homohistidine, α-fluoromethyl-histidine or α-methyl-histidine;
Xaa at position 8 is: Gly, Ala, Val, Leu, Ile, Ser, or Thr;
Xaa at position 12 is: His, Trp, Phe, or Tyr;
Xaa at position 16 is: Leu, Ser, Thr, Trp, His, Phe, Asp, Val, Glu, or Ala;
Xaa at position 22 is: Gly, Asp, Glu, Gln, Asn, Lys, Arg, or Cys;
Xaa at position 23 is: His, Asp, Lys, Glu, or Gln;
Xaa at position 26 is: Asp, Lys, Glu, or His;
Xaa at position 30 is: Ala, Glu, Asp, Ser, or His;
Xaa at position 35 is: Thr, Ser, Lys, Arg, Trp, Tyr, Phe, Asp, Gly, Pro, His, or Glu;
Xaa at position 37 is: Lys, Arg, Thr, Ser, Glu, Asp, Trp, Tyr, Phe, His, $-NH_2$, Gly, Gly-Pro, or Gly-Pro-NH_2, or is deleted.

8. The heterologous fusion protein of Claims 1, 2, or 3 wherein the GLP-1 compound comprises the sequence of formula V (SEQ ID NO: 6)

7	8	9	10	11	12	13	14	15	16	17
Xaa	Xaa	Glu	Gly	Thr	Phe	Thr	Ser	Asp	Val	Ser
18	19	20	21	22	23	24	25	26	27	28
Ser	Tyr	Leu	Glu	Xaa	Xaa	Ala	Ala	Lys	Xaa	Phe
29	30	31	32	33	34	35	36	37		
Ile	Xaa	Trp	Leu	Val	Lys	Gly	Arg	Xaa		

formula V (SEQ ID NO: 6)

wherein:
Xaa at position 7 is: L-histidine, D-histidine, desamino-histidine, 2-amino-histidine, β-hydroxy-histidine, homohistidine, α-fluoromethyl-histidine or α-methyl-histidine;
Xaa at position 8 is: Gly, Ala, Val, Leu, Ile, Ser, or Thr;

Xaa at position 22 is: Gly, Asp, Glu, Gln, Asn, Lys, Arg, or Cys;

Xaa at position 23 is: His, Asp, Lys, Glu, or Gln;

Xaa at position 24 is: Ala, Glu, His, Phe, Tyr, Trp, Arg, or Lys

Xaa at position 30 is: Ala, Glu, Asp, Ser, or His;

Xaa at position 37 is: Lys, Arg, Thr, Ser, Glu, Asp, Trp, Tyr, Phe, His, Gly, Gly-Pro, or is deleted.

9. The heterologous fusion protein of Claims 1, 2, or 3 wherein the GLP-1 compound comprises the sequence of formula VIII (SEQ ID NO:11).

7	8	9	10	11	12	13	14	15	16	17
Xaa	Xaa	Glu	Gly	Thr	Phe	Thr	Ser	Asp	Xaa	Ser

18	19	20	21	22	23	24	25	26	27	28
Xaa	Xaa	Xaa	Glu	Xaa	Xaa	Ala	Xaa	Xaa	Xaa	Phe

29	30	31	32	33	34	35	36	37
Ile	Xaa	Trp	Leu	Xaa	Xaa	Gly	Xaa	Xaa

formula VIII (SEQ ID NO: 11)

wherein:

Xaa at position 7 is: L-histidine, D-histidine, desamino-histidine, 2-amino-histidine, β-hydroxy-histidine, homohistidine, α-fluoromethyl-histidine or α-methyl-histidine;

Xaa at position 8 is: Gly, Ala, or Val;

Xaa at position 16 is: Leu or Val;

Xaa at position 18 is Lys or Ser;

Xaa at position 19 is: Gln or Tyr;

Xaa at position 20 is: Met or Leu;

Xaa at position 22 is: Glu or Gln;

Xaa at position 23 is: Glu, or Gln;

Xaa at position 25 is: Val or Ala;

Xaa at position 26 is: Arg or Lys;

Xaa at position 27 is Leu or Glu;
Xaa at position 30 is: Glu or Ala;
Xaa at position 33 is: Val or Lys;
Xaa at position 34 is: Asn or Lys;
Xaa at position 36 is: Gly or Arg; and
Xaa at position 37 is: Gly, Pro, Pro-Ser-Ser-Gly-Ala-Pro-Pro-Pro-Ser, or is absent.

10. The heterologous fusion protein of claims 1 through 9 wherein the GLP-1 compound has no more than 6 amino acids that are different from the corresponding amino acid in GLP-1(7-37)OH, GLP-1(7-36)OH, or Exendin-4.

11. The heterologous fusion protein of Claim 10 wherein the GLP-1 compound has no more than 5 amino acids that differ from the corresponding amino acid in GLP-1(7-37)OH, GLP-1(7-36)OH, or Exendin-4.

12. The heterologous fusion protein of Claim 11 wherein the GLP-1 compound has no more than 4 amino acids that differ from the corresponding amino acid in GLP-1(7-37)OH, GLP-1(7-36)OH, or Exendin-4.

13. The heterologous fusion protein of Claim 12 wherein the GLP-1 compound has no more than 3 amino acids that differ from the corresponding amino acid in GLP-1(7-37)OH, GLP-1(7-36)OH, or Exendin-4.

14.The heterologous fusion protein of Claim 13 wherein the GLP-1 compound has no more than 2 amino acids that differ from the corresponding amino acid in GLP-1(7-37)OH, GLP-1(7-36)OH, or Exendin-4.

15. The heterologous fusion protein of any one of Claims 1 through 14 wherein Xaa at position 8 is glycine or valine.

16. The heterologous fusion protein of Claim 8 wherein the GLP-1 compound has no more than 2 amino acids that differ from the corresponding amino acid in GLP-1(7-37)OH or GLP-1(7-36)OH and Xaa at position 8 is glycine or valine and Xaa at position 30 is alanine, glutamic acid, aspartic acid, serine, or histidine.

17. The heterologous fusion protein of Claim 16 wherein Xaa at position 30 is Glutamic acid.

18. The heterologous fusion protein of Claim 8 wherein the GLP-1 compound has no more than 2 amino acids that differ from the corresponding amino acid in GLP-1(7-37)OH or GLP-1(7-36)OH and Xaa at position 8 is glycine or valine and Xaa at position 37 is histidine, phenylalanine, tyrosine, tryptophan, aspartic acid, glutamic acid, serine, threonine, arginine, or lysine.

19. The heterologous fusion protein of Claim 18 wherein Xaa at position 37 is histidine.

20. The heterologous fusion protein of Claim 8 wherein the GLP-1 compound has no more than 2 amino acids that differ from the corresponding amino acid in GLP-1(7-37)OH or GLP-1(7-36)OH and Xaa at position 8 is glycine, valine, leucine, isoleucine, serine, threonine, or methionine and Xaa at position 22 is aspartic acid, glutamic acid, lysine, arginine, asparagine, glutamine or histidine.

21. The heterologous fusion protein of Claim 20 wherein Xaa at position 22 is lysine or glutamic acid.

22. The heterologous fusion protein of Claim 8 wherein the GLP-1 compound is Val^{8}-GLP-1(7-37).

23. The heterologous fusion protein of Claim 8 wherein the GLP-1 compound is Gly^8-GLP-1(7-37).

24. The heterologous fusion protein of any one of Claims 1 through 23 wherein the second polypeptide is human albumin.

25. The heterologous fusion protein of Claim 24 wherein the second polypeptide has the sequence of SEQ ID NO: 34.

26. The heterologous fusion protein of any one of Claims 1 through 23 wherein the second polypeptide is an N-terminal fragment of albumin.

27. A heterologous fusion protein comprising a first polypeptide with a N-terminus and a C-terminus fused to a second polypeptide with a N-terminus and a C-terminus wherein the first polypeptide is a GLP-1 compound and the second polypeptide is selected from the group consisting of

a) the Fc portion of an immunoglobulin;

b) an analog of the Fc portion of an immunoglobulin; and

c) fragments of the Fc portion of an immunoglobulin,

and wherein the C-terminus of the first polypeptide is fused to the N-terminus of the second polypeptide.

28. A heterologous fusion protein comprising a first polypeptide with a N-terminus and a C-terminus fused to a second polypeptide with a N-terminus and a C-terminus wherein the first polypeptide is a GLP-1 compound and the second polypeptide is selected from the group consisting of

a) the Fc portion of an immunoglobulin;

b) an analog of the Fc portion of an immunoglobulin; and

c) fragments of the Fc portion of an immunoglobulin,

and wherein the C-terminus of the first polypeptide is fused to the N-terminus of the second polypeptide via a peptide linker.

29. The heterologous fusion protein of the Claim 28 wherein the peptide linker is selected from the group consisting of:

a) a glycine rich peptide;

b) a peptide having the sequence $[Gly\text{-}Gly\text{-}Gly\text{-}Gly\text{-}Ser]_n$ where n is 1, 2, 3, 4, 5, or 6; and

c) a peptide having the sequence $[Gly\text{-}Gly\text{-}Gly\text{-}Gly\text{-}Ser]_3$.

30. The heterologous fusion protein of any one of Claims 27, 28, or 29 wherein the GLP-1 compound comprises the sequence of formula 1 [SEQ ID NO: 2].

```
 7   8   9   10  11  12  13  14  15  16  17
His-Xaa-Xaa-Gly-Xaa-Phe-Thr-Xaa-Asp-Xaa-Xaa-
18  19  20  21  22  23  24  25  26  27  28
Xaa-Xaa-Xaa-Xaa-Xaa-Xaa-Xaa-Xaa-Xaa-Xaa-Phe-
29  30  31  32  33  34  35  36  37  38  39
Ile-Xaa-Xaa-Xaa-Xaa-Xaa-Xaa-Xaa-Xaa-Xaa-Xaa-
40  41  42  43  44  45
Xaa-Xaa-Xaa-Xaa-Xaa-Xaa
```

Formula I (SEQ ID NO: 2)

wherein:

Xaa at position 8 is Ala, Gly, Ser, Thr, Leu, Ile, Val, Glu, Asp, or Lys;

Xaa at position 9 is Glu, Asp, or Lys;

Xaa at position 11 is Thr, Ala, Gly, Ser, Leu, Ile, Val, Glu, Asp, or Lys;

Xaa at position 14 is Ser, Ala, Gly, Thr, Leu, Ile, Val, Glu, Asp, or Lys;

Xaa at position 16 is Val, Ala, Gly, Ser, Thr, Leu, Ile, Tyr, Glu, Asp, Trp, or Lys;
Xaa at position 17 is Ser, Ala, Gly, Thr, Leu, Ile, Val, Glu, Asp, or Lys;
Xaa at position 18 is Ser, Ala, Gly, Thr, Leu, Ile, Val, Glu, Asp, Trp, Tyr, or Lys;
Xaa at position 19 is Tyr, Phe, Trp, Glu, Asp, Gln, or Lys;
Xaa at position 20 is Leu, Ala, Gly, Ser, Thr, Ile, Val, Glu, Asp, Met, Trp, Tyr, or Lys;
Xaa at position 21 is Glu, Asp, or Lys;
Xaa at position 22 is Gly, Ala, Ser, Thr, Leu, Ile, Val, Glu, Asp, or Lys;
Xaa at position 23 is Gln, Asn, Arg, Glu, Asp, or Lys;
Xaa at position 24 is Ala, Gly, Ser, Thr, Leu, Ile, Val, Arg, Glu, Asp, or Lys;
Xaa at position 25 is Ala, Gly, Ser, Thr, Leu, Ile, Val, Glu, Asp, or Lys;
Xaa at position 26 is Lys, Arg, Gln, Glu, Asp, or His;
Xaa at position 27 is Leu, Glu, Asp, or Lys;
Xaa at position 30 is Ala, Gly, Ser, Thr, Leu, Ile, Val, Glu, Asp, or Lys;
Xaa at position 31 is Trp, Phe, Tyr, Glu, Asp, or Lys;
Xaa at position 32 is Leu, Gly, Ala, Ser, Thr, Ile, Val, Glu, Asp, or Lys;
Xaa at position 33 is Val, Gly, Ala, Ser, Thr, Leu, Ile, Glu, Asp, or Lys;
Xaa at position 34 is Asn, Lys, Arg, Glu, Asp, or His;
Xaa at position 35 is Gly, Ala, Ser, Thr, Leu, Ile, Val, Glu, Asp, or Lys;
Xaa at position 36 is Gly, Arg, Lys, Glu, Asp, or His;
Xaa at position 37 is Pro, Gly, Ala, Ser, Thr, Leu, Ile, Val, Glu, Asp, or Lys, or is deleted;
Xaa at position 38 is Ser, Arg, Lys, Glu, Asp, or His, or is deleted;
Xaa at position 39 is Ser, Arg, Lys, Glu, Asp, or His, or

is deleted;
Xaa at position 40 is Gly, Asp, Glu, or Lys, or is deleted;
Xaa at position 41 is Ala, Phe, Trp, Tyr, Glu, Asp, or Lys, or is deleted;
Xaa at position 42 is Ser, Pro, Lys, Glu, or Asp, or is deleted;
Xaa at position 43 is Ser, Pro, Glu, Asp, or Lys, or is deleted;
Xaa at position 44 is Gly, Pro, Glu, Asp, or Lys, or is deleted;
and
Xaa at position 45 is Ala, Ser, Val, Glu, Asp, or Lys, or is deleted;
provided that when the amino acid at position 37, 38, 39, 40, 41, 42, 43, or 44 is deleted, then each amino acid downstream of that amino acid is also deleted.

31. The heterologous fusion protein of Claims 27, 28, or 29 wherein the GLP-1 compound comprises the sequence of formula II (SEQ ID NO: 3):

```
 7   8   9   10  11  12  13  14  15  16  17
Xaa-Xaa-Xaa-Gly-Xaa-Xaa-Thr-Ser-Asp-Xaa-Ser-
18  19  20  21  22  23  24  25  26  27  28
Xaa-Tyr-Leu-Glu-Xaa-Xaa-Xaa-Ala-Xaa-Xaa-Phe-
29  30  31  32  33  34  35  36  37
Ile-Xaa-Xaa-Leu-Xaa-Xaa-Xaa-Xaa-Xaa
```

Formula II (SEQ ID NO: 3)

wherein:
Xaa at position 7 is: L-histidine, D-histidine, desamino-histidine, 2-amino-histidine, β-hydroxy-histidine, homohistidine, α-fluoromethyl-histidine or α-methyl-histidine;
Xaa at position 8 is: Gly, Ala, Val, Leu, Ile, Ser, or Thr;

Xaa at position 9 is: Thr, Ser, Arg, Lys, Trp, Phe, Tyr, Glu, or His;
Xaa at position 11 is: Asp, Glu, Arg, Thr, Ala, Lys, or His;
Xaa at position 12 is: His, Trp, Phe, or Tyr;
Xaa at position 16 is: Leu, Ser, Thr, Trp, His, Phe, Asp, Val, Tyr, Glu, or Ala;
Xaa at position 18 is: His, Pro, Asp, Glu, Arg, Ser, Ala, or Lys;
Xaa at position 19 is: Gly, Asp, Glu, Gln, Asn, Lys, Arg, or Cys;
Xaa at position 23 is: His, Asp, Lys, Glu, Gln, or Arg;
Xaa at position 24 is: Glu, Arg, Ala, or Lys;
Xaa at position 26 is: Trp, Tyr, Phe, Asp, Lys, Glu, or His;
Xaa at position 27 is: Ala, Glu, His, Phe, Tyr, Trp, Arg, or Lys;
Xaa at position 30 is: Ala, Glu, Asp, Ser, or His;
Xaa at position 31 is: Asp, Glu, Ser, Thr, Arg, Trp, or Lys;
Xaa at position 33 is: Asp, Arg, Val, Lys, Ala, Gly, or Glu;
Xaa at position 34 is: Glu, Lys, or Asp;
Xaa at position 35 is: Thr, Ser, Lys, Arg, Trp, Tyr, Phe, Asp, Gly, Pro, His, or Glu;
Xaa at position 36 is: Thr, Ser, Asp, Trp, Tyr, Phe, Arg, Glu, or His;
Xaa at position 37 is: Lys, Arg, Thr, Ser, Glu, Asp, Trp, Tyr, Phe, His, Gly, Gly-Pro, or is deleted.

