcgctcgat gctcgcgggg acagtacttt 540

ggagagcttg ccctggtaac taacaaacct cgagcagctt ctgcccacgc cattgggact 600

gtcaaatgtt tagcaatgga tgtgcaagca tttgaaaggc ttctgggacc ttgcatggaa 660

attatgaaaa ggaacatcgc tacctatgaa gaacagttag ttgccctgta tggaacgaac 720

atggatattg tagggtcagg tggatctgga ggtagctctt ctgatgatca tcactttaag 780

gtgatcctgc actatggcac actggtaatc gacggggtta cgccgaacat gatcgactat 840

ttcggacggc cgtatgaagg catcgccgtg ttcgacggca aaaagatcac tgtaacaggg 900

accctgtgga acggcaacaa aattatcgac gagcgcctga tcaaccccga cggctccctg 960

ctgttccgag taaccatcaa cggagtgacc ggctggcggc tgtgcgaacg cattctggct 1020

<210> 516
<211> 340
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 516

Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala
1 5 10 15

Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu
20 25 30

Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln Arg Ile Val Leu
35 40 45

Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr
50 55 60

Glu Gly Leu Ser Gly Asp Gln Met Gly Gln Ile Glu Lys Ile Phe Lys
65 70 75 80

Val Val Tyr Pro Val Ser Ala Ser Gly Gly Ser Gly Gly Ser Gly Met
85 90 95

Tyr Glu Ser Phe Ile Glu Ser Leu Pro Phe Leu Lys Ser Leu Glu Phe
100 105 110

Ser Ala Arg Leu Lys Val Val Asp Val Ile Gly Thr Lys Val Tyr Asn
115 120 125

Asp Gly Glu Gln Ile Ile Ala Gln Gly Asp Ser Ala Asp Ser Phe Phe
130 135 140

Ile Ile Glu Ser Gly Glu Val Lys Ile Thr Met Lys Arg Lys Gly Lys
145 150 155 160

Ser Glu Val Glu Glu Asn Gly Ala Val Glu Ile Ala Arg Cys Ser Arg
165 170 175

Gly Gln Tyr Phe Gly Glu Leu Ala Leu Val Thr Asn Lys Pro Arg Ala
180 185 190

Ala Ser Ala His Ala Ile Gly Thr Val Lys Cys Leu Ala Met Asp Val
195 200 205

Gln Ala Phe Glu Arg Leu Leu Gly Pro Cys Met Glu Ile Met Lys Arg

210 215 220

Asn Ile Ala Thr Tyr Glu Glu Gln Leu Val Ala Leu Tyr Gly Thr Asn
225 230 235 240

Met Asp Ile Val Gly Ser Gly Gly Ser Gly Gly Ser Ser Ser Asp Asp
245 250 255

His His Phe Lys Val Ile Leu His Tyr Gly Thr Leu Val Ile Asp Gly
260 265 270

Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly Ile
275 280 285

Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr Leu Trp Asn
290 295 300

Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly Ser Leu
305 310 315 320

Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg Leu Cys Glu
325 330 335

Arg Ile Leu Ala
340

<210> 517
<211> 1020
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 517
atggtcttca cactcgaaga tttcgttggg gactggcgac agacagccgg ctacaacctg 60

gaccaagtcc ttgaacaggg aggtgtgtcc agtttgtttc agaatctcgg ggtgtccgta 120

actccgatcc aaaggattgt cctgagcggt gaaaatgggc tgaagatcga catccatgtc 180

atcatcccgt atgaaggtct gagcggcgac caaatgggcc agatcgaaaa aatttttaag 240

gtggtgtacc ctgtggatag cgctagcgga ggttcaggcg gttccggaat gtatgaaagc 300

tttattgagt cactgccatt ccttaaatct ttggagtttt ctgcacgcct gaaagtagta 360

gatgtgatag gcaccaaagt atacaacgat ggagaacaaa tcattgctca gggagattcg 420

gctgattctt ttttcattat tgaatctgga gaagtgaaaa ttactatgaa aagaaagggt 480

aaatcagaag tggaagagaa tggtgcagta gaaatcgctc gatgctcgcg gggacagtac 540

tttggagagc ttgccctggt aactaacaaa cctcgagcag cttctgccca cgccattggg 600

actgtcaaat gtttagcaat ggatgtgcaa gcatttgaaa ggcttctggg accttgcatg 660

gaaattatga aaaggaacat cgctacctat gaagaacagt tagttgccct gtatggaacg 720

aacatggata ttgtagggtc aggtggatct ggaggtagct cttctgatca tcactttaag 780

gtgatcctgc actatggcac actggtaatc gacggggtta cgccgaacat gatcgactat 840

ttcggacggc cgtatgaagg catcgccgtg ttcgacggca aaaagatcac tgtaacaggg 900

accctgtgga acggcaacaa aattatcgac gagcgcctga tcaaccccga cggctccctg 960

ctgttccgag taaccatcaa cggagtgacc ggctggcggc tgtgcgaacg cattctggct 1020

<210> 518
<211> 340
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 518
Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala
1 5 10 15

Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu
20 25 30

Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln Arg Ile Val Leu
35 40 45

Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr
50 55 60

Glu Gly Leu Ser Gly Asp Gln Met Gly Gln Ile Glu Lys Ile Phe Lys
65 70 75 80

Val Val Tyr Pro Val Asp Ser Ala Ser Gly Gly Ser Gly Gly Ser Gly
85 90 95

Met Tyr Glu Ser Phe Ile Glu Ser Leu Pro Phe Leu Lys Ser Leu Glu
100 105 110

Phe Ser Ala Arg Leu Lys Val Val Asp Val Ile Gly Thr Lys Val Tyr
115 120 125

Asn Asp Gly Glu Gln Ile Ile Ala Gln Gly Asp Ser Ala Asp Ser Phe
130 135 140

Phe Ile Ile Glu Ser Gly Glu Val Lys Ile Thr Met Lys Arg Lys Gly
145 150 155 160

Lys Ser Glu Val Glu Glu Asn Gly Ala Val Glu Ile Ala Arg Cys Ser
165 170 175

Arg Gly Gln Tyr Phe Gly Glu Leu Ala Leu Val Thr Asn Lys Pro Arg
180 185 190

```
Ala Ala Ser Ala His Ala Ile Gly Thr Val Lys Cys Leu Ala Met Asp
        195                 200                 205

Val Gln Ala Phe Glu Arg Leu Leu Gly Pro Cys Met Glu Ile Met Lys
    210                 215                 220

Arg Asn Ile Ala Thr Tyr Glu Glu Gln Leu Val Ala Leu Tyr Gly Thr
225                 230                 235                 240

Asn Met Asp Ile Val Gly Ser Gly Gly Ser Gly Gly Ser Ser Ser Asp
                245                 250                 255

His His Phe Lys Val Ile Leu His Tyr Gly Thr Leu Val Ile Asp Gly
            260                 265                 270

Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly Ile
        275                 280                 285

Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr Leu Trp Asn
    290                 295                 300

Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly Ser Leu
305                 310                 315                 320

Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg Leu Cys Glu
                325                 330                 335

Arg Ile Leu Ala
            340
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<210> 519
<211> 1020
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 519

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atggtcttca cactcgaaga tttcgttggg gactggcgac agacagccgg ctacaacctg       60

gaccaagtcc ttgaacaggg aggtgtgtcc agtttgtttc agaatctcgg ggtgtccgta      120

actccgatcc aaaggattgt cctgagcggt gaaaatgggc tgaagatcga catccatgtc      180

atcatcccgt atgaaggtct gagcggcgac caaatgggcc agatcgaaaa aatttttaag      240

gtggtgtacc ctgtggatga tcatcacttt aaggtgatcc tgcactatgg cacactggta      300

atcagcgcta gcggaggttc aggcggttcc ggaatgtatg aaagctttat tgagtcactg      360

ccattcctta aatctttgga gttttctgca cgcctgaaag tagtagatgt gataggcacc      420

aaagtataca acgatggaga acaaatcatt gctcagggag attcggctga ttctttttc       480
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attattgaat ctggagaagt gaaaattact atgaaaagaa agggtaaatc agaagtggaa 540

gagaatggtg cagtagaaat cgctcgatgc tcgcggggac agtactttgg agagcttgcc 600

ctggtaacta acaaacctcg agcagcttct gcccacgcca ttgggactgt caaatgttta 660

gcaatggatg tgcaagcatt tgaaaggctt ctgggacctt gcatggaaat tatgaaaagg 720

aacatcgcta cctatgaaga acagttagtt gccctgtatg gaacgaacat ggatattgta 780

gggtcaggtg gatctggagg tagctcttct gacggggtta cgccgaacat gatcgactat 840

ttcggacggc cgtatgaagg catcgccgtg ttcgacggca aaaagatcac tgtaacaggg 900

accctgtgga acggcaacaa aattatcgac gagcgcctga tcaaccccga cggctccctg 960

ctgttccgag taaccatcaa cggagtgacc ggctggcggc tgtgcgaacg cattctggct 1020

<210> 520
<211> 340
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 520
Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala
1 5 10 15

Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu
20 25 30

Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln Arg Ile Val Leu
35 40 45

Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr
50 55 60

Glu Gly Leu Ser Gly Asp Gln Met Gly Gln Ile Glu Lys Ile Phe Lys
65 70 75 80

Val Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu His Tyr
85 90 95

Gly Thr Leu Val Ile Ser Ala Ser Gly Gly Ser Gly Gly Ser Gly Met
100 105 110

Tyr Glu Ser Phe Ile Glu Ser Leu Pro Phe Leu Lys Ser Leu Glu Phe
115 120 125

Ser Ala Arg Leu Lys Val Val Asp Val Ile Gly Thr Lys Val Tyr Asn
130 135 140

Asp Gly Glu Gln Ile Ile Ala Gln Gly Asp Ser Ala Asp Ser Phe Phe
145 150 155 160

Ile Ile Glu Ser Gly Glu Val Lys Ile Thr Met Lys Arg Lys Gly Lys
165 170 175

Ser Glu Val Glu Glu Asn Gly Ala Val Glu Ile Ala Arg Cys Ser Arg
180 185 190

Gly Gln Tyr Phe Gly Glu Leu Ala Leu Val Thr Asn Lys Pro Arg Ala
195 200 205

Ala Ser Ala His Ala Ile Gly Thr Val Lys Cys Leu Ala Met Asp Val
210 215 220

Gln Ala Phe Glu Arg Leu Leu Gly Pro Cys Met Glu Ile Met Lys Arg
225 230 235 240

Asn Ile Ala Thr Tyr Glu Glu Gln Leu Val Ala Leu Tyr Gly Thr Asn
245 250 255

Met Asp Ile Val Gly Ser Gly Gly Ser Gly Gly Ser Ser Ser Asp Gly
260 265 270

Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly Ile
275 280 285

Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr Leu Trp Asn
290 295 300

Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly Ser Leu
305 310 315 320

Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg Leu Cys Glu
325 330 335

Arg Ile Leu Ala
340

<210> 521
<211> 1020
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 521
atggtcttca cactcgaaga tttcgttggg gactggcgac agacagccgg ctacaacctg 60

gaccaagtcc ttgaacaggg aggtgtgtcc agtttgtttc agaatctcgg ggtgtccgta 120

actccgatcc aaaggattgt cctgagcggt gaaaatgggc tgaagatcga catccatgtc 180

atcatcccgt atgaaggtct gagcggcgac caaatgggcc agatcgaaaa aatttttaag 240

gtggtgtacc ctgtggatga tcatcacttt aaggtgatcc tgcactatgg cacactggta 300

atcgacagcg ctagcggagg ttcaggcggt tccggaatgt atgaaagctt tattgagtca 360

ctgccattcc ttaaatcttt ggagttttct gcacgcctga aagtagtaga tgtgataggc 420

accaaagtat acaacgatgg agaacaaatc attgctcagg gagattcggc tgattctttt 480

ttcattattg aatctggaga agtgaaaatt actatgaaaa gaaagggtaa atcagaagtg 540

gaagagaatg gtgcagtaga aatcgctcga tgctcgcggg gacagtactt tggagagctt 600

gccctggtaa ctaacaaacc tcgagcagct tctgcccacg ccattgggac tgtcaaatgt 660

ttagcaatgg atgtgcaagc atttgaaagg cttctgggac cttgcatgga aattatgaaa 720

aggaacatcg ctacctatga agaacagtta gttgccctgt atggaacgaa catggatatt 780

gtagggtcag gtggatctgg aggtagctct tctggggtta cgccgaacat gatcgactat 840

ttcggacggc cgtatgaagg catcgccgtg ttcgacggca aaaagatcac tgtaacaggg 900

accctgtgga acggcaacaa aattatcgac gagcgcctga tcaaccccga cggctccctg 960

ctgttccgag taaccatcaa cggagtgacc ggctggcggc tgtgcgaacg cattctggct 1020

<210> 522
<211> 340
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 522
Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala
1 5 10 15

Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu
20 25 30

Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln Arg Ile Val Leu
35 40 45

Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr
50 55 60

Glu Gly Leu Ser Gly Asp Gln Met Gly Gln Ile Glu Lys Ile Phe Lys
65 70 75 80

Val Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu His Tyr
85 90 95

Gly Thr Leu Val Ile Asp Ser Ala Ser Gly Gly Ser Gly Gly Ser Gly
100 105 110

Met Tyr Glu Ser Phe Ile Glu Ser Leu Pro Phe Leu Lys Ser Leu Glu
115 120 125

Phe Ser Ala Arg Leu Lys Val Val Asp Val Ile Gly Thr Lys Val Tyr
130 135 140

Asn Asp Gly Glu Gln Ile Ile Ala Gln Gly Asp Ser Ala Asp Ser Phe
145 150 155 160

Phe Ile Ile Glu Ser Gly Glu Val Lys Ile Thr Met Lys Arg Lys Gly
165 170 175

Lys Ser Glu Val Glu Glu Asn Gly Ala Val Glu Ile Ala Arg Cys Ser
180 185 190

Arg Gly Gln Tyr Phe Gly Glu Leu Ala Leu Val Thr Asn Lys Pro Arg
195 200 205

Ala Ala Ser Ala His Ala Ile Gly Thr Val Lys Cys Leu Ala Met Asp
210 215 220

Val Gln Ala Phe Glu Arg Leu Leu Gly Pro Cys Met Glu Ile Met Lys
225 230 235 240

Arg Asn Ile Ala Thr Tyr Glu Glu Gln Leu Val Ala Leu Tyr Gly Thr
245 250 255

Asn Met Asp Ile Val Gly Ser Gly Gly Ser Gly Gly Ser Ser Ser Gly
260 265 270

Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly Ile
275 280 285

Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr Leu Trp Asn
290 295 300

Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly Ser Leu
305 310 315 320

Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg Leu Cys Glu
325 330 335

Arg Ile Leu Ala
340

<210> 523
<211> 1020
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 523
atggtcttca cactcgaaga tttcgttggg gactggcgac agacagccgg ctacaacctg 60

gaccaagtcc ttgaacaggg aggtgtgtcc agtttgtttc agaatctcgg ggtgtccgta 120

actccgatcc aaaggattgt cctgagcggt gaaaatgggc tgaagatcga catccatgtc 180

atcatcccgt atgaaggtct gagcggcgac caaatgggcc agatcgaaaa aatttttaag 240

gtggtgtacc ctgtggatga tcatcacttt aaggtgatcc tgcactatgg cacactggta 300

atcgacggga gcgctagcgg aggttcaggc ggttccggaa tgtatgaaag ctttattgag 360

tcactgccat tccttaaatc tttggagttt tctgcacgcc tgaaagtagt agatgtgata 420

ggcaccaaag tatacaacga tggagaacaa atcattgctc agggagattc ggctgattct 480

tttttcatta ttgaatctgg agaagtgaaa attactatga aaagaaaggg taaatcagaa 540

gtggaagaga atggtgcagt agaaatcgct cgatgctcgc ggggacagta ctttggagag 600

cttgccctgg taactaacaa acctcgagca gcttctgccc acgccattgg gactgtcaaa 660

tgtttagcaa tggatgtgca agcatttgaa aggcttctgg gaccttgcat ggaaattatg 720

aaaaggaaca tcgctaccta tgaagaacag ttagttgccc tgtatggaac gaacatggat 780

attgtagggt caggtggatc tggaggtagc tcttctgtta cgccgaacat gatcgactat 840

ttcggacggc cgtatgaagg catcgccgtg ttcgacggca aaaagatcac tgtaacaggg 900

accctgtgga acggcaacaa aattatcgac gagcgcctga tcaaccccga cggctccctg 960

ctgttccgag taaccatcaa cggagtgacc ggctggcggc tgtgcgaacg cattctggct 1020

<210> 524
<211> 340
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 524
Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala
1 5 10 15

Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu
20 25 30

Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln Arg Ile Val Leu
35 40 45

Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr
50 55 60

Glu Gly Leu Ser Gly Asp Gln Met Gly Gln Ile Glu Lys Ile Phe Lys
65 70 75 80

Val Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu His Tyr
85 90 95

Gly Thr Leu Val Ile Asp Gly Ser Ala Ser Gly Gly Ser Gly Gly Ser

100 105 110

Gly Met Tyr Glu Ser Phe Ile Glu Ser Leu Pro Phe Leu Lys Ser Leu
115 120 125

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

Tyr Asn Asp Gly Glu Gln Ile Ile Ala Gln Gly Asp Ser Ala Asp Ser
145 150 155 160

Phe Phe Ile Ile Glu Ser Gly Glu Val Lys Ile Thr Met Lys Arg Lys
165 170 175

Gly Lys Ser Glu Val Glu Glu Asn Gly Ala Val Glu Ile Ala Arg Cys
180 185 190

Ser Arg Gly Gln Tyr Phe Gly Glu Leu Ala Leu Val Thr Asn Lys Pro
195 200 205

Arg Ala Ala Ser Ala His Ala Ile Gly Thr Val Lys Cys Leu Ala Met
210 215 220

Asp Val Gln Ala Phe Glu Arg Leu Leu Gly Pro Cys Met Glu Ile Met
225 230 235 240

Lys Arg Asn Ile Ala Thr Tyr Glu Glu Gln Leu Val Ala Leu Tyr Gly
245 250 255

Thr Asn Met Asp Ile Val Gly Ser Gly Gly Ser Gly Gly Ser Ser Ser
260 265 270

Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly Ile
275 280 285

Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr Leu Trp Asn
290 295 300

Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly Ser Leu
305 310 315 320

Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg Leu Cys Glu
325 330 335

Arg Ile Leu Ala
340

<210> 525
<211> 1020
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 525
atggtcttca cactcgaaga tttcgttggg gactggcgac agacagccgg ctacaacctg 60

gaccaagtcc ttgaacaggg aggtgtgtcc agtttgtttc agaatctcgg ggtgtccgta 120

actccgatcc aaaggattgt cctgagcggt gaaaatgggc tgaagatcga catccatgtc 180

atcatcccgt atgaaggtct gagcggcgac caaatgggcc agatcgaaaa aatttttaag 240

gtggtgtacc ctgtggatga tcatcacttt aaggtgatcc tgcactatgg cacactggta 300

atcgacgggg ttagcgctag cggaggttca ggcggttccg gaatgtatga aagctttatt 360

gagtcactgc cattccttaa atctttggag ttttctgcac gcctgaaagt agtagatgtg 420

ataggcacca aagtatacaa cgatggagaa caaatcattg ctcagggaga ttcggctgat 480

tctttttca ttattgaatc tggagaagtg aaaattacta tgaaaagaaa gggtaaatca 540

gaagtggaag agaatggtgc agtagaaatc gctcgatgct cgcggggaca gtactttgga 600

gagcttgccc tggtaactaa caaacctcga gcagcttctg cccacgccat tgggactgtc 660

aaatgtttag caatggatgt gcaagcattt gaaaggcttc tgggaccttg catggaaatt 720

atgaaaagga acatcgctac ctatgaagaa cagttagttg ccctgtatgg aacgaacatg 780

gatattgtag ggtcaggtgg atctggaggt agctcttcta cgccgaacat gatcgactat 840

ttcggacggc cgtatgaagg catcgccgtg ttcgacggca aaaagatcac tgtaacaggg 900

accctgtgga acggcaacaa aattatcgac gagcgcctga tcaaccccga cggctccctg 960

ctgttccgag taaccatcaa cggagtgacc ggctggcggc tgtgcgaacg cattctggct 1020

<210> 526
<211> 340
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 526
Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala
1 5 10 15

Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu
20 25 30

Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln Arg Ile Val Leu
35 40 45

Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr
50 55 60

Glu Gly Leu Ser Gly Asp Gln Met Gly Gln Ile Glu Lys Ile Phe Lys
65 70 75 80