32. The heterologous fusion protein of Claims 27, 28, or 29 wherein the GLP-1 compound comprises the sequence of formula III (SEQ ID NO: 4):

```
 7   8   9   10  11  12  13  14  15  16  17
Xaa-Xaa-Glu-Gly-Xaa-Xaa-Thr-Ser-Asp-Xaa-Ser-
18  19  20  21  22  23  24  25  26  27  28
Ser-Tyr-Leu-Glu-Xaa-Xaa-Xaa-Ala-Xaa-Xaa-Phe-
29  30  31  32  33  34  35  36  37
Ile-Ala-Xaa-Leu-Xaa-Xaa-Xaa-Xaa-R
```

formula III (SEQ ID NO: 4)

wherein:

Xaa at position 7 is: L-histidine, D-histidine, desamino-histidine, 2-amino-histidine, β-hydroxy-histidine, homohistidine, α-fluoromethyl-histidine or α-methyl-histidine;

Xaa at position 8 is: Gly, Ala, Val, Leu, Ile, Ser, or Thr;

Xaa at position 11 is: Asp, Glu, Arg, Thr, Ala, Lys, or His;

Xaa at position 12 is: His, Trp, Phe, or Tyr;

Xaa at position 16 is: Leu, Ser, Thr, Trp, His, Phe, Asp, Val, Glu, or Ala;

Xaa at position 22: Gly, Asp, Glu, Gln, Asn, Lys, Arg, or Cys;

Xaa at position 23 is: His, Asp, Lys, Glu, or Gln;

Xaa at position 24 is: Glu, His, Ala, or Lys;

Xaa at position 25 is: Asp, Lys, Glu, or His;

Xaa at position 27 is: Ala, Glu, His, Phe, Tyr, Trp, Arg, or Lys;

Xaa at position 30 is: Ala, Glu, Asp, Ser, or His;

Xaa at position 33 is: Asp, Arg, Val, Lys, Ala, Gly, or Glu;

Xaa at position 34 is: Glu, Lys, or Asp;

Xaa at position 35 is: Thr, Ser, Lys, Arg, Trp, Tyr, Phe, Asp, Gly, Pro, His, or Glu;

Xaa at position 36 is: Arg, Glu, or His;

Xaa at position 37 is: Lys, Arg, Thr, Ser, Glu, Asp, Trp, Tyr, Phe, His, Gly, Gly-Pro, or is deleted.

33. The heterologous fusion protein of Claim 27, 28, or 29 wherein the GLP-1 compound comprises the sequence of formula IV (SEQ ID NO: 5):

7	8	9	10	11	12	13	14	15	16	17
Xaa	Xaa	Glu	Gly	Thr	Xaa	Thr	Ser	Asp	Xaa	Ser

18	19	20	21	22	23	24	25	26	27	28

Ser-Tyr-Leu-Glu-Xaa-Xaa-Ala-Ala-Xaa-Glu-Phe-
29 30 31 32 33 34 35 36 37
Ile-Xaa-Trp-Leu-Val-Lys-Xaa-Arg-Xaa
formula IV (SEQ ID NO: 5)

wherein:
Xaa at position 7 is: L-histidine, D-histidine, desamino-histidine, 2-amino-histidine, β-hydroxy-histidine, homohistidine, α-fluoromethyl-histidine or α-methyl-histidine;
Xaa at position 8 is: Gly, Ala, Val, Leu, Ile, Ser, or Thr;
Xaa at position 12 is: His, Trp, Phe, or Tyr;
Xaa at position 16 is: Leu, Ser, Thr, Trp, His, Phe, Asp, Val, Glu, or Ala;
Xaa at position 22 is: Gly, Asp, Glu, Gln, Asn, Lys, Arg, or Cys;
Xaa at position 23 is: His, Asp, Lys, Glu, or Gln;
Xaa at position 26 is: Asp, Lys, Glu, or His;
Xaa at position 30 is: Ala, Glu, Asp, Ser, or His;
Xaa at position 35 is: Thr, Ser, Lys, Arg, Trp, Tyr, Phe, Asp, Gly, Pro, His, or Glu;
Xaa at position 37 is: Lys, Arg, Thr, Ser, Glu, Asp, Trp, Tyr, Phe, His, Gly, Gly-Pro, or is deleted.

34. The heterologous fusion protein of Claims 27, 28, or 29 wherein the GLP-1 compound comprises the sequence of formula V (SEQ ID NO: 6)

7 8 9 10 11 12 13 14 15 16 17
Xaa-Xaa-Glu-Gly-Thr-Phe-Thr-Ser-Asp-Val-Ser-
18 19 20 21 22 23 24 25 26 27 28
Ser-Tyr-Leu-Glu-Xaa-Xaa-Ala-Ala-Lys-Xaa-Phe-
29 30 31 32 33 34 35 36 37
Ile-Xaa-Trp-Leu-Val-Lys-Gly-Arg-Xaa
formula V (SEQ ID NO: 6)

wherein:
Xaa at position 7 is: L-histidine, D-histidine, desamino-histidine, 2-amino-histidine, β-hydroxy-histidine, homohistidine, α-fluoromethyl-histidine or α-methyl-histidine;
Xaa at position 8 is: Gly, Ala, Val, Leu, Ile, Ser, or Thr;
Xaa at position 22 is: Gly, Asp, Glu, Gln, Asn, Lys, Arg, or Cys;
Xaa at position 23 is: His, Asp, Lys, Glu, or Gln;
Xaa at position 24 is: Ala, Glu, His, Phe, Tyr, Trp, Arg, or Lys
Xaa at position 30 is: Ala, Glu, Asp, Ser, or His;
Xaa at position 37 is: Lys, Arg, Thr, Ser, Glu, Asp, Trp, Tyr, Phe, His, Gly, Gly-Pro, or is deleted.

35. The heterologous fusion protein of Claims 27, 28, or 29 wherein the GLP-1 compound comprises the sequence of formula VIII (SEQ ID NO:11).

7	8	9	10	11	12	13	14	15	16	17
Xaa	Xaa	Glu	Gly	Thr	Phe	Thr	Ser	Asp	Xaa	Ser

18	19	20	21	22	23	24	25	26	27	28
Xaa	Xaa	Xaa	Glu	Xaa	Xaa	Ala	Xaa	Xaa	Xaa	Phe

29	30	31	32	33	34	35	36	37
Ile	Xaa	Trp	Leu	Xaa	Xaa	Gly	Xaa	R

formula VIII (SEQ ID NO: 11)

wherein:
Xaa at position 7 is: L-histidine, D-histidine, desamino-histidine, 2-amino-histidine, β-hydroxy-histidine, homohistidine, α-fluoromethyl-histidine or α-methyl-histidine;
Xaa at position 8 is: Gly, Ala, or Val;
Xaa at position 16 is: Leu or Val;

Xaa at position 18 is Lys or Ser;
Xaa at position 19 is: Gln or Tyr;
Xaa at position 20 is: Met or Leu;
Xaa at position 22 is: Glu or Gln;
Xaa at position 23 is: Glu, or Gln;
Xaa at position 25 is: Val or Ala;
Xaa at position 26 is: Arg or Lys;
Xaa at position 27 is Leu or Glu;
Xaa at position 30 is: Glu or Ala;
Xaa at position 33 is: Val or Lys;
Xaa at position 34 is: Asn or Lys;
Xaa at position 36 is: Gly or Arg; and
Xaa at position 37 is: Gly, Pro, Pro-Ser-Ser-Gly-Ala-Pro-Pro-Pro-Ser, or is absent.

36. The heterologous fusion protein of claims 27 through 35 wherein the GLP-1 compound has no more than 6 amino acids that are different from the corresponding amino acid in GLP-1(7-37)OH, GLP-1(7-36)OH, or Exendin-4.

37. The heterologous fusion protein of Claim 36 wherein the GLP-1 compound has no more than 5 amino acids that differ from the corresponding amino acid in GLP-1(7-37)OH, GLP-1(7-36)OH, or Exendin-4.

38. The heterologous fusion protein of Claim 37 wherein the GLP-1 compound has no more than 4 amino acids that differ from the corresponding amino acid in GLP-1(7-37)OH, GLP-1(7-36)OH, or Exendin-4.

39. The heterologous fusion protein of Claim 38 wherein the GLP-1 compound has no more than 3 amino acids that differ from the corresponding amino acid in GLP-1(7-37)OH, GLP-1(7-36)OH, or Exendin-4.

40. The heterologous fusion protein of Claim 39 wherein the GLP-1 compound has no more than 2 amino acids that differ from the corresponding amino acid in GLP-1(7-37)OH, GLP-1(7-36)OH, or Exendin-4.

41. The heterologous fusion protein of any one of Claims 27 through 40 wherein Xaa at position 8 is glycine or valine.

42. The heterologous fusion protein of Claim 34 wherein the GLP-1 compound has no more than 2 amino acids that differ from the corresponding amino acid in GLP-1(7-37)OH or GLP-1(7-36)OH and Xaa at position 8 is glycine or valine and Xaa at position 30 is alanine, glutamic acid, aspartic acid, serine, or histidine.

43. The heterologous fusion protein of Claim 42 wherein Xaa at position 30 is Glutamic acid.

44. The heterologous fusion protein of Claim 34 wherein the GLP-1 compound has no more than 2 amino acids that differ from the corresponding amino acid in GLP-1(7-37)OH or GLP-1(7-36)OH and Xaa at position 8 is glycine or valine and Xaa at position 37 is histidine, phenylalanine, tyrosine, tryptophan, aspartic acid, glutamic acid, serine, threonine, arginine, or lysine.

45. The heterologous fusion protein of Claim 44 wherein Xaa at position 37 is histidine.

46. The heterologous fusion protein of Claim 34 wherein the GLP-1 compound has no more than 2 amino acids that differ from the corresponding amino acid in GLP-1(7-37)OH or GLP-1(7-36)OH and Xaa at position 8 is glycine, valine, leucine, isoleucine, serine, threonine, or methionine and Xaa at position 22 is aspartic acid, glutamic acid, lysine, arginine, asparagine, glutamine or histidine.

47. The heterologous fusion protein of Claim 46 wherein Xaa at position 22 is lysine or glutamic acid.

48. The heterologous fusion protein of Claim 34 wherein the GLP-1 compound is Val-8-GLP-1(7-37).

49. The heterologous fusion protein of Claim 34 wherein the GLP-1 compound is Gly-8-GLP-1(7-37).

50. The heterologous fusion protein of any one of Claims 27 through 49 wherein the second polypeptide is the Fc portion of an Ig selected from the group consisting of: IgG1, IgG2, IgG3, IgG4, IgE, IgA, IgD, or IgM.

51. The heterologous fusion protein of any one of Claims 27 through 50 wherein the second polypeptide is the Fc portion of an Ig selected from the group consisting of: IgG1, IgG2, IgG3, and IgG4.

52. The heterologous fusion protein of Claim 51 wherein the second polypeptide is the Fc portion of an IgG1 immunoglobulin.

53. The heterologous fusion protein of Claim 51 wherein the second polypeptide is the Fc portion of an IgG4 immunoglobulin.

54. The heterologous fusion protein of Claims 50 through 53 wherein the IgG is human.

55. The heterologous fusion protein of any one of Claims 27 through 54 wherein the Fc portion comprises the hinge, CH2, and CH3 domains.

56. The heterologous fusion protein of Claim 52 wherein the second polypeptide has the sequence of SEQ ID NO: 32.

57. A polynucleotide encoding a heterologous fusion protein of any one of Claims 1 through 56.

58. A vector comprising the polynucleotide of Claim 57.

59. A host cell comprising the vector of Claim 58.

60. A host cell expressing at least one heterologous fusion protein of any one of Claims 1 through 56.

61. The host cell of Claim 60 wherein said host cell is a CHO cell.

62. A process for producing a heterologous fusion protein comprising the steps of transcribing and translating a polynucleotide of Claim 57 under conditions wherein the heterologous fusion protein is expressed in detectable amounts.

63. A method for normalizing blood glucose levels in a mammal in need thereof comprising the administration of a therapeutically effective amount of the heterologous fusion protein of any one of Claims 1 through 56.

64. A method of treating a patient with non-insulin dependent diabetes mellitus comprising the administration of a therapeutically effective amount of the heterologous fusion protein of any one of Claims 1 through 56.

65. A method of treating obesity comprising the administration of a therapeutically effective amount of the heterologous fusion protein of any one of Claims 1 through 56.

66. The use of a heterologous fusion protein as claimed in any one of Claims 1 through 56 for the manufacture of a medicament for the treatment of patients with non-insulin dependent diabetes mellitus.

67. The use of a heterologous fusion protein as claimed in any one of Claims 1 through 56 for the manufacture of a medicament for the treatment of patients with obesity.

68. A pharmaceutical formulation adapted for the treatment of patients with non-insulin dependent diabetes comprising a heterologous fusion protein of any one of Claims 1 through 56.

69. The heterologous fusion protein of Claims 1, 2, or 3 wherein the GLP-1 compound comprises the sequence of formula IX [SEQ ID NO: 12]

Xaa_7-Xaa_8-Glu-Gly-Thr-Xaa_{12}-Thr-Ser-Asp-Xaa_{16}-Ser-
Xaa_{18}-Xaa_{19}-Xaa_{20}-Glu-Xaa_{22}-Gln-Ala-Xaa_{25}-Lys-Xaa_{27}-
Phe-Ile-Xaa_{30}-Trp-Leu-Xaa_{33}-Lys-Gly-Arg-Xaa_{37}

Formula IX (SEQ ID NO: 12)

wherein:

Xaa_7 is: L-histidine, D-histidine, desamino-histidine, 2-

amino-histidine, β-hydroxy-histidine, homohistidine, α-fluoromethyl-histidine, or α-methyl-histidine;

Xaa_8 is: Ala, Gly, Val, Leu, Ile, Ser, or Thr;

Xaa_{12} is: Phe, Trp, or Tyr;

Xaa_{16} is: Val, Trp, Ile, Leu, Phe, or Tyr;

Xaa_{18} is: Ser, Trp, Tyr, Phe, Lys, Ile, Leu, Val;

Xaa_{19} is: Tyr, Trp, or Phe;

Xaa_{20} is: Leu, Phe, Tyr, or Trp;

Xaa_{22} is: Gly, Glu, Asp, or Lys;

Xaa_{25} is: Ala, Val, Ile, or Leu;

Xaa_{27} is: Glu, Ile, or Ala;

Xaa_{30} is: Ala or Glu

Xaa_{33} is: Val, or Ile; and

Xaa_{37} is: Gly, His, NH_2, or is absent.

70. The heterologous fusion protein of Claim 69 wherein the second polypeptide is human albumin.

71. The heterologous fusion protein of Claim 70 wherein the second polypeptide has the sequence of SEQ ID NO: 34.

72. The heterologous fusion protein of Claim 69 wherein the second polypeptide is an N-terminal fragment of albumin.

73. The heterologous fusion protein of any one of Claims 27, 28, or 29 wherein the GLP-1 compound comprises the sequence of formula IX [SEQ ID NO: 12]

Xaa_7-Xaa_8-Glu-Gly-Thr-Xaa_{12}-Thr-Ser-Asp-Xaa_{16}-Ser-Xaa_{18}-Xaa_{19}-Xaa_{20}-Glu-Xaa_{22}-Gln-Ala-Xaa_{25}-Lys-Xaa_{27}-Phe-Ile-Xaa_{30}-Trp-Leu-Xaa_{33}-Lys-Gly-Arg-Xaa_{37}

Formula IX (SEQ ID NO: 12)

wherein:

Xaa_7 is: L-histidine, D-histidine, desamino-histidine, 2-amino-histidine, β-hydroxy-histidine, homohistidine, α-fluoromethyl-histidine, or α-methyl-histidine;

Xaa_8 is: Ala, Gly, Val, Leu, Ile, Ser, or Thr;

Xaa_{12} is: Phe, Trp, or Tyr;

Xaa_{16} is: Val, Trp, Ile, Leu, Phe, or Tyr;

Xaa_{18} is: Ser, Trp, Tyr, Phe, Lys, Ile, Leu, Val;

Xaa_{19} is: Tyr, Trp, or Phe;

Xaa_{20} is: Leu, Phe, Tyr, or Trp;

Xaa_{22} is: Gly, Glu, Asp, or Lys;

Xaa_{25} is: Ala, Val, Ile, or Leu;

Xaa_{27} is: Glu, Ile, or Ala;

Xaa_{30} is: Ala or Glu

Xaa_{33} is: Val, or Ile; and

Xaa_{37} is: Gly, His, NH_2, or is absent.

74. The heterologous fusion protein of Claim 73 wherein the second polypeptide is the Fc portion of an Ig selected from the group consisting of: IgG1, IgG2, IgG3, IgG4, IgE, IgA, IgD, or IgM.

75. The heterologous fusion protein of Claim 73 or 74 wherein the second polypeptide is the Fc portion of an Ig selected from the group consisting of: IgG1, IgG2, IgG3, and IgG4.

76. The heterologous fusion protein of Claim 75 wherein the second polypeptide is the Fc portion of an IgG1 immunoglobulin.

77. The heterologous fusion protein of Claim 75 wherein the second polypeptide is the Fc portion of an IgG4 immunoglobulin.

78. The heterologous fusion protein of Claims 73 through 78 wherein the IgG is human.

79. The heterologous fusion protein of Claim 75 wherein the second polypeptide has the sequence of SEQ ID NO: 32.

80. The heterologous fusion protein of any one of Claims 69 through 79 wherein the GLP-1 compound is selected from the group consisting of Gly^{8}-GLP-1(7-37), Val^{8}-Tyr^{12}-GLP-1(7-37), Val^{8}-Tyr^{12}-GLP-1(7-36), Val^{8}-Trp^{12}-GLP-1(7-37), Val^{8}-Leu^{16}-GLP-1(7-37), Val^{8}-Val^{16}-GLP-1(7-37), Val^{8}-Tyr^{16}-GLP-1(7-37), Gly^{8}-Glu^{22}-GLP-1(7-37), Val^{8}-Glu^{22}-GLP-1(7-37),Val^{8}-Leu^{25}-GLP-1(7-37), Val^{8}-Tyr^{12}-Tyr^{16}-GLP-1(7-37), Val^{8}-Trp^{12}-Glu^{22}-GLP-1(7-37), Val^{8}-Tyr^{12}-Glu^{22}-GLP-1(7-37), Val^{8}-Tyr^{16}-Phe^{19}-GLP-1(7-37), Val^{8}-Tyr^{16}-Glu^{22}-GLP-1(7-37), Val^{8}-Trp^{16}-Glu^{22}-GLP-1(7-37), Val^{8}-Leu^{16}-Glu^{22}-GLP-1(7-37), Val^{8}-Ile^{16}-Glu^{22}-GLP-1(7-37), Val^{8}-Phe^{16}-Glu^{22}-GLP-1(7-37), Val^{8}-Trp^{18}-Glu^{22}-GLP-1(7-37), Val^{8}-Tyr^{18}-Glu^{22}-GLP-1(7-37), Val^{8}-Phe^{18}-Glu^{22}-GLP-1(7-37), Val^{8}-Ile^{18}-Glu^{22}-GLP-1(7-37), Val^{8}-Lys^{18}-Glu^{22}-GLP-1(7-37), Val^{8}-Trp^{19}-Glu^{22}-GLP-1(7-37), Val^{8}-Phe^{19}-Glu^{22}-GLP-1(7-37), Val^{8}-Phe^{20}-Glu^{22}-GLP-1(7-37), Val^{8}-Glu^{22}-Leu^{25}-GLP-1(7-37), Val^{8}-Glu^{22}-Ile^{25}-GLP-1(7-37), Val^{8}-Glu^{22}-Val^{25}-GLP-1(7-37), Val^{8}-Glu^{22}-Ile^{27}-GLP-1(7-37), Val^{8}-Glu^{22}-Ala^{27}-GLP-1(7-37), Val^{8}-Glu^{22}-Ile^{33}-GLP-1(7-37), Val^{8}-Asp^{9}-Ile^{11}-Tyr^{16}-Glu^{22}-GLP-1(7-37), Val^{8}-Tyr^{16}-Trp^{19}-Glu^{22}-GLP-1(7-37), Val^{8}-Trp^{16}-Glu^{22}-Val^{25}-Ile^{33}-GLP-1(7-37), Val^{8}-Trp^{16}-Glu^{22}-Ile^{33}-GLP-1(7-37), Val^{8}-Glu^{22}-Val^{25}-Ile^{33}-GLP-1(7-37), Val^{8}-Trp^{16}-

Glu^{22}-Val^{25}- GLP-1(7-37), and Val^{8}-Cys^{16}-Lys^{26}-GLP-1(7-37).

Fig. 1

```
                  5                  10                  15
Ala Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
                 20                  25                  30
Pro Ala Pro Glu Lys Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
                 35                  40                  45
Lys Pro Lys Asp Thr Lys Met Ile Ser Arg Thr Pro Glu Val Thr
                 50                  55                  60
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
                 65                  70                  75
Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
                 80                  85                  90
Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
                 95                 100                 105
Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
                110                 115                 120
Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
                125                 130                 135
Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
                140                 145                 150
Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
                155                 160                 165
Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
                170                 175                 180
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
                185                 190                 195
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
                200                 205                 210
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
                215                 220                 225
Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
                230
Leu Ser Leu Ser Pro Gly Lys      [SEQ ID NO: 32]
```

Fig. 2

```
                5                   10                  15
Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu Glu Asn
            20                  25                  30                  35
Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln Gln Cys Pro Phe
                        40                  45                  50
Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu Phe Ala Lys Thr Cys Val
55                  60                  65                  70
Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys Ser Leu His Thr Leu Phe Gly Asp
            75                  80                  85                  90
Lys Leu Cys Thr Val Ala Thr Leu Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys
                        95                  100                 105
Cys Ala Lys Gln Glu Pro Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp
            110                 115                 120                 125
Asn Pro Asn Leu Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala
                        130                 135                 140
Phe His Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
145                 150                 155                 160
Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg Tyr Lys
            165                 170                 175                 180
Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala Cys Leu Leu Pro
                        185                 190                 195
Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser Ser Ala Lys Gln Arg Leu
            200                 205                 210                 215
Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu Arg Ala Phe Lys Ala Trp Ala Val
                        220                 225                 230
Ala Arg Leu Ser Gln Arg Phe Pro Lys Ala Glu Phe Ala Glu Val Ser Lys Leu
235                 240                 245                 250
Val Thr Asp Leu Thr Lys Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu
            255                 260                 265                 270
Cys Ala Asp Asp Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser
                        275                 280                 285
Ile Ser Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
            290                 295                 300                 305
Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser Leu Ala
                        310                 315                 320
Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala Glu Ala Lys Asp
325                 330                 335                 340
Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg Arg His Pro Asp Tyr Ser
            345                 350                 355                 360
Val Val Leu Leu Leu Arg Leu Ala Lys Thr Tyr Glu Thr Thr Leu Glu Lys Cys
                        365                 370                 375
Cys Ala Ala Ala Asp Pro His Glu Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys
            380                 385                 390                 395
Pro Leu Val Glu Glu Pro Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu
                        400                 405                 410
Asn Leu Gly Glu Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys
415                 420                 425                 430
Val Pro Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
            435                 440                 445                 450
Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys Ala Glu
                        455                 460                 465
Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His Glu Lys Thr Pro
            470                 475                 480                 485
Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser Leu Val Asn Arg Arg Pro
```