```
Val Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu His Tyr
                85                  90                  95

Gly Thr Leu Val Ile Asp Gly Val Ser Ala Ser Gly Gly Ser Gly Gly
            100                 105                 110

Ser Gly Met Tyr Glu Ser Phe Ile Glu Ser Leu Pro Phe Leu Lys Ser
        115                 120                 125

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

Val Tyr Asn Asp Gly Glu Gln Ile Ile Ala Gln Gly Asp Ser Ala Asp
145                 150                 155                 160

Ser Phe Phe Ile Ile Glu Ser Gly Glu Val Lys Ile Thr Met Lys Arg
                165                 170                 175

Lys Gly Lys Ser Glu Val Glu Glu Asn Gly Ala Val Glu Ile Ala Arg
            180                 185                 190

Cys Ser Arg Gly Gln Tyr Phe Gly Glu Leu Ala Leu Val Thr Asn Lys
        195                 200                 205

Pro Arg Ala Ala Ser Ala His Ala Ile Gly Thr Val Lys Cys Leu Ala
    210                 215                 220

Met Asp Val Gln Ala Phe Glu Arg Leu Leu Gly Pro Cys Met Glu Ile
225                 230                 235                 240

Met Lys Arg Asn Ile Ala Thr Tyr Glu Glu Gln Leu Val Ala Leu Tyr
                245                 250                 255

Gly Thr Asn Met Asp Ile Val Gly Ser Gly Gly Ser Gly Gly Ser Ser
            260                 265                 270

Ser Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly Ile
        275                 280                 285

Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr Leu Trp Asn
    290                 295                 300

Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly Ser Leu
305                 310                 315                 320

Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg Leu Cys Glu
                325                 330                 335

Arg Ile Leu Ala
            340
```

<210> 527
<211> 1020
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 527
atggtcttca cactcgaaga tttcgttggg gactggcgac agacagccgg ctacaacctg 60

gaccaagtcc ttgaacaggg aggtgtgtcc agtttgtttc agaatctcgg ggtgtccgta 120

actccgatcc aaaggattgt cctgagcggt gaaaatgggc tgaagatcga catccatgtc 180

atcatcccgt atgaaggtct gagcggcgac caaatgggcc agatcgaaaa aatttttaag 240

gtggtgtacc ctgtggatga tcatcacttt aaggtgatcc tgcactatgg cacactggta 300

atcgacgggg ttacgccgaa catgatcgac tatttcggac ggccgtatga aggcatcgcc 360

gtgagcgcta gcggaggttc aggcggttcc ggaatgtatg aaagctttat tgagtcactg 420

ccattcctta aatctttgga gttttctgca cgcctgaaag tagtagatgt gataggcacc 480

aaagtataca acgatggaga acaaatcatt gctcagggag attcggctga ttctttttc 540

attattgaat ctggagaagt gaaaattact atgaaaagaa agggtaaatc agaagtggaa 600

gagaatggtg cagtagaaat cgctcgatgc tcgcggggac agtactttgg agagcttgcc 660

ctggtaacta acaaacctcg agcagcttct gcccacgcca ttgggactgt caaatgttta 720

gcaatggatg tgcaagcatt tgaaaggctt ctgggacctt gcatggaaat tatgaaaagg 780

aacatcgcta cctatgaaga acagttagtt gccctgtatg gaacgaacat ggatattgta 840

gggtcaggtg gatctggagg tagctcttct ttcgacggca aaaagatcac tgtaacaggg 900

accctgtgga acggcaacaa aattatcgac gagcgcctga tcaaccccga cggctccctg 960

ctgttccgag taaccatcaa cggagtgacc ggctggcggc tgtgcgaacg cattctggct 1020

<210> 528
<211> 340
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 528
Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala
1 5 10 15

Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu
20 25 30

Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln Arg Ile Val Leu
35 40 45

```
Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr
    50                  55                  60

Glu Gly Leu Ser Gly Asp Gln Met Gly Gln Ile Glu Lys Ile Phe Lys
65                  70                  75                  80

Val Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu His Tyr
                85                  90                  95

Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe
            100                 105                 110

Gly Arg Pro Tyr Glu Gly Ile Ala Val Ser Ala Ser Gly Gly Ser Gly
        115                 120                 125

Gly Ser Gly Met Tyr Glu Ser Phe Ile Glu Ser Leu Pro Phe Leu Lys
    130                 135                 140

Ser Leu Glu Phe Ser Ala Arg Leu Lys Val Val Asp Val Ile Gly Thr
145                 150                 155                 160

Lys Val Tyr Asn Asp Gly Glu Gln Ile Ile Ala Gln Gly Asp Ser Ala
                165                 170                 175

Asp Ser Phe Phe Ile Ile Glu Ser Gly Glu Val Lys Ile Thr Met Lys
            180                 185                 190

Arg Lys Gly Lys Ser Glu Val Glu Glu Asn Gly Ala Val Glu Ile Ala
        195                 200                 205

Arg Cys Ser Arg Gly Gln Tyr Phe Gly Glu Leu Ala Leu Val Thr Asn
    210                 215                 220

Lys Pro Arg Ala Ala Ser Ala His Ala Ile Gly Thr Val Lys Cys Leu
225                 230                 235                 240

Ala Met Asp Val Gln Ala Phe Glu Arg Leu Leu Gly Pro Cys Met Glu
                245                 250                 255

Ile Met Lys Arg Asn Ile Ala Thr Tyr Glu Glu Gln Leu Val Ala Leu
            260                 265                 270

Tyr Gly Thr Asn Met Asp Ile Val Gly Ser Gly Gly Ser Gly Gly Ser
        275                 280                 285

Ser Ser Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr Leu Trp Asn
    290                 295                 300

Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly Ser Leu
305                 310                 315                 320
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Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg Leu Cys Glu
325 330 335

Arg Ile Leu Ala
340

<210> 529
<211> 1020
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 529
atggtcttca cactcgaaga tttcgttggg gactggcgac agacagccgg ctacaacctg 60

gaccaagtcc ttgaacaggg aggtgtgtcc agtttgtttc agaatctcgg ggtgtccgta 120

actccgatcc aaaggattgt cctgagcggt gaaaatgggc tgaagatcga catccatgtc 180

atcatcccgt atgaaggtct gagcggcgac caaatgggcc agatcgaaaa aatttttaag 240

gtggtgtacc ctgtggatga tcatcacttt aaggtgatcc tgcactatgg cacactggta 300

atcgacgggg ttacgccgaa catgatcgac tatttcggac ggccgtatga aggcatcgcc 360

gtgttcgacg gcagcgctag cggaggttca ggcggttccg gaatgtatga aagctttatt 420

gagtcactgc cattccttaa atctttggag ttttctgcac gcctgaaagt agtagatgtg 480

ataggcacca aagtatacaa cgatggagaa caaatcattg ctcagggaga ttcggctgat 540

tctttttca ttattgaatc tggagaagtg aaaattacta tgaaaagaaa gggtaaatca 600

gaagtggaag agaatggtgc agtagaaatc gctcgatgct cgcggggaca gtactttgga 660

gagcttgccc tggtaactaa caaacctcga gcagcttctg cccacgccat tgggactgtc 720

aaatgtttag caatggatgt gcaagcattt gaaaggcttc tgggaccttg catggaaatt 780

atgaaaagga acatcgctac ctatgaagaa cagttagttg ccctgtatgg aacgaacatg 840

gatattgtag ggtcaggtgg atctggaggt agctcttcta aaaagatcac tgtaacaggg 900

accctgtgga acggcaacaa aattatcgac gagcgcctga tcaaccccga cggctccctg 960

ctgttccgag taaccatcaa cggagtgacc ggctggcggc tgtgcgaacg cattctggct 1020

<210> 530
<211> 340
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 530
Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala
1 5 10 15

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Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu
            20                  25                  30

Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln Arg Ile Val Leu
        35                  40                  45

Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr
    50                  55                  60

Glu Gly Leu Ser Gly Asp Gln Met Gly Gln Ile Glu Lys Ile Phe Lys
65                  70                  75                  80

Val Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu His Tyr
                85                  90                  95

Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe
            100                 105                 110

Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Ser Ala Ser Gly
        115                 120                 125

Gly Ser Gly Gly Ser Gly Met Tyr Glu Ser Phe Ile Glu Ser Leu Pro
    130                 135                 140

Phe Leu Lys Ser Leu Glu Phe Ser Ala Arg Leu Lys Val Val Asp Val
145                 150                 155                 160

Ile Gly Thr Lys Val Tyr Asn Asp Gly Glu Gln Ile Ile Ala Gln Gly
                165                 170                 175

Asp Ser Ala Asp Ser Phe Phe Ile Ile Glu Ser Gly Glu Val Lys Ile
            180                 185                 190

Thr Met Lys Arg Lys Gly Lys Ser Glu Val Glu Glu Asn Gly Ala Val
        195                 200                 205

Glu Ile Ala Arg Cys Ser Arg Gly Gln Tyr Phe Gly Glu Leu Ala Leu
    210                 215                 220

Val Thr Asn Lys Pro Arg Ala Ala Ser Ala His Ala Ile Gly Thr Val
225                 230                 235                 240

Lys Cys Leu Ala Met Asp Val Gln Ala Phe Glu Arg Leu Leu Gly Pro
                245                 250                 255

Cys Met Glu Ile Met Lys Arg Asn Ile Ala Thr Tyr Glu Glu Gln Leu
            260                 265                 270

Val Ala Leu Tyr Gly Thr Asn Met Asp Ile Val Gly Ser Gly Gly Ser
        275                 280                 285
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Gly Gly Ser Ser Ser Lys Lys Ile Thr Val Thr Gly Thr Leu Trp Asn
290 295 300

Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly Ser Leu
305 310 315 320

Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg Leu Cys Glu
325 330 335

Arg Ile Leu Ala
340

<210> 531
<211> 1020
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 531
atggtcttca cactcgaaga tttcgttggg gactggcgac agacagccgg ctacaacctg 60

gaccaagtcc ttgaacaggg aggtgtgtcc agtttgtttc agaatctcgg ggtgtccgta 120

actccgatcc aaaggattgt cctgagcggt gaaaatgggc tgaagatcga catccatgtc 180

atcatcccgt atgaaggtct gagcggcgac caaatgggcc agatcgaaaa aatttttaag 240

gtggtgtacc ctgtggatga tcatcacttt aaggtgatcc tgcactatgg cacactggta 300

atcgacgggg ttacgccgaa catgatcgac tatttcggac ggccgtatga aggcatcgcc 360

gtgttcgacg gcaaaagcgc tagcggaggt tcaggcggtt ccggaatgta tgaaagcttt 420

attgagtcac tgccattcct taaatctttg gagttttctg cacgcctgaa agtagtagat 480

gtgataggca ccaaagtata caacgatgga gaacaaatca ttgctcaggg agattcggct 540

gattcttttt tcattattga atctggagaa gtgaaaatta ctatgaaaag aaagggtaaa 600

tcagaagtgg aagagaatgg tgcagtagaa atcgctcgat gctcgcgggg acagtacttt 660

ggagagcttg ccctggtaac taacaaacct cgagcagctt ctgcccacgc cattgggact 720

gtcaaatgtt tagcaatgga tgtgcaagca tttgaaaggc ttctgggacc ttgcatggaa 780

attatgaaaa ggaacatcgc tacctatgaa gaacagttag ttgccctgta tggaacgaac 840

atggatattg tagggtcagg tggatctgga ggtagctctt ctaagatcac tgtaacaggg 900

accctgtgga acggcaacaa aattatcgac gagcgcctga tcaaccccga cggctccctg 960

ctgttccgag taaccatcaa cggagtgacc ggctggcggc tgtgcgaacg cattctggct 1020

<210> 532
<211> 340
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

polypeptide

<400> 532

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Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala
1               5                  10                  15

Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu
            20                  25                  30

Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln Arg Ile Val Leu
        35                  40                  45

Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr
    50                  55                  60

Glu Gly Leu Ser Gly Asp Gln Met Gly Gln Ile Glu Lys Ile Phe Lys
65                  70                  75                  80

Val Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu His Tyr
                85                  90                  95

Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe
            100                 105                 110

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

Gly Gly Ser Gly Gly Ser Gly Met Tyr Glu Ser Phe Ile Glu Ser Leu
    130                 135                 140

Pro Phe Leu Lys Ser Leu Glu Phe Ser Ala Arg Leu Lys Val Val Asp
145                 150                 155                 160

Val Ile Gly Thr Lys Val Tyr Asn Asp Gly Glu Gln Ile Ile Ala Gln
                165                 170                 175

Gly Asp Ser Ala Asp Ser Phe Phe Ile Ile Glu Ser Gly Glu Val Lys
            180                 185                 190

Ile Thr Met Lys Arg Lys Gly Lys Ser Glu Val Glu Glu Asn Gly Ala
        195                 200                 205

Val Glu Ile Ala Arg Cys Ser Arg Gly Gln Tyr Phe Gly Glu Leu Ala
    210                 215                 220

Leu Val Thr Asn Lys Pro Arg Ala Ala Ser Ala His Ala Ile Gly Thr
225                 230                 235                 240

Val Lys Cys Leu Ala Met Asp Val Gln Ala Phe Glu Arg Leu Leu Gly
                245                 250                 255

Pro Cys Met Glu Ile Met Lys Arg Asn Ile Ala Thr Tyr Glu Glu Gln
```

260 265 270

Leu Val Ala Leu Tyr Gly Thr Asn Met Asp Ile Val Gly Ser Gly Gly
275 280 285

Ser Gly Gly Ser Ser Ser Lys Ile Thr Val Thr Gly Thr Leu Trp Asn
290 295 300

Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly Ser Leu
305 310 315 320

Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg Leu Cys Glu
325 330 335

Arg Ile Leu Ala
340

<210> 533
<211> 1020
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 533
atggtcttca cactcgaaga tttcgttggg gactggcgac agacagccgg ctacaacctg 60

gaccaagtcc ttgaacaggg aggtgtgtcc agtttgtttc agaatctcgg ggtgtccgta 120

actccgatcc aaaggattgt cctgagcggt gaaaatgggc tgaagatcga catccatgtc 180

atcatcccgt atgaaggtct gagcggcgac caaatgggcc agatcgaaaa aatttttaag 240

gtggtgtacc ctgtggatga tcatcacttt aaggtgatcc tgcactatgg cacactggta 300

atcgacgggg ttacgccgaa catgatcgac tatttcggac ggccgtatga aggcatcgcc 360

gtgttcgacg gcaaaaagag cgctagcgga ggttcaggcg gttccggaat gtatgaaagc 420

tttattgagt cactgccatt ccttaaatct ttggagtttt ctgcacgcct gaaagtagta 480

gatgtgatag gcaccaaagt atacaacgat ggagaacaaa tcattgctca gggagattcg 540

gctgattctt ttttcattat tgaatctgga gaagtgaaaa ttactatgaa aagaaagggt 600

aaatcagaag tggaagagaa tggtgcagta gaaatcgctc gatgctcgcg gggacagtac 660

tttggagagc ttgccctggt aactaacaaa cctcgagcag cttctgccca cgccattggg 720

actgtcaaat gtttagcaat ggatgtgcaa gcatttgaaa ggcttctggg accttgcatg 780

gaaattatga aaaggaacat cgctacctat gaagaacagt tagttgccct gtatggaacg 840

aacatggata ttgtagggtc aggtggatct ggaggtagct cttctatcac tgtaacaggg 900

accctgtgga acggcaacaa aattatcgac gagcgcctga tcaaccccga cggctccctg 960

ctgttccgag taaccatcaa cggagtgacc ggctggcggc tgtgcgaacg cattctggct 1020

<210> 534
<211> 340
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 534

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Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala
1               5                  10                  15

Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu
            20                  25                  30

Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln Arg Ile Val Leu
        35                  40                  45

Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr
    50                  55                  60

Glu Gly Leu Ser Gly Asp Gln Met Gly Gln Ile Glu Lys Ile Phe Lys
65                  70                  75                  80

Val Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu His Tyr
                85                  90                  95

Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe
            100                 105                 110

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

Ser Gly Gly Ser Gly Gly Ser Gly Met Tyr Glu Ser Phe Ile Glu Ser
    130                 135                 140

Leu Pro Phe Leu Lys Ser Leu Glu Phe Ser Ala Arg Leu Lys Val Val
145                 150                 155                 160

Asp Val Ile Gly Thr Lys Val Tyr Asn Asp Gly Glu Gln Ile Ile Ala
                165                 170                 175

Gln Gly Asp Ser Ala Asp Ser Phe Phe Ile Ile Glu Ser Gly Glu Val
            180                 185                 190

Lys Ile Thr Met Lys Arg Lys Gly Lys Ser Glu Val Glu Glu Asn Gly
        195                 200                 205

Ala Val Glu Ile Ala Arg Cys Ser Arg Gly Gln Tyr Phe Gly Glu Leu
    210                 215                 220

Ala Leu Val Thr Asn Lys Pro Arg Ala Ala Ser Ala His Ala Ile Gly
225                 230                 235                 240
```

Thr Val Lys Cys Leu Ala Met Asp Val Gln Ala Phe Glu Arg Leu Leu
245 250 255

Gly Pro Cys Met Glu Ile Met Lys Arg Asn Ile Ala Thr Tyr Glu Glu
260 265 270

Gln Leu Val Ala Leu Tyr Gly Thr Asn Met Asp Ile Val Gly Ser Gly
275 280 285

Gly Ser Gly Gly Ser Ser Ser Ile Thr Val Thr Gly Thr Leu Trp Asn
290 295 300

Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly Ser Leu
305 310 315 320

Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg Leu Cys Glu
325 330 335

Arg Ile Leu Ala
340

<210> 535
<211> 1020
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 535
atggtcttca cactcgaaga tttcgttggg gactggcgac agacagccgg ctacaacctg 60

gaccaagtcc ttgaacaggg aggtgtgtcc agtttgtttc agaatctcgg ggtgtccgta 120

actccgatcc aaaggattgt cctgagcggt gaaaatgggc tgaagatcga catccatgtc 180

atcatcccgt atgaaggtct gagcggcgac caaatgggcc agatcgaaaa aatttttaag 240

gtggtgtacc ctgtggatga tcatcacttt aaggtgatcc tgcactatgg cacactggta 300

atcgacgggg ttacgccgaa catgatcgac tatttcggac ggccgtatga aggcatcgcc 360

gtgttcgacg gcaaaaagat cactgtaaca gggagcgcta gcggaggttc aggcggttcc 420

ggaatgtatg aaagctttat tgagtcactg ccattcctta aatctttgga gttttctgca 480

cgcctgaaag tagtagatgt gataggcacc aaagtataca acgatggaga acaaatcatt 540

gctcagggag attcggctga ttctttttttc attattgaat ctggagaagt gaaaattact 600

atgaaaagaa agggtaaatc agaagtggaa gagaatggtg cagtagaaat cgctcgatgc 660

tcgcggggac agtactttgg agagcttgcc ctggtaacta acaaacctcg agcagcttct 720

gcccacgcca ttgggactgt caaatgttta gcaatggatg tgcaagcatt tgaaaggctt 780

ctgggacctt gcatggaaat tatgaaaagg aacatcgcta cctatgaaga acagttagtt 840

gccctgtatg gaacgaacat ggatattgta gggtcaggtg gatctggagg tagctcttct 900

accctgtgga acggcaacaa aattatcgac gagcgcctga tcaaccccga cggctccctg 960

ctgttccgag taaccatcaa cggagtgacc ggctggcggc tgtgcgaacg cattctggct 1020

<210> 536
<211> 340
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 536

Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala
1 5 10 15

Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu
20 25 30

Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln Arg Ile Val Leu
35 40 45

Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr
50 55 60

Glu Gly Leu Ser Gly Asp Gln Met Gly Gln Ile Glu Lys Ile Phe Lys
65 70 75 80

Val Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu His Tyr
85 90 95

Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe
100 105 110

Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr
115 120 125

Val Thr Gly Ser Ala Ser Gly Gly Ser Gly Gly Ser Gly Met Tyr Glu
130 135 140

Ser Phe Ile Glu Ser Leu Pro Phe Leu Lys Ser Leu Glu Phe Ser Ala
145 150 155 160

Arg Leu Lys Val Val Asp Val Ile Gly Thr Lys Val Tyr Asn Asp Gly
165 170 175

Glu Gln Ile Ile Ala Gln Gly Asp Ser Ala Asp Ser Phe Phe Ile Ile
180 185 190

Glu Ser Gly Glu Val Lys Ile Thr Met Lys Arg Lys Gly Lys Ser Glu
195 200 205

Val Glu Glu Asn Gly Ala Val Glu Ile Ala Arg Cys Ser Arg Gly Gln
210 215 220

Tyr Phe Gly Glu Leu Ala Leu Val Thr Asn Lys Pro Arg Ala Ala Ser
225 230 235 240

Ala His Ala Ile Gly Thr Val Lys Cys Leu Ala Met Asp Val Gln Ala
245 250 255

Phe Glu Arg Leu Leu Gly Pro Cys Met Glu Ile Met Lys Arg Asn Ile
260 265 270

Ala Thr Tyr Glu Glu Gln Leu Val Ala Leu Tyr Gly Thr Asn Met Asp
275 280 285

Ile Val Gly Ser Gly Gly Ser Gly Gly Ser Ser Ser Thr Leu Trp Asn
290 295 300

Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly Ser Leu
305 310 315 320

Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg Leu Cys Glu
325 330 335

Arg Ile Leu Ala
340

<210> 537
<211> 1020
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 537
atggtcttca cactcgaaga tttcgttggg gactggcgac agacagccgg ctacaacctg 60

gaccaagtcc ttgaacaggg aggtgtgtcc agtttgtttc agaatctcgg ggtgtccgta 120

actccgatcc aaaggattgt cctgagcggt gaaaatgggc tgaagatcga catccatgtc 180

atcatcccgt atgaaggtct gagcggcgac caaatgggcc agatcgaaaa aatttttaag 240

gtggtgtacc ctgtggatga tcatcacttt aaggtgatcc tgcactatgg cacactggta 300

atcgacgggg ttacgccgaa catgatcgac tatttcggac ggccgtatga aggcatcgcc 360

gtgttcgacg gcaaaaagat cactgtaaca gggaccctgt ggaacggcaa cagcgctagc 420

ggaggttcag gcggttccgg aatgtatgaa agctttattg agtcactgcc attccttaaa 480

tctttggagt tttctgcacg cctgaaagta gtagatgtga taggcaccaa agtatacaac 540

gatggagaac aaatcattgc tcagggagat tcggctgatt ctttttttcat tattgaatct 600

ggagaagtga aaattactat gaaaagaaag ggtaaatcag aagtggaaga gaatggtgca 660

gtagaaatcg ctcgatgctc gcggggacag tactttggag agcttgccct ggtaactaac 720

aaacctcgag cagcttctgc ccacgccatt gggactgtca aatgtttagc aatggatgtg 780

caagcatttg aaaggcttct gggaccttgc atggaaatta tgaaaaggaa catcgctacc 840

tatgaagaac agttagttgc cctgtatgga acgaacatgg atattgtagg gtcaggtgga 900

tctggaggta gctcttctaa aattatcgac gagcgcctga tcaaccccga cggctccctg 960

ctgttccgag taaccatcaa cggagtgacc ggctggcggc tgtgcgaacg cattctggct 1020

<210> 538
<211> 340
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 538
Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala
1 5 10 15

Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu
20 25 30

Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln Arg Ile Val Leu
35 40 45

Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr
50 55 60

Glu Gly Leu Ser Gly Asp Gln Met Gly Gln Ile Glu Lys Ile Phe Lys
65 70 75 80

Val Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu His Tyr
85 90 95

Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe
100 105 110

Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr
115 120 125

Val Thr Gly Thr Leu Trp Asn Gly Asn Ser Ala Ser Gly Gly Ser Gly
130 135 140

Gly Ser Gly Met Tyr Glu Ser Phe Ile Glu Ser Leu Pro Phe Leu Lys
145 150 155 160

Ser Leu Glu Phe Ser Ala Arg Leu Lys Val Val Asp Val Ile Gly Thr
165 170 175

Lys Val Tyr Asn Asp Gly Glu Gln Ile Ile Ala Gln Gly Asp Ser Ala
180 185 190

Asp Ser Phe Phe Ile Ile Glu Ser Gly Glu Val Lys Ile Thr Met Lys
195 200 205

Arg Lys Gly Lys Ser Glu Val Glu Glu Asn Gly Ala Val Glu Ile Ala
210 215 220

Arg Cys Ser Arg Gly Gln Tyr Phe Gly Glu Leu Ala Leu Val Thr Asn
225 230 235 240

Lys Pro Arg Ala Ala Ser Ala His Ala Ile Gly Thr Val Lys Cys Leu
245 250 255

Ala Met Asp Val Gln Ala Phe Glu Arg Leu Leu Gly Pro Cys Met Glu
260 265 270

Ile Met Lys Arg Asn Ile Ala Thr Tyr Glu Glu Gln Leu Val Ala Leu
275 280 285

Tyr Gly Thr Asn Met Asp Ile Val Gly Ser Gly Gly Ser Gly Gly Ser
290 295 300

Ser Ser Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly Ser Leu
305 310 315 320

Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg Leu Cys Glu
325 330 335

Arg Ile Leu Ala
340

<210> 539
<211> 1020
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 539
atggtcttca cactcgaaga tttcgttggg gactggcgac agacagccgg ctacaacctg 60

gaccaagtcc ttgaacaggg aggtgtgtcc agtttgtttc agaatctcgg ggtgtccgta 120

actccgatcc aaaggattgt cctgagcggt gaaaatgggc tgaagatcga catccatgtc 180

atcatcccgt atgaaggtct gagcggcgac caaatgggcc agatcgaaaa aatttttaag 240

gtggtgtacc ctgtggatga tcatcacttt aaggtgatcc tgcactatgg cacactggta 300

atcgacgggg ttacgccgaa catgatcgac tatttcggac ggccgtatga aggcatcgcc 360

gtgttcgacg gcaaaaagat cactgtaaca gggaccctgt ggaacggcaa caaaattatc 420

gacgagcgcc tgagcgctag cggaggttca ggcggttccg gaatgtatga aagctttatt 480

gagtcactgc cattccttaa atctttggag ttttctgcac gcctgaaagt agtagatgtg 540

ataggcacca aagtatacaa cgatggagaa caaatcattg ctcagggaga ttcggctgat 600

tctttttca ttattgaatc tggagaagtg aaaattacta tgaaaagaaa gggtaaatca 660

gaagtggaag agaatggtgc agtagaaatc gctcgatgct cgcggggaca gtactttgga 720

gagcttgccc tggtaactaa caaacctcga gcagcttctg cccacgccat tgggactgtc 780

aaatgtttag caatggatgt gcaagcattt gaaaggcttc tgggaccttg catggaaatt 840

atgaaaagga acatcgctac ctatgaagaa cagttagttg ccctgtatgg aacgaacatg 900

gatattgtag ggtcaggtgg atctggaggt agctcttcta tcaaccccga cggctccctg 960

ctgttccgag taaccatcaa cggagtgacc ggctggcggc tgtgcgaacg cattctggct 1020

<210> 540
<211> 340
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 540
Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala
1 5 10 15

Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu
20 25 30

Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln Arg Ile Val Leu
35 40 45

Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr
50 55 60

Glu Gly Leu Ser Gly Asp Gln Met Gly Gln Ile Glu Lys Ile Phe Lys
65 70 75 80

Val Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu His Tyr
85 90 95

Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe
100 105 110

Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr
115 120 125

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

Ser Ala Ser Gly Gly Ser Gly Gly Ser Gly Met Tyr Glu Ser Phe Ile

145 150 155 160

Glu Ser Leu Pro Phe Leu Lys Ser Leu Glu Phe Ser Ala Arg Leu Lys
165 170 175

Val Val Asp Val Ile Gly Thr Lys Val Tyr Asn Asp Gly Glu Gln Ile
180 185 190

Ile Ala Gln Gly Asp Ser Ala Asp Ser Phe Phe Ile Ile Glu Ser Gly
195 200 205

Glu Val Lys Ile Thr Met Lys Arg Lys Gly Lys Ser Glu Val Glu Glu
210 215 220

Asn Gly Ala Val Glu Ile Ala Arg Cys Ser Arg Gly Gln Tyr Phe Gly
225 230 235 240

Glu Leu Ala Leu Val Thr Asn Lys Pro Arg Ala Ala Ser Ala His Ala
245 250 255

Ile Gly Thr Val Lys Cys Leu Ala Met Asp Val Gln Ala Phe Glu Arg
260 265 270

Leu Leu Gly Pro Cys Met Glu Ile Met Lys Arg Asn Ile Ala Thr Tyr
275 280 285

Glu Glu Gln Leu Val Ala Leu Tyr Gly Thr Asn Met Asp Ile Val Gly
290 295 300

Ser Gly Gly Ser Gly Gly Ser Ser Ser Ile Asn Pro Asp Gly Ser Leu
305 310 315 320

Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg Leu Cys Glu
325 330 335

Arg Ile Leu Ala
340

<210> 541
<211> 1020
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 541
atggtcttca cactcgaaga tttcgttggg gactggcgac agacagccgg ctacaacctg 60

gaccaagtcc ttgaacaggg aggtgtgtcc agtttgtttc agaatctcgg ggtgtccgta 120

actccgatcc aaaggattgt cctgagcggt gaaaatgggc tgaagatcga catccatgtc 180

atcatcccgt atgaaggtct gagcggcgac caaatgggcc agatcgaaaa aatttttaag 240

gtggtgtacc ctgtggatga tcatcacttt aaggtgatcc tgcactatgg cacactggta 300

atcgacgggg ttacgccgaa catgatcgac tatttcggac ggccgtatga aggcatcgcc 360

gtgttcgacg gcaaaaagat cactgtaaca gggaccctgt ggaacggcaa caaaattatc 420

gacgagcgcc tgatcaacag cgctagcgga ggttcaggcg gttccggaat gtatgaaagc 480

tttattgagt cactgccatt ccttaaatct ttggagtttt ctgcacgcct gaaagtagta 540

gatgtgatag gcaccaaagt atacaacgat ggagaacaaa tcattgctca gggagattcg 600

gctgattctt ttttcattat tgaatctgga gaagtgaaaa ttactatgaa aagaaagggt 660

aaatcagaag tggaagagaa tggtgcagta gaaatcgctc gatgctcgcg gggacagtac 720

tttggagagc ttgccctggt aactaacaaa cctcgagcag cttctgccca cgccattggg 780

actgtcaaat gtttagcaat ggatgtgcaa gcatttgaaa ggcttctggg accttgcatg 840

gaaattatga aaaggaacat cgctacctat gaagaacagt tagttgccct gtatggaacg 900

aacatggata ttgtagggtc aggtggatct ggaggtagct cttctcccga cggctccctg 960

ctgttccgag taaccatcaa cggagtgacc ggctggcggc tgtgcgaacg cattctggct 1020

<210> 542
<211> 340
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 542
Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala
1 5 10 15

Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu
20 25 30

Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln Arg Ile Val Leu
35 40 45

Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr
50 55 60

Glu Gly Leu Ser Gly Asp Gln Met Gly Gln Ile Glu Lys Ile Phe Lys
65 70 75 80

Val Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu His Tyr
85 90 95

Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe
100 105 110

Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr
115 120 125

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

Ile Asn Ser Ala Ser Gly Gly Ser Gly Gly Ser Gly Met Tyr Glu Ser
145                 150                 155                 160

Phe Ile Glu Ser Leu Pro Phe Leu Lys Ser Leu Glu Phe Ser Ala Arg
                165                 170                 175

Leu Lys Val Val Asp Val Ile Gly Thr Lys Val Tyr Asn Asp Gly Glu
            180                 185                 190

Gln Ile Ile Ala Gln Gly Asp Ser Ala Asp Ser Phe Phe Ile Ile Glu
        195                 200                 205

Ser Gly Glu Val Lys Ile Thr Met Lys Arg Lys Gly Lys Ser Glu Val
    210                 215                 220

Glu Glu Asn Gly Ala Val Glu Ile Ala Arg Cys Ser Arg Gly Gln Tyr
225                 230                 235                 240

Phe Gly Glu Leu Ala Leu Val Thr Asn Lys Pro Arg Ala Ala Ser Ala
                245                 250                 255

His Ala Ile Gly Thr Val Lys Cys Leu Ala Met Asp Val Gln Ala Phe
            260                 265                 270

Glu Arg Leu Leu Gly Pro Cys Met Glu Ile Met Lys Arg Asn Ile Ala
        275                 280                 285

Thr Tyr Glu Glu Gln Leu Val Ala Leu Tyr Gly Thr Asn Met Asp Ile
    290                 295                 300

Val Gly Ser Gly Gly Ser Gly Gly Ser Ser Ser Pro Asp Gly Ser Leu
305                 310                 315                 320

Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg Leu Cys Glu
                325                 330                 335

Arg Ile Leu Ala
            340
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<210> 543
<211> 1020
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 543

atggtcttca cactcgaaga tttcgttggg gactggcgac agacagccgg ctacaacctg 60

gaccaagtcc ttgaacaggg aggtgtgtcc agtttgtttc agaatctcgg ggtgtccgta 120

actccgatcc aaaggattgt cctgagcggt gaaaatgggc tgaagatcga catccatgtc 180

atcatcccgt atgaaggtct gagcggcgac caaatgggcc agatcgaaaa aatttttaag 240

gtggtgtacc ctgtggatga tcatcacttt aaggtgatcc tgcactatgg cacactggta 300

atcgacgggg ttacgccgaa catgatcgac tatttcggac ggccgtatga aggcatcgcc 360

gtgttcgacg gcaaaaagat cactgtaaca gggaccctgt ggaacggcaa caaaattatc 420

gacgagcgcc tgatcaaccc cgacagcgct agcggaggtt caggcggttc cggaatgtat 480

gaaagcttta ttgagtcact gccattcctt aaatctttgg agttttctgc acgcctgaaa 540

gtagtagatg tgataggcac caaagtatac aacgatggag aacaaatcat tgctcaggga 600

gattcggctg attctttttt cattattgaa tctggagaag tgaaaattac tatgaaaaga 660

aagggtaaat cagaagtgga agagaatggt gcagtagaaa tcgctcgatg ctcgcgggga 720

cagtactttg gagagcttgc cctggtaact aacaaacctc gagcagcttc tgcccacgcc 780

attgggactg tcaaatgttt agcaatggat gtgcaagcat ttgaaaggct tctgggacct 840

tgcatggaaa ttatgaaaag gaacatcgct acctatgaag aacagttagt tgccctgtat 900

ggaacgaaca tggatattgt agggtcaggt ggatctggag gtagctcttc tggctccctg 960

ctgttccgag taaccatcaa cggagtgacc ggctggcggc tgtgcgaacg cattctggct 1020

<210> 544
<211> 340
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 544
Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala
1 5 10 15

Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu
20 25 30

Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln Arg Ile Val Leu
35 40 45

Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr
50 55 60

Glu Gly Leu Ser Gly Asp Gln Met Gly Gln Ile Glu Lys Ile Phe Lys
65 70 75 80

Val Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu His Tyr
85 90 95

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Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe
            100                 105                 110

Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr
        115                 120                 125

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

Ile Asn Pro Asp Ser Ala Ser Gly Gly Ser Gly Gly Ser Gly Met Tyr
145                 150                 155                 160

Glu Ser Phe Ile Glu Ser Leu Pro Phe Leu Lys Ser Leu Glu Phe Ser
                165                 170                 175

Ala Arg Leu Lys Val Val Asp Val Ile Gly Thr Lys Val Tyr Asn Asp
            180                 185                 190

Gly Glu Gln Ile Ile Ala Gln Gly Asp Ser Ala Asp Ser Phe Phe Ile
        195                 200                 205

Ile Glu Ser Gly Glu Val Lys Ile Thr Met Lys Arg Lys Gly Lys Ser
    210                 215                 220

Glu Val Glu Glu Asn Gly Ala Val Glu Ile Ala Arg Cys Ser Arg Gly
225                 230                 235                 240

Gln Tyr Phe Gly Glu Leu Ala Leu Val Thr Asn Lys Pro Arg Ala Ala
                245                 250                 255

Ser Ala His Ala Ile Gly Thr Val Lys Cys Leu Ala Met Asp Val Gln
            260                 265                 270

Ala Phe Glu Arg Leu Leu Gly Pro Cys Met Glu Ile Met Lys Arg Asn
        275                 280                 285

Ile Ala Thr Tyr Glu Glu Gln Leu Val Ala Leu Tyr Gly Thr Asn Met
    290                 295                 300

Asp Ile Val Gly Ser Gly Gly Ser Gly Gly Ser Ser Ser Gly Ser Leu
305                 310                 315                 320

Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg Leu Cys Glu
                325                 330                 335

Arg Ile Leu Ala
            340
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<210> 545
<211> 1020
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 545
atggtcttca cactcgaaga tttcgttggg gactggcgac agacagccgg ctacaacctg 60

gaccaagtcc ttgaacaggg aggtgtgtcc agtttgtttc agaatctcgg ggtgtccgta 120

actccgatcc aaaggattgt cctgagcggt gaaaatgggc tgaagatcga catccatgtc 180

atcatcccgt atgaaggtct gagcggcgac caaatgggcc agatcgaaaa aatttttaag 240

gtggtgtacc ctgtggatga tcatcacttt aaggtgatcc tgcactatgg cacactggta 300

atcgacgggg ttacgccgaa catgatcgac tatttcggac ggccgtatga aggcatcgcc 360

gtgttcgacg gcaaaaagat cactgtaaca gggaccctgt ggaacggcaa caaaattatc 420

gacgagcgcc tgatcaaccc cgacggcagc gctagcggag gttcaggcgg ttccggaatg 480

tatgaaagct ttattgagtc actgccattc cttaaatctt tggagttttc tgcacgcctg 540

aaagtagtag atgtgatagg caccaaagta tacaacgatg gagaacaaat cattgctcag 600

ggagattcgg ctgattcttt tttcattatt gaatctggag aagtgaaaat tactatgaaa 660

agaaagggta aatcagaagt ggaagagaat ggtgcagtag aaatcgctcg atgctcgcgg 720

ggacagtact ttggagagct tgccctggta actaacaaac ctcgagcagc ttctgcccac 780

gccattggga ctgtcaaatg tttagcaatg gatgtgcaag catttgaaag gcttctggga 840

ccttgcatgg aaattatgaa aaggaacatc gctacctatg aagaacagtt agttgccctg 900

tatggaacga acatggatat tgtagggtca ggtggatctg gaggtagctc ttcttccctg 960

ctgttccgag taaccatcaa cggagtgacc ggctggcggc tgtgcgaacg cattctggct 1020

<210> 546
<211> 340
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 546
Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala
1 5 10 15

Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu
20 25 30

Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln Arg Ile Val Leu
35 40 45

Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr
50 55 60

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Glu Gly Leu Ser Gly Asp Gln Met Gly Gln Ile Glu Lys Ile Phe Lys
65                  70                  75                  80

Val Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu His Tyr
                85                  90                  95

Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe
            100                 105                 110

Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr
        115                 120                 125

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

Ile Asn Pro Asp Gly Ser Ala Ser Gly Gly Ser Gly Gly Ser Gly Met
145                 150                 155                 160

Tyr Glu Ser Phe Ile Glu Ser Leu Pro Phe Leu Lys Ser Leu Glu Phe
                165                 170                 175

Ser Ala Arg Leu Lys Val Val Asp Val Ile Gly Thr Lys Val Tyr Asn
            180                 185                 190

Asp Gly Glu Gln Ile Ile Ala Gln Gly Asp Ser Ala Asp Ser Phe Phe
        195                 200                 205

Ile Ile Glu Ser Gly Glu Val Lys Ile Thr Met Lys Arg Lys Gly Lys
    210                 215                 220

Ser Glu Val Glu Glu Asn Gly Ala Val Glu Ile Ala Arg Cys Ser Arg
225                 230                 235                 240

Gly Gln Tyr Phe Gly Glu Leu Ala Leu Val Thr Asn Lys Pro Arg Ala
                245                 250                 255

Ala Ser Ala His Ala Ile Gly Thr Val Lys Cys Leu Ala Met Asp Val
            260                 265                 270

Gln Ala Phe Glu Arg Leu Leu Gly Pro Cys Met Glu Ile Met Lys Arg
        275                 280                 285

Asn Ile Ala Thr Tyr Glu Glu Gln Leu Val Ala Leu Tyr Gly Thr Asn
    290                 295                 300

Met Asp Ile Val Gly Ser Gly Gly Ser Gly Gly Ser Ser Ser Ser Leu
305                 310                 315                 320

Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg Leu Cys Glu
                325                 330                 335
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Arg Ile Leu Ala
340

<210> 547
<211> 1020
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 547
atggtcttca cactcgaaga tttcgttggg gactggcgac agacagccgg ctacaacctg 60

gaccaagtcc ttgaacaggg aggtgtgtcc agtttgtttc agaatctcgg ggtgtccgta 120

actccgatcc aaaggattgt cctgagcggt gaaaatgggc tgaagatcga catccatgtc 180

atcatcccgt atgaaggtct gagcggcgac caaatgggcc agatcgaaaa aatttttaag 240

gtggtgtacc ctgtggatga tcatcacttt aaggtgatcc tgcactatgg cacactggta 300

atcgacgggg ttacgccgaa catgatcgac tatttcggac ggccgtatga aggcatcgcc 360

gtgttcgacg gcaaaaagat cactgtaaca gggaccctgt ggaacggcaa caaaattatc 420

gacgagcgcc tgatcaaccc cgacggctcc ctgctgttcc gagtaaccat cagcgctagc 480

ggaggttcag gcggttccgg aatgtatgaa agctttattg agtcactgcc attccttaaa 540

tctttggagt tttctgcacg cctgaaagta gtagatgtga taggcaccaa agtatacaac 600

gatggagaac aaatcattgc tcagggagat tcggctgatt ctttttttcat tattgaatct 660

ggagaagtga aaattactat gaaaagaaag ggtaaatcag aagtggaaga gaatggtgca 720

gtagaaatcg ctcgatgctc gcggggacag tactttggag agcttgccct ggtaactaac 780

aaacctcgag cagcttctgc ccacgccatt gggactgtca aatgtttagc aatggatgtg 840

caagcatttg aaaggcttct gggaccttgc atggaaatta tgaaaaggaa catcgctacc 900

tatgaagaac agttagttgc cctgtatgga acgaacatgg atattgtagg gtcaggtgga 960

tctggaggta gctcttctaa cggagtgacc ggctggcggc tgtgcgaacg cattctggct 1020

<210> 548
<211> 340
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 548
Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala
1 5 10 15

Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu
20 25 30

Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln Arg Ile Val Leu

35 40 45

Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr
50 55 60

Glu Gly Leu Ser Gly Asp Gln Met Gly Gln Ile Glu Lys Ile Phe Lys
65 70 75 80

Val Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu His Tyr
85 90 95

Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe
100 105 110

Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr
115 120 125

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

Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Ser Ala Ser
145 150 155 160

Gly Gly Ser Gly Gly Ser Gly Met Tyr Glu Ser Phe Ile Glu Ser Leu
165 170 175

Pro Phe Leu Lys Ser Leu Glu Phe Ser Ala Arg Leu Lys Val Val Asp
180 185 190

Val Ile Gly Thr Lys Val Tyr Asn Asp Gly Glu Gln Ile Ile Ala Gln
195 200 205

Gly Asp Ser Ala Asp Ser Phe Phe Ile Ile Glu Ser Gly Glu Val Lys
210 215 220

Ile Thr Met Lys Arg Lys Gly Lys Ser Glu Val Glu Glu Asn Gly Ala
225 230 235 240

Val Glu Ile Ala Arg Cys Ser Arg Gly Gln Tyr Phe Gly Glu Leu Ala
245 250 255

Leu Val Thr Asn Lys Pro Arg Ala Ala Ser Ala His Ala Ile Gly Thr
260 265 270

Val Lys Cys Leu Ala Met Asp Val Gln Ala Phe Glu Arg Leu Leu Gly
275 280 285

Pro Cys Met Glu Ile Met Lys Arg Asn Ile Ala Thr Tyr Glu Glu Gln
290 295 300

Leu Val Ala Leu Tyr Gly Thr Asn Met Asp Ile Val Gly Ser Gly Gly

305 310 315 320

Ser Gly Gly Ser Ser Ser Asn Gly Val Thr Gly Trp Arg Leu Cys Glu
325 330 335

Arg Ile Leu Ala
340

<210> 549
<211> 1020
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 549
atggtcttca cactcgaaga tttcgttggg gactggcgac agacagccgg ctacaacctg 60

gaccaagtcc ttgaacaggg aggtgtgtcc agtttgtttc agaatctcgg ggtgtccgta 120

actccgatcc aaaggattgt cctgagcggt gaaaatgggc tgaagatcga catccatgtc 180

atcatcccgt atgaaggtct gagcggcgac caaatgggcc agatcgaaaa aatttttaag 240

gtggtgtacc ctgtggatga tcatcacttt aaggtgatcc tgcactatgg cacactggta 300

atcgacgggg ttacgccgaa catgatcgac tatttcggac ggccgtatga aggcatcgcc 360

gtgttcgacg gcaaaaagat cactgtaaca gggaccctgt ggaacggcaa caaaattatc 420

gacgagcgcc tgatcaaccc cgacggctcc ctgctgttcc gagtaaccat caacagcgct 480

agcggaggtt caggcggttc cggaatgtat gaaagcttta ttgagtcact gccattcctt 540

aaatctttgg agttttctgc acgcctgaaa gtagtagatg tgataggcac caaagtatac 600

aacgatggag aacaaatcat tgctcaggga gattcggctg attctttttt cattattgaa 660

tctggagaag tgaaaattac tatgaaaaga aagggtaaat cagaagtgga agagaatggt 720

gcagtagaaa tcgctcgatg ctcgcgggga cagtactttg gagagcttgc cctggtaact 780

aacaaacctc gagcagcttc tgcccacgcc attgggactg tcaaatgttt agcaatggat 840

gtgcaagcat ttgaaaggct tctgggacct tgcatggaaa ttatgaaaag gaacatcgct 900

acctatgaag aacagttagt tgccctgtat ggaacgaaca tggatattgt agggtcaggt 960

ggatctggag gtagctcttc tggagtgacc ggctggcggc tgtgcgaacg cattctggct 1020

<210> 550
<211> 340
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 550
Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala
1 5 10 15

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Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu
            20                  25                  30

Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln Arg Ile Val Leu
        35                  40                  45

Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr
    50                  55                  60

Glu Gly Leu Ser Gly Asp Gln Met Gly Gln Ile Glu Lys Ile Phe Lys
65                  70                  75                  80

Val Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu His Tyr
                85                  90                  95

Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe
            100                 105                 110

Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr
        115                 120                 125

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

Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Ser Ala
145                 150                 155                 160

Ser Gly Gly Ser Gly Gly Ser Gly Met Tyr Glu Ser Phe Ile Glu Ser
                165                 170                 175

Leu Pro Phe Leu Lys Ser Leu Glu Phe Ser Ala Arg Leu Lys Val Val
            180                 185                 190

Asp Val Ile Gly Thr Lys Val Tyr Asn Asp Gly Glu Gln Ile Ile Ala
        195                 200                 205

Gln Gly Asp Ser Ala Asp Ser Phe Phe Ile Ile Glu Ser Gly Glu Val
    210                 215                 220

Lys Ile Thr Met Lys Arg Lys Gly Lys Ser Glu Val Glu Glu Asn Gly
225                 230                 235                 240

Ala Val Glu Ile Ala Arg Cys Ser Arg Gly Gln Tyr Phe Gly Glu Leu
                245                 250                 255

Ala Leu Val Thr Asn Lys Pro Arg Ala Ala Ser Ala His Ala Ile Gly
            260                 265                 270