Fig. 2 Continued

```
            490                 495                 500
Cys Phe Ser Ala Leu Glu Val Asp Glu Thr Tyr Val Pro Lys Glu Phe Asn Ala
505                 510                 515                 520
Glu Thr Phe Thr Phe His Ala Asp Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln
        525                 530                 535                 540
Ile Lys Lys Gln Thr Ala Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr
                545                 550                 555
Lys Glu Gln Leu Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys
    560                 565                 570                 575
Cys Lys Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
            580                 585
Ala Ala Ser Gln Ala Ala Leu Gly Leu
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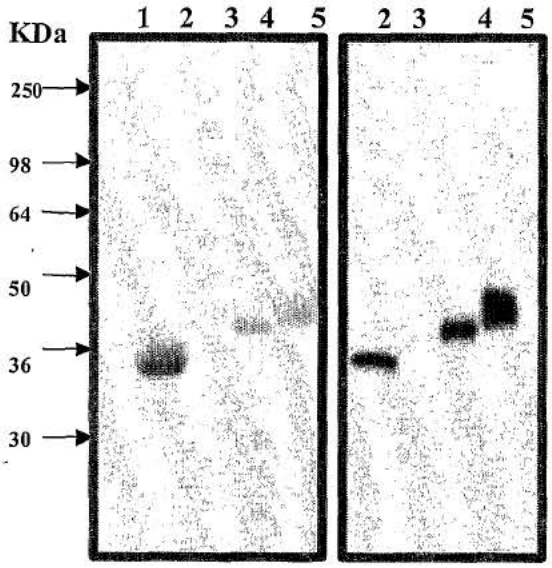
[SEQ ID NO: 34]

Fig. 3

A.


KDa
1 2 3 4 5
2 3 4 5
250
98
64
50
36
30

B.

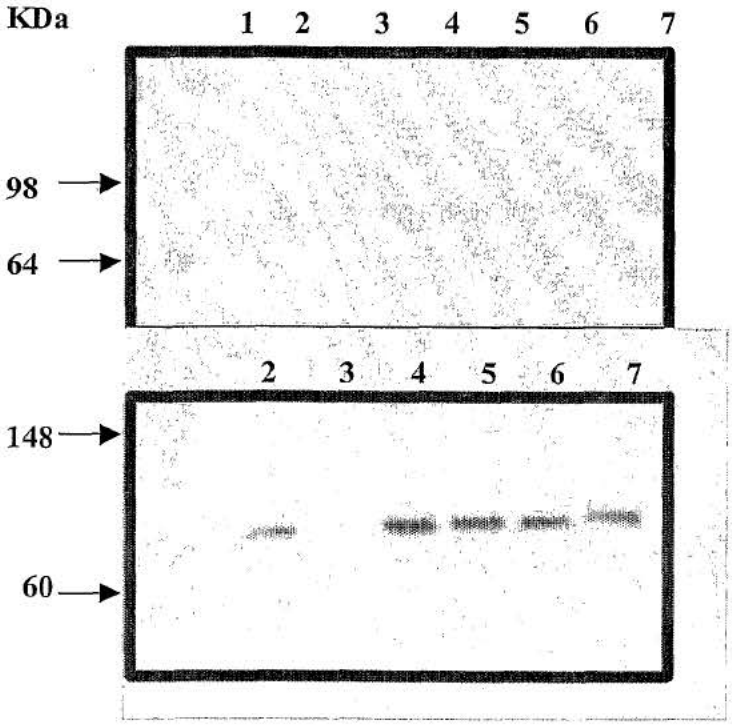

KDa
1 2 3 4 5 6 7
98
64
2 3 4 5 6 7
148
60

Fig. 4

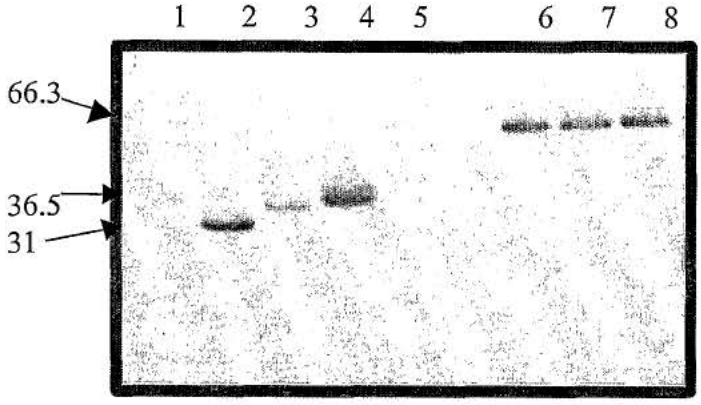
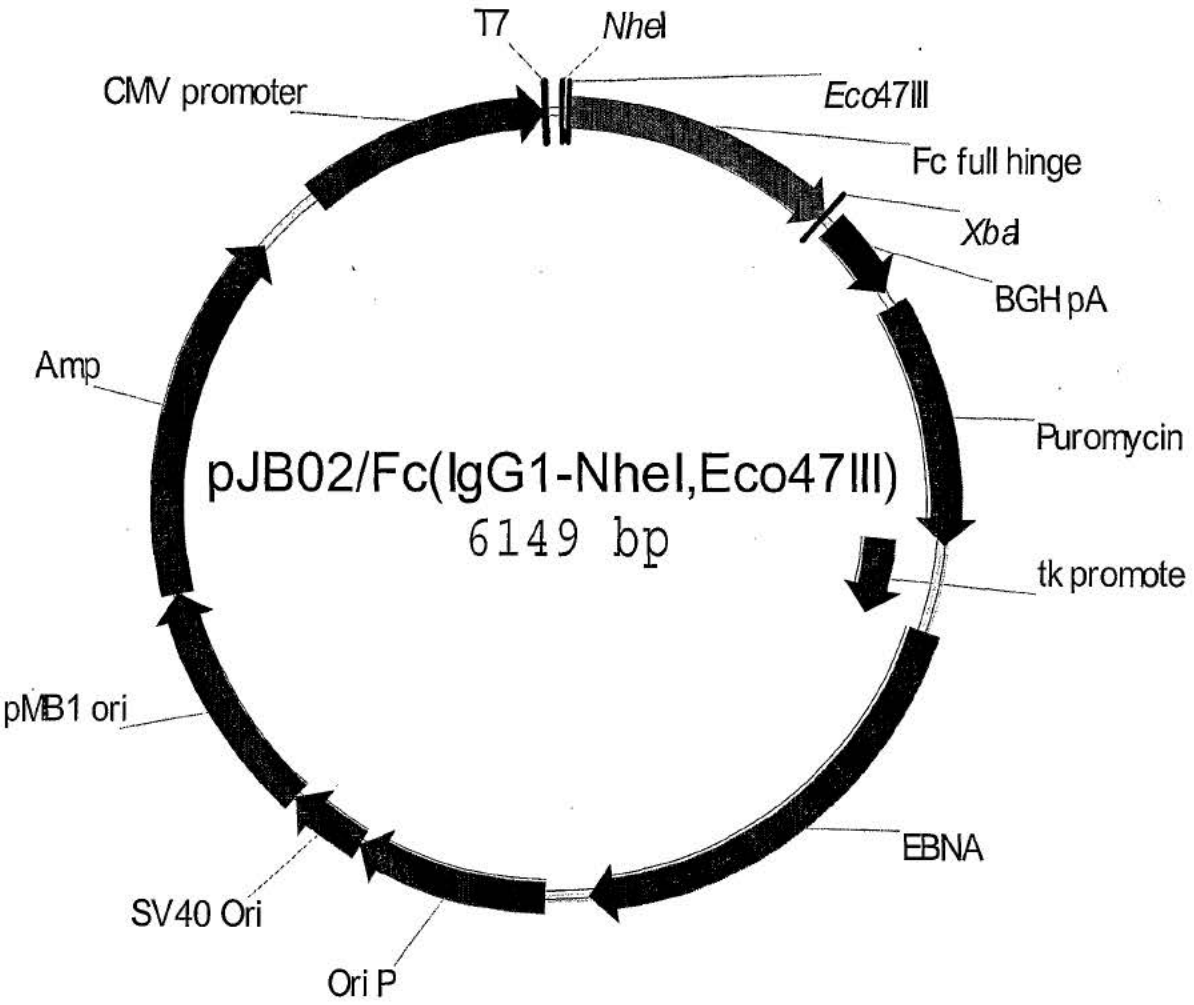


Fig. 5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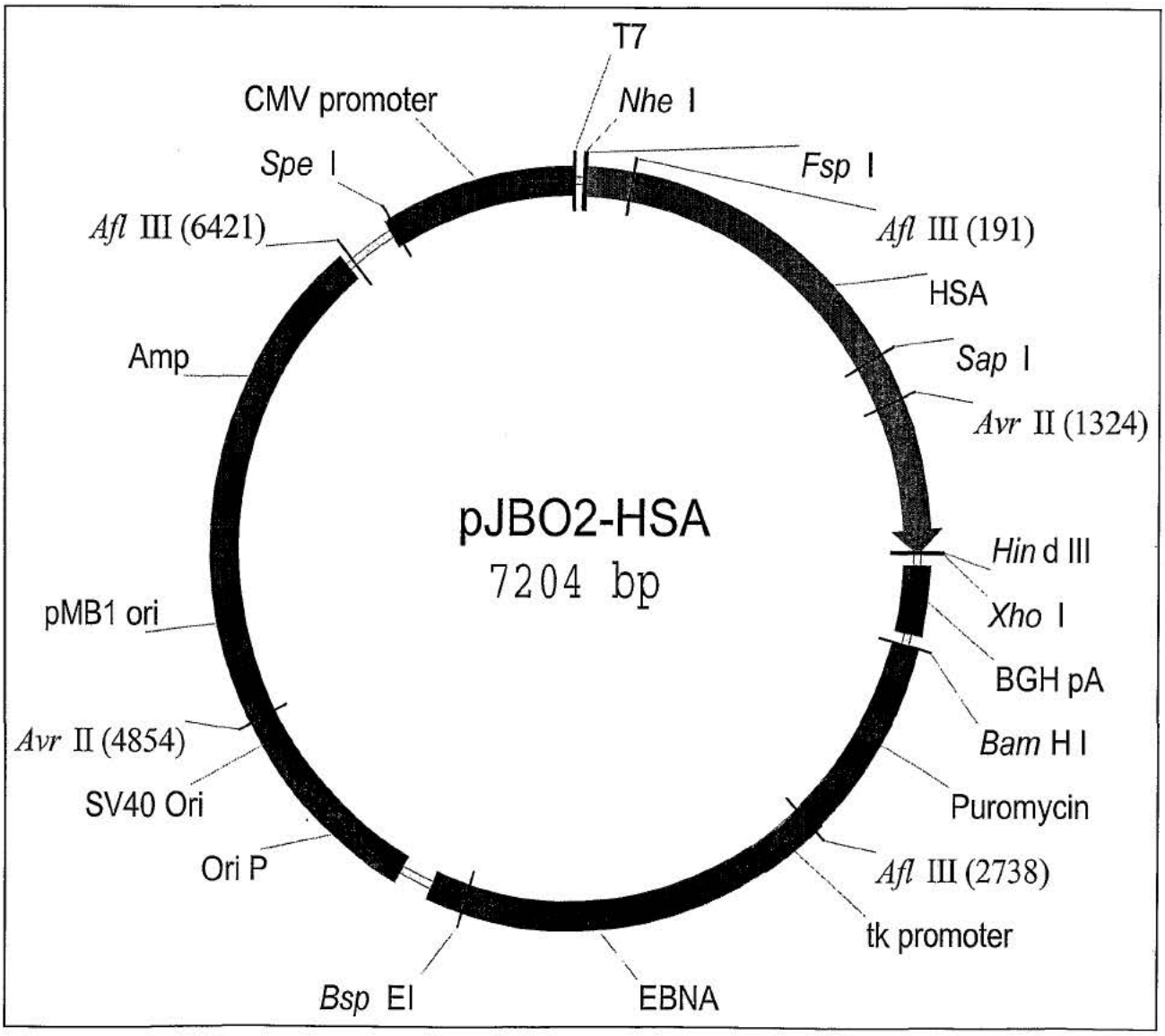
NheI
CMV promoter
Eco47III
Fc full hinge
XbaI
BGH pA
Amp
Puromycin
pJB02/Fc(IgG1-NheI,Eco47III)
6149 bp
tk promote
pMB1 ori
EBNA
SV40 Ori
Ori P

Fig. 6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CMV promoter
Nhe I
Spe I
Fsp I
Afl III (6421)
Afl III (191)
HSA
Amp
Sap I
Avr II (1324)
pJBO2-HSA
7204 bp
Hin d III
Xho I
pMB1 ori
BGH pA
Avr II (4854)
Bam H I
SV40 Ori
Puromycin
Ori P
Afl III (2738)
tk promoter
Bsp EI
EBNA

Fig. 7

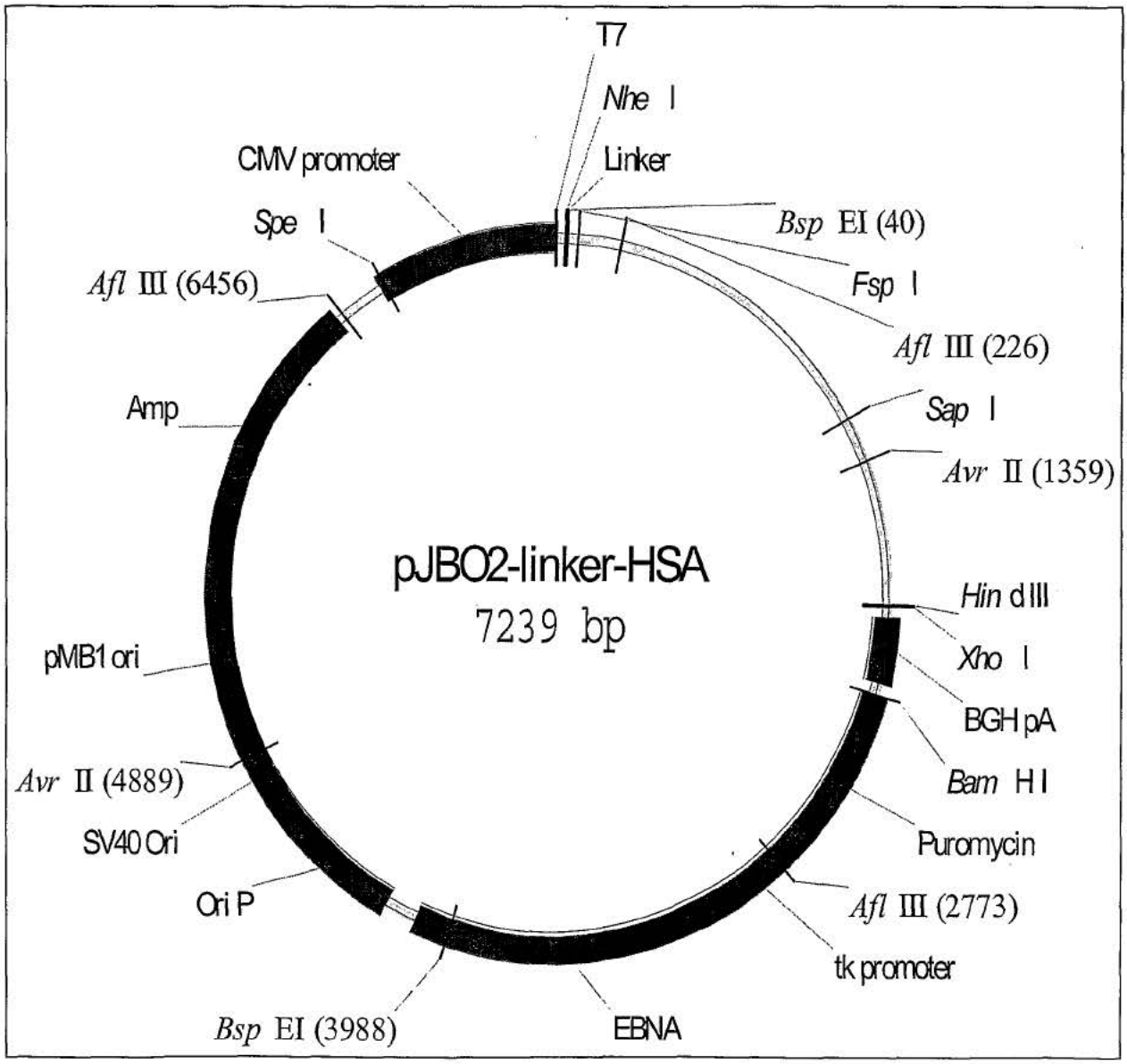

T7
Nhe I
Linker
CMV promoter
Spe I
Bsp EI (40)
Afl III (6456)
Fsp I
Afl III (226)
Amp
Sap I
Avr II (1359)
pJBO2-linker-HSA
7239 bp
Hin d III
Xho I
pMB1 ori
BGH pA
Avr II (4889)
Bam H I
SV40 Ori
Puromycin
Ori P
Afl III (2773)
tk promoter
Bsp EI (3988)
EBNA

Fig. 8

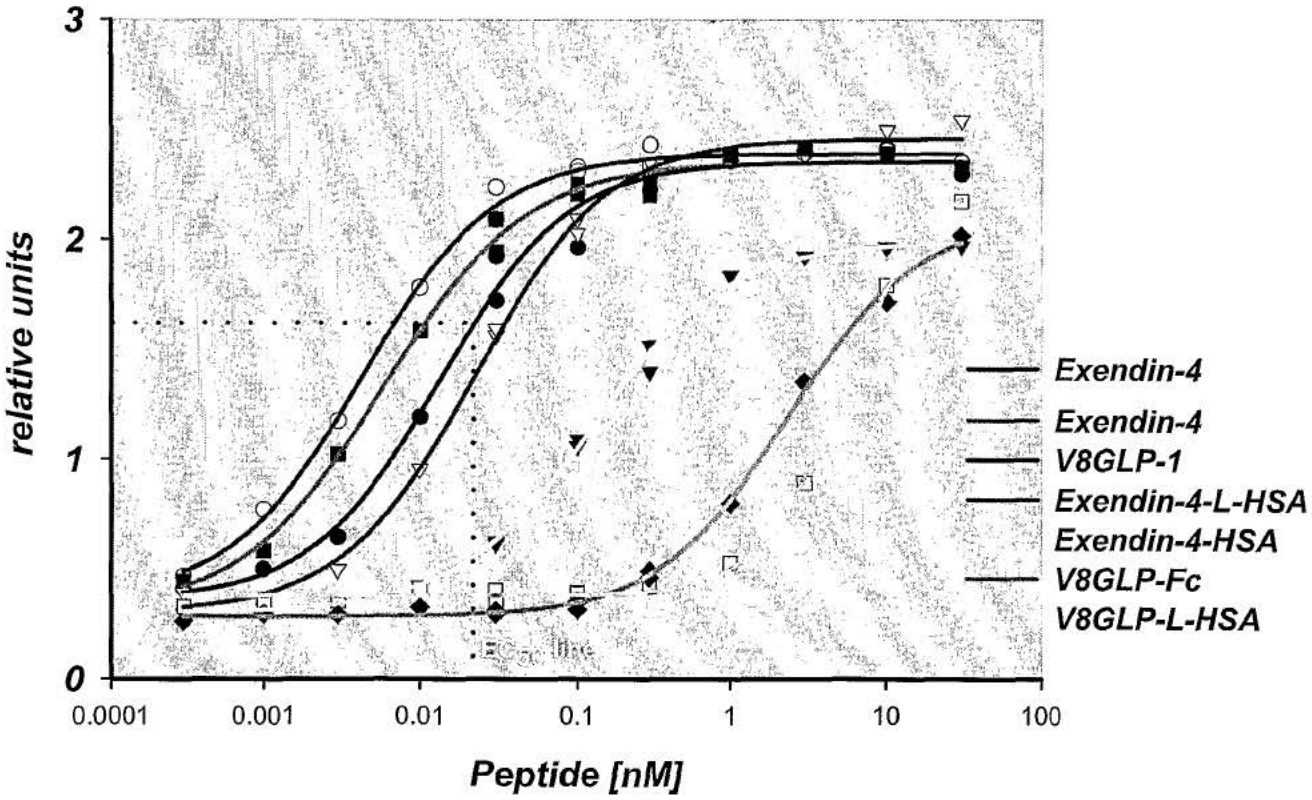
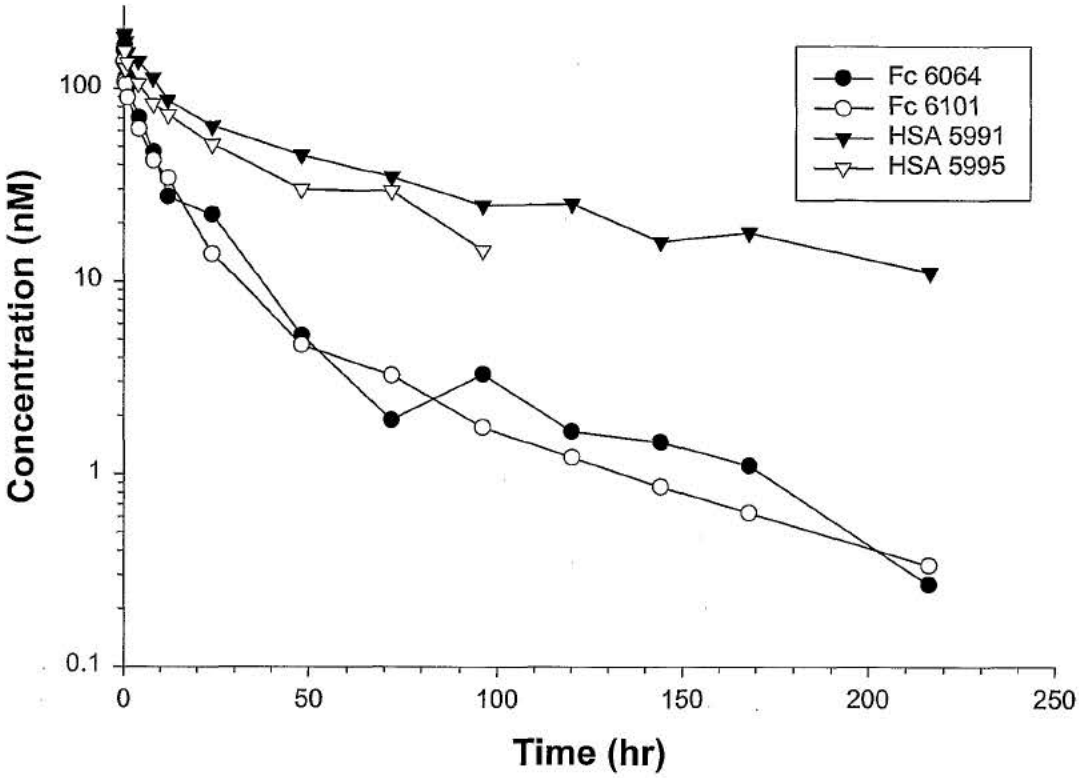

relative units
3
2
1
0
0.0001
0.001
0.01
0.1
1
10
100
Peptide [nM]
Exendin-4
Exendin-4
V8GLP-1
Exendin-4-L-HSA
Exendin-4-HSA
V8GLP-Fc
V8GLP-L-HSA

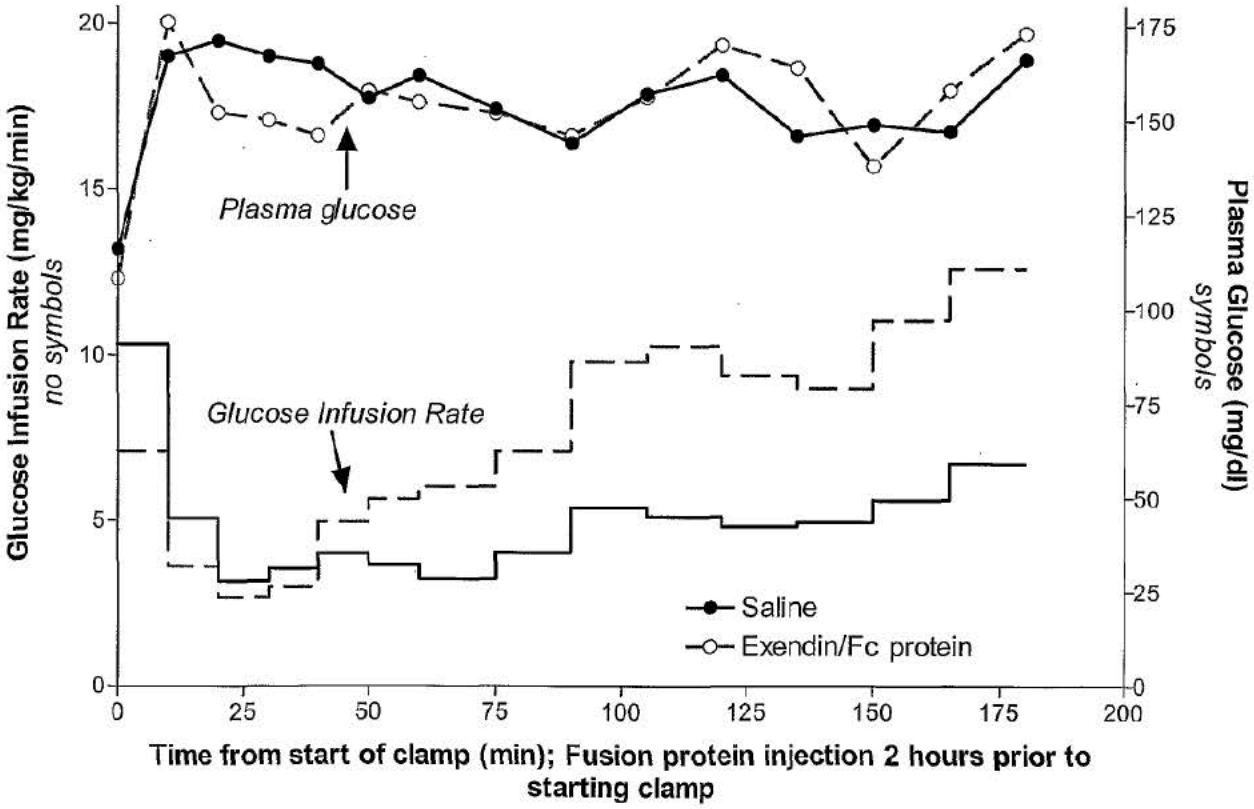
Fig. 9


Fc 6064
Fc 6101
HSA 5991
HSA 5995
Concentration (nM)
100
10
1
0.1
0
50
100
150
200
250
Time (hr)

11/17

Fig. 10

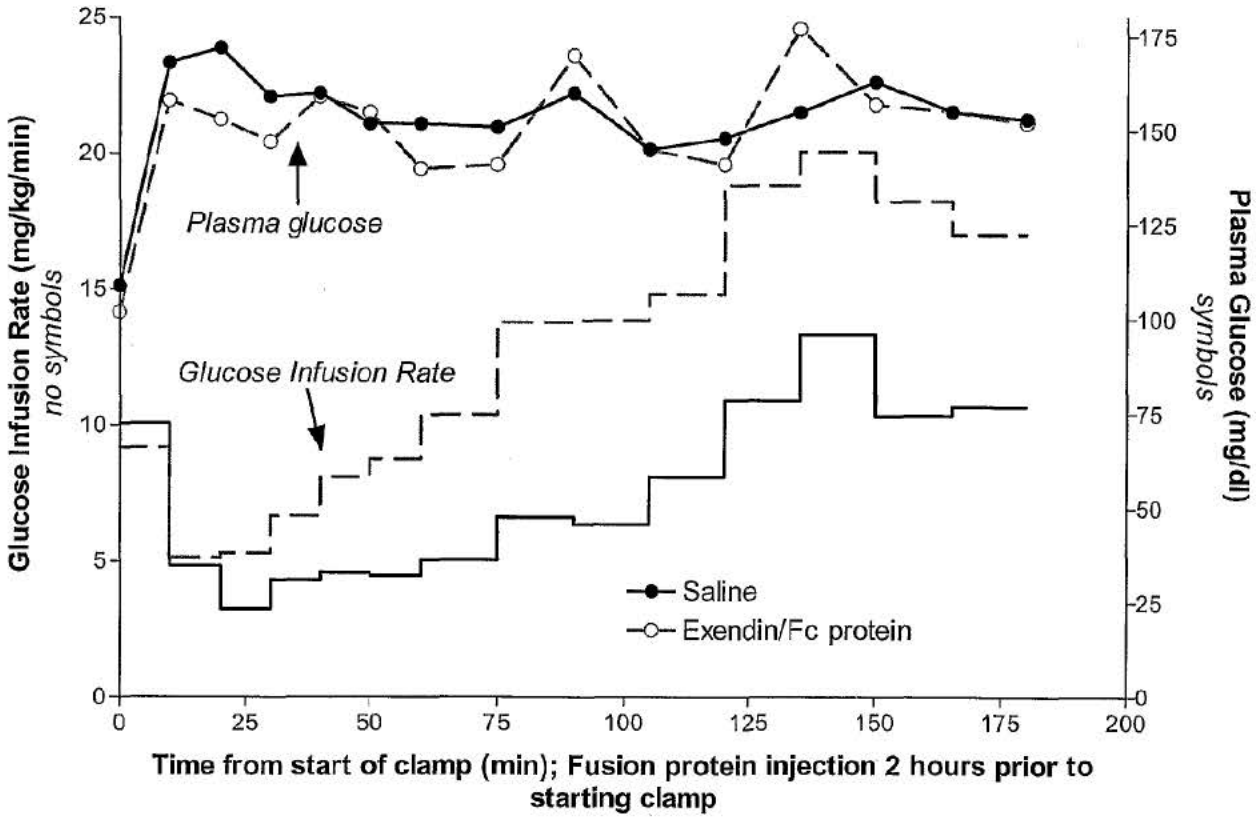
A.


Glucose Infusion Rate (mg/kg/min)
no symbols
Plasma Glucose (mg/dl)
symbols
Plasma glucose
Glucose Infusion Rate
Saline
Exendin/Fc protein
Time from start of clamp (min); Fusion protein injection 2 hours prior to starting clamp
0
5
10
15
20
0
25
50
75
100
125
150
175
200
0
25
50
75
100
125
150
175

12/17

Fig. 10

B.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no symbols
Plasma Glucose (mg/dl)
symbols
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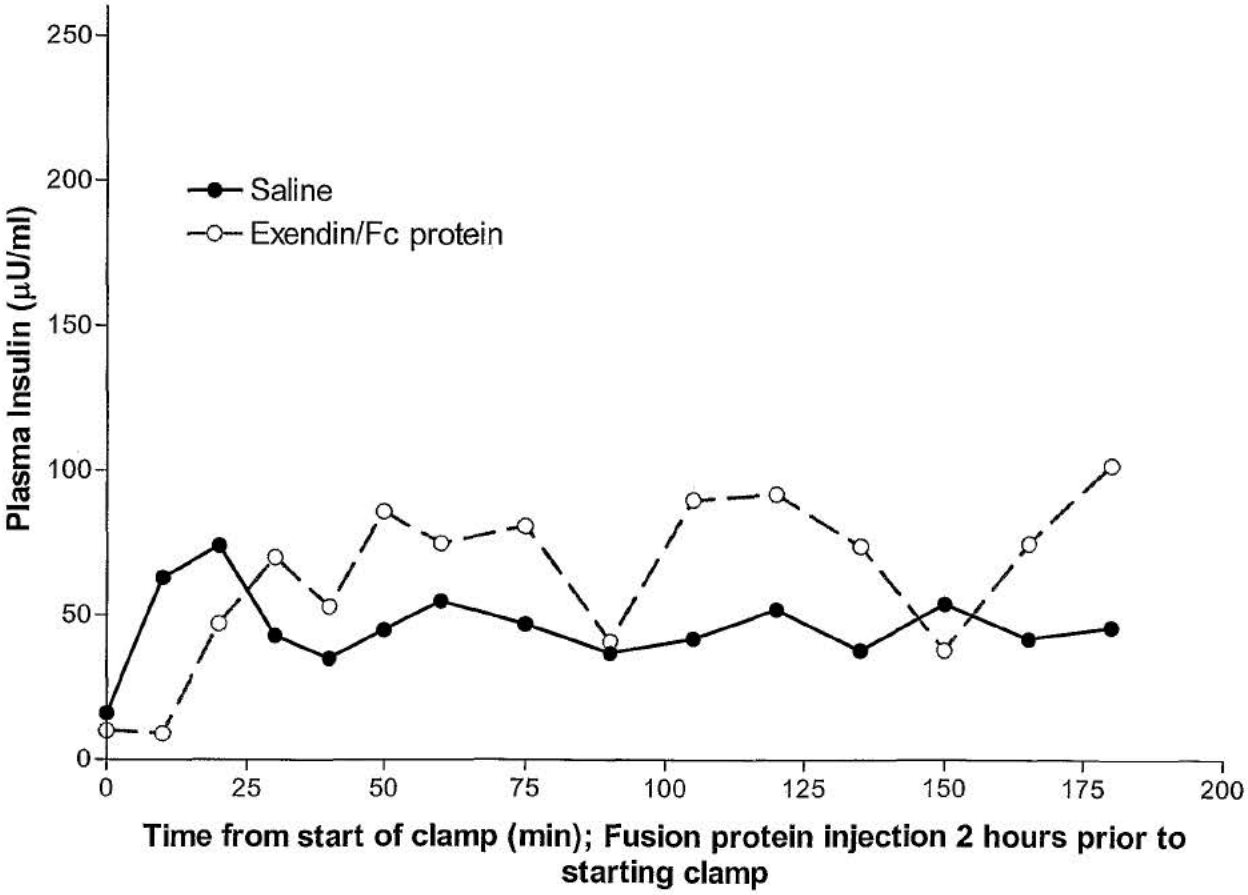
Glucose Infusion Rate
Saline
Exendin/Fc protein
Time from start of clamp (min); Fusion protein injection 2 hours prior to starting clamp

Fig. 11

A.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200
150
100
50
0
Plasma Insulin (μU/ml)
Saline
Exendin/Fc protein
0
25
50
75
100
125
150
175
200
Time from start of clamp (min); Fusion protein injection 2 hours prior to starting clamp

Fig. 11

B.

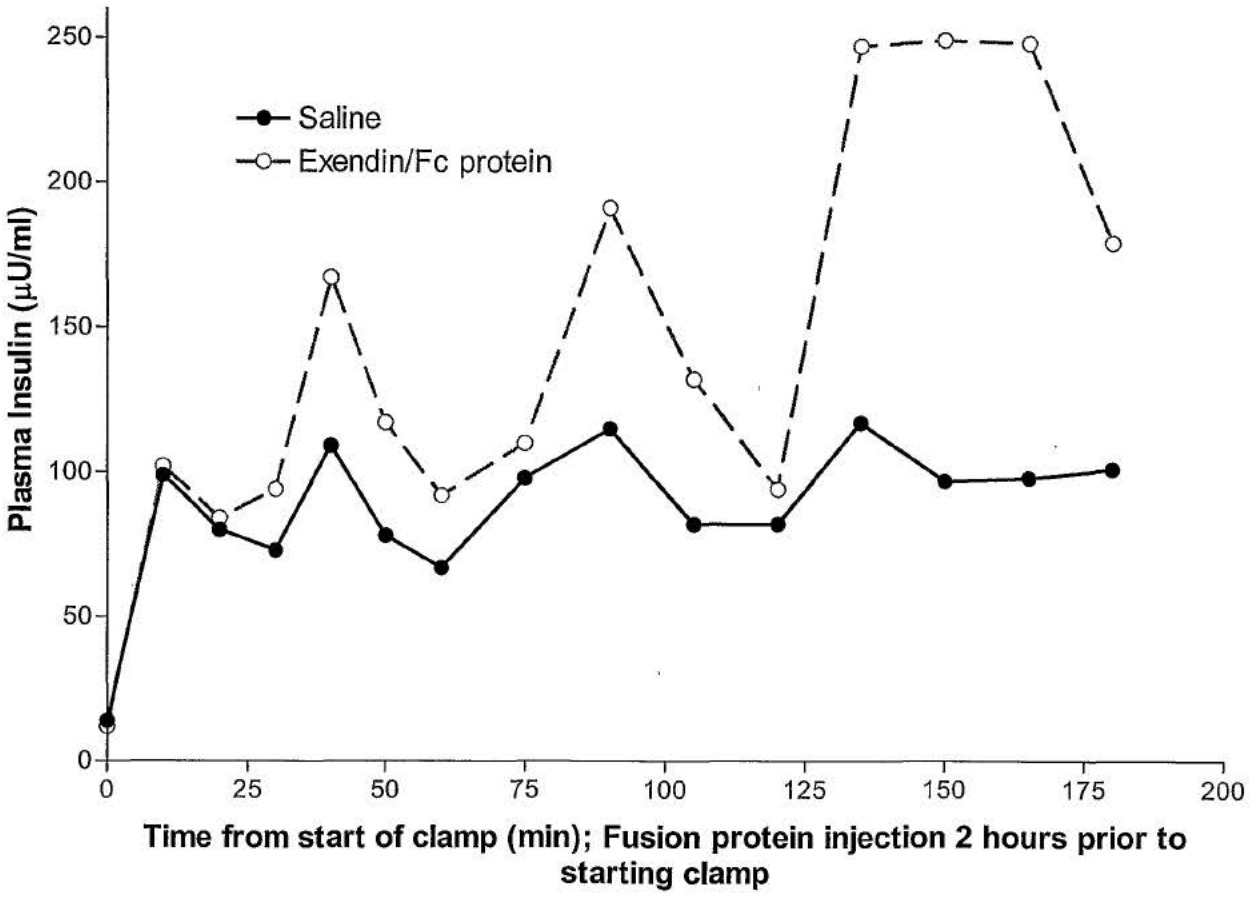
Saline
Exendin/Fc protein
Plasma Insulin (μU/ml)
250
200
150
100
50
0
0
25
50
75
100
125
150
175
200
Time from start of clamp (min); Fusion protein injection 2 hours prior to starting clamp

Fig. 12

1
GAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACC
50
TGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGG
100
ACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGAC
150
GTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGT
200
GGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCA
250
CGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAAT
300
GGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCAT
350
CGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
400
ACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTG
450
ACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGA
500
GAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGG
550
ACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAGAGC
600
AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCT
650
GCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGAT
700
AGT [SEQ ID NO: 33]

Fig. 13

1
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50
AAATTTCAAAGCCTTGGTGTTGATTGCCTTTGCTCAGTATCTTCAGCAGT
100
GTCCATTTGAAGATCATGTAAAATTAGTGAATGAAGTAACTGAATTTGCA
150
AAAACATGTGTTGCTGATGAGTCAGCTGAAAATTGTGACAAATCACTTCA
200
TACCCTTTTTGGAGACAAATTATGCACAGTTGCAACTCTTCGTGAAACCT
250
ATGGTGAAATGGCTGACTGCTGTGCAAAACAAGAACCTGAGAGAAATGAA
300
TGCTTCTTGCAACACAAAGATGACAACCCAAACCTCCCCCGATTGGTGAG
350
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400
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450
GCCCCGGAACTCCTTTTCTTTGCTAAAAGGTATAAAGCTGCTTTTACAGA
500
ATGTTGCCAAGCTGCTGATAAAGCTGCCTGCCTGTTGCCAAAGCTCGATG
550
AACTTCGGGATGAAGGGAAGGCTTCGTCTGCCAAACAGAGACTCAAGTGT
600
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650
TCGCCTGAGCCAGAGATTTCCCAAAGCTGAGTTTGCAGAAGTTTCCAAGT
700
TAGTGACAGATCTTACCAAAGTCCACACGGAATGCTGCCATGGAGATCTG
750
CTTGAATGTGCTGATGACAGGGCGGACCTTGCCAAGTATATCTGTGAAAA
800
TCAAGATTCGATCTCCAGTAAACTGAAGGAATGCTGTGAAAAACCTCTGT
850
TGGAAAAATCCCACTGCATTGCCGAAGTGGAAAATGATGAGATGCCTGCT
900
GACTTGCCTTCATTAGCTGCTGATTTTGTTGAAAGTAAGGATGTTTGCAA
950
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1000
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Fig. 13 Continued

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1100
TGAATGCTATGCCAAAGTGTTCGATGAATTTAAACCTCTTGTGGAAGAGC
1150
CTCAGAATTTAATCAAACAAAATTGTGAGCTTTTTGAGCAGCTTGGAGAG
1200
TACAAATTCCAGAATGCGCTATTAGTTCGTTACACCAAGAAAGTACCCCA
1250
AGTGTCAACTCCAACTCTTGTAGAGGTCTCAAGAAACCTAGGAAAAGTGG
1300
GCAGCAAATGTTGTAAACATCCTGAAGCAAAAAGAATGCCCTGTGCAGAA
1350
GACTATCTATCCGTGGTCCTGAACCAGTTATGTGTGTTGCATGAGAAAAC
1400
GCCAGTAAGTGACAGAGTCACCAAATGCTGCACAGAATCCTTGGTGAACA
1450
GGCGACCATGCTTTTCAGCTCTGGAAGTCGATGAAACATACGTTCCCAAA
1500
GAGTTTAATGCTGAAACATTCACCTTCCATGCAGATATATGCACACTTTC
1550
TGAGAAGGAGAGACAAATCAAGAAACAAACTGCACTTGTTGAGCTCGTGA
1600
AACACAAGCCCAAGGCAACAAAAGAGCAACTGAAAGCTGTTATGGATGAT
1650
TTCGCAGCTTTTGTAGAGAAGTGCTGCAAGGCTGACGATAAGGAGACCTG
1700
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1750
GCTTATAATGAC [SEQ ID NO: 35]

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<150> US 60/251,954
<151> 2000-06-12

<160> 35

<170> PatentIn version 3.1

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<212> PRT
<213> Homo sapiens

<400> 1

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Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Val Lys Gly Arg Gly
            20                  25                  30
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<221> MISC_FEATURE

<222> (12)..(12)

<223> Xaa at position 12 is Ser, Ala, Gly, Thr, Leu, Ile, Val, Glu, Asp , Lys, Trp or Tyr;

<220>

<221> MISC_FEATURE

<222> (13)..(13)

<223> Xaa at position 13 is Tyr, Phe, Trp, Glu, Asp, Gln, or Lys;

<220>

<221> MISC_FEATURE

<222> (14)..(14)

<223> Xaa at position 14 is Leu, Ala, Gly, Ser, Thr, Ile, Val, Glu, Asp , Met, Lys, Trp or Tyr;

<220>

<221> MISC_FEATURE

<222> (15)..(15)

<223> Xaa at position 15 is Glu, Asp, or Lys;

<220>

<221> MISC_FEATURE

<222> (16)..(16)

<223> Xaa at position 16 is Gly, Ala, Ser, Thr, Leu, Ile, Val, Glu, Asp , Trp or Lys;

<220>

<221> MISC_FEATURE

<222> (17)..(17)

<223> Xaa at position 17 is Gln, Asn, Arg, Glu, Asp, or Lys;

<220>

<221> MISC_FEATURE

<222> (18)..(18)

<223> Xaa at position 18 is Ala, Gly, Ser, Thr, Leu, Ile, Val, Arg, Glu , Asp, or Lys;

<220>

<221> MISC_FEATURE

<222> (19)..(19)

<223> Xaa at position 19 is Ala, Gly, Ser, Thr, Leu, Ile, Val, Glu, Asp , or Lys;

<220>

<221> MISC_FEATURE

<222> (20)..(20)

<223> Xaa at position 20 is Lys, Arg, Gln, Glu, Asp, or His;

<220>

<221> MISC_FEATURE

<222> (21)..(21)

<223> Xaa at position 21 is Leu, Glu, Asp, or Lys;

<220>

<221> MISC_FEATURE

<222> (24)..(24)

<223> Xaa at position 24 is Ala, Gly, Ser, Thr, Leu, Ile, Val, Glu, Asp , or Lys;

<220>

<221> MISC_FEATURE

<222> (25)..(25)

<223> Xaa at position 25 is Trp, Phe, Tyr, Glu, Asp, or Lys;

<220>

<221> MISC_FEATURE

<222> (26)..(26)

<223> Xaa at position 26 is Leu, Gly, Ala, Ser, Thr, Ile, Val, Glu, Asp
, or Lys;

<220>

<221> MISC_FEATURE

<222> (27)..(27)

<223> Xaa at position 27 is Val, Gly, Ala, Ser, Thr, Leu, Ile, Glu, Asp
, or Lys;

<220>

<221> MISC_FEATURE

<222> (28)..(28)

<223> Xaa at position 28 is Asn, Lys, Arg, Glu, Asp, or His;

<220>

<221> MISC_FEATURE

<222> (29)..(29)

<223> Xaa at position 29 is Gly, Ala, Ser, Thr, Leu, Ile, Val, Glu, Asp
, or Lys;

<220>

<221> MISC_FEATURE

<222> (30)..(30)

<223> Xaa at position 30 is Gly, Arg, Lys, Glu, Asp, or His;

<220>

<221> MISC_FEATURE

<222> (31)..(31)

<223> Xaa at position 31 is Pro, Gly, Ala, Ser, Thr, Leu, Ile, Val, Glu
, Asp, or Lys, or is deleted;

<220>

<221> MISC_FEATURE

<222> (32)..(32)

<223> Xaa at position 32 is Ser, Arg, Lys, Glu, Asp, or His, or is deleted;

<220>

<221> MISC_FEATURE

<222> (33)..(33)

<223> Xaa at position 33 is Ser, Arg, Lys, Glu, Asp, or His, or is deleted;

<220>

<221> MISC_FEATURE

<222> (34)..(34)

<223> Xaa at position 34 is Gly, Asp, Glu, or Lys, or is deleted;

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa at position 35 is Ala, Phe, Trp, Tyr, Glu, Asp, or Lys, or is deleted;

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa at position 36 is Ser, Pro, Lys, Glu, or Asp, or is deleted;

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa at position 37 is Ser, Pro, Glu, Asp, or Lys, or is deleted;

<220>

<221> MISC_FEATURE

<222> (38)..(38)

<223> Xaa at position 38 is Gly, Pro, Glu, Asp, or Lys, or is deleted;

<220>

<221> MISC_FEATURE

<222> (39)..(39)

<223> Xaa at position 39 is Ala, Ser, Val, Glu, Asp, or Lys, or is deleted;

<400> 2

His Xaa Xaa Gly Xaa Phe Thr Xaa Asp Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15

Xaa Xaa Xaa Xaa Xaa Phe Ile Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
20 25 30

Xaa Xaa Xaa Xaa Xaa Xaa Xaa
35

<210> 3

<211> 32

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic construct

<220>

<221> MISC_FEATURE

<222> (1)..(1)

<223> Xaa at position 1 is L-histidine, D-histidine, or is deleted.

<220>

<221> MISC_FEATURE

<222> (2)..(2)

<223> Xaa at position 2 is Gly, Ala, Val, Leu, Ile, Ser, or Thr;

<220>

<221> MISC_FEATURE

<222> (3)..(3)

<223> Xaa at position 3 is Thr, Ser, Arg, Lys, Trp, Phe, Tyr, Glu, or His;

<220>

<221> MISC_FEATURE

<222> (5)..(5)

<223> Xaa at position 5 is Asp, Glu, Arg, Thr, Ala, Lys, or His;

<220>

<221> MISC_FEATURE

<222> (6)..(6)

<223> Xaa at position 6 is His, Trp, Phe, or Tyr;

<220>

<221> MISC_FEATURE

<222> (10)..(10)

<223> Xaa at position 10 is Leu, Ser, Thr, Trp, His, Phe, Asp, Val, Tyr, Glu, or Ala;

<220>

<221> MISC_FEATURE

<222> (12)..(12)

<223> Xaa at position 12 is His, Pro, Asp, Glu, Arg, Ser, Ala, or Lys;

<220>

<221> MISC_FEATURE

<222> (13)..(13)

<223> Xaa at position 13 is Gly, Asp, Glu, Gln, Asn, Lys, Arg, or Cys;

<220>

<221> MISC_FEATURE
<222> (17)..(17)
<223> Xaa at position 17 is His, Asp, Lys, Glu, Gln, or Arg;

<220>
<221> MISC_FEATURE
<222> (18)..(18)
<223> Xaa at position 18 is Glu, Arg, Ala, or Lys;

<220>
<221> MISC_FEATURE
<222> (20)..(20)
<223> Xaa at position 20 is Trp, Tyr, Phe, Asp, Lys, Glu, or His;

<220>
<221> MISC_FEATURE
<222> (21)..(21)
<223> Xaa at position 21 is Ala, Glu, His, Phe, Tyr, Trp, Arg, or Lys;

<220>
<221> MISC_FEATURE
<222> (24)..(24)
<223> Xaa at position 24 is Ala, Glu, Asp, Ser, or His;

<220>
<221> MISC_FEATURE
<222> (25)..(25)
<223> Xaa at position 25 is Asp, Glu, Ser, Thr, Arg, Trp, or Lys;

<220>
<221> MISC_FEATURE

<222> (27)..(27)

<223> Xaa at position 27 is Asp, Arg, Val, Lys, Ala, Gly, or Glu;

<220>

<221> MISC_FEATURE

<222> (28)..(28)

<223> Xaa at position 28 is Glu, Lys, or Asp;

<220>

<221> MISC_FEATURE

<222> (29)..(29)

<223> Xaa at position 29 is Thr, Ser, Lys, Arg, Trp, Tyr, Phe, Asp, Gly , Pro, His, or Glu;

<220>

<221> MISC_FEATURE

<222> (30)..(30)

<223> Xaa at position 30 is Thr, Ser, Asp, Trp, Tyr, Phe, Arg, Glu, or His;

<220>

<221> MISC_FEATURE

<222> (31)..(31)

<223> Xaa at position 31 is Lys, Arg, Thr, Ser, Glu, Asp, Trp, Tyr, Phe , His, Gly, or is deleted.

<220>

<221> MISC_FEATURE

<222> (32)..(32)

<223> Xaa at position 31 is Pro or is deleted.

<400> 3