Thr Val Lys Cys Leu Ala Met Asp Val Gln Ala Phe Glu Arg Leu Leu
        275                 280                 285
```

Gly Pro Cys Met Glu Ile Met Lys Arg Asn Ile Ala Thr Tyr Glu Glu
290 295 300

Gln Leu Val Ala Leu Tyr Gly Thr Asn Met Asp Ile Val Gly Ser Gly
305 310 315 320

Gly Ser Gly Gly Ser Ser Ser Gly Val Thr Gly Trp Arg Leu Cys Glu
325 330 335

Arg Ile Leu Ala
340

<210> 551
<211> 1020
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 551
atggtcttca cactcgaaga tttcgttggg gactggcgac agacagccgg ctacaacctg 60

gaccaagtcc ttgaacaggg aggtgtgtcc agtttgtttc agaatctcgg ggtgtccgta 120

actccgatcc aaaggattgt cctgagcggt gaaaatgggc tgaagatcga catccatgtc 180

atcatcccgt atgaaggtct gagcggcgac caaatgggcc agatcgaaaa aatttttaag 240

gtggtgtacc ctgtggatga tcatcacttt aaggtgatcc tgcactatgg cacactggta 300

atcgacgggg ttacgccgaa catgatcgac tatttcggac ggccgtatga aggcatcgcc 360

gtgttcgacg gcaaaaagat cactgtaaca gggaccctgt ggaacggcaa caaaattatc 420

gacgagcgcc tgatcaaccc cgacggctcc ctgctgttcc gagtaaccat caacggaagc 480

gctagcggag gttcaggcgg ttccggaatg tatgaaagct ttattgagtc actgccattc 540

cttaaatctt tggagtttc tgcacgcctg aaagtagtag atgtgatagg caccaaagta 600

tacaacgatg gagaacaaat cattgctcag ggagattcgg ctgattcttt tttcattatt 660

gaatctggag aagtgaaaat tactatgaaa agaaagggta aatcagaagt ggaagagaat 720

ggtgcagtag aaatcgctcg atgctcgcgg ggacagtact ttggagagct tgccctggta 780

actaacaaac ctcgagcagc ttctgcccac gccattggga ctgtcaaatg tttagcaatg 840

gatgtgcaag catttgaaag gcttctggga ccttgcatgg aaattatgaa aaggaacatc 900

gctacctatg aagaacagtt agttgccctg tatggaacga acatggatat tgtagggtca 960

ggtggatctg gaggtagctc ttctgtgacc ggctggcggc tgtgcgaacg cattctggct 1020

<210> 552
<211> 340
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 552

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Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala
1               5                  10                  15

Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu
            20                  25                  30

Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln Arg Ile Val Leu
        35                  40                  45

Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr
    50                  55                  60

Glu Gly Leu Ser Gly Asp Gln Met Gly Gln Ile Glu Lys Ile Phe Lys
65                  70                  75                  80

Val Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu His Tyr
                85                  90                  95

Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe
            100                 105                 110

Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr
        115                 120                 125

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

Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Ser
145                 150                 155                 160

Ala Ser Gly Gly Ser Gly Gly Ser Gly Met Tyr Glu Ser Phe Ile Glu
                165                 170                 175

Ser Leu Pro Phe Leu Lys Ser Leu Glu Phe Ser Ala Arg Leu Lys Val
            180                 185                 190

Val Asp Val Ile Gly Thr Lys Val Tyr Asn Asp Gly Glu Gln Ile Ile
        195                 200                 205

Ala Gln Gly Asp Ser Ala Asp Ser Phe Phe Ile Ile Glu Ser Gly Glu
    210                 215                 220

Val Lys Ile Thr Met Lys Arg Lys Gly Lys Ser Glu Val Glu Glu Asn
225                 230                 235                 240

Gly Ala Val Glu Ile Ala Arg Cys Ser Arg Gly Gln Tyr Phe Gly Glu
                245                 250                 255
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Leu Ala Leu Val Thr Asn Lys Pro Arg Ala Ala Ser Ala His Ala Ile
260 265 270

Gly Thr Val Lys Cys Leu Ala Met Asp Val Gln Ala Phe Glu Arg Leu
275 280 285

Leu Gly Pro Cys Met Glu Ile Met Lys Arg Asn Ile Ala Thr Tyr Glu
290 295 300

Glu Gln Leu Val Ala Leu Tyr Gly Thr Asn Met Asp Ile Val Gly Ser
305 310 315 320

Gly Gly Ser Gly Gly Ser Ser Ser Val Thr Gly Trp Arg Leu Cys Glu
325 330 335

Arg Ile Leu Ala
340

<210> 553
<211> 1020
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 553
atggtcttca cactcgaaga tttcgttggg gactggcgac agacagccgg ctacaacctg 60

gaccaagtcc ttgaacaggg aggtgtgtcc agtttgtttc agaatctcgg ggtgtccgta 120

actccgatcc aaaggattgt cctgagcggt gaaaatgggc tgaagatcga catccatgtc 180

atcatcccgt atgaaggtct gagcggcgac caaatgggcc agatcgaaaa aatttttaag 240

gtggtgtacc ctgtggatga tcatcacttt aaggtgatcc tgcactatgg cacactggta 300

atcgacgggg ttacgccgaa catgatcgac tatttcggac ggccgtatga aggcatcgcc 360

gtgttcgacg gcaaaaagat cactgtaaca gggaccctgt ggaacggcaa caaaattatc 420

gacgagcgcc tgatcaaccc cgacggctcc ctgctgttcc gagtaaccat caacggagtg 480

accggctggc ggctgtgcga aagcgctagc ggaggttcag gcggttccgg aatgtatgaa 540

agctttattg agtcactgcc attccttaaa tctttggagt tttctgcacg cctgaaagta 600

gtagatgtga taggcaccaa agtatacaac gatggagaac aaatcattgc tcagggagat 660

tcggctgatt ctttttttcat tattgaatct ggagaagtga aaattactat gaaaagaaag 720

ggtaaatcag aagtggaaga gaatggtgca gtagaaatcg ctcgatgctc gcggggacag 780

tactttggag agcttgccct ggtaactaac aaacctcgag cagcttctgc ccacgccatt 840

gggactgtca aatgtttagc aatggatgtg caagcatttg aaaggcttct gggaccttgc 900

atggaaatta tgaaaaggaa catcgctacc tatgaagaac agttagttgc cctgtatgga 960

acgaacatgg atattgtagg gtcaggtgga tctggaggta gctcttctcg cattctggct 1020

<210> 554
<211> 340
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 554
Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala
1 5 10 15

Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu
20 25 30

Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln Arg Ile Val Leu
35 40 45

Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr
50 55 60

Glu Gly Leu Ser Gly Asp Gln Met Gly Gln Ile Glu Lys Ile Phe Lys
65 70 75 80

Val Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu His Tyr
85 90 95

Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe
100 105 110

Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr
115 120 125

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

Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val
145 150 155 160

Thr Gly Trp Arg Leu Cys Glu Ser Ala Ser Gly Gly Ser Gly Gly Ser
165 170 175

Gly Met Tyr Glu Ser Phe Ile Glu Ser Leu Pro Phe Leu Lys Ser Leu
180 185 190

Glu Phe Ser Ala Arg Leu Lys Val Val Asp Val Ile Gly Thr Lys Val
195 200 205

Tyr Asn Asp Gly Glu Gln Ile Ile Ala Gln Gly Asp Ser Ala Asp Ser
210 215 220

Phe Phe Ile Ile Glu Ser Gly Glu Val Lys Ile Thr Met Lys Arg Lys
225 230 235 240

Gly Lys Ser Glu Val Glu Glu Asn Gly Ala Val Glu Ile Ala Arg Cys
245 250 255

Ser Arg Gly Gln Tyr Phe Gly Glu Leu Ala Leu Val Thr Asn Lys Pro
260 265 270

Arg Ala Ala Ser Ala His Ala Ile Gly Thr Val Lys Cys Leu Ala Met
275 280 285

Asp Val Gln Ala Phe Glu Arg Leu Leu Gly Pro Cys Met Glu Ile Met
290 295 300

Lys Arg Asn Ile Ala Thr Tyr Glu Glu Gln Leu Val Ala Leu Tyr Gly
305 310 315 320

Thr Asn Met Asp Ile Val Gly Ser Gly Gly Ser Gly Gly Ser Ser Ser
325 330 335

Arg Ile Leu Ala
340

<210> 555
<211> 1023
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 555
atgggtgtgt ccagtttgtt tcagaatctc ggggtgtccg taactccgat ccaaaggatt 60

gtcctgagcg gtgaaaatgg gctgaagatc gacatccatg tcatcatccc gtatgaaggt 120

ctgagcggcg accaaatggg ccagatcgaa aaaatttta aggtggtgta ccctgtggat 180

gatcatcact ttaaggtgat cctgcactat ggcacactgg taatcgacgg ggttacgccg 240

aacatgatcg actatttcgg acggccgtat gaaggcatcg ccgtgttcga cggcaaaaag 300

atcactgtaa cagggaccct gtggaacggc aacaaaatta tcgacgagcg cctgatcaac 360

cccgacggct ccctgctgtt ccgagtaacc atcaacggag tgaccggctg gcggctgtgc 420

gaacgcattc tggctagctc aagcggaggt tcaggcggtt ccggaatgta tgaaagcttt 480

attgagtcac tgccattcct taaatctttg gagttttctg cacgcctgaa agtagtagat 540

gtgataggca ccaaagtata caacgatgga gaacaaatca ttgctcaggg agattcggct 600

gattcttttt tcattattga atctggagaa gtgaaaatta ctatgaaaag aaagggtaaa 660

tcagaagtgg aagagaatgg tgcagtagaa atcgctcgat gctcgcgggg acagtacttt 720

ggagagcttg ccctggtaac taacaaacct cgagcagctt ctgcccacgc cattgggact 780

gtcaaatgtt tagcaatgga tgtgcaagca tttgaaaggc ttctgggacc ttgcatggaa 840

attatgaaaa ggaacatcgc tacctatgaa gaacagttag ttgccctgta tggaacgaac 900

atggatattg tagggtcagg tggatctgga ggtagctctt ctatggtctt cacactcgaa 960

gatttcgttg gggactggcg acagacagcc ggctacaacc tggaccaagt ccttgaacag 1020

gga 1023

<210> 556
<211> 341
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 556

| | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Met | Gly | Val | Ser | Ser | Leu | Phe | Gln | Asn | Leu | Gly | Val | Ser | Val | Thr | Pro |
| 1 | | | | 5 | | | | 10 | | | | | 15 | | |
| Ile | Gln | Arg | Ile | Val | Leu | Ser | Gly | Glu | Asn | Gly | Leu | Lys | Ile | Asp | Ile |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| His | Val | Ile | Ile | Pro | Tyr | Glu | Gly | Leu | Ser | Gly | Asp | Gln | Met | Gly | Gln |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Ile | Glu | Lys | Ile | Phe | Lys | Val | Val | Tyr | Pro | Val | Asp | Asp | His | His | Phe |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Lys | Val | Ile | Leu | His | Tyr | Gly | Thr | Leu | Val | Ile | Asp | Gly | Val | Thr | Pro |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Asn | Met | Ile | Asp | Tyr | Phe | Gly | Arg | Pro | Tyr | Glu | Gly | Ile | Ala | Val | Phe |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Asp | Gly | Lys | Lys | Ile | Thr | Val | Thr | Gly | Thr | Leu | Trp | Asn | Gly | Asn | Lys |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Ile | Ile | Asp | Glu | Arg | Leu | Ile | Asn | Pro | Asp | Gly | Ser | Leu | Leu | Phe | Arg |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Val | Thr | Ile | Asn | Gly | Val | Thr | Gly | Trp | Arg | Leu | Cys | Glu | Arg | Ile | Leu |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Ala | Ser | Ser | Ser | Gly | Gly | Ser | Gly | Gly | Ser | Gly | Met | Tyr | Glu | Ser | Phe |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| Ile | Glu | Ser | Leu | Pro | Phe | Leu | Lys | Ser | Leu | Glu | Phe | Ser | Ala | Arg | Leu |
| | | | | 165 | | | | | 170 | | | | | 175 | |
| Lys | Val | Val | Asp | Val | Ile | Gly | Thr | Lys | Val | Tyr | Asn | Asp | Gly | Glu | Gln |
| | | | 180 | | | | | 185 | | | | | 190 | | |

Ile Ile Ala Gln Gly Asp Ser Ala Asp Ser Phe Phe Ile Ile Glu Ser
195 200 205

Gly Glu Val Lys Ile Thr Met Lys Arg Lys Gly Lys Ser Glu Val Glu
210 215 220

Glu Asn Gly Ala Val Glu Ile Ala Arg Cys Ser Arg Gly Gln Tyr Phe
225 230 235 240

Gly Glu Leu Ala Leu Val Thr Asn Lys Pro Arg Ala Ala Ser Ala His
245 250 255

Ala Ile Gly Thr Val Lys Cys Leu Ala Met Asp Val Gln Ala Phe Glu
260 265 270

Arg Leu Leu Gly Pro Cys Met Glu Ile Met Lys Arg Asn Ile Ala Thr
275 280 285

Tyr Glu Glu Gln Leu Val Ala Leu Tyr Gly Thr Asn Met Asp Ile Val
290 295 300

Gly Ser Gly Gly Ser Gly Gly Ser Ser Ser Met Val Phe Thr Leu Glu
305 310 315 320

Asp Phe Val Gly Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln
325 330 335

Val Leu Glu Gln Gly
340

<210> 557
<211> 1023
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 557
atggtcctga gcggtgaaaa tgggctgaag atcgacatcc atgtcatcat cccgtatgaa 60

ggtctgagcg gcgaccaaat gggccagatc gaaaaaattt ttaaggtggt gtaccctgtg 120

gatgatcatc actttaaggt gatcctgcac tatggcacac tggtaatcga cggggttacg 180

ccgaacatga tcgactattt cggacggccg tatgaaggca tcgccgtgtt cgacggcaaa 240

aagatcactg taacagggac cctgtggaac ggcaacaaaa ttatcgacga gcgcctgatc 300

aaccccgacg gctccctgct gttccgagta accatcaacg gagtgaccgg ctggcggctg 360

tgcgaacgca ttctggctag ctcaagcgga ggttcaggcg gttccggaat gtatgaaagc 420

tttattgagt cactgccatt ccttaaatct ttggagtttt ctgcacgcct gaaagtagta 480

gatgtgatag gcaccaaagt atacaacgat ggagaacaaa tcattgctca gggagattcg 540

gctgattctt ttttcattat tgaatctgga gaagtgaaaa ttactatgaa aagaaagggt 600

aaatcagaag tggaagagaa tggtgcagta gaaatcgctc gatgctcgcg gggacagtac 660

tttggagagc ttgccctggt aactaacaaa cctcgagcag cttctgccca cgccattggg 720

actgtcaaat gtttagcaat ggatgtgcaa gcatttgaaa ggcttctggg accttgcatg 780

gaaattatga aaaggaacat cgctacctat gaagaacagt tagttgccct gtatggaacg 840

aacatggata ttgtagggtc aggtggatct ggaggtagct cttctatggt cttcacactc 900

gaagatttcg ttggggactg gcgacagaca gccggctaca acctggacca agtccttgaa 960

cagggaggtg tgtccagttt gtttcagaat ctcggggtgt ccgtaactcc gatccaaagg 1020

att 1023

<210> 558
<211> 341
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 558
Met Val Leu Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile
1 5 10 15

Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln Met Gly Gln Ile Glu Lys
20 25 30

Ile Phe Lys Val Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile
35 40 45

Leu His Tyr Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile
50 55 60

Asp Tyr Phe Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys
65 70 75 80

Lys Ile Thr Val Thr Gly Thr Leu Trp Asn Gly Asn Lys Ile Ile Asp
85 90 95

Glu Arg Leu Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile
100 105 110

Asn Gly Val Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala Ser Ser
115 120 125

Ser Gly Gly Ser Gly Gly Ser Gly Met Tyr Glu Ser Phe Ile Glu Ser
130 135 140

Leu Pro Phe Leu Lys Ser Leu Glu Phe Ser Ala Arg Leu Lys Val Val
145 150 155 160

Asp Val Ile Gly Thr Lys Val Tyr Asn Asp Gly Glu Gln Ile Ile Ala
165 170 175

Gln Gly Asp Ser Ala Asp Ser Phe Phe Ile Ile Glu Ser Gly Glu Val
180 185 190

Lys Ile Thr Met Lys Arg Lys Gly Lys Ser Glu Val Glu Glu Asn Gly
195 200 205

Ala Val Glu Ile Ala Arg Cys Ser Arg Gly Gln Tyr Phe Gly Glu Leu
210 215 220

Ala Leu Val Thr Asn Lys Pro Arg Ala Ala Ser Ala His Ala Ile Gly
225 230 235 240

Thr Val Lys Cys Leu Ala Met Asp Val Gln Ala Phe Glu Arg Leu Leu
245 250 255

Gly Pro Cys Met Glu Ile Met Lys Arg Asn Ile Ala Thr Tyr Glu Glu
260 265 270

Gln Leu Val Ala Leu Tyr Gly Thr Asn Met Asp Ile Val Gly Ser Gly
275 280 285

Gly Ser Gly Gly Ser Ser Ser Met Val Phe Thr Leu Glu Asp Phe Val
290 295 300

Gly Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val Leu Glu
305 310 315 320

Gln Gly Gly Val Ser Ser Leu Phe Gln Asn Leu Gly Val Ser Val Thr
325 330 335

Pro Ile Gln Arg Ile
340

<210> 559
<211> 1026
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 559
atggacgggg ttacgccgaa catgatcgac tatttcggac ggccgtatga aggcatcgcc 60

gtgttcgacg gcaaaaagat cactgtaaca gggaccctgt ggaacggcaa caaaattatc 120

gacgagcgcc tgatcaaccc cgacggctcc ctgctgttcc gagtaaccat caacggagtg 180

accggctggc ggctgtgcga acgcattctg gctagctcaa gcggaggttc aggcggttcc 240

ggaatgtatg aaagctttat tgagtcactg ccattcctta aatctttgga gttttctgca 300

cgcctgaaag tagtagatgt gataggcacc aaagtataca acgatggaga acaaatcatt 360

gctcagggag attcggctga ttctttttc attattgaat ctggagaagt gaaaattact 420

atgaaaagaa agggtaaatc agaagtggaa gagaatggtg cagtagaaat cgctcgatgc 480

tcgcggggac agtactttgg agagcttgcc ctggtaacta acaaacctcg agcagcttct 540

gcccacgcca ttgggactgt caaatgttta gcaatggatg tgcaagcatt tgaaaggctt 600

ctgggacctt gcatggaaat tatgaaaagg aacatcgcta cctatgaaga acagttagtt 660

gccctgtatg gaacgaacat ggatattgta gggtcaggtg gatctggagg tagctcttct 720

atggtcttca cactcgaaga tttcgttggg gactggcgac agacagccgg ctacaacctg 780

gaccaagtcc ttgaacaggg aggtgtgtcc agtttgtttc agaatctcgg ggtgtccgta 840

actccgatcc aaaggattgt cctgagcggt gaaaatgggc tgaagatcga catccatgtc 900

atcatcccgt atgaaggtct gagcggcgac caaatgggcc agatcgaaaa aatttttaag 960

gtggtgtacc ctgtggatga tcatcacttt aaggtgatcc tgcactatgg cacactggta 1020

atcgac 1026

<210> 560
<211> 342
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 560
Met Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr
1 5 10 15

Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr
20 25 30

Leu Trp Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp
35 40 45

Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg
50 55 60

Leu Cys Glu Arg Ile Leu Ala Ser Ser Ser Gly Gly Ser Gly Gly Ser
65 70 75 80

Gly Met Tyr Glu Ser Phe Ile Glu Ser Leu Pro Phe Leu Lys Ser Leu
85 90 95

Glu Phe Ser Ala Arg Leu Lys Val Val Asp Val Ile Gly Thr Lys Val
100 105 110

Tyr Asn Asp Gly Glu Gln Ile Ile Ala Gln Gly Asp Ser Ala Asp Ser

115 120 125

Phe Phe Ile Ile Glu Ser Gly Glu Val Lys Ile Thr Met Lys Arg Lys
130 135 140

Gly Lys Ser Glu Val Glu Glu Asn Gly Ala Val Glu Ile Ala Arg Cys
145 150 155 160

Ser Arg Gly Gln Tyr Phe Gly Glu Leu Ala Leu Val Thr Asn Lys Pro
165 170 175

Arg Ala Ala Ser Ala His Ala Ile Gly Thr Val Lys Cys Leu Ala Met
180 185 190

Asp Val Gln Ala Phe Glu Arg Leu Leu Gly Pro Cys Met Glu Ile Met
195 200 205

Lys Arg Asn Ile Ala Thr Tyr Glu Glu Gln Leu Val Ala Leu Tyr Gly
210 215 220

Thr Asn Met Asp Ile Val Gly Ser Gly Gly Ser Gly Gly Ser Ser Ser
225 230 235 240

Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala
245 250 255

Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu
260 265 270

Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln Arg Ile Val Leu
275 280 285

Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr
290 295 300

Glu Gly Leu Ser Gly Asp Gln Met Gly Gln Ile Glu Lys Ile Phe Lys
305 310 315 320

Val Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu His Tyr
325 330 335

Gly Thr Leu Val Ile Asp
340

<210> 561
<211> 1026
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 561
atgggggtta cgccgaacat gatcgactat ttcggacggc cgtatgaagg catcgccgtg 60

ttcgacggca aaaagatcac tgtaacaggg accctgtgga acggcaacaa aattatcgac 120

gagcgcctga tcaaccccga cggctccctg ctgttccgag taaccatcaa cggagtgacc 180

ggctggcggc tgtgcgaacg cattctggct agctcaagcg gaggttcagg cggttccgga 240

atgtatgaaa gctttattga gtcactgcca ttccttaaat ctttggagtt ttctgcacgc 300

ctgaaagtag tagatgtgat aggcaccaaa gtatacaacg atggagaaca aatcattgct 360

cagggagatt cggctgattc ttttttcatt attgaatctg gagaagtgaa aattactatg 420

aaaagaaagg gtaaatcaga agtggaagag aatggtgcag tagaaatcgc tcgatgctcg 480

cggggacagt actttggaga gcttgccctg gtaactaaca aacctcgagc agcttctgcc 540

cacgccattg ggactgtcaa atgtttagca atggatgtgc aagcatttga aaggcttctg 600

ggaccttgca tggaaattat gaaaaggaac atcgctacct atgaagaaca gttagttgcc 660

ctgtatggaa cgaacatgga tattgtaggg tcaggtggat ctggaggtag ctcttctatg 720

gtcttcacac tcgaagattt cgttggggac tggcgacaga cagccggcta caacctggac 780

caagtccttg aacagggagg tgtgtccagt ttgtttcaga atctcggggt gtccgtaact 840

ccgatccaaa ggattgtcct gagcggtgaa aatgggctga agatcgacat ccatgtcatc 900

atcccgtatg aaggtctgag cggcgaccaa atgggccaga tcgaaaaaat ttttaaggtg 960

gtgtaccctg tggatgatca tcactttaag gtgatcctgc actatggcac actggtaatc 1020

gacggg 1026

<210> 562
<211> 342
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 562
Met Gly Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu
1 5 10 15

Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr Leu
20 25 30

Trp Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly
35 40 45

Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg Leu
50 55 60

Cys Glu Arg Ile Leu Ala Ser Ser Ser Gly Gly Ser Gly Gly Ser Gly
65 70 75 80

```
Met Tyr Glu Ser Phe Ile Glu Ser Leu Pro Phe Leu Lys Ser Leu Glu
                85                  90                  95

Phe Ser Ala Arg Leu Lys Val Val Asp Val Ile Gly Thr Lys Val Tyr
            100                 105                 110

Asn Asp Gly Glu Gln Ile Ile Ala Gln Gly Asp Ser Ala Asp Ser Phe
        115                 120                 125

Phe Ile Ile Glu Ser Gly Glu Val Lys Ile Thr Met Lys Arg Lys Gly
    130                 135                 140

Lys Ser Glu Val Glu Glu Asn Gly Ala Val Glu Ile Ala Arg Cys Ser
145                 150                 155                 160

Arg Gly Gln Tyr Phe Gly Glu Leu Ala Leu Val Thr Asn Lys Pro Arg
                165                 170                 175

Ala Ala Ser Ala His Ala Ile Gly Thr Val Lys Cys Leu Ala Met Asp
            180                 185                 190

Val Gln Ala Phe Glu Arg Leu Leu Gly Pro Cys Met Glu Ile Met Lys
        195                 200                 205

Arg Asn Ile Ala Thr Tyr Glu Glu Gln Leu Val Ala Leu Tyr Gly Thr
    210                 215                 220

Asn Met Asp Ile Val Gly Ser Gly Gly Ser Gly Gly Ser Ser Ser Met
225                 230                 235                 240

Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala Gly
                245                 250                 255

Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu Phe
            260                 265                 270

Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln Arg Ile Val Leu Ser
        275                 280                 285

Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr Glu
    290                 295                 300

Gly Leu Ser Gly Asp Gln Met Gly Gln Ile Glu Lys Ile Phe Lys Val
305                 310                 315                 320

Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu His Tyr Gly
                325                 330                 335