```
Xaa Xaa Xaa Gly Xaa Xaa Thr Ser Asp Xaa Ser Xaa Xaa Leu Glu Gly
1               5                   10                  15

Xaa Xaa Ala Xaa Xaa Phe Ile Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa
            20                  25                  30
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<210> 4

<211> 32

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic construct

<220>

<221> MISC_FEATURE

<222> (1)..(1)

<223> Xaa at position 1 is L-histidine, D-histidine, or is deleted.

<220>

<221> MISC_FEATURE

<222> (2)..(2)

<223> Xaa at position 2 is Gly, Ala, Val, Leu, Ile, Ser, or Thr;

<220>

<221> MISC_FEATURE

<222> (5)..(5)

<223> Xaa at position 5 is Asp, Glu, Arg, Thr, Ala, Lys, or His;

<220>

<221> MISC_FEATURE

<222> (6)..(6)

<223> Xaa at position 6 is His, Trp, Phe, or Tyr;

<220>

<221> MISC_FEATURE

<222> (10)..(10)

<223> Xaa at position 10 is Leu, Ser, Thr, Trp, His, Phe, Asp, Val, Glu
, or Ala;

<220>

<221> MISC_FEATURE

<222> (16)..(16)

<223> Xaa at position 16 is Gly, Asp, Glu, Gln, Asn, Lys, Arg, or Cys;

<220>

<221> MISC_FEATURE

<222> (17)..(17)

<223> Xaa at position 17 is His, Asp, Lys, Glu, or Gln;

<220>

<221> MISC_FEATURE

<222> (18)..(18)

<223> Xaa at position 18 is Glu, His, Ala, or Lys;

<220>

<221> MISC_FEATURE

<222> (19)..(19)

<223> Xaa at position 19 is Asp, Lys, Glu, or His;

<220>

<221> MISC_FEATURE

<222> (21)..(21)

<223> Xaa at position 21 is Ala, Glu, His, Phe, Tyr, Trp, Arg, or Lys;

<220>

<221> MISC_FEATURE

<222> (24)..(24)

<223> Xaa at position 24 is Ala, Glu, Asp, Ser, or His;

<220>

<221> MISC_FEATURE

<222> (27)..(27)

<223> Xaa at position 27 is Asp, Arg, Val, Lys, Ala, Gly, or Glu;

<220>

<221> MISC_FEATURE

<222> (28)..(28)

<223> Xaa at position 28 is Glu, Lys, or Asp;

<220>

<221> MISC_FEATURE

<222> (29)..(29)

<223> Xaa at position 29 is Thr, Ser, Lys, Arg, Trp, Tyr, Phe, Asp, Gly
, Pro, His, or Glu;

<220>

<221> MISC_FEATURE

<222> (30)..(30)

<223> Xaa at position 30 is Arg, Glu, or His;

<220>

<221> MISC_FEATURE

<222> (31)..(31)

<223> Xaa at position 31 is Lys, Arg, Thr, Ser, Glu, Asp, Trp, Tyr, Phe
, His, Gly, or is deleted.

<220>

<221> MISC_FEATURE

<222> (32)..(32)

<223> Xaa at position 32 is Pro, or is deleted.

<400> 4

Xaa Xaa Glu Gly Xaa Xaa Thr Ser Asp Xaa Ser Ser Tyr Leu Glu Xaa
1 5 10 15

Xaa Xaa Xaa Lys Xaa Phe Ile Xaa Trp Leu Xaa Xaa Xaa Xaa Xaa Xaa
20 25 30

<210> 5

<211> 32

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic construct

<220>

<221> MISC_FEATURE

<222> (1)..(1)

<223> Xaa at position 1 is L-histidine, D-histidine, or is deleted.

<220>

<221> MISC_FEATURE

<222> (2)..(2)

<223> Xaa at position 2 is Gly, Ala, Val, Leu, Ile, Ser, Met, or Thr;

<220>

<221> MISC_FEATURE

<222> (6)..(6)

<223> Xaa at position 6 is His, Trp, Phe, or Tyr;

<220>

<221> MISC_FEATURE

<222> (10)..(10)

<223> Xaa at position 10 is Leu, Ser, Thr, Trp, His, Phe, Asp, Val, Glu
, or Ala;

<220>

<221> MISC_FEATURE

<222> (16)..(16)

<223> Xaa at position 16 is Gly, Asp, Glu, Gln, Asn, Lys, Arg, or Cys;

<220>

<221> MISC_FEATURE

<222> (17)..(17)

<223> Xaa at position 17 is His, Asp, Lys, Glu, or Gln;

<220>

<221> MISC_FEATURE

<222> (20)..(20)

<223> Xaa at position 20 is Asp, Lys, Glu, or His;

<220>

<221> MISC_FEATURE

<222> (24)..(24)

<223> Xaa at position 24 is Ala, Glu, Asp, Ser, or His;

<220>

<221> MISC_FEATURE

<222> (29)..(29)

<223> Xaa at position 29 is Thr, Ser, Lys, Arg, Trp, Tyr, Phe, Asp, Gly
, Pro, His, or Glu;

<220>

<221> MISC_FEATURE

<222> (31)..(31)

<223> Xaa at position 31 is Lys, Arg, Thr, Ser, Glu, Asp, Trp, Tyr, Phe
, His, Gly, or is deleted.

<220>

<221> MISC_FEATURE

<222> (32)..(32)

<223> Xaa at position 32 is Pro or is deleted.

<400> 5

Xaa Xaa Glu Gly Thr Xaa Thr Ser Asp Xaa Ser Ser Tyr Leu Glu Xaa
1 5 10 15

Xaa Ala Ala Xaa Glu Phe Ile Xaa Trp Leu Val Lys Xaa Arg Xaa Xaa
20 25 30

<210> 6

<211> 32

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic construct

<220>

<221> MISC_FEATURE

<222> (1)..(1)

<223> Xaa at position 1 is L-histidine, D-histidine, or is deleted.

<220>

<221> MISC_FEATURE

<222> (2)..(2)

<223> Xaa at position 2 is Gly, Ala, Val, Leu, Ile, Ser, or Thr;

<220>

<221> MISC_FEATURE

<222> (16)..(16)

<223> Xaa at position 16 is Gly, Asp, Glu, Gln, Asn, Lys, Arg, or Cys;

<220>

<221> MISC_FEATURE

<222> (17)..(17)

<223> Xaa at position 17 is His, Asp, Lys, Glu, or Gln;

<220>

<221> MISC_FEATURE

<222> (18)..(18)

<223> Xaa at position 18 is Ala, Glu, His, Phe, Tyr, Trp, Arg, or Lys;

<220>

<221> MISC_FEATURE

<222> (24)..(24)

<223> Xaa at position 24 is Ala, Glu, Asp, Ser, or His;

<220>

<221> MISC_FEATURE

<222> (31)..(31)

<223> Xaa at position 31 is Lys, Arg, Thr, Ser, Glu, Asp, Trp, Tyr, Phe
, His, Gly, Gly-Pro, or is deleted.

<220>

<221> MISC_FEATURE

<222> (32)..(32)

<223> Xaa at position 32 is Pro or is deleted.

<400> 6

Xaa Xaa Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu Xaa
1 5 10 15

Xaa Xaa Ala Lys Glu Phe Ile Xaa Trp Leu Val Lys Gly Arg Xaa Xaa
20 25 30

<210> 7

<211> 31

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic construct

<220>

<221> MISC_FEATURE

<222> (1)..(1)

<223> Xaa at position 1 is L-histidine, D-histidine, or is deleted.

<220>

<221> MISC_FEATURE

<222> (2)..(2)

<223> Xaa at position 2 is Ala, Gly, Val, Thr, Ile, and alpha-methyl-Al
a;

<220>

<221> MISC_FEATURE

<222> (15)..(15)

<223> Xaa at position 15 is Glu, Gln, Ala, Thr, Ser, and Gly;

<220>

<221> MISC_FEATURE

<222> (21)..(21)

<223> Xaa at position 21 is Glu, Gln, Ala, Thr, Ser, and Gly;

<400> 7

Xaa Xaa Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Xaa Gly
1 5 10 15

Gln Ala Ala Lys Xaa Phe Ile Ala Trp Leu Val Lys Gly Arg Gly
20 25 30

<210> 8

<211> 30

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic construct

<220>

<221> MISC_FEATURE

<222> (19)..(19)

<223> Xaa at position 19 is Lys or Arg;

<220>

<221> MOD_RES

<222> (27)..(27)

<223> ACETYLATION

<220>

<221> MISC_FEATURE

<222> (30)..(30)

<223> Xaa at position 30 is Gly;

<220>

<221> MOD_RES

<222> (30)..(30)

<223> AMIDATION

<400> 8

```
Ala Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu Gly Gln
1               5                   10                  15

Ala Ala Xaa Glu Phe Ile Ala Trp Leu Val Lys Gly Arg Xaa
            20                  25                  30
```

<210> 9

<211> 39

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 9

```
His Ser Asp Gly Thr Phe Thr Ser Asp Leu Ser Lys Gln Met Glu Glu
1               5                   10                  15

Glu Ala Val Arg Leu Phe Ile Glu Trp Leu Lys Asn Gly Gly Pro Ser
            20                  25                  30
```

Ser Gly Ala Pro Pro Pro Ser
35

<210> 10

<211> 39

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 10

His Gly Glu Gly Thr Phe Thr Ser Asp Leu Ser Lys Gln Met Glu Glu
1 5 10 15

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

Ser Gly Ala Pro Pro Pro Ser
35

<210> 11

<211> 39

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic construct

<220>

<221> MISC_FEATURE

<222> (1)..(1)

<223> Xaa at position 1 is L-histidine, D-histidine, or is deleted.

<220>

<221> MISC_FEATURE

<222> (2)..(2)

<223> Xaa at position 2 is Gly, Ala, or Val;

<220>

<221> MISC_FEATURE
<222> (10)..(10)
<223> Xaa at position 10 is Leu or Val;

<220>
<221> MISC_FEATURE
<222> (12)..(12)
<223> Xaa at position 12 is Lys or Ser;

<220>
<221> MISC_FEATURE
<222> (13)..(13)
<223> Xaa at position 13 is Gln or Tyr;

<220>
<221> MISC_FEATURE
<222> (14)..(14)
<223> Xaa at position 14 is Met or Leu;

<220>
<221> MISC_FEATURE
<222> (16)..(16)
<223> Xaa at position 16 is Glu or Gln;

<220>
<221> MISC_FEATURE
<222> (17)..(17)
<223> Xaa at position 17 is Glu or Gln;

<220>
<221> MISC_FEATURE
<222> (19)..(19)
<223> Xaa at position 19 is Val or Ala;

<220>

<221> MISC_FEATURE

<222> (20)..(20)

<223> Xaa at position 20 is Arg or Lys;

<220>

<221> MISC_FEATURE

<222> (21)..(21)

<223> Xaa at position 21 is Leu or Glu;

<220>

<221> MISC_FEATURE

<222> (24)..(24)

<223> Xaa at position 24 is Glu or Ala;

<220>

<221> MISC_FEATURE

<222> (27)..(27)

<223> Xaa at position 27 is Val or Lys;

<220>

<221> MISC_FEATURE

<222> (28)..(28)

<223> Xaa at position 28 is Asn or Lys;

<220>

<221> MISC_FEATURE

<222> (30)..(30)

<223> Xaa at position 30 is Gly or Arg; and

<220>

<221> MISC_FEATURE

<222> (31)..(31)

<223> Xaa at position 31 is Gly, or Pro;

<220>
<221> MISC_FEATURE
<222> (32)..(32)
<223> Xaa at position 32 is Ser, or is absent.

<220>
<221> MISC_FEATURE
<222> (33)..(33)
<223> Xaa at position 33 is Ser, or is absent.

<220>
<221> MISC_FEATURE
<222> (34)..(34)
<223> Xaa at position 34 is Gly, or is absent.

<220>
<221> MISC_FEATURE
<222> (35)..(35)
<223> Xaa at position 35 is Ala, or is absent.

<220>
<221> MISC_FEATURE
<222> (36)..(36)
<223> Xaa at position 36 is Pro, or is absent.

<220>
<221> MISC_FEATURE
<222> (37)..(37)
<223> Xaa at position 37 is Pro, or is absent.

<220>
<221> MISC_FEATURE
<222> (38)..(38)

<223> Xaa at position 38 is Pro, or is absent.

<220>

<221> MISC_FEATURE

<222> (39)..(39)

<223> Xaa at position 39 is Pro, or is absent.

<220>

<221> MISC_FEATURE

<222> (39)..(39)

<223> Xaa at position 39 is Ser, or is absent.

<400> 11

Xaa Xaa Glu Glu Thr Phe Thr Ser Asp Xaa Ser Xaa Xaa Xaa Glu Xaa
1 5 10 15

Xaa Ala Xaa Xaa Xaa Phe Ile Xaa Trp Leu Xaa Xaa Gly Xaa Xaa Xaa
20 25 30

Xaa Xaa Xaa Xaa Xaa Xaa Xaa
35

<210> 12

<211> 31

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic construct

<220>

<221> MISC_FEATURE

<222> (1)..(1)

<223> Xaa at position 1 is L-histidine, D-histidine, or is deleted.