Thr Leu Val Ile Asp Gly
            340
```

<210> 563
<211> 1026
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 563
atggttacgc cgaacatgat cgactatttc ggacggccgt atgaaggcat cgccgtgttc 60

gacggcaaaa agatcactgt aacagggacc ctgtggaacg gcaacaaaat tatcgacgag 120

cgcctgatca accccgacgg ctccctgctg ttccgagtaa ccatcaacgg agtgaccggc 180

tggcggctgt gcgaacgcat tctggctagc tcaagcggag gttcaggcgg ttccggaatg 240

tatgaaagct ttattgagtc actgccattc cttaaatctt tggagttttc tgcacgcctg 300

aaagtagtag atgtgatagg caccaaagta tacaacgatg gagaacaaat cattgctcag 360

ggagattcgg ctgattcttt tttcattatt gaatctggag aagtgaaaat tactatgaaa 420

agaaagggta aatcagaagt ggaagagaat ggtgcagtag aaatcgctcg atgctcgcgg 480

ggacagtact ttggagagct tgccctggta actaacaaac ctcgagcagc ttctgcccac 540

gccattggga ctgtcaaatg tttagcaatg gatgtgcaag catttgaaag gcttctggga 600

ccttgcatgg aaattatgaa aaggaacatc gctacctatg aagaacagtt agttgccctg 660

tatggaacga acatggatat tgtagggtca ggtggatctg gaggtagctc ttctatggtc 720

ttcacactcg aagatttcgt tggggactgg cgacagacag ccggctacaa cctggaccaa 780

gtccttgaac agggaggtgt gtccagtttg tttcagaatc tcggggtgtc cgtaactccg 840

atccaaagga ttgtcctgag cggtgaaaat gggctgaaga tcgacatcca tgtcatcatc 900

ccgtatgaag gtctgagcgg cgaccaaatg ggccagatcg aaaaaatttt taaggtggtg 960

taccctgtgg atgatcatca ctttaaggtg atcctgcact atggcacact ggtaatcgac 1020

ggggtt 1026

<210> 564
<211> 342
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 564
Met Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly
1 5 10 15

Ile Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr Leu Trp
20 25 30

Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly Ser
35 40 45

```
Leu Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp Arg Leu Cys
    50                  55                  60

Glu Arg Ile Leu Ala Ser Ser Ser Gly Gly Ser Gly Gly Ser Gly Met
65                  70                  75                  80

Tyr Glu Ser Phe Ile Glu Ser Leu Pro Phe Leu Lys Ser Leu Glu Phe
                85                  90                  95

Ser Ala Arg Leu Lys Val Val Asp Val Ile Gly Thr Lys Val Tyr Asn
            100                 105                 110

Asp Gly Glu Gln Ile Ile Ala Gln Gly Asp Ser Ala Asp Ser Phe Phe
        115                 120                 125

Ile Ile Glu Ser Gly Glu Val Lys Ile Thr Met Lys Arg Lys Gly Lys
    130                 135                 140

Ser Glu Val Glu Glu Asn Gly Ala Val Glu Ile Ala Arg Cys Ser Arg
145                 150                 155                 160

Gly Gln Tyr Phe Gly Glu Leu Ala Leu Val Thr Asn Lys Pro Arg Ala
                165                 170                 175

Ala Ser Ala His Ala Ile Gly Thr Val Lys Cys Leu Ala Met Asp Val
            180                 185                 190

Gln Ala Phe Glu Arg Leu Leu Gly Pro Cys Met Glu Ile Met Lys Arg
        195                 200                 205

Asn Ile Ala Thr Tyr Glu Glu Gln Leu Val Ala Leu Tyr Gly Thr Asn
    210                 215                 220

Met Asp Ile Val Gly Ser Gly Gly Ser Gly Gly Ser Ser Ser Met Val
225                 230                 235                 240

Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala Gly Tyr
                245                 250                 255

Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu Phe Gln
            260                 265                 270

Asn Leu Gly Val Ser Val Thr Pro Ile Gln Arg Ile Val Leu Ser Gly
        275                 280                 285

Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr Glu Gly
    290                 295                 300

Leu Ser Gly Asp Gln Met Gly Gln Ile Glu Lys Ile Phe Lys Val Val
305                 310                 315                 320
```

Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu His Tyr Gly Thr
325 330 335

Leu Val Ile Asp Gly Val
340

<210> 565
<211> 1026
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 565
atgatcaacc ccgacggctc cctgctgttc cgagtaacca tcaacggagt gaccggctgg 60

cggctgtgcg aacgcattct ggctagctca agcggaggtt caggcggttc cggaatgtat 120

gaaagcttta ttgagtcact gccattcctt aaatctttgg agttttctgc acgcctgaaa 180

gtagtagatg tgataggcac caaagtatac aacgatggag aacaaatcat tgctcaggga 240

gattcggctg attctttttt cattattgaa tctggagaag tgaaaattac tatgaaaaga 300

aagggtaaat cagaagtgga agagaatggt gcagtagaaa tcgctcgatg ctcgcgggga 360

cagtactttg gagagcttgc cctggtaact aacaaacctc gagcagcttc tgcccacgcc 420

attgggactg tcaaatgttt agcaatggat gtgcaagcat ttgaaaggct tctgggacct 480

tgcatggaaa ttatgaaaag gaacatcgct acctatgaag aacagttagt tgccctgtat 540

ggaacgaaca tggatattgt agggtcaggt ggatctggag gtagctcttc tatggtcttc 600

acactcgaag atttcgttgg ggactggcga cagacagccg gctacaacct ggaccaagtc 660

cttgaacagg gaggtgtgtc cagtttgttt cagaatctcg gggtgtccgt aactccgatc 720

caaaggattg tcctgagcgg tgaaaatggg ctgaagatcg acatccatgt catcatcccg 780

tatgaaggtc tgagcggcga ccaaatgggc cagatcgaaa aaatttttaa ggtggtgtac 840

cctgtggatg atcatcactt taaggtgatc ctgcactatg gcacactggt aatcgacggg 900

gttacgccga acatgatcga ctatttcgga cggccgtatg aaggcatcgc cgtgttcgac 960

ggcaaaaaga tcactgtaac agggaccctg tggaacggca acaaaattat cgacgagcgc 1020

ctgatc 1026

<210> 566
<211> 342
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 566
Met Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly
1 5 10 15

```
Val Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala Ser Ser Ser Gly
            20                  25                  30

Gly Ser Gly Gly Ser Gly Met Tyr Glu Ser Phe Ile Glu Ser Leu Pro
        35                  40                  45

Phe Leu Lys Ser Leu Glu Phe Ser Ala Arg Leu Lys Val Val Asp Val
    50                  55                  60

Ile Gly Thr Lys Val Tyr Asn Asp Gly Glu Gln Ile Ile Ala Gln Gly
65                  70                  75                  80

Asp Ser Ala Asp Ser Phe Phe Ile Ile Glu Ser Gly Glu Val Lys Ile
                85                  90                  95

Thr Met Lys Arg Lys Gly Lys Ser Glu Val Glu Glu Asn Gly Ala Val
            100                 105                 110

Glu Ile Ala Arg Cys Ser Arg Gly Gln Tyr Phe Gly Glu Leu Ala Leu
        115                 120                 125

Val Thr Asn Lys Pro Arg Ala Ala Ser Ala His Ala Ile Gly Thr Val
    130                 135                 140

Lys Cys Leu Ala Met Asp Val Gln Ala Phe Glu Arg Leu Leu Gly Pro
145                 150                 155                 160

Cys Met Glu Ile Met Lys Arg Asn Ile Ala Thr Tyr Glu Glu Gln Leu
                165                 170                 175

Val Ala Leu Tyr Gly Thr Asn Met Asp Ile Val Gly Ser Gly Gly Ser
            180                 185                 190

Gly Gly Ser Ser Ser Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp
        195                 200                 205

Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly
    210                 215                 220

Gly Val Ser Ser Leu Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile
225                 230                 235                 240

Gln Arg Ile Val Leu Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His
                245                 250                 255

Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln Met Gly Gln Ile
            260                 265                 270

Glu Lys Ile Phe Lys Val Val Tyr Pro Val Asp Asp His His Phe Lys
        275                 280                 285
```

Val Ile Leu His Tyr Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn
290 295 300

Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp
305 310 315 320

Gly Lys Lys Ile Thr Val Thr Gly Thr Leu Trp Asn Gly Asn Lys Ile
325 330 335

Ile Asp Glu Arg Leu Ile
340

<210> 567
<211> 1026
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 567
atgggctccc tgctgttccg agtaaccatc aacggagtga ccggctggcg gctgtgcgaa 60

cgcattctgg ctagctcaag cggaggttca ggcggttccg gaatgtatga aagctttatt 120

gagtcactgc cattccttaa atctttggag ttttctgcac gcctgaaagt agtagatgtg 180

ataggcacca aagtatacaa cgatggagaa caaatcattg ctcagggaga ttcggctgat 240

tctttttca ttattgaatc tggagaagtg aaaattacta tgaaaagaaa gggtaaatca 300

gaagtggaag agaatggtgc agtagaaatc gctcgatgct cgcggggaca gtactttgga 360

gagcttgccc tggtaactaa caaacctcga gcagcttctg cccacgccat tgggactgtc 420

aaatgtttag caatggatgt gcaagcattt gaaaggcttc tgggaccttg catggaaatt 480

atgaaaagga acatcgctac ctatgaagaa cagttagttg ccctgtatgg aacgaacatg 540

gatattgtag ggtcaggtgg atctggaggt agctcttcta tggtcttcac actcgaagat 600

ttcgttgggg actggcgaca gacagccggc tacaacctgg accaagtcct tgaacaggga 660

ggtgtgtcca gtttgtttca gaatctcggg gtgtccgtaa ctccgatcca aaggattgtc 720

ctgagcggtg aaaatgggct gaagatcgac atccatgtca tcatcccgta tgaaggtctg 780

agcggcgacc aaatgggcca gatcgaaaaa atttttaagg tggtgtaccc tgtggatgat 840

catcacttta aggtgatcct gcactatggc acactggtaa tcgacggggt tacgccgaac 900

atgatcgact atttcggacg gccgtatgaa ggcatcgccg tgttcgacgg caaaaagatc 960

actgtaacag ggaccctgtg gaacggcaac aaaattatcg acgagcgcct gatcaacccc 1020

gacggc 1026

<210> 568
<211> 342
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 568
Met Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly Trp
1 5 10 15

Arg Leu Cys Glu Arg Ile Leu Ala Ser Ser Ser Gly Gly Ser Gly Gly
20 25 30

Ser Gly Met Tyr Glu Ser Phe Ile Glu Ser Leu Pro Phe Leu Lys Ser
35 40 45

Leu Glu Phe Ser Ala Arg Leu Lys Val Val Asp Val Ile Gly Thr Lys
50 55 60

Val Tyr Asn Asp Gly Glu Gln Ile Ile Ala Gln Gly Asp Ser Ala Asp
65 70 75 80

Ser Phe Phe Ile Ile Glu Ser Gly Glu Val Lys Ile Thr Met Lys Arg
85 90 95

Lys Gly Lys Ser Glu Val Glu Glu Asn Gly Ala Val Glu Ile Ala Arg
100 105 110

Cys Ser Arg Gly Gln Tyr Phe Gly Glu Leu Ala Leu Val Thr Asn Lys
115 120 125

Pro Arg Ala Ala Ser Ala His Ala Ile Gly Thr Val Lys Cys Leu Ala
130 135 140

Met Asp Val Gln Ala Phe Glu Arg Leu Leu Gly Pro Cys Met Glu Ile
145 150 155 160

Met Lys Arg Asn Ile Ala Thr Tyr Glu Glu Gln Leu Val Ala Leu Tyr
165 170 175

Gly Thr Asn Met Asp Ile Val Gly Ser Gly Gly Ser Gly Gly Ser Ser
180 185 190

Ser Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr
195 200 205

Ala Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser
210 215 220

Leu Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln Arg Ile Val
225 230 235 240

Leu Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro

245 250 255

Tyr Glu Gly Leu Ser Gly Asp Gln Met Gly Gln Ile Glu Lys Ile Phe
260 265 270

Lys Val Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu His
275 280 285

Tyr Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr
290 295 300

Phe Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile
305 310 315 320

Thr Val Thr Gly Thr Leu Trp Asn Gly Asn Lys Ile Ile Asp Glu Arg
325 330 335

Leu Ile Asn Pro Asp Gly
340

<210> 569
<211> 1026
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 569
atgaacggag tgaccggctg gcggctgtgc gaacgcattc tggctagctc aagcggaggt 60

tcaggcggtt ccggaatgta tgaaagcttt attgagtcac tgccattcct taaatctttg 120

gagttttctg cacgcctgaa agtagtagat gtgataggca ccaaagtata caacgatgga 180

gaacaaatca ttgctcaggg agattcggct gattcttttt tcattattga atctggagaa 240

gtgaaaatta ctatgaaaag aaagggtaaa tcagaagtgg aagagaatgg tgcagtagaa 300

atcgctcgat gctcgcgggg acagtacttt ggagagcttg ccctggtaac taacaaacct 360

cgagcagctt ctgcccacgc cattgggact gtcaaatgtt tagcaatgga tgtgcaagca 420

tttgaaaggc ttctgggacc ttgcatggaa attatgaaaa ggaacatcgc tacctatgaa 480

gaacagttag ttgccctgta tggaacgaac atggatattg tagggtcagg tggatctgga 540

ggtagctctt ctatggtctt cacactcgaa gatttcgttg gggactggcg acagacagcc 600

ggctacaacc tggaccaagt ccttgaacag ggaggtgtgt ccagtttgtt tcagaatctc 660

ggggtgtccg taactccgat ccaaaggatt gtcctgagcg gtgaaaatgg gctgaagatc 720

gacatccatg tcatcatccc gtatgaaggt ctgagcggcg accaaatggg ccagatcgaa 780

aaaatttta aggtggtgta ccctgtggat gatcatcact ttaaggtgat cctgcactat 840

ggcacactgg taatcgacgg ggttacgccg aacatgatcg actatttcgg acggccgtat 900

gaaggcatcg ccgtgttcga cggcaaaaag atcactgtaa cagggaccct gtggaacggc 960

aacaaaatta tcgacgagcg cctgatcaac cccgacggct ccctgctgtt ccgagtaacc 1020

atcaac 1026

<210> 570
<211> 342
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 570
Met Asn Gly Val Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala Ser
1 5 10 15

Ser Ser Gly Gly Ser Gly Gly Ser Gly Met Tyr Glu Ser Phe Ile Glu
20 25 30

Ser Leu Pro Phe Leu Lys Ser Leu Glu Phe Ser Ala Arg Leu Lys Val
35 40 45

Val Asp Val Ile Gly Thr Lys Val Tyr Asn Asp Gly Glu Gln Ile Ile
50 55 60

Ala Gln Gly Asp Ser Ala Asp Ser Phe Phe Ile Ile Glu Ser Gly Glu
65 70 75 80

Val Lys Ile Thr Met Lys Arg Lys Gly Lys Ser Glu Val Glu Glu Asn
85 90 95

Gly Ala Val Glu Ile Ala Arg Cys Ser Arg Gly Gln Tyr Phe Gly Glu
100 105 110

Leu Ala Leu Val Thr Asn Lys Pro Arg Ala Ala Ser Ala His Ala Ile
115 120 125

Gly Thr Val Lys Cys Leu Ala Met Asp Val Gln Ala Phe Glu Arg Leu
130 135 140

Leu Gly Pro Cys Met Glu Ile Met Lys Arg Asn Ile Ala Thr Tyr Glu
145 150 155 160

Glu Gln Leu Val Ala Leu Tyr Gly Thr Asn Met Asp Ile Val Gly Ser
165 170 175

Gly Gly Ser Gly Gly Ser Ser Ser Met Val Phe Thr Leu Glu Asp Phe
180 185 190

Val Gly Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val Leu
195 200 205

Glu Gln Gly Gly Val Ser Ser Leu Phe Gln Asn Leu Gly Val Ser Val
210 215 220

Thr Pro Ile Gln Arg Ile Val Leu Ser Gly Glu Asn Gly Leu Lys Ile
225 230 235 240

Asp Ile His Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln Met
245 250 255

Gly Gln Ile Glu Lys Ile Phe Lys Val Val Tyr Pro Val Asp Asp His
260 265 270

His Phe Lys Val Ile Leu His Tyr Gly Thr Leu Val Ile Asp Gly Val
275 280 285

Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly Ile Ala
290 295 300

Val Phe Asp Gly Lys Lys Ile Thr Val Thr Gly Thr Leu Trp Asn Gly
305 310 315 320

Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly Ser Leu Leu
325 330 335

Phe Arg Val Thr Ile Asn
340

<210> 571
<211> 1026
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 571
atggtgaccg gctggcggct gtgcgaacgc attctggcta gctcaagcgg aggttcaggc 60

ggttccggaa tgtatgaaag ctttattgag tcactgccat tccttaaatc tttggagttt 120

tctgcacgcc tgaaagtagt agatgtgata ggcaccaaag tatacaacga tggagaacaa 180

atcattgctc agggagattc ggctgattct tttttcatta ttgaatctgg agaagtgaaa 240

attactatga aaagaaaggg taaatcagaa gtggaagaga atggtgcagt agaaatcgct 300

cgatgctcgc ggggacagta ctttggagag cttgccctgg taactaacaa acctcgagca 360

gcttctgccc acgccattgg gactgtcaaa tgtttagcaa tggatgtgca agcatttgaa 420

aggcttctgg gaccttgcat ggaaattatg aaaaggaaca tcgctaccta tgaagaacag 480

ttagttgccc tgtatggaac gaacatggat attgtagggt caggtggatc tggaggtagc 540

tcttctatgg tcttcacact cgaagatttc gttggggact ggcgacagac agccggctac 600

aacctggacc aagtccttga acagggaggt gtgtccagtt tgtttcagaa tctcggggtg 660

tccgtaactc cgatccaaag gattgtcctg agcggtgaaa atgggctgaa gatcgacatc 720

catgtcatca tcccgtatga aggtctgagc ggcgaccaaa tgggccagat cgaaaaaatt 780

tttaaggtgg tgtaccctgt ggatgatcat cactttaagg tgatcctgca ctatggcaca 840

ctggtaatcg acggggttac gccgaacatg atcgactatt tcggacggcc gtatgaaggc 900

atcgccgtgt tcgacggcaa aaagatcact gtaacaggga ccctgtggaa cggcaacaaa 960

attatcgacg agcgcctgat caaccccgac ggctccctgc tgttccgagt aaccatcaac 1020

ggagtg 1026

<210> 572
<211> 342
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 572

Met Val Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala Ser Ser Ser
1 5 10 15

Gly Gly Ser Gly Gly Ser Gly Met Tyr Glu Ser Phe Ile Glu Ser Leu
20 25 30

Pro Phe Leu Lys Ser Leu Glu Phe Ser Ala Arg Leu Lys Val Val Asp
35 40 45

Val Ile Gly Thr Lys Val Tyr Asn Asp Gly Glu Gln Ile Ile Ala Gln
50 55 60

Gly Asp Ser Ala Asp Ser Phe Phe Ile Ile Glu Ser Gly Glu Val Lys
65 70 75 80

Ile Thr Met Lys Arg Lys Gly Lys Ser Glu Val Glu Glu Asn Gly Ala
85 90 95

Val Glu Ile Ala Arg Cys Ser Arg Gly Gln Tyr Phe Gly Glu Leu Ala
100 105 110

Leu Val Thr Asn Lys Pro Arg Ala Ala Ser Ala His Ala Ile Gly Thr
115 120 125

Val Lys Cys Leu Ala Met Asp Val Gln Ala Phe Glu Arg Leu Leu Gly
130 135 140

Pro Cys Met Glu Ile Met Lys Arg Asn Ile Ala Thr Tyr Glu Glu Gln
145 150 155 160

Leu Val Ala Leu Tyr Gly Thr Asn Met Asp Ile Val Gly Ser Gly Gly
165 170 175

Ser Gly Gly Ser Ser Ser Met Val Phe Thr Leu Glu Asp Phe Val Gly
180 185 190

Asp Trp Arg Gln Thr Ala Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln
195 200 205

Gly Gly Val Ser Ser Leu Phe Gln Asn Leu Gly Val Ser Val Thr Pro
210 215 220

Ile Gln Arg Ile Val Leu Ser Gly Glu Asn Gly Leu Lys Ile Asp Ile
225 230 235 240

His Val Ile Ile Pro Tyr Glu Gly Leu Ser Gly Asp Gln Met Gly Gln
245 250 255

Ile Glu Lys Ile Phe Lys Val Val Tyr Pro Val Asp Asp His His Phe
260 265 270

Lys Val Ile Leu His Tyr Gly Thr Leu Val Ile Asp Gly Val Thr Pro
275 280 285

Asn Met Ile Asp Tyr Phe Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe
290 295 300

Asp Gly Lys Lys Ile Thr Val Thr Gly Thr Leu Trp Asn Gly Asn Lys
305 310 315 320

Ile Ile Asp Glu Arg Leu Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg
325 330 335

Val Thr Ile Asn Gly Val
340

<210> 573
<211> 1026
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 573
atgcgcattc tggctagctc aagcggaggt tcaggcggtt ccggaatgta tgaaagcttt 60

attgagtcac tgccattcct taaatctttg gagttttctg cacgcctgaa agtagtagat 120

gtgataggca ccaaagtata caacgatgga gaacaaatca ttgctcaggg agattcggct 180

gattcttttt tcattattga atctggagaa gtgaaaatta ctatgaaaag aaagggtaaa 240

tcagaagtgg aagagaatgg tgcagtagaa atcgctcgat gctcgcgggg acagtacttt 300

ggagagcttg ccctggtaac taacaaacct cgagcagctt ctgcccacgc cattgggact 360

gtcaaatgtt tagcaatgga tgtgcaagca tttgaaaggc ttctgggacc ttgcatggaa 420

attatgaaaa ggaacatcgc tacctatgaa gaacagttag ttgccctgta tggaacgaac 480

atggatattg tagggtcagg tggatctgga ggtagctctt ctatggtctt cacactcgaa 540

gatttcgttg gggactggcg acagacagcc ggctacaacc tggaccaagt ccttgaacag 600

ggaggtgtgt ccagtttgtt tcagaatctc ggggtgtccg taactccgat ccaaaggatt 660

gtcctgagcg gtgaaaatgg gctgaagatc gacatccatg tcatcatccc gtatgaaggt 720

ctgagcggcg accaaatggg ccagatcgaa aaaatttta aggtggtgta ccctgtggat 780

gatcatcact ttaaggtgat cctgcactat ggcacactgg taatcgacgg ggttacgccg 840

aacatgatcg actatttcgg acggccgtat gaaggcatcg ccgtgttcga cggcaaaaag 900

atcactgtaa cagggaccct gtggaacggc aacaaaatta tcgacgagcg cctgatcaac 960

cccgacggct ccctgctgtt ccgagtaacc atcaacggag tgaccggctg gcggctgtgc 1020

gaacgc 1026

<210> 574
<211> 342
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 574
Met Arg Ile Leu Ala Ser Ser Ser Gly Gly Ser Gly Gly Ser Gly Met
1 5 10 15

Tyr Glu Ser Phe Ile Glu Ser Leu Pro Phe Leu Lys Ser Leu Glu Phe
20 25 30

Ser Ala Arg Leu Lys Val Val Asp Val Ile Gly Thr Lys Val Tyr Asn
35 40 45

Asp Gly Glu Gln Ile Ile Ala Gln Gly Asp Ser Ala Asp Ser Phe Phe
50 55 60

Ile Ile Glu Ser Gly Glu Val Lys Ile Thr Met Lys Arg Lys Gly Lys
65 70 75 80

Ser Glu Val Glu Glu Asn Gly Ala Val Glu Ile Ala Arg Cys Ser Arg
85 90 95

Gly Gln Tyr Phe Gly Glu Leu Ala Leu Val Thr Asn Lys Pro Arg Ala
100 105 110

Ala Ser Ala His Ala Ile Gly Thr Val Lys Cys Leu Ala Met Asp Val
115 120 125

Gln Ala Phe Glu Arg Leu Leu Gly Pro Cys Met Glu Ile Met Lys Arg
130 135 140

Asn Ile Ala Thr Tyr Glu Glu Gln Leu Val Ala Leu Tyr Gly Thr Asn
145 150 155 160

Met Asp Ile Val Gly Ser Gly Gly Ser Gly Gly Ser Ser Ser Met Val
165 170 175

Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala Gly Tyr
180 185 190

Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu Phe Gln
195 200 205

Asn Leu Gly Val Ser Val Thr Pro Ile Gln Arg Ile Val Leu Ser Gly
210 215 220

Glu Asn Gly Leu Lys Ile Asp Ile His Val Ile Ile Pro Tyr Glu Gly
225 230 235 240

Leu Ser Gly Asp Gln Met Gly Gln Ile Glu Lys Ile Phe Lys Val Val
245 250 255

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

Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe Gly Arg
275 280 285

Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr Val Thr
290 295 300

Gly Thr Leu Trp Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu Ile Asn
305 310 315 320

Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val Thr Gly
325 330 335

Trp Arg Leu Cys Glu Arg
340

<210> 575
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 575
gggtcaggtg gatctggagg tagctcttct 30

<210> 576

<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 576
agctcaagcg gaggttcagg cggttccgga 30

<210> 577
<211> 377
<212> DNA
<213> Homo sapiens

<400> 577
atgccgtccg agaagacctt caaacagcgc cggagcttcg aacaaagagt ggaagatgtc 60

cggctcatcc gggagcagca ccccaccaag atcccagtga ttatagagcg atacaagggt 120

gagaagcagc tgcccgtcct ggacaagacc agttccttgt acctgatcac gtgaatatga 180

gcgaactcat caagataatt agaaggcgcc tgcagctcaa tgctaaccaa gccttcttcc 240

tcctggtgaa tgggcacagc atggtgagtg tgtccacacc catctctgaa gtgtacgaga 300

gcgagagaga tgaagacggc ttcctgtaca tggtctatgc ctcccaggag acgttcggga 360

cagcactggc tgtgtaa 377

<210> 578
<211> 125
<212> PRT
<213> Homo sapiens

<400> 578
Met Pro Ser Glu Lys Thr Phe Lys Gln Arg Arg Ser Phe Glu Gln Arg
1 5 10 15

Val Glu Asp Val Arg Leu Ile Arg Glu Gln His Pro Thr Lys Ile Pro
20 25 30

Val Ile Ile Glu Arg Tyr Lys Gly Glu Lys Gln Leu Pro Val Leu Asp
35 40 45

Lys Thr Lys Phe Leu Val Pro Asp His Val Asn Met Ser Glu Leu Ile
50 55 60

Lys Ile Ile Arg Arg Arg Leu Gln Leu Asn Ala Asn Gln Ala Phe Phe
65 70 75 80

Leu Leu Val Asn Gly His Ser Met Val Ser Val Ser Thr Pro Ile Ser
85 90 95

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

Tyr Ala Ser Gln Glu Thr Phe Gly Thr Ala Leu Ala Val

115 120 125

<210> 579
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 579
Met Lys Ala Leu
1

<210> 580
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 580
His Gln His Gln His Gln
1 5

<210> 581
<211> 4
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Caspase-3 cleavage sequence

<400> 581
Asp Glu Val Asp
1

<210> 582

<400> 582
000

<210> 583

<400> 583
000

<210> 584

<400> 584
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<210> 585

<400> 585
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<210> 586

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<210> 587

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<210> 588

<400> 588
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<210> 589

<400> 589
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<210> 590

<400> 590
000

<210> 591

<400> 591
000

<210> 592
<211> 936
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 592
atggtgttta cactcgaaga tttcgtaggg gactggcggc agacagccgg ctacaacctg 60

gaccaagtcc ttgagcaggg cggtgtgtcc agtttgtttc agaatctcgg ggtgtccgta 120

actccgatcc aaaggattgt cctgagcggt gaaaacggcc tgaagatcga catccatgtc 180

atcatcccgt atgaaggtct gagcggcgat cagatgggcc agatcgaaaa aatttttaag 240

gtggtgtacc ctgtggatga tcatcacttt aaggtgattc tgcactatgg cacactggta 300

atcgacgggg ttacgccgaa catgatcgac tatttcggac ggccgtatga aggcatcgcc 360

gtgttcgacg gcaaaaagat cactgtaacc gggaccctgt ggaacggcaa caaaattatc 420

gacgagcgcc tgatcaaccc cgacggctcc ctgctgttcc gcgtaaccat caacggagtg 480

accggctggc ggctgtgcga gagaattttg gcgggctcga gcggaggtgg aggttcaggt 540

ggtggcggga gcggtggaat gccgtccgag aagaccttca aacagcgccg gagcttcgaa 600

caaagagtgg aagatgtccg gctcatccgg gagcagcacc ccaccaagat cccagtgatt 660

atagagcgat acaagggtga gaagcagctg cccgtcctgg acaagaccaa gttccttgta 720

cctgatcacg tgaatatgag cgaactcatc aagataatta gaaggcgcct gcagctcaat 780

gctaaccaag ccttcttcct cctggtgaat gggcacagca tggtgagtgt gtccacaccc 840

atctctgaag tgtacgagag cgagagagat gaagacggct tcctgtacat ggtctatgcc 900

tcccaggaga cgttcgggac agcactggct gtgtaa 936

<210> 593
<211> 311
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 593

| | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Met | Val | Phe | Thr | Leu | Glu | Asp | Phe | Val | Gly | Asp | Trp | Arg | Gln | Thr | Ala |
| 1 | | | | 5 | | | | 10 | | | | | 15 | | |
| Gly | Tyr | Asn | Leu | Asp | Gln | Val | Leu | Glu | Gln | Gly | Gly | Val | Ser | Ser | Leu |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Phe | Gln | Asn | Leu | Gly | Val | Ser | Val | Thr | Pro | Ile | Gln | Arg | Ile | Val | Leu |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Ser | Gly | Glu | Asn | Gly | Leu | Lys | Ile | Asp | Ile | His | Val | Ile | Ile | Pro | Tyr |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Glu | Gly | Leu | Ser | Gly | Asp | Gln | Met | Gly | Gln | Ile | Glu | Lys | Ile | Phe | Lys |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Val | Val | Tyr | Pro | Val | Asp | Asp | His | His | Phe | Lys | Val | Ile | Leu | His | Tyr |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Gly | Thr | Leu | Val | Ile | Asp | Gly | Val | Thr | Pro | Asn | Met | Ile | Asp | Tyr | Phe |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Gly | Arg | Pro | Tyr | Glu | Gly | Ile | Ala | Val | Phe | Asp | Gly | Lys | Lys | Ile | Thr |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Val | Thr | Gly | Thr | Leu | Trp | Asn | Gly | Asn | Lys | Ile | Ile | Asp | Glu | Arg | Leu |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Ile | Asn | Pro | Asp | Gly | Ser | Leu | Leu | Phe | Arg | Val | Thr | Ile | Asn | Gly | Val |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| Thr | Gly | Trp | Arg | Leu | Cys | Glu | Arg | Ile | Leu | Ala | Gly | Ser | Ser | Gly | Gly |
| | | | | 165 | | | | | 170 | | | | | 175 | |
| Gly | Gly | Ser | Gly | Gly | Gly | Gly | Ser | Gly | Gly | Met | Pro | Ser | Glu | Lys | Thr |
| | | | 180 | | | | | 185 | | | | | 190 | | |

```
Phe Lys Gln Arg Arg Ser Phe Glu Gln Arg Val Glu Asp Val Arg Leu
        195                 200                 205

Ile Arg Glu Gln His Pro Thr Lys Ile Pro Val Ile Ile Glu Arg Tyr
    210                 215                 220

Lys Gly Glu Lys Gln Leu Pro Val Leu Asp Lys Thr Lys Phe Leu Val
225                 230                 235                 240

Pro Asp His Val Asn Met Ser Glu Leu Ile Lys Ile Ile Arg Arg Arg
                245                 250                 255

Leu Gln Leu Asn Ala Asn Gln Ala Phe Phe Leu Leu Val Asn Gly His
            260                 265                 270

Ser Met Val Ser Val Ser Thr Pro Ile Ser Glu Val Tyr Glu Ser Glu
        275                 280                 285

Arg Asp Glu Asp Gly Phe Leu Tyr Met Val Tyr Ala Ser Gln Glu Thr
    290                 295                 300

Phe Gly Thr Ala Leu Ala Val
305                 310
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