<220>

<221> MISC_FEATURE

<222> (2)..(2)

<223> Xaa at position 2 is Ala, Gly, Val, Leu, Ile, Ser, or Thr;

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> Xaa at position 6 is Phe, Trp, or Tyr;

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> Xaa at position 10 is Val, Trp, Ile, Leu, Phe, or Tyr;

<220>
<221> MISC_FEATURE
<222> (12)..(12)
<223> Xaa at position 12 is Ser, Trp, Tyr, Phe, Lys, Ile, Leu, Val;

<220>
<221> MISC_FEATURE
<222> (13)..(13)
<223> Xaa at position 13 is Tyr, Trp, or Phe;

<220>
<221> MISC_FEATURE
<222> (14)..(14)
<223> Xaa at position 14 is Leu, Phe, Tyr, or Trp;

<220>
<221> MISC_FEATURE
<222> (16)..(16)
<223> Xaa at position 16 is Gly, Glu, Asp, or Lys;

<220>
<221> MISC_FEATURE

<222> (19)..(19)

<223> Xaa at position 19 is Ala, Val, Ile, or Leu;

<220>

<221> MISC_FEATURE

<222> (21)..(21)

<223> Xaa at position 21 is Glu, Ile, or Ala;

<220>

<221> MISC_FEATURE

<222> (24)..(24)

<223> Xaa at position 24 is Ala or Glu;

<220>

<221> MISC_FEATURE

<222> (27)..(27)

<223> Xaa at position 27 is Val or Ile; and

<220>

<221> MOD_RES

<222> (30)..(30)

<223> AMIDATION

<220>

<221> MISC_FEATURE

<222> (31)..(31)

<223> Xaa at position 31 is Gly, His or is absent.

<400> 12

Xaa Xaa Glu Gly Thr Xaa Thr Ser Asp Xaa Ser Xaa Xaa Xaa Glu Xaa
1 5 10 15

Gln Ala Xaa Lys Xaa Phe Ile Xaa Trp Leu Xaa Lys Gly Arg Xaa
20 25 30

<210> 13

<211> 616

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 13

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His Val Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu Gly
1               5                  10                  15

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

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

Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln Gln
    50                  55                  60

Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu Phe
65                  70                  75                  80

Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys Ser
                85                  90                  95

Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu Arg
            100                 105                 110

Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro Glu
        115                 120                 125

Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu Pro
    130                 135                 140

Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His Asp
145                 150                 155                 160

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

His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg Tyr
            180                 185                 190

Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala Cys
        195                 200                 205

Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser Ser
    210                 215                 220
```

Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu Arg
225 230 235 240

Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro Lys
245 250 255

Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys Val
260 265 270

His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp Arg
275 280 285

Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser Ser
290 295 300

Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His Cys
305 310 315 320

Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser Leu
325 330 335

Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala Glu
340 345 350

Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg Arg
355 360 365

His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr Tyr
370 375 380

Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu Cys
385 390 395 400

Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro Gln
405 410 415

Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu Tyr
420 425 430

Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro Gln
435 440 445

Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys Val
450 455 460

Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys Ala
465 470 475 480

Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His Glu
485 490 495

```
Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser Leu
            500                 505                 510

Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr Tyr
        515                 520                 525

Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp Ile
    530                 535                 540

Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala Leu
545                 550                 555                 560

Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu Lys
                565                 570                 575

Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys Ala
            580                 585                 590

Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val Ala
        595                 600                 605

Ala Ser Gln Ala Ala Leu Gly Leu
    610                 615
```

<210> 14

<211> 631

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 14

```
His Val Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu Gly
1               5                   10                  15

Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Val Lys Gly Arg Gly Gly
            20                  25                  30

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ala
        35                  40                  45

His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu Glu Asn
    50                  55                  60

Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln Gln Cys
65                  70                  75                  80
```

```
Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu Phe Ala
                85                  90                  95

Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys Ser Leu
            100                 105                 110

His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu Arg Glu
        115                 120                 125

Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro Glu Arg
    130                 135                 140

Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu Pro Arg
145                 150                 155                 160

Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His Asp Asn
                165                 170                 175

Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg Arg His
            180                 185                 190

Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg Tyr Lys
        195                 200                 205

Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala Cys Leu
    210                 215                 220

Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser Ser Ala
225                 230                 235                 240

Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu Arg Ala
                245                 250                 255

Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro Lys Ala
            260                 265                 270

Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys Val His
        275                 280                 285

Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp Arg Ala
    290                 295                 300

Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser Ser Lys
305                 310                 315                 320

Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His Cys Ile
                325                 330                 335

Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser Leu Ala
            340                 345                 350
```

Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala Glu Ala
355 360 365

Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg Arg His
370 375 380

Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr Tyr Glu
385 390 395 400

Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu Cys Tyr
405 410 415

Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro Gln Asn
420 425 430

Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu Tyr Lys
435 440 445

Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro Gln Val
450 455 460

Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys Val Gly
465 470 475 480

Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys Ala Glu
485 490 495

Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His Glu Lys
500 505 510

Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser Leu Val
515 520 525

Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr Tyr Val
530 535 540

Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp Ile Cys
545 550 555 560

Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala Leu Val
565 570 575

Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu Lys Ala
580 585 590

Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys Ala Asp
595 600 605

Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val Ala Ala
610 615 620

```
Ser Gln Ala Ala Leu Gly Leu
625                 630
```

<210> 15

<211> 640

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 15

```
His Gly Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu Glu
1               5                  10                  15

Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Val Lys Gly Arg Gly Ser
            20                  25                  30

Ser Gly Ala Pro Pro Pro Ser Gly Gly Gly Gly Gly Ser Gly Gly Gly
        35                  40                  45

Gly Ser Gly Gly Gly Gly Ser Asp Ala His Lys Ser Glu Val Ala His
    50                  55                  60

Arg Phe Lys Asp Leu Gly Glu Glu Asn Phe Lys Ala Leu Val Leu Ile
65                  70                  75                  80

Ala Phe Ala Gln Tyr Leu Gln Gln Cys Pro Phe Glu Asp His Val Lys
                85                  90                  95

Leu Val Asn Glu Val Thr Glu Phe Ala Lys Thr Cys Val Ala Asp Glu
            100                 105                 110

Ser Ala Glu Asn Cys Asp Lys Ser Leu His Thr Leu Phe Gly Asp Lys
        115                 120                 125

Leu Cys Thr Val Ala Thr Leu Arg Glu Thr Tyr Gly Glu Met Ala Asp
    130                 135                 140

Cys Cys Ala Lys Gln Glu Pro Glu Arg Asn Glu Cys Phe Leu Gln His
145                 150                 155                 160

Lys Asp Asp Asn Pro Asn Leu Pro Arg Leu Val Arg Pro Glu Val Asp
                165                 170                 175

Val Met Cys Thr Ala Phe His Asp Asn Glu Glu Thr Phe Leu Lys Lys
            180                 185                 190
```

```
Tyr Leu Tyr Glu Ile Ala Arg Arg His Pro Tyr Phe Tyr Ala Pro Glu
        195                 200                 205

Leu Leu Phe Phe Ala Lys Arg Tyr Lys Ala Ala Phe Thr Glu Cys Cys
    210                 215                 220

Gln Ala Ala Asp Lys Ala Ala Cys Leu Leu Pro Lys Leu Asp Glu Leu
225                 230                 235                 240

Arg Asp Glu Gly Lys Ala Ser Ser Ala Lys Gln Arg Leu Lys Cys Ala
                245                 250                 255

Ser Leu Gln Lys Phe Gly Glu Arg Ala Phe Lys Ala Trp Ala Val Ala
            260                 265                 270

Arg Leu Ser Gln Arg Phe Pro Lys Ala Glu Phe Ala Glu Val Ser Lys
        275                 280                 285

Leu Val Thr Asp Leu Thr Lys Val His Thr Glu Cys Cys His Gly Asp
    290                 295                 300

Leu Leu Glu Cys Ala Asp Asp Arg Ala Asp Leu Ala Lys Tyr Ile Cys
305                 310                 315                 320

Glu Asn Gln Asp Ser Ile Ser Ser Lys Leu Lys Glu Cys Cys Glu Lys
                325                 330                 335

Pro Leu Leu Glu Lys Ser His Cys Ile Ala Glu Val Glu Asn Asp Glu
            340                 345                 350

Met Pro Ala Asp Leu Pro Ser Leu Ala Ala Asp Phe Val Glu Ser Lys
        355                 360                 365

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

Phe Leu Tyr Glu Tyr Ala Arg Arg His Pro Asp Tyr Ser Val Val Leu
385                 390                 395                 400

Leu Leu Arg Leu Ala Lys Thr Tyr Glu Thr Thr Leu Glu Lys Cys Cys
                405                 410                 415

Ala Ala Ala Asp Pro His Glu Cys Tyr Ala Lys Val Phe Asp Glu Phe
            420                 425                 430

Lys Pro Leu Val Glu Glu Pro Gln Asn Leu Ile Lys Gln Asn Cys Glu
        435                 440                 445

Leu Phe Glu Gln Leu Gly Glu Tyr Lys Phe Gln Asn Ala Leu Leu Val
    450                 455                 460
```

```
Arg Tyr Thr Lys Lys Val Pro Gln Val Ser Thr Pro Thr Leu Val Glu
465                 470                 475                 480

Val Ser Arg Asn Leu Gly Lys Val Gly Ser Lys Cys Cys Lys His Pro
                485                 490                 495

Glu Ala Lys Arg Met Pro Cys Ala Glu Asp Tyr Leu Ser Val Val Leu
            500                 505                 510

Asn Gln Leu Cys Val Leu His Glu Lys Thr Pro Val Ser Asp Arg Val
        515                 520                 525

Thr Lys Cys Cys Thr Glu Ser Leu Val Asn Arg Arg Pro Cys Phe Ser
    530                 535                 540

Ala Leu Glu Val Asp Glu Thr Tyr Val Pro Lys Glu Phe Asn Ala Glu
545                 550                 555                 560

Thr Phe Thr Phe His Ala Asp Ile Cys Thr Leu Ser Glu Lys Glu Arg
                565                 570                 575

Gln Ile Lys Lys Gln Thr Ala Leu Val Glu Leu Val Lys His Lys Pro
            580                 585                 590

Lys Ala Thr Lys Glu Gln Leu Lys Ala Val Met Asp Asp Phe Ala Ala
        595                 600                 605

Phe Val Glu Lys Cys Cys Lys Ala Asp Asp Lys Glu Thr Cys Phe Ala
    610                 615                 620

Glu Glu Gly Lys Lys Leu Val Ala Ala Ser Gln Ala Ala Leu Gly Leu
625                 630                 635                 640
```

<210> 16

<211> 624

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 16

```
His Gly Glu Gly Thr Phe Thr Ser Asp Leu Ser Lys Gln Met Glu Glu
1               5                   10                  15

Glu Ala Val Arg Leu Phe Ile Glu Trp Leu Lys Asn Gly Gly Pro Ser
            20                  25                  30
```

```
Ser Gly Ala Pro Pro Pro Ser Asp Ala His Lys Ser Glu Val Ala His
        35                  40                  45

Arg Phe Lys Asp Leu Gly Glu Glu Asn Phe Lys Ala Leu Val Leu Ile
    50                  55                  60

Ala Phe Ala Gln Tyr Leu Gln Gln Cys Pro Phe Glu Asp His Val Lys
65                  70                  75                  80

Leu Val Asn Glu Val Thr Glu Phe Ala Lys Thr Cys Val Ala Asp Glu
                85                  90                  95

Ser Ala Glu Asn Cys Asp Lys Ser Leu His Thr Leu Phe Gly Asp Lys
            100                 105                 110

Leu Cys Thr Val Ala Thr Leu Arg Glu Thr Tyr Gly Glu Met Ala Asp
        115                 120                 125

Cys Cys Ala Lys Gln Glu Pro Glu Arg Asn Glu Cys Phe Leu Gln His
    130                 135                 140

Lys Asp Asp Asn Pro Asn Leu Pro Arg Leu Val Arg Pro Glu Val Asp
145                 150                 155                 160

Val Met Cys Thr Ala Phe His Asp Asn Glu Glu Thr Phe Leu Lys Lys
                165                 170                 175

Tyr Leu Tyr Glu Ile Ala Arg Arg His Pro Tyr Phe Tyr Ala Pro Glu
            180                 185                 190

Leu Leu Phe Phe Ala Lys Arg Tyr Lys Ala Ala Phe Thr Glu Cys Cys
        195                 200                 205

Gln Ala Ala Asp Lys Ala Ala Cys Leu Leu Pro Lys Leu Asp Glu Leu
    210                 215                 220

Arg Asp Glu Gly Lys Ala Ser Ser Ala Lys Gln Arg Leu Lys Cys Ala
225                 230                 235                 240

Ser Leu Gln Lys Phe Gly Glu Arg Ala Phe Lys Ala Trp Ala Val Ala
                245                 250                 255

Arg Leu Ser Gln Arg Phe Pro Lys Ala Glu Phe Ala Glu Val Ser Lys
            260                 265                 270

Leu Val Thr Asp Leu Thr Lys Val His Thr Glu Cys Cys His Gly Asp
        275                 280                 285

Leu Leu Glu Cys Ala Asp Asp Arg Ala Asp Leu Ala Lys Tyr Ile Cys
    290                 295                 300
```

Glu Asn Gln Asp Ser Ile Ser Ser Lys Leu Lys Glu Cys Cys Glu Lys
305 310 315 320

Pro Leu Leu Glu Lys Ser His Cys Ile Ala Glu Val Glu Asn Asp Glu
325 330 335

Met Pro Ala Asp Leu Pro Ser Leu Ala Ala Asp Phe Val Glu Ser Lys
340 345 350

Asp Val Cys Lys Asn Tyr Ala Glu Ala Lys Asp Val Phe Leu Gly Met
355 360 365

Phe Leu Tyr Glu Tyr Ala Arg Arg His Pro Asp Tyr Ser Val Val Leu
370 375 380

Leu Leu Arg Leu Ala Lys Thr Tyr Glu Thr Thr Leu Glu Lys Cys Cys
385 390 395 400

Ala Ala Ala Asp Pro His Glu Cys Tyr Ala Lys Val Phe Asp Glu Phe
405 410 415

Lys Pro Leu Val Glu Glu Pro Gln Asn Leu Ile Lys Gln Asn Cys Glu
420 425 430

Leu Phe Glu Gln Leu Gly Glu Tyr Lys Phe Gln Asn Ala Leu Leu Val
435 440 445

Arg Tyr Thr Lys Lys Val Pro Gln Val Ser Thr Pro Thr Leu Val Glu
450 455 460

Val Ser Arg Asn Leu Gly Lys Val Gly Ser Lys Cys Cys Lys His Pro
465 470 475 480

Glu Ala Lys Arg Met Pro Cys Ala Glu Asp Tyr Leu Ser Val Val Leu
485 490 495

Asn Gln Leu Cys Val Leu His Glu Lys Thr Pro Val Ser Asp Arg Val
500 505 510

Thr Lys Cys Cys Thr Glu Ser Leu Val Asn Arg Arg Pro Cys Phe Ser
515 520 525

Ala Leu Glu Val Asp Glu Thr Tyr Val Pro Lys Glu Phe Asn Ala Glu
530 535 540

Thr Phe Thr Phe His Ala Asp Ile Cys Thr Leu Ser Glu Lys Glu Arg
545 550 555 560

Gln Ile Lys Lys Gln Thr Ala Leu Val Glu Leu Val Lys His Lys Pro
565 570 575

```
Lys Ala Thr Lys Glu Gln Leu Lys Ala Val Met Asp Asp Phe Ala Ala
            580                 585                 590

Phe Val Glu Lys Cys Cys Lys Ala Asp Asp Lys Glu Thr Cys Phe Ala
        595                 600                 605

Glu Glu Gly Lys Lys Leu Val Ala Ala Ser Gln Ala Ala Leu Gly Leu
    610                 615                 620
```

<210> 17

<211> 640

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 17

```
His Gly Glu Gly Thr Phe Thr Ser Asp Leu Ser Lys Gln Met Glu Glu
1               5                   10                  15

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

Ser Gly Ala Pro Pro Pro Ser Gly Gly Gly Gly Gly Ser Gly Gly Gly
        35                  40                  45

Gly Ser Gly Gly Gly Gly Ser Asp Ala His Lys Ser Glu Val Ala His
    50                  55                  60

Arg Phe Lys Asp Leu Gly Glu Glu Asn Phe Lys Ala Leu Val Leu Ile
65                  70                  75                  80

Ala Phe Ala Gln Tyr Leu Gln Gln Cys Pro Phe Glu Asp His Val Lys
                85                  90                  95

Leu Val Asn Glu Val Thr Glu Phe Ala Lys Thr Cys Val Ala Asp Glu
            100                 105                 110

Ser Ala Glu Asn Cys Asp Lys Ser Leu His Thr Leu Phe Gly Asp Lys
        115                 120                 125

Leu Cys Thr Val Ala Thr Leu Arg Glu Thr Tyr Gly Glu Met Ala Asp
    130                 135                 140

Cys Cys Ala Lys Gln Glu Pro Glu Arg Asn Glu Cys Phe Leu Gln His
145                 150                 155                 160
```

```
Lys Asp Asp Asn Pro Asn Leu Pro Arg Leu Val Arg Pro Glu Val Asp
                165                 170                 175

Val Met Cys Thr Ala Phe His Asp Asn Glu Glu Thr Phe Leu Lys Lys
            180                 185                 190

Tyr Leu Tyr Glu Ile Ala Arg Arg His Pro Tyr Phe Tyr Ala Pro Glu
        195                 200                 205

Leu Leu Phe Phe Ala Lys Arg Tyr Lys Ala Ala Phe Thr Glu Cys Cys
    210                 215                 220

Gln Ala Ala Asp Lys Ala Ala Cys Leu Leu Pro Lys Leu Asp Glu Leu
225                 230                 235                 240

Arg Asp Glu Gly Lys Ala Ser Ser Ala Lys Gln Arg Leu Lys Cys Ala
                245                 250                 255

Ser Leu Gln Lys Phe Gly Glu Arg Ala Phe Lys Ala Trp Ala Val Ala
            260                 265                 270

Arg Leu Ser Gln Arg Phe Pro Lys Ala Glu Phe Ala Glu Val Ser Lys
        275                 280                 285

Leu Val Thr Asp Leu Thr Lys Val His Thr Glu Cys Cys His Gly Asp
    290                 295                 300

Leu Leu Glu Cys Ala Asp Asp Arg Ala Asp Leu Ala Lys Tyr Ile Cys
305                 310                 315                 320

Glu Asn Gln Asp Ser Ile Ser Ser Lys Leu Lys Glu Cys Cys Glu Lys
                325                 330                 335

Pro Leu Leu Glu Lys Ser His Cys Ile Ala Glu Val Glu Asn Asp Glu
            340                 345                 350

Met Pro Ala Asp Leu Pro Ser Leu Ala Ala Asp Phe Val Glu Ser Lys
        355                 360                 365

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

Phe Leu Tyr Glu Tyr Ala Arg Arg His Pro Asp Tyr Ser Val Val Leu
385                 390                 395                 400

Leu Leu Arg Leu Ala Lys Thr Tyr Glu Thr Thr Leu Glu Lys Cys Cys
                405                 410                 415

Ala Ala Ala Asp Pro His Glu Cys Tyr Ala Lys Val Phe Asp Glu Phe
            420                 425                 430
```

Lys Pro Leu Val Glu Glu Pro Gln Asn Leu Ile Lys Gln Asn Cys Glu
435 440 445

Leu Phe Glu Gln Leu Gly Glu Tyr Lys Phe Gln Asn Ala Leu Leu Val
450 455 460

Arg Tyr Thr Lys Lys Val Pro Gln Val Ser Thr Pro Thr Leu Val Glu
465 470 475 480

Val Ser Arg Asn Leu Gly Lys Val Gly Ser Lys Cys Cys Lys His Pro
485 490 495

Glu Ala Lys Arg Met Pro Cys Ala Glu Asp Tyr Leu Ser Val Val Leu
500 505 510

Asn Gln Leu Cys Val Leu His Glu Lys Thr Pro Val Ser Asp Arg Val
515 520 525

Thr Lys Cys Cys Thr Glu Ser Leu Val Asn Arg Arg Pro Cys Phe Ser
530 535 540

Ala Leu Glu Val Asp Glu Thr Tyr Val Pro Lys Glu Phe Asn Ala Glu
545 550 555 560

Thr Phe Thr Phe His Ala Asp Ile Cys Thr Leu Ser Glu Lys Glu Arg
565 570 575

Gln Ile Lys Lys Gln Thr Ala Leu Val Glu Leu Val Lys His Lys Pro
580 585 590

Lys Ala Thr Lys Glu Gln Leu Lys Ala Val Met Asp Asp Phe Ala Ala
595 600 605

Phe Val Glu Lys Cys Cys Lys Ala Asp Asp Lys Glu Thr Cys Phe Ala
610 615 620

Glu Glu Gly Lys Lys Leu Val Ala Ala Ser Gln Ala Ala Leu Gly Leu
625 630 635 640

<210> 18

<211> 264

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 18

```
His Val Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu Gly
1               5                  10                  15

Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Val Lys Gly Arg Gly Ala
            20                  25                  30

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
        35                  40                  45

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
    50                  55                  60

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
65                  70                  75                  80

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
                85                  90                  95

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
            100                 105                 110

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
        115                 120                 125

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
    130                 135                 140

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
145                 150                 155                 160

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
                165                 170                 175

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
            180                 185                 190

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
        195                 200                 205

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
    210                 215                 220

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
225                 230                 235                 240

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
                245                 250                 255

Ser Leu Ser Leu Ser Pro Gly Lys
            260
```

<210> 19

<211> 272

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 19

```
His Val Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu Gly
1               5                  10                  15

Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Val Lys Gly Arg Gly Ser
            20                  25                  30

Ser Gly Ala Pro Pro Pro Ser Ala Glu Pro Lys Ser Cys Asp Lys Thr
        35                  40                  45

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
    50                  55                  60

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
65                  70                  75                  80

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
                85                  90                  95

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
            100                 105                 110

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
        115                 120                 125

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
    130                 135                 140

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
145                 150                 155                 160

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
                165                 170                 175

Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
            180                 185                 190

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
        195                 200                 205
```

```
Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
    210                 215                 220

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
225                 230                 235                 240

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
                245                 250                 255

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
            260                 265                 270
```

<210> 20

<211> 264

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 20

```
His Val Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu Glu
1               5                   10                  15

Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Val Lys Gly Arg Gly Ala
            20                  25                  30

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
        35                  40                  45

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
    50                  55                  60

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
65                  70                  75                  80

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
                85                  90                  95

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
            100                 105                 110

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
        115                 120                 125

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
    130                 135                 140
```

```
Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
145                 150                 155                 160

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
                165                 170                 175

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
            180                 185                 190

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
        195                 200                 205

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
    210                 215                 220

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
225                 230                 235                 240

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
                245                 250                 255

Ser Leu Ser Leu Ser Pro Gly Lys
            260
```

<210> 21

<211> 272

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 21

```
His Val Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu Glu
1               5                   10                  15

Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Val Lys Gly Arg Gly Ser
            20                  25                  30

Ser Gly Ala Pro Pro Pro Ser Ala Glu Pro Lys Ser Cys Asp Lys Thr
        35                  40                  45

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
    50                  55                  60

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
65                  70                  75                  80
```


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Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
85 90 95

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
100 105 110

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
115 120 125

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
130 135 140

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
145 150 155 160

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
165 170 175

Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
180 185 190

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
195 200 205

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

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
225 230 235 240

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
245 250 255

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
260 265 270

<210> 22

<211> 272

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 22

His Gly Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu Glu
1 5 10 15

```
Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Val Lys Gly Arg Gly Ser
            20                  25                  30

Ser Gly Ala Ser Ser Gly Ala Ala Glu Pro Lys Ser Cys Asp Lys Thr
        35                  40                  45

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
    50                  55                  60

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
65                  70                  75                  80

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
                85                  90                  95

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
            100                 105                 110

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
        115                 120                 125

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
    130                 135                 140

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
145                 150                 155                 160

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
                165                 170                 175

Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
            180                 185                 190

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
        195                 200                 205

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

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
225                 230                 235                 240

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
                245                 250                 255

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
            260                 265                 270
```

<210> 23

<211> 287

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 23

His Gly Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu Glu
1 5 10 15

Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Val Lys Gly Arg Gly Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
35 40 45

Ser Gly Gly Gly Gly Ser Ala Glu Pro Lys Ser Cys Asp Lys Thr His
50 55 60

Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
65 70 75 80

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
85 90 95

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
100 105 110

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
115 120 125

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
130 135 140

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
145 150 155 160

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
165 170 175

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
180 185 190

Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
195 200 205

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
210 215 220

```
Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
225                 230                 235                 240

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
                245                 250                 255

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
            260                 265                 270

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        275                 280                 285
```

<210> 24

<211> 284

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 24

```
His Gly Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu Glu
1               5                   10                  15

Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Val Lys Gly Arg Gly Ser
            20                  25                  30

Ser Gly Ala Pro Pro Pro Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        35                  40                  45

Ser Gly Gly Gly Gly Ser Ala Glu Ser Lys Tyr Gly Pro Pro Cys Pro
    50                  55                  60

Ser Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe
65                  70                  75                  80

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
                85                  90                  95

Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe
            100                 105                 110

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
        115                 120                 125

Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
    130                 135                 140
```

```
Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
145                 150                 155                 160

Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala
                165                 170                 175

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln
            180                 185                 190

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
        195                 200                 205

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
    210                 215                 220

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
225                 230                 235                 240

Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu
                245                 250                 255

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
            260                 265                 270

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
        275                 280
```

<210> 25

<211> 302

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 25

```
His Gly Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu Glu
1               5                   10                  15

Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Val Lys Gly Arg Gly Ser
            20                  25                  30

Ser Gly Ala Pro Pro Pro Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        35                  40                  45

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


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```
Gly Gly Gly Gly Ser Ala Glu Pro Lys Ser Cys Asp Lys Thr His Thr
65                  70                  75                  80

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
                85                  90                  95

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
            100                 105                 110

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
        115                 120                 125

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
    130                 135                 140

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

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
                165                 170                 175

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
            180                 185                 190

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
        195                 200                 205

Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
    210                 215                 220

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
225                 230                 235                 240

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
                245                 250                 255

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

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
        275                 280                 285

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
    290                 295                 300
```

<210> 26

<211> 294

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 26

```
His Gly Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu Glu
1               5                  10                  15

Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Val Lys Gly Arg Gly Gly
            20                  25                  30

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

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Glu Pro
    50                  55                  60

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
65                  70                  75                  80

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
                85                  90                  95

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
            100                 105                 110

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
        115                 120                 125

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
    130                 135                 140

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
145                 150                 155                 160

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
                165                 170                 175

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
            180                 185                 190

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
        195                 200                 205

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
    210                 215                 220

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
225                 230                 235                 240
                                        50
```

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
245 250 255

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
260 265 270

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
275 280 285

Ser Leu Ser Pro Gly Lys
290

<210> 27

<211> 280

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 27

His Gly Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu Glu
1 5 10 15

Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Val Lys Gly Arg Gly Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Ser Ser Gly Ala Pro Pro Pro Ser Ala
35 40 45

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
50 55 60

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
65 70 75 80

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
85 90 95

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
100 105 110

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
115 120 125

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
130 135 140

```
Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
145                 150                 155                 160

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
                165                 170                 175

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
            180                 185                 190

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
        195                 200                 205

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
    210                 215                 220

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

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
                245                 250                 255

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
            260                 265                 270

Ser Leu Ser Leu Ser Pro Gly Lys
        275                 280
```

<210> 28

<211> 287

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 28

```
His Gly Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu Glu
1               5                   10                  15

Gln Ala Val Lys Glu Phe Ile Ala Trp Leu Ile Lys Gly Arg Gly Ser
            20                  25                  30

Ser Gly Ala Pro Pro Pro Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        35                  40                  45

Ser Gly Gly Gly Gly Ser Ala Glu Pro Lys Ser Cys Asp Lys Thr His
    50                  55                  60
```

```
Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
65                  70                  75                  80

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
                85                  90                  95

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
            100                 105                 110

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
        115                 120                 125

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
    130                 135                 140

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
145                 150                 155                 160

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
                165                 170                 175

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
            180                 185                 190

Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
        195                 200                 205

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
    210                 215                 220

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
225                 230                 235                 240

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
                245                 250                 255

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
            260                 265                 270

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        275                 280                 285
```

<210> 29

<211> 272

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 29

```
His Gly Glu Gly Thr Phe Thr Ser Asp Leu Ser Lys Gln Met Glu Glu
1               5                  10                  15

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

Ser Gly Ala Pro Pro Pro Ser Ala Glu Pro Lys Ser Cys Asp Lys Thr
        35                  40                  45

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
    50                  55                  60

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
65                  70                  75                  80

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
                85                  90                  95

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
            100                 105                 110

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
        115                 120                 125

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
    130                 135                 140

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
145                 150                 155                 160

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
                165                 170                 175

Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
            180                 185                 190

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
        195                 200                 205

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

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
225                 230                 235                 240

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
                245                 250                 255
```

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
260 265 270

<210> 30

<211> 272

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 30

His Gly Glu Gly Thr Phe Thr Ser Asp Leu Ser Lys Gln Met Glu Glu
1 5 10 15

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

Ser Gly Ala Ser Ser Gly Ala Ala Glu Pro Lys Ser Cys Asp Lys Thr
35 40 45

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
50 55 60

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
65 70 75 80

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
85 90 95

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
100 105 110

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
115 120 125

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
130 135 140

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
145 150 155 160

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
165 170 175

Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
180 185 190

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
195 200 205

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

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
225 230 235 240

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
245 250 255

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
260 265 270

<210> 31

<211> 287

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 31

His Gly Glu Gly Thr Phe Thr Ser Asp Leu Ser Lys Gln Met Glu Glu
1 5 10 15

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

Ser Gly Ala Pro Pro Pro Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
35 40 45

Ser Gly Gly Gly Gly Ser Ala Glu Pro Lys Ser Cys Asp Lys Thr His
50 55 60

Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
65 70 75 80

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
85 90 95

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
100 105 110

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
115 120 125

```
Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
    130                 135                 140

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
145                 150                 155                 160

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
                165                 170                 175

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
            180                 185                 190

Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
        195                 200                 205

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
    210                 215                 220

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
225                 230                 235                 240

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
                245                 250                 255

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
            260                 265                 270

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        275                 280                 285

<210>  32

<211>  232

<212>  PRT

<213>  Homo sapiens


<400>  32

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

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

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

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

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys
225 230

<210> 33

<211> 703

<212> DNA

<213> Homo sapiens

<400> 33
gagcccaaat cttgtgacaa aactcacaca tgcccaccgt gcccagcacc tgaactcctg 60

gggggaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 120

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 180

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 240

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 300

ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagccccat cgagaaaacc 360

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 420

gaggagatga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc 480

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 540

cccgtgctgg actccgacgg ctccttcttc ctctatagca agctcaccgt ggacaagagc 600

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 660

tacacgcaga agagcctctc cctgtctccg ggtaaatgat agt 703

<210> 34

<211> 585

<212> PRT

<213> Homo sapiens

<400> 34

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

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
20 25 30

Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
165 170 175

```
Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
            180                 185                 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
        195                 200                 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
    210                 215                 220

Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys
225                 230                 235                 240

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
                245                 250                 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
            260                 265                 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
        275                 280                 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
    290                 295                 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305                 310                 315                 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
                325                 330                 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
            340                 345                 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
        355                 360                 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
    370                 375                 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Asn Leu Gly Glu
385                 390                 395                 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
                405                 410                 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
            420                 425                 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
        435                 440                 445
```

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
530 535 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
565 570 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu
580 585

<210> 35

<211> 1762

<212> DNA

<213> Homo sapiens

<400> 35
gatgcgcaca agagtgaggt tgctcatcgg tttaaagatt tgggagaaga aaatttcaaa 60

gccttggtgt tgattgcctt tgctcagtat cttcagcagt gtccatttga agatcatgta 120

aaattagtga atgaagtaac tgaatttgca aaaacatgtg ttgctgatga gtcagctgaa 180

aattgtgaca aatcacttca tacccttttt ggagacaaat tatgcacagt tgcaactctt 240

cgtgaaacct atggtgaaat ggctgactgc tgtgcaaaac aagaacctga gagaaatgaa 300

tgcttcttgc aacacaaaga tgacaaccca aacctccccc gattggtgag accagaggtt 360

gatgtgatgt gcactgcttt tcatgacaat gaagagacat ttttgaaaaa atacttatat 420

gaaattgcca gaagacatcc ttacttttat gccccggaac tccttttctt tgctaaaagg 480

tataaagctg cttttacaga atgttgccaa gctgctgata aagctgcctg cctgttgcca 540

aagctcgatg aacttcggga tgaagggaag gcttcgtctg ccaaacagag actcaagtgt 600

gccagtctcc aaaaatttgg agaaagagct ttcaaagcat gggcagtagc tcgcctgagc 660

cagagatttc ccaaagctga gtttgcagaa gtttccaagt tagtgacaga tcttaccaaa 720

gtccacacgg aatgctgcca tggagatctg cttgaatgtg ctgatgacag ggcggacctt 780

gccaagtata tctgtgaaaa tcaagattcg atctccagta aactgaagga atgctgtgaa 840

aaacctctgt tggaaaaatc ccactgcatt gccgaagtgg aaaatgatga gatgcctgct 900

gacttgcctt cattagctgc tgattttgtt gaaagtaagg atgtttgcaa aaactatgct 960

gaggcaaagg atgtcttcct gggcatgttt ttgtatgaat atgcaagaag gcatcctgat 1020

tactctgtcg tgctgctgct gagacttgcc aagacatatg aaaccactct agagaagtgc 1080

tgtgccgctg cagatcctca tgaatgctat gccaaagtgt tcgatgaatt taaacctctt 1140

gtggaagagc ctcagaattt aatcaaacaa aattgtgagc tttttgagca gcttggagag 1200

tacaaattcc agaatgcgct attagttcgt tacaccaaga aagtacccca agtgtcaact 1260

ccaactcttg tagaggtctc aagaaaccta ggaaaagtgg gcagcaaatg ttgtaaacat 1320

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